


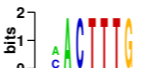


| Optimized motif | location | MI (bits) | z-score | robustness | position bias | orientation bias | conservation index | seed | Motif name | Protein array |
|--|----------|-----------|---------|------------|---------------|------------------|--------------------|---------|----------------------------|---------------|
|  | 5' | 0.004 | 21.8 | 10/10 | - | ↔ | 1.00 | CTCCGCC | SPTF_3 | - |
|  | 5' | 0.003 | 12.1 | 7/10 | - | ← | 0.92 | AGATGAG | PIE_1 | - |
|  | 5' | 0.003 | 11.8 | 8/10 | - | ← | 1.00 | AATCGAT | CEH-28, CEH_28, CEH-38 ... | - |
|  | 5' | 0.003 | 11.6 | 8/10 | - | → | 0.61 | AACTTTG | NHR_69, NHR_64, PIE_1 ... | - |