


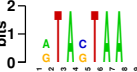




optimized motif	location	MI (bits)	z-score	robustness	position bias	orientation bias	conservation index	seed	motif name	protein array
	5'	0.005	22.7	10/10	-	↔	1.00	AATCGAT	CEH_28, CEH-28, CEH_38 ...	-
	5'	0.003	16.1	9/10	-	←	0.98	ACGATGA	PIE_1	-
	5'	0.003	12.2	8/10	-	-	0.99	CACTCTC	PIE_1	-
	5'	0.004	17.0	10/10	-	→	0.69	ATAGTAA	DAF_19, PIE_1, MEF_2 ...	-
	5'	0.003	15.0	10/10	-	←	0.99	ACAGGTG	-	-
	5'	0.003	11.4	7/10	-	→	0.94	CCACGCC	SPTF_3	-