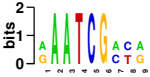
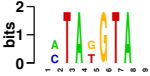
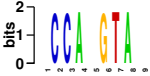
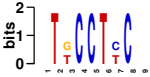


Optimized motif	location	MI (bits)	z-score	robustness	Position bias	orientation bias	conservation index	seed	motif name	protein array
	5'	0.005	24.3	10/10	-	↔	1.00	AATCGAT	PIE_1	-
	5'	0.003	17.0	10/10	-	↔	0.48	ATATGTA	-	-
	5'	0.003	12.3	7/10	-	→	0.65	CCAAGTA	-	-
	5'	0.002	12.2	8/10	-	→	0.75	TTCCTCC	PIE_1	-