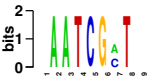
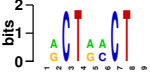
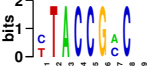


optimized motif	location	MI (bits)	z-score	robustness	position bias	orientation bias	conservation index	seed	motif name	protein array
	5'	0.003	15.3	10/10	-	←	1.00	AATCGAT	CEH_28, PIE_1, CEH-28	-
	5'	0.003	14.6	9/10	-	←	0.71	ACTAACT	-	-
	5'	0.002	11.7	6/10	-	-	0.38	TACCGAC	-	-