

label	size	typical GO terms	p-value
0	4	ribosomal subunit export from nucleus	8.78E-03
7	3	NA	NA
36	5	NA	NA
40	7	NA	NA
41	13	NA	NA
42	2	NA	NA
54	15	urea cycle	3.14E-02
		heteroduplex formation	4.61E-02
		telomere maintenance via recombination	1.58E-02
		glutamine family amino acid metabolic p	6.34E-03
		alpha-amino acid biosynthetic process	2.99E-03
		aromatic compound biosynthetic proces	1.35E-02
		heterocycle biosynthetic process	1.26E-02
		organic cyclic compound biosynthetic pr	1.56E-02
63	28	cellular response to phosphate starvation	1.01E-02
		regulation of glycolytic process by positiv	1.72E-02
		gluconeogenesis	1.62E-04
		glycolytic process	1.95E-05
		cytoplasmic translation	2.23E-04
67	3	urea cycle	1.99E-02
		'de novo' pyrimidine nucleobase biosynt	1.31E-02
		arginine biosynthetic process	1.39E-02
77	14	vesicle fusion	3.44E-05
		Golgi to plasma membrane transport	1.89E-02
		exocytosis	1.68E-03
84	2	NA	NA
101	2	termination of RNA polymerase III transc	3.64E-02
		tRNA transcription by RNA polymerase II	2.26E-02
		transcription by RNA polymerase I	3.52E-02
113	5	NA	NA
126	19	galactose catabolic process via UDP-gal	2.97E-06
		positive regulation of transcription from	1.85E-02
		sucrose metabolic process	4.36E-02
133	2	NA	NA
175	11	NA	NA
201	20	NA	NA
249	2	NA	NA
253	4	NLS-bearing protein import into nucleus	1.13E-02
		nuclear pore organization	1.40E-02
		mRNA transport	4.83E-03
260	2	NA	NA
271	10	response to DNA damage checkpoint sig	1.70E-02
		negative regulation of glycogen biosynt	1.98E-02
		negative regulation of macroautophagy	2.38E-02
		negative regulation of DNA binding tran	2.55E-02
		mRNA polyadenylation	2.01E-02
		pre-mRNA cleavage required for polyad	4.30E-02
		regulation of protein stability	4.17E-02
282	3	rRNA 2'-O-methylation	8.90E-06
319	2	early endosome to Golgi transport	1.85E-02
331	4	translational elongation	8.23E-04
332	19	cytoplasmic translational initiation	1.72E-03
333	5	NA	NA
335	26	C-terminal protein lipidation	2.09E-05
		galactose transmembrane transport	3.46E-02
		late nucleophagy	2.92E-04
		glycogen metabolic process	1.47E-03

		autophagosome assembly	1.68E-03
		regulation of phosphoprotein phosphatase activity	2.04E-03
		autophagy of mitochondrion	1.90E-03
		piecemeal microautophagy of the nucleus	2.45E-03
		protein localization by the Cvt pathway	4.38E-03
336	9	NA	NA
337	7	NA	NA
338	4	L-serine biosynthetic process	4.99E-03
339	3	NA	NA
340	3	ribosome-associated ubiquitin-dependent proteolysis	2.56E-02
		positive regulation of protein localization	1.28E-02
		negative regulation of telomerase activity	1.07E-02
		retrograde protein transport, ER to cytosol	6.41E-03
		cytoplasm protein quality control by the chaperone	6.53E-03
		ER-associated misfolded protein catabolic pathway	6.94E-03
		nonfunctional rRNA decay	1.52E-02
		ubiquitin-dependent ERAD pathway	4.71E-02
342	7	protein import into peroxisome matrix, docking and targeting	1.98E-07
		fatty acid beta-oxidation	2.15E-02
343	8	ribosomal large subunit assembly	7.37E-03
		cytoplasmic translation	1.28E-05
347	9	NA	NA
348	9	NA	NA
349	3	NA	NA
350	2	tryptophan biosynthetic process	6.65E-03
351	5	glucose mediated signaling pathway	2.13E-02
		cell morphogenesis	2.88E-02
354	3	NA	NA
355	24	negative regulation of mating-type specific gene expression	2.10E-05
		negative regulation of dipeptide transport	3.19E-02
		regulation of fatty acid biosynthetic process	2.67E-02
		regulation of mating type switching	3.80E-02
		regulation of growth of unicellular organism	3.13E-02
		cellular response to pheromone	2.78E-02
		mitotic cell cycle phase transition	3.14E-02
		positive regulation of reproductive process	2.86E-02
		positive regulation of cellular process	2.56E-02
356	2	arsenate ion transmembrane transport	1.43E-03
		iron assimilation by reduction and transmembrane transport	1.78E-03
		iron ion transmembrane transport	3.27E-03