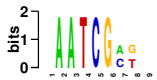
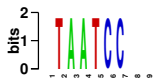
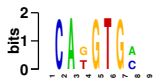
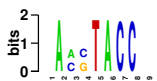
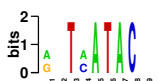
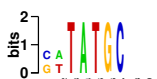
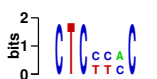




optimized motif	location	MI (bits)	z-score	robustness	position bias	orientation bias	conservation index	seed	motif name	protein array
	5'	0.007	37.3	10/10	-	↔	0.99	AATCGAT	CEH_28, PIE_1	-
	5'	0.006	30.7	10/10	Y	↔	0.98	TAATCCC	UNC-30 UNC_30, CEH_45, CEH_37 ...	-
	5'	0.003	15.7	10/10	-	↔	0.98	CAGGTGA	SNAI_1, HLH_25, MDL_1 ...	-
	5'	0.003	13.2	8/10	-	↔	0.57	ACGTACC	-	-
	5'	0.003	12.8	9/10	-	→	0.61	ATCATAC	-	-
	5'	0.003	11.9	7/10	-	-	0.64	ATATGCT	UNC-86, UNC_86	-
	5'	0.003	15.8	10/10	-	→	0.96	CTCTTCC	PIE_1	-
	5'	0.003	13.1	9/10	-	←	0.99	CACTCCG	PIE_1	-
	5'	0.003	11.7	9/10	-	→	1.00	CGCAGAC	PIE_1	-