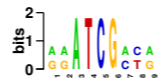

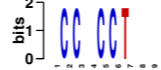


optimized motif	location	MI (bits)	z-score	robustness	position bias	orientation bias	conservation index	seed	motif name	protein array
	5'	0.005	24.9	10/10	-	↔	1.00	AATCGAT	PIE_1	-
	5'	0.003	14.9	9/10	-	←	0.55	CTATGAA	-	-
	5'	0.003	12.9	9/10	Y	→	0.98	CCACCTC	ZTF_14	-