

"p.value"	"term_goid"	"term_category"	"term_name"
"1"	0.000274503133841	"GO:1990381"	"m" "ubiquitin-specific protease binding"
"2"	0.000500267892008	"GO:0032550"	"m" "purine ribonucleoside binding"
"3"	0.00053222237287	"GO:1904029"	"b" "regulation of cyclin-dependent protein kinase activity"
"4"	0.000754752783805	"GO:0022408"	"b" "negative regulation of cell-cell adhesion"
"5"	0.000863642885657	"GO:0045786"	"b" "negative regulation of cell cycle"
"6"	0.000904280970111	"GO:0006591"	"b" "ornithine metabolic process"
"7"	0.000964643345232	"GO:0070201"	"b" "regulation of establishment of protein localization"
"8"	0.00104696335435	"GO:0030855"	"b" "epithelial cell differentiation"
"9"	0.00128985401214	"GO:0051129"	"b" "negative regulation of cellular component organization"
"10"	0.00173178855607	"GO:0030554"	"m" "adenyl nucleotide binding"
"11"	0.00177665256278	"GO:0030133"	"c" "transport vesicle"
"12"	0.00201477938283	"GO:0010482"	"b" "regulation of epidermal cell division"
"13"	0.00233682935688	"GO:0006281"	"b" "DNA repair"
"14"	0.00251264034563	"GO:0097106"	"b" "postsynaptic density organization"
"15"	0.00278393091893	"GO:0097479"	"b" "synaptic vesicle localization"
"16"	0.00286535783216	"GO:0050866"	"b" "negative regulation of cell activation"
"17"	0.00293828747833	"GO:0034620"	"b" "cellular response to unfolded protein"
"18"	0.00364443463439	"GO:0043566"	"m" "structure-specific DNA binding"
"19"	0.00395968855205	"GO:0034287"	"b" "detection of monosaccharide stimulus"
"20"	0.00395968855205	"GO:0060283"	"b" "negative regulation of oocyte development"
"21"	0.00421525987826	"GO:0016310"	"b" "phosphorylation"
"22"	0.00440884045968	"GO:0051223"	"b" "regulation of protein transport"
"23"	0.0044776601323	"GO:0009119"	"b" "ribonucleoside metabolic process"
"24"	0.00453676759395	"GO:0006461"	"b" "protein complex assembly"
"25"	0.0048488503079	"GO:0031344"	"b" "regulation of cell projection organization"
"26"	0.00512526147812	"GO:0003684"	"m" "damaged DNA binding"
"27"	0.0057632700004	"GO:0016538"	"m" "cyclin-dependent protein serine/threonine kinase regulator activity"
"28"	0.00585431165563	"GO:0010942"	"b" "positive regulation of cell death"
"29"	0.00592121206667	"GO:0097480"	"b" "establishment of synaptic vesicle localization"

"30"	0.00592121206667	"GO:0099003"	"b"	"vesicle-mediated transport in synapse"
"31"	0.00640212346772	"GO:0008285"	"b"	"negative regulation of cell proliferation"
"32"	0.00647375832797	"GO:0006906"	"b"	"vesicle fusion"
"33"	0.00648529965197	"GO:0000268"	"m"	"peroxisome targeting sequence binding"
"34"	0.00654950071427	"GO:0016339"	"b"	"calcium-dependent cell-cell adhesion via plasma membrane cell adhesion molecules"
"35"	0.0065505338418	"GO:0009411"	"b"	"response to UV"
"36"	0.00750963326254	"GO:0004252"	"m"	"serine-type endopeptidase activity"
"37"	0.00778129898563	"GO:0031532"	"b"	"actin cytoskeleton reorganization"
"38"	0.00793365905828	"GO:0008017"	"m"	"microtubule binding"
"39"	0.00825114774636	"GO:0051046"	"b"	"regulation of secretion"
"40"	0.00843236048907	"GO:0050954"	"b"	"sensory perception of mechanical stimulus"
"41"	0.00876124561119	"GO:0032963"	"b"	"collagen metabolic process"
"42"	0.00921569982471	"GO:0042069"	"b"	"regulation of catecholamine metabolic process"
"43"	0.00921569982471	"GO:0022842"	"m"	"narrow pore channel activity"
"44"	0.00956001057409	"GO:2001300"	"b"	"lipoxin metabolic process"
"45"	0.00956001057409	"GO:1900193"	"b"	"regulation of oocyte maturation"
"46"	0.00956001057409	"GO:0004645"	"m"	"phosphorylase activity"
"47"	0.00956001057409	"GO:0034991"	"c"	"nuclear meiotic cohesin complex"
"48"	0.00956001057409	"GO:0001739"	"c"	"sex chromatin"
"49"	0.00963755055864	"GO:1903827"	"b"	"regulation of cellular protein localization"
"50"	0.00975281493122	"GO:0042278"	"b"	"purine nucleoside metabolic process"