



optimized motif	location	MI (bits)	z-score	robustness	position bias	orientation bias	conservation index	seed	motif name	protein array
	3'UTR	0.008	41.2	10/10	Y	↔	0.97	AAAAAUU	-	-
	5'	0.003	12.3	8/10	-	←	0.94	ATGATCA	NHR_1_NHR_10_NHR_101_NHR_17_NHR_40_NHR_47_NHR_68, NHR_119_NHR_31	-
	5'	0.004	21.8	10/10	-	↔	1.00	AATCGAT	CEH_28, CEH-28, CEH_38 ...	-
	3'UTR	0.004	20.6	10/10	-	→	0.99	AUCCCCC	-	-
	5'	0.003	12.4	8/10	Y	→	0.90	CTCTTCC	EOR_1.2, EOR-1, PIE_1	-
	5'	0.003	13.7	9/10	-	←	0.70	TATGCTA	-	-
	5'	0.002	10.8	8/10	-	-	0.68	ACCAAAC	PIE_1	-
	5'	0.003	14.1	10/10	-	↔	0.83	TAAGATA	-	-