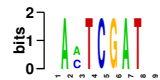
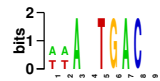
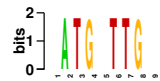
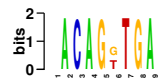
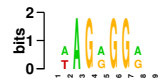


optimized motif	location	MI (bits)	z-score	robustness	position bias	orientation bias	conservation index	seed	motif name	protein array
	5'	0.003	17.9	10/10	-	↔	1.00	AATCGAT	CEH_28, CEH-28, CEH-38 ...	-
	5'	0.002	10.1	6/10	-	-	0.73	AAATGAC	PIE_1	-
	5'	0.002	11.6	7/10	-	-	0.97	ATGTTTG	PIE_1	-
	5'	0.002	10.6	6/10	-	-	0.85	ACAGTTG	SNAI_1, PIE_1, HLH_1.5	-
	5'	0.002	10.9	7/10	-	←	0.85	AAGGGGG	-	-