
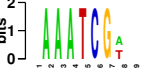
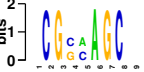
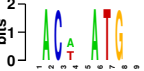
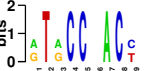






optimized motif	location	MI (bits)	z-score	robustness	position bias	orientation bias	conservation index	seed	motif name	protein array
	3'UTR	0.012	61.5	10/10	Y	↔	0.99	UUUCAGA	-	-
	5'	0.005	23.9	10/10	-	↔	0.99	AAATCGA	CEH-38, PIE_1, CEH_28	-
	5'	0.004	19.4	10/10	-	↔	0.93	CGGAAGC	ETS_5, HAM_2	-
	5'	0.004	18.2	10/10	-	↔	0.71	ACAAATG	-	-
	5'	0.003	13.2	10/10	-	←	0.39	TGCCTAC	-	-
	3'UTR	0.003	12.7	9/10	-	→	0.98	UUCCCCC	-	-
	5'	0.003	12.3	8/10	-	↔	0.97	CTTCTTC	PIE_1	-
	5'	0.002	10.7	6/10	Y	-	1.00	CCGCCCA	SPTF_3, EGRH_1_EGRH_2, KLF_1 ...	-
	5'	0.002	10.5	7/10	-	←	0.99	CGCAGAC	-	-