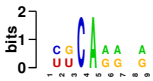
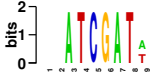
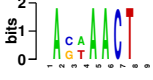
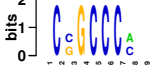


Optimized motif	location	MI (bits)	z-score	robustness	position bias	orientation bias	conservation index	seed	motif name	protein array
	3'UTR	0.006	32.0	10/10	-	↔	0.85	UUCAGAA	-	-
	5'	0.004	24.9	10/10	-	↔	1.00	AATCGAT	CEH_28, CEH-28, CEH_38 ...	-
	5'	0.002	13.3	7/10	-	→	0.42	ACAAACT	ZTF_11, PIE_1	-
	5'	0.002	12.1	8/10	-	↔	1.00	CCGCCCC	SPTF_3, EGRH_1_EGRH_2	-