










optimized motif	location	MI (bits)	z-score	robustness	position bias	orientation bias	conservation index	seed	motif name	protein array
	3'UTR	0.006	52.7	10/10	-	→	0.75	AGAUUAG	-	-
	3'UTR	0.005	47.0	10/10	-	→	0.54	UAAGGU	-	-
	3'UTR	0.005	45.5	10/10	-	→	0.81	CUAACAA	-	-
	3'UTR	0.006	49.7	10/10	-	→	0.20	CCAUCGC	-	-
	3'UTR	0.005	48.3	10/10	Y	→	0.58	GGUCAA	-	-
	3'UTR	0.004	35.1	10/10	Y	→	0.78	GUCGAUC	-	-
	3'UTR	0.003	28.8	10/10	-	→	0.74	CAUGUAC	-	-
	3'UTR	0.003	22.6	8/10	-	→	0.58	GUGAGUA	-	-
	3'UTR	0.002	21.9	8/10	-	→	0.35	CGACCAA	-	-