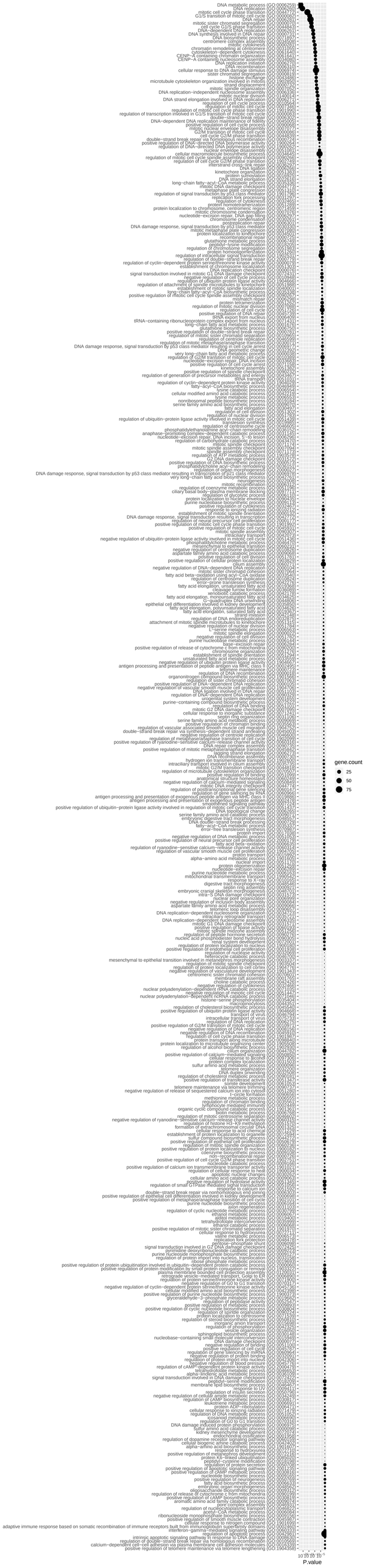
DNA metabolic process (GO:0006259)
DNA repair (GO:0006281)
mitotic cell cycle phase transition (GO:0044772)
G1/S transition of mitotic cell cycle (GO:0000082)
DNA repair (GO:0006281)
mitotic sister chromatid segregation (GO:0000070)
cell cycle G1/S phase transition (GO:0044843)
DNA-dependent DNA replication (GO:0006261)
DNA synthesis involved in DNA repair (GO:0000731)
DNA repair (GO:0006281)
centromere complex assembly (GO:0034508)
mitotic cytokinesis (GO:0000281)
chromatin remodeling at centromere (GO:0006338)
cytoskeleton-dependent cytokinesis (GO:0061640)
CENP-A containing chromatin organization (GO:0034080)
CENP-A containing nucleosome assembly (GO:0034080)
DNA repair (GO:0006281)
DNA recombination (GO:0006310)
cellular response to DNA damage stimulus (GO:0006974)
sister chromatid segregation (GO:0000819)
histone exchange (GO:0043486)
microtubule cytoskeleton organization involved in mitosis (GO:0000226)
strand displacement (GO:0006309)
mitotic cytokinesis (GO:0000281)
DNA replication-independent nucleosome assembly (GO:0006336)
mitotic nuclear division (GO:0140014)
DNA strand elongation involved in DNA replication (GO:0006271)
regulation of cell cycle process (GO:0010564)
mitotic cell cycle (GO:0000278)
regulation of mitotic cell cycle phase transition (GO:0045930)
regulation of transcription involved in G1/S transition of mitotic cell cycle (GO:0000083)
double-strand break repair (GO:0006302)
DNA-dependent DNA replication maintenance of fidelity (GO:0045005)
positive regulation of cell cycle process (GO:0010604)
mitotic nuclear envelope disassembly (GO:0000737)
cell cycle G1/S phase transition (GO:0044843)
cell cycle G2/M phase transition (GO:0044839)
double-strand break repair via homologous recombination (GO:0000724)
positive regulation of DNA-directed DNA polymerase activity (GO:0034104)
regulation of DNA-directed DNA polymerase activity (GO:0034654)
nuclear envelope disassembly (GO:0051081)
cellular macromolecule biosynthetic process (GO:0034645)
regulation of mitotic cell cycle spindle assembly checkpoint (GO:0090231)
regulation of cell cycle G2/M phase transition (GO:0010389)
interstrand cross-link repair (GO:0036297)
DNA ligation (GO:0006266)
kinetochore organization (GO:0051383)
protein sumoylation (GO:0016925)
DNA strand elongation (GO:0022616)
long-chain fatty-acyl-CoA metabolic process (GO:0035337)
mitotic DNA damage checkpoint (GO:0007093)
metaphase plate congression (GO:0051310)
regulation of signal transduction by p53 class mediator (GO:0010165)
replication fork processing (GO:0031297)
regulation of cytokinesis (GO:0032465)
protein homotetramerization (GO:0051289)
protein localization to chromosome (GO:0034502)
mitotic chromosome condensation (GO:0007076)
nucleotide-excision repair, DNA gap filling (GO:0006297)
chromosome condensation (GO:0030261)
postreplication repair (GO:0006301)
DNA damage response, signal transduction by p53 class mediator (GO:0030330)
mitotic metaphase plate congression (GO:0007080)
protein K63-linked ubiquitination (GO:0070534)
recombinational repair (GO:0000725)
glutathione metabolic process (GO:0006749)
peptidyl-lysine modification (GO:0018205)
regulation of chromosome segregation (GO:0051983)
protein homodimerization (GO:0042803)
regulation of intracellular signal transduction (GO:1902531)
regulation of cell cycle phase transition (GO:1901987)
regulation of cyclin-dependent protein serine/threonine kinase activity (GO:0045737)
establishment of chromosome localization (GO:0051303)
DNA replication checkpoint (GO:0000076)
signal transduction involved in mitotic G1 DNA damage checkpoint (GO:0072403)
negative regulation of cell cycle process (GO:0010948)
regulation of ubiquitin-protein ligase activity (GO:0051436)
regulation of attachment of mitotic spindle to kinetochore (GO:0051988)
establishment of mitotic spindle localization (GO:0040001)
long-chain fatty-acyl-CoA biosynthetic process (GO:0035338)
positive regulation of mitotic cell cycle spindle assembly checkpoint (GO:0090266)
mismatch repair (GO:0006298)
protein localization (GO:0045184)
regulation of mitotic nuclear division (GO:0007087)
regulation of cell cycle (GO:0051726)
positive regulation of DNA repair (GO:0045739)
tRNA export from nucleus (GO:0006409)
tRNA-containing ribonucleoprotein complex export from nucleus (GO:0000970)
long-chain fatty acid metabolic process (GO:0001676)
regulation of cell cycle phase transition (GO:1901988)
positive regulation of double-strand break repair (GO:0010792)
regulation of mitotic sister chromatid separation (GO:0010965)
regulation of centrosome cohesion (GO:0010826)
regulation of mitotic metaphase/anaphase transition (GO:0007091)
DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest (GO:0006977)
DNA geometric change (GO:0032392)
very long-chain fatty acid metabolic process (GO:0000038)
regulation of G2/M transition of mitotic cell cycle (GO:0010389)
nucleotide-excision repair, DNA incision (GO:0006289)
positive regulation of cell cycle arrest (GO:0071158)
kinetochore assembly (GO:0051382)
positive regulation of spindle checkpoint (GO:0090263)
regulation of generation of precursor metabolites and energy (GO:0043467)
mitotic spindle assembly (GO:0007052)
regulation of cyclin-dependent protein kinase activity (GO:0000079)
fatty-acyl-CoA biosynthetic process (GO:0046949)
lysine catabolic process (GO:0019475)
cellular modified amino acid catabolic process (GO:0042219)
lysine metabolic process (GO:0006553)
nonribosomal peptide biosynthetic process (GO:0019184)
serine family amino acid catabolic process (GO:0009071)
fatty acid elongation (GO:0019367)
regulation of cell division (GO:0051301)
regulation of nuclear division (GO:0051784)
regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle (GO:0051439)
transversion synthesis (GO:0070987)
regulation of centrosome cycle (GO:0046605)
phosphatidylethanolamine metabolic process (GO:0046337)
anaphase-promoting complex-dependent catabolic process (GO:0031145)
nucleotide-excision repair, DNA incision, 5'-to lesion (GO:0006297)
regulation of carbohydrate catabolic process (GO:0043471)
mitotic spindle checkpoint (GO:0071174)
mitotic spindle assembly checkpoint (GO:0071173)
spindle assembly checkpoint (GO:0071174)
regulation of G2/M transition (GO:0010389)
G2 DNA damage checkpoint (GO:0031572)
positive regulation of DNA biosynthetic process (GO:2000573)
phosphatidylcholine acyl-chain remodeling (GO:0036151)
regulation of organ morphogenesis (GO:0009887)
DNA damage response, signal transduction by p53 class mediator resulting in transcription of p21 class mediator (GO:0006979)
very long-chain fatty acid biosynthetic process (GO:0042761)
DNA repair (GO:0006281)
mitotic recombination (GO:0006312)
regulation of coenzyme metabolic process (GO:0051196)
ciliary basal body-plasma membrane docking (GO:0097711)
regulation of glycolytic process (GO:0006110)
protein localization to nuclear envelope (GO:0090150)
purine nucleobase biosynthetic process (GO:0009113)
protein localization (GO:0045184)
response to ionizing radiation (GO:0010212)
establishment of mitotic spindle orientation (GO:0000132)
DNA damage response, signal transduction resulting in transcription (GO:0042770)
regulation of neural precursor cell proliferation (GO:0061101)
positive regulation of mitotic cell cycle (GO:0045930)
positive regulation of cell cycle (GO:0045787)
mitotic spindle assembly (GO:0007052)
pituitary transport (GO:0051574)
negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle (GO:0051436)
phosphatidylcholine metabolic process (GO:0046470)
mesenchymal to epithelial transition (GO:0060231)
negative regulation of cell cycle process (GO:0010948)
aspartate family amino acid catabolic process (GO:0009068)
positive regulation of cell division (GO:0051781)
positive regulation of cellular protein localization (GO:0070727)
cilium assembly (GO:0060271)
negative regulation of DNA-dependent DNA replication (GO:0045814)
mitotic sister chromatid cohesion (GO:0007064)
fatty acid beta-oxidation (GO:0006635)
regulation of centrosome duplication (GO:0010824)
error-prone translesion synthesis (GO:0070987)
fatty acid elongation, unsaturated fatty acid (GO:0019367)
cleavage furrow formation (GO:0036089)
xenobiotic catabolic process (GO:0042178)
fatty acid elongation, monounsaturated fatty acid (GO:0034625)
cellular response to DNA damage (GO:0006974)
epithelial cell differentiation involved in kidney development (GO:0072243)
fatty acid elongation, polyunsaturated fatty acid (GO:0034626)
fatty acid elongation, saturated fatty acid (GO:0019367)
strand invasion (GO:0000150)
regulation of DNA endoreduplication (GO:0032875)
attachment of mitotic spindle microtubules to kinetochore (GO:0051315)
negative regulation of cell cycle (GO:0045786)
L-serine metabolic process (GO:0006563)
mitotic spindle elongation (GO:0000022)
negative regulation of cell division (GO:0051782)
purine nucleobase metabolic process (GO:0006144)
base-excision repair (GO:0006284)
positive regulation of release of cytochrome c from mitochondria (GO:0090200)
cilium organization (GO:0044782)
establishment of spindle orientation (GO:0051294)
unsaturated fatty acid metabolic process (GO:0033559)
negative regulation of ubiquitin protein ligase activity (GO:0051438)
antigen processing and presentation of peptide antigen via MHC class I (GO:0019885)
telomere maintenance (GO:0000723)
regulation of DNA recombination (GO:0000018)
organonitrogen compound catabolic process (GO:1901565)
regulation of sister chromatid cohesion (GO:0051984)
positive regulation of DNA-dependent DNA replication (GO:0045740)
negative regulation of vascular smooth muscle cell proliferation (GO:1904754)
DNA ligation involved in DNA repair (GO:0051103)
regulation of DNA-dependent DNA replication (GO:0006275)
chromatin system development (GO:0061982)
purine-containing compound metabolic process (GO:0072521)
regulation of DNA binding (GO:0051101)
mitotic G2 DNA damage checkpoint (GO:0007095)
cellular response to inorganic substance (GO:0071241)
septin ring organization (GO:0031106)
serine family amino acid metabolic process (GO:0006563)
positive regulation of chromatin binding (GO:0035561)
regulation of vascular associated smooth muscle cell migration (GO:1904752)
double-strand break repair via synthesis-dependent strand annealing (GO:0000731)
negative regulation of centriole replication (GO:0046600)
regulation of metaphase/anaphase transition of cell cycle (GO:0044772)
positive regulation of ryanodine-sensitive calcium-release channel activity (GO:0060315)
DNA-dependent DNA replication (GO:0006261)
positive regulation of mitotic metaphase/anaphase transition (GO:0045842)
lagging strand elongation (GO:0006273)
DNA recombinase assembly (GO:0000730)
hydrogen ion transmembrane transport (GO:1902600)
intraciliary transport involved in cilium assembly (GO:0044458)
regulation of microtubule polymerization (GO:0032886)
positive regulation of binding (GO:0030695)
anatomical structure homeostasis (GO:0060249)
negative regulation of calcium-mediated signaling (GO:0050848)
mitotic DNA integrity checkpoint (GO:0044774)
regulation of posttranscriptional gene silencing (GO:0060147)
regulation of gene silencing by RNA (GO:0060966)
antigen processing and presentation of exogenous peptide antigen (GO:0019884)
antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-independent (GO:0002479)
smoothened signaling pathway (GO:0007224)
positive regulation of ubiquitin-protein ligase activity involved in regulation of mitotic cell cycle transition (GO:0031929)
DNA topological change (GO:0006265)
serine family amino acid catabolic process (GO:0009071)
embryonic digestive tract morphogenesis (GO:0048557)
DNA repair (GO:0006281)
fatty-acyl-CoA metabolic process (GO:0035337)
error-free translesion synthesis (GO:0070987)
protein import (GO:0017038)
negative regulation of DNA metabolic process (GO:0051052)
positive regulation of neural precursor cell proliferation (GO:0061101)
fatty acid beta-oxidation (GO:0006635)
regulation of ryanodine-sensitive calcium-release channel activity (GO:0060314)
regulation of vascular smooth muscle cell proliferation (GO:1904705)
protein transport (GO:0015031)
alpha-amino acid metabolic process (GO:0006520)
nuclear import (GO:0051170)
protein oligomerization (GO:0051259)
nucleotide-excision repair (GO:0006289)
purine nucleotide metabolic process (GO:0006163)
mitochondrial transmembrane transport (GO:0006839)
response to X-ray (GO:0010165)
digestive tract morphogenesis (GO:0048557)
septin ring assembly (GO:0000921)
embryonic cranial skeleton morphogenesis (GO:0048701)
intra-S DNA damage checkpoint (GO:0031573)
nucleus organization (GO:0006997)
negative regulation of inclusion body assembly (GO:0090084)
aspartate family amino acid metabolic process (GO:0009068)
telomeric loop disassembly (GO:0070929)
DNA replication-dependent nucleosome organization (GO:0034723)
intracisternal retrograde transport (GO:0061816)
DNA replication-dependent nucleosome assembly (GO:0034723)
cellular response to ionizing radiation (GO:0071479)
positive regulation of lipase activity (GO:0010884)
mitotic spindle midzone assembly (GO:0051256)
regulation of peptide hormone secretion (GO:0002791)
nucleic acid phosphodiester bond hydrolysis (GO:0090305)
negative regulation of protein binding (GO:0032091)
regulation of protein localization to nucleus (GO:1904772)
positive regulation of endothelial cell proliferation (GO:1903588)
regulation of nucleobase activity (GO:0019208)
heterocycle catabolic process (GO:0046700)
mesenchymal to epithelial transition involved in metanephros morphogenesis (GO:0072179)
regulation of mitotic spindle checkpoint (GO:1903504)
regulation of protein localization (GO:0032880)
negative regulation of vasculature development (GO:1904018)
centromeric sister chromatid cohesion (GO:0070601)
membrane cell assembly (GO:0071666)
choline catabolic process (GO:0042426)
negative regulation of cytokinesis (GO:0061640)
nucleotide metabolic process (GO:0009117)
nuclear polyadenylation-dependent rRNA catabolic process (GO:0071051)
negative regulation of ubiquitin protein ligase activity (GO:0051438)
nuclear polyadenylation-dependent tRNA catabolic process (GO:0071044)
histone-serine phosphorylation (GO:0035404)
macropinocytosis (GO:0044351)
regulation of cholesterol biosynthetic process (GO:0045540)
positive regulation of ubiquitin protein ligase activity (GO:0051439)
intracellular transport of virus (GO:0046790)
regulation of DNA replication (GO:0006275)
positive regulation of G2/M transition of mitotic cell cycle (GO:0010971)
negative regulation of DNA replication (GO:0045814)
negative regulation of DNA recombination (GO:0045910)
regulation of cell cycle phase transition (GO:1901987)
protein localization to chromosome, telomeric region (GO:0070525)
regulation of alcohol biosynthetic process (GO:0046519)
cilium organization (GO:0044782)
positive regulation of calcium-mediated signaling (GO:0050850)
cellular response to biotin (GO:0071522)
protein complex localization (GO:0031365)
sulfur amino acid metabolic process (GO:0006790)
DNA duplex unwinding (GO:0032508)
regulation of cholesterol metabolic process (GO:0090181)
positive regulation of transferase activity (GO:0051347)
somite development (GO:0061053)
telomere maintenance via telomere trimming (GO:0090166)
negative regulation of release of sequestered calcium ion into cytosol (GO:0051279)
sulfur compound metabolic process (GO:0006790)
methionine metabolic process (GO:0009086)
regulation of chromatin binding (GO:0120183)
lymphocyte mediated immunity (GO:0002449)
organic cyclic compound catabolic process (GO:1901361)
biotin metabolic process (GO:0006768)
regulation of mitotic centrosome separation (GO:0060236)
negative regulation of ryanodine-sensitive calcium-release channel activity (GO:0060316)
regulation of histone H3-K9 methylation (GO:0051570)
formation of extrachromosomal circular DNA (GO:0001124)
cellular response to acid chemical (GO:0071229)
establishment of protein localization to organelle (GO:0072594)
sulfur amino acid catabolic process (GO:0000096)
positive regulation of endothelial cell proliferation (GO:1903588)
regulation of mitotic spindle organization (GO:0060236)
positive regulation of protein localization to nucleus (GO:1904772)
coenzyme biosynthetic process (GO:0009108)
non-recombinational repair (GO:0000726)
positive regulation of cell cycle G2/M phase transition (GO:1902751)
nucleoside catabolic process (GO:0009164)
positive regulation of calcium ion transmembrane transport activity (GO:1903553)
regulation of apoptosis (GO:0042981)
apoptotic nuclear changes (GO:0030262)
cellular amino acid catabolic process (GO:0009063)
positive regulation of hydrolase activity (GO:0051345)
positive regulation of small GTPase mediated signal transduction (GO:0051056)
cellular response to biotin (GO:0071522)
double-strand break repair via nonhomologous end joining (GO:0006303)
positive regulation of epithelial cell differentiation involved in kidney development (GO:0072243)
positive regulation of metaphase/anaphase transition of cell cycle (GO:0045842)
purine nucleotide biosynthetic process (GO:0006164)
axon regeneration (GO:0031103)
regulation of cyclic nucleotide metabolic process (GO:0030799)
cellular response to acid (GO:0071229)
alditol metabolic process (GO:0019400)
tetrahydrofolate interconversion (GO:0035999)
ethanol catabolic process (GO:0006068)
positive regulation of mitotic sister chromatid separation (GO:1901970)
cellular response to hydroxyurea (GO:0071479)
valine metabolic process (GO:0006573)
nucleotide biosynthetic process (GO:0009165)
pentose-phosphate shunt (GO:0009052)
signal transduction involved in G2 DNA damage checkpoint (GO:0072422)
pyrimidine deoxyribonucleotide catabolic process (GO:0046386)
purine nucleoside monophosphate biosynthetic process (GO:0009127)
regulation of protein import into nucleus, translocation (GO:0060080)
ribose phosphate metabolic process (GO:0019693)
positive regulation of protein ubiquitination involved in ubiquitin-dependent protein catabolic process (GO:0031398)
positive regulation of protein modification by small protein conjugation or removal (GO:0070534)
plasma membrane bounded cell projection assembly (GO:0120031)
retrograde vesicle-mediated transport, Golgi to ER (GO:0006886)
regulation of protein serine/threonine kinase activity (GO:0071900)
negative regulation of G0 to G1 transition (GO:0070316)
negative regulation of cyclin-dependent protein serine/threonine kinase activity (GO:0045736)
regulation of G0 to G1 transition (GO:0070314)
positive regulation of purine nucleotide biosynthetic process (GO:0010918)
glyceraldehyde-3-phosphate metabolic process (GO:0019682)
regulation of peptidase activity (GO:0052547)
positive regulation of metabolic process (GO:0009893)
positive regulation of cell cycle (GO:0045787)
regulation of spindle organization (GO:0051988)
regulation of cell cycle phase transition (GO:1901987)
regulation of steroid biosynthetic process (GO:0010894)
inorganic anion transport (GO:0015698)
regulation of phosphorylation (GO:0042325)
vesicle organization (GO:0016050)
sphingolipid biosynthetic process (GO:0030148)
nucleobase-containing small molecule interconversion (GO:0015949)
DNA repair (GO:0006281)
negative regulation of binding (GO:0051100)
positive regulation of cell cycle (GO:0045787)
regulation of gene silencing by miRNA (GO:0060964)
negative regulation of protein binding (GO:0032091)
regulation of protein import into nucleus (GO:0051170)
negative regulation of blood pressure (GO:0045776)
regulation of cAMP-mediated protein kinase activity (GO:0034199)
tetrahydrofolate metabolic process (GO:0046653)
alpha-linolenic acid metabolic process (GO:0036109)
signal transduction involved in DNA damage checkpoint (GO:0072401)
peptidyl-serine modification (GO:0018209)
membrane lipid biosynthetic process (GO:0046467)
response to UV (GO:0009411)
regulation of insulin secretion (GO:0050796)
negative regulation of cellular amide metabolic process (GO:0034249)
regulation of cAMP biosynthetic process (GO:0030817)
leukotriene metabolic process (GO:0006691)
protein ADP-ribosylation (GO:0006471)
cellular response to hydroxyurea (GO:0071479)
regulation of DNA metabolic process (GO:0051052)
icosanoid metabolic process (GO:0006690)
regulation of G0 to G1 transition (GO:0070316)
DNA damage induced protein phosphorylation (GO:0006975)
sulfur amino acid catabolic process (GO:0000096)
kidney mesenchyme development (GO:0072179)
regulation of cell cycle phase transition (GO:1901987)
regulation of dopamine receptor signaling pathway (GO:0010795)
cellular biogenic amine catabolic process (GO:0042402)
alpha-linolenic acid biosynthetic process (GO:0036108)
response to hydroxyurea (GO:0071479)
positive regulation of metanephros development (GO:0072215)
protein K6-linked ubiquitination (GO:0085020)
regulation of ATP biosynthesis (GO:0046034)
regulation of protein secretion (GO:0050708)
positive regulation of lipoprotein signaling pathway (GO:0075101)
positive regulation of cAMP metabolic process (GO:0030818)
nucleotide biosynthetic process (GO:0009165)
positive regulation of neurogenesis (GO:0050769)
fatty acid biosynthetic process (GO:0006633)
embryonic organ development (GO:0048568)
oligosaccharide biosynthetic process (GO:0009312)
regulation of release of cytochrome c from mitochondria (GO:0090199)
positive regulation of cAMP biosynthetic process (GO:0030819)
aromatic amino acid family catabolic process (GO:0009074)
pore complex assembly (GO:0046931)
regulation of nucleocytoplasmic transport (GO:0046825)
regulation of ATP biosynthetic process (GO:0046034)
ribonucleoside monophosphate biosynthetic process (GO:0009156)
positive regulation of smooth muscle contraction (GO:0045987)
cellular response to hydroxyurea (GO:0071479)
adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains (GO:0002460)
interferon-gamma-mediated signaling pathway (GO:0060333)
regulation of adaptive immune response (GO:0002819)
intrinsic apoptotic signaling pathway (GO:0070228)
regulation of double-strand break repair via homologous recombination (GO:0010569)
calcium-dependent cell-cell adhesion via plasma membrane cell adhesion molecules (GO:0016339)
positive regulation of telomere maintenance via telomere lengthening (GO:1904358)
gene.count
25
50
75
10
10
10
10
P.value