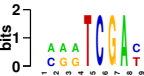
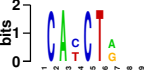
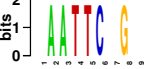


optimized motif	location	MI (bits)	z-score	robustness	position bias	orientation bias	conservation index	seed	motif name	protein array
	5'	0.003	21.6	10/10	-	↔	1.00	AAATCGA	CEH_28, PIE_1, CEH_38	-
	5'	0.003	16.0	8/10	Y	→	0.90	CACCTGC	SNAI_1, TBX_43	-
	5'	0.002	13.6	8/10	-	↔	0.23	AATTCTG	PIE_1	-