Pathways
carbohydrate derivative transport (GO:1901264)
translational initiation (GO:0006413)
cysteine metabolic process (GO:0006534)
cellular response to drug (GO:0035690)
negative regulation of growth (GO:0045926)
organophosphate ester transport (GO:0015748)
viral transcription (GO:0019083)
acylglycerol homeostasis (GO:0055090)
early endosome to late endosome transport (GO:0045022)
response to insulin (GO:0032868)
organic acid transmembrane transport (GO:1903825)
carnitine metabolic process (GO:0009437)
carbohydrate transmembrane transport (GO:0034219)
adaptive thermogenesis (GO:1990845)
flavonoid metabolic process (GO:0009812)
organophosphate catabolic process (GO:0046434)
protein targeting to peroxisome (GO:0006625)
intestinal absorption (GO:0050892)
lipid transport (GO:0006869)
negative regulation of protein phosphorylation (GO:0001933)
carbohydrate transport (GO:0008643)
vitamin metabolic process (GO:0006766)
peroxisome organization (GO:0007031)
response to metal ion (GO:0010038)
peroxisomal transport (GO:0043574)
fatty acid derivative metabolic process (GO:1901568)
digestion (GO:0007586)
lipid homeostasis (GO:0055088)
antibiotic metabolic process (GO:0016999)
lipid localization (GO:0010876)
cellular aldehyde metabolic process (GO:0006081)
cellular ketone metabolic process (GO:0042180)
cellular response to oxidative stress (GO:0034599)
sulfur compound metabolic process (GO:0006790)
response to oxidative stress (GO:0006979)
nucleoside bisphosphate metabolic process (GO:0033865)
cellular modified amino acid metabolic process (GO:0006575)
alcohol metabolic process (GO:0006066)
response to xenobiotic stimulus (GO:0009410)
detoxification (GO:0098754)
organic acid transport (GO:0015849)
hormone metabolic process (GO:0042445)
response to nutrient levels (GO:0031667)
monosaccharide metabolic process (GO:0005996)
protein localization to endoplasmic reticulum (GO:0070972)
coenzyme metabolic process (GO:0006732)
xenobiotic metabolic process (GO:0006805)
organic anion transport (GO:0015711)
ammonium ion metabolic process (GO:0097164)
fatty acid metabolic process (GO:0006631)
DOWNREGULATED_GENES
regulation of I−kappaB kinase/NF−kappaB signaling (GO:0043122)
protein localization to chromosome, centromeric region (GO:0071459)
antigen processing and presentation of exogenous peptide antigen (GO:0002478)
signal transduction by p53 class mediator (GO:0072331)
histone phosphorylation (GO:0016572)
humoral immune response (GO:0006959)
mitotic nuclear envelope disassembly (GO:0007077)
leukocyte cell−cell adhesion (GO:0007159)
chromatin remodeling at centromere (GO:0031055)
oocyte maturation (GO:0001556)
tolerance induction (GO:0002507)
response to virus (GO:0009615)
leukocyte proliferation (GO:0070661)
positive regulation of interleukin−1 beta production (GO:0032731)
mitotic cytokinesis (GO:0000281)
anaphase−promoting complex−dependent catabolic process (GO:0031145)
signal transduction in response to DNA damage (GO:0042770)
phagocytosis (GO:0006909)
production of molecular mediator of immune response (GO:0002440)
immunoglobulin production (GO:0002377)
ciliary basal body−plasma membrane docking (GO:0097711)
membrane invagination (GO:0010324)
protein localization to microtubule cytoskeleton (GO:0072698)
establishment of chromosome localization (GO:0051303)
cellular response to interferon−gamma (GO:0071346)
lymphocyte mediated immunity (GO:0002449)
adaptive immune response based on .. (GO:0002460)
regulation of lymphocyte activation (GO:0051249)
centrosome cycle (GO:0007098)
DNA replication (GO:0006260)
sister chromatid segregation (GO:0000819)
organelle fission (GO:0048285)
chromosome segregation (GO:0007059)
nuclear division (GO:0000280)
UPREGULATED_GENES
p.adjust
0.0004
0.0008
0.0012
0.0016
GeneRatio
0.025
0.050
0.075