



ribonucleoprotein complex,  $p < 0.01$

GTP binding,  $p < 0.01$

motif name	seed	conservation index	orientation bias	position bias	$z\text{-score}$	robustness	$MI$ (bits)	location	optimized motif
-	UCCCCAU	1.00	$\rightarrow$	-	12.4	10/10	0.018	3' UTR	
-	CGAGACC	1.00	$\uparrow$	-	11.5	10/10	0.017	5'	
-	UUCCCUU	0.86	$\rightarrow$	-	7.9	10/10	0.015	3' UTR	
-	CGAAGAA	0.83	-	-	7.2	6/10	0.013	5'	