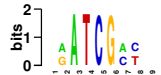

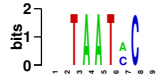
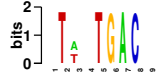
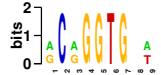


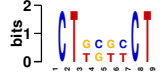


optimized motif	location	MI (bits)	z-score	robustness	position bias	orientation bias	conservation index	seed	motif name	protein array
	5'	0.006	29.6	10/10	-	↔	1.00	AATCGAT	PIE_1	-
	5'	0.004	19.0	10/10	Y	→	0.65	CATAGCA	ZTF_9	-
	5'	0.004	17.8	9/10	-	→	0.92	CTAATCC	CEH_45, UNC-30 UNC_30, CEH_53 ...	-
	5'	0.003	16.1	10/10	-	↔	0.81	TTGTGAC	NHR_102_NHR_142_NHR_170_NHR_213_NHR_218_NHR_54, NHR_84, NHR_216 ...	-
	5'	0.003	12.8	8/10	Y	-	0.99	CAGGTGA	SNAI_1	-
	5'	0.003	12.5	8/10	-	-	0.74	AGTAGTA	CEH-22	-
	5'	0.003	11.4	7/10	-	←	0.27	AAGTTGG	PIE_1	-
	5'	0.003	15.8	10/10	-	→	1.00	CTTCTTC	-	-