



optimized motif	location	MI (bits)	z-score	robustness	position bias	orientation bias	conservation index	seed	motif name	protein array
	3'UTR	0.005	28.0	10/10	Y	↔	0.97	AAUCAAA	-	-
	5'	0.004	21.0	10/10	-	↔	0.99	AATCGAT	CEH_28, CEH-28, PIE_1	-
	5'	0.003	16.6	10/10	-	↔	0.99	CCCCGCC	-	-
	5'	0.003	13.3	8/10	-	→	0.86	AACCACT	-	-
	5'	0.003	16.1	10/10	-	→	0.05	CAGTATA	PIE_1	-
	5'	0.003	13.2	7/10	-	→	0.57	TAGTAAC	DAF_19, DMD_8, MAB_3 ...	-