

Jump to: Multiple Alignment Motif Tree Motif Matching

Input file: 8 motifs loaded

Settings: Metric=PCC, Alignment=SWU, Gap-open=1000, Gap-extend=1000, -nooverlapalign Multiple Alignment=IR, Tree=UPGMA, Matching against: user-defined Note: All results files are removed nightly at midnight EST. Please save your results by saving "Webpage, complete".

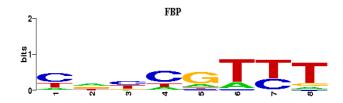
<u>Download results as a PDF</u> <u>Click here to run STAMP again.</u>

Multiple Alignment

(Consensus sequence representations shown, but multiple alignment was carried out on the matrices)

Motif1:	TCGTCTGCT-
Motif2:	YTTWTATA
Motif3:	TCAGTY
Motif4:	CGCCATCT
Motif5:	CARCGTTGCC
Motif6:	KTGTTTAT
Motif7:	-CCCWCCYYCY
Motif8:	ANNTATCGATT

Familial Profile: (click for matrix)

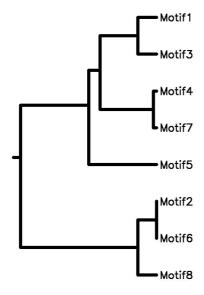


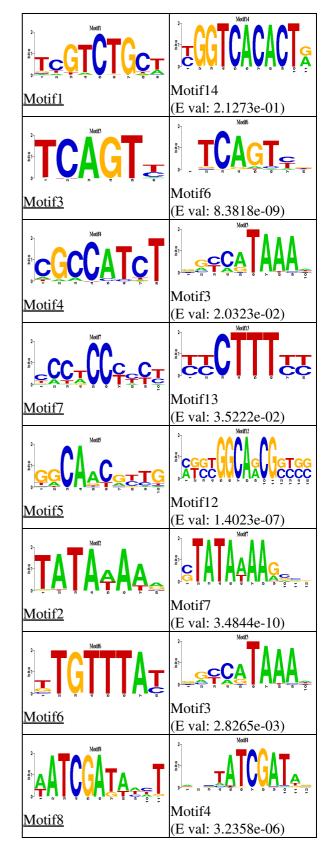
Motif Tree

Tree (drawn by Phylip)
Click here for Newick-format tree (viewable with MEGA)

Input Motif

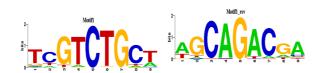
Best match in user-defined





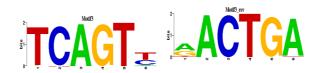
Motif Similarity Matches

Motif1



	forward	reverse compliment	
Name	E value	Alignment	Motif
Motif14	2.1273e-01	AGCAGACGA YGGTCACACTR	
Motif8	2.3233e-01	AGCAGACGA RGWYNT	Modf8 No
Motif9	2.4445e-01	TCGTCTGCT GTTSSGYTSG-	
Motif6	2.7437e-01	TCGTCTGCT -NRACTGAN	TCAGT
Motif5	2.8216e-01	TCGTCTGCT NNRNCAGCTGNN	Modification of the second of

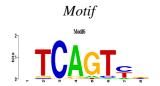
Motif3



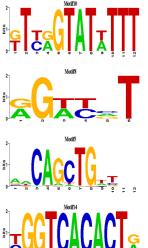
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reverse compliment

Name	E value	Alignment
Motif6	8.3818e-09	-TCAGTY- NTCAGTYN



Motif10	1.2708e-02	RACTGA- AAAWATACYRAM	F CAU
Motif8	6.5127e-02	RACTGA ANRWCY	Modis Modis
Motif5	6.9027e-02	TCAGTY NNRNCAGCTGNN	E A CAGO TO
Motif14	8.1892e-02	TCAGTYYAGTGTGACCR	E COLOR MORTH



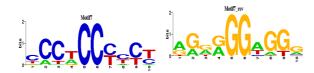
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Motif4

EGCCATCT AGATGGCG

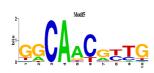
	forward	reverse compliment	
Name	E value	Alignment	Motif
Motif3	2.0323e-02	AGATGGCG NTTTATGRCN	E CA TAAA
Motif2	2.1885e-02	AGATGGCG GGCGYSS	2 North Cocc
Motif12	1.6974e-01	CGCCATCT SSRSCGYTGCCRSMK	CGGT WWW. A VICE CCC
Motif8	1.9820e-01	CGCCATCT ANRWCY	Modified To the Control of the Contr
Motif5	2.8226e-01	-CGCCATCT NNRNCAGCTGNN	2 Age To Modif

Motif7



		forward re	verse compliment	
Name	E value		Alignment	Motif
Motif	13 3.5222e	2 -02	GRRGGWGGG -RRAAAGRR	
Motif	14 4.5639e	<u>^_() </u>	RGRRGGWGGG AGTGTGACCR	E COTOA CACTE
Motif	2 5.3817e	: -()	GRRGGWGGG -GGCGYSS-	ESSECCE CE
Motif	8 6.1491e	:-()	CCWCCYYCY NRWCY	Modified Towns of the Control of the
Motif	12 7.3517e	: -()	RRGGWGGG 7GGCARCGSYSS	CGGT LA LEGGE COLOR

Motif5





forward

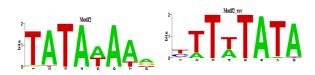
reverse compliment

Name	E value	Alignment	Motif
Motif12	1.4023e-07	GGCAACGYTG- MKSYGGCARCGSYSS	
Motif14	2.0678e-02	CARCGTTGCC- YAGTGTGACCR	EGGT CACACTE

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Motif11	1.4543e-01	GGCAACGYTG RNYAGNGMTGNNM	
Motif9	2.3786e-01	-CARCGTTGCC CSARCSSAAC-	
Motif13	3.7526e-01	CARCGTTGCC YYCTTTYY	

Motif2



	forward	reverse compliment	
Name	E value	Alignment	Motif
Motif7	3.4844e-10	-TATAWAAR STATAAAAGSNN	
Motif3	9.4605e-03	YTTWTATANTTTATGRCN	E CA TAAA
Motif10	6.0196e-02	TATAWAARAAAWATACYRAM	
Motif13	1.2250e-01	TATAWAAR RRAAAGRR	
Motif4	2.2214e-01	-TATAWAAR NTATCGATANNN	TATOGALA.

Motif6



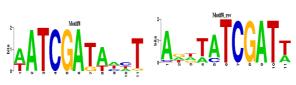
forward



reverse compliment

Name	E value	Alignment	Motif
Motif3	2.8265e-03	KTGTTTAT NTTTATGRCN	SECONDARY AND SECONDARY SE
Motif7	1.2291e-02	KTGTTTAT NNSCTTTTATAS	S A A A A A A A A A A A A A A A A A A A
Motif13	3.7056e-02	ATAAACAM RRAAAGRR	
Motif1	9.3000e-02	ATAAACAM- MMMMNAY	Modfin Section 1
Motif10	9.8876e-02	KTGTTTAT KTYRGTATWTTT	

Motif8





forward

reverse compliment

Name	E value	Alignment	Motif
Motif4	3.2358e-06	-AATCGATANNT NTATCGATANNN	STATEGAL A
Motif10	1.4592e-02	ANNTATCGATT AAAWATACYRAM-	F TRUM A TIME

Motif8	4.4804e-02	AATCGATANNT ANRWCY	Modifs
Motif11	2.7816e-01	ANNTATCGATTRNYAGNGMTGNNM	
Motif7	2.9399e-01	ANNTATCGATT NNSCTTTTATAS	E North Moult

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