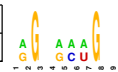
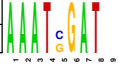
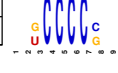
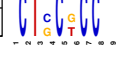
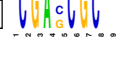
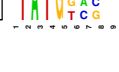


optimized motif	location	MI (bits)	z-score	robustness	position bias	orientation bias	conservation index	seed	motif name	protein array
	3'UTR	0.006	29.9	10/10	-	↔	0.99	AGAAAUG	-	-
	5'	0.003	17.1	10/10	-	↔	0.99	AATCGAT	CEH_28, CEH-38, CEH-28 ...	-
	3'UTR	0.003	14.9	10/10	-	→	1.00	CUCCCCC	-	-
	5'	0.003	17.0	10/10	-	→	1.00	CTCCGCC	-	-
	5'	0.002	11.5	8/10	-	-	0.95	CGACCGC	PIE_1	-
	5'	0.002	11.1	7/10	-	→	0.39	TATGTAC	-	-