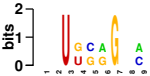
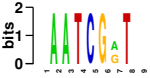
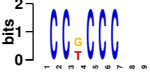

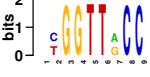
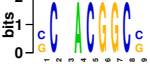


optimized motif	location	MI (bits)	z-score	robustness	position bias	orientation bias	conservation index	seed	motif name	protein array
	3'UTR	0.007	39.3	10/10	-	↔	0.93	UUUCAGA	-	-
	5'	0.005	28.0	10/10	-	↔	1.00	AATCGAT	CEH_28, CEH-28, CEH-38 ...	-
	5'	0.006	33.1	10/10	-	→	1.00	CCGCCCC	KLF_3, KLF_1, SPTF_3	-
	5'	0.003	15.4	8/10	-	→	0.04	TTTAGAC	-	-
	5'	0.002	13.1	7/10	-	-	0.92	TGGTTGC	PIE_1	-
	5'	0.002	11.6	6/10	-	←	0.89	CCACGGC	-	-