

	"p.value"	"term_goid"	"term_category"	"term_name"
"1"	1.50528447927e-05	"GO:0010647"	"b"	"positive regulation of cell communication"
"2"	2.91114085404e-05	"GO:0009967"	"b"	"positive regulation of signal transduction"
"3"	6.13351622493e-05	"GO:0030033"	"b"	"microvillus assembly"
"4"	0.000125564990642	"GO:0010604"	"b"	"positive regulation of macromolecule metabolic process"
"5"	0.000179023052873	"GO:0000975"	"m"	"regulatory region DNA binding"
"6"	0.000226353991561	"GO:0042612"	"c"	"MHC class I protein complex"
"7"	0.000302472252746	"GO:1903522"	"b"	"regulation of blood circulation"
"8"	0.000350247797198	"GO:0034341"	"b"	"response to interferon-gamma"
"9"	0.000352388126167	"GO:1902531"	"b"	"regulation of intracellular signal transduction"
"10"	0.000476728950817	"GO:0032608"	"b"	"interferon-beta production"
"11"	0.000518340413149	"GO:0032981"	"b"	"mitochondrial respiratory chain complex I assembly"
"12"	0.000638893434296	"GO:0019885"	"b"	"antigen processing and presentation of endogenous peptide antigen via MHC class I"
"13"	0.00064385627971	"GO:0003725"	"m"	"double-stranded RNA binding"
"14"	0.000661801365182	"GO:0006461"	"b"	"protein complex assembly"
"15"	0.000662272918632	"GO:0001819"	"b"	"positive regulation of cytokine production"
"16"	0.000686171054835	"GO:0060047"	"b"	"heart contraction"
"17"	0.000867050844667	"GO:0002476"	"b"	"antigen processing and presentation of endogenous peptide antigen via MHC class Ib"
"18"	0.00102579924309	"GO:0060333"	"b"	"interferon-gamma-mediated signaling pathway"
"19"	0.00107071421737	"GO:0030855"	"b"	"epithelial cell differentiation"
"20"	0.00124097244193	"GO:0003690"	"m"	"double-stranded DNA binding"
"21"	0.00126244194127	"GO:0031325"	"b"	"positive regulation of cellular metabolic process"
"22"	0.00134310080018	"GO:0060479"	"b"	"lung cell differentiation"
"23"	0.001356314282	"GO:0038180"	"b"	"nerve growth factor signaling pathway"
"24"	0.00150928090065	"GO:0005509"	"m"	"calcium ion binding"
"25"	0.00158323235938	"GO:0071556"	"c"	"integral component of lumenal side of endoplasmic reticulum membrane"
"26"	0.00159110169215	"GO:0009890"	"b"	"negative regulation of biosynthetic process"
"27"	0.00169064947762	"GO:0030133"	"c"	"transport vesicle"
"28"	0.00191045981383	"GO:0032479"	"b"	"regulation of type I interferon production"
"29"	0.00198912721172	"GO:0048194"	"b"	"Golgi vesicle budding"
"30"	0.00209441593385	"GO:0030135"	"c"	"coated vesicle"

"31" 0.00217420646132 "GO:0050136" (quinone) activity"	"m"	"NADH dehydrogenase
"32" 0.0021870576881 "GO:0005768"	"c"	"endosome"
"33" 0.00229827505608 "GO:0051092" kappaB transcription factor activity"	"b"	"positive regulation of NF-
"34" 0.00243668950099 "GO:0043565" binding"	"m"	"sequence-specific DNA
"35" 0.00265861779341 "GO:0010979" 24-hydroxylase activity"	"b"	"regulation of vitamin D
"36" 0.00265861779341 "GO:0034344" interferon production"	"b"	"regulation of type III
"37" 0.00323189645145 "GO:0032607" production"	"b"	"interferon-alpha
"38" 0.00336594815155 "GO:0010605" macromolecule metabolic process"	"b"	"negative regulation of
"39" 0.00344602584237 "GO:0051173" nitrogen compound metabolic process"	"b"	"positive regulation of
"40" 0.003735381812 "GO:0046719" viral protein levels in host cell"	"b"	"regulation by virus of
"41" 0.00385727815612 "GO:0071010"	"c"	"prespliceosome"
"42" 0.00444070784182 "GO:0051345" hydrolase activity"	"b"	"positive regulation of
"43" 0.00447238364669 "GO:0001649" differentiation"	"b"	"osteoblast
"44" 0.00472405984143 "GO:0032268" protein metabolic process"	"b"	"regulation of cellular
"45" 0.00521117856584 "GO:0021553" development"	"b"	"olfactory nerve
"46" 0.00521117856584 "GO:0034441" particle oxidation"	"b"	"plasma lipoprotein
"47" 0.00521117856584 "GO:0023029" binding"	"m"	"MHC class Ib protein
"48" 0.0054976670815 "GO:0009891" biosynthetic process"	"b"	"positive regulation of
"49" 0.00552466770798 "GO:0050688" response to virus"	"b"	"regulation of defense
"50" 0.00568608034424 "GO:0051172" nitrogen compound metabolic process"	"b"	"negative regulation of
"51" 0.00598877034979 "GO:0002687" leukocyte migration"	"b"	"positive regulation of
"52" 0.00619079669054 "GO:0038202"	"b"	"TORC1 signaling"
"53" 0.00619079669054 "GO:0016580"	"c"	"Sin3 complex"
"54" 0.00658551616223 "GO:0010556" macromolecule biosynthetic process"	"b"	"regulation of
"55" 0.00664217875107 "GO:0051246" metabolic process"	"b"	"regulation of protein
"56" 0.00680684979769 "GO:0005791" reticulum"	"c"	"rough endoplasmic
"57" 0.00716994730573 "GO:0001106" transcription corepressor activity"	"m"	"RNA polymerase II
"58" 0.00732100149639 "GO:0006338"	"b"	"chromatin remodeling"
"59" 0.00740757309213 "GO:0070252" contraction"	"b"	"actin-mediated cell
"60" 0.00770495212406 "GO:0051383"	"b"	"kinetochore organization"

"61"	0.00772783954084	"GO:0034620"	"b"	"cellular response to unfolded protein"
"62"	0.00815440699344	"GO:0019219"	"b"	"regulation of nucleobase-containing compound metabolic process"
"63"	0.00823555666766	"GO:0060428"	"b"	"lung epithelium development"
"64"	0.00823555666766	"GO:0004407"	"m"	"histone deacetylase activity"
"65"	0.00842953565803	"GO:0051252"	"b"	"regulation of RNA metabolic process"
"66"	0.00845313068004	"GO:0001885"	"b"	"endothelial cell development"
"67"	0.00851249953299	"GO:0070842"	"b"	"aggresome assembly"
"68"	0.00851249953299	"GO:0045159"	"m"	"myosin II binding"
"69"	0.00851249953299	"GO:0004301"	"m"	"epoxide hydrolase activity"
"70"	0.00851249953299	"GO:0046923"	"m"	"ER retention sequence binding"
"71"	0.00886868350522	"GO:0044409"	"b"	"entry into host"
"72"	0.00886868350522	"GO:0051806"	"b"	"entry into cell of other organism involved in symbiotic interaction"
"73"	0.0091072963588	"GO:0031324"	"b"	"negative regulation of cellular metabolic process"
"74"	0.00919562203072	"GO:0002221"	"b"	"pattern recognition receptor signaling pathway"
"75"	0.00974206465986	"GO:0001077"	"m"	"transcriptional activator activity, RNA polymerase II core promoter proximal region sequence-specific binding"
"76"	0.00990787888944	"GO:0032677"	"b"	"regulation of interleukin-8 production"