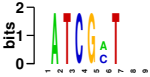
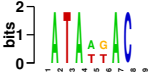
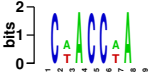



Optimized motif	location	MI (bits)	z-score	robustness	Position bias	orientation bias	conservation index	seed	motif name	protein array
	5'	0.003	15.8	10/10	-	↔	1.00	ATCGATA	CEH_28, CEH-28, CEH_38 ...	-
	5'	0.003	13.4	9/10	-	-	0.23	ATATGAC	-	-
	5'	0.003	12.4	8/10	-	→	0.52	CAACCAA	-	-
	5'	0.002	10.9	6/10	-	←	0.44	CTCTCTA	EOR_1.2, EOR-1, PIE_1	-