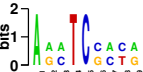
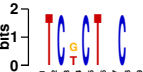



optimized motif	location	MI (bits)	z-score	robustness	position bias	orientation bias	conservation index	seed	motif name	protein array
	5'	0.004	17.7	10/10	-	↔	0.98	AATCGAT	PIE_1	-
	5'	0.003	11.7	6/10	-	→	0.91	TCTCTTC	EOR_1.2, EOR-1, PIE_1	-
	5'	0.003	11.2	10/10	-	-	0.21	ACATTTC	-	-