
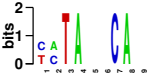

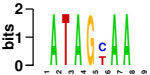







| optimized motif | location | MI (bits) | z-score | robustness | position bias | orientation bias | conservation index | seed | motif name | protein array |
|---|----------|-----------|---------|------------|---------------|------------------|--------------------|---------|----------------------------------|---------------|
|  | 5' | 0.006 | 28.8 | 10/10 | Y | ↔ | 1.00 | CACCTGC | SNAI_1, HLH_1.4 | - |
|  | 5' | 0.005 | 23.5 | 10/10 | - | ↔ | 0.33 | CTAATCA | - | - |
|  | 5' | 0.003 | 13.8 | 10/10 | - | ↔ | 0.24 | TGGTAAC | - | - |
|  | 5' | 0.003 | 12.4 | 9/10 | - | - | 0.52 | ATAGTAA | DAF_19, MEF_2, PIE_1 | - |
|  | 5' | 0.003 | 12.6 | 7/10 | - | - | 0.29 | TCTGACA | NHR_216, NHR-6_NHR_6, NHR_91 ... | - |
|  | 5' | 0.003 | 11.4 | 6/10 | Y | ← | 0.95 | TTTGATC | PIE_1, NHR_216 | - |
|  | 5' | 0.006 | 28.3 | 10/10 | - | ↔ | 1.00 | AATCGAT | PIE_1, CEH_28, CEH_38 ... | - |
|  | 5' | 0.004 | 18.1 | 10/10 | - | ↔ | 0.96 | CTCTCTC | PIE_1 | - |
|  | 5' | 0.004 | 15.6 | 10/10 | - | → | 0.98 | CTTCTTC | PIE_1 | - |