

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".

Download results as a PDF Click here to run STAMP again.

Multiple Alignment

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

AGACCACK: ----AGACCACK
GCAGACGA: --GCAGACGA-GTCTGCTA: TAGCAGAC--CGTCTGTA: -TACAGACG---

Familial Profile: (click for matrix)

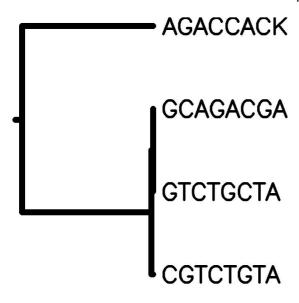


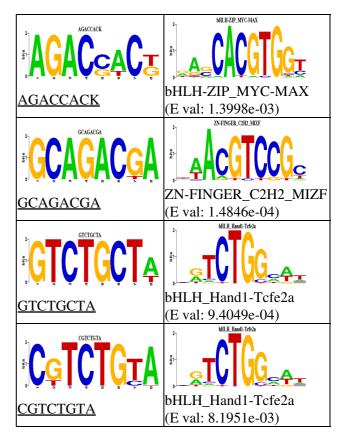
Motif Tree

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





| | forward | reverse compliment | |
|------------------|------------|----------------------|--|
| Name | E value | Alignment | Motif |
| bHLH-ZIP_MYC-MAX | 1.3998e-03 | AGACCACKACCACGTGSTN | E CACCIO |
| bHLH-ZIP_MAX | 3.3369e-03 | AGACCACKNANCACGTGN | STATE OF THE PARTY |
| bZIP_EMBP1 | 1.1639e-02 | AGACCACK CCACGTST | ACGTGG |

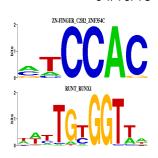
ZN-FINGER_C2H2_ZNF354C 1.2680e-02

MGTGGTCT -GTGGAK-

RUNT_RUNX1

1.4490e-02

AGACCACK--NAACCACARWW

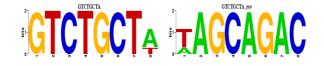


GCAGACGA



| | forward | reverse compliment | |
|---------------------|------------|------------------------|----------------------------------|
| Name | E value | Alignment | Motif ZN-FINGER CERE MIZE |
| ZN-FINGER_C2H2_MIZF | 1.4846e-04 | TCGTCTGC NAACGTCCGC | ACCTCCC _E |
| bHLH_Hand1-Tcfe2a | 6.9255e-03 | TCGTCTGCNRTCTGGNWN | E TOTOG A |
| bZIP_bZIP910 | 8.6824e-03 | TCGTCTGC ACGTCAK- | TGACGT |
| ETS_SPIB | 1.0128e-02 | -TCGTCTGC TTCCKST | |
| bZIP_TGA1a | 2.2477e-02 | -TCGTCTGC NACGTCA | E ACGTCA |

GTCTGCTA

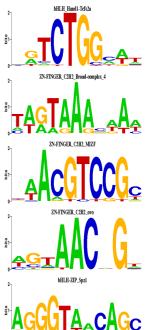


forward

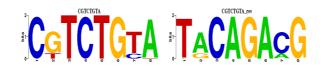
reverse compliment

Name E value Alignment Motif

| bHLH_Hand1-Tcfe2a | 9.4049e-04 | -TAGCAGAC- NWNCCAGAYN | 6- |
|-------------------------------|--------------|--------------------------|----------------------------------|
| ZN-FINGER_C2H2_Broad-complex_ | 4 6.7311e-03 | GTCTGCTA WTWNTTTACTA | 2- 2 - 2 1- 0- |
| ZN-FINGER_C2H2_MIZF | 1.4612e-02 | GTCTGCTA | 3 1- 2- |
| ZN-FINGER_C2H2_ovo | 2.3087e-02 | TAGCAGAC WGTAACNGN- | 2- \$\frac{8}{4}1- 0- |
| bHLH-ZIP_Spz1 | 2.8443e-02 | TAGCAGAC AGGGTAWCAGC- | 2- \$\frac{\pi}{2}\frac{1}{2} |



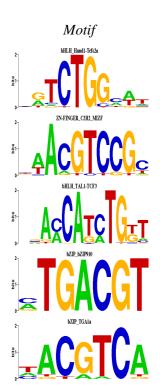
CGTCTGTA



reverse compliment

| | jornana | reverse compriment |
|---------------------|--------------|--------------------------|
| Name | E value | Alignment |
| bHLH_Hand1-Tcfe2a | 8.1951e-03 | TACAGACG NWNCCAGAYN |
| ZN-FINGER_C2H2_MIZI | F 8.3176e-03 | CGTCTGTA NAACGTCCGC- |
| bHLH_TAL1-TCF3 | 8.3517e-03 | CGTCTGTA NNAMCATCTGKT |
| bZIP_bZIP910 | 9.5945e-03 | -CGTCTGTA ACGTCAK |
| bZIP_TGA1a | 2.5826e-02 | TACAGACG TGACGTN |

forward



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