

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".

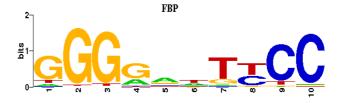
<u>Download results as a PDF</u> <u>Click here to run STAMP again.</u>

Multiple Alignment

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

motif_raw_refined: GGGGNNTYCCmotif2_raw: GGGGNNTYCCmotif_merged: GGGGNWTYCCC

Familial Profile: (click for matrix)

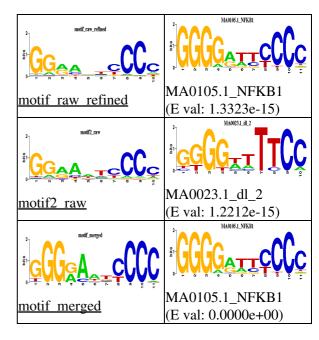


Motif Tree

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



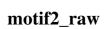
| | forward | reverse compliment | |
|--------------------|--------------|----------------------------|--|
| Name | E value | Alignment | Motif |
| MA0105.1_NFKB1 | 1.3323e-15 | -GGRANNCCCC GGGGAATCCCC | E COLOR DE LA COLO |
| MA0061.1_NF-kappaB | 3 1.8319e-14 | GGRANNCCCC GGRAAKTCCC | MAWGLI_WF-bappaB |
| MA0107.1_RELA | 1.8985e-14 | GGRANNCCCC GGAAANTCCC | MADIOTAL RELA |
| MA0101.1_REL | 8.4488e-14 | GGGGNNTYCC NGGRNWTTCC | MADIOLI REL |

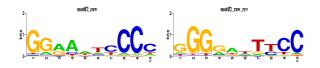
MA0023.1_dl_2

1.0492e-13

GGRANNCCCC GGAAAWCCCC

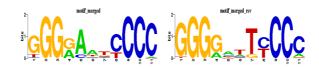






| | forward | reverse compliment | |
|-------------------|--------------|----------------------------|--------------------|
| Name | E value | Alignment | Motif |
| MA0023.1_dl_2 | 1.2212e-15 | GGGGNNTYCC GGGGWTTTCC | GGGGTT TCC |
| MA0107.1_RELA | 5.3291e-15 | GGGGNNTYCC GGGANTTTCC | AMAIOT.L.RELA TICC |
| MA0101.1_REL | 7.8826e-15 | GGGGNNTYCC NGGRNWTTCC | MADOUL REL |
| MA0061.1_NF-kappa | B 3.1974e-14 | GGRANNCCCC GGRAAKTCCC | MANOLLN LappaB |
| MA0105.1_NFKB1 | 3.3418e-14 | -GGRANNCCCC GGGGAATCCCC | MADIOLIVIKBI |

motif_merged



| jorwara | reverse | сотритені |
|---------|---------|-----------|
| | | |

Name E value Alignment

MA0105.1_NFKB1 0.0000e+00 GGGGNWTYCCC GGGGATTCCCC



| MA0061.1_NF-kappa | nB 7.4385e-15 | GGGRAWNCCCC -GGRAAKTCCC | |
|-------------------|---------------|----------------------------|------------------|
| MA0107.1_RELA | 1.5632e-13 | GGGRAWNCCCC -GGAAANTCCC | MANOVILEZIA TICC |
| MA0101.1_REL | 1.9773e-13 | GGGGNWTYCCC NGGRNWTTCC- | MANINIL REL |
| MA0023.1_dl_2 | 2.4734e-12 | GGGGNWTYCCC GGGGWTTTCC- | GGGGTT TCC |

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