over-representation

under-representation

RNA processing, p<0.001

nucleoside-triphosphatase activity, p<0.01

ribonucleoprotein complex biogenesis, p<1e-05

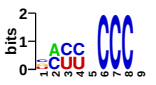
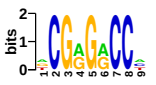
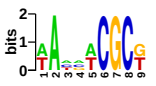
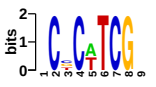
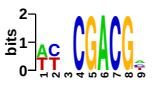
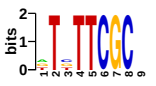
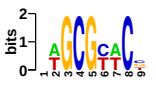
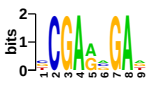
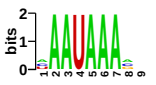
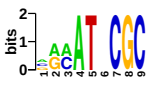
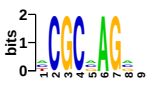
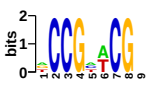
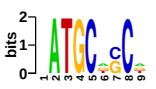
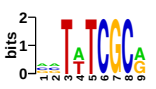
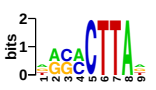
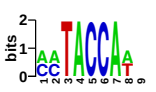
intracellular anatomical structure, p<1e-06

5770

1907

1

0

optimized motif	location	MI (bits)	z-score	robustness	position bias	orientation bias	conservation index	seed	motif name
	5′	0.027	23.2	10/10	Y	–	1.00	CGCGCTC	–
	3′UTR	0.023	18.7	10/10	Y	→	1.00	CUUUCCC	–
	5′	0.022	17.7	10/10	–	–	1.00	CGAGACC	–
	3′UTR	0.019	14.0	10/10	–	→	0.99	UAUUUAU	–
	5′	0.016	10.0	10/10	–	→	0.75	AAATCGC	–
	5′	0.022	17.0	10/10	–	–	1.00	AATCGAT	–
	5′	0.017	11.5	10/10	–	←	0.93	ACGAGAA	–
	5′	0.015	9.1	9/10	–	→	0.93	CTCTTCG	–
	5′	0.015	8.8	10/10	–	←	0.97	CACGACG	–
	5′	0.018	12.2	10/10	Y	→	0.95	TTTTCGC	–
	5′	0.017	11.8	10/10	–	–	0.98	TGCGTAC	–
	5′	0.014	7.5	7/10	–	←	0.75	CGAGAGA	–
	3′UTR	0.017	11.0	10/10	–	→	1.00	AAUAAAA	–
	5′	0.015	9.5	10/10	–	–	0.82	AAATGCG	–
	3′UTR	0.015	8.4	7/10	–	→	0.84	AUUCCUC	–
	5′	0.014	8.0	8/10	–	–	0.94	CACCTAC	–
	3′UTR	0.014	8.0	10/10	–	→	0.94	UUGUUAU	miR-44/miR-45/miR-61/miR-247
	5′	0.014	8.0	7/10	–	→	0.64	AACTTTG	–
	5′	0.014	7.9	10/10	–	←	0.97	ACCGTAG	–
	5′	0.014	7.5	6/10	–	←	1.00	CTTATCA	–
	5′	0.013	7.3	6/10	–	–	0.71	CGCCAGC	–
	5′	0.013	7.3	6/10	–	–	0.93	CCGCACG	–
	5′	0.013	7.1	7/10	–	–	0.95	ATGCGGC	–
	5′	0.013	7.1	7/10	–	←	0.94	ATTTCGC	–
	5′	0.013	6.9	6/10	–	–	0.21	AGACTTA	–
	5′	0.013	7.0	6/10	–	–	0.98	GTCCGCC	–
	5′	0.013	6.7	8/10	–	–	0.22	ATACCAA	–
	5′	0.012	5.9	6/10	–	←	0.83	AGTATGA	–