

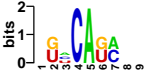


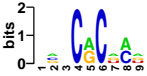






Optimized motif	location	MI (bits)	z-score	robustness	position bias	orientation bias	conservation index	seed	motif name	protein array
	3'UTR	0.012	112.1	10/10	-	-	0.93	ACUGGAG	-	-
	3'UTR	0.009	86.1	10/10	-	→	0.96	AAUGUGG	-	-
	3'UTR	0.007	64.6	10/10	-	-	0.90	UUCAUAC	-	-
	3'UTR	0.010	93.3	10/10	-	-	1.00	GGGGGGG	miR-532-3p, miR-377, miR-603 ...	-
	3'UTR	0.010	89.1	10/10	-	-	0.97	CCCCCCC	-	-
	3'UTR	0.008	76.4	10/10	-	-	0.94	AUCACUC	-	-
	3'UTR	0.003	27.6	10/10	-	-	0.52	UCUCUCA	-	-
	3'UTR	0.005	50.9	10/10	-	→	0.99	UUUUUUU	miR-3613-3p, miR-3148, miR-548f ...	-
	3'UTR	0.004	31.8	10/10	-	→	0.35	GAGGAAG	-	-
	3'UTR	0.003	27.1	10/10	-	→	0.96	GGCCCAG	-	-