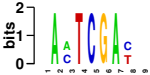
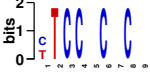
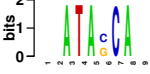



Optimized motif	location	MI (bits)	z-score	robustness	Position bias	orientation bias	conservation index	seed	motif name	protein array
	5'	0.003	14.9	9/10	-	↔	1.00	AATCGAT	CEH_28, CEH-28, PIE_1	-
	5'	0.003	13.9	9/10	-	→	0.99	TCCCCC	PIE_1	-
	5'	0.003	14.0	10/10	-	←	0.37	CATAGCA	-	-
	5'	0.002	11.4	7/10	-	-	0.13	CTCTGTA	-	-