



# 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 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)

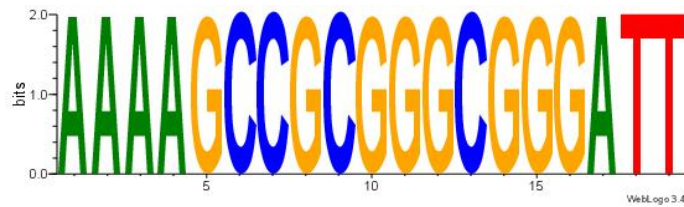
Motif ID:	<a href="#">MA0290.1</a>
Motif name:	DAL81
Taxon:	Fungi
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	11
Number of overlap:	8
Similarity score:	0.0497454

Alignment:

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

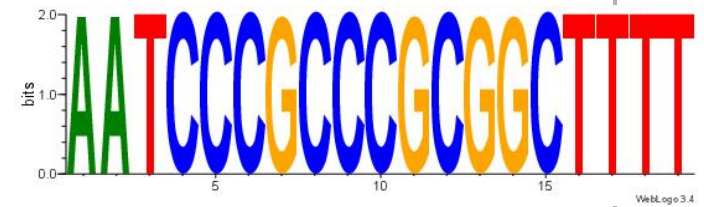
Original motif

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

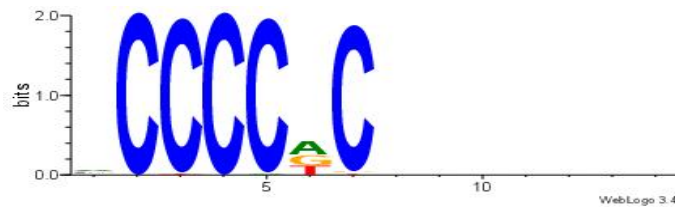


Motif ID: [MA0425.1](#)  
Motif name: YGR067C  
Taxon: Fungi  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Original Motif  
Direction: Backward  
Position number: 7

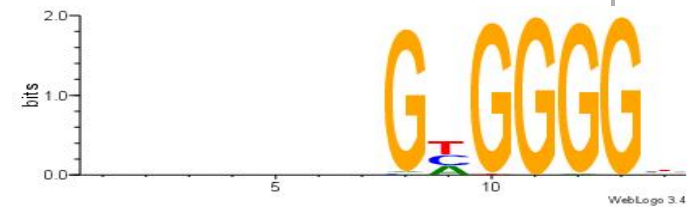
Number of overlap: 8  
Similarity score: 0.0654186

Alignment:  
VCCCCDCHHHDDBD  
GCCCGCC-----

Original motif  
Consensus sequence: VCCCCDCHHHDDBD



Reverse complement motif  
Consensus sequence: DBDDHHHGDGGGGG



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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  
GCCCGCC-

Original motif

Reverse complement motif

Consensus sequence: VCCCCDCWH



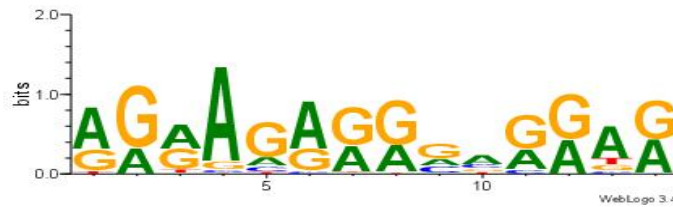
Consensus sequence: DWGHGGGGB



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

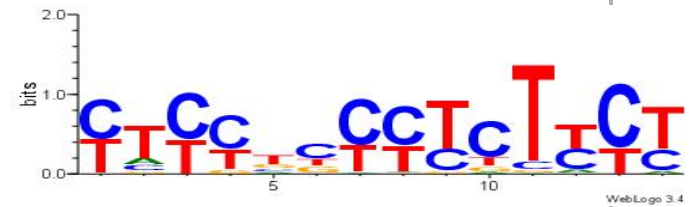
Original motif

Consensus sequence: RGRAGARRGARRAR



Reverse complement motif

Consensus sequence: MTMMTCMMTCTKCK



### Best Matches for Motif ID 2 (Highest to Lowest)

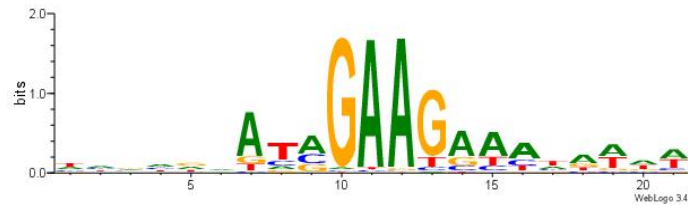
Motif ID:	<a href="#">MA0377.1</a>
Motif name:	SFL1
Taxon:	Fungi
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	3
Number of overlap:	14
Similarity score:	0.0351315

Alignment:

HHVHDHATMGAAGAAHDWDW  
-----RGRAGARRGARRAR--

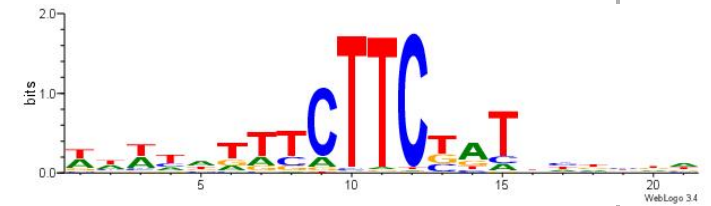
Original motif

Consensus sequence: HHVHDHATMGAAGAAHDWDW



Reverse complement motif

Consensus sequence: WDWDHTTTCTTCYATHHHVHH



Motif ID: [MA0308.1](#)  
Motif name: GSM1  
Taxon: Fungi  
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: 0.0437372

Alignment:

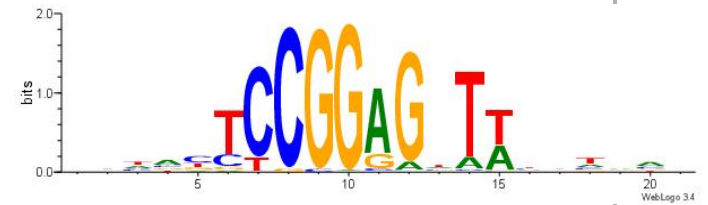
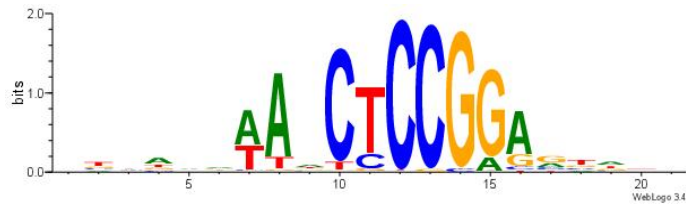
HDDVVTCCGGAGDTWDDDHVH  
MTMMTCMMTCTKCK-----

Original motif

Consensus sequence: HBHDDDWADCTCCGGAVBDDH

Reverse complement motif

Consensus sequence: HDDVVTCCGGAGDTWDDDHVH

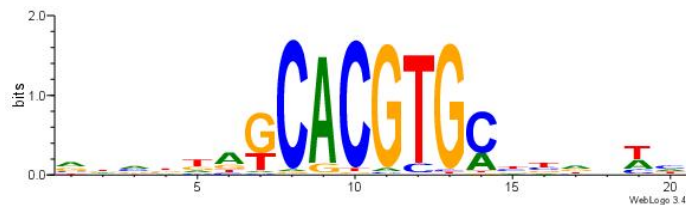


Motif ID: [MA0376.1](#)  
 Motif name: RTG3  
 Taxon: Fungi  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 6  
 Number of overlap: 14  
 Similarity score: 0.0450939

Alignment:  
 DWVDVVGACGTGCTDVBDB  
 -MTMMTCMMTCTKCK-----

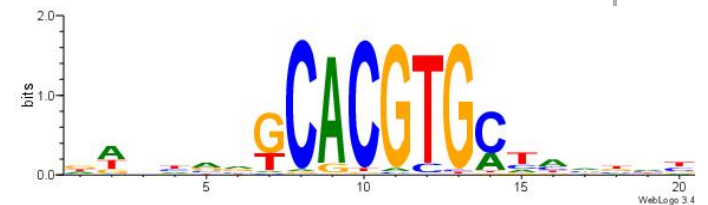
Original motif

Consensus sequence: VDVBDAGCACGTGCBBDVWH



Reverse complement motif

Consensus sequence: DWVDVVGACGTGCTDVBDB



Motif ID: [MA0346.1](#)



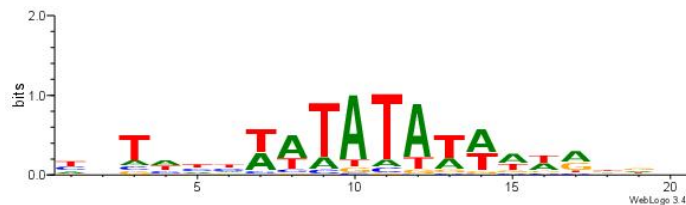
Motif name: NHP6B  
 Taxon: Fungi  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 7  
 Number of overlap: 14  
 Similarity score: 0.0451102

**Alignment:**

HHTHHHWATATATWWWRDDV  
 MTMMTCMMTCTKCK-----

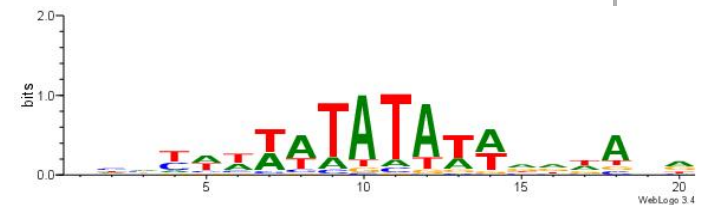
**Original motif**

Consensus sequence: HHTHHHWATATATWWWRDDV



**Reverse complement motif**

Consensus sequence: BHDKWWWATATATWHHHAHH




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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: 7  
 Number of overlap: 14

Similarity score:

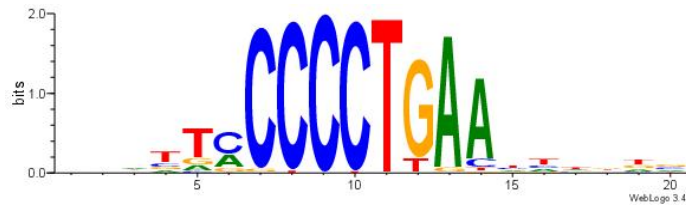
0.0452242

Alignment:

```
DDDTMCCCCTGAAHHBDV  
MTMMTCMMTCTKCK-----
```

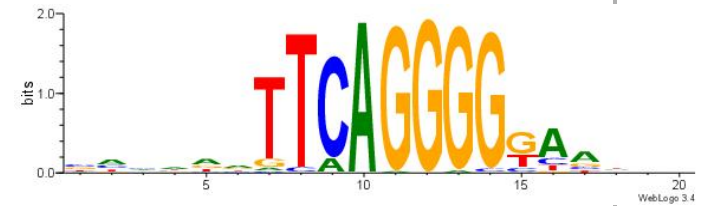
Original motif

Consensus sequence: DDDTMCCCCTGAAHHBDV



Reverse complement motif

Consensus sequence: VBDHHTTCAGGGGRAADDD



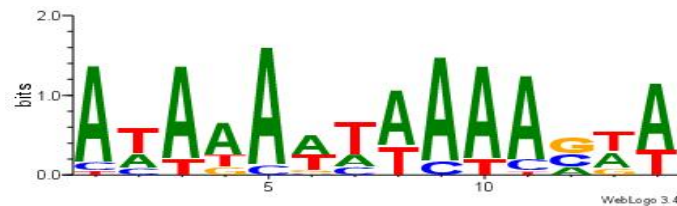
**Dataset #: 2**

**Motif ID: 3**

**Motif name: Motif 3**

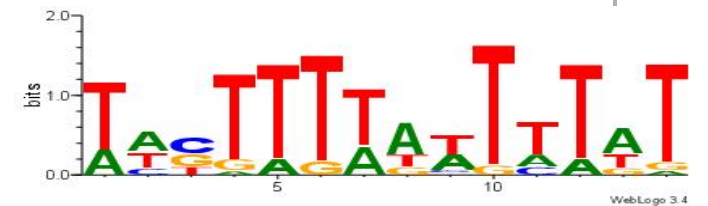
Original motif

Consensus sequence: AWAAAWTWAASWA



Reverse complement motif

Consensus sequence: TWSTTTWAWTTTWT



### Best Matches for Motif ID 3 (Highest to Lowest)

Motif ID:	<a href="#">MA0346.1</a>
Motif name:	NHP6B
Taxon:	Fungi
Matching format of first motif:	Original Motif

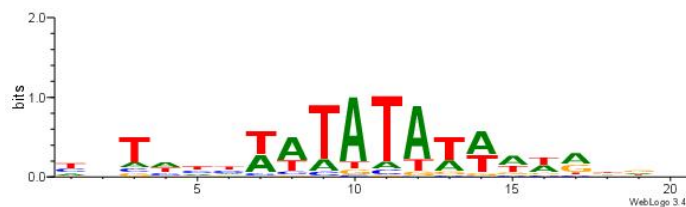
Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 5  
 Number of overlap: 14  
 Similarity score: 0.0383354

Alignment:

BHDKWWWATATATWHHHAHH  
 ----AWAAAWTWAAASWA--

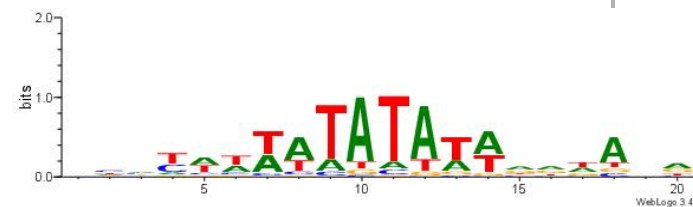
Original motif

Consensus sequence: HHTHHHWATATATWWWRRDDV



Reverse complement motif

Consensus sequence: BHDKWWWATATATWHHHAHH




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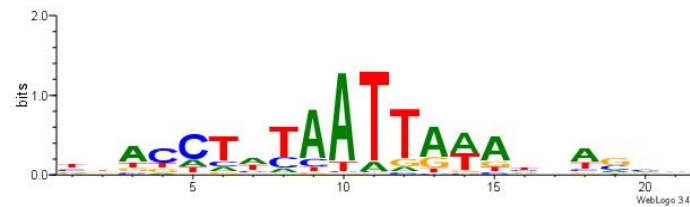
Motif ID: [MA0383.1](#)  
 Motif name: SMP1  
 Taxon: Fungi  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 5  
 Number of overlap: 14  
 Similarity score: 0.0440227

Alignment:

BDACCTWTAATTAWAHBWVVD  
----AWAAAWTWAAASWA----

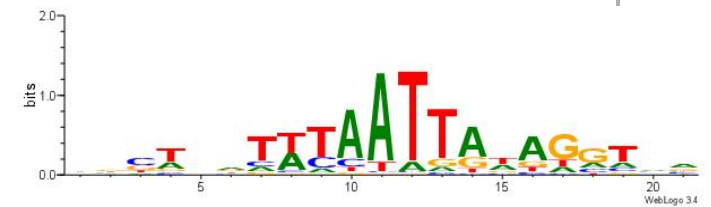
Original motif

Consensus sequence: BDACCTWTAATTAWAHBWVVD



Reverse complement motif

Consensus sequence: DVVWVHTWTAATTAWAGGTDV



Motif ID: [MA0345.1](#)  
Motif name: NHP6A  
Taxon: Fungi  
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: 0.0465457

Alignment:

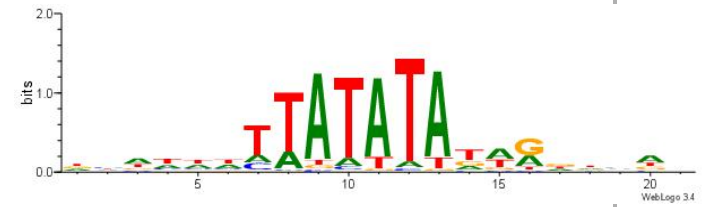
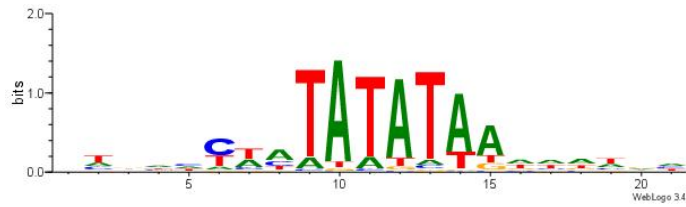
VHDHHYWHTATATAADDDHDH  
-----AWAAAWTWAAASWA

Original motif

Consensus sequence: VHDHHYWHTATATAADDDHDH

Reverse complement motif

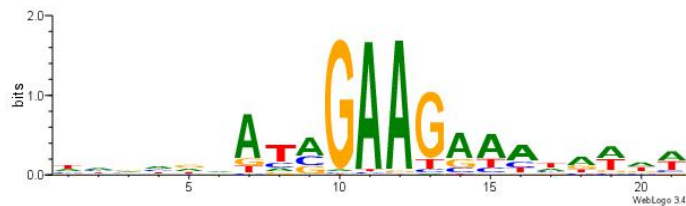
Consensus sequence: HHHDDTTATATAHWKDHHDH



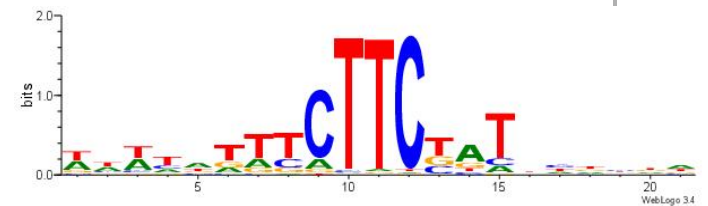
Motif ID: [MA0377.1](#)  
 Motif name: SFL1  
 Taxon: Fungi  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 2  
 Number of overlap: 14  
 Similarity score: 0.0479921

Alignment:  
 HHVHDHATMGAAGAAHDWDW  
 -----AWAAAWTWAAASWA-

Original motif  
 Consensus sequence: HHVHDHATMGAAGAAHDWDW



Reverse complement motif  
 Consensus sequence: WDWDHTTTCTTCYATHHHVHH



Motif ID: [MA0296.1](#)

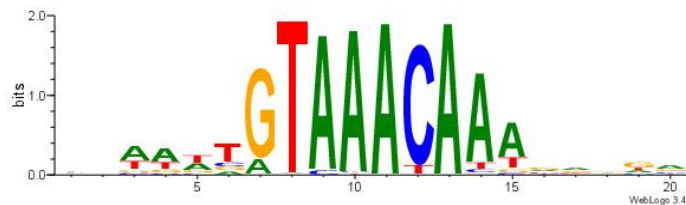
Motif name: FKH1  
 Taxon: Fungi  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 1  
 Number of overlap: 14  
 Similarity score: 0.0507283

Alignment:

BHHDVTTTGTTTACAWWWHV  
 -----TWSTTTWAWTTTWT

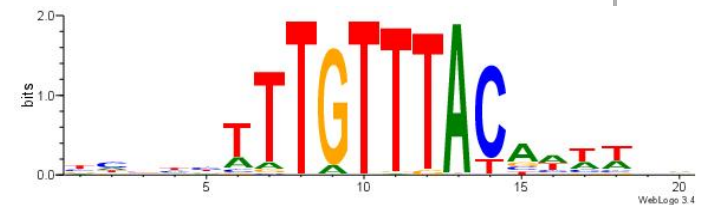
Original motif

Consensus sequence: BDWWWTGTAAACAAVDDDDV



Reverse complement motif

Consensus sequence: BHHDVTTTGTTTACAWWWHV



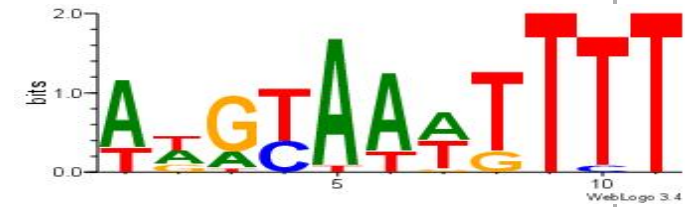
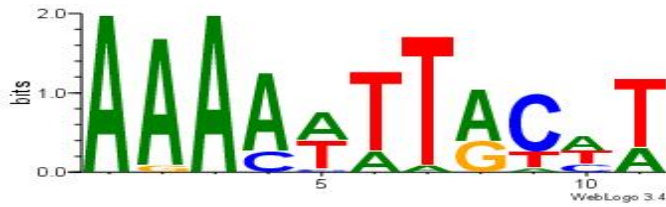
**Dataset #: 2      Motif ID: 4      Motif name: Motif 4**

Original motif

Consensus sequence: AAAAWTTRCWT

Reverse complement motif

Consensus sequence: AWGKAAWTTTT



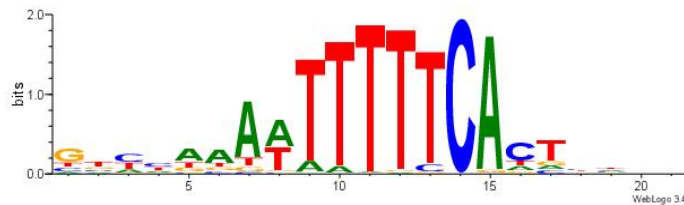
**Best Matches for Motif ID 4 (Highest to Lowest)**

Motif ID: [MA0390.1](#)  
 Motif name: STB3  
 Taxon: Fungi  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 2  
 Number of overlap: 11  
 Similarity score: 0.00483292

Alignment:  
 GBYHAAAWTTTTTCACTBHDD  
 -AWGKAAWTTTT-----

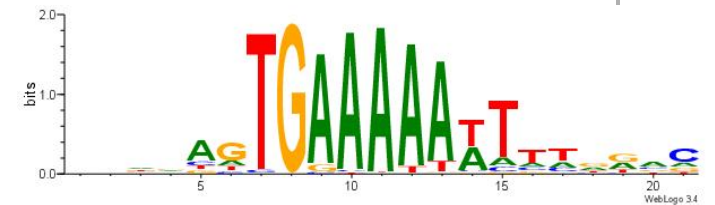
**Original motif**

Consensus sequence: GBYHAAAWTTTTTCACTBHDD



**Reverse complement motif**

Consensus sequence: HHHBAGTGAAAAAWTTTDDKVC



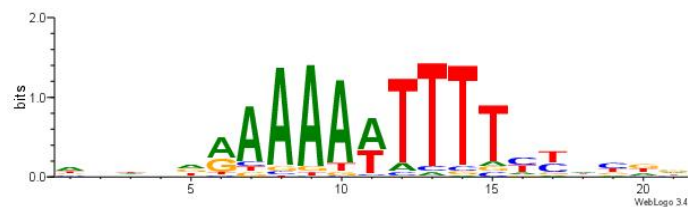
Motif ID: [MA0378.1](#)  
 Motif name: SFP1  
 Taxon: Fungi  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 7  
 Number of overlap: 11  
 Similarity score: 0.0107712

Alignment:

DHDDDRAAAAWTTTTYYHBDD  
 -----AAAWTTRCWT-----

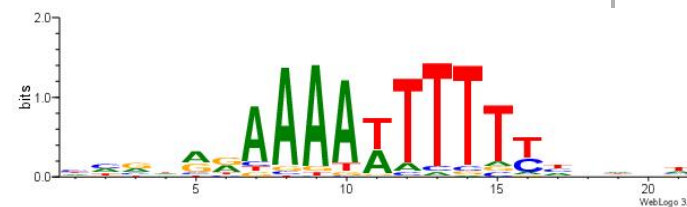
Original motif

Consensus sequence: DHDDDRAAAAWTTTTYYHBDD



Reverse complement motif

Consensus sequence: HHBHMKAAAAWTTTTKDHDHD



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



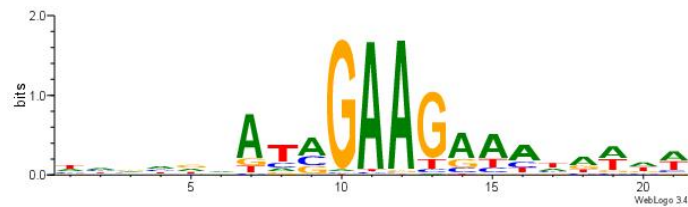
Number of overlap: 11  
Similarity score: 0.0282258

Alignment:

WDWDHTTTCTTCYATHHHVHH  
AWGKAAWTTTT-----

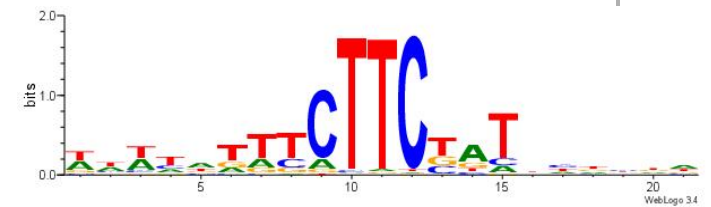
Original motif

Consensus sequence: HHVHDHATMGAAGAAHDWDW



Reverse complement motif

Consensus sequence: WDWDHTTTCTTCYATHHHVHH



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Motif ID: [MA0336.1](#)  
Motif name: MGA1  
Taxon: Fungi  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Reverse Complement  
Direction: Backward  
Position number: 11  
Number of overlap: 11  
Similarity score: 0.0394154

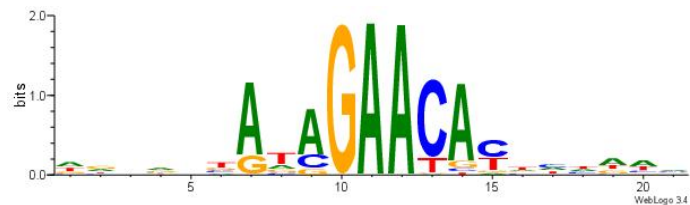
Alignment:

BHDHDDKTGTTCTATVDBVHD  
AWGKAAWTTTT-----

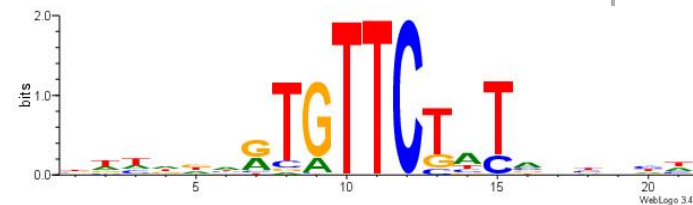
Original motif

Reverse complement motif

Consensus sequence: DDVVHBATAGAACAYDHHDHV



Consensus sequence: BHDHDDKTGTTCTATVDBVHD



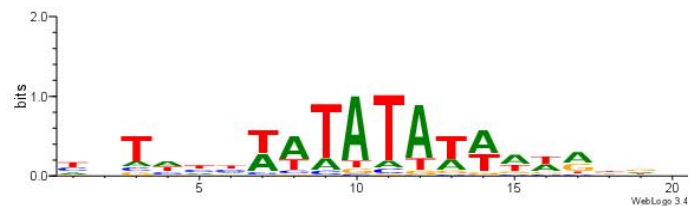
Motif ID: [MA0346.1](#)  
Motif name: NHP6B  
Taxon: Fungi  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Reverse Complement  
Direction: Backward  
Position number: 10  
Number of overlap: 11  
Similarity score: 0.0409802

Alignment:

```
BHKWWWATATATWHHHAHH  
AWGKAATTTT-----
```

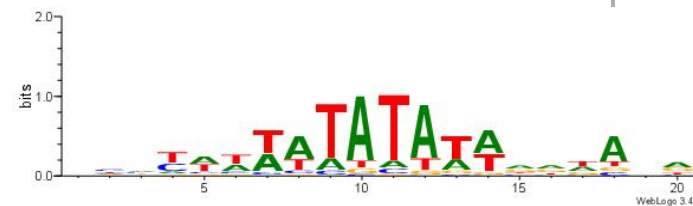
Original motif

Consensus sequence: HHTHHHWATATATWWWRRDDV



Reverse complement motif

Consensus sequence: BHDKWWWATATATWHHHAHH



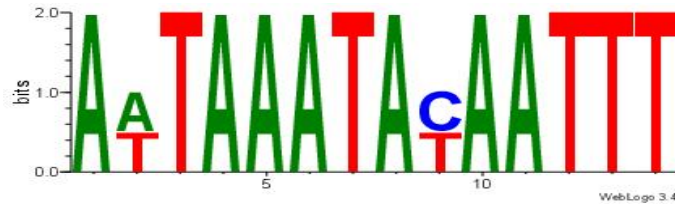
**Dataset #: 2**

**Motif ID: 5**

**Motif name: Motif 5**

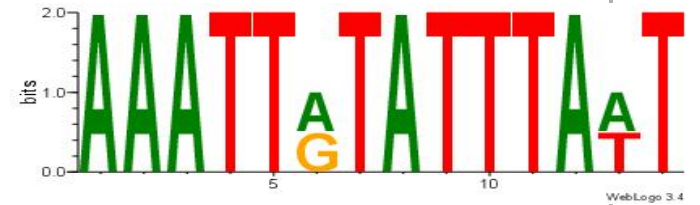
Original motif

Consensus sequence: AWTAATAYAATTT



Reverse complement motif

Consensus sequence: AAATTKTATTTAWT



**Best Matches for Motif ID 5 (Highest to Lowest)**

Motif ID:	<a href="#">MA0378.1</a>
Motif name:	SFP1
Taxon:	Fungi
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	8
Number of overlap:	14
Similarity score:	0.0787324

Alignment:

```

HHBHMKAAAAWTTTTKDHDHD
-----AAATTKTATTTAWT

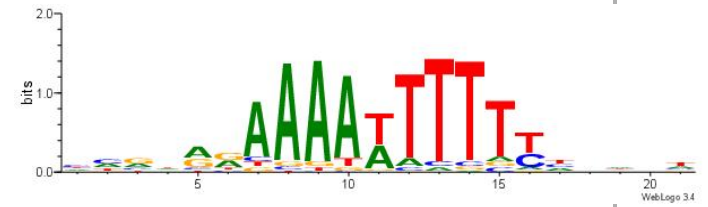
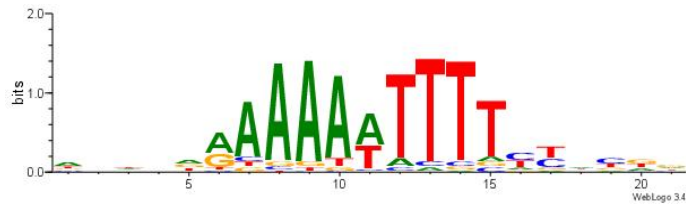
```

Original motif

Consensus sequence: DHDDDRAAAATTTTTYYHBDD

Reverse complement motif

Consensus sequence: HHBHMKAAAAWTTTTKDHDHD

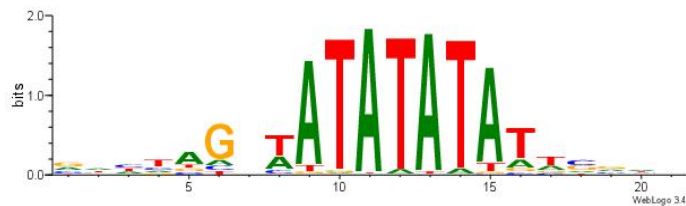


Motif ID: [MA0386.1](#)  
 Motif name: SPT15  
 Taxon: Fungi  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 5  
 Number of overlap: 14  
 Similarity score: 0.0787361

Alignment:  
 DHVSDATATATATWDCTHDHV  
 ----AWTAAATAYAATTT----

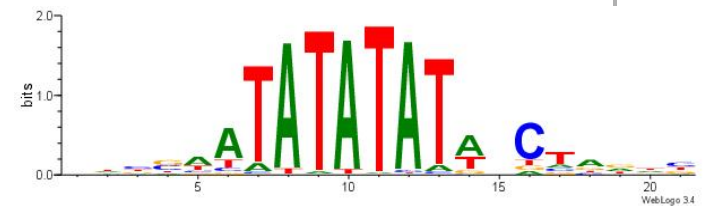
Original motif

Consensus sequence: VHHHAGDWATATATATDSVHD



Reverse complement motif

Consensus sequence: DHVSDATATATATWDCTHDHV



Motif ID: [MA0345.1](#)

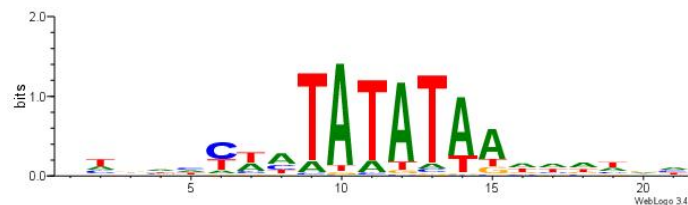
Motif name: NHP6A  
 Taxon: Fungi  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 2  
 Number of overlap: 14  
 Similarity score: 0.0815545

Alignment:

HHHDDDTTATATAHWKDHHHB  
 -AAATTKTATTTAWT-----

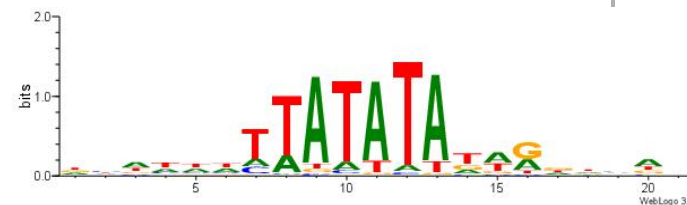
Original motif

Consensus sequence: VHDHHYWHTATATAADDDHDH



Reverse complement motif

Consensus sequence: HHHDDDTTATATAHWKDHHHB




---

Motif ID: [MA0296.1](#)  
 Motif name: FKH1  
 Taxon: Fungi  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 6  
 Number of overlap: 14

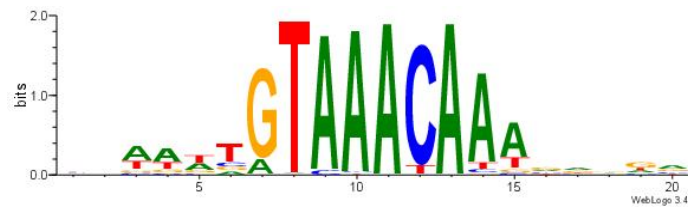
Similarity score: 0.0932265

Alignment:

BHHDVTTTGTTTACAWWWHV  
-AAATTKTATTTAWT-----

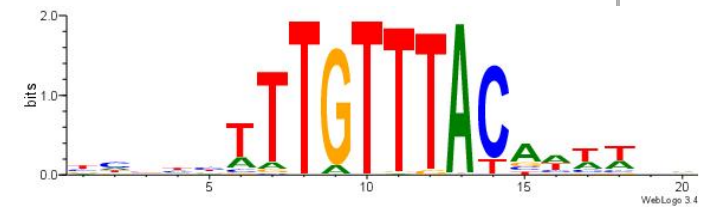
Original motif

Consensus sequence: BDWWWTGTAAACAAVDDDDV



Reverse complement motif

Consensus sequence: BHHDVTTTGTTTACAWWWHV



Motif ID: [MA0383.1](#)  
Motif name: SMP1  
Taxon: Fungi  
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: 0.0950567

Alignment:

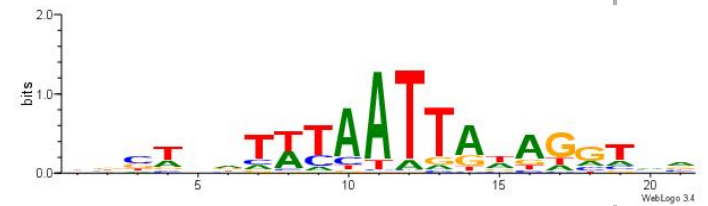
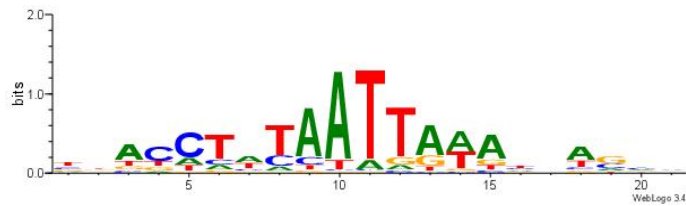
DVVVHTWTAATTAWAGGTDV  
-----AWTAAATAYAATTT-

Original motif

Consensus sequence: BDACCTWTAATTAWAHBWVVD

Reverse complement motif

Consensus sequence: DVVVHTWTAATTAWAGGTDV



**Dataset #: 2      Motif ID: 6      Motif name: Motif 6**

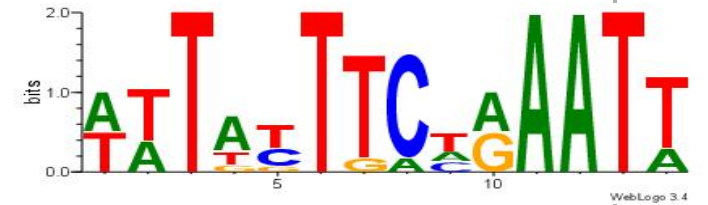
Original motif

Consensus sequence: AATTYDGAARTAWW



Reverse complement motif

Consensus sequence: WWTAKTTCDKAATT



**Best Matches for Motif ID 6 (Highest to Lowest)**

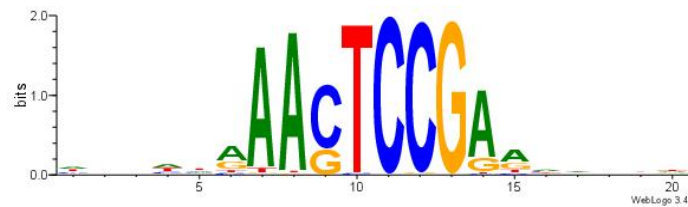
Motif ID:	<a href="#">MA0400.1</a>
Motif name:	SUT2
Taxon:	Fungi
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	7
Number of overlap:	14
Similarity score:	0.0673673

Alignment:

DVDHHTTCGGAGTTKHHHDH  
WWTAKTTCDKAATT-----

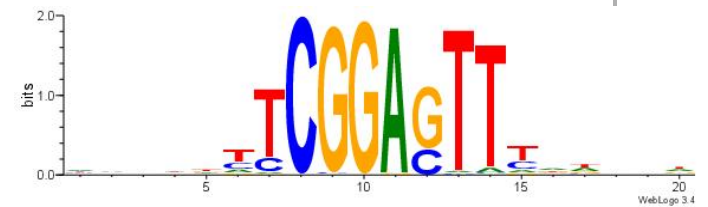
Original motif

Consensus sequence: HDDHHRAACTCCGAAHHDBD



Reverse complement motif

Consensus sequence: DVDHHTTCGGAGTTKHHHDH



Motif ID: [MA0377.1](#)  
Motif name: SFL1  
Taxon: Fungi  
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: 0.0693729

Alignment:

HHVHDHATMGAAGAAHDWDW  
---AATTYDGAARTAWW----

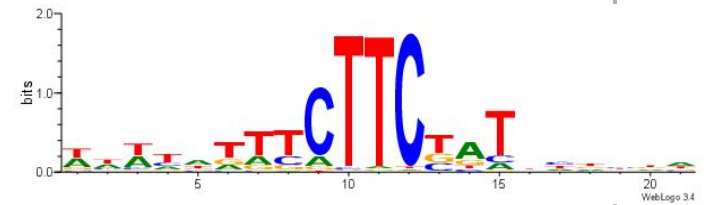
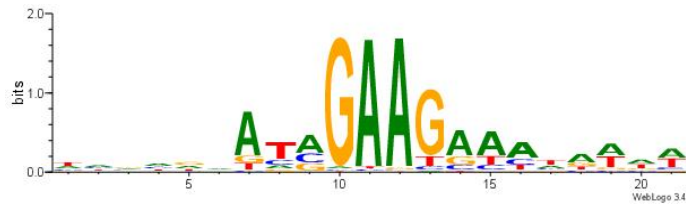
Original motif

Consensus sequence: HHVHDHATMGAAGAAHDWDW

Reverse complement motif

Consensus sequence: WDWDHTTTCTTCYATHHHVHH



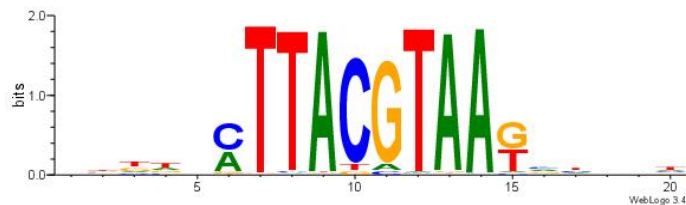


Motif ID: [MA0415.1](#)  
 Motif name: YAP1  
 Taxon: Fungi  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 5  
 Number of overlap: 14  
 Similarity score: 0.0741794

Alignment:  
 HBDDDMTTACGTAAKVHHVH  
 --WWTAKTTCDKAATT----

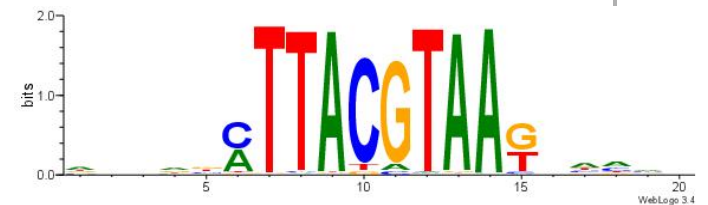
Original motif

Consensus sequence: HBDDDMTTACGTAAKVHHVH



Reverse complement motif

Consensus sequence: HVDHVYTTACGTAARHDDVH



Motif ID: [MA0296.1](#)

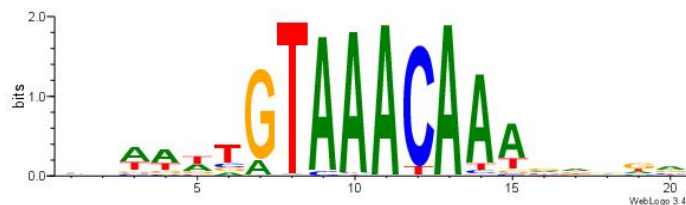
Motif name: FKH1  
 Taxon: Fungi  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 6  
 Number of overlap: 14  
 Similarity score: 0.0778093

**Alignment:**

BDWWWTGTAAACAAVDDD  
 -AATTYDGAARTAWW-----

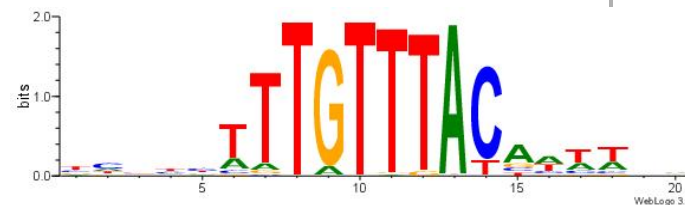
**Original motif**

Consensus sequence: BDWWWTGTAAACAAVDDD



**Reverse complement motif**

Consensus sequence: BHHDVTTTGTTTACAWWHV



Motif ID: [MA0390.1](#)  
 Motif name: STB3  
 Taxon: Fungi  
 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:

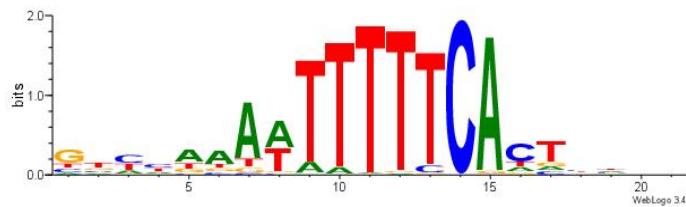
0.0793696

Alignment:

GBYHAAAWTTTTTCACTBHDD  
-----AATTYDGAARTAWW-

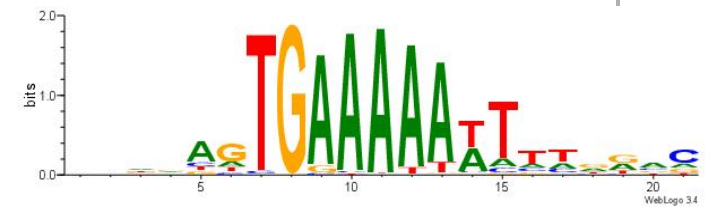
Original motif

Consensus sequence: GBYHAAAWTTTTTCACTBHDD



Reverse complement motif

Consensus sequence: HHHBAGTGAAAAWTTTDDKVC



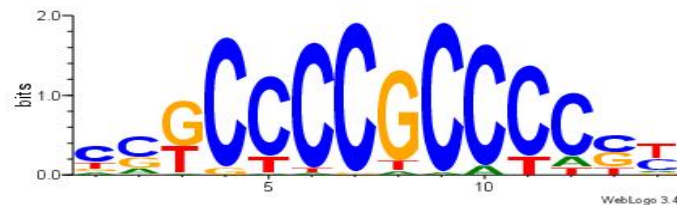
**Dataset #: 2**

**Motif ID: 7**

**Motif name: Motif 7**

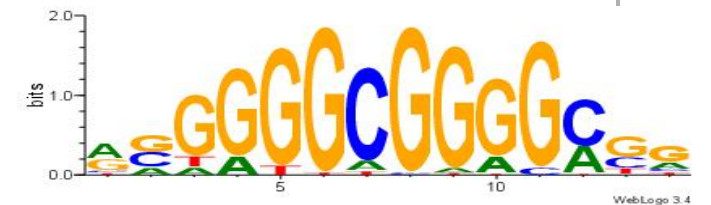
Original motif

Consensus sequence: CSKCCCCGCCCSY



Reverse complement motif

Consensus sequence: MSGGGCGGGGYSG



### Best Matches for Motif ID 7 (Highest to Lowest)

Motif ID:

[MA0395.1](#)

Motif name:

STP2

Taxon:

Fungi

Matching format of first motif:

Reverse Complement

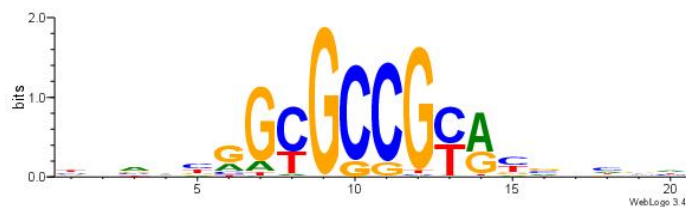
Matching format of second motif: Original Motif  
Direction: Forward  
Position number: 4  
Number of overlap: 14  
Similarity score: 0.0478852

Alignment:

HVVHBBGGCGCCGYRYVHHBH  
---MSGGGGCGGGYSG---

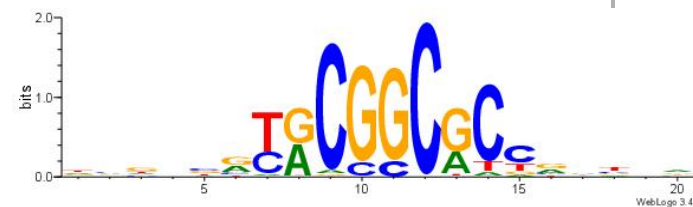
Original motif

Consensus sequence: HVVHBBGGCGCCGYRYVHHBH



Reverse complement motif

Consensus sequence: HBDHVKKKCGGCGCCBHBVH



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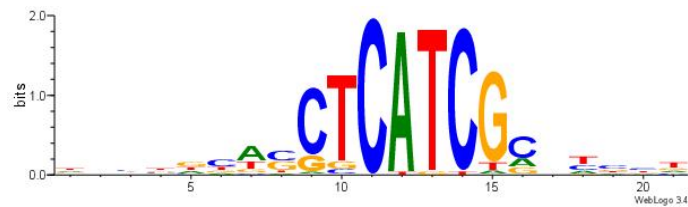
Motif ID: [MA0351.1](#)  
Motif name: DOT6  
Taxon: Fungi  
Matching format of first motif: Original Motif  
Matching format of second motif: Original Motif  
Direction: Forward  
Position number: 8  
Number of overlap: 14  
Similarity score: 0.0530075

Alignment:

DBBBDBWSCTCATCGCVHBBB  
-----CSKCCCCGCCCSY

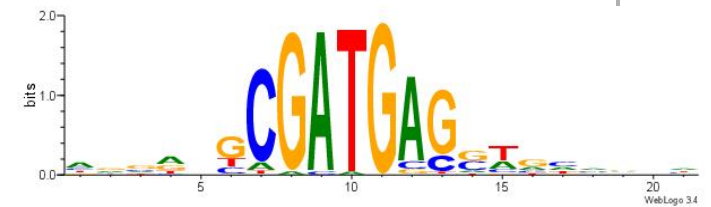
Original motif

Consensus sequence: DBBBDBWSCTCATCGCVHBBB



Reverse complement motif

Consensus sequence: DBBHBGCGATGAGSWBHVBVD



Motif ID: [MA0350.1](#)  
Motif name: TOD6  
Taxon: Fungi  
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: 0.0615081

Alignment:

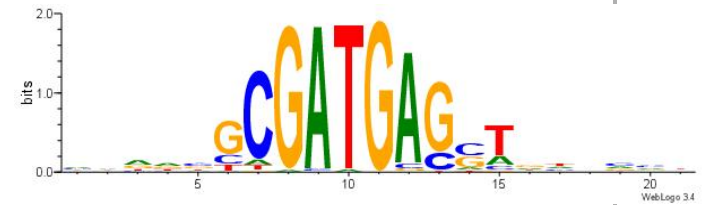
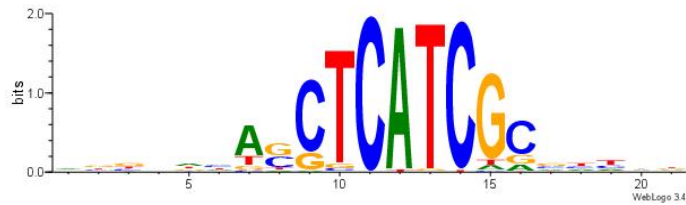
DBBHDHASCTCATCGCVHHHD  
-----CSKCCCCGCCCSY

Original motif

Consensus sequence: DBBHDHASCTCATCGCVHHHD

Reverse complement motif

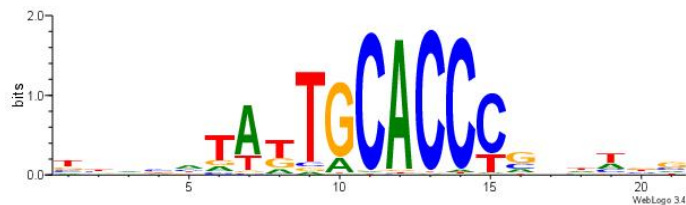
Consensus sequence: DHHHVCGATGAGSTDDDBBD



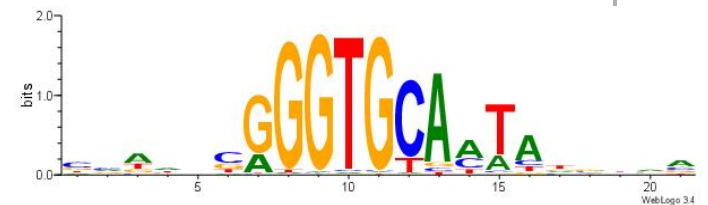
Motif ID: [MA0269.1](#)  
 Motif name: AFT1  
 Taxon: Fungi  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 3  
 Number of overlap: 14  
 Similarity score: 0.0669459

Alignment:  
 VBWDBSGGGTGCARTAHBDVV  
 -----MSGGGGCGGGGYSG--

Original motif  
 Consensus sequence: BBDBHTAKTGCACCCSVDWBV



Reverse complement motif  
 Consensus sequence: VBWDBSGGGTGCARTAHBDVV



Motif ID: [MA0425.1](#)

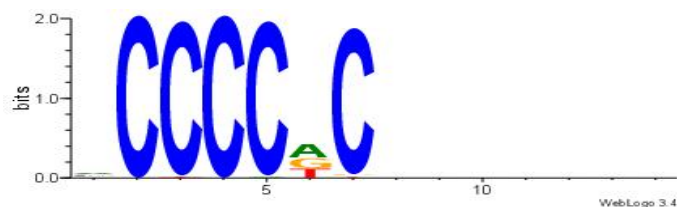
Motif name: YGR067C  
 Taxon: Fungi  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 14  
 Similarity score: 0.0706512

**Alignment:**

DBDDHHHGDGGGGGB  
 MSGGGGCGGGGYSG

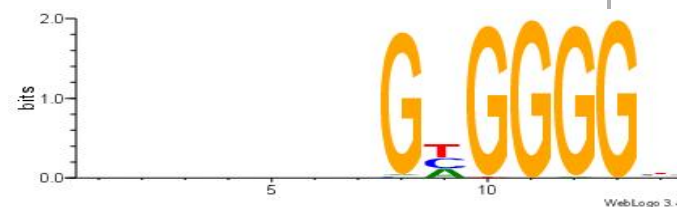
**Original motif**

Consensus sequence: VCCCCDCHHHDDBD



**Reverse complement motif**

Consensus sequence: DBDDHHHGDGGGGGB




---

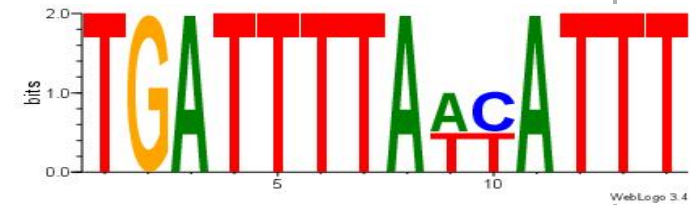
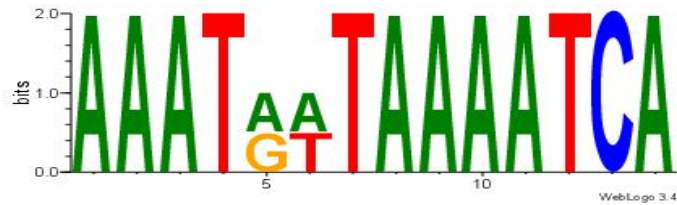
**Dataset #: 2      Motif ID: 8      Motif name: Motif 8**

**Original motif**

Consensus sequence: AAATRWATAAATCA

**Reverse complement motif**

Consensus sequence: TGATTTAWKATTT



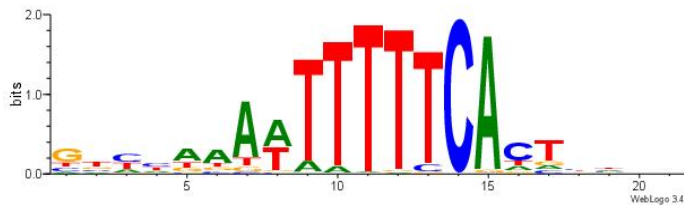
**Best Matches for Motif ID 8 (Highest to Lowest)**

Motif ID: [MA0390.1](#)  
 Motif name: STB3  
 Taxon: Fungi  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 5  
 Number of overlap: 14  
 Similarity score: 0.0751523

Alignment:  
 HHHBAGTGAAAAWTTTDDKVC  
 ---AAATRWTA AAAATCA----

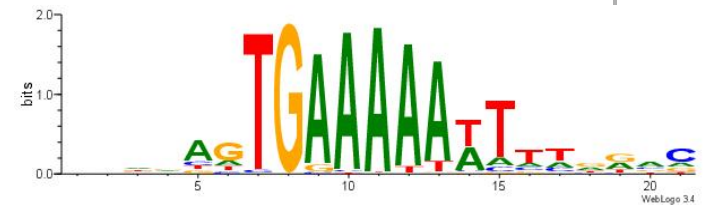
**Original motif**

Consensus sequence: GBYHAAWTTTTTCACTBHDD



**Reverse complement motif**

Consensus sequence: HHHBAGTGAAAAWTTTDDKVC





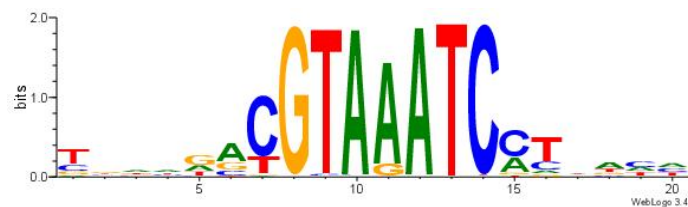
Motif ID: [MA0435.1](#)  
 Motif name: YPR015C  
 Taxon: Fungi  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 2  
 Number of overlap: 14  
 Similarity score: 0.075789

**Alignment:**

TBDHDACGTAAATCMTDDHH  
 -AAATRWTAATAATCA-----

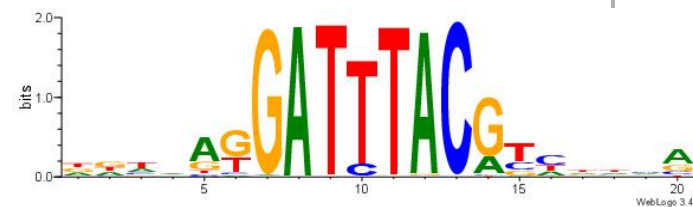
**Original motif**

Consensus sequence: TBDHDACGTAAATCMTDDHH



**Reverse complement motif**

Consensus sequence: HDDDARGATTTACGTHHDBA



Motif ID: [MA0369.1](#)  
 Motif name: RLM1  
 Taxon: Fungi  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 2  
 Number of overlap: 13

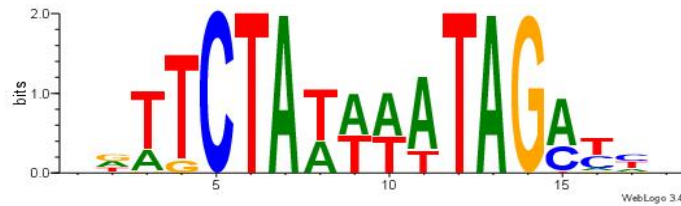
Similarity score: 0.564575

Alignment:

VKMYCTATWWWTAGAAHB-  
-TGATTTTAWKATTT----

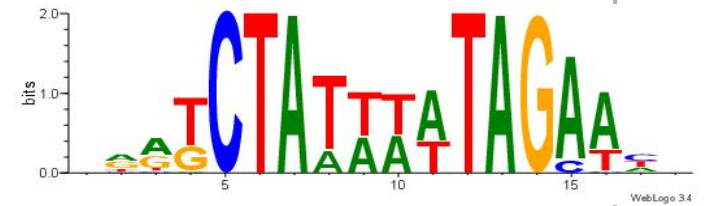
Original motif

Consensus sequence: VDTTCTAWWWATAGMYVV



Reverse complement motif

Consensus sequence: VKMYCTATWWWTAGAAHB



Motif ID: [MA0407.1](#)  
Motif name: THI2  
Taxon: Fungi  
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: 0.570221

Alignment:

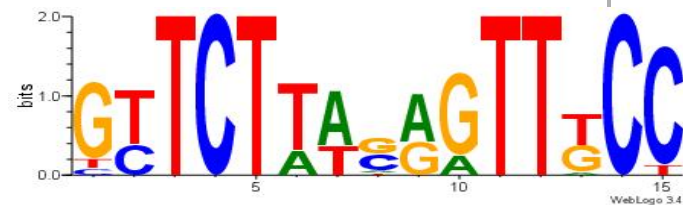
-GGMAACYSWAAGARC  
-AAATRWTAAAATCA-

Original motif

Consensus sequence: GGMAACYSWAAGARC

Reverse complement motif

Consensus sequence: GKTCTTWSMGTTYCC



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: 2  
 Number of overlap: 13  
 Similarity score: 0.575864

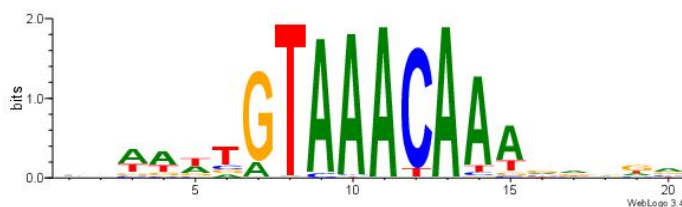
Alignment:

```

BDWWWTGTAAACAAVDDDDV-
-AAATRWTAAAATCA-----
  
```

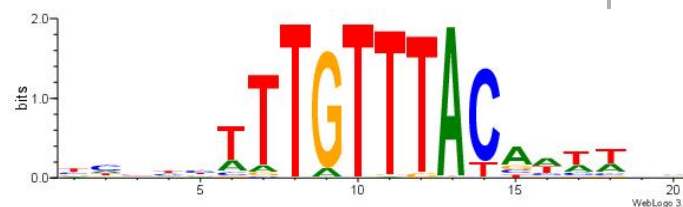
Original motif

Consensus sequence: BDWWWTGTAAACAAVDDDDV



Reverse complement motif

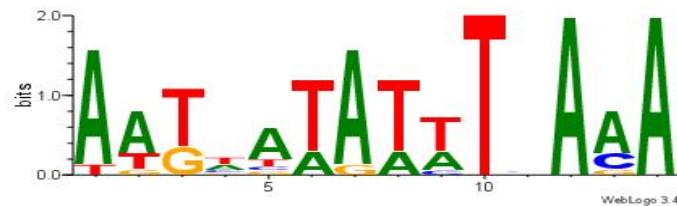
Consensus sequence: BHHDVTTTGTTCACAWWWHV



**Dataset #: 2**      **Motif ID: 9**      **Motif name: Motif 9**

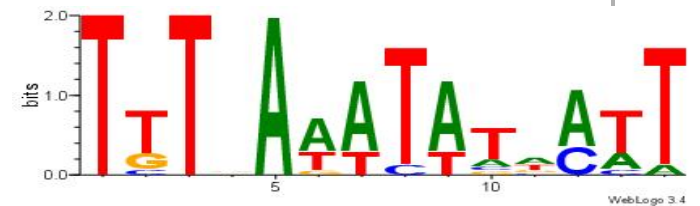
Original motif

Consensus sequence: AATHATATWTHAAA



Reverse complement motif

Consensus sequence: TTTDAWATATHATT



### Best Matches for Motif ID 9 (Highest to Lowest)

Motif ID: [MA0345.1](#)  
Motif name: NHP6A  
Taxon: Fungi  
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: 0.0354375

Alignment:

HHHDDDTTATATAHWKDH H B

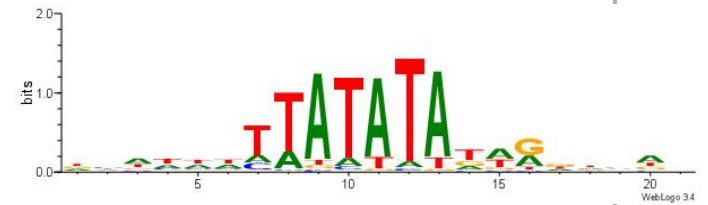
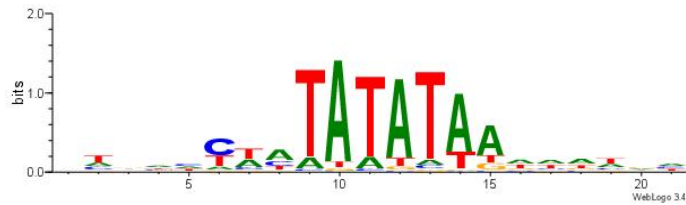
----TTTDAWATATHATT---

Original motif

Consensus sequence: VHDHHYWHTATATAADDDHDH

Reverse complement motif

Consensus sequence: HHHDDDTTATATAHWKDH H B

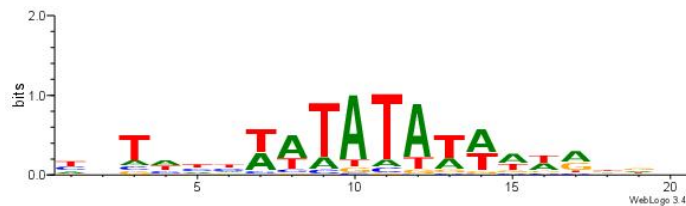


Motif ID: [MA0346.1](#)  
 Motif name: NHP6B  
 Taxon: Fungi  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 4  
 Number of overlap: 14  
 Similarity score: 0.041212

Alignment:  
 HHTHHHWATATATWWWRDDV  
 ---AATHATATWTHAAA---

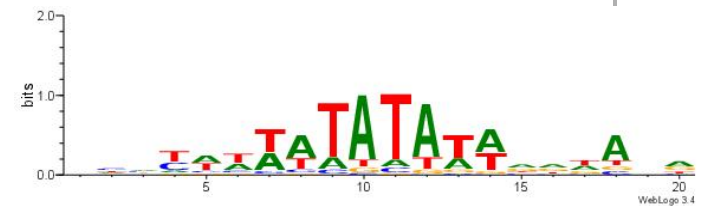
Original motif

Consensus sequence: HHTHHHWATATATWWWRDDV



Reverse complement motif

Consensus sequence: BHDKWWWATATATWHHHAAHH



Motif ID: [MA0383.1](#)

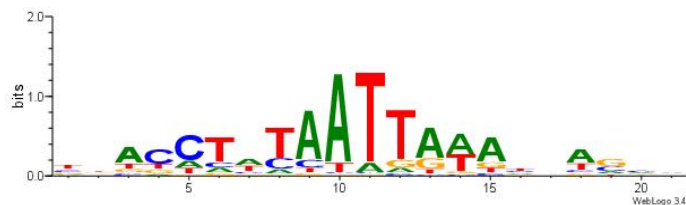
Motif name: SMP1  
 Taxon: Fungi  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 6  
 Number of overlap: 14  
 Similarity score: 0.0513433

**Alignment:**

DVVWVHTWTAATTAWAGGTDV  
 -----TTTDAWATATHATT--

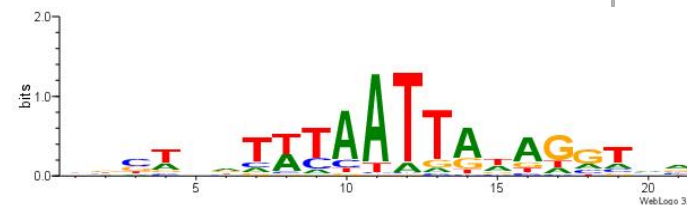
**Original motif**

Consensus sequence: BDACCTWTAATTAWAHBWVVD



**Reverse complement motif**

Consensus sequence: DVVWVHTWTAATTAWAGGTDV




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Motif ID: [MA0386.1](#)  
 Motif name: SPT15  
 Taxon: Fungi  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 2  
 Number of overlap: 14

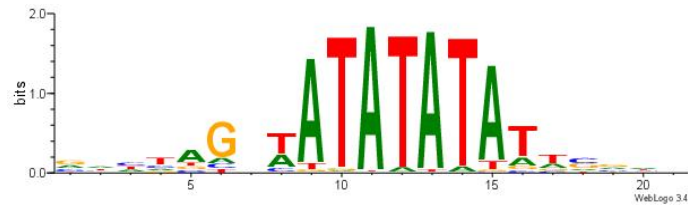
Similarity score: 0.0562045

Alignment:

VHHHAGDWATATATATDSVHD  
-----TTTDAWATATHATT-

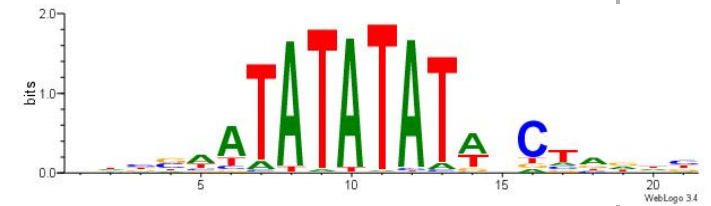
Original motif

Consensus sequence: VHHHAGDWATATATATDSVHD



Reverse complement motif

Consensus sequence: DHVSDATATATATWDCCTHDHV



Motif ID: [MA0369.1](#)  
Motif name: RLM1  
Taxon: Fungi  
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: 0.0619139

Alignment:

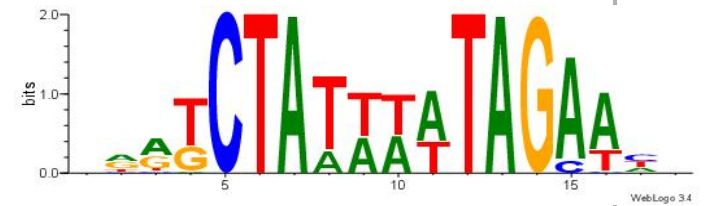
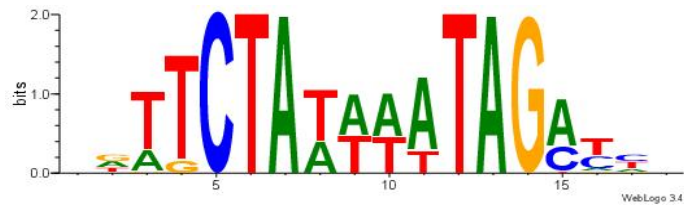
VDTTCTAWWWATAGMYV  
--TTTDAWATATHATT--

Original motif

Consensus sequence: VDTTCTAWWWATAGMYV

Reverse complement motif

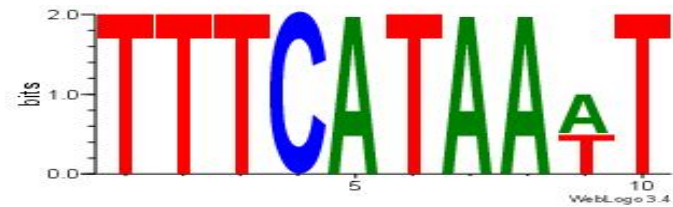
Consensus sequence: VKMYCTATWWWTAGAAHB



**Dataset #: 2      Motif ID: 10      Motif name: Motif 10**

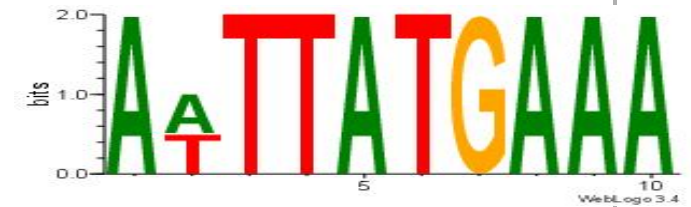
Original motif

Consensus sequence: TTTCATAAWT



Reverse complement motif

Consensus sequence: AWTTATGAAA



### Best Matches for Motif ID 10 (Highest to Lowest)

Motif ID:	<a href="#">MA0415.1</a>
Motif name:	YAP1
Taxon:	Fungi
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	7
Number of overlap:	10
Similarity score:	0.0643778

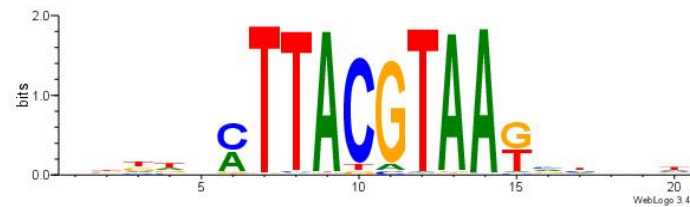
Alignment:



HVDHVYTTACGTAARHDDVH  
-----AWTTATGAAA-----

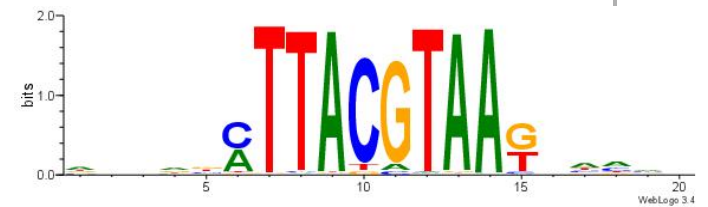
Original motif

Consensus sequence: HBDDDMTTACGTAAKVHHVH



Reverse complement motif

Consensus sequence: HVDHVYTTACGTAARHDDVH



Motif ID: [MA0387.1](#)  
Motif name: SPT2  
Taxon: Fungi  
Matching format of first motif: Original Motif  
Matching format of second motif: Reverse Complement  
Direction: Backward  
Position number: 1  
Number of overlap: 10  
Similarity score: 0.0680925

Alignment:

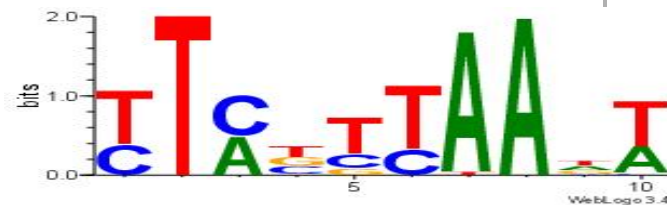
KTYBTAAHW  
TTCATAAWT

Original motif

Consensus sequence: WHTTAAVKAR

Reverse complement motif

Consensus sequence: KTYBTAAHW



Motif ID: [MA0390.1](#)  
 Motif name: STB3  
 Taxon: Fungi  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 2  
 Number of overlap: 10  
 Similarity score: 0.0721515

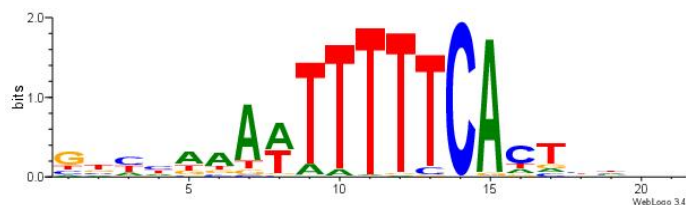
Alignment:

```

HHHBAGTGAAAAWTTTDDKVC
-AWTTATGAAA-----
  
```

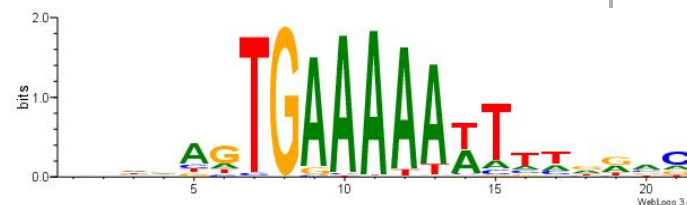
Original motif

Consensus sequence: GBYHAAWTTTTTCACTBHDD



Reverse complement motif

Consensus sequence: HHHBAGTGAAAAWTTTDDKVC



Motif ID: [MA0369.1](#)

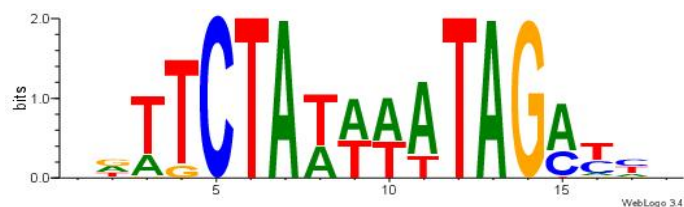
Motif name: RLM1  
 Taxon: Fungi  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 3  
 Number of overlap: 10  
 Similarity score: 0.0782947

**Alignment:**

VKMYCTATWWWTAGAAHB  
 -----AWTTATGAAA--

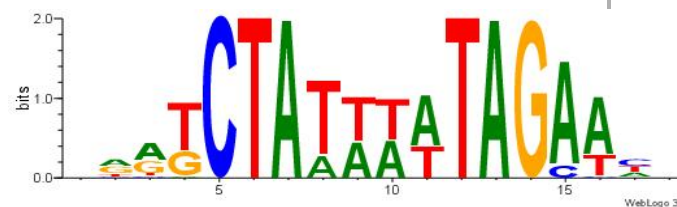
**Original motif**

Consensus sequence: VDTTCTAWWWATAGMYVV



**Reverse complement motif**

Consensus sequence: VKMYCTATWWWTAGAAHB




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Motif ID: [MA0418.1](#)  
 Motif name: YAP6  
 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:

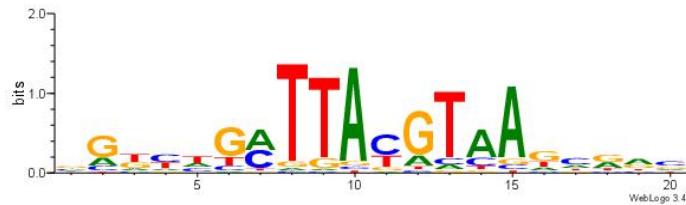
0.0840819

Alignment:

VGKYHGMTTAYGTAAKHRDV  
-----AWTTATGAAA-----

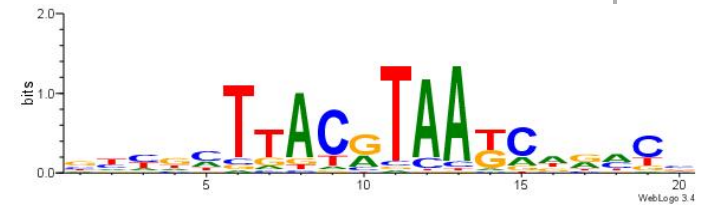
Original motif

Consensus sequence: VGKYHGMTTAYGTAAKHRDV



Reverse complement motif

Consensus sequence: VDMDYTTACKTAAYCHKRCV



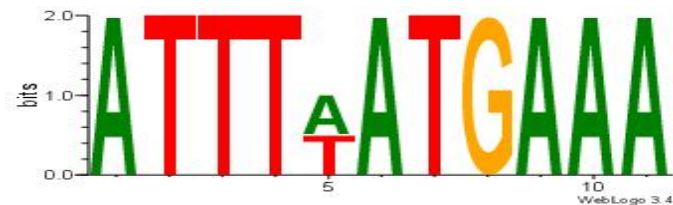
**Dataset #: 2**

**Motif ID: 11**

**Motif name: Motif 11**

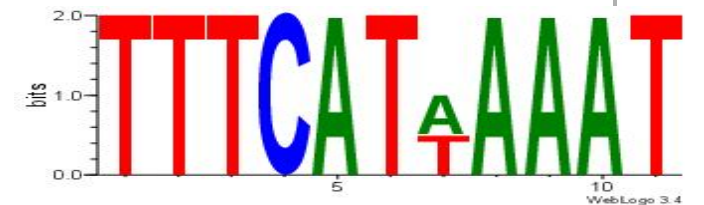
Original motif

Consensus sequence: ATTTWATGAAA



Reverse complement motif

Consensus sequence: TTTCATWAAAT



### Best Matches for Motif ID 11 (Highest to Lowest)

Motif ID:

[MA0390.1](#)

Motif name:

STB3

Taxon:

Fungi

Matching format of first motif:

Original Motif

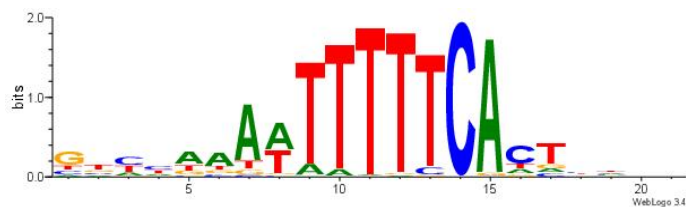
Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 11  
 Similarity score: 0.0759198

Alignment:

HHHBAGTGAAAAWTTTDDKVC  
 ATTTWATGAAA-----

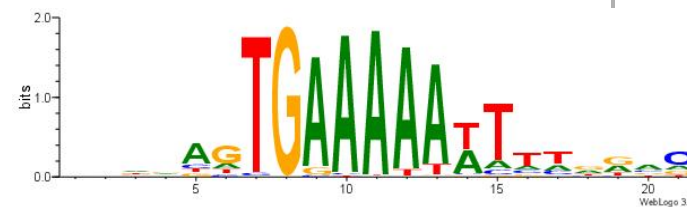
Original motif

Consensus sequence: GBYHAAWTTTTTCACTBHDD



Reverse complement motif

Consensus sequence: HHHBAGTGAAAAWTTTDDKVC




---

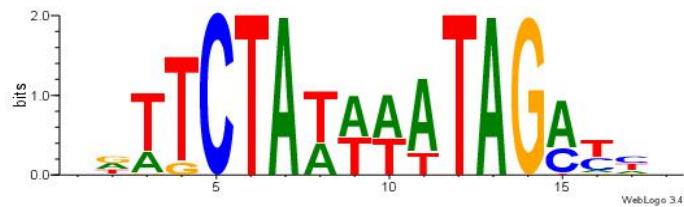
Motif ID: [MA0369.1](#)  
 Motif name: RLM1  
 Taxon: Fungi  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 2  
 Number of overlap: 11  
 Similarity score: 0.0779159

Alignment:

VKMYCTATWWWTAGAAHB  
-----ATTTWATGAAA-

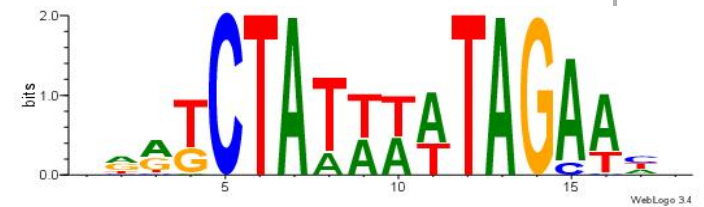
Original motif

Consensus sequence: VDTTCTAWWWATAGMYVV



Reverse complement motif

Consensus sequence: VKMYCTATWWWTAGAAHB



Motif ID: [MA0415.1](#)  
Motif name: YAP1  
Taxon: Fungi  
Matching format of first motif: Original Motif  
Matching format of second motif: Reverse Complement  
Direction: Forward  
Position number: 4  
Number of overlap: 11  
Similarity score: 0.0864254

Alignment:

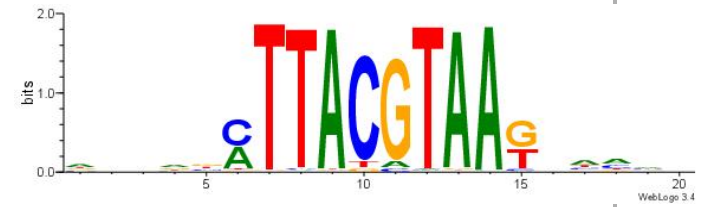
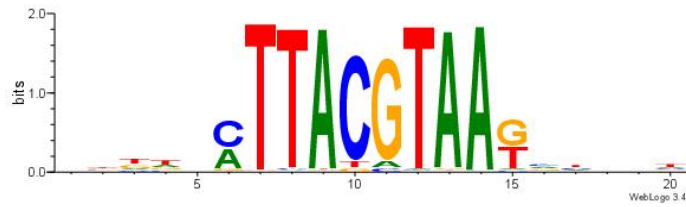
HVDHVYTTACGTAARHDDVH  
---ATTTWATGAAA-----

Original motif

Consensus sequence: HBDDDMTTACGTAAKVHHVH

Reverse complement motif

Consensus sequence: HVDHVYTTACGTAARHDDVH

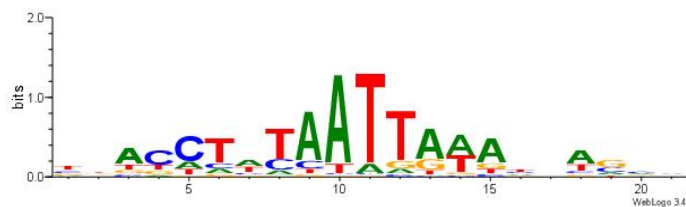


Motif ID: [MA0383.1](#)  
 Motif name: SMP1  
 Taxon: Fungi  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 6  
 Number of overlap: 11  
 Similarity score: 0.087477

Alignment:  
 BDACCTWTAATTAWAHBWVVD  
 -----TTTCATWAAAT-----

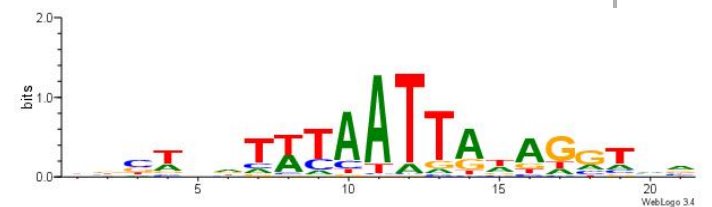
Original motif

Consensus sequence: BDACCTWTAATTAWAHBWVVD



Reverse complement motif

Consensus sequence: DVVWVHTWTAATTAWAGGTDV



Motif ID: [MA0407.1](#)

Motif name: THI2  
 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: 0.0885853

Alignment:

GGMAACYSWAAGARC  
 ----ATTWATGAAA

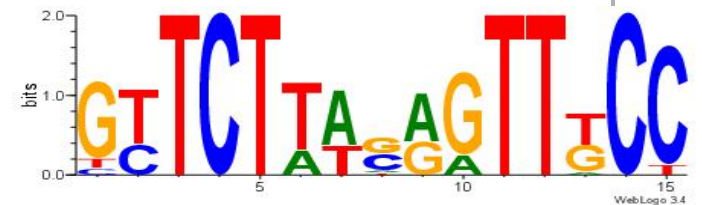
Original motif

Consensus sequence: GGMAACYSWAAGARC



Reverse complement motif

Consensus sequence: GKTCTTWSMGTTYCC



**Dataset #: 2      Motif ID: 12      Motif name: Motif 12**

Original motif

Consensus sequence: AAAACAAA

Reverse complement motif

Consensus sequence: TTTGTTTT





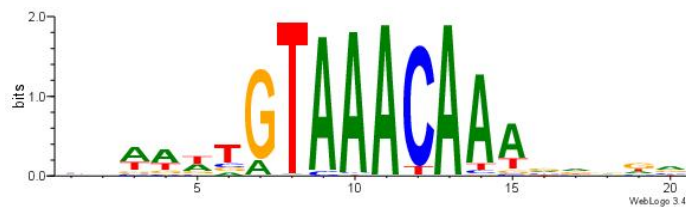
### Best Matches for Motif ID 12 (Highest to Lowest)

Motif ID: [MA0296.1](#)  
 Motif name: FKH1  
 Taxon: Fungi  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 6  
 Number of overlap: 8  
 Similarity score: 0.00812138

Alignment:  
 BHHDVTTTGTTTACAWWWHV  
 -----TTTGTTTT-----

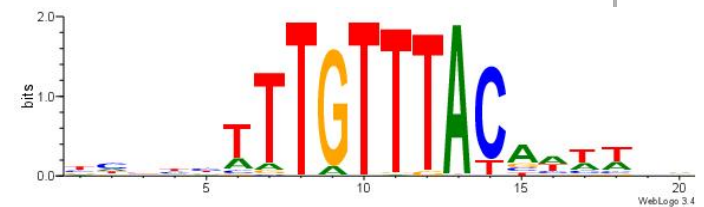
#### Original motif

Consensus sequence: BDWWWTGTAAACAAVDDDDV



#### Reverse complement motif

Consensus sequence: BHHDVTTTGTTTACAWWWHV

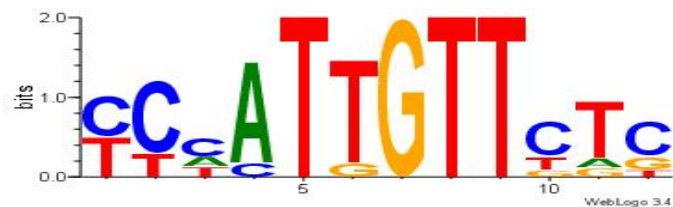


Motif ID: [MA0371.1](#)  
 Motif name: ROX1  
 Taxon: Fungi  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 4  
 Number of overlap: 8  
 Similarity score: 0.0247396

Alignment:  
 YCHATTGTTCTC  
 ---TTTGTTTT-

Original motif

Consensus sequence: YCHATTGTTCTC



Reverse complement motif

Consensus sequence: GAGAACAATDGK



Motif ID: [MA0277.1](#)  
 Motif name: AZF1  
 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: 0.0259235

Alignment:

AAAAAGAAA  
-AAAACAAA

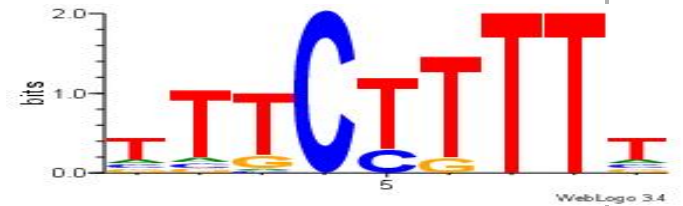
Original motif

Consensus sequence: AAAAAGAAA



Reverse complement motif

Consensus sequence: TTTCTTTTT



Motif ID: [MA0343.1](#)  
Motif name: NDT80  
Taxon: Fungi  
Matching format of first motif: Original Motif  
Matching format of second motif: Original Motif  
Direction: Backward  
Position number: 8  
Number of overlap: 8  
Similarity score: 0.0382796

Alignment:

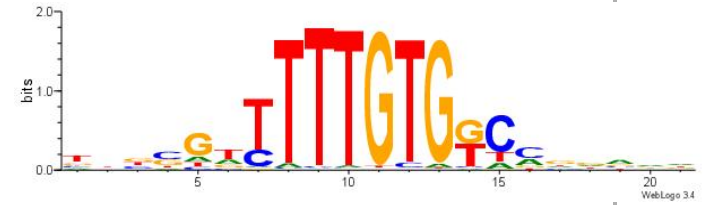
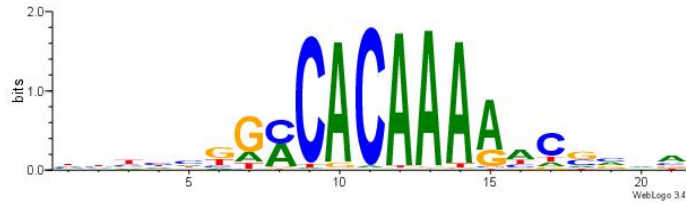
HHBHHKGMCACAAAHCSDV  
-----AAAACAAA-----

Original motif

Consensus sequence: HHBHHKGMCACAAAHCSDV

Reverse complement motif

Consensus sequence: BDVSGHTTTTGTGRCYDDVHH



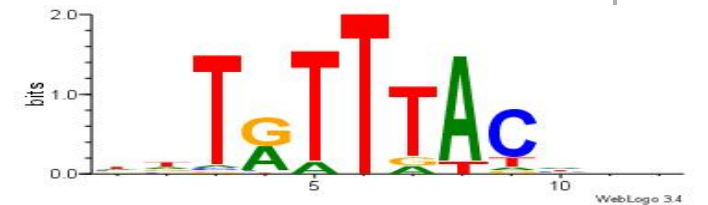
Motif ID: [MA0929.1](#)  
 Motif name: NCU00019  
 Taxon: Fungi  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 1  
 Number of overlap: 8  
 Similarity score: 0.0487695

Alignment:  
 DBDGTAAAYAHD  
 ----AAAACAAA

Original motif  
 Consensus sequence: DBDGTAAAYAHD



Reverse complement motif  
 Consensus sequence: BHTKTTTACDDB



**Dataset #: 2      Motif ID: 13      Motif name: Motif 13**

Original motif

Consensus sequence: AAAGATTT



Reverse complement motif

Consensus sequence: AAATCTTT



### Best Matches for Motif ID 13 (Highest to Lowest)

Motif ID: [MA0435.1](#)  
Motif name: YPR015C  
Taxon: Fungi  
Matching format of first motif: Original Motif  
Matching format of second motif: Reverse Complement  
Direction: Backward  
Position number: 10  
Number of overlap: 8  
Similarity score: 0.0140145

Alignment:

HDDDARGATTTACGTHHDBA

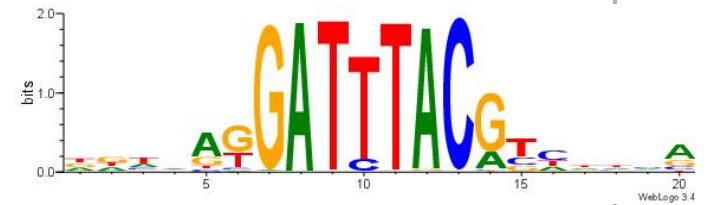
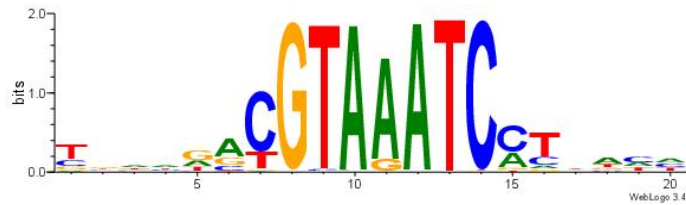
---AAAGATTT-----

Original motif

Consensus sequence: TBDHDACGTAAATCMTDDHH

Reverse complement motif

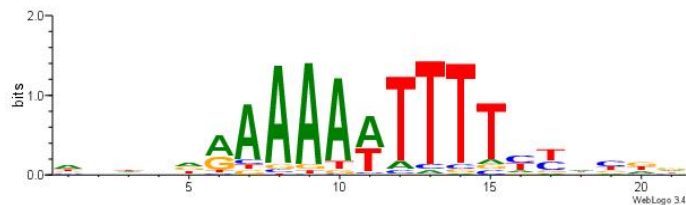
Consensus sequence: HDDDARGATTTACGTHHDBA



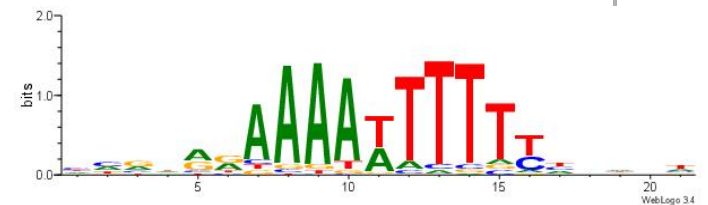
Motif ID: [MA0378.1](#)  
 Motif name: SFP1  
 Taxon: Fungi  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 7  
 Number of overlap: 8  
 Similarity score: 0.0232736

Alignment:  
 DHDDDRAAAWTTTTYYHBDD  
 -----AAAGATTT-----

Original motif  
 Consensus sequence: DHDDDRAAAWTTTTYYHBDD



Reverse complement motif  
 Consensus sequence: HHBHMKAAAATTTTKDHDHD



Motif ID: [MA0390.1](#)

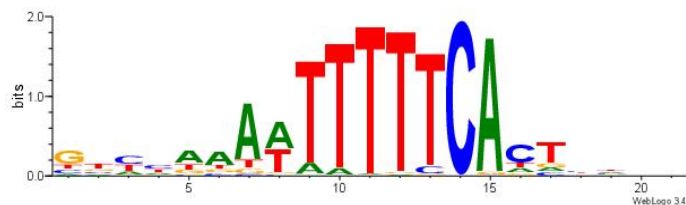
Motif name: STB3  
 Taxon: Fungi  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 6  
 Number of overlap: 8  
 Similarity score: 0.030962

**Alignment:**

GBYHAAAWTTTTTCACTBHDD  
 -----AAATCTTT-----

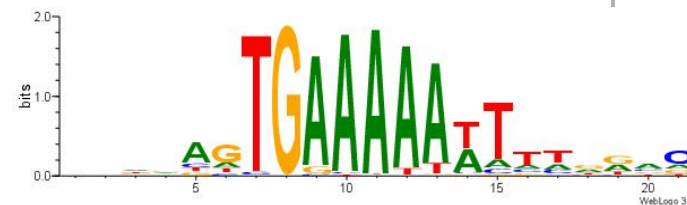
**Original motif**

Consensus sequence: GBYHAAAWTTTTTCACTBHDD



**Reverse complement motif**

Consensus sequence: HHHBAGTGAAAAAWTTTIDKVC




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Motif ID: [MA0398.1](#)  
 Motif name: SUM1  
 Taxon: Fungi  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 8

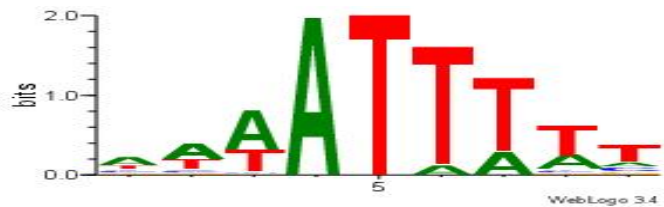
Similarity score: 0.0460574

Alignment:

AAAAATWWD  
AAAGATTT-

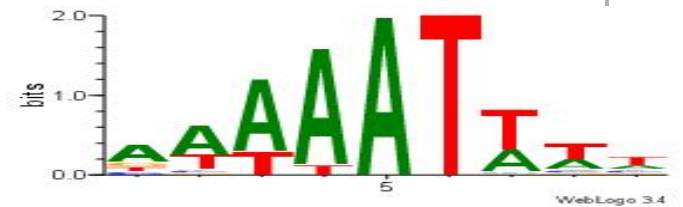
Original motif

Consensus sequence: DWWATTTTT



Reverse complement motif

Consensus sequence: AAAAATWWD



Motif ID: [MA0302.1](#)  
Motif name: GAT4  
Taxon: Fungi  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Reverse Complement  
Direction: Forward  
Position number: 4  
Number of overlap: 8  
Similarity score: 0.0477168

Alignment:

BBBAGATCTHB  
---AAATCTTT

Original motif

Consensus sequence: VHAGATCTVH

Reverse complement motif

Consensus sequence: BBBAGATCTHB





**Dataset #: 2      Motif ID: 14      Motif name: Motif 14**

Original motif

Consensus sequence: AWAATAA



Reverse complement motif

Consensus sequence: TTATTTWT



**Best Matches for Motif ID 14 (Highest to Lowest)**

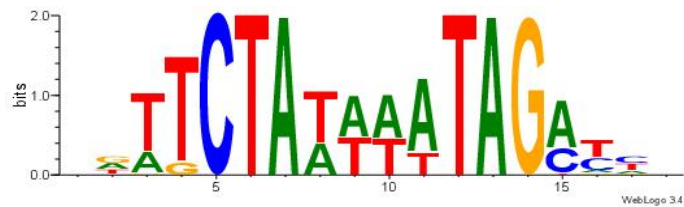
Motif ID:	<a href="#">MA0369.1</a>
Motif name:	RLM1
Taxon:	Fungi
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	5
Number of overlap:	8
Similarity score:	0.0179286

Alignment:

VKMYCTATWWWTAGAAHB  
-----TTATTTWT-----

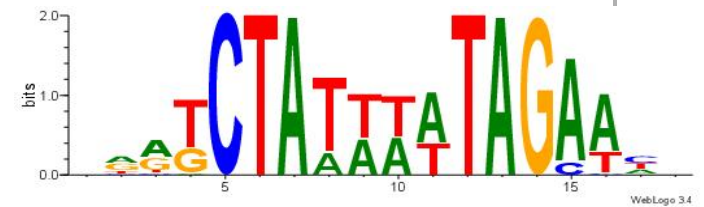
Original motif

Consensus sequence: VDTTCTAWWWATAGMYVV



Reverse complement motif

Consensus sequence: VKMYCTATWWWTAGAAHB

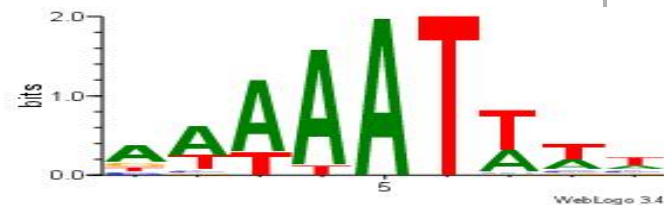


Motif ID: [MA0398.1](#)  
Motif name: SUM1  
Taxon: Fungi  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Original Motif  
Direction: Forward  
Position number: 2  
Number of overlap: 8  
Similarity score: 0.0179741

Alignment:  
DWWATTTTT  
-TTATTTWT

Original motif  
Consensus sequence: DWWATTTTT

Reverse complement motif  
Consensus sequence: AAAAATWWD



Motif ID: [MA0433.1](#)  
 Motif name: YOX1  
 Taxon: Fungi  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 8  
 Similarity score: 0.0225467

Alignment:  
 TTAATTA  
 AWAATA

Original motif

Consensus sequence: TTAATTA



Reverse complement motif

Consensus sequence: TTAATTA



Motif ID: [MA0317.1](#)

Motif name: HCM1  
 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: 0.0233838

Alignment:  
 ATAAACAA  
 AWAATAA

Original motif

Consensus sequence: ATAAACAA



Reverse complement motif

Consensus sequence: TTGTTTAT




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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: 7  
 Number of overlap: 8

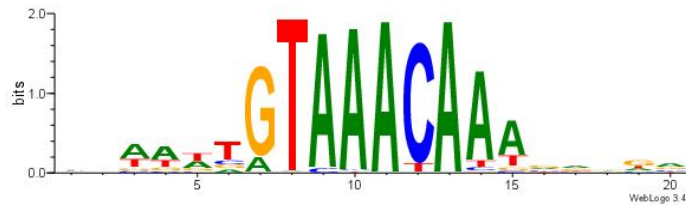
Similarity score: 0.0238432

Alignment:

BDWWWTGTAAACAAVDDD  
-----AWAAATAA-----

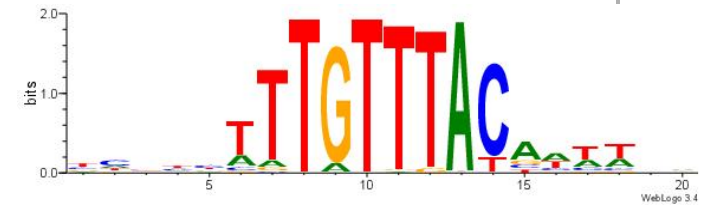
Original motif

Consensus sequence: BDWWWTGTAAACAAVDDD



Reverse complement motif

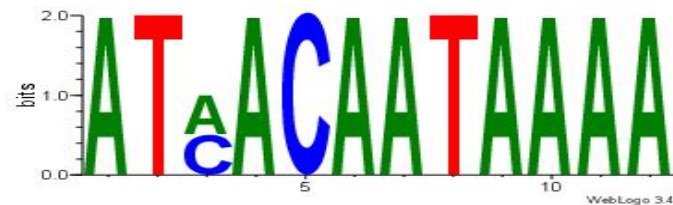
Consensus sequence: BHHDVTTTGTTCACAWWHV



**Dataset #: 2 Motif ID: 15 Motif name: Motif 15**

Original motif

Consensus sequence: ATMACAATAAAA



Reverse complement motif

Consensus sequence: TTTTATTGTAT



### Best Matches for Motif ID 15 (Highest to Lowest)

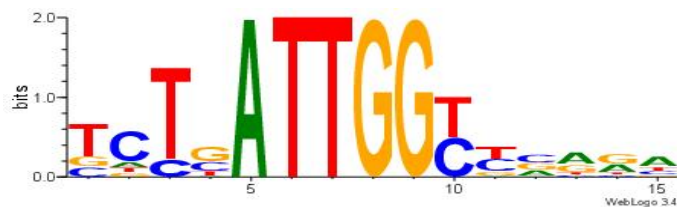
Motif ID: [MA0314.1](#)  
Motif name: HAP3  
Taxon: Fungi  
Matching format of first motif: Original Motif

Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 1  
 Number of overlap: 12  
 Similarity score: 0.106236

Alignment:  
 TMKVMMCCAATSAGA  
 ---ATMACAATAAAA

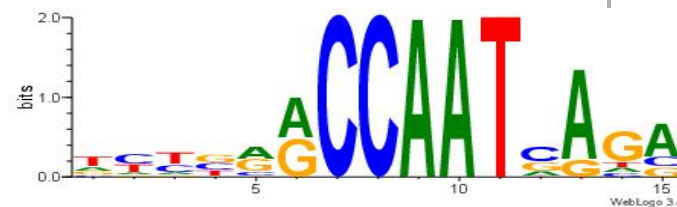
Original motif

Consensus sequence: TCTSATTGGYYVRRRA



Reverse complement motif

Consensus sequence: TMKVMMCCAATSAGA




---

Motif ID: [MA0440.1](#)  
 Motif name: ZAP1  
 Taxon: Fungi  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 2  
 Number of overlap: 12  
 Similarity score: 0.109512

Alignment:

ACCYTMAAGGTBATG  
--TTTTATTGTYAT-

Original motif

Consensus sequence: ACCYTMAAGGTBATG



Reverse complement motif

Consensus sequence: CATBACCTTYAMGGT



Motif ID: [MA0369.1](#)  
Motif name: RLM1  
Taxon: Fungi  
Matching format of first motif: Original Motif  
Matching format of second motif: Reverse Complement  
Direction: Forward  
Position number: 5  
Number of overlap: 12  
Similarity score: 0.116071

Alignment:

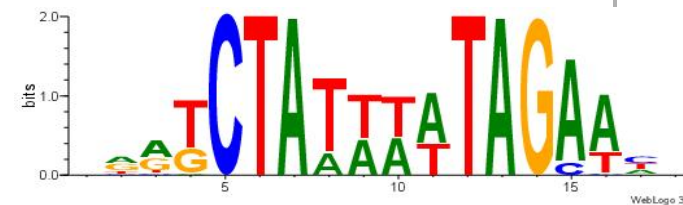
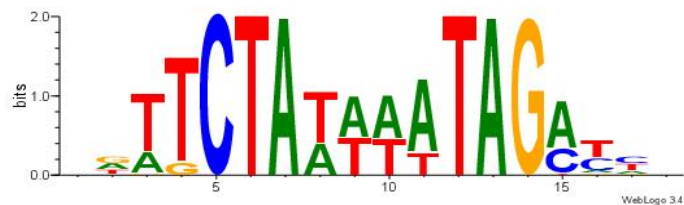
VKMYCTATWWWTAGAAHB  
----ATMACAATAAAA--

Original motif

Consensus sequence: VDTTCTAWWWATAGMYVV

Reverse complement motif

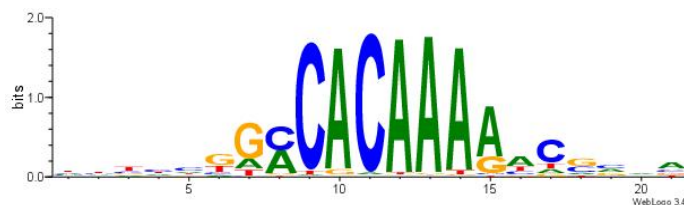
Consensus sequence: VKMYCTATWWWTAGAAHB



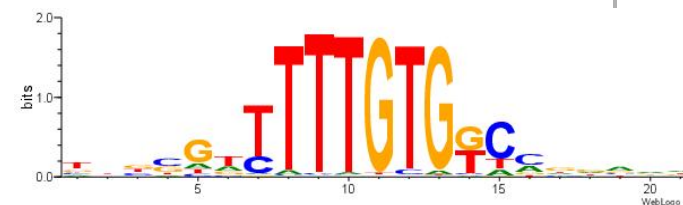
Motif ID: [MA0343.1](#)  
 Motif name: NDT80  
 Taxon: Fungi  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 4  
 Number of overlap: 12  
 Similarity score: 0.116213

Alignment:  
 BDVSGHTTTTGTGRCYDDVHH  
 -----TTTTATTGTYAT---

Original motif  
 Consensus sequence: HHBHHKGMCACAAAHCSDV



Reverse complement motif  
 Consensus sequence: BDVSGHTTTTGTGRCYDDVHH



Motif ID: [MA0296.1](#)



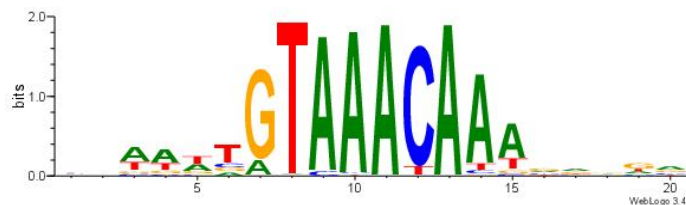
Motif name: FKH1  
 Taxon: Fungi  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 5  
 Number of overlap: 12  
 Similarity score: 0.122106

Alignment:

BHHDVTTTGTTTACAWWWHV  
 ----TTTTATTGTYAT----

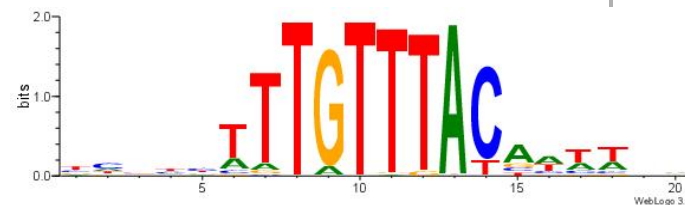
Original motif

Consensus sequence: BDWWWTGTAAACAAVDDDDV



Reverse complement motif

Consensus sequence: BHHDVTTTGTTTACAWWWHV



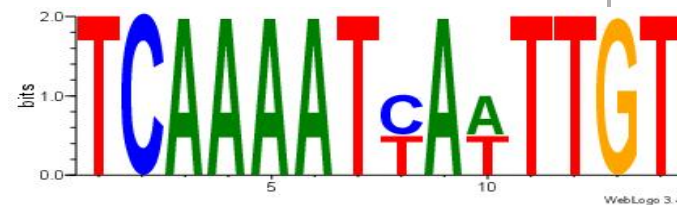
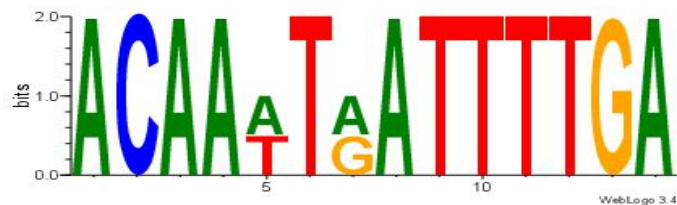
**Dataset #: 2      Motif ID: 16      Motif name: Motif 16**

Original motif

Consensus sequence: ACAAWTRATTTTGA

Reverse complement motif

Consensus sequence: TCAAAATKAWTTGT



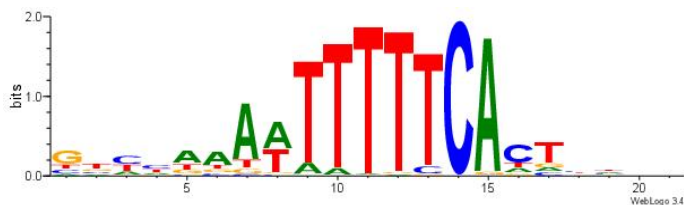
### Best Matches for Motif ID 16 (Highest to Lowest)

Motif ID: [MA0390.1](#)  
 Motif name: STB3  
 Taxon: Fungi  
 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: 0.0889454

Alignment:  
 HHHBAGTGAAAAWTTT DKVC  
 -----TCAAAATKAWTTGT-

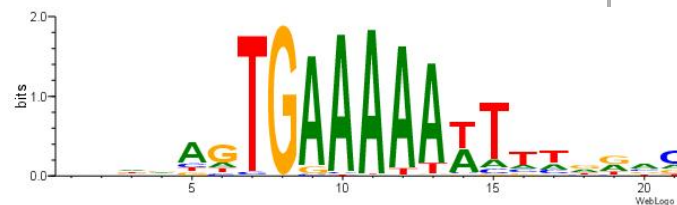
#### Original motif

Consensus sequence: GBYHAAWTTTTTCACTBHDD



#### Reverse complement motif

Consensus sequence: HHHBAGTGAAAAWTTT DKVC



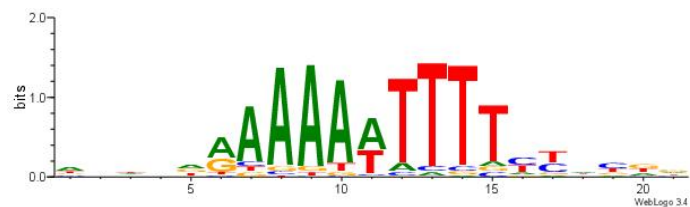
Motif ID: [MA0378.1](#)  
 Motif name: SFP1  
 Taxon: Fungi  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 5  
 Number of overlap: 14  
 Similarity score: 0.0980629

Alignment:

HHBHMKAAAAWTTTTKDHDHD  
 ----TCAAATKAWTTGT---

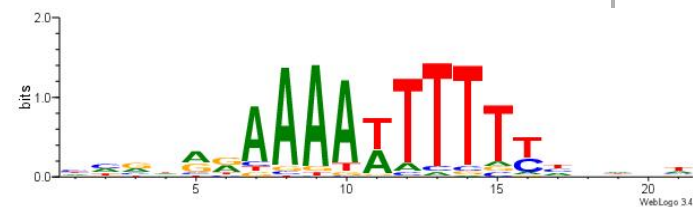
Original motif

Consensus sequence: DHDDDRAAAWTTTTYYHBDD



Reverse complement motif

Consensus sequence: HHBHMKAAAAWTTTTKDHDHD



Motif ID: [MA0343.1](#)  
 Motif name: NDT80  
 Taxon: Fungi  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 10

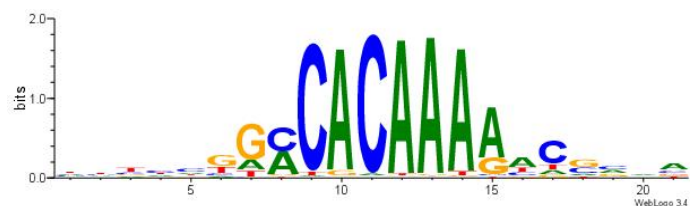
Number of overlap: 12  
Similarity score: 1.0933

Alignment:

--BDVSGHTTTTGTGRCYDDVHH  
ACAAWTRATTTTGA-----

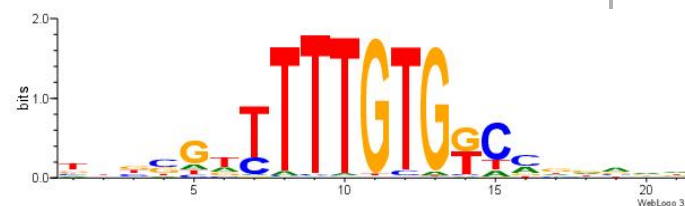
Original motif

Consensus sequence: HHBHHKGMCACAAAHCSDVDV



Reverse complement motif

Consensus sequence: BDVSGHTTTTGTGRCYDDVHH



---

Motif ID: [MA0440.1](#)  
Motif name: ZAP1  
Taxon: Fungi  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Original Motif  
Direction: Backward  
Position number: 4  
Number of overlap: 11  
Similarity score: 1.59678

Alignment:

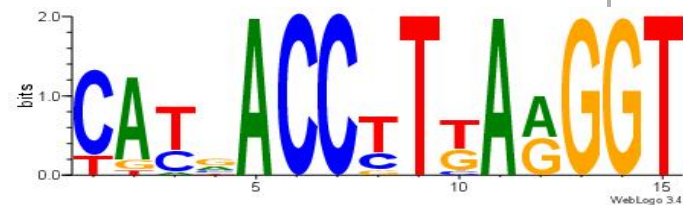
---CATBACCTTYAMGGT  
-TCAAAATKAWTTGT---

Original motif

Consensus sequence: ACCYTMAAGGTBATG

Reverse complement motif

Consensus sequence: CATBACCTTYAMGGT



Motif ID: [MA0296.1](#)  
 Motif name: FKH1  
 Taxon: Fungi  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 5  
 Number of overlap: 10  
 Similarity score: 2.07585

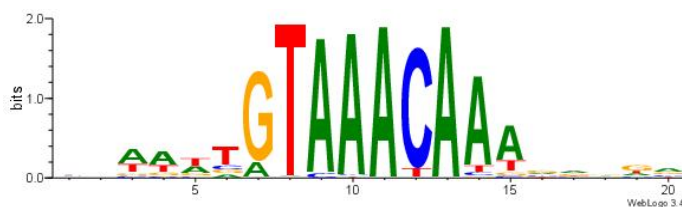
Alignment:

```

----BDWWWTGTAAACAAVDDDDV
-----ACAAWTRATTTTGA-----
  
```

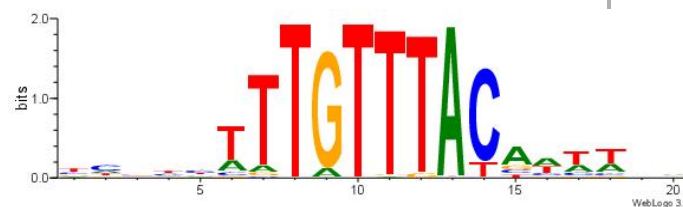
Original motif

Consensus sequence: BDWWWTGTAAACAAVDDDDV



Reverse complement motif

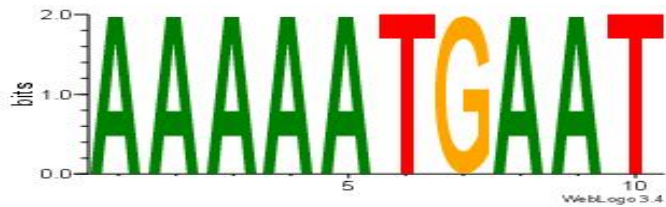
Consensus sequence: BHHDVTTTGTTTACAWWWHV



**Dataset #: 2      Motif ID: 17      Motif name: Motif 17**

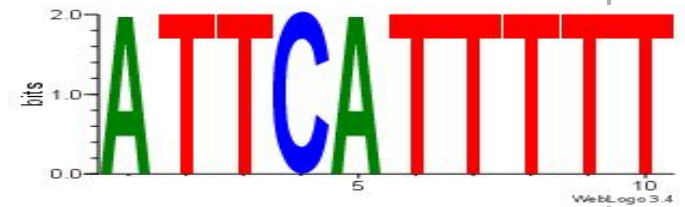
Original motif

Consensus sequence: AAAAATGAAT



Reverse complement motif

Consensus sequence: ATTCATTTT



### Best Matches for Motif ID 17 (Highest to Lowest)

Motif ID: [MA0390.1](#)  
Motif name: STB3  
Taxon: Fungi  
Matching format of first motif: Original Motif  
Matching format of second motif: Reverse Complement  
Direction: Forward  
Position number: 9  
Number of overlap: 10  
Similarity score: 0.0496392

Alignment:

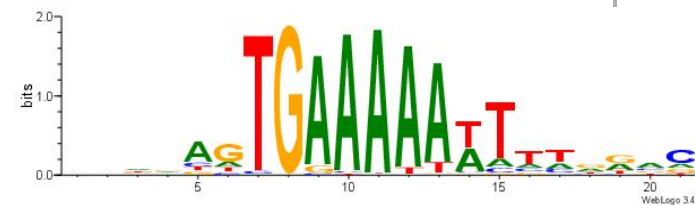
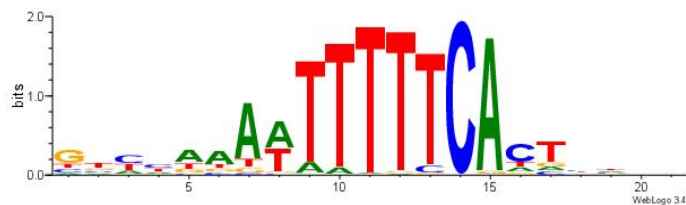
```
HHHBAGTGAAAAWTTT DKVC  
-----AAAAATGAAT---
```

Original motif

Consensus sequence: GBYHAAWTTTTTCACTBHDD

Reverse complement motif

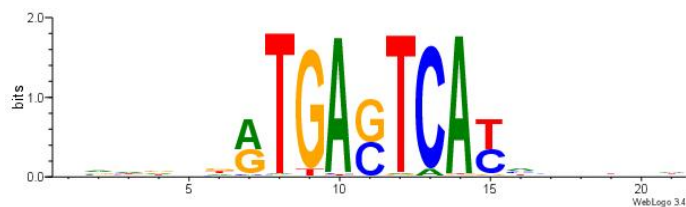
Consensus sequence: HHHBAGTGAAAAWTTT DKVC



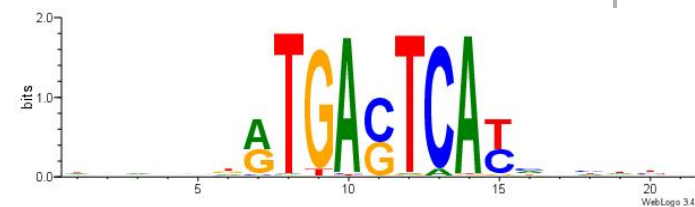
Motif ID: [MA0303.1](#)  
 Motif name: GCN4  
 Taxon: Fungi  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 10  
 Number of overlap: 10  
 Similarity score: 0.0605292

Alignment:  
 DVHDDHMTGASTCAKHHHHBB  
 -----ATTCATTTTT--

Original motif  
 Consensus sequence: BVHDDDR TGASTCAYHHHHVD



Reverse complement motif  
 Consensus sequence: DVHDDHMTGASTCAKHHHHBB



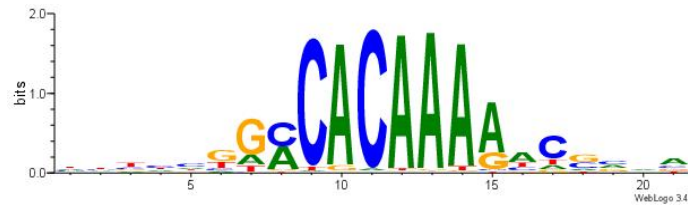
Motif ID: [MA0343.1](#)

Motif name: NDT80  
 Taxon: Fungi  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 1  
 Number of overlap: 10  
 Similarity score: 0.0620677

Alignment:  
 HHBHHKGMCACAAAHCSDV  
 -----AAAAATGAAT

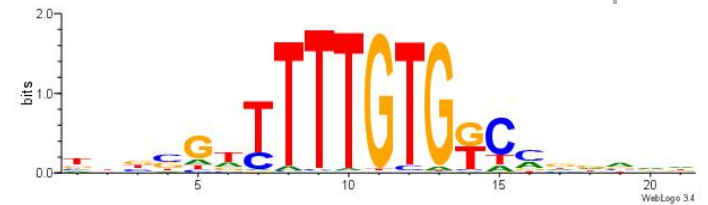
Original motif

Consensus sequence: HHBHHKGMCACAAAHCSDV



Reverse complement motif

Consensus sequence: BDVSGHTTTTGTGRCYDDVHH




---

Motif ID: [MA0378.1](#)  
 Motif name: SFP1  
 Taxon: Fungi  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 6  
 Number of overlap: 10  
 Similarity score: 0.0653327

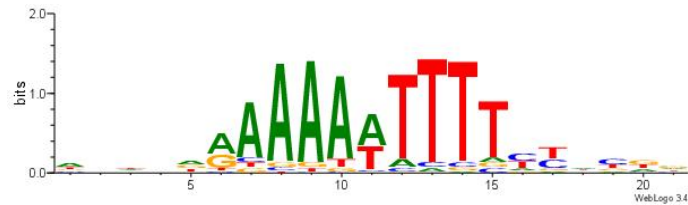


Alignment:

```
HHBHMKAAAAWTTTTKDHDHD  
-----AAAAATGAAT-----
```

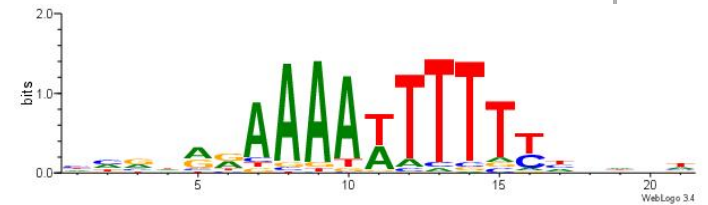
Original motif

Consensus sequence: DHDDDRAAAATTTTTYYHBDD



Reverse complement motif

Consensus sequence: HHBHMKAAAAWTTTTKDHDHD



---

Motif ID:	<a href="#">MA0369.1</a>
Motif name:	RLM1
Taxon:	Fungi
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	3
Number of overlap:	10
Similarity score:	0.0663763

Alignment:

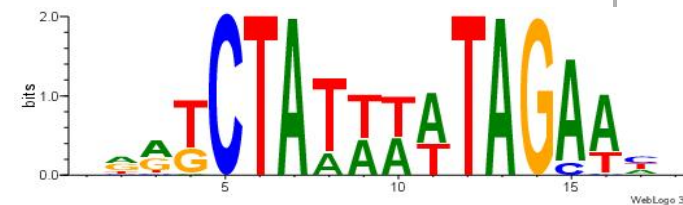
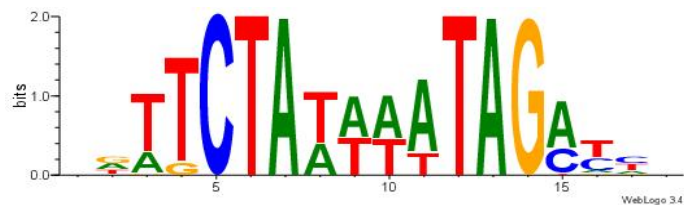
```
VKMYCTATWWWTAGAAHB  
--ATTCATTTTT-----
```

Original motif

Consensus sequence: VDTTCTAWWWATAGMYYY

Reverse complement motif

Consensus sequence: VKMYCTATWWWTAGAAHB



**Dataset #: 2      Motif ID: 18      Motif name: Motif 18**

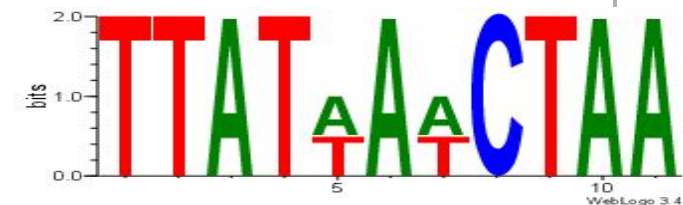
Original motif

Consensus sequence: TTAGWTWATAA



Reverse complement motif

Consensus sequence: TTATWAWCTAA



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

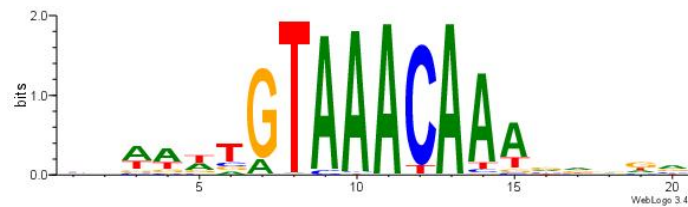
Motif ID:	<a href="#">MA0296.1</a>
Motif name:	FKH1
Taxon:	Fungi
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	5
Number of overlap:	11
Similarity score:	0.0529918

Alignment:

BDWWWTGTAACAAVDDDDV  
----TTATWAWCTAA-----

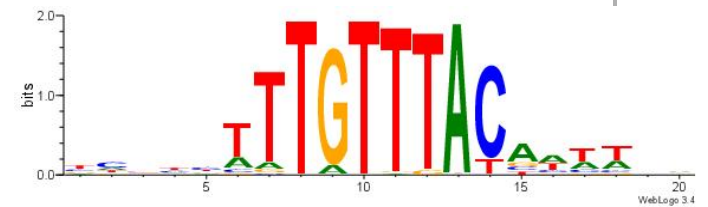
Original motif

Consensus sequence: BDWWWTGTAACAAVDDDDV



Reverse complement motif

Consensus sequence: BHHDVTTTGTTCACAWWHV



Motif ID: [MA0415.1](#)  
Motif name: YAP1  
Taxon: Fungi  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Original Motif  
Direction: Backward  
Position number: 7  
Number of overlap: 11  
Similarity score: 0.0535956

Alignment:

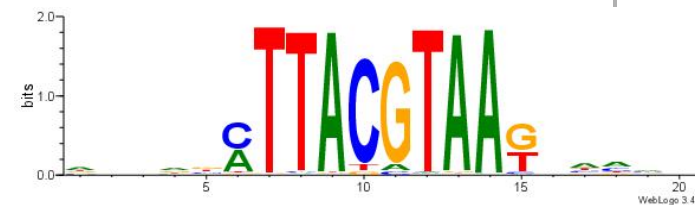
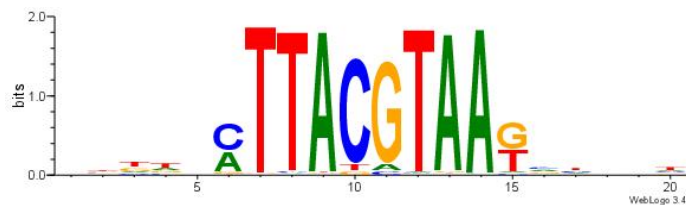
HBDDDMTTACGTAAKVHHVH  
----TTATWAWCTAA-----

Original motif

Consensus sequence: HBDDDMTTACGTAAKVHHVH

Reverse complement motif

Consensus sequence: HVDHVYTTACGTAARHDDVH

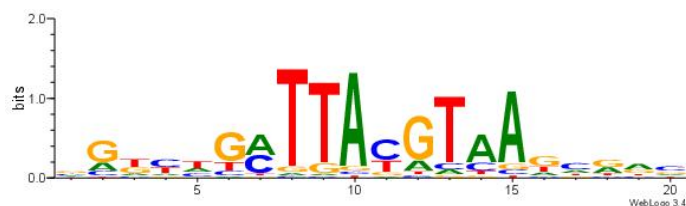


Motif ID: [MA0418.1](#)  
 Motif name: YAP6  
 Taxon: Fungi  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 5  
 Number of overlap: 11  
 Similarity score: 0.0641812

Alignment:  
 VGKYHGTTAYGTAAKHRDV  
 ----TTATWAWCTAA-----

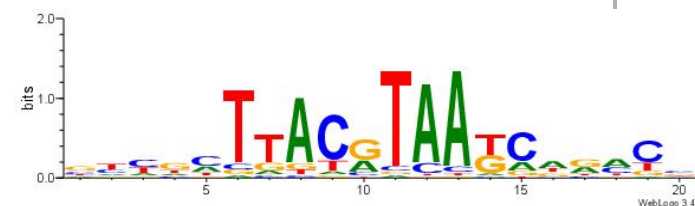
Original motif

Consensus sequence: VGKYHGTTAYGTAAKHRDV



Reverse complement motif

Consensus sequence: VDMDYTTACKTAAYCHKRCV



Motif ID: [MA0346.1](#)

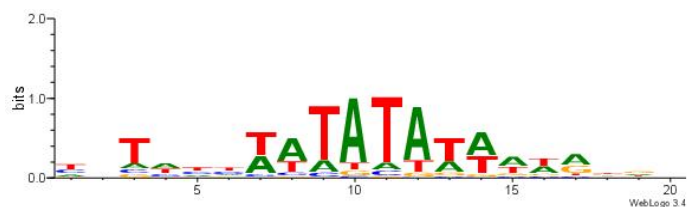
Motif name: NHP6B  
 Taxon: Fungi  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 8  
 Number of overlap: 11  
 Similarity score: 0.0671782

**Alignment:**

BHDKWWWATATATWHHHAHH  
 -----TTATWAWCTAA--

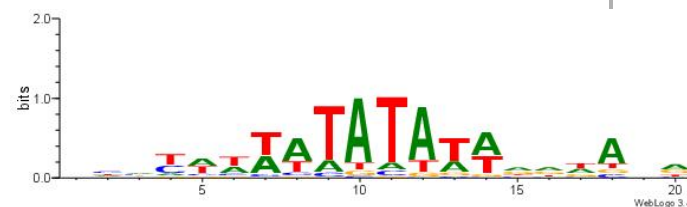
**Original motif**

Consensus sequence: HHTHHHWATATATWWWRRDDV



**Reverse complement motif**

Consensus sequence: BHDKWWWATATATWHHHAHH




---

Motif ID: [MA0345.1](#)  
 Motif name: NHP6A  
 Taxon: Fungi  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 8  
 Number of overlap: 11

Similarity score:

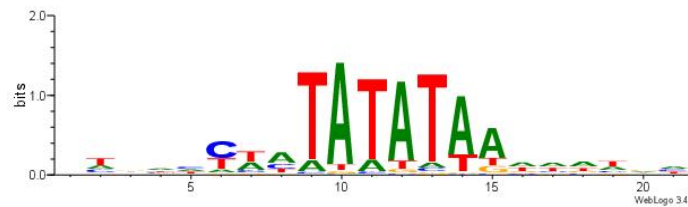
0.0678808

Alignment:

```
HHHDDDTTATATAHWKDH H B
---TTATWAWCTAA-----
```

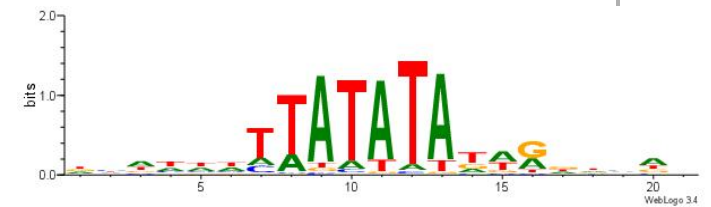
Original motif

Consensus sequence: VHDHHYWHTATATAADDDH D H



Reverse complement motif

Consensus sequence: HHHDDDTTATATAHWKDH H B



**Dataset #: 2**

**Motif ID: 19**

**Motif name: Motif 19**

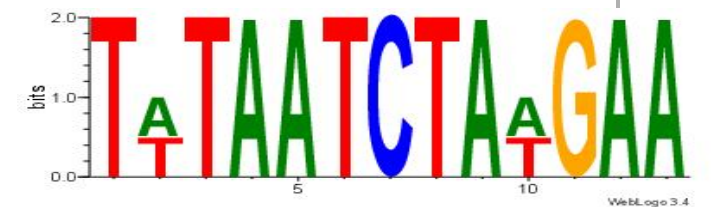
Original motif

Consensus sequence: TTCWTAGATTAWA



Reverse complement motif

Consensus sequence: TWTAACTAWGAA



### Best Matches for Motif ID 19 (Highest to Lowest)

Motif ID:

[MA0407.1](#)

Motif name:

THI2

Taxon:

Fungi

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: 0.0781943

Alignment:  
 GKTCTTWSMGTTYCC  
 -TTCWTAGATTAWA-

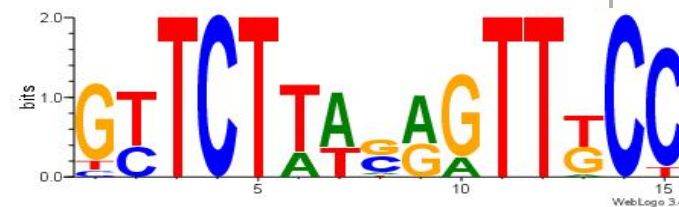
Original motif

Consensus sequence: GGMAACYSWAAGARC



Reverse complement motif

Consensus sequence: GKTCTTWSMGTTYCC




---

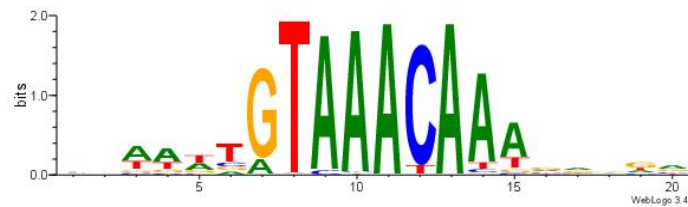
Motif ID: [MA0296.1](#)  
 Motif name: FKH1  
 Taxon: Fungi  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 3  
 Number of overlap: 13  
 Similarity score: 0.0790099

Alignment:

BDWWWTGTAAACAAVDDDDV  
-----TWTAACTAWGAA--

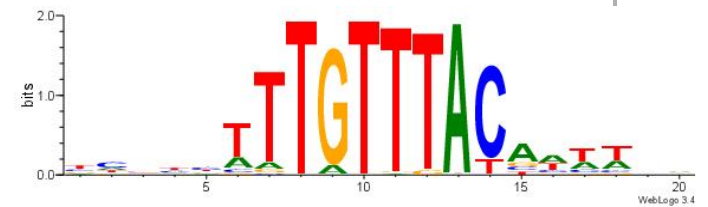
Original motif

Consensus sequence: BDWWWTGTAAACAAVDDDDV



Reverse complement motif

Consensus sequence: BHHDVTTTGTTCACAWWHV



Motif ID: [MA0369.1](#)  
Motif name: RLM1  
Taxon: Fungi  
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: 0.0859661

Alignment:

VDTTCTAWWWATAGMYV  
--TTCWTAGATTAWA---

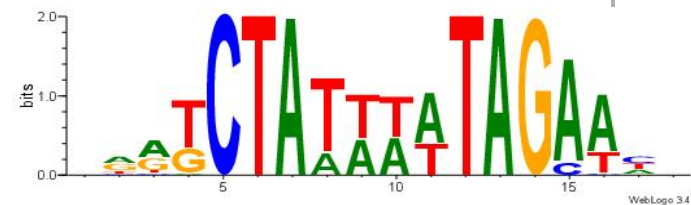
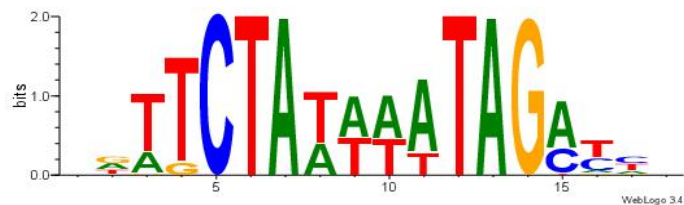
Original motif

Consensus sequence: VDTTCTAWWWATAGMYV

Reverse complement motif

Consensus sequence: VKMYCTATWWWTAGAAHB

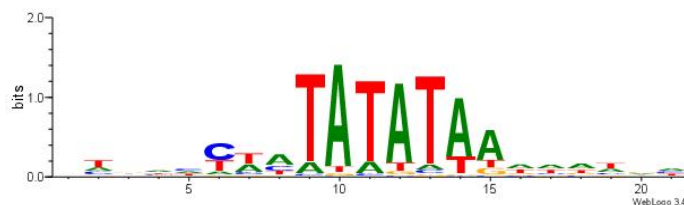




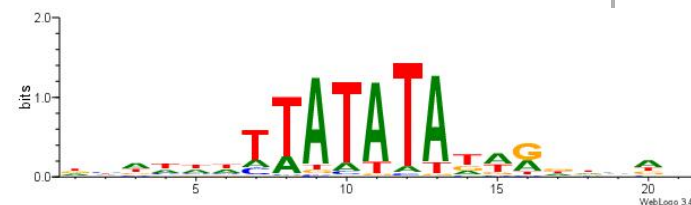
Motif ID: [MA0345.1](#)  
 Motif name: NHP6A  
 Taxon: Fungi  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 5  
 Number of overlap: 13  
 Similarity score: 0.0862971

Alignment:  
 VHDHHYWHTATATAADDDHDH  
 ----TTCWTAGATTAWA----

Original motif  
 Consensus sequence: VHDHHYWHTATATAADDDHDH



Reverse complement motif  
 Consensus sequence: HHHDDTTATATAHWKDH HHB



Motif ID: [MA0400.1](#)

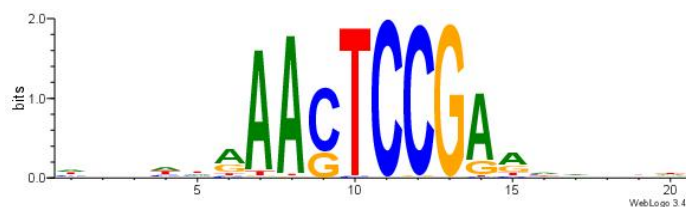
Motif name: SUT2  
 Taxon: Fungi  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 3  
 Number of overlap: 13  
 Similarity score: 0.0872006

**Alignment:**

DVDHHTTCGGAGTTKHHHDH  
 -----TTCWTAGATTAWA--

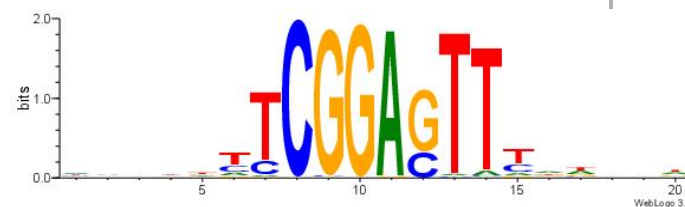
**Original motif**

Consensus sequence: HDDHHRAACTCCGAAHHDBD



**Reverse complement motif**

Consensus sequence: DVDHHTTCGGAGTTKHHHDH



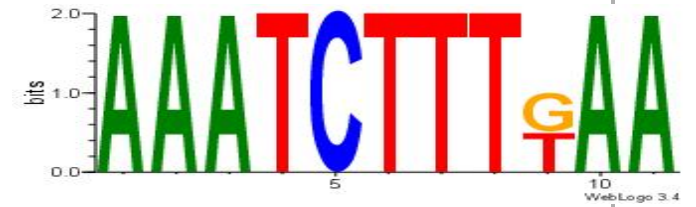
**Dataset #: 2      Motif ID: 20      Motif name: Motif 20**

**Original motif**

Consensus sequence: TTMAAAGATTT

**Reverse complement motif**

Consensus sequence: AAATCTTTYAA



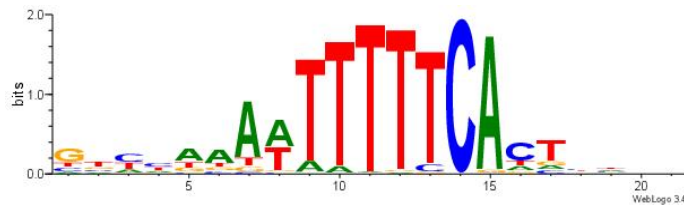
### Best Matches for Motif ID 20 (Highest to Lowest)

Motif ID: [MA0390.1](#)  
 Motif name: STB3  
 Taxon: Fungi  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 6  
 Number of overlap: 11  
 Similarity score: 0.0477023

Alignment:  
 GBYHAAAWTTTTTCACTBHDD  
 -----AAATCTTTYAA-----

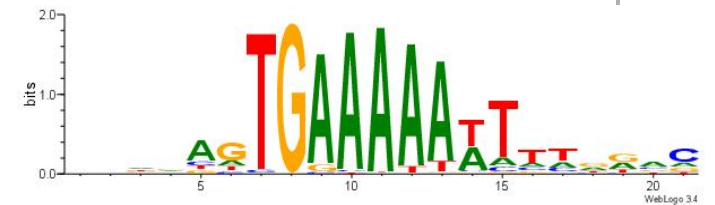
#### Original motif

Consensus sequence: GBYHAAAWTTTTTCACTBHDD



#### Reverse complement motif

Consensus sequence: HHHBAGTGAAAAWTTTSDKVC

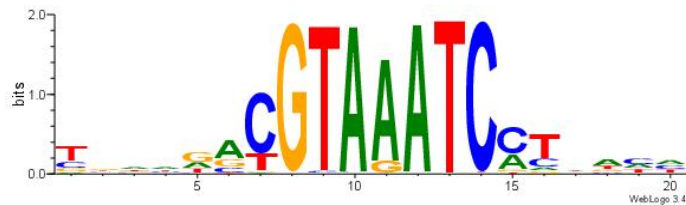


Motif ID: [MA0435.1](#)  
 Motif name: YPR015C  
 Taxon: Fungi  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 11  
 Similarity score: 0.0501411

Alignment:  
 TBDHDACGTAAATCMTDDHH  
 TTMAAAGATTT-----

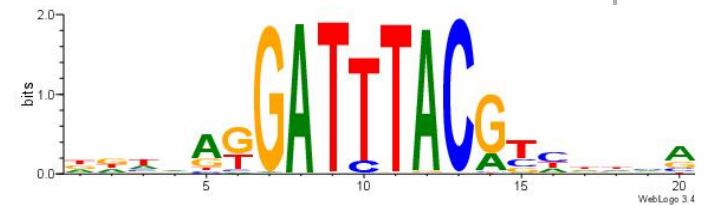
Original motif

Consensus sequence: TBDHDACGTAAATCMTDDHH



Reverse complement motif

Consensus sequence: HDDDARGATTTACGTHHDBA



Motif ID: [MA0378.1](#)  
 Motif name: SFP1  
 Taxon: Fungi  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 4  
 Number of overlap: 11

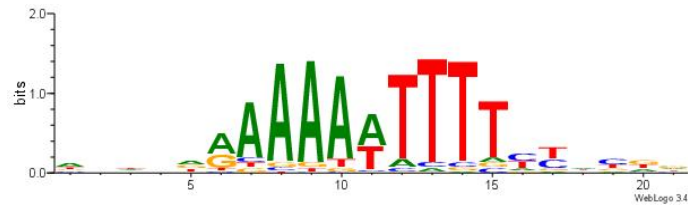
Similarity score: 0.0548685

Alignment:

DHDDDRAAAATTTTTYYHBDD  
-----AAATCTTTYAA---

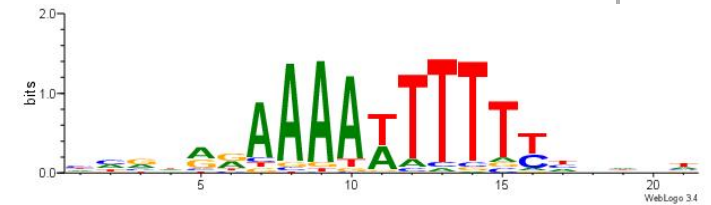
Original motif

Consensus sequence: DHDDDRAAAATTTTTYYHBDD



Reverse complement motif

Consensus sequence: HHBHMKAAAATTTTKDHDHD



Motif ID: [MA0407.1](#)  
Motif name: THI2  
Taxon: Fungi  
Matching format of first motif: Original Motif  
Matching format of second motif: Reverse Complement  
Direction: Backward  
Position number: 4  
Number of overlap: 11  
Similarity score: 0.0682282

Alignment:

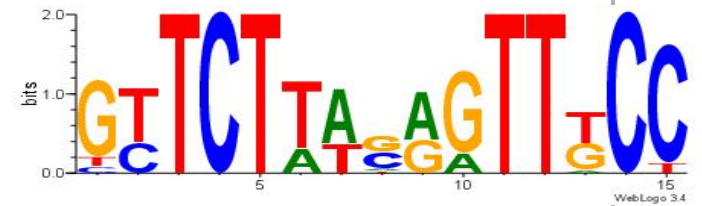
GKTCTTWSMGTTYCC  
-TTMAAGATTT---

Original motif

Consensus sequence: GMAACYSWAAGARC

Reverse complement motif

Consensus sequence: GKTCTTWSMGTTYCC



Motif ID: [MA0440.1](#)  
 Motif name: ZAP1  
 Taxon: Fungi  
 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: 0.0708025

Alignment:  
 ACCYTMAAGGTBATG  
 ---TTMAAAGATTT-

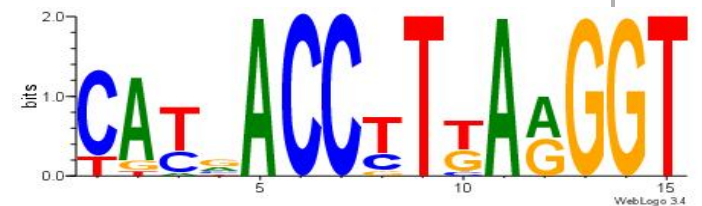
Original motif

Consensus sequence: ACCYTMAAGGTBATG



Reverse complement motif

Consensus sequence: CATBACCTTYAMGGT



**Dataset #: 2**

**Motif ID: 21**

**Motif name: Motif 21**

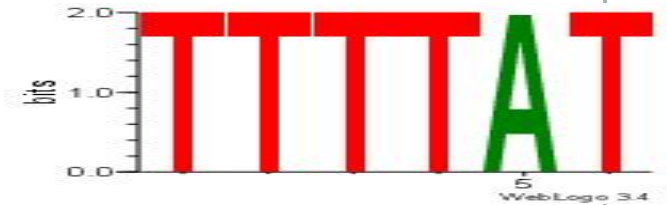
Original motif

Consensus sequence: ATAAAA



Reverse complement motif

Consensus sequence: TTTTAT



### Best Matches for Motif ID 21 (Highest to Lowest)

Motif ID: [MA0343.1](#)  
Motif name: NDT80  
Taxon: Fungi  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Reverse Complement  
Direction: Backward  
Position number: 10  
Number of overlap: 6  
Similarity score: 0.0600039

Alignment:

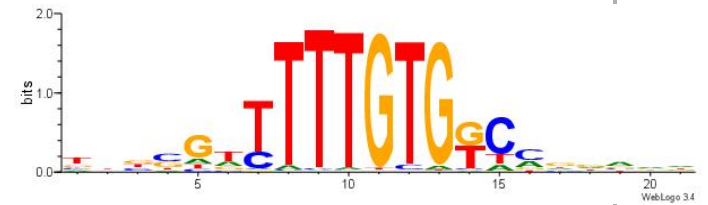
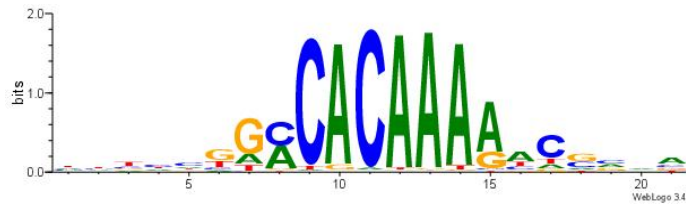
```
BDVSGHTTTTGTGRCYDDVHH  
-----TTTTAT-----
```

Original motif

Consensus sequence: HHBHHKGMCAAAAHCSDV

Reverse complement motif

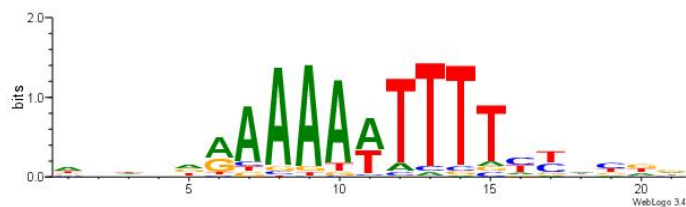
Consensus sequence: BDVSGHTTTTGTGRCYDDVHH



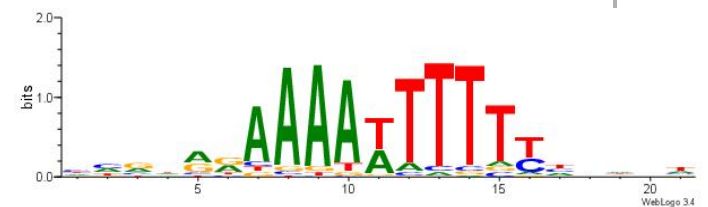
Motif ID: [MA0378.1](#)  
 Motif name: SFP1  
 Taxon: Fungi  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 5  
 Number of overlap: 6  
 Similarity score: 0.0715567

Alignment:  
 HHBHMKAAAAWTTTTKDHDHD  
 ----ATAAAA-----

Original motif  
 Consensus sequence: DHDDDRAAA WTTTTYYHBDD



Reverse complement motif  
 Consensus sequence: HHBHMKAAA WTTTTKDHDHD



Motif ID: [MA0369.1](#)



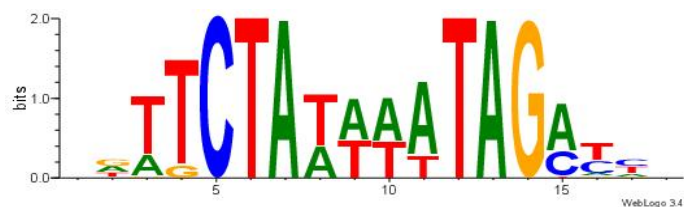
Motif name: RLM1  
 Taxon: Fungi  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 3  
 Number of overlap: 6  
 Similarity score: 0.0744048

**Alignment:**

VDTTCTAWWWATAGMYV  
 --TTTTAT-----

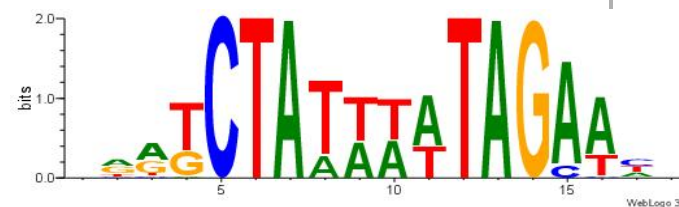
**Original motif**

Consensus sequence: VDTTCTAWWWATAGMYV



**Reverse complement motif**

Consensus sequence: VKMYCTATWWWTAGAAHB




---

Motif ID: [MA0390.1](#)  
 Motif name: STB3  
 Taxon: Fungi  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 8  
 Number of overlap: 6

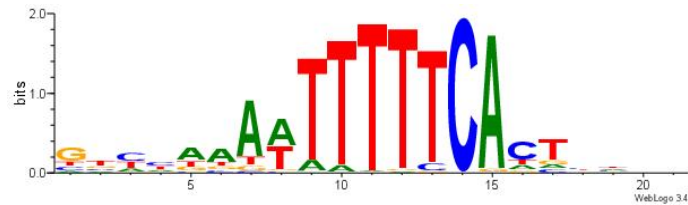
Similarity score: 0.0757497

Alignment:

HHHBAGTGAAAAWTTT DKVC  
-----ATAAAA-----

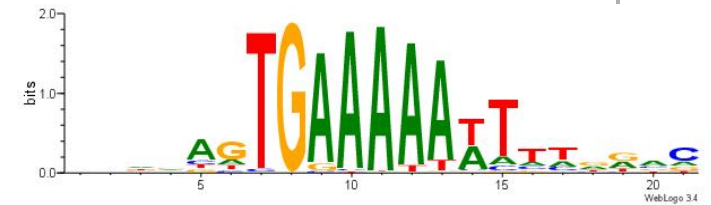
Original motif

Consensus sequence: GBYHAAWTTTTTCACTBHDD



Reverse complement motif

Consensus sequence: HHHBAGTGAAAAWTTT DKVC



Motif ID: [MA0309.1](#)  
Motif name: GZF3  
Taxon: Fungi  
Matching format of first motif: Original Motif  
Matching format of second motif: Original Motif  
Direction: Forward  
Position number: 3  
Number of overlap: 6  
Similarity score: 0.0766832

Alignment:

YGATAASV  
--ATAAAA

Original motif

Consensus sequence: YGATAASV

Reverse complement motif

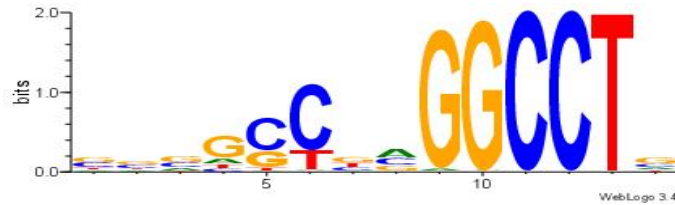
Consensus sequence: BSTTATCM



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

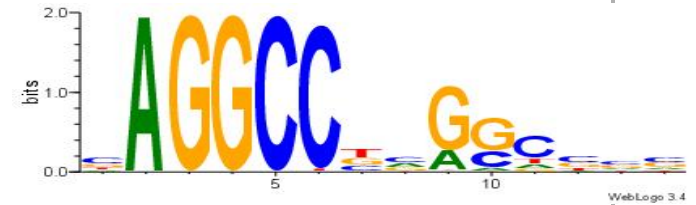
Original motif

Consensus sequence: BBVGCCBVGGCCTV



Reverse complement motif

Consensus sequence: VAGGCCBBGGCVBB



### Best Matches for Motif ID 22 (Highest to Lowest)

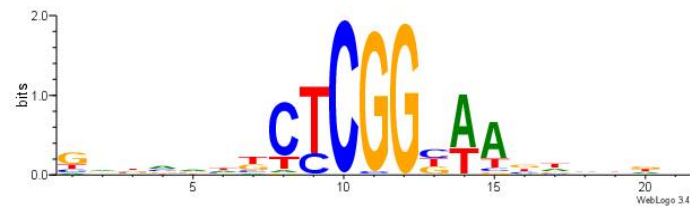
Motif ID:	<a href="#">MA0273.1</a>
Motif name:	ARO80
Taxon:	Fungi
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	6
Number of overlap:	14
Similarity score:	0.0605125

Alignment:

GVBVVHKCTCGGBAABDHHDH  
--BBVGCCBVGGCCTV-----

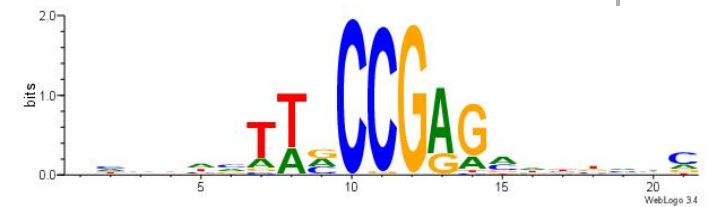
Original motif

Consensus sequence: GVBVVHKCTCGGBAABDHHDH



Reverse complement motif

Consensus sequence: HHHHDBTTBCCGAGRHHBBVBC



Motif ID: [MA0395.1](#)  
Motif name: STP2  
Taxon: Fungi  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Original Motif  
Direction: Forward  
Position number: 6  
Number of overlap: 14  
Similarity score: 0.0610807

Alignment:

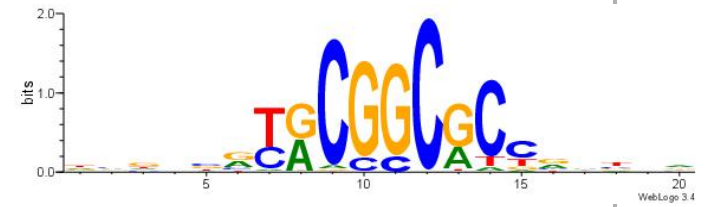
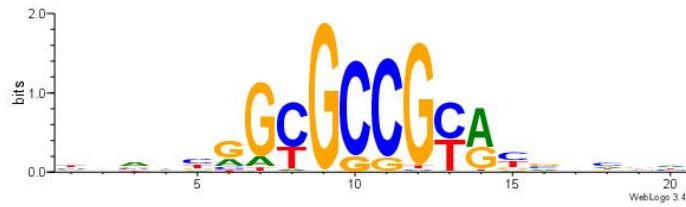
HVVHBBGGCGCCGYRYVHHBH  
-----VAGGCCBBGGCVBB-

Original motif

Consensus sequence: HVVHBBGGCGCCGYRYVHHBH

Reverse complement motif

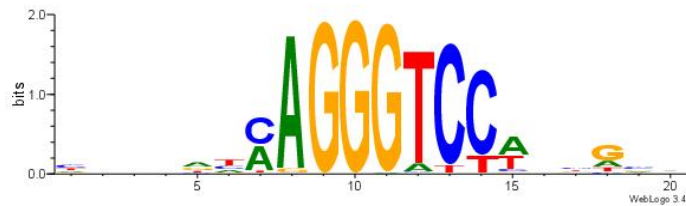
Consensus sequence: HBDHVKKKCGGCGCCBHBVH



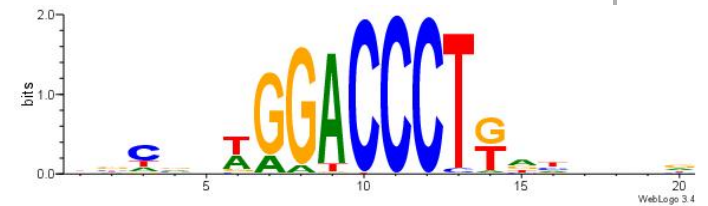
Motif ID: [MA0347.1](#)  
 Motif name: NRG1  
 Taxon: Fungi  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 1  
 Number of overlap: 14  
 Similarity score: 0.0633057

Alignment:  
 DVCBDWGGACCCTRHDVBHD  
 -----VAGGCCBBGGCVBB

Original motif  
 Consensus sequence: HHVVDHMAGGGTCCWDBGVD



Reverse complement motif  
 Consensus sequence: DVCBDWGGACCCTRHDVBHD



Motif ID: [MA0278.1](#)  
 Motif name: BAS1

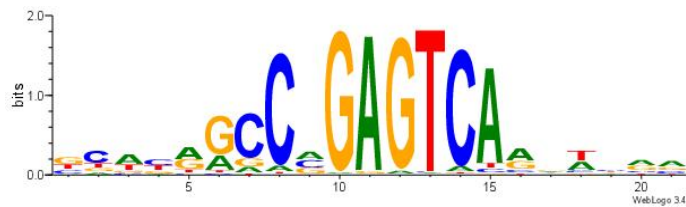
Taxon:	Fungi
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	3
Number of overlap:	14
Similarity score:	0.0666116

**Alignment:**

```
BBBWHKTGACTCBGGCKBWGB
-----VAGGCCBBGGCVBB--
```

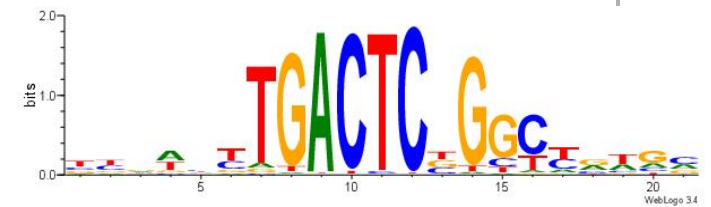
**Original motif**

Consensus sequence: BCWBRGCCVAGTTCARDWBVV



**Reverse complement motif**

Consensus sequence: BBBWHKTGACTCBGGCKBWGB




---

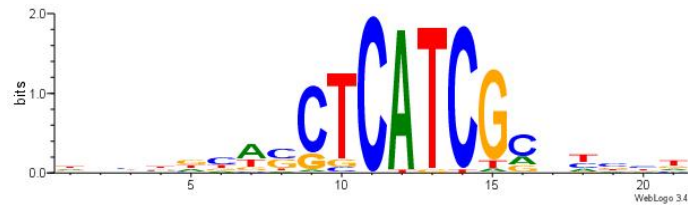
Motif ID:	<a href="#">MA0351.1</a>
Motif name:	DOT6
Taxon:	Fungi
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	8
Number of overlap:	14
Similarity score:	0.0714887

Alignment:

DBBHBGCGATGAGSWBHVBD  
-----VAGGCCBBGGCVBB

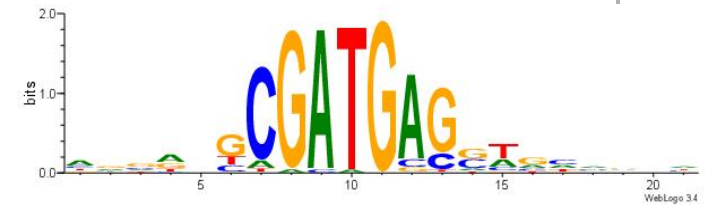
Original motif

Consensus sequence: DBBBDBWSCTCATCGCVHBB



Reverse complement motif

Consensus sequence: DBBHBGCGATGAGSWBHVBD



**Dataset #: 3**

**Motif ID: 23**

**Motif name: Egr1**

Original motif

Consensus sequence: HGCGTGGGCGK



Reverse complement motif

Consensus sequence: YCGCCCACGCH



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

Motif ID:	<a href="#">MA0290.1</a>
Motif name:	DAL81
Taxon:	Fungi
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement

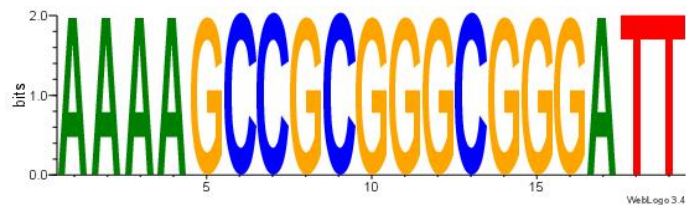
Direction: Forward  
Position number: 5  
Number of overlap: 11  
Similarity score: 0.0310356

Alignment:

AATCCCGCCCGGGCTTTT  
----YCGCCACGCH----

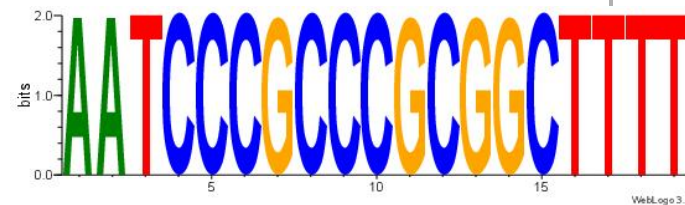
Original motif

Consensus sequence: AAAAGCCGCGGGCGGGATT



Reverse complement motif

Consensus sequence: AATCCCGCCCGGGCTTTT



Motif ID: [MA0376.1](#)  
Motif name: RTG3  
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: 0.0552565

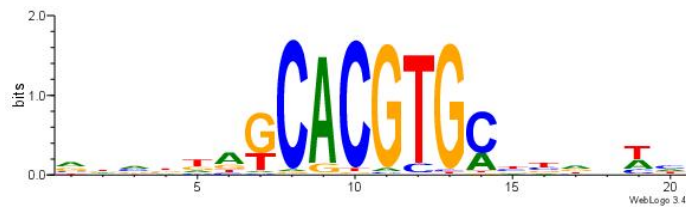
Alignment:



VDVBDAGCACGTGCBBDVWH  
-----YCGCCCACGCH-----

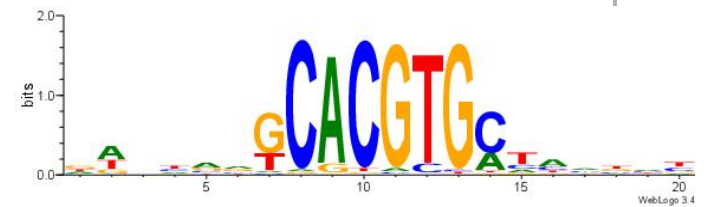
Original motif

Consensus sequence: VDVBDAGCACGTGCBBDVWH



Reverse complement motif

Consensus sequence: DWVDVVGACACGTGCTDVBDB



Motif ID: [MA0425.1](#)  
Motif name: YGR067C  
Taxon: Fungi  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Original Motif  
Direction: Forward  
Position number: 4  
Number of overlap: 11  
Similarity score: 0.0562067

Alignment:

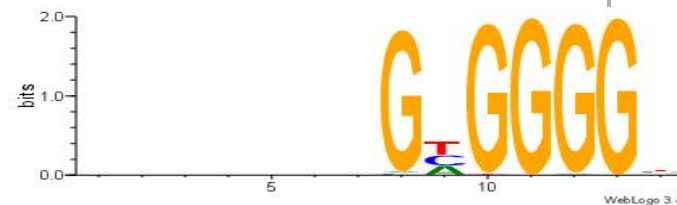
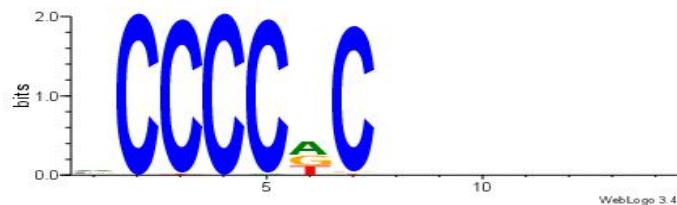
VCCCCDCHHHDDDBD  
---YCGCCCACGCH

Original motif

Consensus sequence: VCCCCDCHHHDDDBD

Reverse complement motif

Consensus sequence: DBDDHHHGDGGGGB

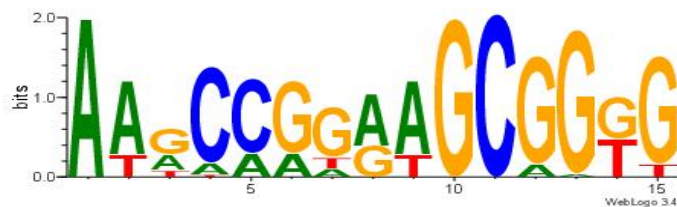


Motif ID: [MA0323.1](#)  
 Motif name: IXR1  
 Taxon: Fungi  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 3  
 Number of overlap: 11  
 Similarity score: 0.056625

Alignment:  
 AARCCGGRAGCGGKG  
 --HCCGTGGGCGK--

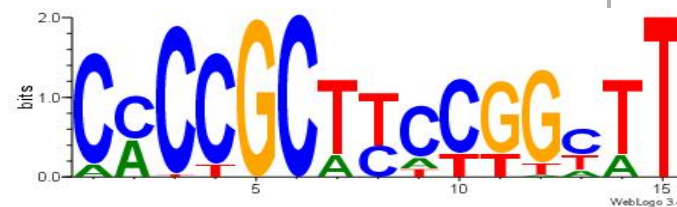
Original motif

Consensus sequence: AARCCGGRAGCGGKG



Reverse complement motif

Consensus sequence: CYCCGCTKCCGGMTT



Motif ID: [MA0400.1](#)

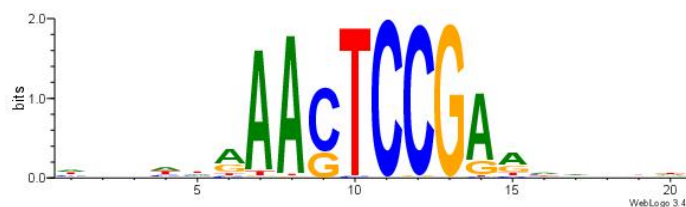
Motif name: SUT2  
 Taxon: Fungi  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 3  
 Number of overlap: 11  
 Similarity score: 0.059616

**Alignment:**

DVDHHTTCGGAGTTKHHHDH  
 --HGCGTGGGCGK-----

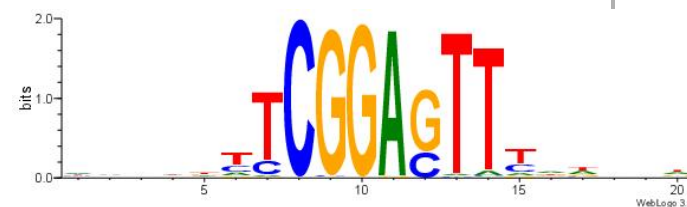
**Original motif**

Consensus sequence: HDDHHRAACTCCGAAHHDBD



**Reverse complement motif**

Consensus sequence: DVDHHTTCGGAGTTKHHHDH



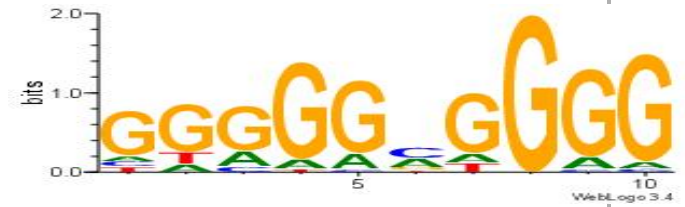
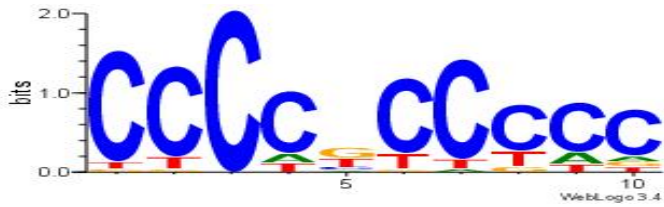
**Dataset #: 3      Motif ID: 24      Motif name: SP1**

**Original motif**

Consensus sequence: CCCCKCCCCC

**Reverse complement motif**

Consensus sequence: GGGGYGGGG



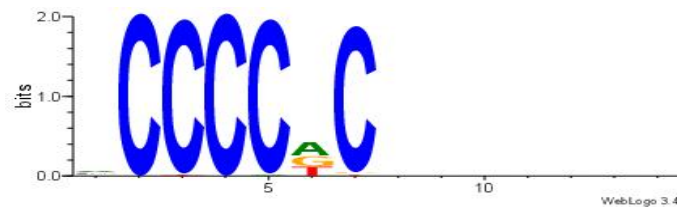
### Best Matches for Motif ID 24 (Highest to Lowest)

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:  
 VCCCCDCHHHDDBD  
 -CCCCKCCCC---

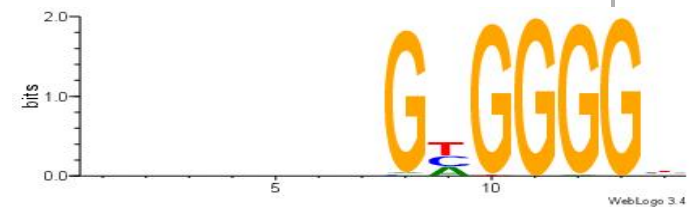
#### Original motif

Consensus sequence: VCCCCDCHHHDDBD



#### Reverse complement motif

Consensus sequence: DBDDHHHGDGGGGG



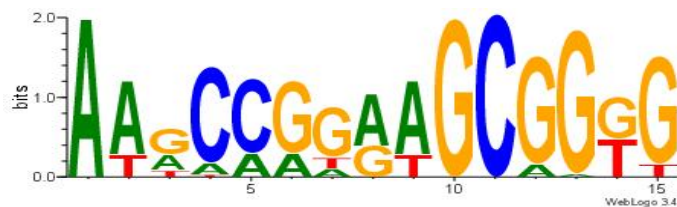
Motif ID: [MA0323.1](#)  
 Motif name: IXR1  
 Taxon: Fungi  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 6  
 Number of overlap: 10  
 Similarity score: 0.0418489

Alignment:

AARCCGGRAGCGGKG  
 -----GGGGYGGGG

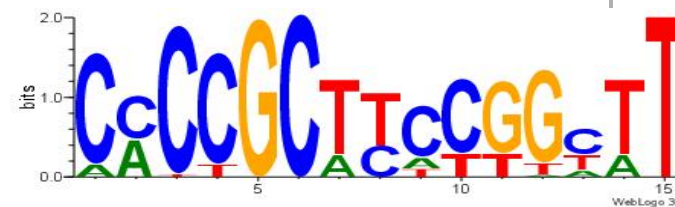
Original motif

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

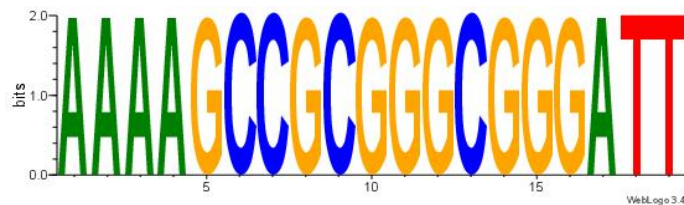
Number of overlap: 10  
Similarity score: 0.059697

Alignment:

AATCCCGCCCGCGGCTTTT  
--CCCKCCCC-----

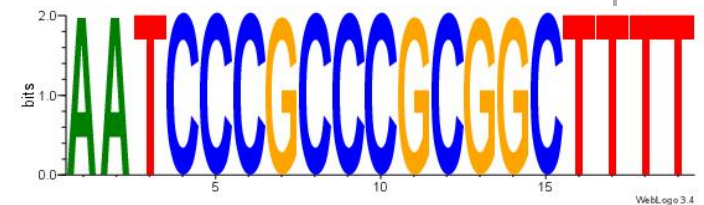
Original motif

Consensus sequence: AAAAGCCGCGGGCGGGATT



Reverse complement motif

Consensus sequence: AATCCCGCCCGCGGCTTTT



---

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

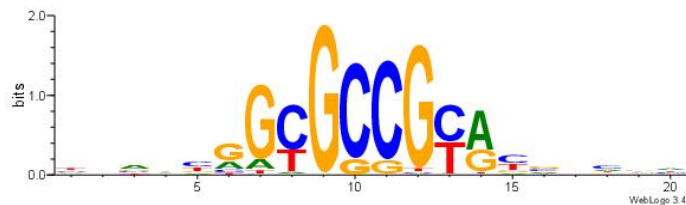
Alignment:

HBDHVKKKCGGCGCCBHBVH  
---GGGGYGGGG-----

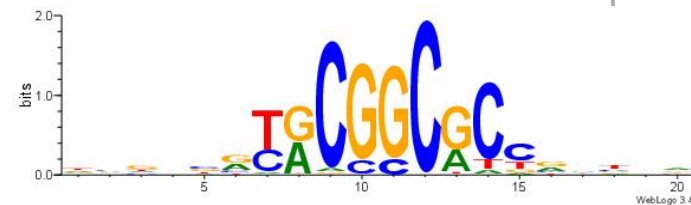
Original motif

Reverse complement motif

Consensus sequence: HVVHBGGCGCCGYRYVHHBH



Consensus sequence: HBDHVKKKCGGCGCCBHBVH



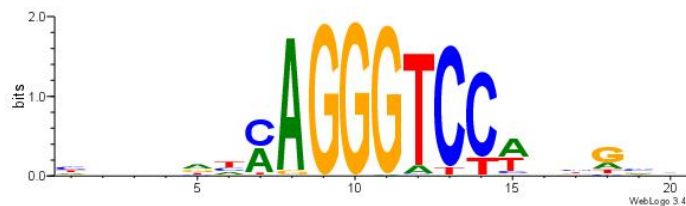
Motif ID: [MA0347.1](#)  
Motif name: NRG1  
Taxon: Fungi  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Original Motif  
Direction: Backward  
Position number: 10  
Number of overlap: 10  
Similarity score: 0.0720885

Alignment:

```
HHVVDHMAGGGTCCWDBGVD  
-GGGGGYGGGG-----
```

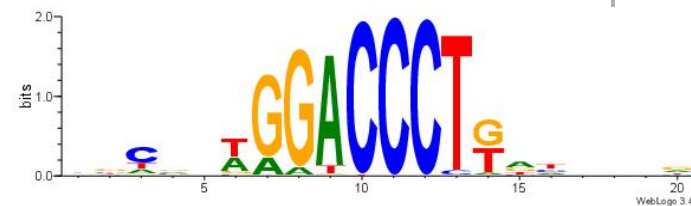
Original motif

Consensus sequence: HHVVDHMAGGGTCCWDBGVD



Reverse complement motif

Consensus sequence: DVCBDWGGACCCTRHDBHD



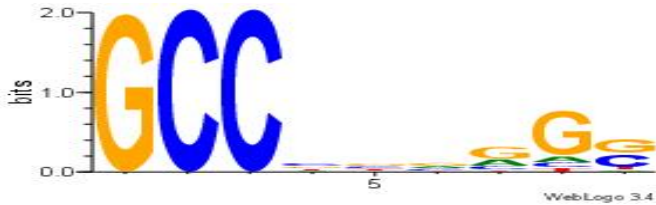
**Dataset #: 3**

**Motif ID: 25**

**Motif name: TFAP2A**

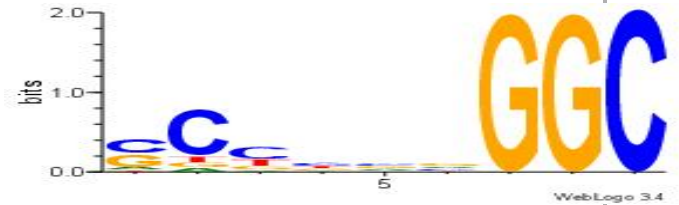
Original motif

Consensus sequence: GCCBBVRGS



Reverse complement motif

Consensus sequence: SCMVBBGGC



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

Motif ID:	<a href="#">MA0395.1</a>
Motif name:	STP2
Taxon:	Fungi
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	12
Number of overlap:	9
Similarity score:	0.0523356

Alignment:

```
HBDHVKKKCGGCGCCBHBVH  
SCMVBBGGC-----
```

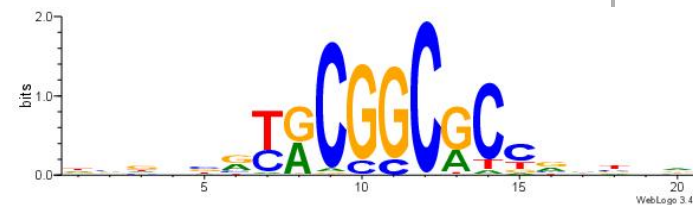
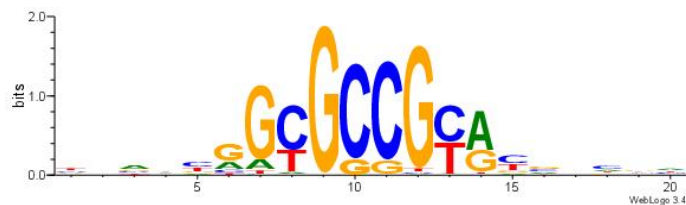
Original motif

Consensus sequence: HVVHBGGCGCCGYRYVHHBH

Reverse complement motif

Consensus sequence: HBDHVKKKCGGCGCCBHBVH



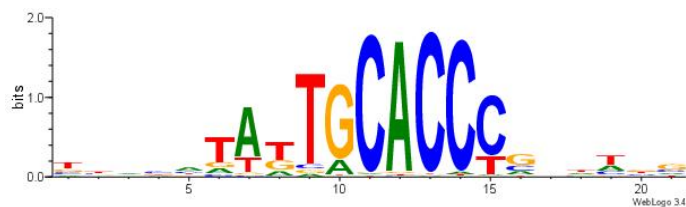


Motif ID: [MA0269.1](#)  
 Motif name: AFT1  
 Taxon: Fungi  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 13  
 Number of overlap: 9  
 Similarity score: 0.0531916

Alignment:  
 VBWDBSGGGTGCARTAHBDVV  
 SCMVBGGC-----

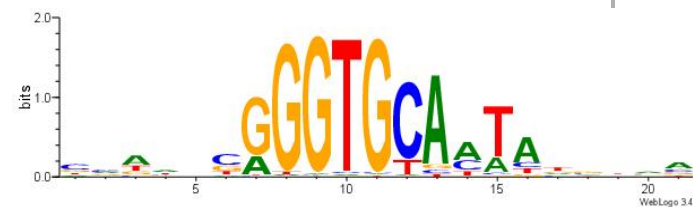
Original motif

Consensus sequence: BBDBHTAKTGCACCCSVDWBV



Reverse complement motif

Consensus sequence: VBWDBSGGGTGCARTAHBDVV



Motif ID: [MA0347.1](#)

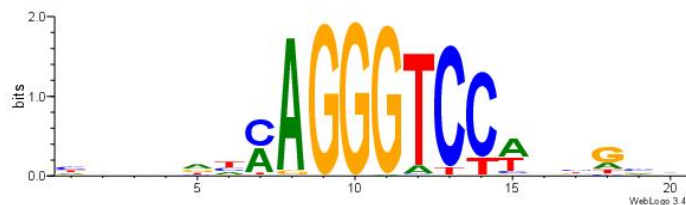
Motif name: NRG1  
 Taxon: Fungi  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 2  
 Number of overlap: 9  
 Similarity score: 0.0537997

**Alignment:**

DVCBDWGGACCCTRHDVBHD  
 -SCMVBBGGC-----

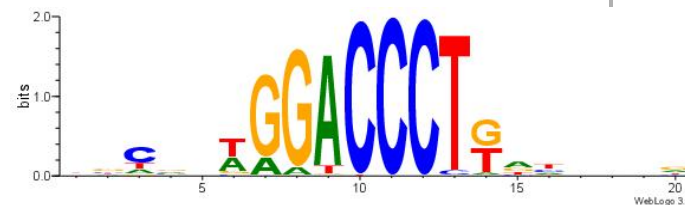
**Original motif**

Consensus sequence: HHVVDHMAGGGTCCWDBGVD



**Reverse complement motif**

Consensus sequence: DVCBDWGGACCCTRHDVBHD




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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: 6  
 Number of overlap: 9

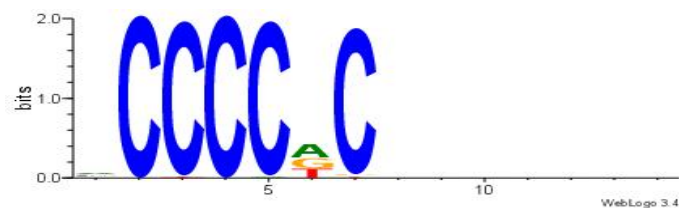
Similarity score: 0.055572

Alignment:

VCCCCDCHHHDDDBD  
-----GCCBBVRGS

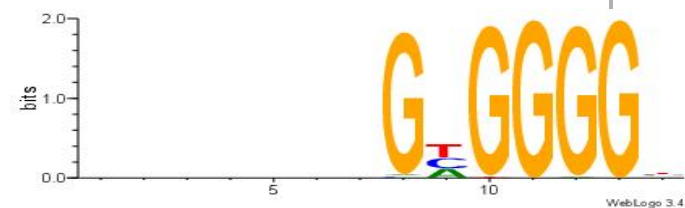
Original motif

Consensus sequence: VCCCCDCHHHDDDBD



Reverse complement motif

Consensus sequence: DBDDHHHGDGGGGG



Motif ID: [MA0343.1](#)  
Motif name: NDT80  
Taxon: Fungi  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Original Motif  
Direction: Backward  
Position number: 13  
Number of overlap: 9  
Similarity score: 0.0585669

Alignment:

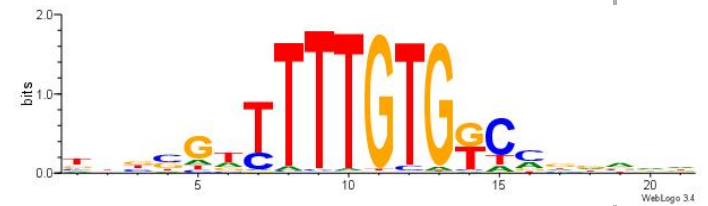
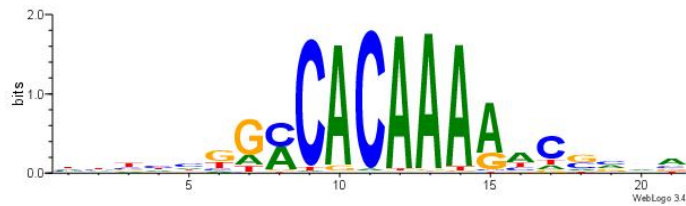
HHBHHKGMCAAAAHCSDV  
SCMVBBGCC-----

Original motif

Consensus sequence: HHBHHKGMCAAAAHCSDV

Reverse complement motif

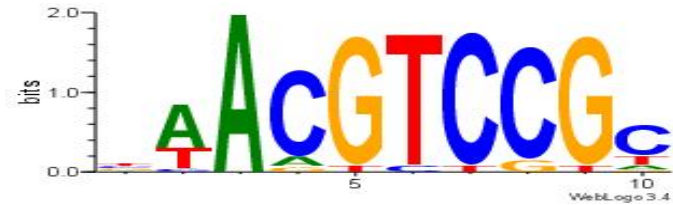
Consensus sequence: BDVSGHTTTTGTGRCYDDVHH



**Dataset #: 3      Motif ID: 26      Motif name: MIZF**

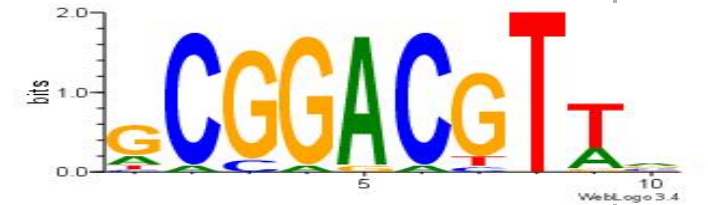
Original motif

Consensus sequence: BAACGTCCGC



Reverse complement motif

Consensus sequence: GCGGACGTTV



**Best Matches for Motif ID 26 (Highest to Lowest)**

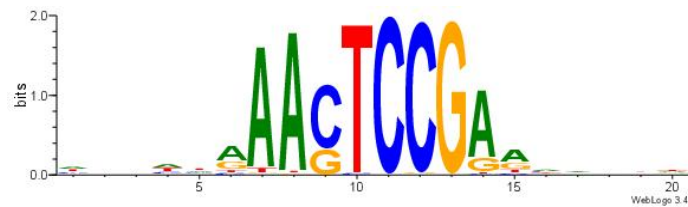
Motif ID:	<a href="#">MA0400.1</a>
Motif name:	SUT2
Taxon:	Fungi
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	5
Number of overlap:	10
Similarity score:	0.0463449

Alignment:

DVDHHTTCGGAGTTKHHHDH  
-----GCGGACGTTV-----

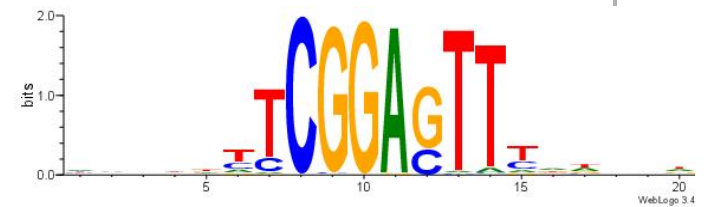
Original motif

Consensus sequence: HDDHHRAACTCCGAAHHDBD



Reverse complement motif

Consensus sequence: DVDHHTTCGGAGTTKHHHDH

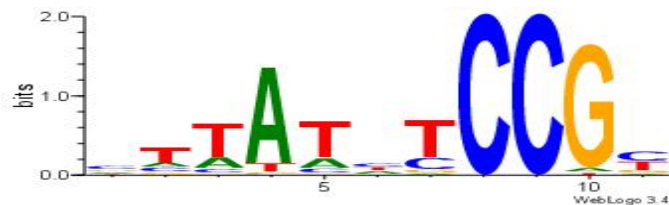


Motif ID: [MA0439.1](#)  
Motif name: YRR1  
Taxon: Fungi  
Matching format of first motif: Original Motif  
Matching format of second motif: Original Motif  
Direction: Backward  
Position number: 1  
Number of overlap: 10  
Similarity score: 0.0501225

Alignment:  
VTTATHHTCCGY  
-BAACGTCCGC

Original motif  
Consensus sequence: VTTATHHTCCGY

Reverse complement motif  
Consensus sequence: KCGGADATAAV



Motif ID: [MA0308.1](#)  
 Motif name: GSM1  
 Taxon: Fungi  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 6  
 Number of overlap: 10  
 Similarity score: 0.052838

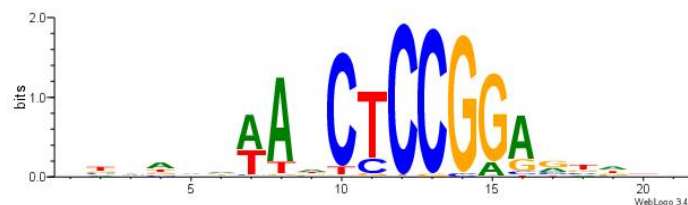
**Alignment:**

```

HDDVVTCCGGAGDTWDDDHVH
-----GCGGACGTTV-----
  
```

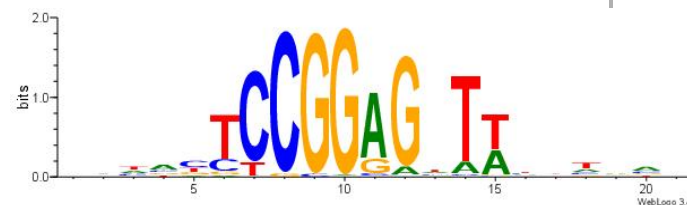
**Original motif**

Consensus sequence: HBHDDDWADCTCCGGAVBDDH



**Reverse complement motif**

Consensus sequence: HDDVVTCCGGAGDTWDDDHVH



Motif ID: [MA0422.1](#)

Motif name: URC2  
Taxon: Fungi  
Matching format of first motif: Original Motif  
Matching format of second motif: Reverse Complement  
Direction: Backward  
Position number: 1  
Number of overlap: 10  
Similarity score: 0.0613126

Alignment:

HCGGAVWTAH  
BAACGTCCGC

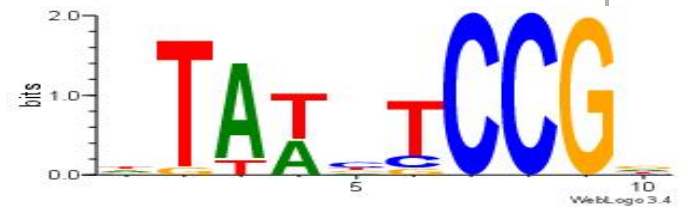
Original motif

Consensus sequence: HCGGAVWTAH



Reverse complement motif

Consensus sequence: HTAWVTCCGD



---

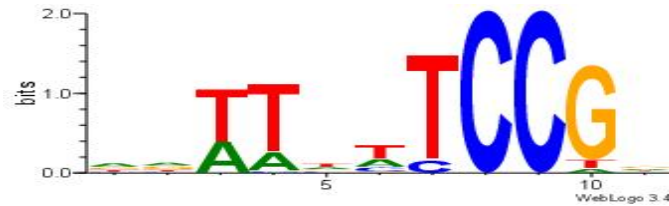
Motif ID: [MA0367.1](#)  
Motif name: RGT1  
Taxon: Fungi  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Reverse Complement  
Direction: Backward  
Position number: 2  
Number of overlap: 10  
Similarity score: 0.0625248

Alignment:

HCGGAWDAWDD  
GCGGACGTTV-

Original motif

Consensus sequence: DDWTDWTCCGD



Reverse complement motif

Consensus sequence: HCGGAWDAWDD



**Dataset #: 3**

**Motif ID: 27**

**Motif name: Klf4**

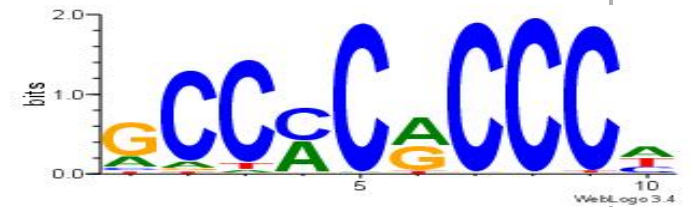
Original motif

Consensus sequence: DGGGYGKGGC



Reverse complement motif

Consensus sequence: GCCYCMCCCD



### Best Matches for Motif ID 27 (Highest to Lowest)

Motif ID:	<a href="#">MA0425.1</a>
Motif name:	YGR067C
Taxon:	Fungi
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif



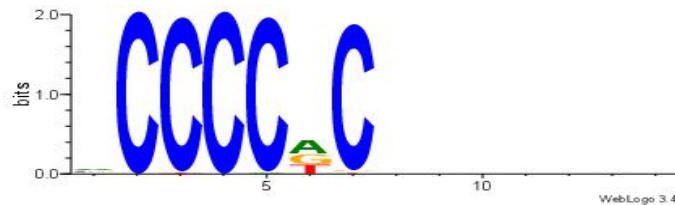
Direction: Backward  
Position number: 5  
Number of overlap: 10  
Similarity score: 0.0377858

Alignment:

VCCCCDCHHHDDDBD  
GCCYCMCCCD-----

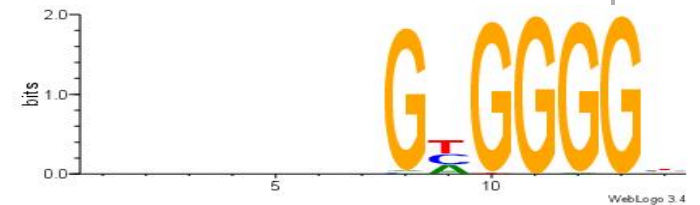
Original motif

Consensus sequence: VCCCCDCHHHDDDBD



Reverse complement motif

Consensus sequence: DBDDHHHGDGGGGG



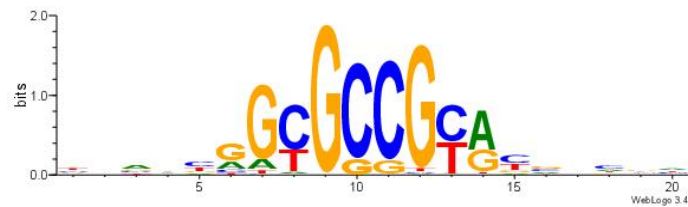
Motif ID: [MA0395.1](#)  
Motif name: STP2  
Taxon: Fungi  
Matching format of first motif: Original Motif  
Matching format of second motif: Original Motif  
Direction: Backward  
Position number: 8  
Number of overlap: 10  
Similarity score: 0.0479742

Alignment:

HVVHBGGCGCCGYRYVHHBH  
---DGGGYGKGGC-----

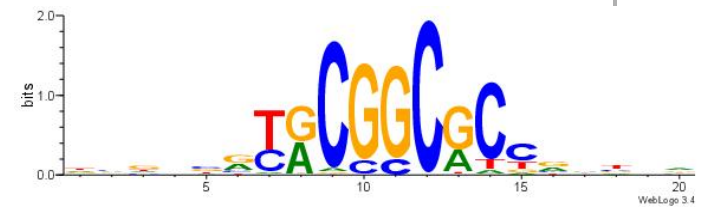
Original motif

Consensus sequence: HVVHBGGCGCCGYRYVHHBH



Reverse complement motif

Consensus sequence: HBDHVKKKCGGCGCCBHBVH

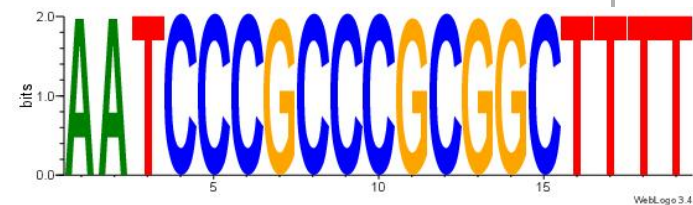
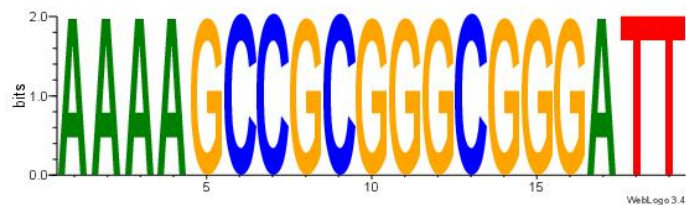


Motif ID: [MA0290.1](#)  
Motif name: DAL81  
Taxon: Fungi  
Matching format of first motif: Original Motif  
Matching format of second motif: Original Motif  
Direction: Forward  
Position number: 9  
Number of overlap: 10  
Similarity score: 0.0512896

Alignment:  
AAAAGCCGCGGGCGGGATT  
-----DGGGYGKGGC--

Original motif  
Consensus sequence: AAAAGCCGCGGGCGGGATT

Reverse complement motif  
Consensus sequence: AATCCCGCCGCGGCTTTT

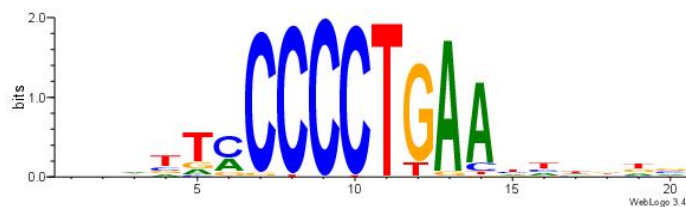


Motif ID: [MA0413.1](#)  
 Motif name: USV1  
 Taxon: Fungi  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 10  
 Number of overlap: 10  
 Similarity score: 0.0518653

Alignment:  
 DDDTTMCCCCTGAAHHDBDV  
 -GCCYCMCCCD-----

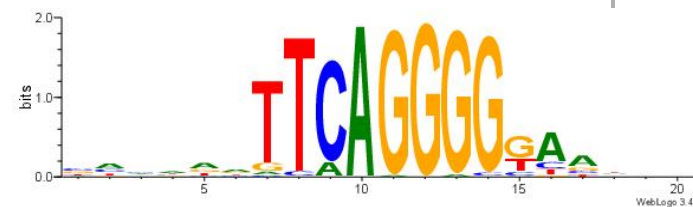
Original motif

Consensus sequence: DDDTTMCCCCTGAAHHDBDV



Reverse complement motif

Consensus sequence: VDBDHHTTCAGGGGRAADDD



Motif ID: [MA0269.1](#)

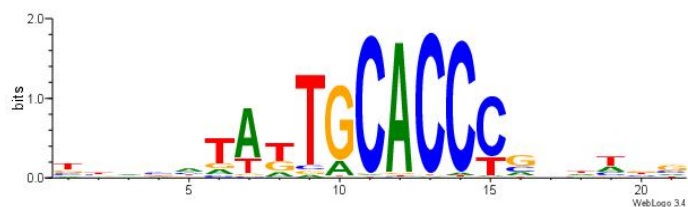
Motif name: AFT1  
 Taxon: Fungi  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 6  
 Number of overlap: 10  
 Similarity score: 0.0608491

Alignment:

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

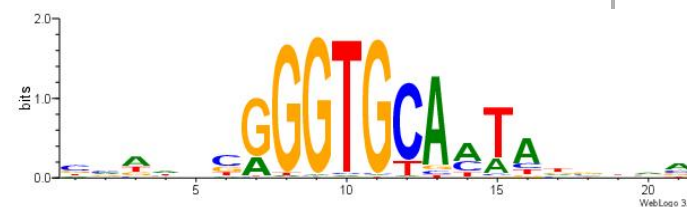
Original motif

Consensus sequence: BBDBHTAKTGCACCCSVDWBV



Reverse complement motif

Consensus sequence: VBWDBSGGGTGCARTAHBDVV



**Dataset #: 3      Motif ID: 28      Motif name: E2F1**

Original motif

Consensus sequence: TTTSGCGC

Reverse complement motif

Consensus sequence: GCGCSAAA



**Best Matches for Motif ID 28 (Highest to Lowest)**

Motif ID: [MA0401.1](#)  
 Motif name: SWI4  
 Taxon: Fungi  
 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: 0.047828

Alignment:  
 ACGCGAAA  
 GCGCSAAA

Original motif  
 Consensus sequence: ACGCGAAA



Reverse complement motif  
 Consensus sequence: TTTCGCGT



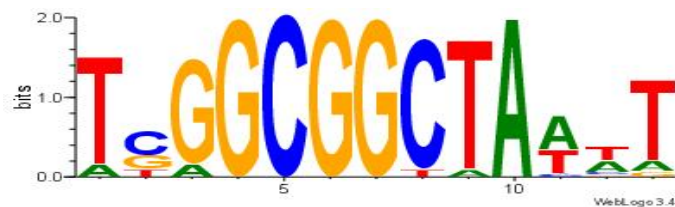
Motif ID: [MA0412.1](#)  
 Motif name: UME6  
 Taxon: Fungi  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 4  
 Number of overlap: 8  
 Similarity score: 0.0641639

Alignment:

AWWTAGCCGCCGA  
 --TTTSGCGC---

Original motif

Consensus sequence: TCGGCGGCTA



Reverse complement motif

Consensus sequence: AWWTAGCCGCCGA

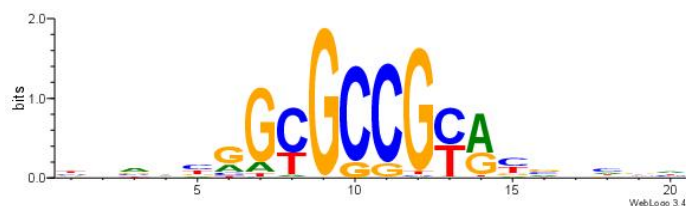


Motif ID: [MA0395.1](#)  
 Motif name: STP2  
 Taxon: Fungi  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 7

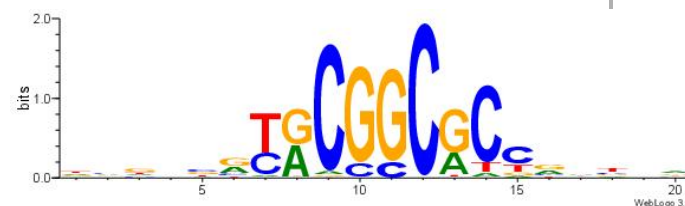
Number of overlap: 8  
Similarity score: 0.0656133

Alignment:  
HBDHVKKKCGGCGCCBHBVH  
-----TTTSGCGC-----

Original motif  
Consensus sequence: HVVHBGGCGCCGYRYVHHBH



Reverse complement motif  
Consensus sequence: HBDHVKKKCGGCGCCBHBVH



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Motif ID: [MA0384.1](#)  
Motif name: SNT2  
Taxon: Fungi  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Reverse Complement  
Direction: Backward  
Position number: 2  
Number of overlap: 8  
Similarity score: 0.069239

Alignment:  
MGGCGCTAMCA  
--GCGCSAAA--

Original motif

Reverse complement motif

Consensus sequence: TGRTAGCGCCR



Consensus sequence: MGGCGCTAMCA



Motif ID: [MA0396.1](#)  
Motif name: STP3  
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: 0.0748236

Alignment:  
DGGCGTABH  
-GCGCSAAA

Original motif

Consensus sequence: DBTAGCGCD



Reverse complement motif

Consensus sequence: DGGCGTABH





**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: [MA0357.1](#)  
Motif name: PHO4  
Taxon: Fungi  
Matching format of first motif: Original Motif  
Matching format of second motif: Original Motif  
Direction: Forward  
Position number: 1  
Number of overlap: 8  
Similarity score: 0.00818914

Alignment:  
SCACGTGS  
VBACGTGV

Original motif

Consensus sequence: SCACGTGS

Reverse complement motif

Consensus sequence: SCACGTGS



Motif ID: [MA0376.1](#)  
 Motif name: RTG3  
 Taxon: Fungi  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 7  
 Number of overlap: 8  
 Similarity score: 0.0129728

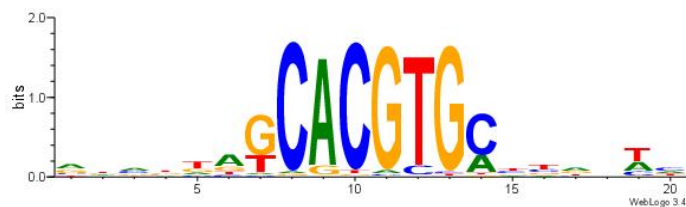
Alignment:

```

VDVBDAGCACGTGCBBDVWH
-----VCACGTBV-----
  
```

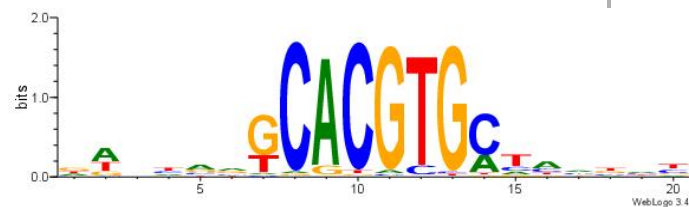
Original motif

Consensus sequence: VDVBDAGCACGTGCBBDVWH



Reverse complement motif

Consensus sequence: DWVDVVGACGTGCTDVBDB



Motif ID: [MA0281.1](#)

Motif name: CBF1  
 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: 0.0134372

Alignment:  
 GCACGTGA  
 VBACGTGV

Original motif

Consensus sequence: GCACGTGA



Reverse complement motif

Consensus sequence: TCACGTGC




---

Motif ID: [MA0321.1](#)  
 Motif name: INO2  
 Taxon: Fungi  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 8

Similarity score: 0.0403872

Alignment:

GCATGTGAA

VCACGTBV-

Original motif

Consensus sequence: GCATGTGAA



Reverse complement motif

Consensus sequence: TTCACATGC



Motif ID: [MA0286.1](#)  
Motif name: CST6  
Taxon: Fungi  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Reverse Complement  
Direction: Backward  
Position number: 2  
Number of overlap: 8  
Similarity score: 0.0442236

Alignment:

DHACGTCAK

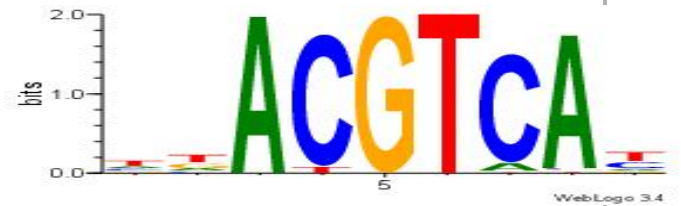
VCACGTBV-

Original motif

Consensus sequence: RTGACGTHD

Reverse complement motif

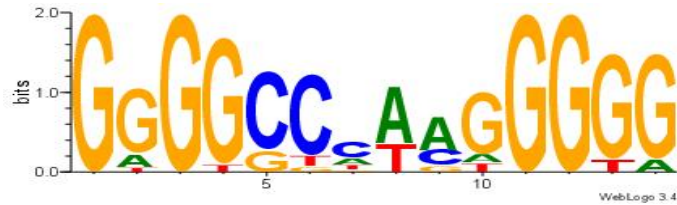
Consensus sequence: DHACGTCAK



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

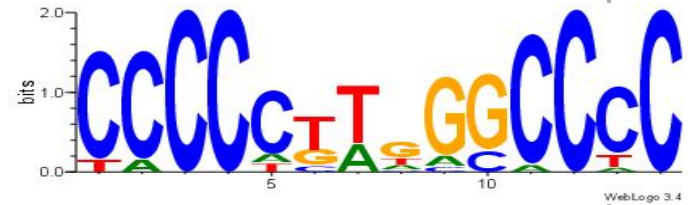
Original motif

Consensus sequence: GGGCCCAAGGGG



Reverse complement motif

Consensus sequence: CCCCTTGGCCCC



**Best Matches for Motif ID 30 (Highest to Lowest)**

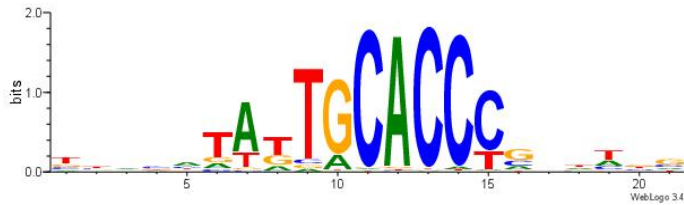
Motif ID:	<a href="#">MA0269.1</a>
Motif name:	AFT1
Taxon:	Fungi
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	14
Similarity score:	0.100886

Alignment:

```
VBWDBSGGGTGCARTAHBDVV
CCCCCTTGGGCCCC-----
```

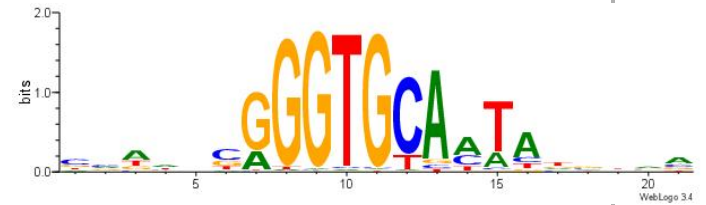
Original motif

Consensus sequence: BBDBHTAKTGCACCCSVDWBV



Reverse complement motif

Consensus sequence: VBWDBSGGGTGCARTAHBDVV



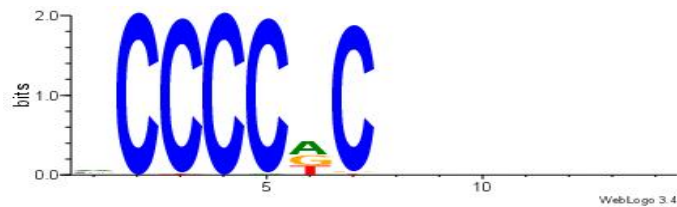
Motif ID: [MA0425.1](#)  
 Motif name: YGR067C  
 Taxon: Fungi  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 14  
 Similarity score: 0.102193

Alignment:

DBDDHHHGDGGGGB  
 GGGCCCAAGGGGG

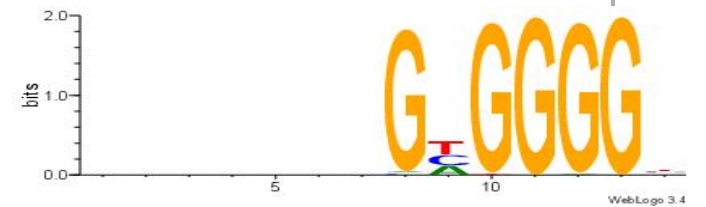
Original motif

Consensus sequence: VCCCCDCHHDDBD



Reverse complement motif

Consensus sequence: DBDDHHHGDGGGGB



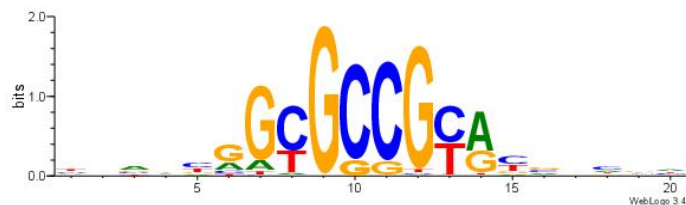
Motif ID: [MA0395.1](#)  
Motif name: STP2  
Taxon: Fungi  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Reverse Complement  
Direction: Backward  
Position number: 6  
Number of overlap: 14  
Similarity score: 0.103695

Alignment:

HBDHVKKKCGGCGCCBHBVH  
-CCCCCTTGGGCCCC-----

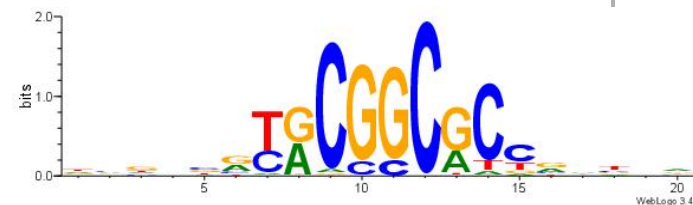
Original motif

Consensus sequence: HVVHBGGCGCCGYRYVHHBH



Reverse complement motif

Consensus sequence: HBDHVKKKCGGCGCCBHBVH



Motif ID: [MA0347.1](#)  
Motif name: NRG1  
Taxon: Fungi  
Matching format of first motif: Original Motif  
Matching format of second motif: Original Motif  
Direction: Forward

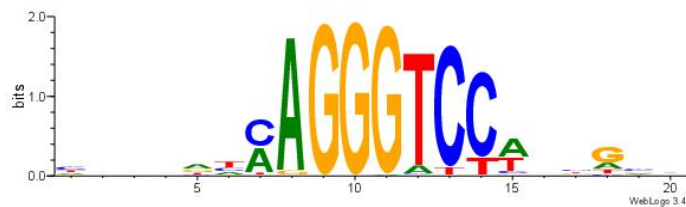
Position number: 8  
Number of overlap: 13  
Similarity score: 0.590746

Alignment:

HHVVDHMAGGGTCCWDBGVD-  
-----GGGGCCCAAGGGGG

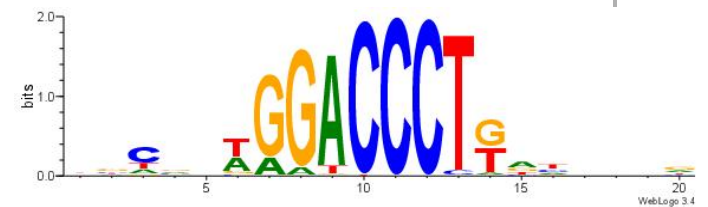
Original motif

Consensus sequence: HHVVDHMAGGGTCCWDBGVD



Reverse complement motif

Consensus sequence: DVCBDWGGACCCTRHDBHD



Motif ID: [MA0323.1](#)  
Motif name: IXR1  
Taxon: Fungi  
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: 0.606398

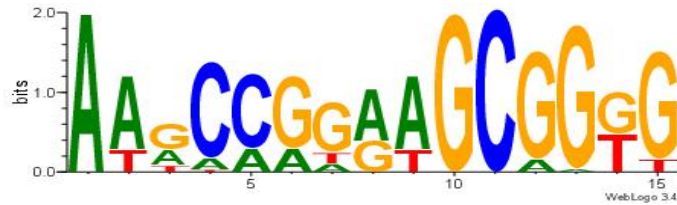
Alignment:

-AARCCGGRAGCGGKG  
GGGGCCCAAGGGGG--



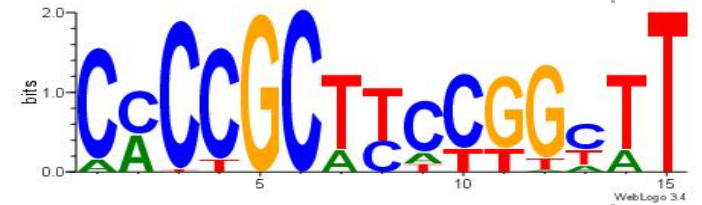
Original motif

Consensus sequence: AARCCGGRAGCGGKG



Reverse complement motif

Consensus sequence: CYCCGCTKCCGGMTT



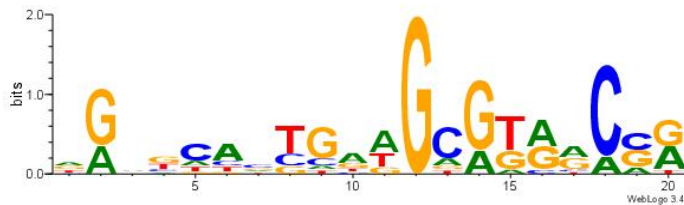
**Dataset #: 3**

**Motif ID: 31**

**Motif name: Pax5**

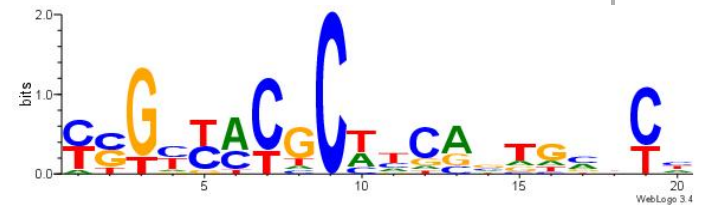
Original motif

Consensus sequence: DGVBCABTGDWGCGRRCR



Reverse complement motif

Consensus sequence: MSGKKRCGCWDCABTGBBBD



### Best Matches for Motif ID 31 (Highest to Lowest)

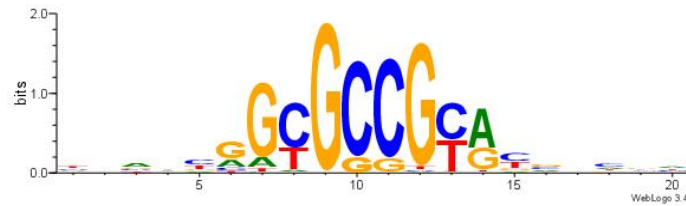
Motif ID:	<a href="#">MA0395.1</a>
Motif name:	STP2
Taxon:	Fungi
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	20
Similarity score:	0.0474871

**Alignment:**

HVVHBBGGCGCCGYRYVHHBH  
DGVBCABTGDWCGCKRRCSR

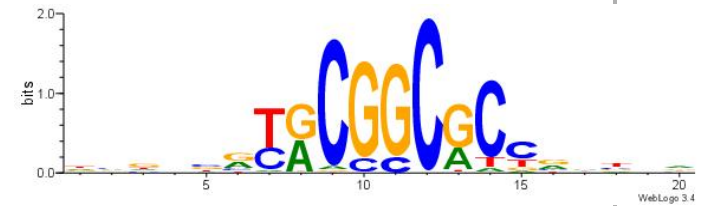
**Original motif**

Consensus sequence: HVVHBBGGCGCCGYRYVHHBH



**Reverse complement motif**

Consensus sequence: HBDHVKKKCGGCGCCBHBVH



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Motif ID:	<a href="#">MA0351.1</a>
Motif name:	DOT6
Taxon:	Fungi
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	20
Similarity score:	0.0524078

**Alignment:**

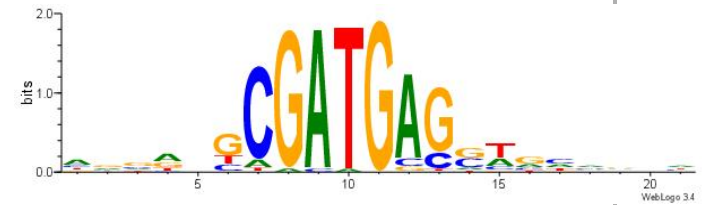
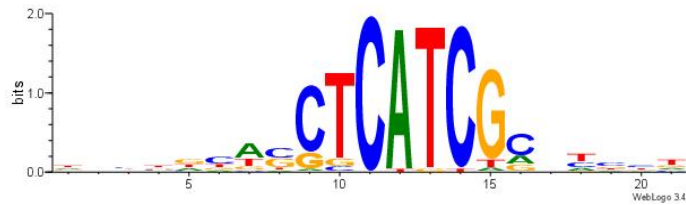
DBBHBGCGATGAGSWBHVVD  
MSGKKRCGCWDCABTGBBCD-

**Original motif**

Consensus sequence: DBBDBWSCTCATCGCVHBB

**Reverse complement motif**

Consensus sequence: DBBHBGCGATGAGSWBHVVD

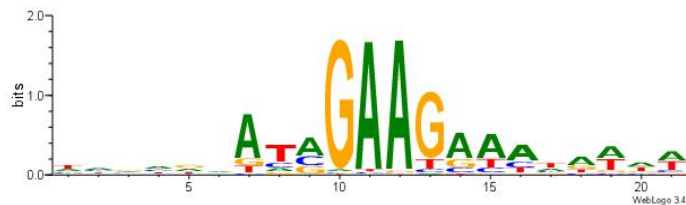


Motif ID: [MA0377.1](#)  
 Motif name: SFL1  
 Taxon: Fungi  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 20  
 Similarity score: 0.0533034

Alignment:  
 WDWDHTTTCTTCYATHHHVHH  
 MSGKKRCGCWDCABTGBCD-

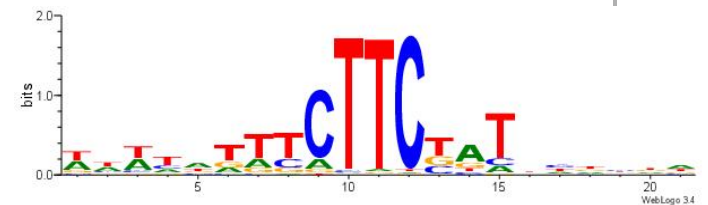
Original motif

Consensus sequence: HHVHDHATMGAAGAAHDWDW



Reverse complement motif

Consensus sequence: WDWDHTTTCTTCYATHHHVHH



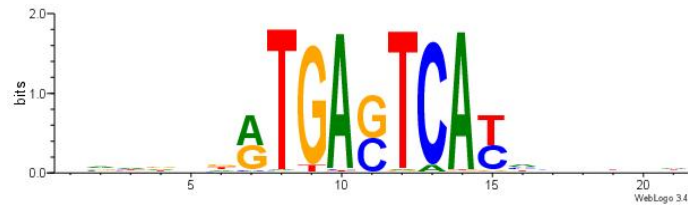
Motif ID: [MA0303.1](#)

Motif name: GCN4  
 Taxon: Fungi  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 1  
 Number of overlap: 20  
 Similarity score: 0.0547496

Alignment:  
 DVHHDHMTGASTCAKHHHHBB  
 -MSGKKRCGCWDCABTGBBCD

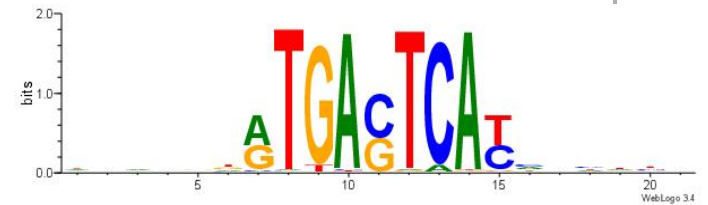
Original motif

Consensus sequence: BVHDDDRTGASTCAYHHHHVD



Reverse complement motif

Consensus sequence: DVHHDHMTGASTCAKHHHHBB




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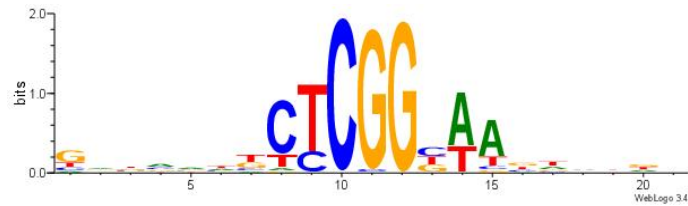
Motif ID: [MA0273.1](#)  
 Motif name: ARO80  
 Taxon: Fungi  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 2  
 Number of overlap: 20  
 Similarity score: 0.0582152

Alignment:

GVBVVHKCTCGGBAABDHHDH  
-MSGKKRCGCWDCABTGBBCD

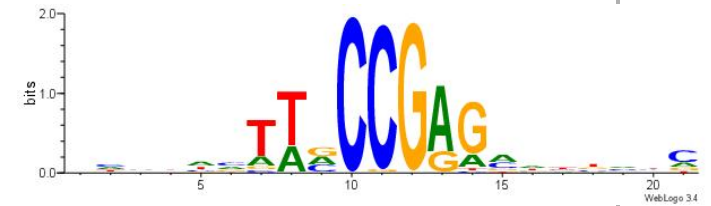
Original motif

Consensus sequence: GVBVVHKCTCGGBAABDHHDH



Reverse complement motif

Consensus sequence: HHHHDBTTBCCGAGRHHBBVBC



**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:	<a href="#">MA0310.1</a>
Motif name:	HAC1
Taxon:	Fungi
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif

Direction: Forward  
Position number: 3  
Number of overlap: 6  
Similarity score: 0.0161785

Alignment:  
GACACGTV  
--CACGCM

Original motif

Consensus sequence: GACACGTV



Reverse complement motif

Consensus sequence: VACGTGTC



---

Motif ID: [MA0270.1](#)  
Motif name: AFT2  
Taxon: Fungi  
Matching format of first motif: Original Motif  
Matching format of second motif: Reverse Complement  
Direction: Forward  
Position number: 1  
Number of overlap: 6  
Similarity score: 0.017883

Alignment:

BGGGTGTB  
YGCGTG--

Original motif

Consensus sequence: BACACCCB



Reverse complement motif

Consensus sequence: BGGGTGTB



Motif ID: [MA0295.1](#)  
Motif name: FHL1  
Taxon: Fungi  
Matching format of first motif: Original Motif  
Matching format of second motif: Reverse Complement  
Direction: Backward  
Position number: 1  
Number of overlap: 6  
Similarity score: 0.0196507

Alignment:  
GACGCAVA  
--YGCGTG

Original motif  
Consensus sequence: GACGCAVA

Reverse complement motif  
Consensus sequence: TBTGCGTC



Motif ID: [MA0281.1](#)  
 Motif name: CBF1  
 Taxon: Fungi  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 2  
 Number of overlap: 6  
 Similarity score: 0.0277434

Alignment:  
 GCACGTGA  
 -YGCGTG-

Original motif

Consensus sequence: GCACGTGA



Reverse complement motif

Consensus sequence: TCACGTGC



Motif ID: [MA0269.1](#)



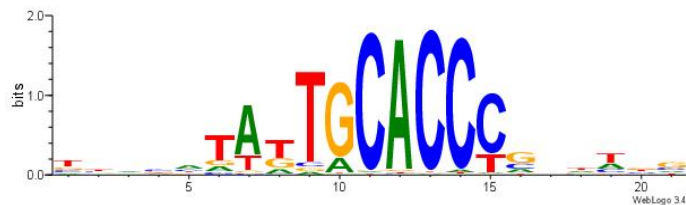
Motif name: AFT1  
 Taxon: Fungi  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 11  
 Number of overlap: 6  
 Similarity score: 0.0290394

Alignment:

VBWDBSGGGTGCARTAHBDVV  
 -----YGCGTG-----

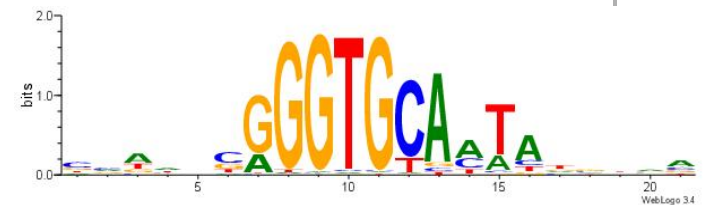
Original motif

Consensus sequence: BBDBHTAKTGCACCCSVDWBV



Reverse complement motif

Consensus sequence: VBWDBSGGGTGCARTAHBDVV



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

Original motif

Consensus sequence: HSCACGTGGC

Reverse complement motif

Consensus sequence: GCCACGTGSD



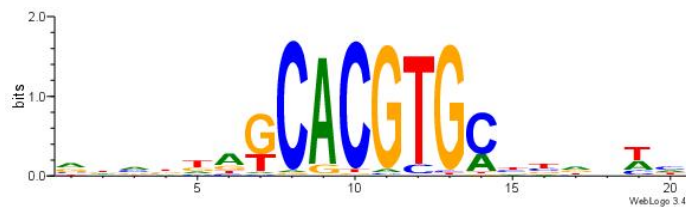
### Best Matches for Motif ID 33 (Highest to Lowest)

Motif ID: [MA0376.1](#)  
 Motif name: RTG3  
 Taxon: Fungi  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 6  
 Number of overlap: 10  
 Similarity score: 0.0219866

Alignment:  
 VDVBDAGCACGTGCBBDVWH  
 -----HSCACGTGGC-----

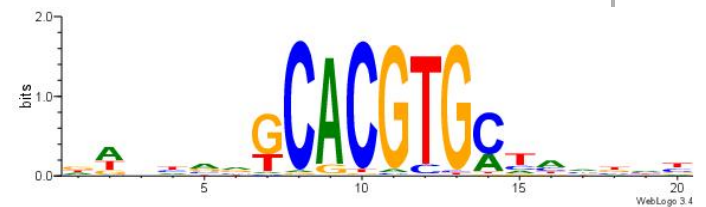
#### Original motif

Consensus sequence: VDVBDAGCACGTGCBBDVWH



#### Reverse complement motif

Consensus sequence: DWVDVVGACACGTGCTDVBDB



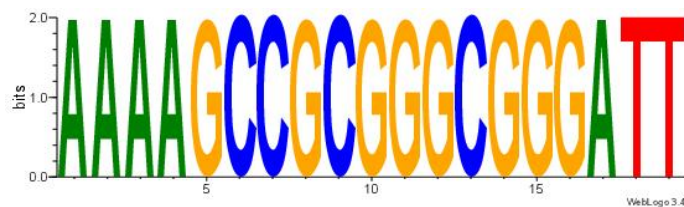
Motif ID: [MA0290.1](#)  
 Motif name: DAL81  
 Taxon: Fungi  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 6  
 Number of overlap: 10  
 Similarity score: 0.0657718

Alignment:

AATCCCGCCC GCGGCTTTT  
 -----HSCACGTGGC-----

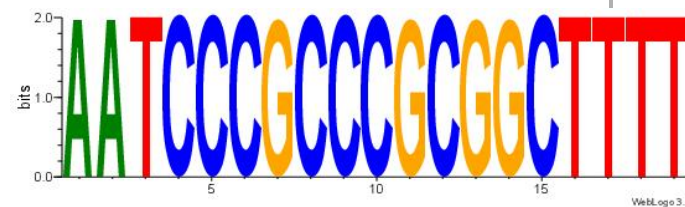
Original motif

Consensus sequence: AAAAGCCGCGGGCGGGATT



Reverse complement motif

Consensus sequence: AATCCCGCCC GCGGCTTTT



Motif ID: [MA0395.1](#)  
 Motif name: STP2  
 Taxon: Fungi  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 7

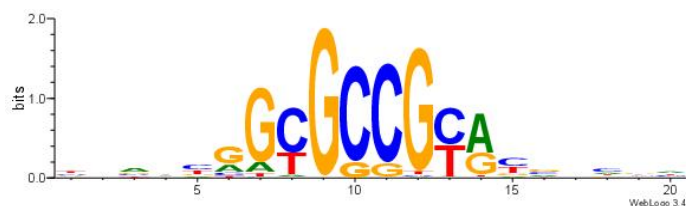
Number of overlap: 10  
Similarity score: 0.0693996

Alignment:

HVVHBGGCGCCGYRYVHHBH  
-----GCCACGTGSD-----

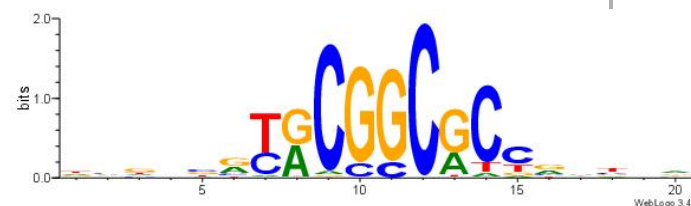
Original motif

Consensus sequence: HVVHBGGCGCCGYRYVHHBH



Reverse complement motif

Consensus sequence: HBDHVKKKCGGCGCCBHBVH



Motif ID: [MA0350.1](#)  
Motif name: TOD6  
Taxon: Fungi  
Matching format of first motif: Original Motif  
Matching format of second motif: Original Motif  
Direction: Forward  
Position number: 7  
Number of overlap: 10  
Similarity score: 0.0710797

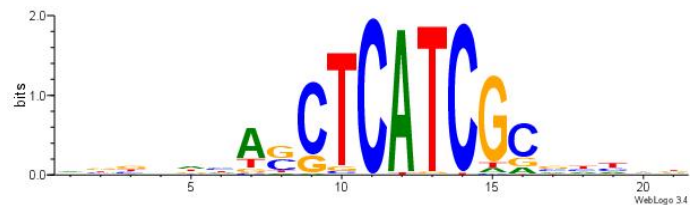
Alignment:

DBBHDHASCTCATCGCVHHHD  
-----HSCACGTGGC-----

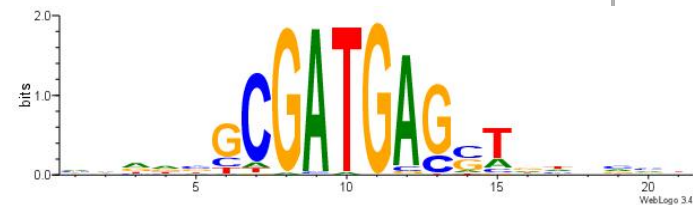
Original motif

Reverse complement motif

Consensus sequence: DBBHDHASCTCATCGCVHHHD



Consensus sequence: DHHHVCGGATGAGSTDDDBBD



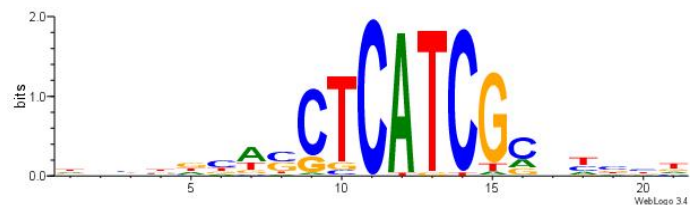
Motif ID: [MA0351.1](#)  
Motif name: DOT6  
Taxon: Fungi  
Matching format of first motif: Original Motif  
Matching format of second motif: Original Motif  
Direction: Backward  
Position number: 6  
Number of overlap: 10  
Similarity score: 0.0713738

Alignment:

DBBBDBWSCTCATCGCVHBB  
-----HSCACGTGGC-----

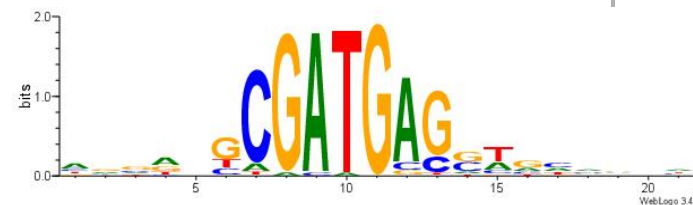
Original motif

Consensus sequence: DBBBDBWSCTCATCGCVHBB



Reverse complement motif

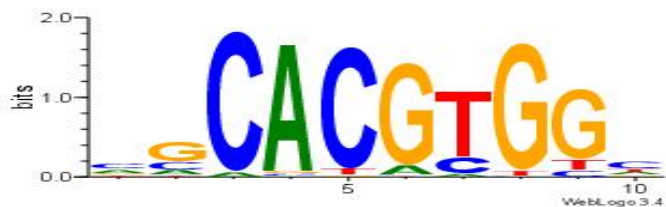
Consensus sequence: DBBBHBCGATGAGSWBHVBD



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

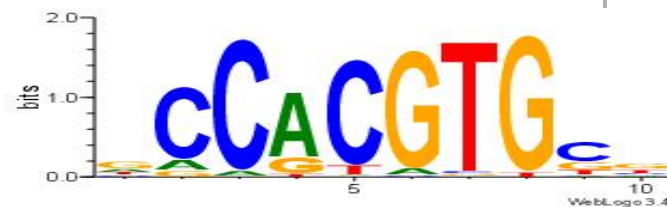
Original motif

Consensus sequence: VGCACGTGGH



Reverse complement motif

Consensus sequence: DCCACGTGCV



### Best Matches for Motif ID 34 (Highest to Lowest)

Motif ID:	<a href="#">MA0376.1</a>
Motif name:	RTG3
Taxon:	Fungi
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	6
Number of overlap:	10
Similarity score:	0.0185747

Alignment:

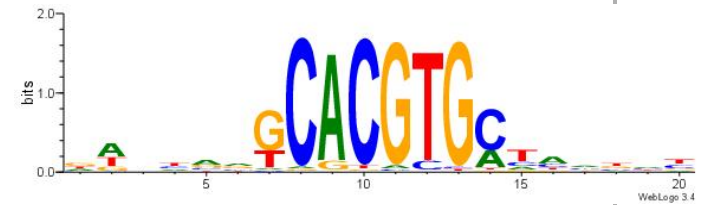
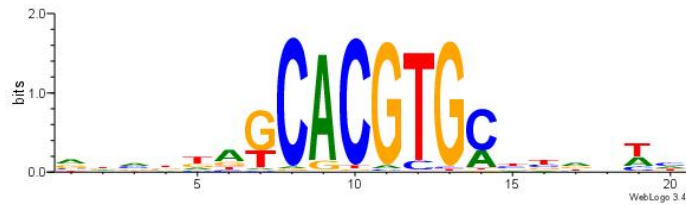
```
DWVDVVGACACGTGCTDVBDB  
-----VGCACGTGGH-----
```

Original motif

Consensus sequence: VDVBDAGCACGTGCBBDVWH

Reverse complement motif

Consensus sequence: DWVDVVGACACGTGCTDVBDB

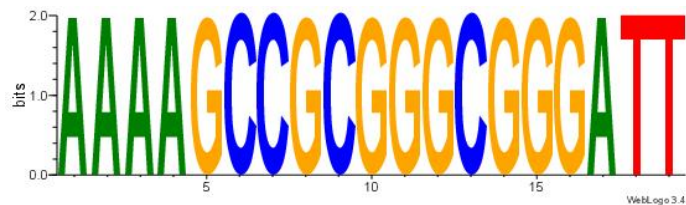


Motif ID: [MA0290.1](#)  
 Motif name: DAL81  
 Taxon: Fungi  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 6  
 Number of overlap: 10  
 Similarity score: 0.0632131

Alignment:  
 AATCCCGCCCGGGCTTTT  
 -----VGCACGTGGH-----

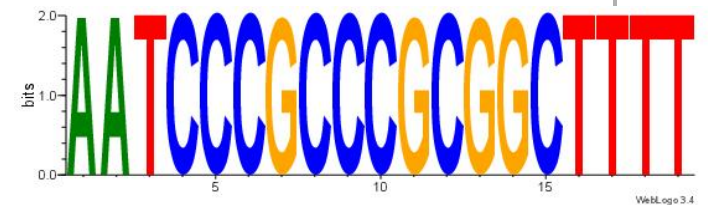
Original motif

Consensus sequence: AAAAGCCGCGGGCGGGATT



Reverse complement motif

Consensus sequence: AATCCCGCCCGGGCTTTT



Motif ID: [MA0269.1](#)

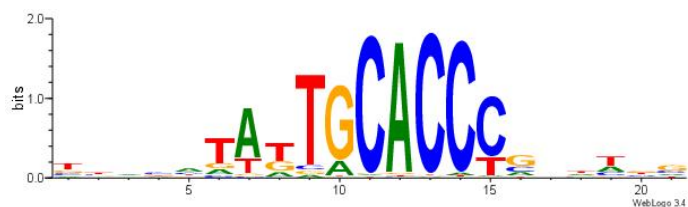
Motif name: AFT1  
 Taxon: Fungi  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 4  
 Number of overlap: 10  
 Similarity score: 0.0677837

**Alignment:**

BBDBHTAKTGCACCCSVDWBV  
 -----VGCACGTGGH---

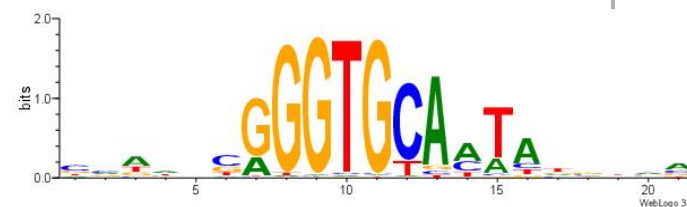
**Original motif**

Consensus sequence: BBDBHTAKTGCACCCSVDWBV



**Reverse complement motif**

Consensus sequence: VBWDBSGGGTGCARTAHBDVV




---

Motif ID: [MA0395.1](#)  
 Motif name: STP2  
 Taxon: Fungi  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 7  
 Number of overlap: 10



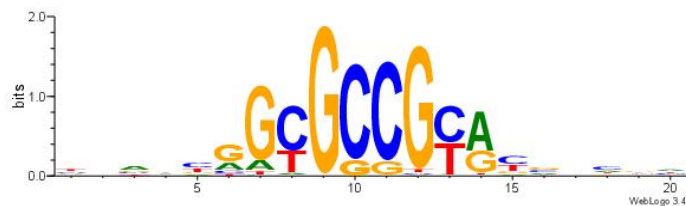
Similarity score: 0.0717569

Alignment:

HVVHBGGCGCCGYRYVHHBH  
-----DCCACGTGCV-----

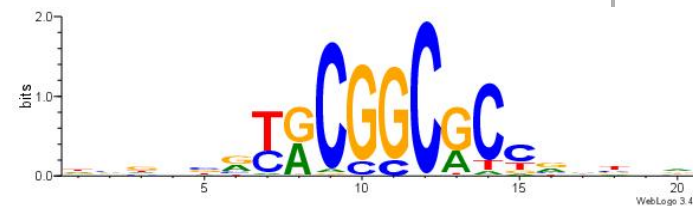
Original motif

Consensus sequence: HVVHBGGCGCCGYRYVHHBH



Reverse complement motif

Consensus sequence: HBDHVKKKCGGCGCCBHBVH



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: 7  
Number of overlap: 10  
Similarity score: 0.0738781

Alignment:

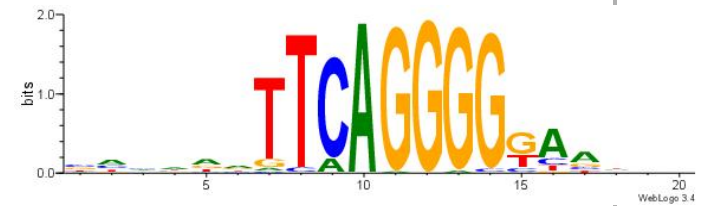
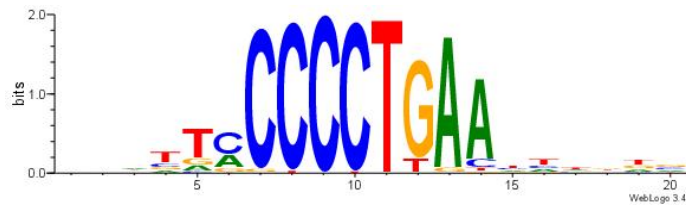
DDDTMCCCCTGAAHHDBDV  
----DCCACGTGCV-----

Original motif

Consensus sequence: DDDTMCCCCTGAAHHDBDV

Reverse complement motif

Consensus sequence: VDBDHHTTCAGGGGRAADDD



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

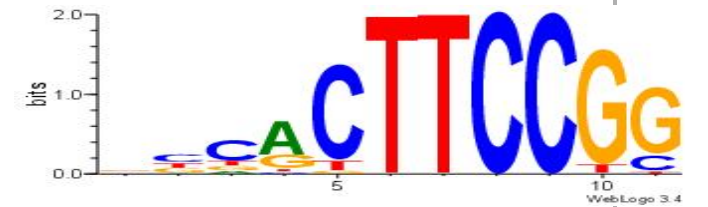
Original motif

Consensus sequence: CCGGAAGTGVV



Reverse complement motif

Consensus sequence: VVCACTTCCGG



**Best Matches for Motif ID 35 (Highest to Lowest)**

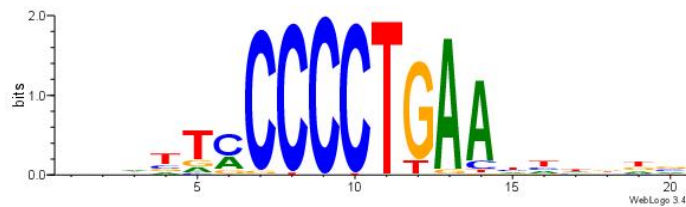
Motif ID:	<a href="#">MA0413.1</a>
Motif name:	USV1
Taxon:	Fungi
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	9
Number of overlap:	11
Similarity score:	0.0573253

Alignment:

VDBDHHTTCAGGGGRAADDD  
-VVCACTCCGG-----

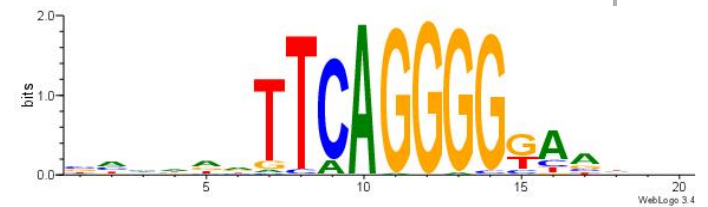
Original motif

Consensus sequence: DDDTTMCCCCTGAAHHDBDV



Reverse complement motif

Consensus sequence: VDBDHHTTCAGGGGRAADDD



Motif ID: [MA0308.1](#)  
Motif name: GSM1  
Taxon: Fungi  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Original Motif  
Direction: Backward  
Position number: 7  
Number of overlap: 11  
Similarity score: 0.0620377

Alignment:

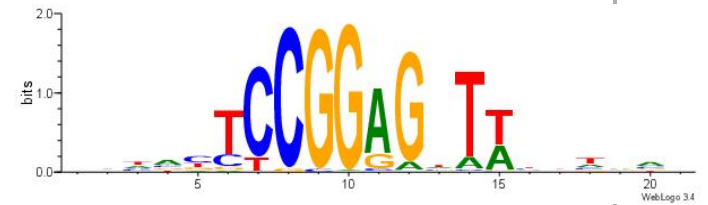
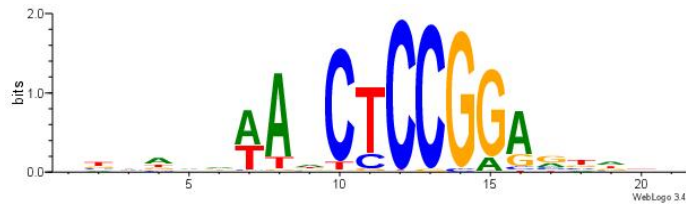
HBHDDDWADCTCCGGAVBDDH  
----VVCACTCCGG-----

Original motif

Consensus sequence: HBHDDDWADCTCCGGAVBDDH

Reverse complement motif

Consensus sequence: HDDVVTCCGGAGDTWDDDHVH

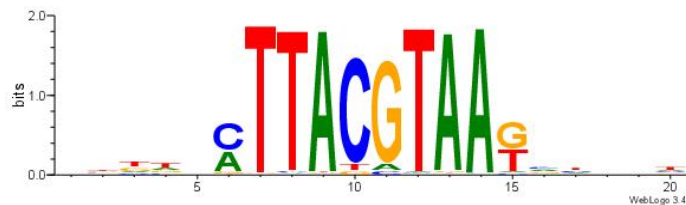


Motif ID: [MA0415.1](#)  
 Motif name: YAP1  
 Taxon: Fungi  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 2  
 Number of overlap: 11  
 Similarity score: 0.0640651

Alignment:  
 HVDHVYTTACGTAARHDDVH  
 -VCACTTCCGG-----

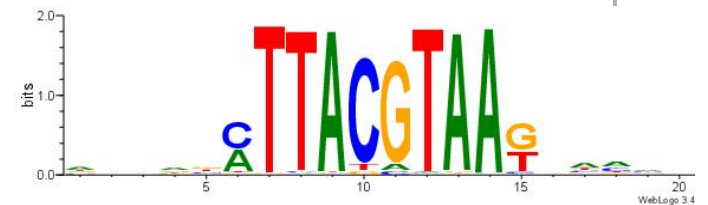
Original motif

Consensus sequence: HBDDDMTTACGTAAKVHHVH



Reverse complement motif

Consensus sequence: HVDHVYTTACGTAARHDDVH



Motif ID: [MA0323.1](#)

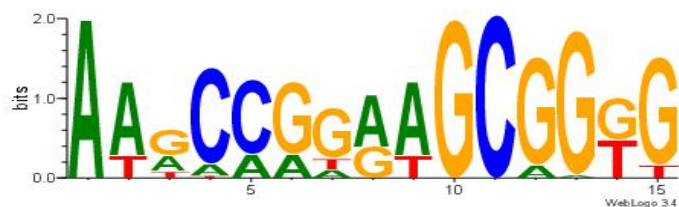
Motif name: IXR1  
 Taxon: Fungi  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 4  
 Number of overlap: 11  
 Similarity score: 0.0672647

Alignment:

AARCCGGRAGCGGKG  
 ---CCGGAAGTGVV-

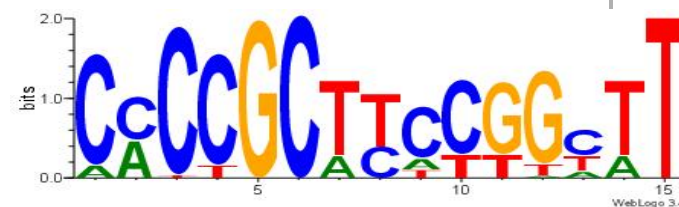
Original motif

Consensus sequence: AARCCGGRAGCGGKG



Reverse complement motif

Consensus sequence: CYCCGCTKCCGGMTT




---

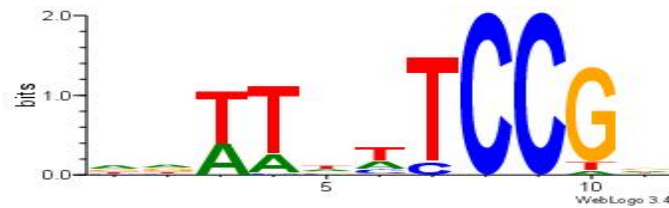
Motif ID: [MA0367.1](#)  
 Motif name: RGT1  
 Taxon: Fungi  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 11  
 Similarity score: 0.0701765

Alignment:

DDWTDWTCCGD  
CCGGAAGTGVV

Original motif

Consensus sequence: DDWTDWTCCGD



Reverse complement motif

Consensus sequence: HCGGAWDAWDD



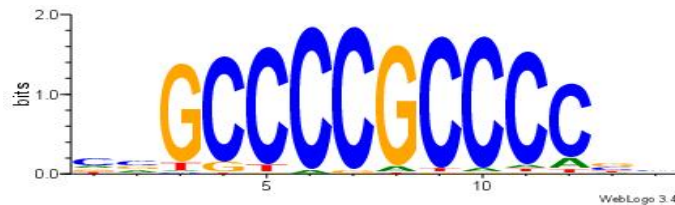
**Dataset #: 4**

**Motif ID: 36**

**Motif name: csGCCCCGCCCCsc**

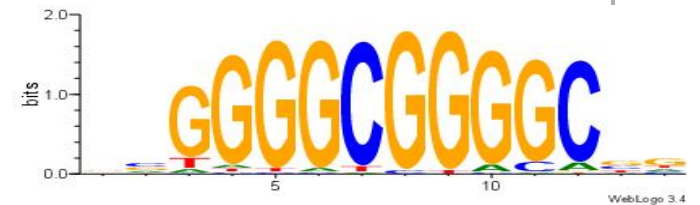
Original motif

Consensus sequence: HVGCCCCGCCCCBB



Reverse complement motif

Consensus sequence: BBGGGGCGGGGCVD



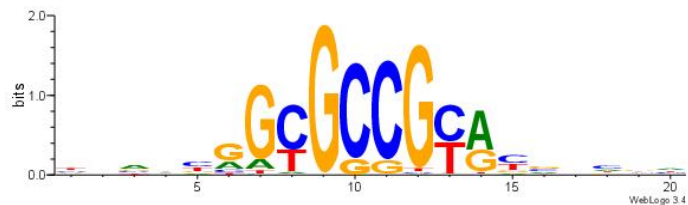
### Best Matches for Motif ID 36 (Highest to Lowest)

Motif ID:	<a href="#">MA0395.1</a>
Motif name:	STP2
Taxon:	Fungi
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement

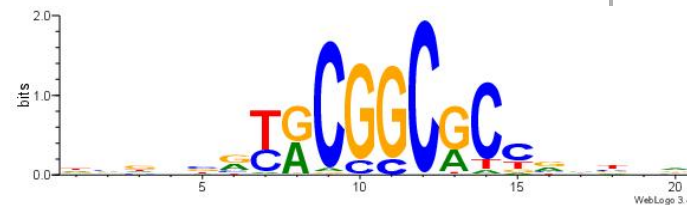
Direction: Backward  
 Position number: 5  
 Number of overlap: 14  
 Similarity score: 0.0443426

Alignment:  
 HBDHVKKKCGGCGCCBHBVH  
 --BBGGGGCGGGGCVD----

Original motif  
 Consensus sequence: HVVHBGGCGCCGYRYVHHBH



Reverse complement motif  
 Consensus sequence: HBDHVKKKCGGCGCCBHBVH



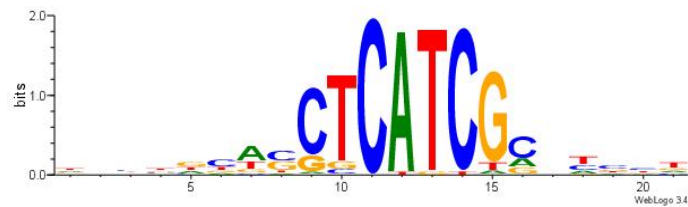
Motif ID: [MA0351.1](#)  
 Motif name: DOT6  
 Taxon: Fungi  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 8  
 Number of overlap: 14  
 Similarity score: 0.0711355

Alignment:

DBBBDBWSCTCATCGCVHBBB  
-----HVGCCCGCCCB

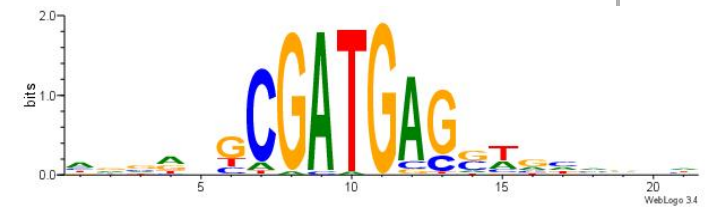
Original motif

Consensus sequence: DBBBDBWSCTCATCGCVHBBB



Reverse complement motif

Consensus sequence: DBBHBGCGATGAGSWBHVBVD



Motif ID: [MA0376.1](#)  
Motif name: RTG3  
Taxon: Fungi  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Original Motif  
Direction: Forward  
Position number: 4  
Number of overlap: 14  
Similarity score: 0.0750988

Alignment:

VDVBDAGCACGTGCBBDVWH  
---BBGGGGCGGGCVD---

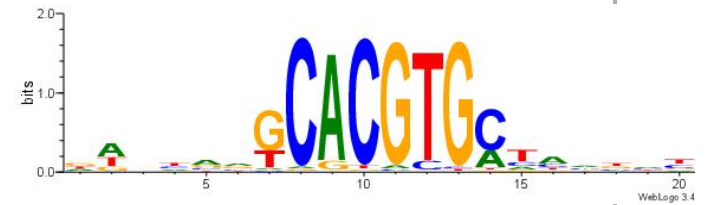
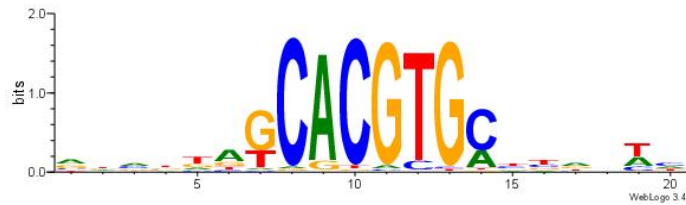
Original motif

Consensus sequence: VDVBDAGCACGTGCBBDVWH

Reverse complement motif

Consensus sequence: DWVDVVGACGTGCTDVBB

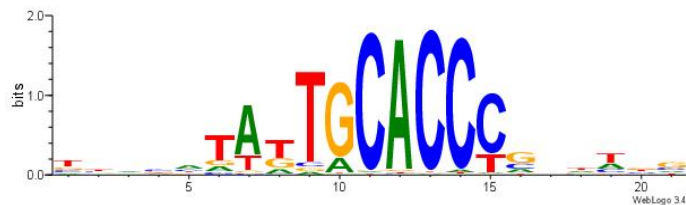




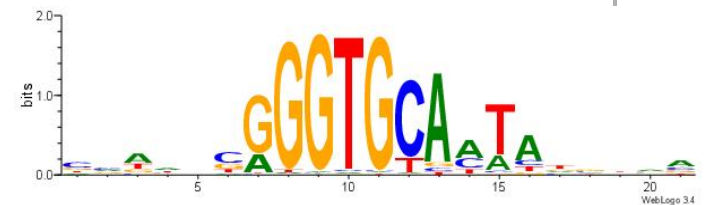
Motif ID: [MA0269.1](#)  
 Motif name: AFT1  
 Taxon: Fungi  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 3  
 Number of overlap: 14  
 Similarity score: 0.0753304

Alignment:  
 VBWDBSGGGTGCARTAHBDVV  
 -----BBGGGGCGGGGCVD--

Original motif  
 Consensus sequence: BBDBHTAKTGCACCCSVDWBV



Reverse complement motif  
 Consensus sequence: VBWDBSGGGTGCARTAHBDVV



Motif ID: [MA0350.1](#)

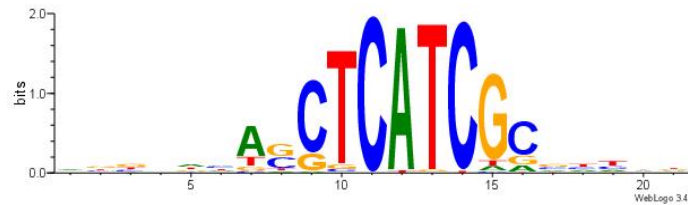
Motif name: TOD6  
 Taxon: Fungi  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 1  
 Number of overlap: 14  
 Similarity score: 0.0758122

**Alignment:**

DBBHDHASCTCATCGCVHHHD  
 -----HVGCCCGCCCCBB

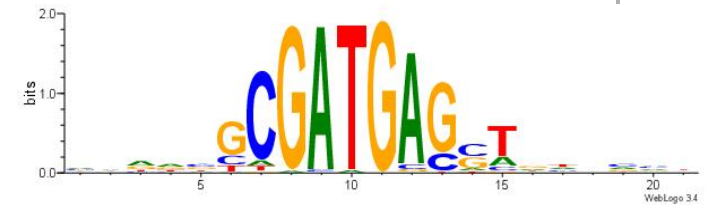
**Original motif**

Consensus sequence: DBBHDHASCTCATCGCVHHHD



**Reverse complement motif**

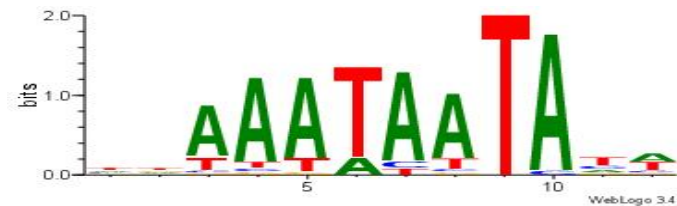
Consensus sequence: DHHHVGCATGAGSTDDDBBD



**Dataset #: 4      Motif ID: 37      Motif name: tkAAATAATAtw**

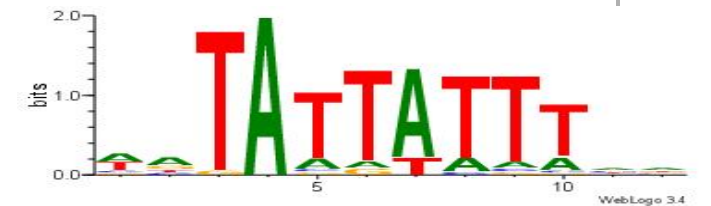
**Original motif**

Consensus sequence: HDAAATAATAHW



**Reverse complement motif**

Consensus sequence: WHTATTATTTDH



## Best Matches for Motif ID 37 (Highest to Lowest)

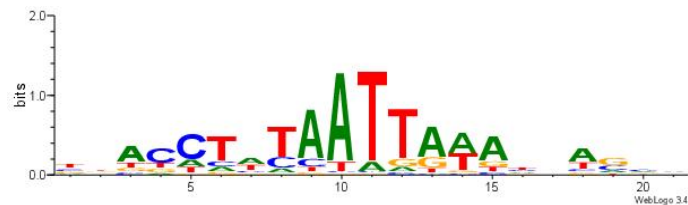
Motif ID: [MA0383.1](#)  
Motif name: SMP1  
Taxon: Fungi  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Reverse Complement  
Direction: Forward  
Position number: 5  
Number of overlap: 12  
Similarity score: 0.0286836

### Alignment:

```
DV\VVVHTWTAATTAWAGGTDV  
----WHTATTATTTDH-----
```

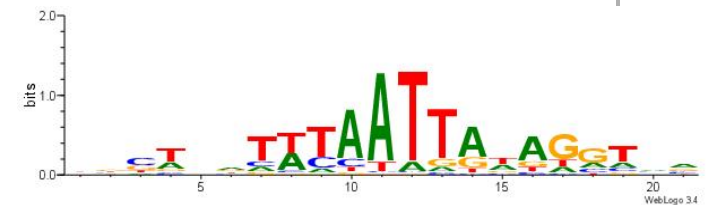
### Original motif

Consensus sequence: BDACCTWTAATTAWAHBWVVD



### Reverse complement motif

Consensus sequence: DV\VVVHTWTAATTAWAGGTDV



---

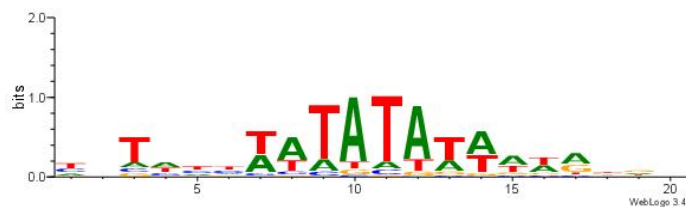
Motif ID: [MA0346.1](#)  
Motif name: NHP6B  
Taxon: Fungi  
Matching format of first motif: Reverse Complement

Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 6  
 Number of overlap: 12  
 Similarity score: 0.0302485

Alignment:  
 HHTHHHWATATATWWWRDDV  
 ---WHTATTATTTDH-----

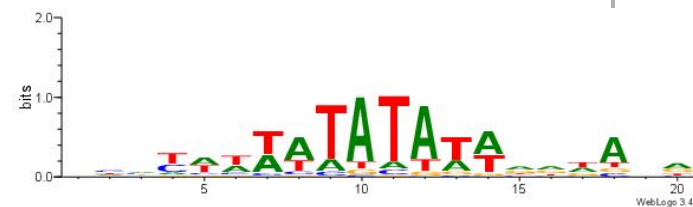
Original motif

Consensus sequence: HHTHHHWATATATWWWRDDV



Reverse complement motif

Consensus sequence: BHDKWWWATATATWHHHAAHH




---

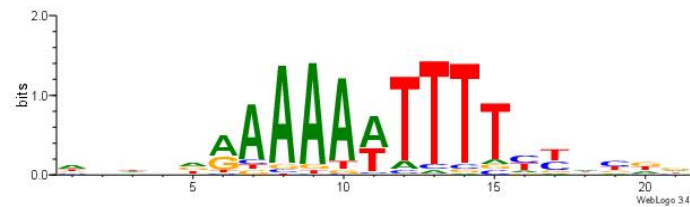
Motif ID: [MA0378.1](#)  
 Motif name: SFP1  
 Taxon: Fungi  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 7  
 Number of overlap: 12  
 Similarity score: 0.0314807

Alignment:

HHBHMKAAAAWTTTTKDHDHD  
-----WHTATTATTTDH---

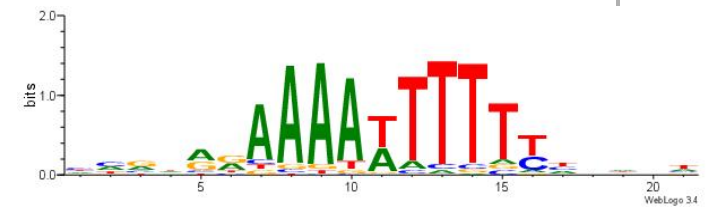
Original motif

Consensus sequence: DHDDDRAAAWTTTTYYHBDD



Reverse complement motif

Consensus sequence: HHBHMKAAAAWTTTTKDHDHD



Motif ID: [MA0345.1](#)  
Motif name: NHP6A  
Taxon: Fungi  
Matching format of first motif: Original Motif  
Matching format of second motif: Original Motif  
Direction: Forward  
Position number: 8  
Number of overlap: 12  
Similarity score: 0.0324864

Alignment:

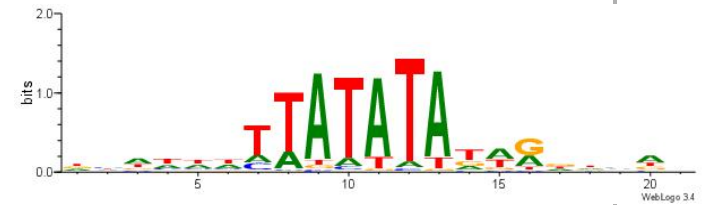
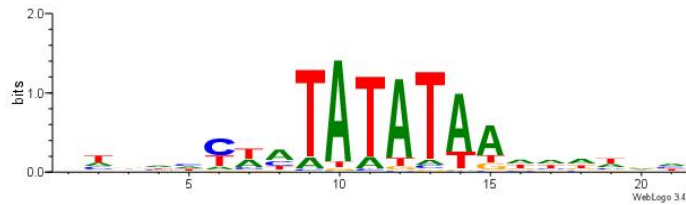
VHDHHYWHTATATAADDDHDH  
-----HDAAATAATAHW--

Original motif

Consensus sequence: VHDHHYWHTATATAADDDHDH

Reverse complement motif

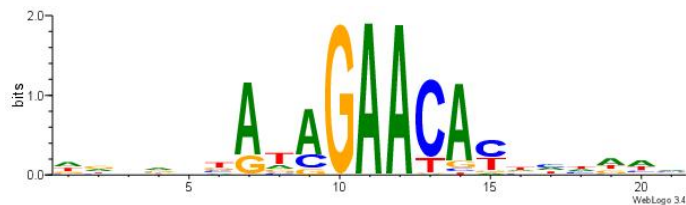
Consensus sequence: HHHDDTTATATAHWKDHBB



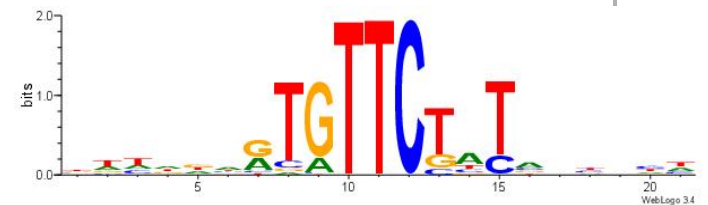
Motif ID: [MA0336.1](#)  
 Motif name: MGA1  
 Taxon: Fungi  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 6  
 Number of overlap: 12  
 Similarity score: 0.0399294

Alignment:  
 DDVVHBATAGAACAYDHHHDHV  
 ----HDAAATAATAHW-----

Original motif  
 Consensus sequence: DDVVHBATAGAACAYDHHHDHV



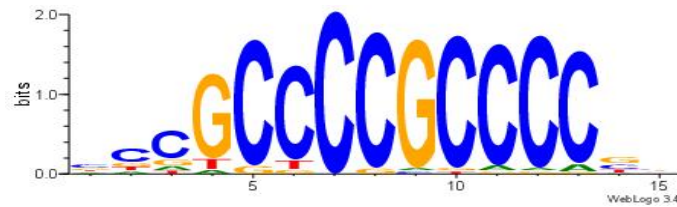
Reverse complement motif  
 Consensus sequence: BHDHDDKTGTTCTATVDBVHD



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

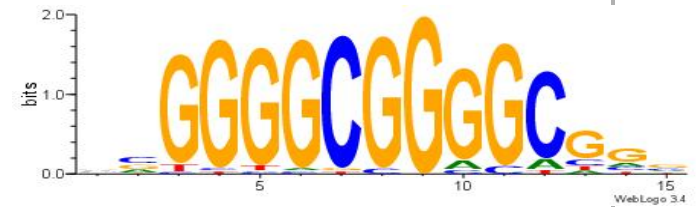
Original motif

Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif

Consensus sequence: BBGGGGCGGGGCGGB



### Best Matches for Motif ID 38 (Highest to Lowest)

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: 3  
Number of overlap: 15  
Similarity score: 0.0578957

Alignment:

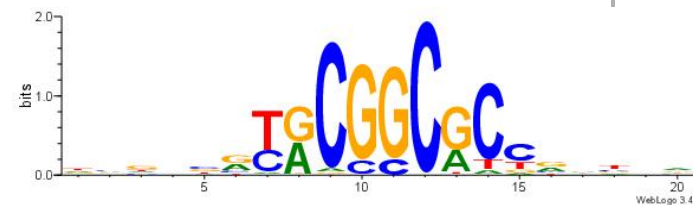
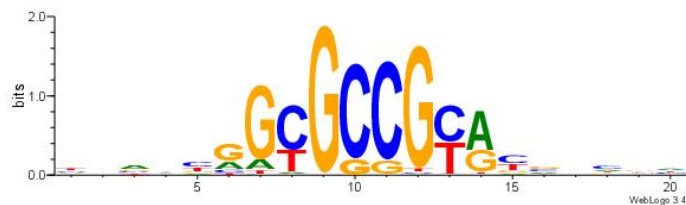
```
HBDHVKKKCGGCGCCBHBVH  
--BBGGGGCGGGGCGGB---
```

Original motif

Consensus sequence: HVVHBGGCGCCGYRYVHHBH

Reverse complement motif

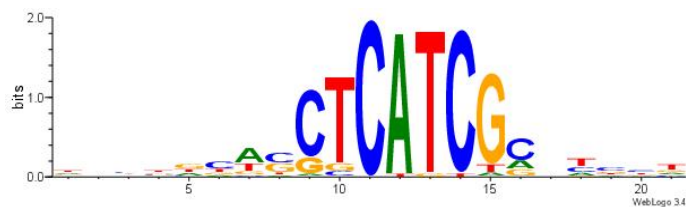
Consensus sequence: HBDHVKKKCGGCGCCBHBVH



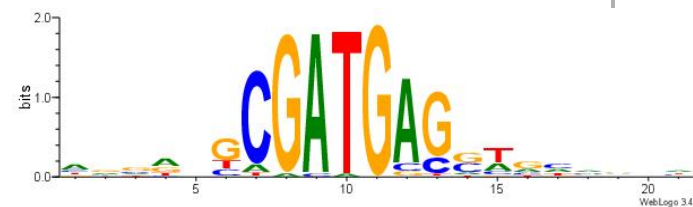
Motif ID: [MA0351.1](#)  
 Motif name: DOT6  
 Taxon: Fungi  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 1  
 Number of overlap: 15  
 Similarity score: 0.0771995

Alignment:  
 DBBBDBWSCTCATCGCVHBB  
 -----BCCGCCCGCCCCBB

Original motif  
 Consensus sequence: DBBBDBWSCTCATCGCVHBB



Reverse complement motif  
 Consensus sequence: DBBBDBWSCTCATCGCVHBB



Motif ID: [MA0269.1](#)



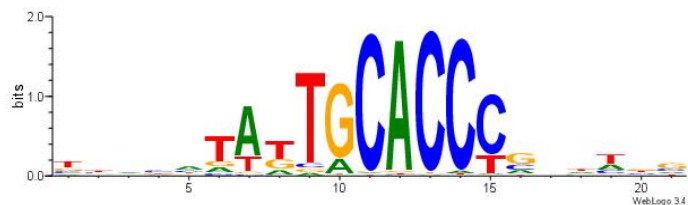
Motif name: AFT1  
 Taxon: Fungi  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 6  
 Number of overlap: 15  
 Similarity score: 0.0809779

**Alignment:**

VBWDBSGGGTGCARTAHBDVV  
 -----BBGGGGCGGGGCGGB-

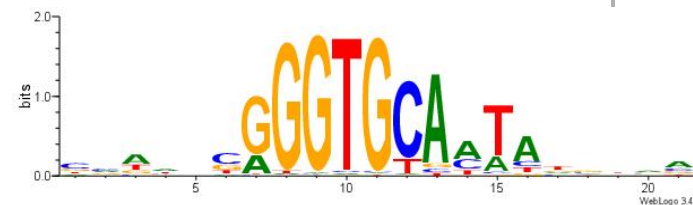
**Original motif**

Consensus sequence: BBDBHTAKTGCACCCSVDWBV



**Reverse complement motif**

Consensus sequence: VBWDBSGGGTGCARTAHBDVV




---

Motif ID: [MA0350.1](#)  
 Motif name: TOD6  
 Taxon: Fungi  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 1  
 Number of overlap: 15

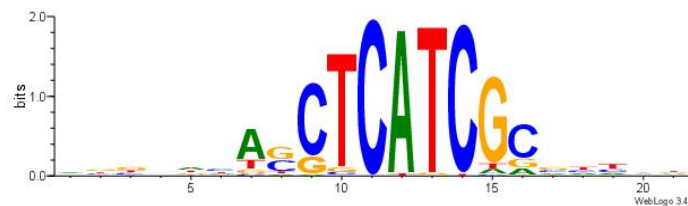
Similarity score: 0.081315

Alignment:

DBBHDHASCTCATCGCVHHHD  
-----BCCGCCCCGCCCCBB

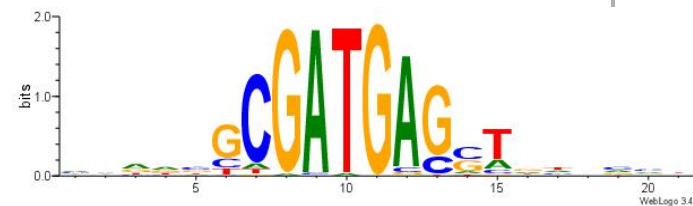
Original motif

Consensus sequence: DBBHDHASCTCATCGCVHHHD



Reverse complement motif

Consensus sequence: DHHHVGCATGAGSTDDDBBD



Motif ID: [MA0376.1](#)  
Motif name: RTG3  
Taxon: Fungi  
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: 0.0831289

Alignment:

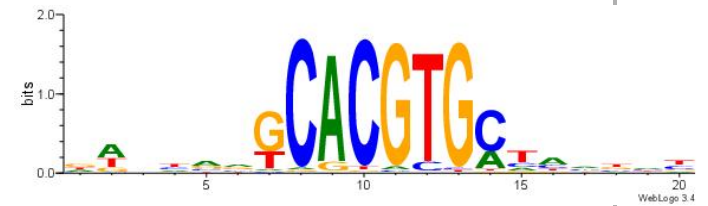
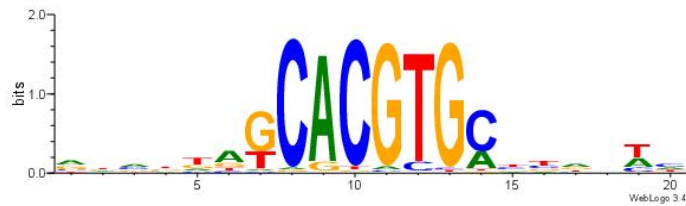
VDVBDAGCACGTGCBBDVWH  
---BBGGGGCGGGCGGB--

Original motif

Consensus sequence: VDVBDAGCACGTGCBBDVWH

Reverse complement motif

Consensus sequence: DWVDVVGACGTGCTDVBB



**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)

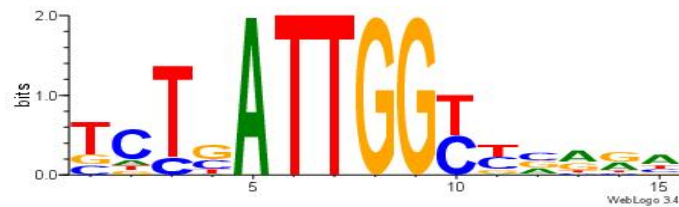
Motif ID:	<a href="#">MA0314.1</a>
Motif name:	HAP3
Taxon:	Fungi
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	3
Number of overlap:	11
Similarity score:	0.0335999

Alignment:

TCTSATTGGYYVRRRA  
--MBATTGGCTGH--

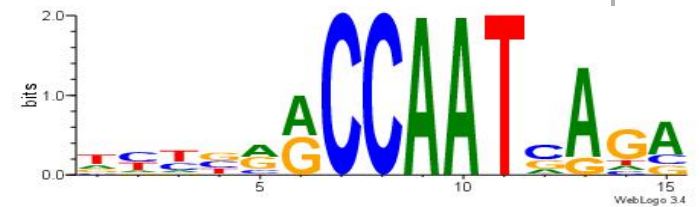
Original motif

Consensus sequence: TCTSATTGGYYVRRRA



Reverse complement motif

Consensus sequence: TMKVMCCAATSAGA



Motif ID: [MA0278.1](#)  
Motif name: BAS1  
Taxon: Fungi  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Reverse Complement  
Direction: Backward  
Position number: 9  
Number of overlap: 11  
Similarity score: 0.0653972

Alignment:

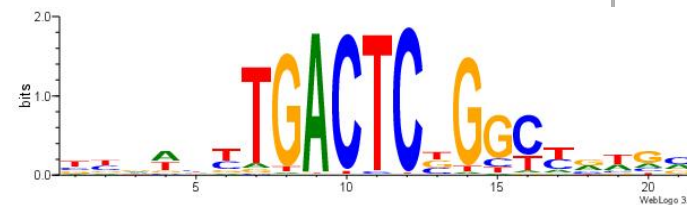
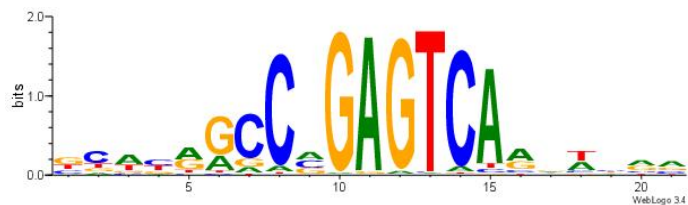
BBBWHKTGACTCBGGCKBWGB  
--MBATTGGCTGH-----

Original motif

Consensus sequence: BCWBRGCCV GAGTCARDWBVV

Reverse complement motif

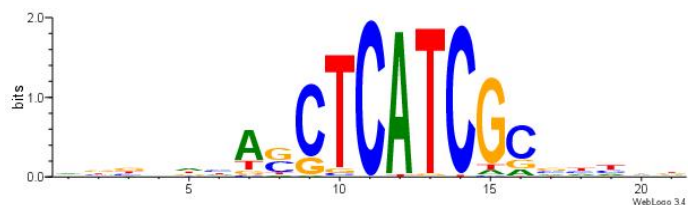
Consensus sequence: BBBWHKTGACTCBGGCKBWGB



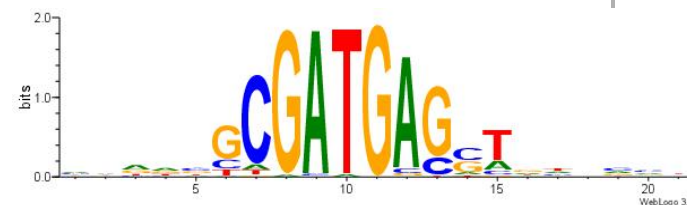
Motif ID: [MA0350.1](#)  
 Motif name: TOD6  
 Taxon: Fungi  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 7  
 Number of overlap: 11  
 Similarity score: 0.0758689

Alignment:  
 DBBHDHASCTCATCGCVHHHD  
 ----DCAGCCAATVR-----

Original motif  
 Consensus sequence: DBBHDHASCTCATCGCVHHHD



Reverse complement motif  
 Consensus sequence: DHHHVGCATGAGSTDDDBBD



Motif ID: [MA0351.1](#)

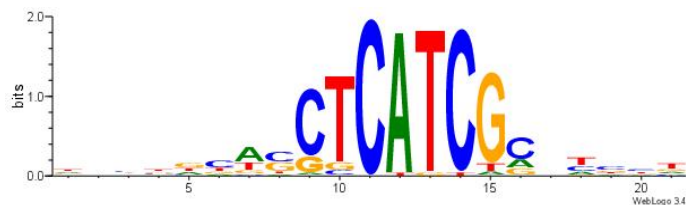
Motif name: DOT6  
 Taxon: Fungi  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 5  
 Number of overlap: 11  
 Similarity score: 0.0769469

**Alignment:**

DBBBDBWSCTCATCGCVHBB  
 ----DCAGCCAATVR-----

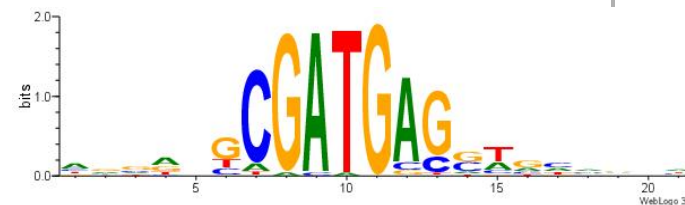
**Original motif**

Consensus sequence: DBBBDBWSCTCATCGCVHBB



**Reverse complement motif**

Consensus sequence: DBBHBGCGATGAGSWBHVBVD




---

Motif ID: [MA0435.1](#)  
 Motif name: YPR015C  
 Taxon: Fungi  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 6  
 Number of overlap: 11

Similarity score:

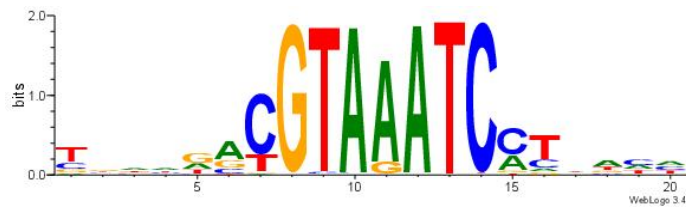
0.0778865

Alignment:

HDDDARGATTTACGTHHDBA  
-----MBATTGGCTGH-----

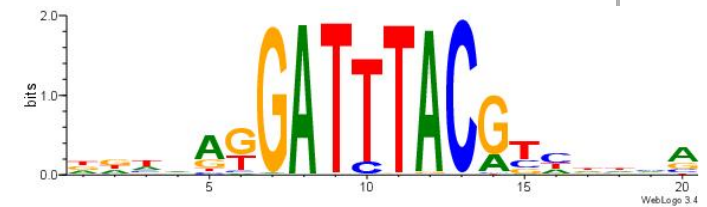
Original motif

Consensus sequence: TBDHDACGTAAATCMTDDHH



Reverse complement motif

Consensus sequence: HDDDARGATTTACGTHHDBA



**Dataset #: 4**

**Motif ID: 40**

**Motif name: kcACCTGCAGc**

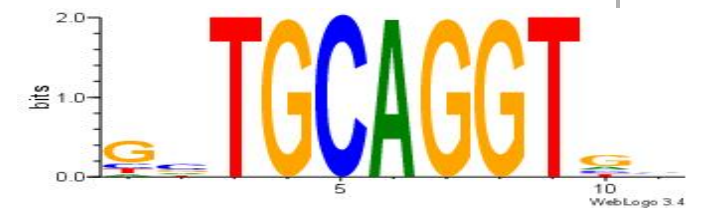
Original motif

Consensus sequence: BCACCTGCABC



Reverse complement motif

Consensus sequence: GBTGCAGGTGB



### Best Matches for Motif ID 40 (Highest to Lowest)

Motif ID:

[MA0376.1](#)

Motif name:

RTG3

Taxon:

Fungi

Matching format of first motif:

Reverse Complement

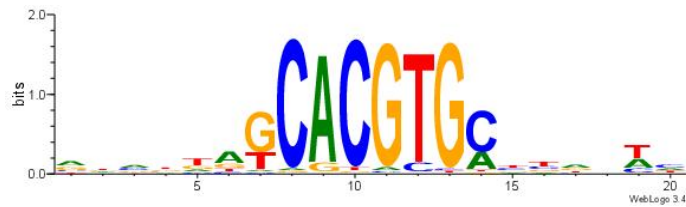
Matching format of second motif: Reverse Complement  
Direction: Backward  
Position number: 7  
Number of overlap: 11  
Similarity score: 0.0263419

Alignment:

DWVDVVGCACGTGCTDVBDB  
---GBTGCAGGTGB-----

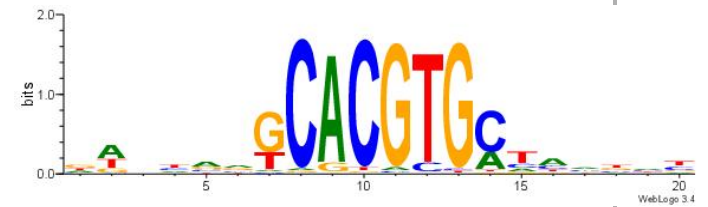
Original motif

Consensus sequence: VDVBDAGCACGTGCBBDVWH



Reverse complement motif

Consensus sequence: DWVDVVGCACGTGCTDVBDB



---

Motif ID: [MA0413.1](#)  
Motif name: USV1  
Taxon: Fungi  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Reverse Complement  
Direction: Forward  
Position number: 5  
Number of overlap: 11  
Similarity score: 0.0285119

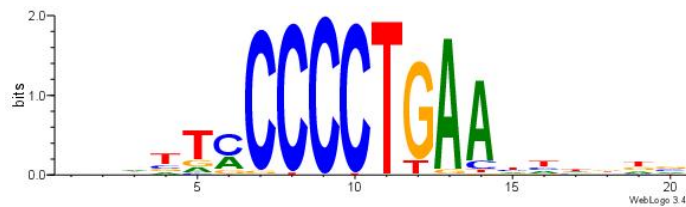
Alignment:



VDBDHHTTCAGGGGRAADDD  
----GBTGCAGGTGB-----

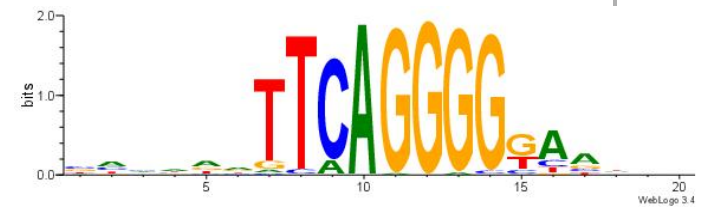
Original motif

Consensus sequence: DDDTTMCCCCTGAAHHDBDV



Reverse complement motif

Consensus sequence: VDBDHHTTCAGGGGRAADDD



Motif ID: [MA0440.1](#)  
Motif name: ZAP1  
Taxon: Fungi  
Matching format of first motif: Original Motif  
Matching format of second motif: Reverse Complement  
Direction: Forward  
Position number: 3  
Number of overlap: 11  
Similarity score: 0.0342832

Alignment:  
CATBACCTTYAMGGT  
--BCACCTGCABC--

Original motif  
Consensus sequence: ACCYTMAAGGTBATG

Reverse complement motif  
Consensus sequence: CATBACCTTYAMGGT



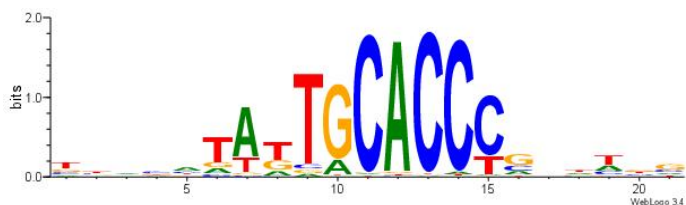
Motif ID: [MA0269.1](#)  
 Motif name: AFT1  
 Taxon: Fungi  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 7  
 Number of overlap: 11  
 Similarity score: 0.0417278

Alignment:

BBDBHTAKTGCACCCSVDWBV  
 -----GBTGCAGGTGB-----

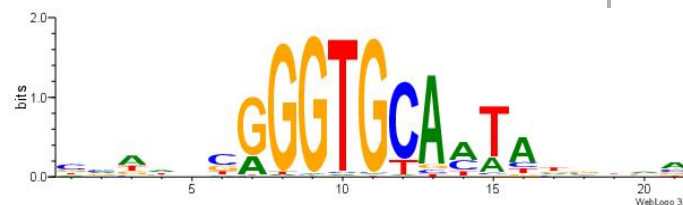
Original motif

Consensus sequence: BBDBHTAKTGCACCCSVDWBV



Reverse complement motif

Consensus sequence: VBWDBSGGGTGCARTAHBDVV



Motif ID: [MA0400.1](#)

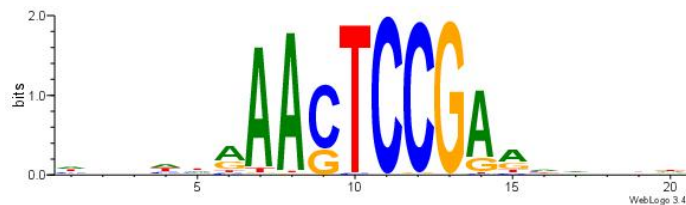
Motif name: SUT2  
 Taxon: Fungi  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 6  
 Number of overlap: 11  
 Similarity score: 0.0531282

Alignment:

DVDHHTTCGGAGTTKHHHDH  
 -----GBTGCAGGTGB-----

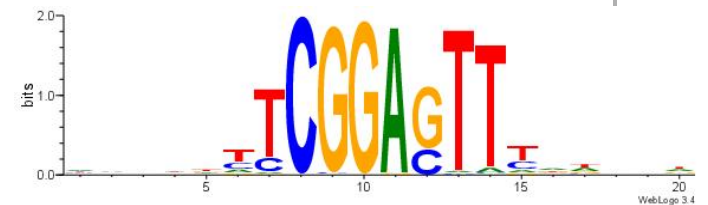
Original motif

Consensus sequence: HDDHHRAACTCCGAAHHDBD



Reverse complement motif

Consensus sequence: DVDHHTTCGGAGTTKHHHDH



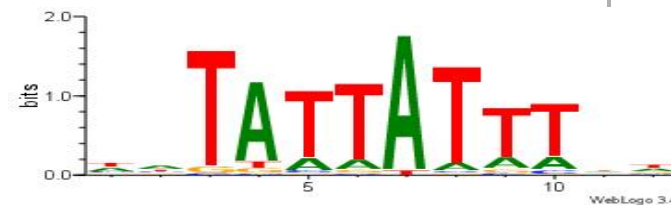
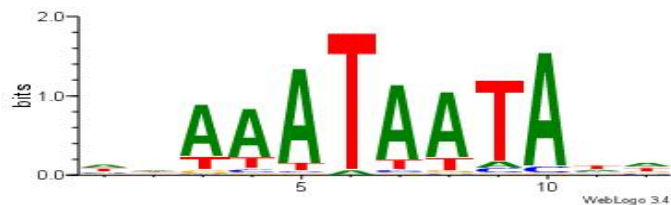
**Dataset #: 4      Motif ID: 41      Motif name: wwAAATAATAtw**

Original motif

Consensus sequence: HDAAATAATADD

Reverse complement motif

Consensus sequence: DDTATTATTTDH



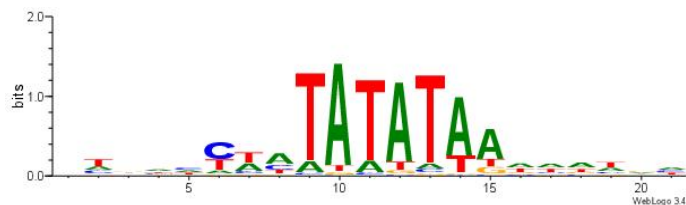
### Best Matches for Motif ID 41 (Highest to Lowest)

Motif ID: [MA0345.1](#)  
 Motif name: NHP6A  
 Taxon: Fungi  
 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: 0.0160013

Alignment:  
 VHDHHYWHTATATAADDDHDH  
 -----HDAAATAATADD--

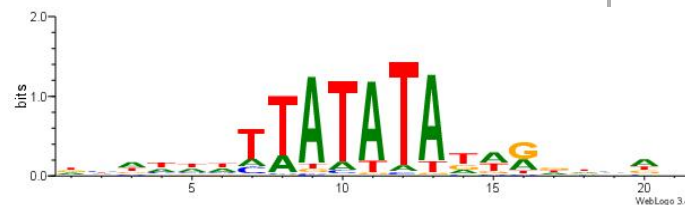
#### Original motif

Consensus sequence: VHDHHYWHTATATAADDDHDH



#### Reverse complement motif

Consensus sequence: HHHDDTTATATAHWKDHBB



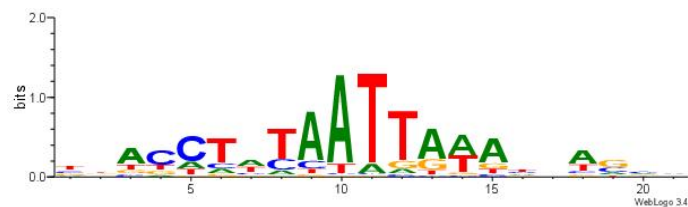
Motif ID: [MA0383.1](#)  
 Motif name: SMP1  
 Taxon: Fungi  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 5  
 Number of overlap: 12  
 Similarity score: 0.0173741

Alignment:

BDACCTWTAATTAWAHBWVVD  
 -----HDAAATAATADD-----

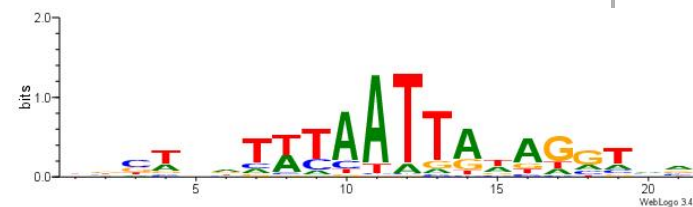
Original motif

Consensus sequence: BDACCTWTAATTAWAHBWVVD



Reverse complement motif

Consensus sequence: DVVWVHTWTAATTAWAGGTDV




---

Motif ID: [MA0346.1](#)  
 Motif name: NHP6B  
 Taxon: Fungi  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 4

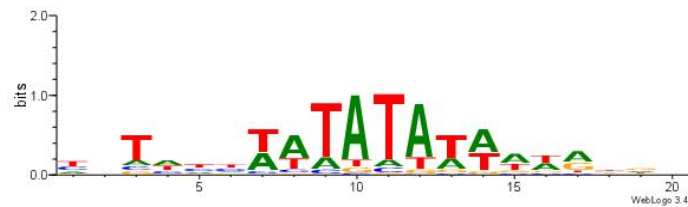
Number of overlap: 12  
Similarity score: 0.0175581

Alignment:

HHTHHHWATATATWWWRDDV  
---DDTATTATTTDH-----

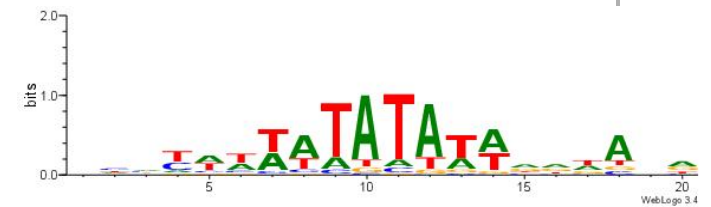
Original motif

Consensus sequence: HHTHHHWATATATWWWRDDV



Reverse complement motif

Consensus sequence: BHDKWWWATATATWHHHHH



---

Motif ID: [MA0378.1](#)  
Motif name: SFP1  
Taxon: Fungi  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Reverse Complement  
Direction: Forward  
Position number: 7  
Number of overlap: 12  
Similarity score: 0.0272758

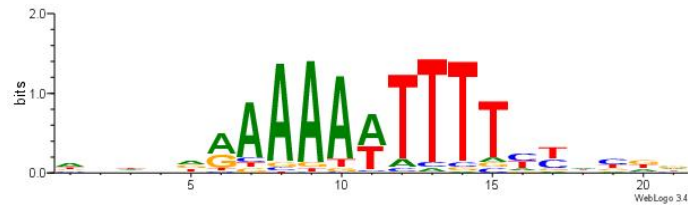
Alignment:

HHBHMKAAAAWTTTTKDHDHD  
-----DDTATTATTTDH---

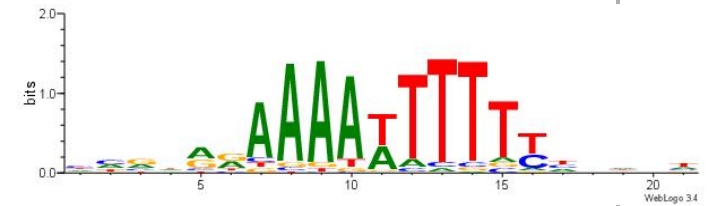
Original motif

Reverse complement motif

Consensus sequence: DHDDDRAAAATTTTTYYHBDD



Consensus sequence: HHBHMKAAAATTTTTKDHDHD



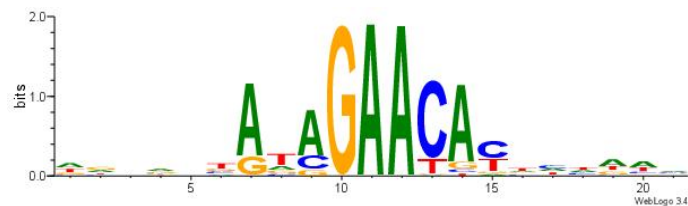
Motif ID: [MA0336.1](#)  
Motif name: MGA1  
Taxon: Fungi  
Matching format of first motif: Original Motif  
Matching format of second motif: Original Motif  
Direction: Backward  
Position number: 6  
Number of overlap: 12  
Similarity score: 0.032139

Alignment:

```
DDVVHBBATAGAACAYDHHHDHV  
-----HDAAATAATADD-----
```

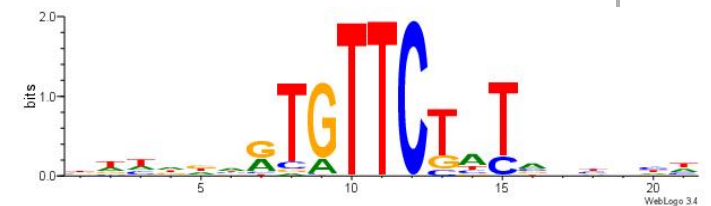
Original motif

Consensus sequence: DDVVHBBATAGAACAYDHHHDHV



Reverse complement motif

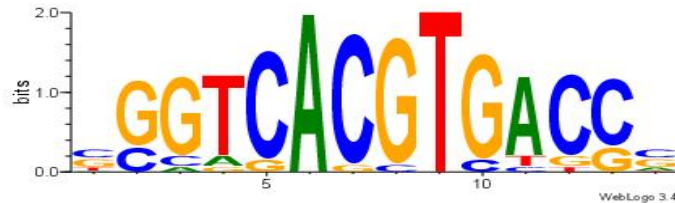
Consensus sequence: BHDHDDKTGTTCTATVDBVHD



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

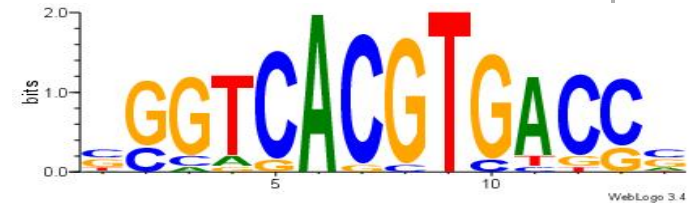
Original motif

Consensus sequence: SGGTCACGTGACCS



Reverse complement motif

Consensus sequence: SGGTCACGTGACCS



### Best Matches for Motif ID 42 (Highest to Lowest)

Motif ID:	<a href="#">MA0376.1</a>
Motif name:	RTG3
Taxon:	Fungi
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:	0.0699483

Alignment:

```
VDVBDAGCACGTGCBBDVWH  
---SGGTCACGTGACCS---
```

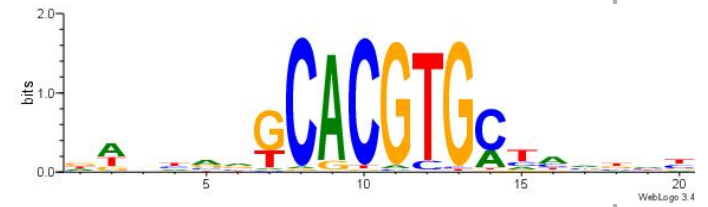
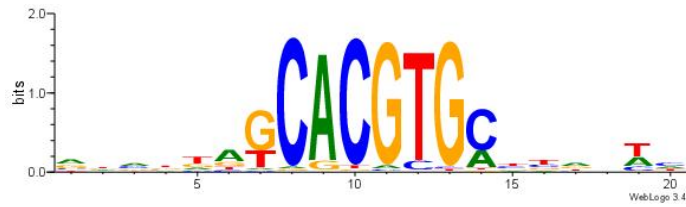
Original motif

Consensus sequence: VDVBDAGCACGTGCBBDVWH

Reverse complement motif

Consensus sequence: DWVDVVGACGTGCTDVVDB



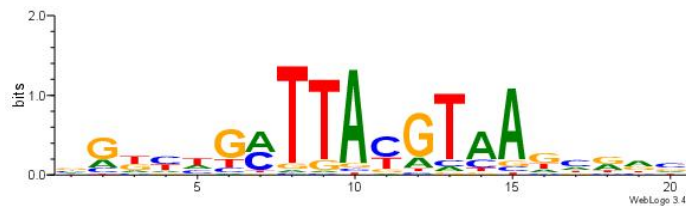


Motif ID: [MA0418.1](#)  
 Motif name: YAP6  
 Taxon: Fungi  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 3  
 Number of overlap: 14  
 Similarity score: 0.0812819

Alignment:  
 VDMDYTTACKTAAYCHKRCV  
 --SGGTCACGTGACCS-----

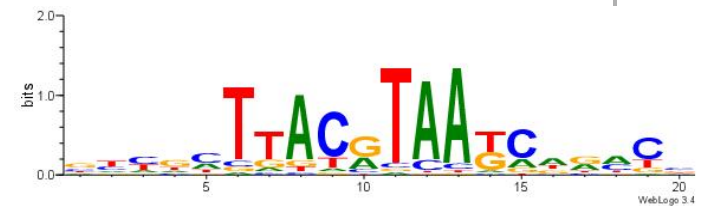
Original motif

Consensus sequence: VGKYHGTTAYGTAAKHRDV



Reverse complement motif

Consensus sequence: VDMDYTTACKTAAYCHKRCV



Motif ID: [MA0415.1](#)

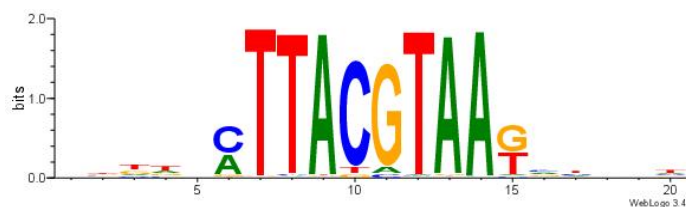
Motif name: YAP1  
Taxon: Fungi  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Reverse Complement  
Direction: Backward  
Position number: 4  
Number of overlap: 14  
Similarity score: 0.088253

Alignment:

HVDHVYTTACGTAARHDDVH  
---SGGTCACGTGACCS---

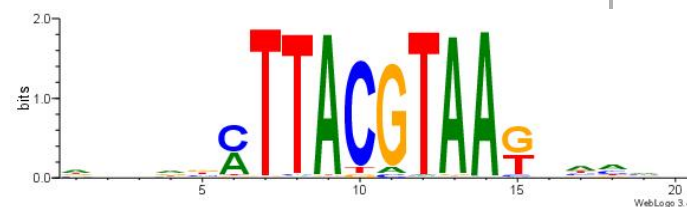
Original motif

Consensus sequence: HBDDDMTTACGTAAKVHHVH



Reverse complement motif

Consensus sequence: HVDHVYTTACGTAARHDDVH



Motif ID: [MA0343.1](#)  
Motif name: NDT80  
Taxon: Fungi  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Reverse Complement  
Direction: Forward  
Position number: 4  
Number of overlap: 14

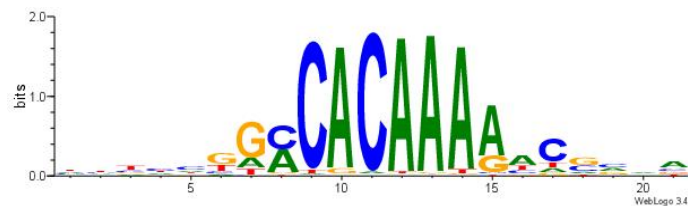
Similarity score: 0.090505

Alignment:

```
BDVSGHTTTTGTGRCYDDVHH  
---SGGTCACGTGACCS----
```

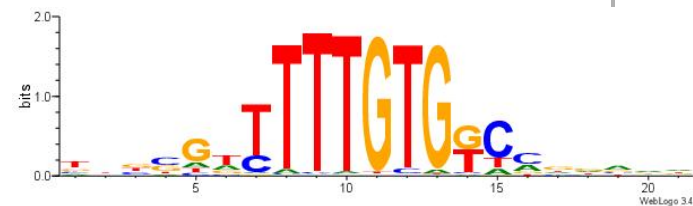
Original motif

Consensus sequence: HHBHHKGMCACAAAHCSDV



Reverse complement motif

Consensus sequence: BDVSGHTTTTGTGRCYDDVHH



Motif ID: [MA0395.1](#)  
Motif name: STP2  
Taxon: Fungi  
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: 0.103029

Alignment:

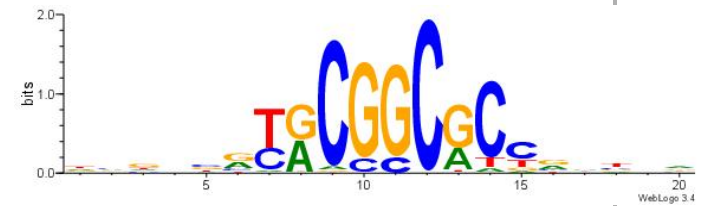
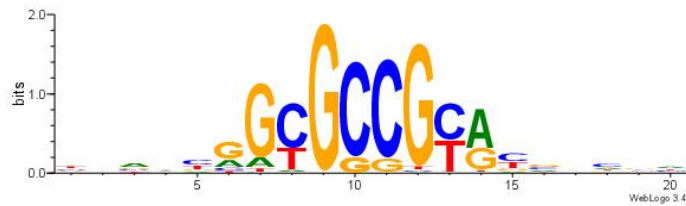
```
HVVHBGGCGCCGYRYVHHBH  
----SGGTCACGTGACCS--
```

Original motif

Consensus sequence: HVVHBGGCGCCGYRYVHHBH

Reverse complement motif

Consensus sequence: HBDHVKKKCGGCGCCBHBVH



**Dataset #: 4      Motif ID: 43      Motif name: wsTACwGTAsw**

Original motif

Consensus sequence: HVTACWGATABD



Reverse complement motif

Consensus sequence: DBTACWGTA VH



**Best Matches for Motif ID 43 (Highest to Lowest)**

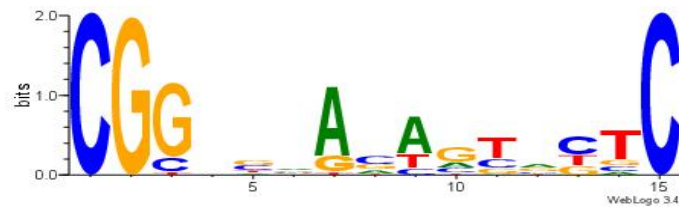
Motif ID:	<a href="#">MA0299.1</a>
Motif name:	GAL4
Taxon:	Fungi
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	4
Number of overlap:	11
Similarity score:	0.04133

Alignment:

GAKBACTVTBBHCCG  
-DBTACWGTAVH---

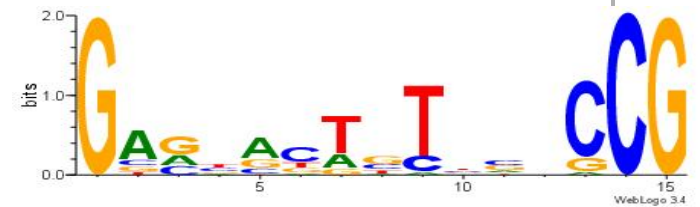
Original motif

Consensus sequence: CGGDBVAVAGTVYTC



Reverse complement motif

Consensus sequence: GAKBACTVTBBHCCG



Motif ID: [MA0296.1](#)  
Motif name: FKH1  
Taxon: Fungi  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Reverse Complement  
Direction: Backward  
Position number: 1  
Number of overlap: 11  
Similarity score: 0.0426543

Alignment:

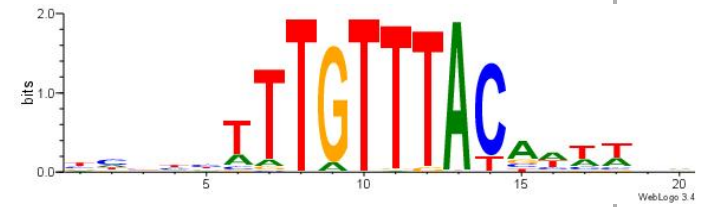
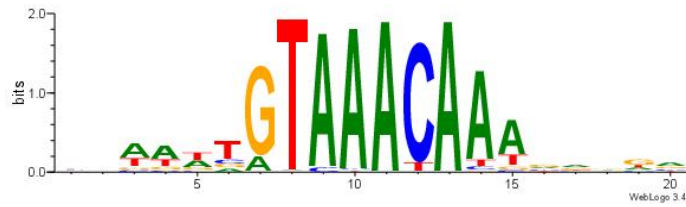
BHHDVTTTGTTCACAWWHV  
-----DBTACWGTAVH

Original motif

Consensus sequence: BDWWWTGTAAACAAVDDDDV

Reverse complement motif

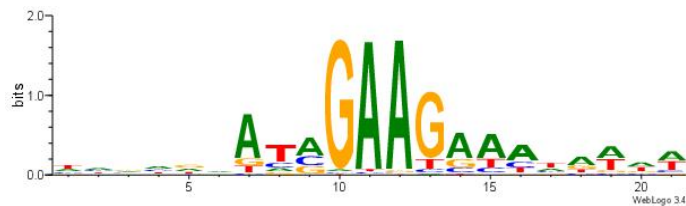
Consensus sequence: BHHDVTTTGTTCACAWWHV



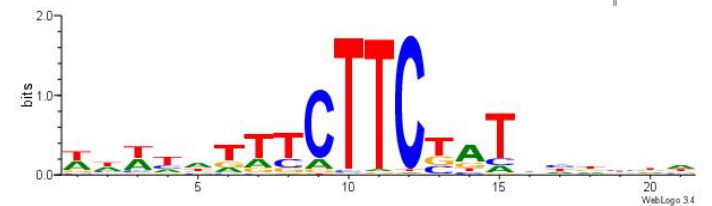
Motif ID: [MA0377.1](#)  
 Motif name: SFL1  
 Taxon: Fungi  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 8  
 Number of overlap: 11  
 Similarity score: 0.045564

Alignment:  
 HHVHDHATMGAAGAAHDWDW  
 ---HVTACWG TABD-----

Original motif  
 Consensus sequence: HHVHDHATMGAAGAAHDWDW



Reverse complement motif  
 Consensus sequence: WDWDHTTTCTTCYATHHHVHH



Motif ID: [MA0336.1](#)

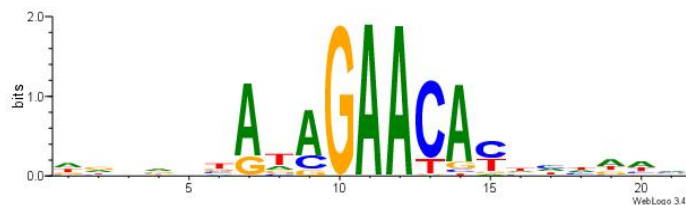
Motif name: MGA1  
 Taxon: Fungi  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 8  
 Number of overlap: 11  
 Similarity score: 0.0471974

**Alignment:**

BHDHDDKTGTTCTATVDBVHD  
 -----HVTACWGTTABD---

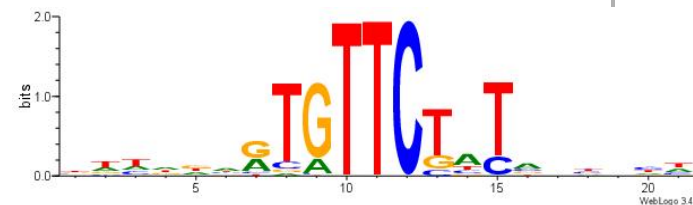
**Original motif**

Consensus sequence: DDVHBBATAGAACAYDHHDHV



**Reverse complement motif**

Consensus sequence: BHDHDDKTGTTCTATVDBVHD




---

Motif ID: [MA0345.1](#)  
 Motif name: NHP6A  
 Taxon: Fungi  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 10  
 Number of overlap: 11

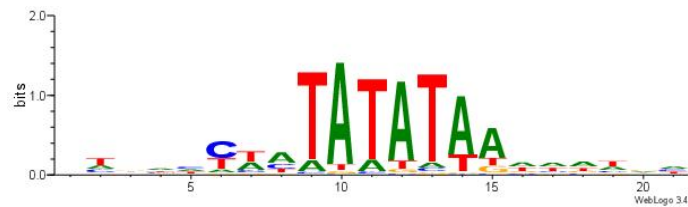
Similarity score: 0.0507352

Alignment:

```
HHHDDDTTATATAHWKDH H B  
-----DBTACWGTAVH-
```

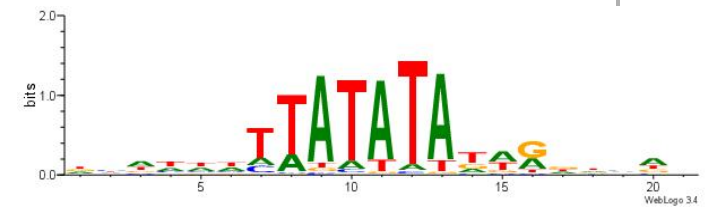
Original motif

Consensus sequence: VHDHHYWHTATATAADDDH D H



Reverse complement motif

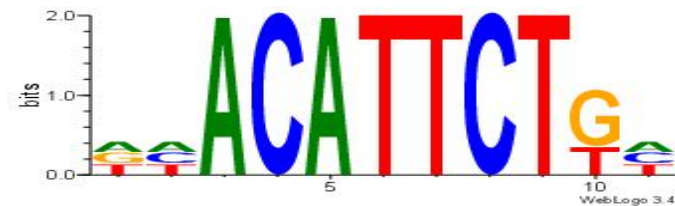
Consensus sequence: HHHDDDTTATATAHWKDH H B



**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:	<a href="#">MA0377.1</a>
Motif name:	SFL1
Taxon:	Fungi
Matching format of first motif:	Reverse Complement



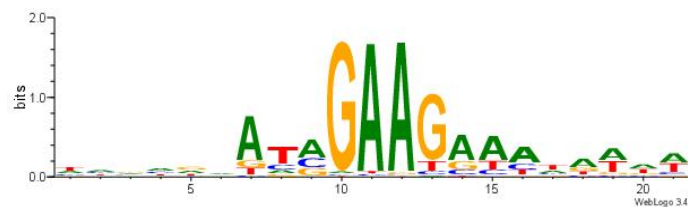
Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 5  
 Number of overlap: 11  
 Similarity score: 0.0436478

Alignment:

HHVHDHATMGAAGAAAHDWDW  
 -----HCAGAATGTHD-----

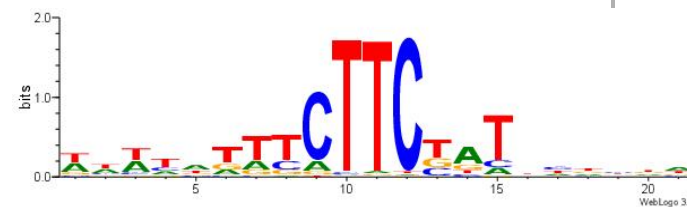
Original motif

Consensus sequence: HHVHDHATMGAAGAAAHDWDW



Reverse complement motif

Consensus sequence: WDWDHTTTCTTCYATHHHVHH




---

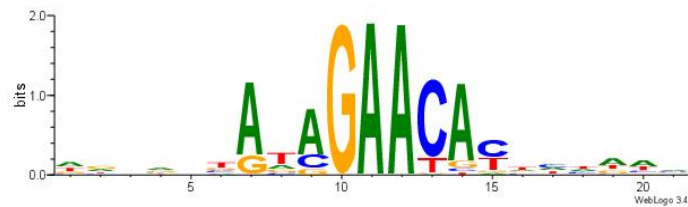
Motif ID: [MA0336.1](#)  
 Motif name: MGA1  
 Taxon: Fungi  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 7  
 Number of overlap: 11  
 Similarity score: 0.0439501

Alignment:

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

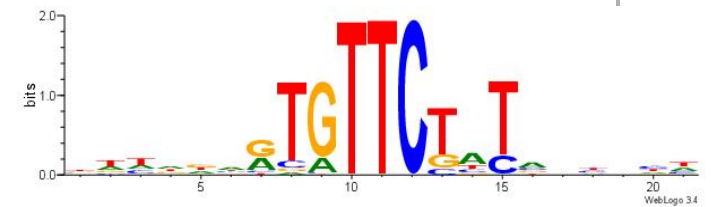
Original motif

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:

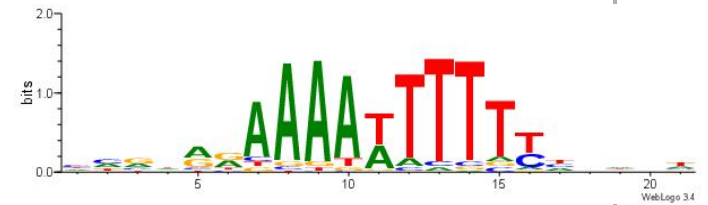
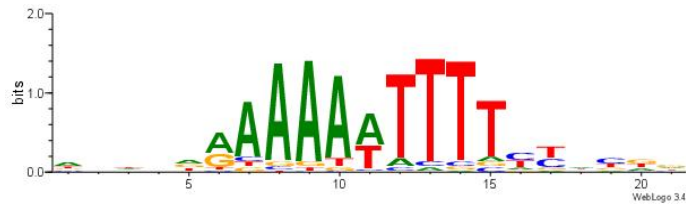
DHDDDRAAAWTTTTYYHBDD  
-----DHACATTCTGH-----

Original motif

Consensus sequence: DHDDDRAAAWTTTTYYHBDD

Reverse complement motif

Consensus sequence: HHBMKAAAATTTTKDHDHD



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--

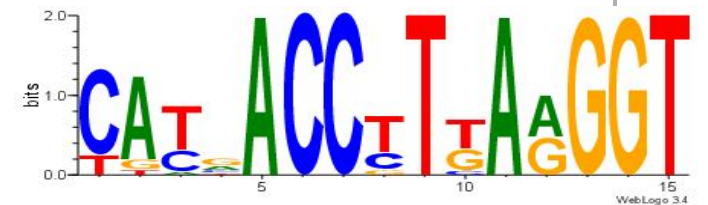
Original motif

Consensus sequence: ACCYTMAAGGTBATG



Reverse complement motif

Consensus sequence: CATBACCTTYAMGGT



Motif ID: [MA0345.1](#)

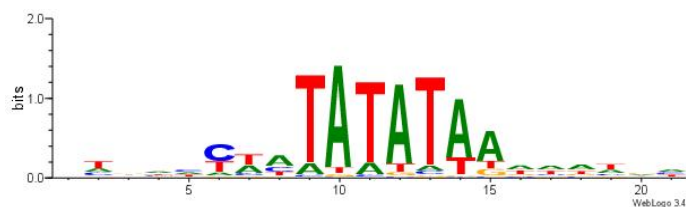
Motif name: NHP6A  
 Taxon: Fungi  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 5  
 Number of overlap: 11  
 Similarity score: 0.0504146

Alignment:

VHDHHYWHTATATAADDDHDH  
 ----HCAGAATGTHD-----

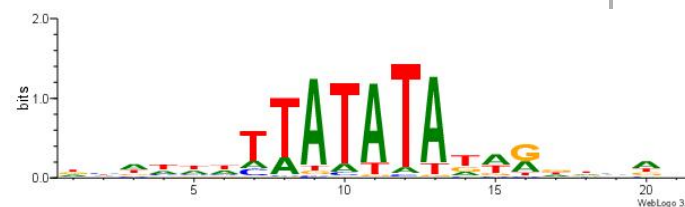
Original motif

Consensus sequence: VHDHHYWHTATATAADDDHDH



Reverse complement motif

Consensus sequence: HHHDDTTATATAHWKDHBB



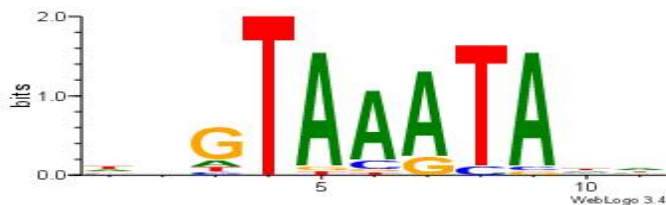
**Dataset #: 4      Motif ID: 45      Motif name: wbgTAAATAww**

Original motif

Consensus sequence: DBGTAATAHD

Reverse complement motif

Consensus sequence: DHTATTTACBD

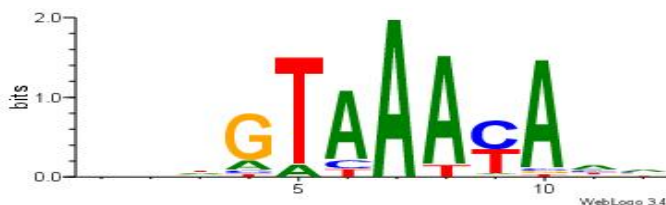


### Best Matches for Motif ID 45 (Highest to Lowest)

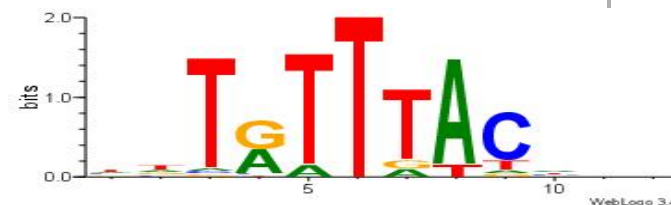
Motif ID: [MA0929.1](#)  
 Motif name: NCU00019  
 Taxon: Fungi  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 1  
 Number of overlap: 11  
 Similarity score: 0

Alignment:  
 DBDGTAAAYAHD  
 -DBGTAAATAHD

Original motif  
 Consensus sequence: DBDGTAAAYAHD



Reverse complement motif  
 Consensus sequence: BHTKTTTACDDB




---

Motif ID: [MA0345.1](#)

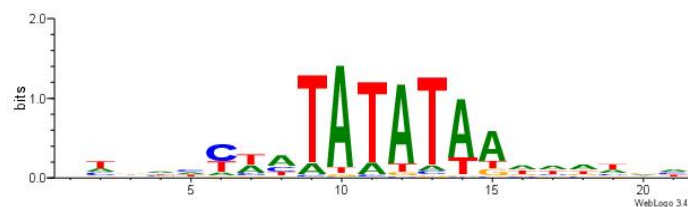
Motif name: NHP6A  
 Taxon: Fungi  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 5  
 Number of overlap: 11  
 Similarity score: 0.0222559

Alignment:

HHHDDDTTATATAHWKDHHHB  
 ----DBGTAAATAHD-----

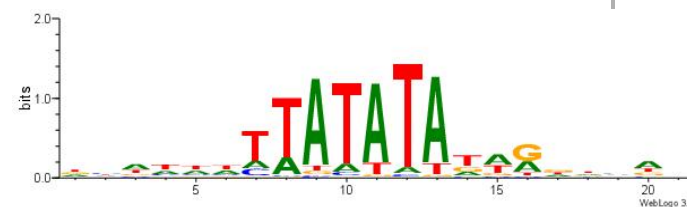
Original motif

Consensus sequence: VHDHHYWHTATATAADDDHDH



Reverse complement motif

Consensus sequence: HHHDDDTTATATAHWKDHHHB




---

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

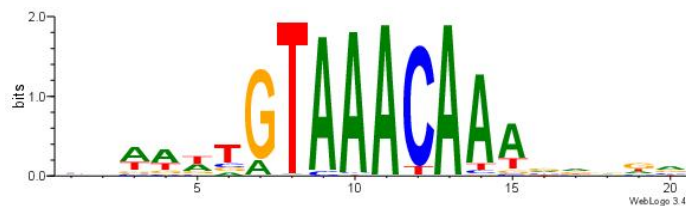
Similarity score: 0.024745

Alignment:

BDWWWTGTAAACAAVDDD  
----DBGTAAATAHD-----

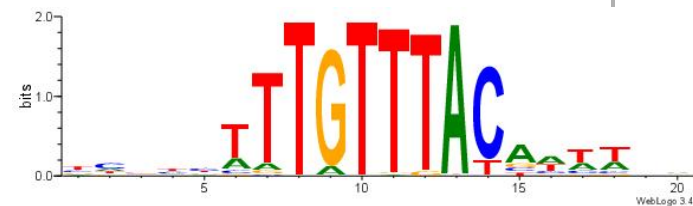
Original motif

Consensus sequence: BDWWWTGTAAACAAVDDD



Reverse complement motif

Consensus sequence: BHHDVTTTGTTCACAWWWHV



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:

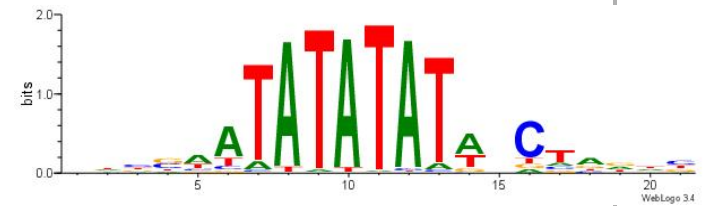
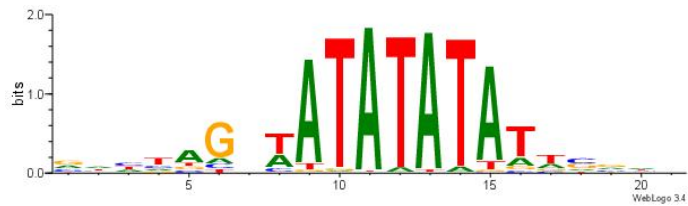
VHHHAGDWATATATATDSVHD  
-----DBGTAAATAHD-----

Original motif

Consensus sequence: VHHHAGDWATATATATDSVHD

Reverse complement motif

Consensus sequence: DHVSDATATATATWDCTHDHV



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

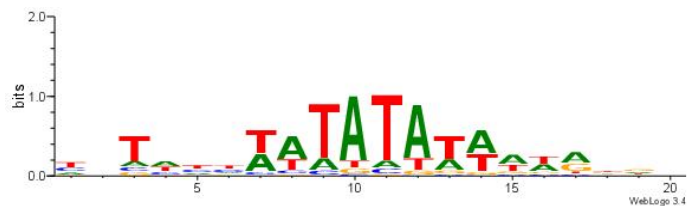
**Alignment:**

```

BHDKWWWATATATWHHHAHH
-----DHTATTTACBD----
  
```

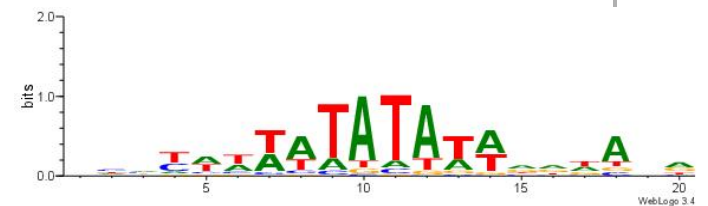
**Original motif**

Consensus sequence: HHTHHHWATATATWWWRRDDV



**Reverse complement motif**

Consensus sequence: BHDKWWWATATATWHHHAHH





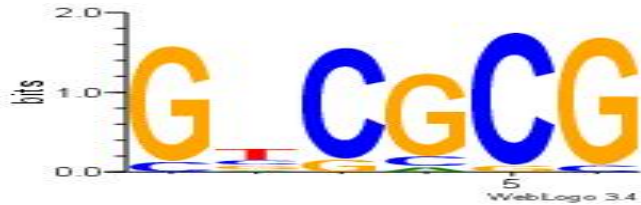
**Dataset #: 5**

**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: [MA0290.1](#)  
Motif name: DAL81  
Taxon: Fungi  
Matching format of first motif: Original Motif  
Matching format of second motif: Original Motif  
Direction: Backward  
Position number: 10  
Number of overlap: 6  
Similarity score: 0.0317132

Alignment:

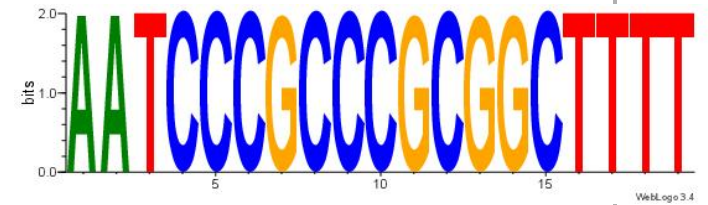
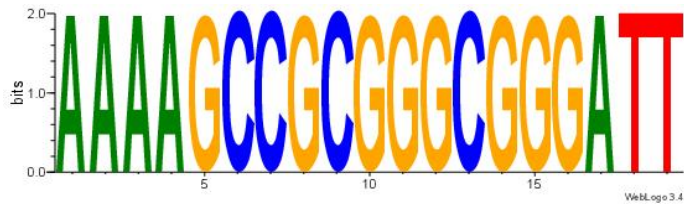
```
AAAAGCCGCGGGCGGGATT  
----GTCGCG-----
```

Original motif

Consensus sequence: AAAAGCCGCGGGCGGGATT

Reverse complement motif

Consensus sequence: AATCCCGCCGCGGCTTTT



Motif ID: [MA0374.1](#)  
 Motif name: RSC3  
 Taxon: Fungi  
 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: 0.035812

Alignment:  
 VVGCGCG  
 -GTCGCG

Original motif  
 Consensus sequence: CGCGCVV



Reverse complement motif  
 Consensus sequence: VVGCGCG



Motif ID: [MA0375.1](#)

Motif name: RSC30  
Taxon: Fungi  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Reverse Complement  
Direction: Backward  
Position number: 1  
Number of overlap: 6  
Similarity score: 0.0365344

Alignment:  
CGCGCGSV  
--CGCGAC

Original motif

Consensus sequence: VSCGCGCG



Reverse complement motif

Consensus sequence: CGCGCGSV



---

Motif ID: [MA0329.1](#)  
Motif name: MBP1  
Taxon: Fungi  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Original Motif  
Direction: Forward  
Position number: 2  
Number of overlap: 6  
Similarity score: 0.0377355

Alignment:  
ACGCGHH  
-CGCGAC

Original motif

Consensus sequence: ACGCGHH



Reverse complement motif

Consensus sequence: BHCGCGT



---

Motif ID:	<a href="#">MA0330.1</a>
Motif name:	MBP1::SWI6
Taxon:	Fungi
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	2
Number of overlap:	6
Similarity score:	0.0502588

Alignment:  
ACGCGTY  
-CGCGAC

Original motif

Consensus sequence: ACGCGTY

Reverse complement motif

Consensus sequence: MACGCGT



**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)

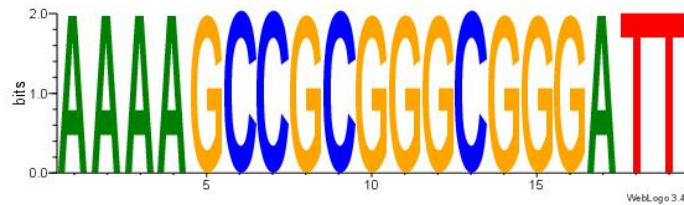
Motif ID:	<a href="#">MA0290.1</a>
Motif name:	DAL81
Taxon:	Fungi
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	5
Number of overlap:	8
Similarity score:	0.0420825

Alignment:

AATCCCGCCCGCGGCTTTT  
-----CCGCGCGS-----

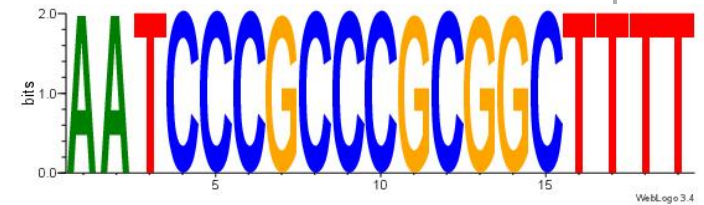
Original motif

Consensus sequence: AAAAGCCGCGGGCGGGATT



Reverse complement motif

Consensus sequence: AATCCCGCCCGCGGCTTTT



Motif ID: [MA0395.1](#)  
Motif name: STP2  
Taxon: Fungi  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Original Motif  
Direction: Forward  
Position number: 10  
Number of overlap: 8  
Similarity score: 0.0502501

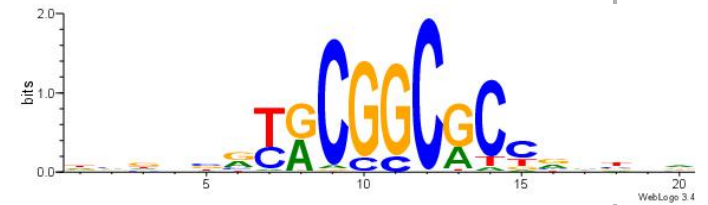
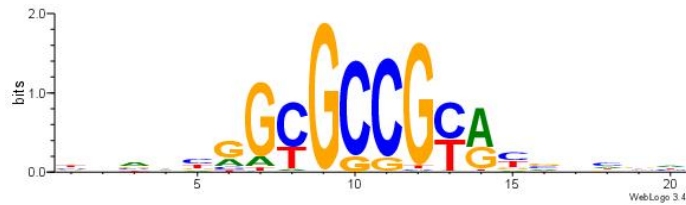
Alignment:  
HVVHBGGCGCCGYRYVHHBH  
-----CCGCGCGS----

Original motif

Consensus sequence: HVVHBGGCGCCGYRYVHHBH

Reverse complement motif

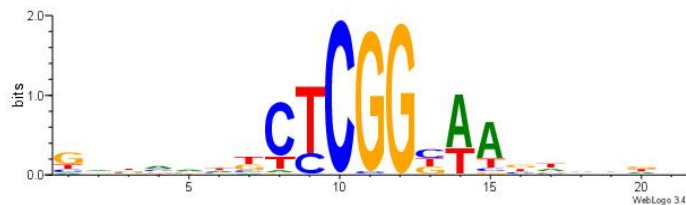
Consensus sequence: HBDHVKKKCGGCGCCBHBVH



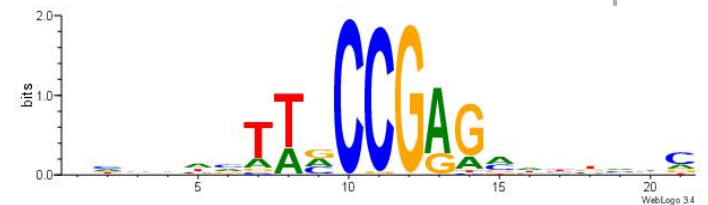
Motif ID: [MA0273.1](#)  
 Motif name: ARO80  
 Taxon: Fungi  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 5  
 Number of overlap: 8  
 Similarity score: 0.0651707

Alignment:  
 GVBVVKCTCGGBAABDHHDH  
 ----SCGCGCGG-----

Original motif  
 Consensus sequence: GVBVVKCTCGGBAABDHHDH



Reverse complement motif  
 Consensus sequence: HHHHDBTTCCGAGRHHBBVBC



Motif ID: [MA0357.1](#)

Motif name: PHO4  
Taxon: Fungi  
Matching format of first motif: Original Motif  
Matching format of second motif: Reverse Complement  
Direction: Forward  
Position number: 1  
Number of overlap: 8  
Similarity score: 0.0659131

Alignment:  
SCACGTGS  
SCGCGCGG

Original motif

Consensus sequence: SCACGTGS



Reverse complement motif

Consensus sequence: SCACGTGS



---

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: 6  
Number of overlap: 8



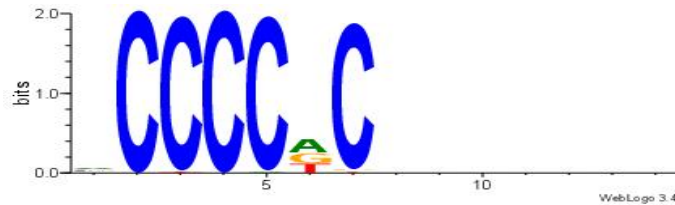
Similarity score: 0.0667998

Alignment:

VCCCCDCHHHDDDBD  
-CCGCGCGS-----

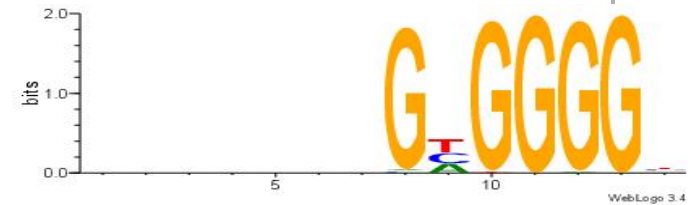
Original motif

Consensus sequence: VCCCCDCHHHDDDBD



Reverse complement motif

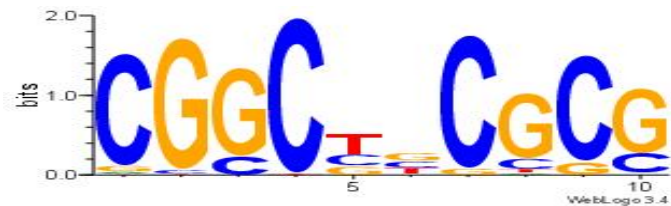
Consensus sequence: DBDDHHHGDGGGGG



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

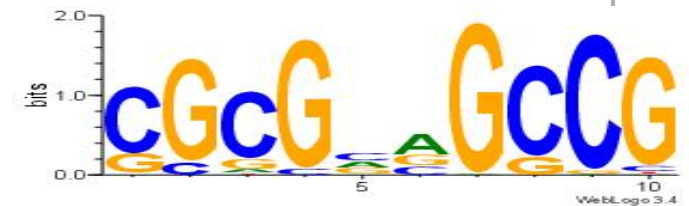
Original motif

Consensus sequence: CGGCYBCGCG



Reverse complement motif

Consensus sequence: CGCGBMGCCG



### Best Matches for Motif ID 48 (Highest to Lowest)

Motif ID: [MA0395.1](#)  
Motif name: STP2  
Taxon: Fungi  
Matching format of first motif: Original Motif

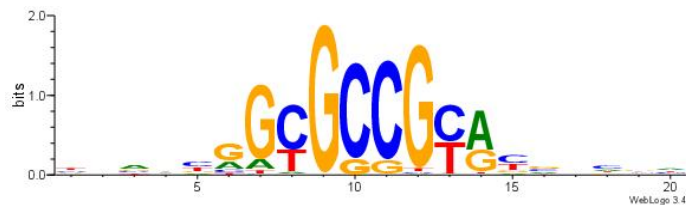
Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 3  
 Number of overlap: 10  
 Similarity score: 0.0494805

Alignment:

HBDHVKKKCGGCGCCBHBVH  
 -----CGGCYBCGCG--

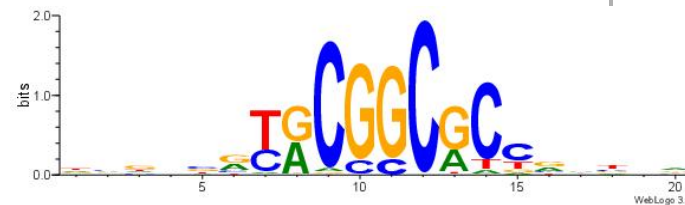
Original motif

Consensus sequence: HVVHBGGCGCCGYRYVHHBH



Reverse complement motif

Consensus sequence: HBDHVKKKCGGCGCCBHBVH



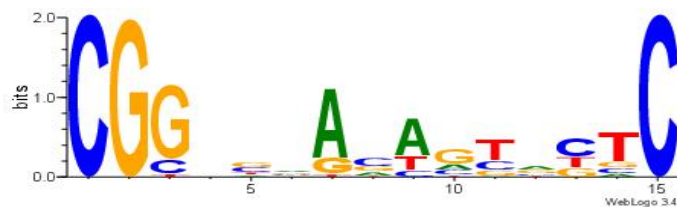
Motif ID: [MA0299.1](#)  
 Motif name: GAL4  
 Taxon: Fungi  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 1  
 Number of overlap: 10  
 Similarity score: 0.0660923

Alignment:

GAKBACTVTBBHCCG  
 -----CGCGBMGCCG

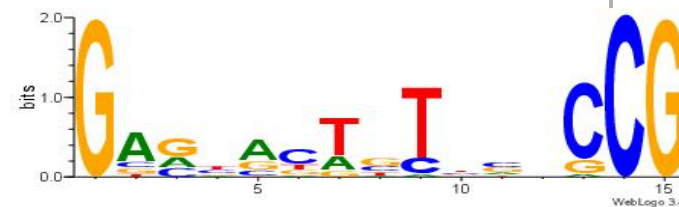
Original motif

Consensus sequence: CGGDBVAVAGTVYTC



Reverse complement motif

Consensus sequence: GAKBACTVTBBHCCG



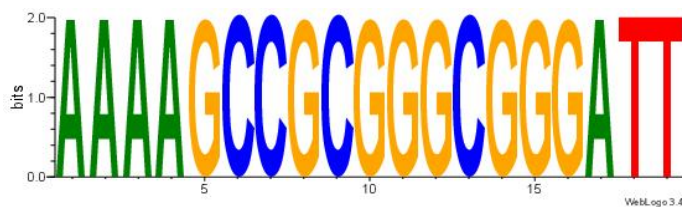
Motif ID: [MA0290.1](#)  
Motif name: DAL81  
Taxon: Fungi  
Matching format of first motif: Original Motif  
Matching format of second motif: Reverse Complement  
Direction: Backward  
Position number: 5  
Number of overlap: 10  
Similarity score: 0.0731045

Alignment:

```
AATCCCGCCCGGGCTTTT  
-----CGGCYBCGCG-----
```

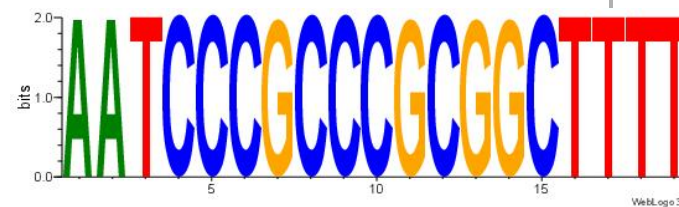
Original motif

Consensus sequence: AAAAGCCGCGGGCGGGATT



Reverse complement motif

Consensus sequence: AATCCCGCCCGGGCTTTT



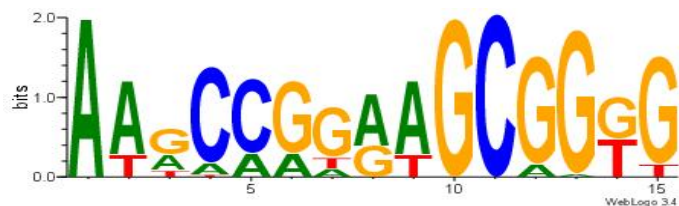
Motif ID: [MA0323.1](#)  
Motif name: IXR1  
Taxon: Fungi  
Matching format of first motif: Original Motif  
Matching format of second motif: Reverse Complement  
Direction: Forward  
Position number: 3  
Number of overlap: 10  
Similarity score: 0.0735542

Alignment:

```
CYCCGCTKCCGGMTT  
--CGGCYBCGCG---
```

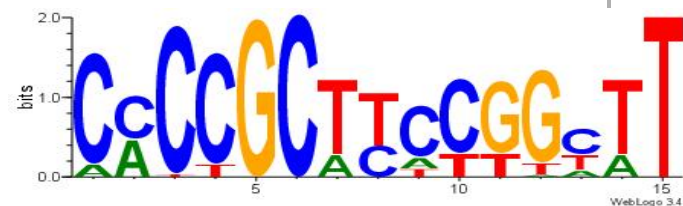
Original motif

Consensus sequence: AARCCGGRAGCGGKG



Reverse complement motif

Consensus sequence: CYCCGCTKCCGGMTT



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

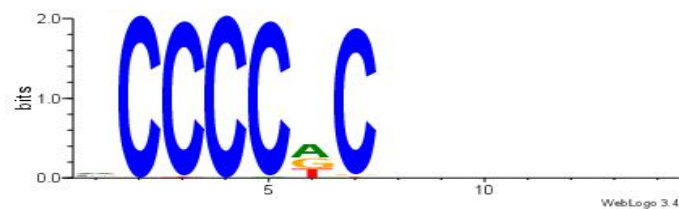
Position number: 4  
Number of overlap: 10  
Similarity score: 0.0830377

Alignment:

VCCCCDCHHHDDDBD  
---CGGCYBCGCG-

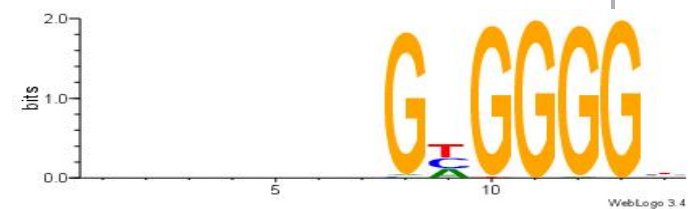
Original motif

Consensus sequence: VCCCCDCHHHDDDBD



Reverse complement motif

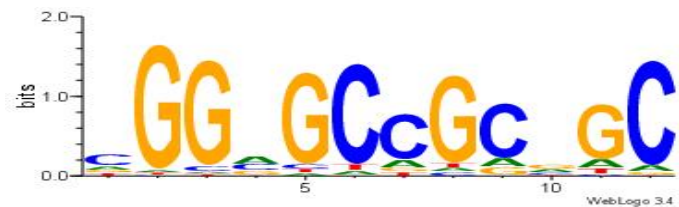
Consensus sequence: DBDDHHHGDGGGGG



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

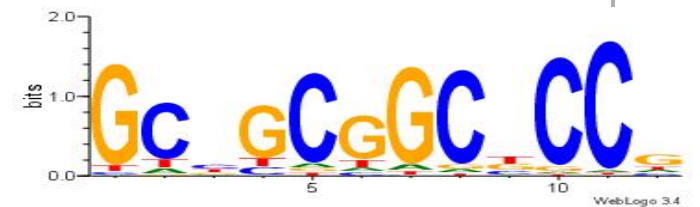
Original motif

Consensus sequence: CGGVGCCGCVGC



Reverse complement motif

Consensus sequence: GCVGCCGCBCCG



**Best Matches for Motif ID 49 (Highest to Lowest)**

Motif ID: [MA0395.1](#)  
Motif name: STP2

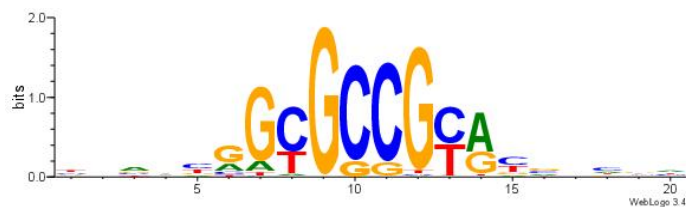
Taxon:	Fungi
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	5
Number of overlap:	12
Similarity score:	0.0423489

**Alignment:**

```
HVVHBGGCGCCGYRYVHHBH
----CGGVGCCGCVGC----
```

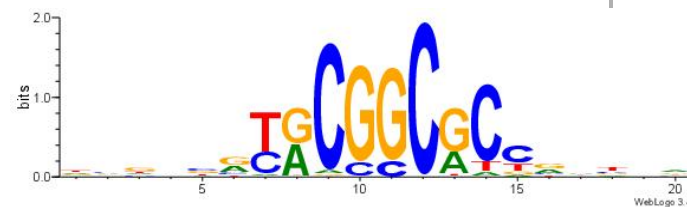
**Original motif**

Consensus sequence: HVVHBGGCGCCGYRYVHHBH



**Reverse complement motif**

Consensus sequence: HBDHVKKKCGGCGCCBHBVH




---

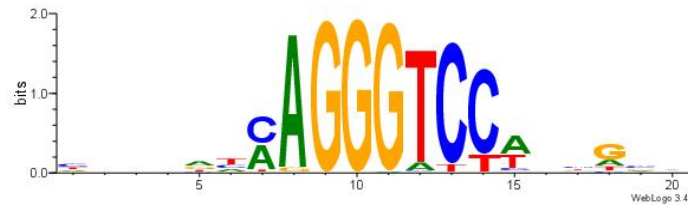
Motif ID:	<a href="#">MA0347.1</a>
Motif name:	NRG1
Taxon:	Fungi
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	2
Number of overlap:	12
Similarity score:	0.0692583

Alignment:

DVCBDWGGACCCTRHDVBHD  
-GCVGCGGCBCCG-----

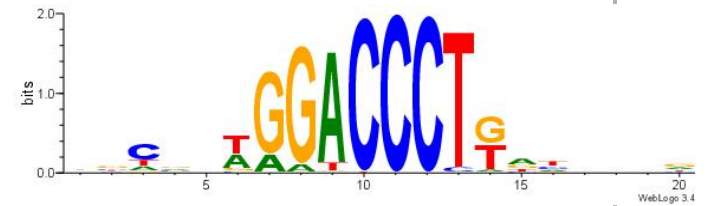
Original motif

Consensus sequence: HHVVDHMAGGGTCCWDBGVD



Reverse complement motif

Consensus sequence: DVCBDWGGACCCTRHDVBHD



Motif ID: [MA0308.1](#)  
Motif name: GSM1  
Taxon: Fungi  
Matching format of first motif: Original Motif  
Matching format of second motif: Reverse Complement  
Direction: Forward  
Position number: 2  
Number of overlap: 12  
Similarity score: 0.0733694

Alignment:

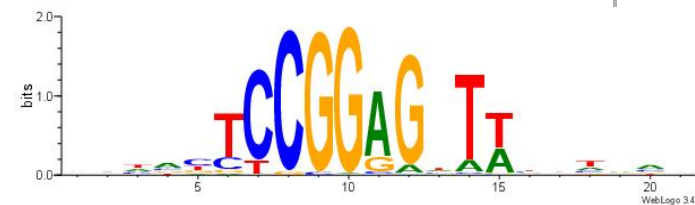
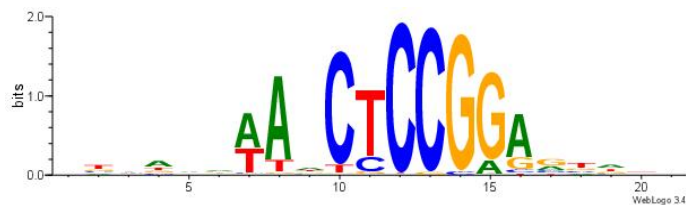
HDDVVTCCGGAGDTWDDDHVH  
-CGGVGCCGCVGC-----

Original motif

Consensus sequence: HBHDDDWADCTCCGGAVBDDH

Reverse complement motif

Consensus sequence: HDDVVTCCGGAGDTWDDDHVH

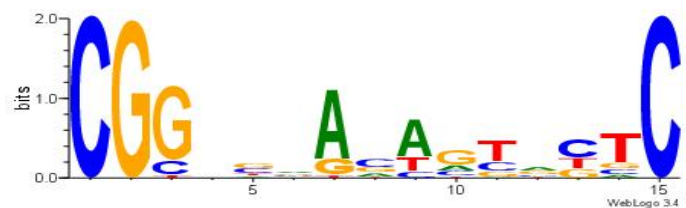


Motif ID: [MA0299.1](#)  
 Motif name: GAL4  
 Taxon: Fungi  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 4  
 Number of overlap: 12  
 Similarity score: 0.0735331

Alignment:  
 GAKBACTVTBBHCCG  
 ---GCVGCGGCBCCG

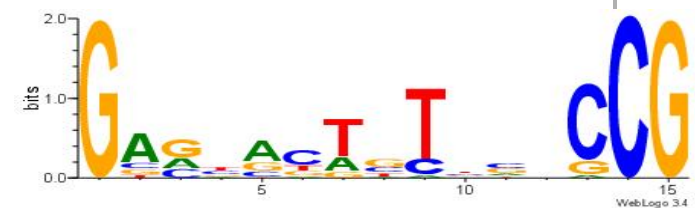
Original motif

Consensus sequence: CGGDBVAVAGTVYTC



Reverse complement motif

Consensus sequence: GAKBACTVTBBHCCG



Motif ID: [MA0273.1](#)



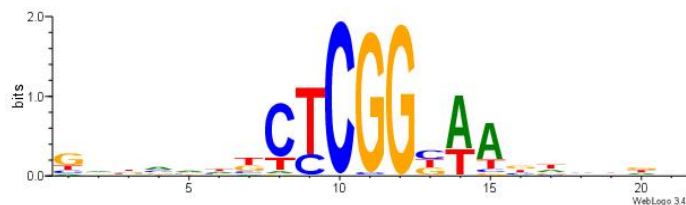
Motif name: ARO80  
 Taxon: Fungi  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 10  
 Number of overlap: 12  
 Similarity score: 0.074724

Alignment:

HHHHDBTTBCCGAGRHHBBVBC  
 -----CGGVGCCGCVGC

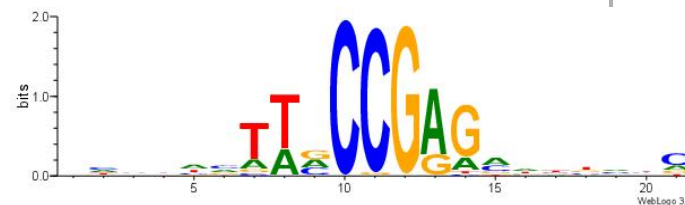
Original motif

Consensus sequence: GVBVHKCTCGGBAABDHHDH



Reverse complement motif

Consensus sequence: HHHHDBTTBCCGAGRHHBBVBC



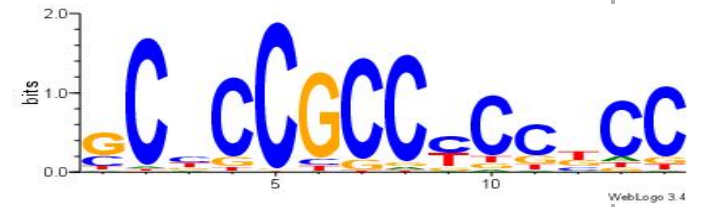
**Dataset #: 5      Motif ID: 50      Motif name: TFF11**

Original motif

Consensus sequence: GGMGGRGGCGGVGC

Reverse complement motif

Consensus sequence: GCVCCGCCMCCYCC

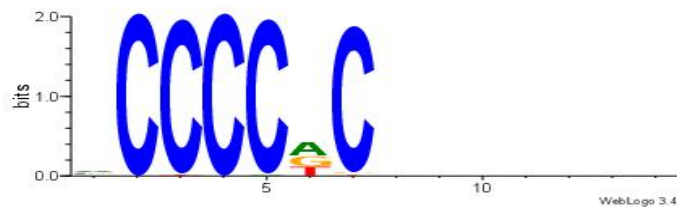


**Best Matches for Motif ID 50 (Highest to Lowest)**

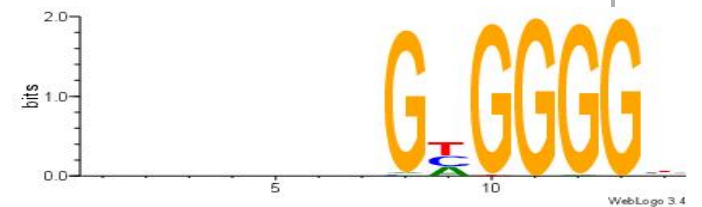
Motif ID: [MA0425.1](#)  
 Motif name: YGR067C  
 Taxon: Fungi  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 14  
 Similarity score: 0.0442772

Alignment:  
 VCCCCDCHHHDDDBD  
 GCVCCGCCMCCYCC

Original motif  
 Consensus sequence: VCCCCDCHHHDDDBD



Reverse complement motif  
 Consensus sequence: DBDDHHHGDGGGGG



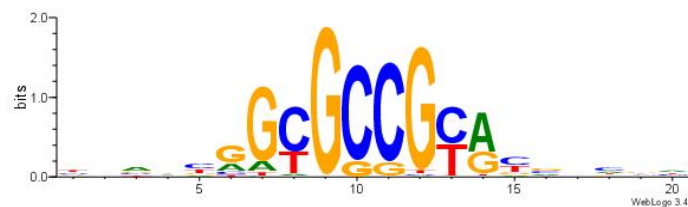
Motif ID: [MA0395.1](#)  
 Motif name: STP2  
 Taxon: Fungi  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 7  
 Number of overlap: 14  
 Similarity score: 0.0513557

**Alignment:**

HBDHVKKKCGGCGCCBHBVH  
 GGMGGRGGCGGVGC-----

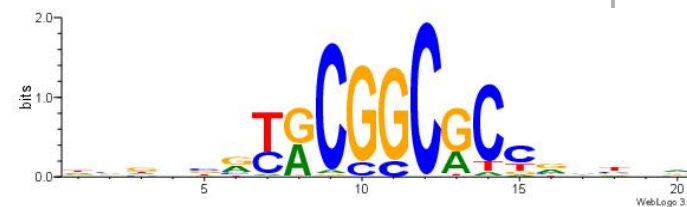
**Original motif**

Consensus sequence: HVVHBGGCGCCGYRYVHHBH



**Reverse complement motif**

Consensus sequence: HBDHVKKKCGGCGCCBHBVH



Motif ID: [MA0376.1](#)  
 Motif name: RTG3  
 Taxon: Fungi  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 7

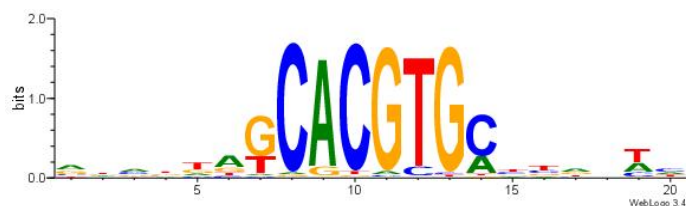
Number of overlap: 14  
Similarity score: 0.065682

Alignment:

VDVBDAGCACGTGCBBDVWH  
GGMGGRGGCGGVGC-----

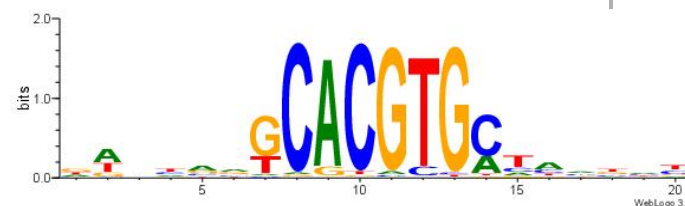
Original motif

Consensus sequence: VDVBDAGCACGTGCBBDVWH



Reverse complement motif

Consensus sequence: DWVDVVGACGTGCTDVBB



Motif ID: [MA0278.1](#)  
Motif name: BAS1  
Taxon: Fungi  
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: 0.0674206

Alignment:

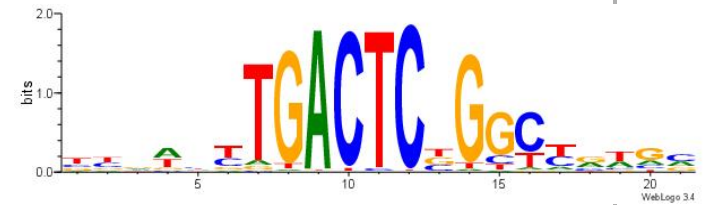
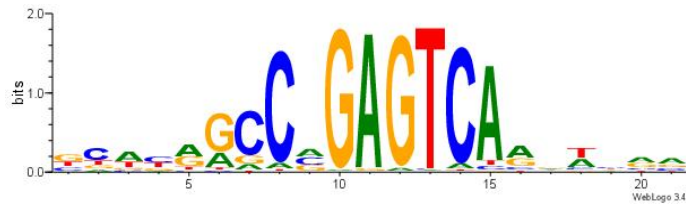
BBBWHKTGACTCBGGCKBWGB  
GCVCCGCCMCCYCC-----

Original motif

Consensus sequence: BCWBRGCCVAGTCARDWBVV

Reverse complement motif

Consensus sequence: BBBWHKTGACTCBGGCKBWGB



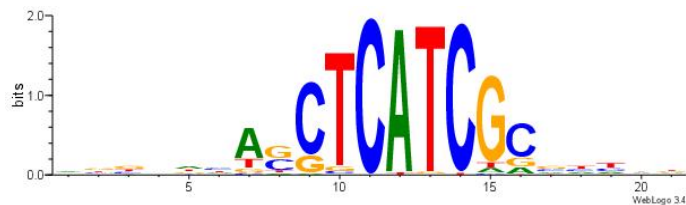
Motif ID: [MA0350.1](#)  
 Motif name: TOD6  
 Taxon: Fungi  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 8  
 Number of overlap: 14  
 Similarity score: 0.0684329

Alignment:

DHHHVCGGATGAGSTDDDBBD  
 GGMGGRGGCGGVGC-----

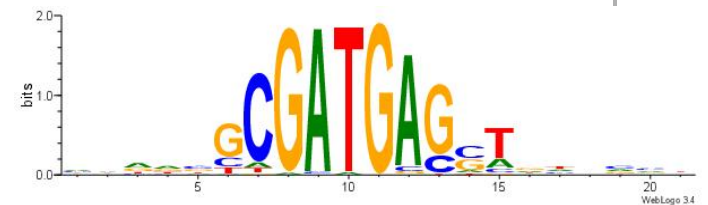
Original motif

Consensus sequence: DBBHDHASCTCATCGCVHHHD



Reverse complement motif

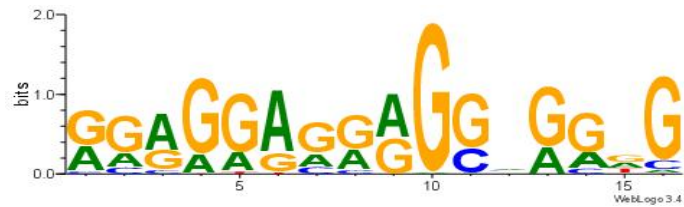
Consensus sequence: DHHHVCGGATGAGSTDDDBBD



**Dataset #: 5      Motif ID: 51      Motif name: TFM2**

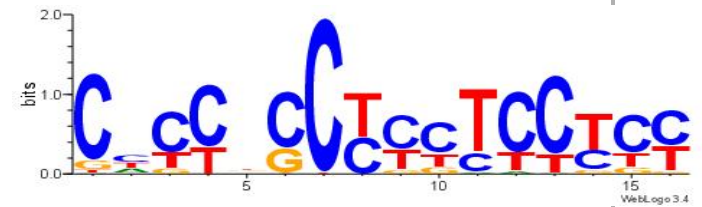
Original motif

Consensus sequence: RGRGGAGRRGGHGGDG



Reverse complement motif

Consensus sequence: CHCCBCKMCTCCKCM



### Best Matches for Motif ID 51 (Highest to Lowest)

Motif ID: [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: 3  
Number of overlap: 16  
Similarity score: 0.0415781

Alignment:

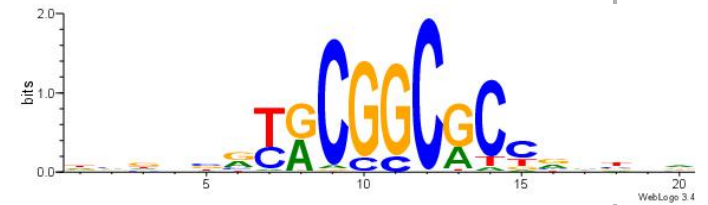
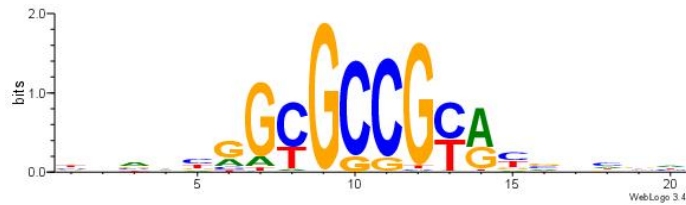
```
HBDHVKKKCGGCGCCBHBVH  
--CHCCBCKMCTCCKCM--
```

Original motif

Consensus sequence: HVVHBGGCGCCGYRYVHHBH

Reverse complement motif

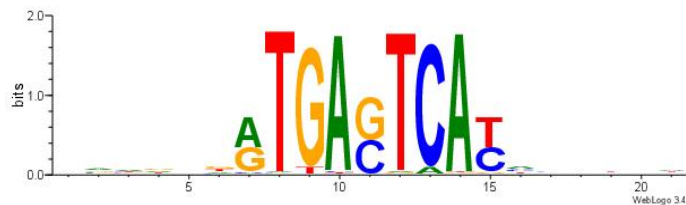
Consensus sequence: HBDHVKKKCGGCGCCBHBVH



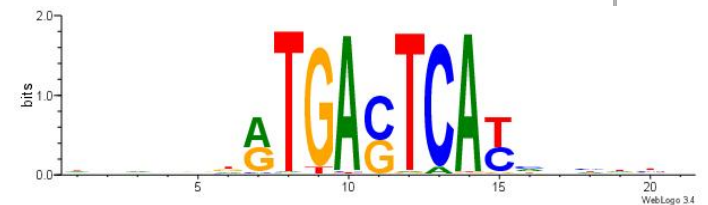
Motif ID: [MA0303.1](#)  
 Motif name: GCN4  
 Taxon: Fungi  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 2  
 Number of overlap: 16  
 Similarity score: 0.0417084

Alignment:  
 DVHHDHMTGASTCAKHHHHBB  
 -CHCCBCKMCTCCKCM----

Original motif  
 Consensus sequence: BVHDDDRTGASTCAYHHHHVD



Reverse complement motif  
 Consensus sequence: DVHHDHMTGASTCAKHHHHBB



Motif ID: [MA0351.1](#)

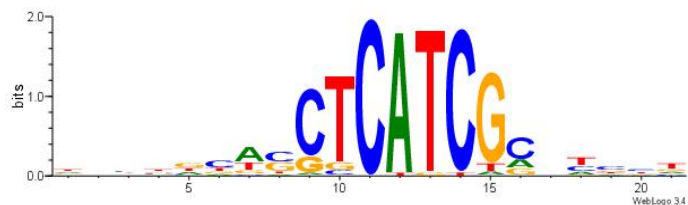
Motif name: DOT6  
 Taxon: Fungi  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 4  
 Number of overlap: 16  
 Similarity score: 0.0417741

**Alignment:**

DBBHBGCGATGAGSWBHVBVD  
 ---RGRGGAGRRGGHGGDG--

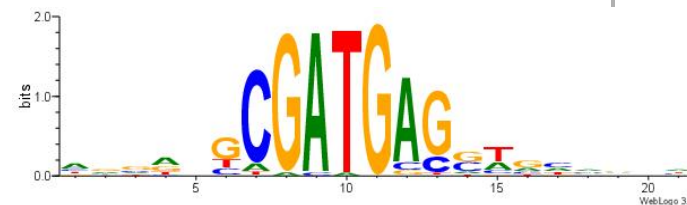
**Original motif**

Consensus sequence: DBBBDBWSCTCATCGCVHBB



**Reverse complement motif**

Consensus sequence: DBBHBGCGATGAGSWBHVBVD




---

Motif ID: [MA0350.1](#)  
 Motif name: TOD6  
 Taxon: Fungi  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 4  
 Number of overlap: 16



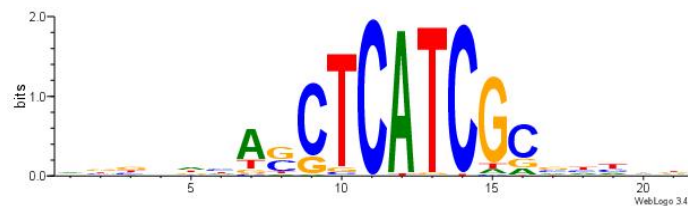
Similarity score: 0.0433269

Alignment:

DHHHVCGGATGAGSTDDDBBD  
---RGRGGAGRRGGHGGDG---

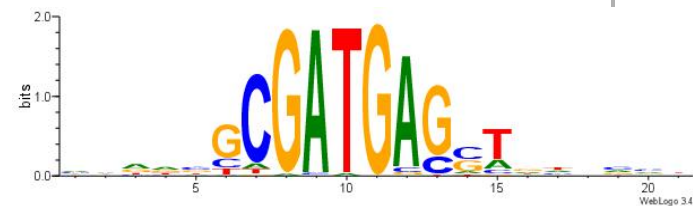
Original motif

Consensus sequence: DBBHDHASCTCATCGCVHHHD



Reverse complement motif

Consensus sequence: DHHHVCGGATGAGSTDDDBBD



Motif ID: [MA0377.1](#)  
Motif name: SFL1  
Taxon: Fungi  
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: 0.0500315

Alignment:

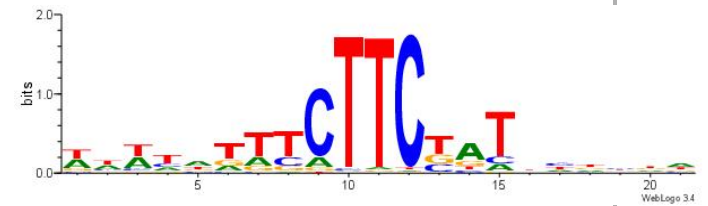
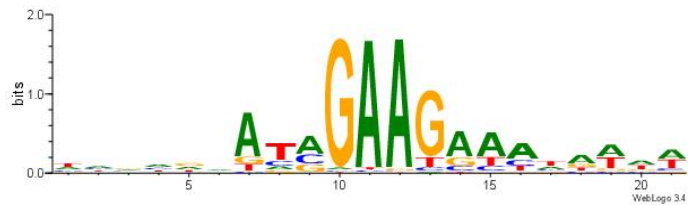
HHVHDHATMGAAGAAHDWDW  
---RGRGGAGRRGGHGGDG---

Original motif

Consensus sequence: HHVHDHATMGAAGAAHDWDW

Reverse complement motif

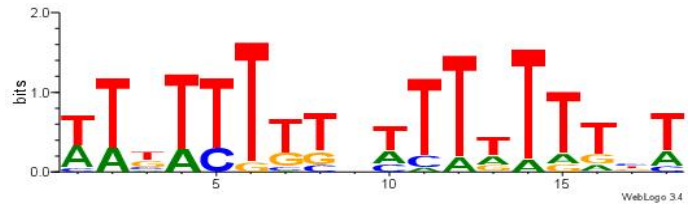
Consensus sequence: WDWDHTTTCTTCYATHHHVHH



**Dataset #: 5      Motif ID: 52      Motif name: TFM1**

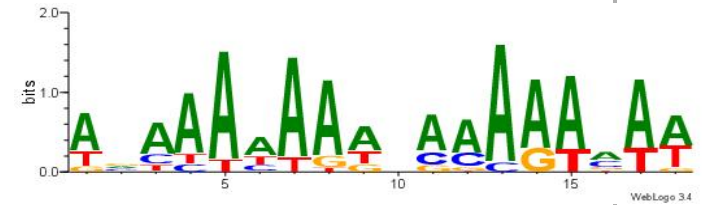
Original motif

Consensus sequence: WTKTTTTTHWTTTTTBT



Reverse complement motif

Consensus sequence: ABAAAAAWHAAAAARAW



**Best Matches for Motif ID 52 (Highest to Lowest)**

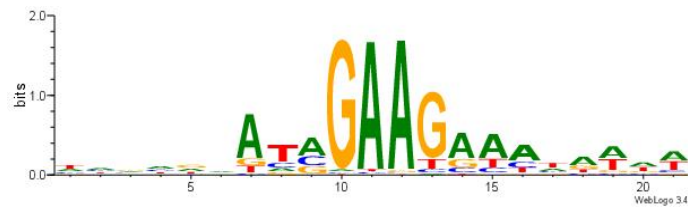
Motif ID:	<a href="#">MA0377.1</a>
Motif name:	SFL1
Taxon:	Fungi
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	4
Number of overlap:	18
Similarity score:	0.0314002

Alignment:

WDWDHTTTCTTCYATHHHVHH  
WKTTTTTHWTTTTTBT---

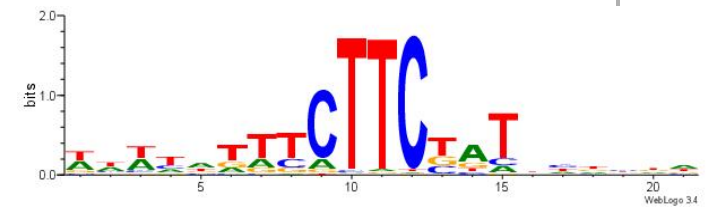
Original motif

Consensus sequence: HHVHDHATMGAAGAAAHDDWDW



Reverse complement motif

Consensus sequence: WDWDHTTTCTTCYATHHHVHH



Motif ID: [MA0346.1](#)  
Motif name: NHP6B  
Taxon: Fungi  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Reverse Complement  
Direction: Forward  
Position number: 3  
Number of overlap: 18  
Similarity score: 0.0404368

Alignment:

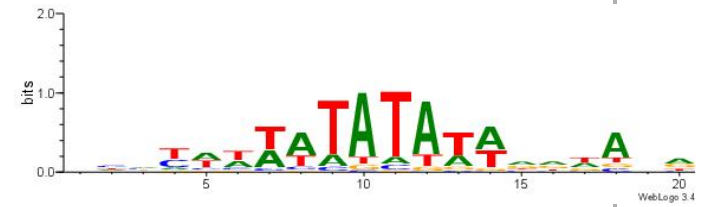
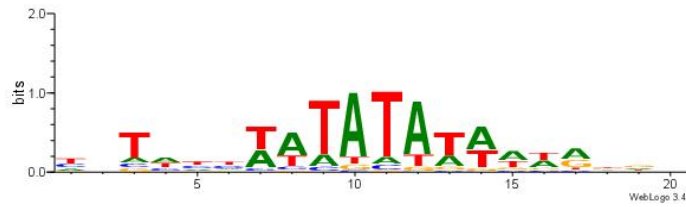
BHDKWWWATATATWHHHAHH  
--ABAAAAAAWHAAAAARAW

Original motif

Consensus sequence: HHTHHHWATATATWWWRRDDV

Reverse complement motif

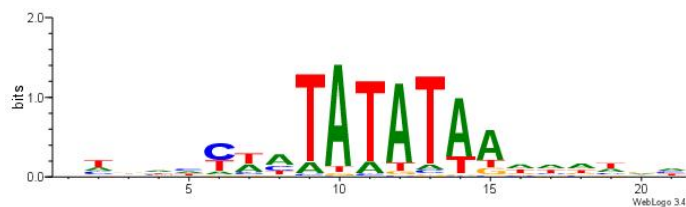
Consensus sequence: BHDKWWWATATATWHHHAHH



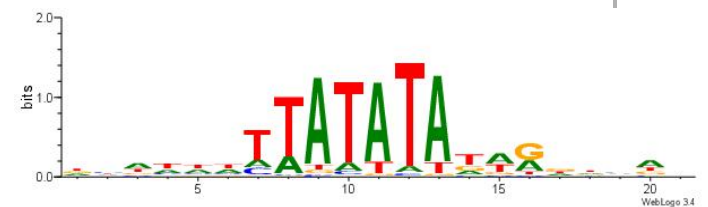
Motif ID: [MA0345.1](#)  
 Motif name: NHP6A  
 Taxon: Fungi  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 18  
 Similarity score: 0.0405522

Alignment:  
 HHHDDDTTATATAHWKDH H B  
 WKTTTTTTHWTTTTTBT ---

Original motif  
 Consensus sequence: VHDHHYWHTATATAADDDH D H



Reverse complement motif  
 Consensus sequence: HHHDDDTTATATAHWKDH H B



Motif ID: [MA0383.1](#)

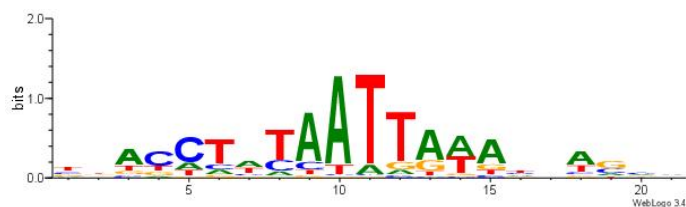
Motif name: SMP1  
 Taxon: Fungi  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 18  
 Similarity score: 0.0419477

**Alignment:**

BDACCTWTAATTAWAHBWVVD  
 WKTTTTTTHWTTTTTTTBT---

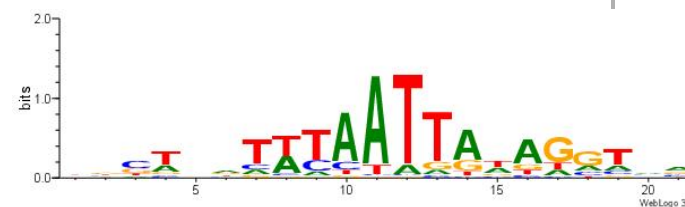
**Original motif**

Consensus sequence: BDACCTWTAATTAWAHBWVVD



**Reverse complement motif**

Consensus sequence: DVVWVHTWTAATTAWAGGTDV




---

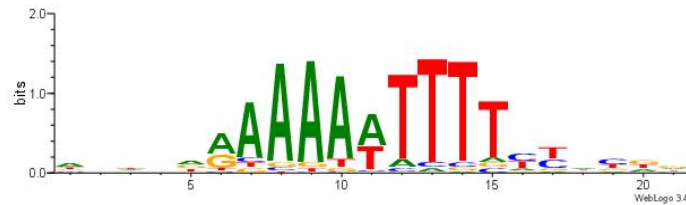
Motif ID: [MA0378.1](#)  
 Motif name: SFP1  
 Taxon: Fungi  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 18  
 Similarity score: 0.0436589

Alignment:

```
DHDDDRAAAAWTTTTYYHBDD  
WKTTTTTHWTTTTTBT---
```

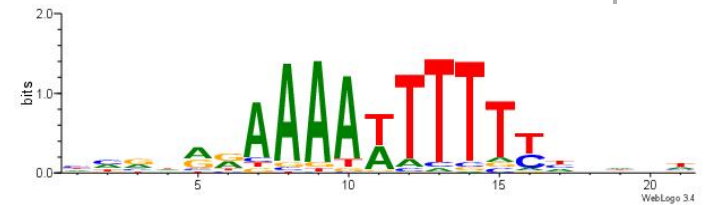
Original motif

Consensus sequence: DHDDDRAAAAWTTTTYYHBDD



Reverse complement motif

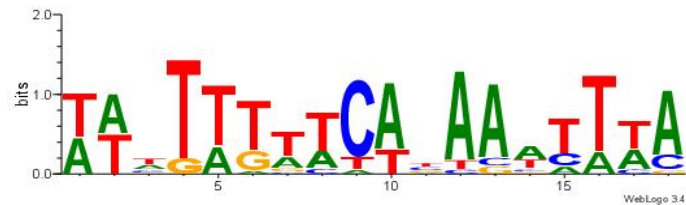
Consensus sequence: HHBMKAAAAWTTTTKDHDHD



**Dataset #: 5      Motif ID: 53      Motif name: TFM3**

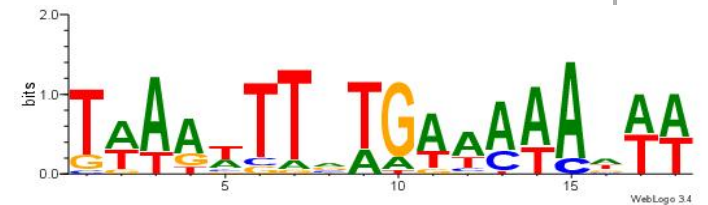
Original motif

Consensus sequence: WWHTTTTTCABAAWTTWA



Reverse complement motif

Consensus sequence: TAAWTTVTGAAAAHWW



### Best Matches for Motif ID 53 (Highest to Lowest)

Motif ID:	<a href="#">MA0346.1</a>
Motif name:	NHP6B
Taxon:	Fungi
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif

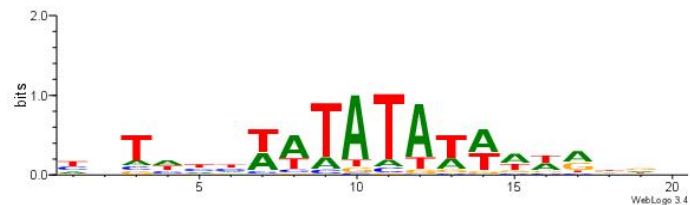
Direction: Forward  
Position number: 3  
Number of overlap: 18  
Similarity score: 0.0343553

Alignment:

HHTHHHWATATATWWWRDDV  
--TWAAWTTVTGAAAAHWW

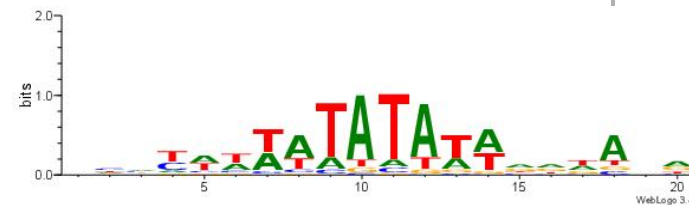
Original motif

Consensus sequence: HHTHHHWATATATWWWRDDV



Reverse complement motif

Consensus sequence: BHDKWWWATATATWHHHAAH



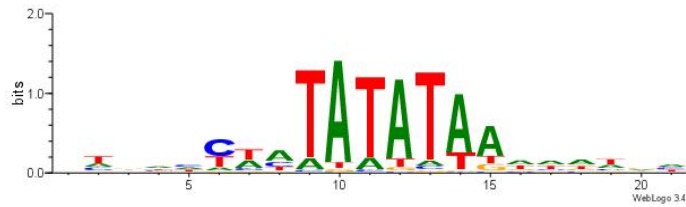
Motif ID: [MA0345.1](#)  
Motif name: NHP6A  
Taxon: Fungi  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Original Motif  
Direction: Forward  
Position number: 3  
Number of overlap: 18  
Similarity score: 0.0370702

Alignment:

VHDHHYWHTATATAADDDHDH  
--TWAAWTTVTGAAAAHWW-

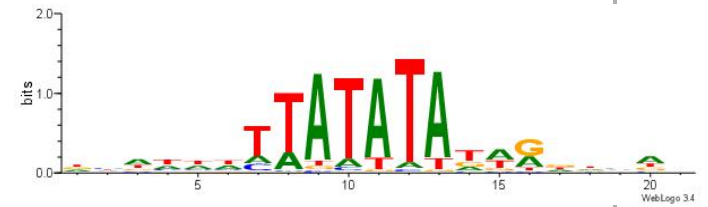
Original motif

Consensus sequence: VHDHHYWHTATATAADDDHDH



Reverse complement motif

Consensus sequence: HHHDDTTATATAHWKDH H B



Motif ID: [MA0377.1](#)  
Motif name: SFL1  
Taxon: Fungi  
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: 0.0412997

Alignment:

HHVHDHATMGAAGAAHDWDW  
WWHTTTTTCABAAWTTWA---

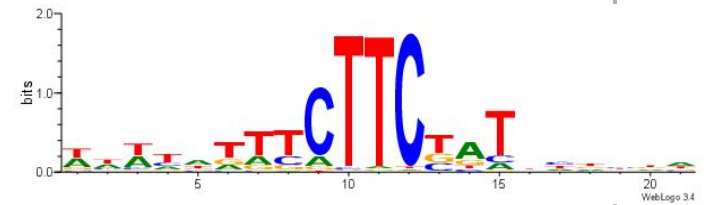
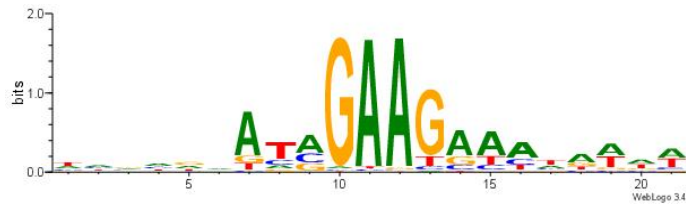
Original motif

Consensus sequence: HHVHDHATMGAAGAAHDWDW

Reverse complement motif

Consensus sequence: WDWDHTTTCTTCYATHHHVHH

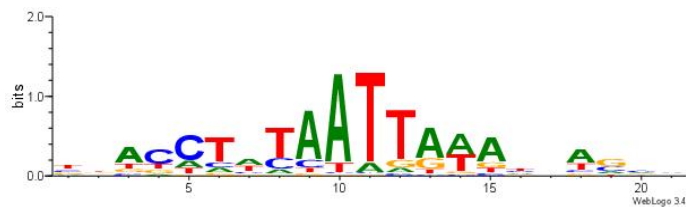




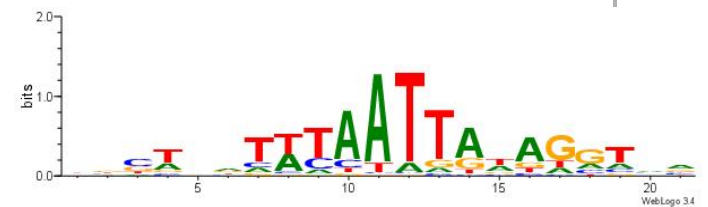
Motif ID: [MA0383.1](#)  
 Motif name: SMP1  
 Taxon: Fungi  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 1  
 Number of overlap: 18  
 Similarity score: 0.0471804

Alignment:  
 BDACCTWTAATTAWAHBWVVD  
 ---WWHTTTTTTCABAATTWA

Original motif  
 Consensus sequence: BDACCTWTAATTAWAHBWVVD



Reverse complement motif  
 Consensus sequence: DVVWVHTWTAATTAWAGGTDV



Motif ID: [MA0418.1](#)  
 Motif name: YAP6

Taxon:	Fungi
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	3
Number of overlap:	18
Similarity score:	0.0519178

**Alignment:**

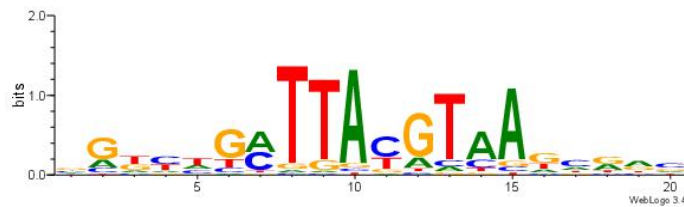
```

VDMDYTTACKTAAYCHKRCV
WWHTTTTTTCABAAWTTWA--

```

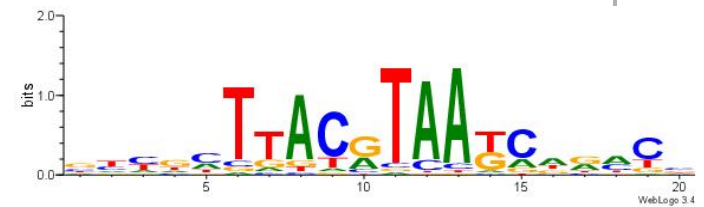
**Original motif**

Consensus sequence: VGKYHGMTTAYGTAAKHRDV



**Reverse complement motif**

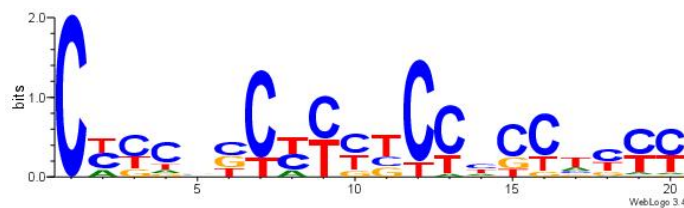
Consensus sequence: VDMDYTTACKTAAYCHKRCV



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

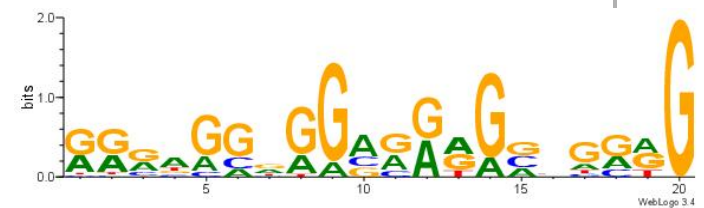
**Original motif**

Consensus sequence: CYYCBBYYYTCCHCCTYYY



**Reverse complement motif**

Consensus sequence: KKKAGGDGGAKKMGBBGKMG



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

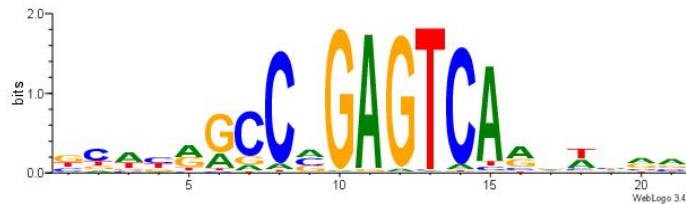
Motif ID: [MA0278.1](#)  
Motif name: BAS1  
Taxon: Fungi  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Reverse Complement  
Direction: Forward  
Position number: 1  
Number of overlap: 20  
Similarity score: 0.0588509

### Alignment:

BBBWHKTGACTCBGGCKBWGB  
KKKAGGDGGAKKMGBBGKMG-

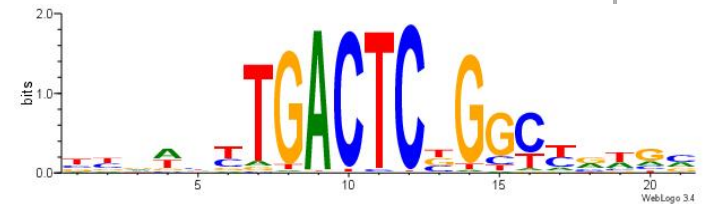
### Original motif

Consensus sequence: BCWBRGCCV GAGTCARDWBVV



### Reverse complement motif

Consensus sequence: BBBWHKTGACTCBGGCKBWGB



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Motif ID: [MA0303.1](#)  
Motif name: GCN4  
Taxon: Fungi  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Original Motif  
Direction: Forward  
Position number: 1

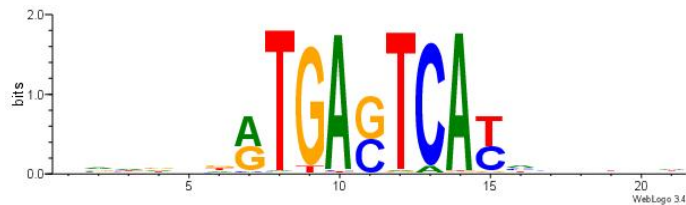
Number of overlap: 20  
Similarity score: 0.060319

**Alignment:**

DVHHDHMTGASTCAKHHHHBB  
KKKAGGDGGAKKMGBBGKMG-

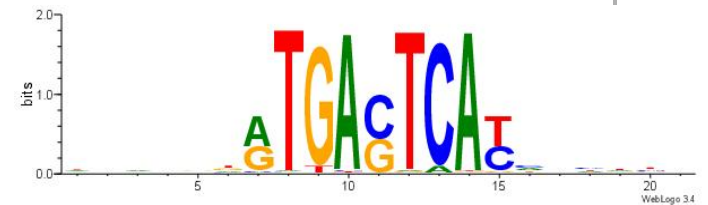
**Original motif**

Consensus sequence: BVHDDDRTGASTCAYHHHHVD



**Reverse complement motif**

Consensus sequence: DVHHDHMTGASTCAKHHHHBB



Motif ID: [MA0395.1](#)  
Motif name: STP2  
Taxon: Fungi  
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: 0.0604525

**Alignment:**

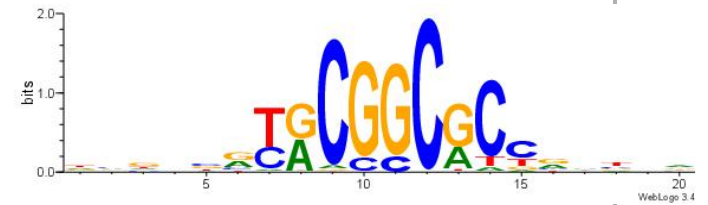
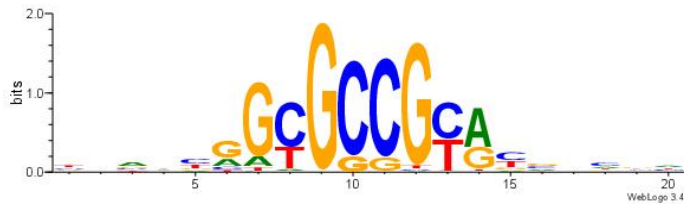
HVVHBGGCGCCGYRYVHHBH  
CYYCBBCYYYTCCHCCTYYY

**Original motif**

Consensus sequence: HVVHBGGCGCCGYRYVHHBH

**Reverse complement motif**

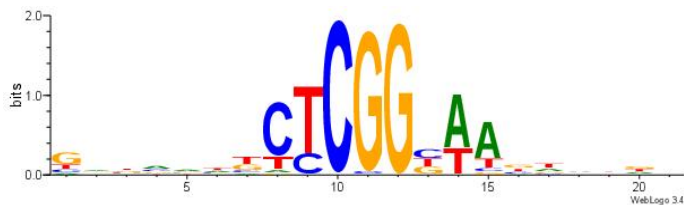
Consensus sequence: HBDHVKKKCGGCGCCBHBVH



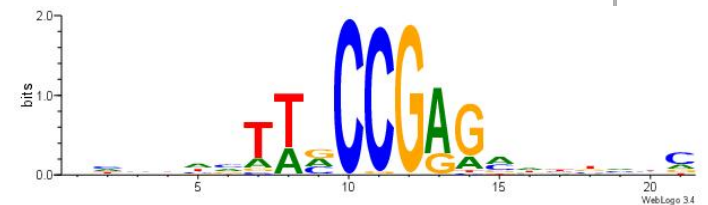
Motif ID: [MA0273.1](#)  
 Motif name: ARO80  
 Taxon: Fungi  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 2  
 Number of overlap: 20  
 Similarity score: 0.0624127

Alignment:  
 HHHHDBTTBCCGAGRHHBBVBC  
 KKKAGGDGGAKKMGBBGKMG-

Original motif  
 Consensus sequence: GVBVHKCTCGGBAABDHHDH



Reverse complement motif  
 Consensus sequence: HHHHDBTTBCCGAGRHHBBVBC



Motif ID: [MA0377.1](#)

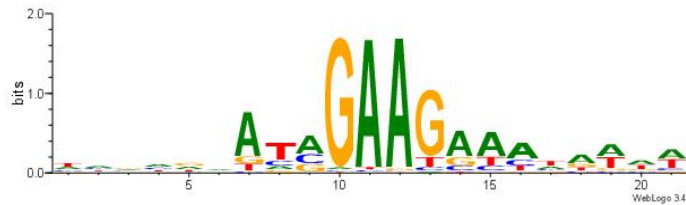
Motif name: SFL1  
 Taxon: Fungi  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 20  
 Similarity score: 0.0630527

**Alignment:**

HHVHDHATMGAAGAAHDWDW  
 CYYCBBCYYYTCCHCCTYYY-

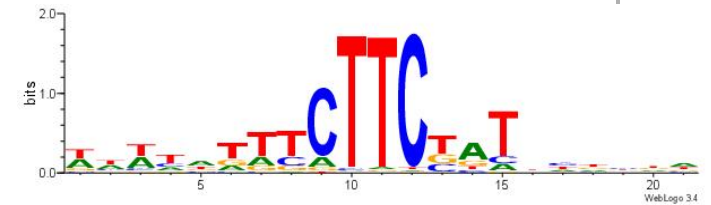
**Original motif**

Consensus sequence: HHVHDHATMGAAGAAHDWDW



**Reverse complement motif**

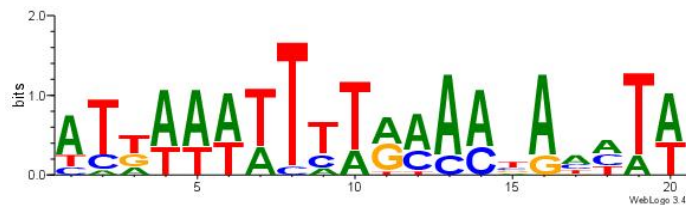
Consensus sequence: WDWHTTTCTTCYATHHHVHH



**Dataset #: 5      Motif ID: 55      Motif name: TFM13**

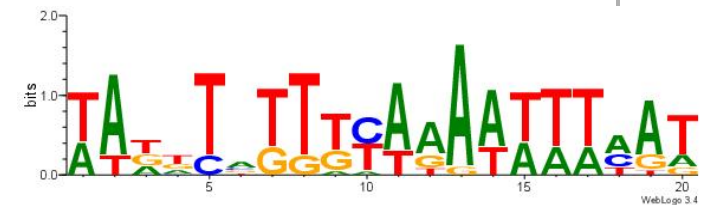
**Original motif**

Consensus sequence: ATKAAWTTTTRMAABAHTW



**Reverse complement motif**

Consensus sequence: WAHHTVTTYKAAAATTRAT



## Best Matches for Motif ID 55 (Highest to Lowest)

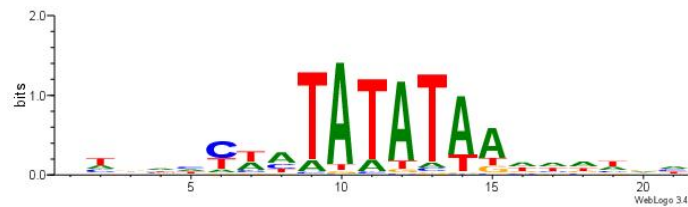
Motif ID: [MA0345.1](#)  
Motif name: NHP6A  
Taxon: Fungi  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Original Motif  
Direction: Backward  
Position number: 1  
Number of overlap: 20  
Similarity score: 0.0402024

### Alignment:

```
VHDHHYWHTATATAADDDHDH  
-WAHHTVTTYKAAAATTRAT
```

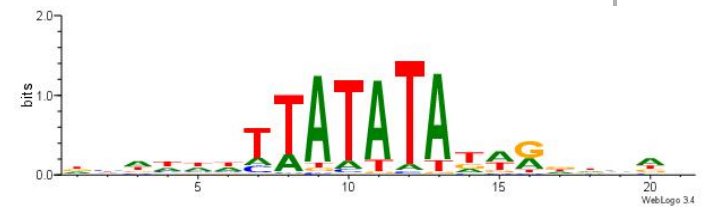
### Original motif

Consensus sequence: VHDHHYWHTATATAADDDHDH



### Reverse complement motif

Consensus sequence: HHHDDTTATATAHWKDH H B



---

Motif ID: [MA0377.1](#)  
Motif name: SFL1  
Taxon: Fungi  
Matching format of first motif: Reverse Complement

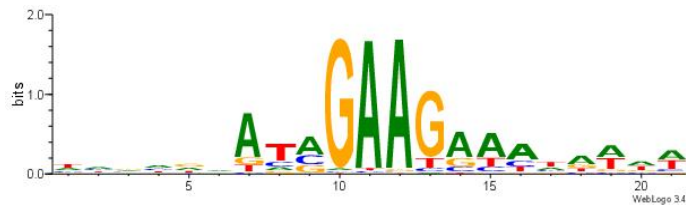
Matching format of second motif: Original Motif  
Direction: Backward  
Position number: 2  
Number of overlap: 20  
Similarity score: 0.0437557

Alignment:

HHVHDHATMGAAGAAHDWDW  
WAHHTVTTYKAAAATTRAT-

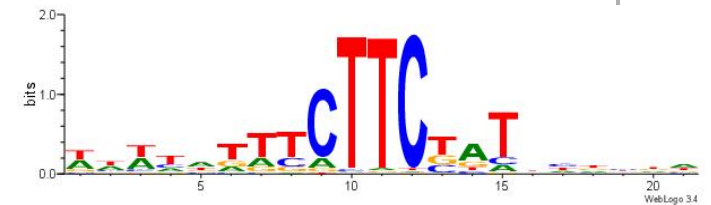
Original motif

Consensus sequence: HHVHDHATMGAAGAAHDWDW



Reverse complement motif

Consensus sequence: WDWDHTTTCTTCYATHHHVHH



---

Motif ID: [MA0383.1](#)  
Motif name: SMP1  
Taxon: Fungi  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Original Motif  
Direction: Forward  
Position number: 2  
Number of overlap: 20  
Similarity score: 0.0465576

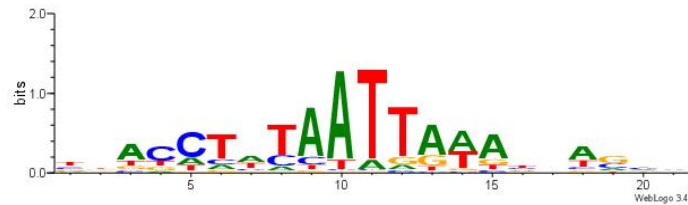
Alignment:



BDACCTWTAATTAWAHBWVVD  
-WAHHTVTTYKAAAATTRAT

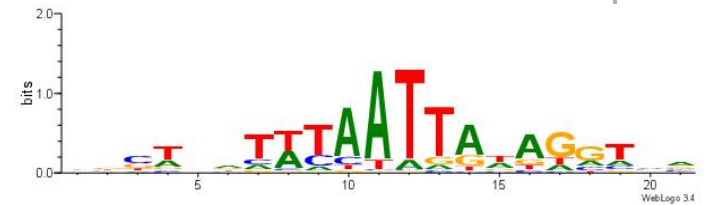
Original motif

Consensus sequence: BDACCTWTAATTAWAHBWVVD



Reverse complement motif

Consensus sequence: DVVWVHTWTAATTAWAGGTDV



Motif ID: [MA0390.1](#)  
Motif name: STB3  
Taxon: Fungi  
Matching format of first motif: Original Motif  
Matching format of second motif: Original Motif  
Direction: Forward  
Position number: 2  
Number of overlap: 20  
Similarity score: 0.0479924

Alignment:

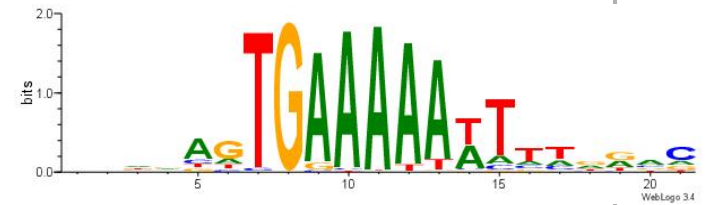
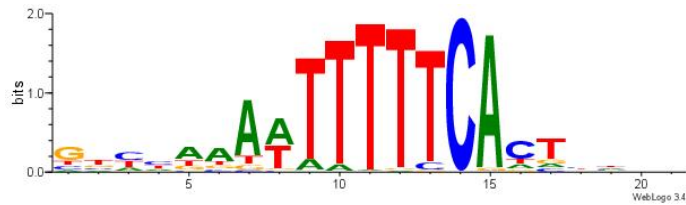
GBYHAAWTTTTCTACTBHDD  
-ATKAAWTTTTTRMAABAHTW

Original motif

Consensus sequence: GBYHAAWTTTTCTACTBHDD

Reverse complement motif

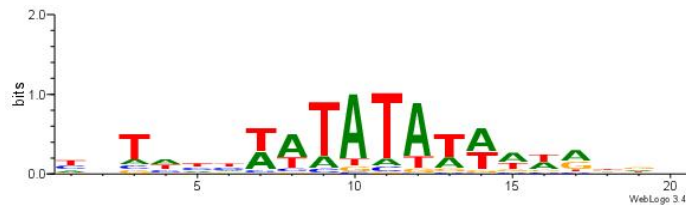
Consensus sequence: HHHBAGTGAAAAWTTTDDKVC



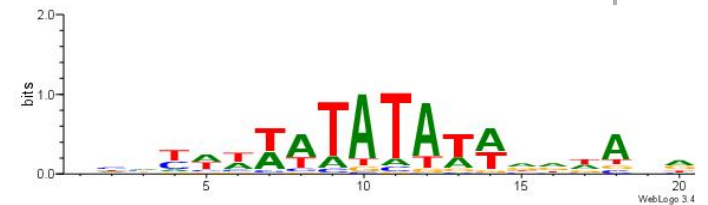
Motif ID: [MA0346.1](#)  
 Motif name: NHP6B  
 Taxon: Fungi  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 20  
 Similarity score: 0.0485472

Alignment:  
 HHTHHHWATATATWWWRDDV  
 ATKAAWTTTTRMAABAHHTW

Original motif  
 Consensus sequence: HHTHHHWATATATWWWRDDV



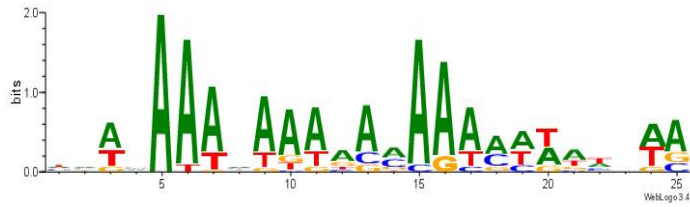
Reverse complement motif  
 Consensus sequence: BHDKWWWATATATWHHHAHH



**Dataset #: 5      Motif ID: 56      Motif name: TFM11**

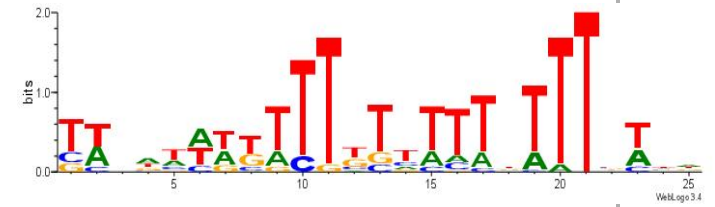
Original motif

Consensus sequence: HDWVAAAHAAAAAMAAAMWWWHBWA



Reverse complement motif

Consensus sequence: TWVHWWYTTTTYTTTTHTTTTVW



Best Matches for Motif ID 56 (Highest to Lowest)

Motif ID: [MA0377.1](#)  
 Motif name: SFL1  
 Taxon: Fungi  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 2  
 Number of overlap: 21  
 Similarity score: 0.0547631

Alignment:

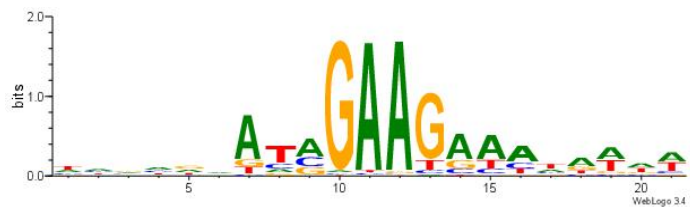
```

----HHVHDHATMGAAGAAHDWDW
HDWVAAAHAAAAAMAAAMWWWHBWA-

```

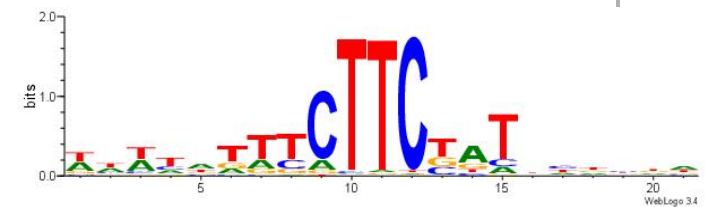
Original motif

Consensus sequence: HHVHDHATMGAAGAAHDWDW



Reverse complement motif

Consensus sequence: WDWHTTTCTTCYATHHHVHH



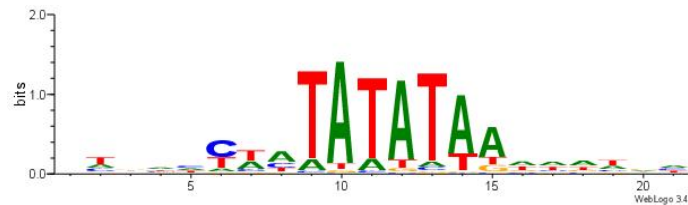
Motif ID: [MA0345.1](#)  
 Motif name: NHP6A  
 Taxon: Fungi  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 2  
 Number of overlap: 21  
 Similarity score: 0.0599871

Alignment:

HHHDDDDTTATATAHWKDHHHB-----  
 -TWVHWWWYTTTTYTTTTHTTTVWBH

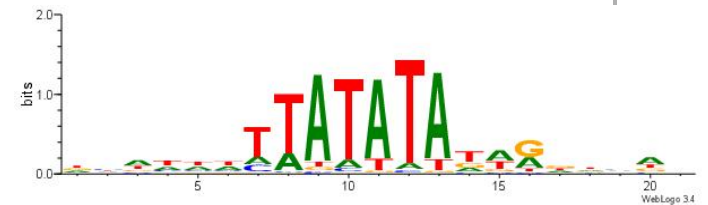
Original motif

Consensus sequence: VHDHHYWHTATATAADDDHDH



Reverse complement motif

Consensus sequence: HHHDDDDTTATATAHWKDHHHB



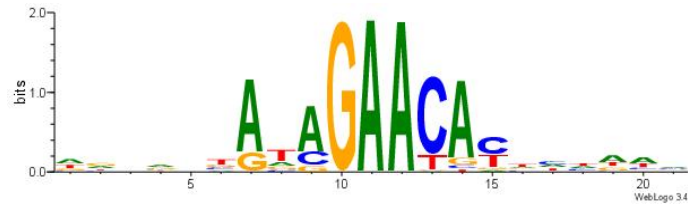
Motif ID: [MA0336.1](#)  
 Motif name: MGA1  
 Taxon: Fungi  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 5  
 Number of overlap: 21  
 Similarity score: 0.0605282

Alignment:

DDVVHBATAGAACAYDHHHDHV-----  
-----HDWVAAAHAAAAAMAAAMWWWHBWA

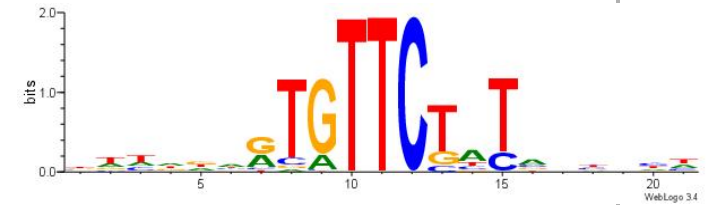
Original motif

Consensus sequence: DDVVHBATAGAACAYDHHHDHV



Reverse complement motif

Consensus sequence: BHDHDDKTGTTCTATVDBVHD



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Motif ID:	<a href="#">MA0390.1</a>
Motif name:	STB3
Taxon:	Fungi
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	21
Similarity score:	0.069776

Alignment:

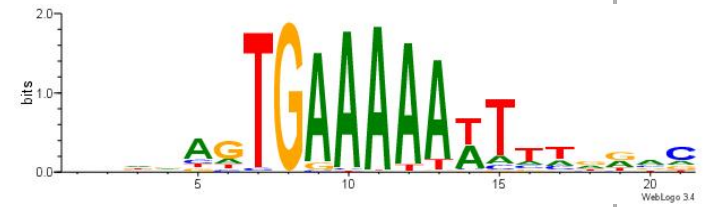
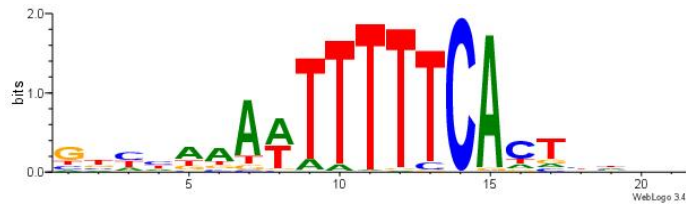
GBYHAAAWTTTTTCACTBHDD-----  
TWVHWWWYTTTTYTTTTTHTTTVWBH

Original motif

Consensus sequence: GBYHAAAWTTTTTCACTBHDD

Reverse complement motif

Consensus sequence: HHHBAGTGAAAAWTTTSDKVC



Motif ID: [MA0383.1](#)  
 Motif name: SMP1  
 Taxon: Fungi  
 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: 0.0708423

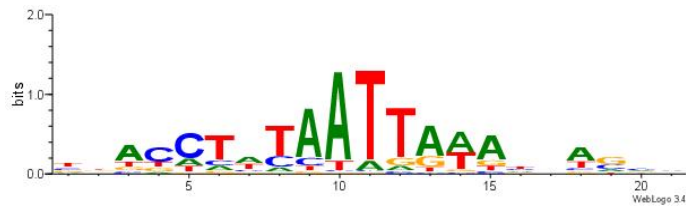
**Alignment:**

```

BDACCTWTAATTAWAHBWVVD----
HDWVAAAHA AAAAAMAAAMWWWHBWA
  
```

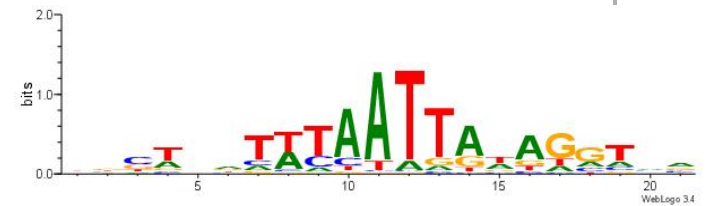
**Original motif**

Consensus sequence: BDACCTWTAATTAWAHBWVVD



**Reverse complement motif**

Consensus sequence: DVVWVHTWTAATTAWAGGTDV



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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