

over-representation



under-representation



extrinsic to membrane, p<0.01

phosphatase, transport<0.001, cytoskeleton, cell cycle, PS1, PS2, PS3, PS4, PS5, PS6, PS7, PS8, PS9, PS10, PS11, PS12, PS13, PS14, PS15, PS16, PS17, PS18, PS19, PS20, PS21, PS22, PS23, PS24, PS25, PS26, PS27, PS28, PS29, PS30, PS31, PS32, PS33, PS34, PS35, PS36, PS37, PS38, PS39, PS40, PS41, PS42, PS43, PS44, PS45, PS46, PS47, PS48, PS49, PS50, PS51, PS52, PS53, PS54, PS55, PS56, PS57, PS58, PS59, PS60, PS61, PS62, PS63, PS64, PS65, PS66, PS67, PS68, PS69, PS70, PS71, PS72, PS73, PS74, PS75, PS76, PS77, PS78, PS79, PS80, PS81, PS82, PS83, PS84, PS85, PS86, PS87, PS88, PS89, PS90, PS91, PS92, PS93, PS94, PS95, PS96, PS97, PS98, PS99, PS100

optimized motif	location	MI (bits)	z-score	robustness	position bias	orientation bias	conservation index	seed	motif name
	5'	0.018	13.3	10/10	-	←	0.97	AGAGAGA	-
	3'UTR	0.017	11.8	10/10	-	→	1.00	UCUUUCC	-
	5'	0.016	10.4	10/10	-	-	1.00	ATCGATA	-
	5'	0.016	10.7	10/10	Y	-	1.00	CTTATCA	-
	5'	0.013	7.0	6/10	-	→	0.96	TGATAAC	-
	5'	0.016	10.7	10/10	-	-	1.00	AACGCGC	-
	3'UTR	0.015	9.8	9/10	-	→	1.00	GAAUAAA	-
	3'UTR	0.015	9.6	10/10	-	→	0.98	UUUCCCU	-
	5'	0.015	9.1	10/10	-	→	0.95	TCCCTCC	-
	5'	0.014	7.8	7/10	-	→	0.89	AAGTTCA	-
	3'UTR	0.013	7.4	6/10	-	→	1.00	AAAUAAA	-