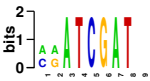
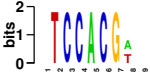
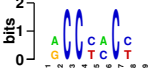



Optimized motif	location	MI (bits)	z-score	robustness	Position bias	orientation bias	conservation index	seed	motif name	protein array
	5'	0.007	38.1	10/10	-	↔	1.00	AATCGAT	PIE_1, CEH_28, CEH-28 ...	-
	5'	0.003	13.6	8/10	-	→	1.00	TCCACGA	MXL_3, REF_1, PIE_1 ...	-
	5'	0.003	15.8	10/10	Y	→	0.98	ACCTACC	-	-
	5'	0.003	13.3	9/10	-	←	0.10	CTCTAAA	PIE_1	-