

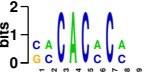
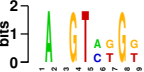
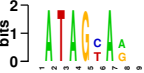



optimized motif	location	MI (bits)	z-score	robustness	position bias	orientation bias	conservation index	seed	motif name	protein array
	5'	0.007	41.2	10/10	-	↔	1.00	AATCGAT	CEH_28, CEH-28, CEH-38 ...	-
	5'	0.004	20.2	10/10	Y	↔	0.99	CGCGCCA	-	-
	5'	0.004	19.7	10/10	-	→	0.96	ACACACA	ZTF_3	-
	5'	0.003	13.2	9/10	-	←	0.50	ATGTATG	-	-
	5'	0.004	19.8	10/10	-	↔	0.72	ATAGTAA	MEF_2, DAF_19	-
	5'	0.003	12.3	8/10	-	←	0.55	ACTTCTG	PIE_1	-