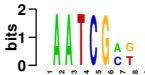
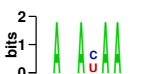
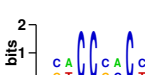
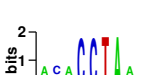

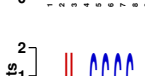
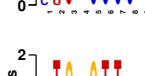
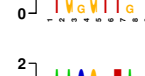


optimized motif	location	MI (bits)	z-score	robustness	position bias	orientation bias	conservation index	seed	motif name	protein array
	5'	0.008	50.6	10/10	-	↔	0.99	AATCGAT	CEH_28, PIE_1	-
	3'UTR	0.008	43.8	10/10	Y	↔	0.99	AAAUAAA	-	-
	5'	0.004	24.4	10/10	Y	→	1.00	CTCCGCC	-	-
	5'	0.004	24.2	10/10	-	↔	0.22	TGCCTAC	MAB_9	-
	5'	0.002	13.0	7/10	-	←	0.54	CTGAACA	NHR_1_NHR_10_NHR_101_NHR_17_NHR_40_NHR_47_NHR_68, PIE_1	-
	3'UTR	0.004	19.3	10/10	-	→	0.98	UUUCCCC	-	-
	5'	0.003	15.4	9/10	-	←	0.42	TGAGTTC	PIE_1	-
	5'	0.002	10.8	6/10	-	→	0.03	AACGATA	PIE_1	-