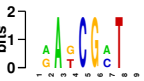





Optimized motif	location	MI (bits)	z-score	robustness	position bias	orientation bias	conservation index	seed	Motif name	Protein array
	5'	0.006	30.3	10/10	-	↔	1.00	AATCGAT	PIE_1, CEH_28, CEH_38	-
	5'	0.003	14.4	8/10	-	→	0.99	CTCTCTC	PIE_1	-
	5'	0.005	22.8	10/10	-	↔	0.90	TACCAAA	TBX_40	-
	5'	0.003	14.8	10/10	-	←	0.32	TACTAGA	-	-