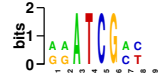
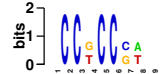
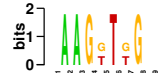


optimized motif	location	MI (bits)	z-score	robustness	position bias	orientation bias	conservation index	seed	motif name	protein array
	5'	0.004	18.7	10/10	-	↔	1.00	AATCGAT	PIE_1, CEH_28, CEH_38	-
	5'	0.003	15.4	9/10	-	→	0.97	CCGCCCA	ZTF_27	-
	5'	0.003	14.1	8/10	-	←	0.28	AAGTTTG	TBX_39, PIE_1, NSY_7	-