
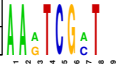
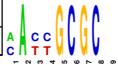
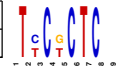
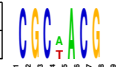






optimized motif	location	MI (bits)	z-score	robustness	position bias	orientation bias	conservation index	seed	motif name	protein array
	3'UTR	0.011	58.1	10/10	Y	↔	0.99	UUGGAAA	-	-
	5'	0.007	36.6	10/10	-	↔	1.00	AATCGAT	CEH_28, PIE_1, CEH-38	-
	5'	0.004	18.7	9/10	-	↔	0.91	ATCGCGC	Y44A6D.3	-
	5'	0.003	16.9	10/10	Y	↔	0.96	TTCTCTC	PIE_1	-
	5'	0.003	13.9	7/10	-	↔	0.97	CGCAACG	ZIP_8, CES_2	-
	5'	0.002	10.7	8/10	-	←	0.92	AATGGCG	-	-
	5'	0.003	14.8	8/10	Y	↔	0.96	ACAGTAA	LSL_1, ODD_2, LSY_2	-
	5'	0.003	12.9	8/10	-	←	0.47	ATATGAT	-	-
	5'	0.003	12.7	6/10	-	↔	0.41	AGGTAAG	-	-