

GOBP

GOCC

GOMF

	C2	C3	C4	C5	C6	C8
defense response to oomycetes	3.85e-04					
response to oomycetes	3.85e-04					
phloem or xylem histogenesis	1.04e-02					
S-glycoside metabolic process	1.04e-02					
obsolete glycosinolate metabolic process	1.04e-02					
glucosinolate metabolic process	1.04e-02					
response to ethylene	1.04e-02					
lead ion transport	1.04e-02					
isoprenoid transport	1.2e-02					
terpenoid transport	1.2e-02					
abscisic acid transport	1.2e-02					
ethylene-activated signaling pathway	2.18e-02					
response to jasmonic acid	2.2e-02					
glycosyl compound metabolic process	2.52e-02					
phosphorelay signal transduction system	2.68e-02					
cellular response to ethylene stimulus	2.71e-02					
monocarboxylic acid transport	3.36e-02					
organic hydroxy compound transport	3.81e-02					
cellular response to iron ion	4.05e-02					
carbon-sulfur lyase activity	1.14e-02					
arginyl-tRNA aminoacylation		2.88e-02				
arginine-tRNA ligase activity		5.43e-03				
aminoacyl-tRNA ligase activity		1.25e-02				
ligase activity, forming carbon-oxygen bonds		1.25e-02				
catalytic activity, acting on a tRNA		1.85e-02				
neuron differentiation			1.61e-02			
generation of neurons			1.61e-02			
liver development			1.61e-02			
hepaticobiliary system development			1.61e-02			
neurogenesis			1.61e-02			
eye development			1.61e-02			
sensory organ morphogenesis			1.61e-02			
appendage morphogenesis			1.61e-02			
appendage development			1.61e-02			
proteasome assembly			1.61e-02			
gland development			1.61e-02			
leaf senescence			1.61e-02			
plant organ senescence			1.61e-02			
post-translational protein modification			1.61e-02			
nervous system development			1.79e-02			
epithelial tube morphogenesis			1.79e-02			
animal organ development			1.84e-02			
sensory organ development			2.06e-02			
chordate embryonic development			2.06e-02			
protein-containing complex assembly			2.41e-02			
response to misfolded protein			2.41e-02		2.65e-02	
spermatogenesis			2.41e-02			
positive regulation of apoptotic process			2.41e-02			
morphogenesis of an epithelium			2.41e-02			
embryo development ending in birth or egg hatching			2.41e-02			
positive regulation of flower development			2.41e-02			
tissue morphogenesis			2.41e-02			
protein-containing complex organization			2.57e-02			
tube morphogenesis			2.57e-02			
obsolete aging			2.57e-02			
animal organ morphogenesis			2.59e-02			
behavior			2.85e-02			
positive regulation of programmed cell death			3.12e-02			
central nervous system development			3.67e-02			
protein modification by small protein removal			3.67e-02			
tube development			3.95e-02			
positive regulation of reproductive process			4.4e-02			
obsolete positive regulation of cell death			4.4e-02			
response to topologically incorrect protein			4.4e-02		1.19e-02	
positive regulation of hydrolase activity			4.46e-02			
embryonic morphogenesis			4.46e-02			
epithelium development			4.46e-02			
positive regulation of cell population proliferation			4.73e-02			
perinuclear region of cytoplasm			3.49e-02			
proteasome complex			3.49e-02			
endopeptidase complex			3.49e-02			
peptidase complex			3.49e-02			
polyubiquitin modification-dependent protein binding			4.84e-02			
nucleotide binding			4.84e-02			
nucleoside phosphate binding			4.84e-02			
adenyl nucleotide binding			4.84e-02			
adenyl ribonucleotide binding			4.84e-02			
DNA strand invasion				2.54e-03		
double-strand break repair via synthesis-dependent strand annealing				2.54e-03		
mitotic recombination				2.54e-03		
purine nucleoside triphosphate biosynthetic process				2.75e-02		
purine ribonucleoside triphosphate biosynthetic process				2.75e-02		
ribonucleoside triphosphate biosynthetic process				2.75e-02		
response to ionizing radiation				2.75e-02		
nucleoside triphosphate biosynthetic process				2.76e-02		
double-strand break repair via homologous recombination				3.22e-02		
recombinational repair				3.22e-02		
purine ribonucleoside triphosphate metabolic process				3.22e-02		
purine nucleoside triphosphate metabolic process				3.22e-02		
ribonucleoside triphosphate metabolic process				3.22e-02		
nucleoside triphosphate metabolic process				3.83e-02		
purine ribonucleotide biosynthetic process				4.11e-02		
purine nucleotide biosynthetic process				4.21e-02		
purine-containing compound biosynthetic process				4.43e-02		
protein-DNA complex assembly				4.43e-02		
four-way junction DNA binding				6.77e-04		
DNA secondary structure binding				2.66e-03		
single-stranded DNA binding				1.9e-02		
obsolete negative regulation of cellular macromolecule biosynthetic process						1.9e-03
negative regulation of macromolecule biosynthetic process						1.9e-03
negative regulation of gene expression						1.9e-03
negative regulation of cellular biosynthetic process						1.9e-03
negative regulation of biosynthetic process						1.9e-03
obsolete negative regulation of nitrogen compound metabolic process						3.64e-03
negative regulation of macromolecule metabolic process						3.64e-03
nuclear-transcribed mRNA catabolic process						3.64e-03
negative regulation of cellular metabolic process						5.32e-03
mRNA catabolic process						5.47e-03
negative regulation of translation						5.47e-03
obsolete regulation of histone modification						5.47e-03
negative regulation of amide metabolic process						5.47e-03
RNA catabolic process						7.99e-03
negative regulation of protein metabolic process						8.85e-03
obsolete regulation of histone H3-K27 methylation						1.05e-02
regulation of translation						1.75e-02
nuclear-transcribed mRNA poly(A) tail shortening						1.75e-02
regulation of chromatin organization						1.75e-02
obsolete RNA phosphodiester bond hydrolysis, exonucleolytic						1.77e-02
regulation of amide metabolic process						1.77e-02
nucleobase-containing compound catabolic process						1.77e-02
negative regulation of nucleobase-containing compound metabolic process						1.77e-02
obsolete RNA phosphodiester bond hydrolysis						2.37e-02
regulation of protein metabolic process						2.47e-02
regulation of mRNA stability						2.63e-02
negative regulation of long-day photoperiodism, flowering						2.63e-02
obsolete cellular nitrogen compound catabolic process						2.63e-02
mRNA metabolic process						2.63e-02
obsolete heterocycle catabolic process						2.63e-02
obsolete regulation of histone methylation						2.63e-02
obsolete aromatic compound catabolic process						2.63e-02
regulation of RNA stability						2.92e-02
nuclear-transcribed mRNA catabolic process, deadenylation-dependent decay						2.97e-02
regulation of mRNA catabolic process						2.97e-02
obsolete organic cyclic compound catabolic process						3.12e-02
regulation of organelle organization						3.12e-02
regulation of long-day photoperiodism, flowering						3.37e-02
negative regulation of cellular component organization						3.44e-02
regulation of chromosome organization						4.02e-02
chromosome						4.04e-04
chromatin						8.9e-04
obsolete chromosomal part						2.74e-02
small-subunit processome						2.74e-02
obsolete nuclear chromosome part						4.39e-02
nuclear chromosome						4.39e-02