

Typical GO terms	p-value
xenobiotic transport	2.50E-05
glycine biosynthetic process from serine	2.34E-02
mannosyl-inositol phosphorylceramide biosynthetic process	2.34E-02
pre-miRNA processing	2.34E-02
box H/ACA snoRNA processing	2.34E-02
production of siRNA involved in RNA interference	2.34E-02
cellular response to tetrahydrofolate	2.34E-02
N-acetylglucosamine metabolic process	2.34E-02
microtubule anchoring	2.34E-02
arsenate ion transmembrane transport	2.34E-02
plasma membrane acetate transport	3.11E-02
positive regulation of G1 to G0 transition	3.11E-02
L-serine catabolic process	3.11E-02
primary miRNA processing	3.11E-02
response to cycloheximide	3.11E-02
water transport	3.88E-02
morphogenesis checkpoint	3.88E-02
post-chaperonin tubulin folding pathway	3.88E-02
putrescine transport	3.88E-02
pentose transmembrane transport	3.88E-02
positive regulation of cellular response to drug	3.88E-02
cellular response to phosphate starvation	3.88E-02
spermidine transmembrane transport	3.88E-02
spermine transmembrane transport	3.88E-02
positive regulation of transcription involved in meiotic cell cycle	3.88E-02
sterol import	3.19E-03
tubulin complex assembly	3.81E-03
drug export	8.25E-04
regulation of cell size	2.59E-02
positive regulation of autophagy	2.59E-02
septin ring organization	3.06E-02
regulation of cyclin-dependent protein serine/threonine kinase activity	3.56E-02
divalent inorganic cation transport	3.92E-02
organelle assembly	1.11E-02
cation homeostasis	3.71E-02
cellular macromolecule metabolic process	1.35E-02

