| optimized motif | location | MI (bits) | z-score | robustness | position bias | orientation bias | conservation index | seed | motif name | protein array |
|---|---|---|---|---|---|---|---|---|---|---|
|  | 3'UTR | 0.006 | 28.6 | 10/10 | Y | ↔ | 0.97 | AAAAAAU | – | – |
|  | 5' | 0.003 | 17.5 | 10/10 | – | ↔ | 0.99 | AATCGAT | PIE_1, CEH_28, CEH-28 ... | – |
|  | 5' | 0.003 | 12.8 | 10/10 | – | ← | 0.91 | ATGTACA | DAF-16, PHA_4.3, FKH_8 | – |
|  | 5' | 0.002 | 10.3 | 8/10 | – | ← | 0.99 | AAGGTCA | NHR_91, SEX_1, NHR_84 ... | – |