

Jump to: Multiple Alignment Motif Tree Motif Matching

Input file: 3 motifs loaded

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

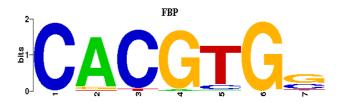
Note: All results files are removed nightly at midnight EST. Please save your results by saving "Webpage, complete".

<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)

Familial Profile: (click for matrix)

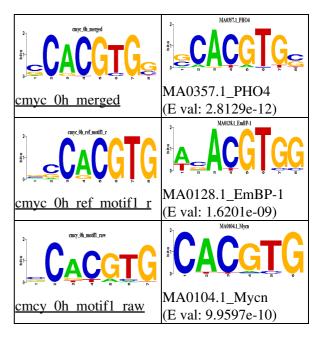


Motif Tree

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



Motif Similarity Matches



forward

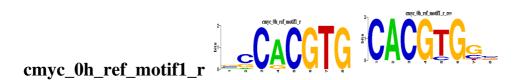
	y · · · · · ·	reverse compliment	
Name	E value	Alignment	Motif
MA0357.1_PHO4	2.8129e-12	SCACGTGG SCACGTGS	CACGTG
MA0059.1_MYC_MAX	1.1303e-11	-CCACGTGS ACCACGTGSTN	MAGOSAL MYC MAX CACCET CE A CACCET CE CACCET CACC
MA0147.1_Myc	2.7176e-10	-SCACGTGG- NSCACGTGGN	EACGTGG
MA0128.1_EmBP-1	1.3325e-09	CCACGTGS CCACGTST	A A C G T GG

MA0104.1_Mycn

4.0652e-09

CCACGTGS
-CACGTG-





jorwara	reverse compliment

Name	E value	Alignment	Motif
MA0128.1_EmBP-1	1.6201e-09	NCCACGTG- -CCACGTST	A ACCUTED
MA0104.1_Mycn	3.8769e-09	NCCACGTG CACGTG	E CACGT C
MA0357.1_PHO4	4.8121e-09	NCCACGTG- -SCACGTGS	MANOST, LPHO4 Particular of the control of the con
MA0004.1_Arnt	5.2670e-09	CACGTGGN CACGTG	EACGTG
MA0147.1_Myc	1.3391e-08	NCCACGTG NCCACGTGSN	CACGIGG



forward

reverse compliment

Name E value Alignment Motif

MA0104.1_Mycn	9.9597e-10	NCACGTG -CACGTG	AMANNAL Myra CACGTG
MA0004.1_Arnt	1.4494e-09	CACGTGN CACGTG-	EACGTG
MA0093.1_USF1	2.9071e-08	-CACGTGN NCACGTG-	E CACGTG
MA0409.1_TYE7	3.5152e-08	NCACGTG TCACGTG	E CACETGA
MA0357.1_PHO4	1.6868e-07	-CACGTGN SCACGTGS	EL CACCTC

Stamp Results

Sequence logo generation powered by weblogo STAMP is written by Shaun Mahony

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