glutamate−5−semialdehyde dehydrogenase activity
glutamate 5−kinase activity
catalytic activity

proline catabolic process
ornithine biosynthetic process
methionyl−tRNA aminoacylation
methionine catabolic process
citrulline biosynthetic process
4−hydroxyproline catabolic process
cellular amino acid metabolic process

amide biosynthetic process
cellular nitrogen compound

negative regulation of cytoplasmic translational initiation in response to stress
cytoplasmic translation

catalysis of the reaction: 2 L−glutamate + NAD+ = 2−oxoglutarate + L−glutamine + H+ + NADH
glutamate synthase (NADH) activity

glutamate dehydrogenase [NAD(P)+] activity
catalysis of the formation of L−glutamine and 2−oxoglutarate from L−glutamate
glutamate synthase activity

catalysis of the reaction: ATP + L−glutamate + NH4+ = ADP + H+ + L−glutamine + phosphate
glutamine synthetase activity

the directed movement of glutamine, 2−amino−4−carbamoylbutanoic acid
glutamine transport

Hsp90 protein binding
Hsp70 protein binding
heat shock protein binding

spermine acetylation
spermidine acetylation
regulation of protein metabolic process
putrescine acetylation
positive regulation of RNA biosynthetic process
nor−spermidine metabolic process
nitrogen compound metabolic process

protein phosphorylation
protein metabolic process

response to melanocyte−stimulating hormone
cellular response to histidine
cellular response to gonadotropin−releasing hormone
cellular response to diamide
cellular response to cGMP
cellular response to benomyl
response to nitrogen compound

response to food
positive regulation of cellular response to amino acid starvation
negative regulation of appetite
chemotaxis to folate
response to nutrient levels

response to hypoxia
response to heat
eiF2alpha phosphorylation in response to endoplasmic reticulum stress
cellular stress response to acidic pH
response to stress

DEG.GO.terms
DMG.GO.terms
Method

Number of Genes
500
1000
1500
2000

Adjusted p−value
0.04
0.03
0.02
0.01