Biological Processes	Subprocess	Sub-subprocess	Sub-subprocess	# genes	Percent of gene hit against total # genes	Percent of gene hit against total # Pathway hits
metabolic process (GO:0008152)				109	56.80%	30.20%
	primary metabolic process (GO:0044238)			83	76.10%	68.60%
		lipid metabolic process (GO:0006629)		15	18.10%	14.00%
			steroid metabolic process (GO:0008202)	5	33.30%	41.70%
			phospholipid metabolic process (GO:0006644)	1	6.70%	8.30%
			fatty acid metabolic process (GO:0006631)	6	40.00%	50.00%
		cellular amino acid metabolic process (GO:0006520)		6	7.20%	5.60%
		protein metabolic process (GO:0019538)		37	44.60%	34.60%
			proteolysis (GO:0006508)	11	29.70%	30.60%
			translation (GO:0006412)	7	18.90%	19.40%
			protein complex assembly (GO:0006461)	2	5.40%	5.60%
			protein folding (GO:0006457)	4	10.80%	11.10%
			cellular protein modification process (GO:0006464)	12	32.40%	33.30%
		nucleobase-containing compound metabolic process (GO:0006139)		31	37.30%	29.00%
		tricarboxylic acid cycle (GO:0006099)		3	3.60%	2.80%
		carbohydrate metabolic process (GO:0005975)		15	18.10%	14.00%
	phosphate-containing compound metabolic process (GO:0006796)			5	4.60%	4.10%
	biosynthetic process (GO:0009058)			2	1.80%	1.70%
	vitamin metabolic process (GO:0006766)			3	2.80%	2.50%
	catabolic process (GO:0009056)			2	1.80%	1.70%
	sulfur compound metabolic process (GO:0006790)			1	0.90%	0.80%
	coenzyme metabolic process (GO:0006732)			8	7.30%	6.60%
	nitrogen compound metabolic process (GO:0006807)			6	5.50%	5.00%
	generation of precursor metabolites and energy (GO:0006091)			11	10.10%	9.10%
cellular component organization or biogenesis (GO:0071840)				35	18.20%	9.70%
cellular process (GO:0009987)				64	33.30%	17.70%
localization (GO:0051179)				25	13.00%	6.90%
apoptotic process (GO:0006915)				4	2.10%	1.10%
reproduction (GO:0000003)				4	2.10%	1.10%
biological regulation (GO:0065007)				27	14.10%	7.50%
response to stimulus (GO:0050896)				15	7.80%	4.20%
developmental process (GO:0032502)				33	17.20%	9.10%
multicellular organismal process (GO:0032501)				16	8.30%	4.40%
biological adhesion (GO:0022610)				10	5.20%	2.80%
immune system process (GO:0002376)				19	9.90%	5.30%

Molecular Function		# genes	Percent of gene hit against total # genes	Percent of gene hit against total # Pathway hits
catalytic activity (GO:0003824)		85	44.30%	37.30%
	helicase activity (GO:0004386)	4	4.70%	3.70%
	ligase activity (GO:0016874)	8	9.40%	7.40%
	oxidoreductase activity (GO:0016491)	21	24.70%	19.40%
	transferase activity (GO:0016740)	23	27.10%	21.30%
	enzyme regulator activity (GO:0030234)	15	17.60%	13.90%
	hydrolase activity (GO:0016787)	29	34.10%	26.90%
	lyase activity (GO:0016829)	4	4.70%	3.70%
	isomerase activity (GO:0016853)	4	4.70%	3.70%
transporter activity (GO:0005215)		11	5.70%	4.80%
translation regulator activity (GO:0045182)		3	1.60%	1.30%
protein binding transcription factor activity (GO:0000988)		3	1.60%	1.30%
enzyme regulator activity (GO:0030234)		15	7.80%	6.60%
receptor activity (GO:0004872)		12	6.30%	5.30%
nucleic acid binding transcription factor activity (GO:0001071)		7	3.60%	3.10%
antioxidant activity (GO:0016209)		1	0.50%	0.40%
structural molecule activity (GO:0005198)		27	14.10%	11.80%
binding (GO:0005488)		64	33.30%	28.10%