



optimized motif	location	MI (bits)	z-score	robustness	position bias	orientation bias	conservation index	seed	motif name	protein array
	3'UTR	0.011	55.5	10/10	Y	↔	0.95	UCAAAAA	-	-
	5'	0.003	15.0	9/10	Y	→	0.99	CAGGTGA	SNAI_1	-
	5'	0.003	13.6	8/10	-	→	0.95	TTGTGAC	NHR_102_NHR_142_NHR_170_NHR_213_NHR_218_NHR_54, ATF_7, PIE_1 ...	-
	5'	0.003	12.4	8/10	-	←	0.61	ATTATAG	-	-
	5'	0.003	11.6	10/10	-	-	0.44	AACTGAT	NHR_46, PIE_1, EGL_27 ...	-
	5'	0.006	28.6	10/10	-	↔	1.00	AATCGAT	PIE_1	-
	5'	0.003	15.0	10/10	-	↔	1.00	CTTCTTC	PIE_1, EOR-1	-
	5'	0.002	11.0	7/10	-	←	0.45	AAAAGGG	PIE_1, FEZF_1	-