

Jump to: Multiple Alignment Motif Tree Motif Matching

Input file: 4 motifs loaded

Settings: Metric=PCC, Alignment=SWU, Gap-open=1000, Gap-extend=1000, -nooverlapalign Multiple Alignment=IR, Tree=UPGMA, Matching against: JASPAR_Fams

Note: All results files are removed nightly at midnight EST. Please save your results by saving "Webpage, complete".

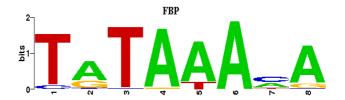
<u>Download results as a PDF</u> <u>Click here to run STAMP again.</u>

Multiple Alignment

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

TATAWAAA: -TATAWANRGTATAAAA: GTATAAAA-CTGTTTAT: --ATAAACAG
TGTTTACA: -TGTAAACA-

Familial Profile: (click for matrix)

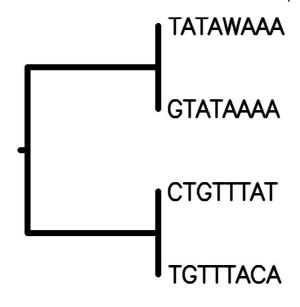


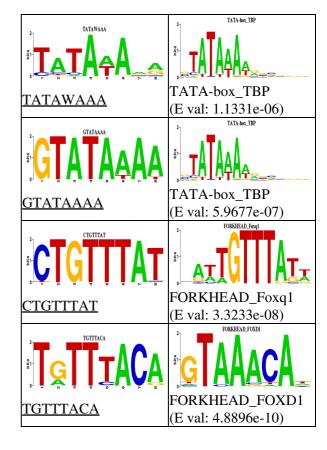
Motif Tree

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

Input Motif

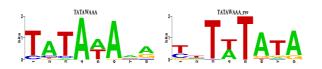
Best match in JASPAR_Fams





Motif Similarity Matches

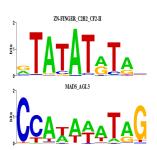
TATAWAAA



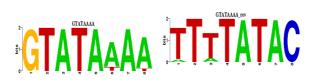
	forward	reverse compliment	
Name	E value	Alignment	Motif
TATA-box_TBP	1.1331e-06	YNTWTATA- NNNNNYWTTTATAN	TATA-box, TBP
ZN-FINGER_C2H2_hb	3.6111e-06	-YNTWTATA- NTTTTTNYKS	ZN-FINGER, CHR. 360
MADS_MEF2A	8.8489e-06	-YNTWTATA- CTATTTATAG	E-CTATTATAG

ZN-FINGER_C2H2_CF2-II 4.3873e-05
-YNTWTATANTAYATATAY

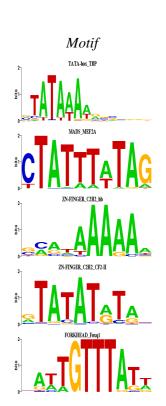
MADS_AGL3 3.8595e-04 -YNTWTATA-CTATWTWTGG



GTATAAAA



	forward	reverse compliment
Name	E value	Alignment
TATA-box_TBP	5.9677e-07	TTTTATAC
MADS_MEF2A	3.6428e-05	TTTTATAC CTATTTATAG
ZN-FINGER_C2H2_hb	5.6788e-05	TTTTATAC NTTTTTNYKS
ZN-FINGER_C2H2_CF2-	-II 7.5147e-04	TTTTATAC NTAYATATAY
FORKHEAD_Foxq1	1.8255e-03	GTATAAAA -WATAAACAATN



CTGTTTAT



forward

reverse compliment

Name	E value	Alignment	Motif
FORKHEAD_Foxq1	3.3233e-08	-ATAAACAG WATAAACAATN	FORKHEAD Food
MADS_MEF2A	5.2183e-07	ATAAACAG CTATAAATAG	ETATITA AG
FORKHEAD_FOXD1	1.1940e-06	CTGTTTAT NTGTTTAC	FORMHAD FORM
FORKHEAD_FOXI1	1.0175e-05	ATAAACAG AWAYAAAYANNN	FORRHEAD FOXII
ZN-FINGER_C2H2_Broad-complex_	_1 1.7552e-05	CTGTTTAT NWYTTGTYTATNAN	ZN-FINGER CH2 Broad-complex.1

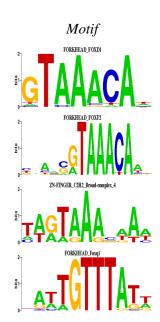


reverse compliment

TGTTTACA

J		1
Name	E value	Alignment
FORKHEAD_FOXD1	4.8896e-10	-TGTTTACA NTGTTTAC-
FORKHEAD_FOXF2	2.5893e-07	TGTAAACA NNANSGTAAACANN
ZN-FINGER_C2H2_Broad-complex_	_4 2.6265e-07	TGTTTACA- WTWNTTTACTA
FORKHEAD_Foxq1	4.3297e-05	TGTTTACA NATTGTTTATW

forward



MADS_MEF2A

3.6999e-04

-TGTAAACA-CTATAAATAG



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