

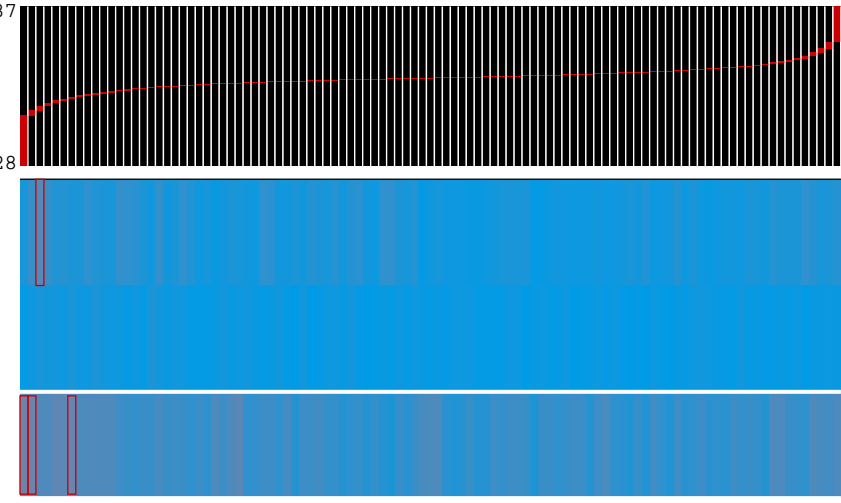
ation



over-representation

0

structural constituent of cytoskeleton
 nucleoside diphosphate
 phosphoric hydrolase activity, p<0.01
 phosphate metabolism, p<0.01



bits	optimized motif	location	MI (bits)	z-score	robustness	position bias	orientation bias	conservation index	seed	motif name
	5'	0.017	9.8	8/10	Y	→	0.99	ACGTGAA	-	
	5'	0.016	8.0	6/10	-	-	0.81	AACGTGA	-	
	3' UTR	0.016	9.0	9/10	Y	→	0.99	AAUAAA	-	