

Ontology	Biological role	p-value	Fold	Genes	Binding sites
GO Molecular Function	structural constituent of ribosome	1.5×10^{-27}	3.3	104	118
	unfolded protein binding	4.2×10^{-9}	2.5	49	54
	translation factor activity, nucleic acid binding	4.5×10^{-9}	2.3	56	60
	translation initiation factor activity	6.3×10^{-9}	2.9	36	41
	ribonucleoprotein binding	1.3×10^{-8}	4.0	24	25
GO Biological Process	RNA processing	1.3×10^{-39}	2.2	298	342
	translation	4.1×10^{-36}	2.7	185	205
	ncRNA metabolic process	9.3×10^{-29}	2.9	130	145
	ribonucleoprotein complex biogenesis	2.1×10^{-26}	2.8	131	142
	ncRNA processing	3.4×10^{-25}	3.0	109	122
GO Cellular Component	ribonucleoprotein complex	1.5×10^{-57}	2.6	302	351
	ribosome	6.2×10^{-27}	2.8	129	146
	ribosomal subunit	2.9×10^{-23}	3.4	81	92
	spliceosomal complex	1.5×10^{-19}	2.8	86	102
	large ribosomal subunit	1.9×10^{-17}	4.1	48	55
Mouse Phenotypes	-				
PANTHER Pathway	General transcription by RNA polymerase I	3.3×10^{-6}	6.1	10	11
	Transcription regulation by bZIP transcription factor	1.2×10^{-5}	2.7	23	26
Pathway Commons	mRNA Splicing	3.5×10^{-60}	4.2	164	192
	mRNA Splicing - Major Pathway	3.5×10^{-60}	4.2	164	192
	Transcription	2.8×10^{-50}	3.2	196	223
	Elongation arrest and recovery	1.7×10^{-49}	4.2	142	161
	Pausing and recovery of elongation	1.7×10^{-49}	4.2	142	161
BioCyc Pathway	tRNA charging pathway	1.3×10^{-4}	2.4	21	24
TreeFam	Zinc finger protein	1.0×10^{-18}	22.8	16	18
HGNC Gene Families	MRPL	3.1×10^{-16}	5.1	33	40
	PSM	8.6×10^{-11}	4.6	21	28
	ZSCANK	2.2×10^{-7}	5.5	12	15
	PSM, ATP, AATP	3.7×10^{-7}	12.6	6	8
	DDX	3.7×10^{-5}	2.4	22	28