



- 1: 2.37 GO:0042623-ATPase activity,coupled
- 2: 2.58 GO:0043452-ATPase activity,coupled to movement of substances
- 3: 2.58 GO:0042626-ATPase activity,coupled to transmembrane movement of substances
- 4: 2.47 GO:0016820-hydrolase activity,acting on acid anhydrides,catalyzing transmembrane movement of substances
- 5: 2.37 GO:0015405-P-P bond hydrolysis-driven transmembrane transporter activity
- 6: 2.37 GO:0015398-primary active transmembrane transporter activity
- 7: 3.6 egg0260.glycine,serine and threonine metabolism
- 8: 1.43 GO:0017036-purine nucleotide binding
- 9: 1.34 GO:0001066-nucleotide binding
- 10: 1.38 GO:0030504-adenyl nucleotide binding
- 11: 1.38 GO:0001883-purine nucleoside binding
- 12: 1.38 GO:0032505-purine ribonucleotide binding
- 13: 1.38 GO:0032553-ribonucleotide binding
- 14: 1.37 GO:0001882-nucleoside binding
- 15: 1.35 GO:0005524-ATP binding
- 16: 1.35 GO:0032509-adenyl ribonucleotide binding
- 17: 1.22 atp-binding
- 18: 1.2 nucleotide binding
- 19: 2.72 GO:0042398-cellular amino acid derivative biosynthetic process
- 20: 2.15 GO:0006075-cellular amino acid derivative metabolic process
- 21: 1.57 GO:0009309-amine biosynthetic process
- 22: 1.54 GO:0046394-carboxylic acid biosynthetic process
- 23: 1.54 GO:0016053-organic acid biosynthetic process
- 24: 1.56 GO:0008652-cellular amino acid biosynthetic process
- 25: 4.18 domain ABC transporter 1
- 26: 4.18 domain ABC transporter 2
- 27: 1.7 GO:0011090-organelle membrane
- 28: 1.9 GO:0030312-external encapsulating structure
- 29: 1.7 GO:0009274-peptidoglycan-based cell wall
- 30: 1.9 GO:000918-cell wall
- 31: 5.82 GO:0016226-iron-sulfur cluster assembly
- 32: 5.82 GO:0011163-metallo-sulfur cluster assembly
- 33: 1.27 GO:0011090-organelle membrane
- 34: 1.24 GO:0011067-organelle envelope
- 35: 1.24 GO:0019866-organelle inner membrane
- 36: 1.14 GO:001975-envelope

- group 1: 1.63
- group 2: 1.44
- group 3: 1.29
- group 4: 1.27
- group 5: 1.25
- group 6: 1.18
- group 7: 1.18
- group 8: 1.05
- group 9: 1.04