

Supp Data 3 : TTCC Motif comparison and structural alignment

Starick, Ibn-Salem, Jurk et al *ChIP-exo signal associated with DNA-binding motifs provide insights into the genomic binding of the glucocorticoid receptor and cooperating transcription factors.*

One-to-n motif alignment with RSAT compare-matrices (www.rsat.eu); reference motif: TTCC ; Database: Jaspas Vertebrates ; 25 matrices
4 classes: Zinc-coordinating,Winged Helix-Turn-Helix,Helix-Turn-Helix,Ig-fold
6 families : BetaBetaAlpha-zinc finger, E2f, Ets,homeo,Rel,Stat

Matrix name	Class	Family	Aligned logos	PDB structure	Structural alignment result
TTCC motif query	-	-	...atrices_query_matrices.tab_1_shift4 matrix1.1 100 sites		
MA0056.1_rc_shift7 (MZFI_1-4_rc)	Zinc-coordinating	BetaBetaAlpha-zinc finger	MA0056.1_rc_shift7 MZF1_1-4_rc 20 sites	no structure	
MA0471.1_rc_shift4 (E2F6_rc)	Winged Helix-Turn-Helix	E2F	MA0471.1_rc_shift4 E2F6_rc 2757 sites		
MA0470.1_rc_shift4 (E2F4_rc)	Winged Helix-Turn-Helix	E2F	MA0470.1_rc_shift4 E2F4_rc 1878 sites		
MA0081.1_rc_shift6 (SPIB_rc)	Winged Helix-Turn-Helix	Ets	MA0081.1_rc_shift6 SPIB_rc 49 sites		
MA0136.1_shift3 (ELF5)	Winged Helix-Turn-Helix	Ets	MA0136.1_shift3 ELF5 44 sites		
MA0076.2_shift2 (ELK4)	Winged Helix-Turn-Helix	Ets	MA0076.2_shift2 ELK4 3427 sites		
MA0028.1_rc_shift5 (ELK1_rc)	Winged Helix-Turn-Helix	Ets	MA0028.1_rc_shift5 ELK1_rc 28 sites	1DUX	
MA0598.1_shift4 (EHF)	Winged Helix-Turn-Helix	Ets	MA0598.1_shift4 EHF 1427 sites		
MA0475.1_rc_shift2 (FLI1_rc)	Winged Helix-Turn-Helix	Ets	MA0475.1_rc_shift2 FLI1_rc 3667 sites		
MA0474.1_rc_shift2 (Erg_rc)	Winged Helix-Turn-Helix	Ets	MA0474.1_rc_shift2 Erg_rc 16727 sites		
MA0080.3_rc_shift2 (Spi1_rc)	Winged Helix-Turn-Helix	Ets	MA0080.3_rc_shift2 Spi1_rc 63715 sites		
MA0156.1_rc_shift4 (FEV_rc)	Winged Helix-Turn-Helix	Ets	MA0156.1_rc_shift4 FEV_rc 13 sites		
MA0473.1_rc_shift3 (ELF1_rc)	Winged Helix-Turn-Helix	Ets	MA0473.1_rc_shift3 ELF1_rc 13518 sites		
MA0062.2_rc_shift1 (GABPA_rc)	Winged Helix-Turn-Helix	Ets	MA0062.2_rc_shift1 GABPA_rc 993 sites		
MA0098.2_shift1 (Ets1)	Winged Helix-Turn-Helix	Ets	MA0098.2_shift1 Ets1 1868 sites	1K79	

MA0090.1_shift2 (TEAD1)	Helix-Turn-Helix	Homeo	MA0090.1_shift2 TEAD1 bits 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 12 sites	2HZD	
MA0101.1_shift0 (REL)	Ig-fold	Rel	MA0101.1_shift0 REL bits 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 17 sites		
MA0152.1_shift4 (NFATC2)	Ig-fold	Rel	MA0152.1_shift4 NFATC2 bits 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 26 sites		
MA0107.1_shift0 (RELA)	Ig-fold	Rel	MA0107.1_shift0 RELA bits 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 18 sites		
MA0105.3_shift0 (NFKB1)	Ig-fold	Rel	MA0105.3_shift0 NFKB1 bits 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 5112 sites	1SVC (p50) 2O61 (p65)	
MA0519.1_shift4 (Stat5a::Stat5b)	Ig-fold (other)	STAT	MA0519.1_shift4 Stat5a::Stat5b bits 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16507 sites		
MA0520.1_shift3 (Stat6)	Ig-fold (other)	STAT	MA0520.1_shift3 Stat6 bits 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 1852 sites		
MA0518.1_rc_shift2 (Stat4_rc)	Ig-fold (other)	STAT	MA0518.1_rc_shift2 Stat4_rc bits 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 2873 sites		
MA0137.3_rc_shift5 (STAT1_rc)	Ig-fold	Stat	MA0137.3_rc_shift5 STAT1_rc bits 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 3629 sites	1BF5	
MA0144.2_rc_shift5 (STAT3_rc)	Ig-fold	Stat	MA0144.2_rc_shift5 STAT3_rc bits 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 21620 sites		