



optimized motif	location	MI (bits)	z-score	robustness	position bias	orientation bias	conservation index	seed	motif name	protein array
	3'UTR	0.012	65.1	10/10	Y	↔	0.99	AGAAAAU	RSP_3	-
	5'	0.004	21.7	10/10	-	↔	0.65	ATATGTA	UNC-86, UNC_86	-
	5'	0.006	31.6	10/10	-	↔	1.00	AATCGAT	CEH_28, CEH-38, CEH-28 ...	-
	3'UTR	0.004	17.6	10/10	-	→	0.99	UUUCCCC	-	-
	5'	0.003	12.8	10/10	-	→	0.99	TTCTCTC	EOR-1, EOR_1.2, PIE_1	-
	5'	0.003	16.4	10/10	Y	↔	0.99	CAGGTGA	SNAI_1, PIE_1, UNC-62	-
	5'	0.003	13.0	8/10	-	→	0.87	CATGGCA	-	-
	5'	0.002	9.9	6/10	-	-	0.95	TGACCTC	PIE_1	-