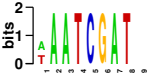
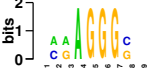
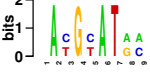



Optimized motif	location	MI (bits)	z-score	robustness	position bias	orientation bias	conservation index	seed	motif name	protein array
	5'	0.004	21.9	10/10	-	↔	1.00	AATCGAT	CEH-28, CEH_28, CEH-38 ...	-
	5'	0.004	20.3	10/10	-	↔	0.93	AGAGGGG	PIE_1	-
	5'	0.003	16.2	10/10	-	↔	0.59	ATGTATA	UNC_86, UNC-86, M03D4.4	-
	5'	0.002	11.8	7/10	-	←	0.47	ATCTTAC	PIE_1, CEH_32	-