






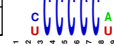



optimized motif	location	MI (bits)	z-score	robustness	position bias	orientation bias	conservation index	seed	motif name	protein array
	3'UTR	0.017	90.1	10/10	Y	↔	0.99	AAAAAUA	-	-
	5'	0.005	26.5	10/10	-	↔	0.41	AATTATA	CEH_1, CEH_2, CEH_23 ...	-
	5'	0.005	24.7	10/10	Y	↔	0.98	CAGGTGA	HLH_30, HLH-30, MDL_1 ...	-
	5'	0.004	18.1	10/10	-	←	0.15	AGTCAGA	-	-
	5'	0.008	41.8	10/10	-	↔	0.99	CGTCGTC	-	-
	5'	0.007	37.8	10/10	-	↔	0.99	AATCGAT	CEH_28, CEH-28, CEH-38 ...	-
	3'UTR	0.006	29.3	10/10	-	→	0.99	UUCCCCC	-	-
	5'	0.004	18.3	9/10	-	→	0.44	GTCCCCC	PIE_1	-
	5'	0.003	14.2	8/10	-	→	0.37	ATAGGGA	-	-