



- 1: 2.66 GO:0016053~organic acid biosynthetic process
- 2: 2.66 GO:0046394~carboxylic acid biosynthetic process
- 3: 2.82 GO:0008652~cellular amino acid biosynthetic process
- 4: 2.72 GO:0009309~amine biosynthetic process
- 5: 6.9 amino-acid transport
- 6: 3.82 GO:0006865~amino acid transport
- 7: 3.54 GO:0015837~amine transport
- 8: 2.86 GO:0046942~carboxylic acid transport
- 9: 2.86 GO:0015849~organic acid transport
- 10: 11.59 PIRSF002740:lysine-arginine-ornithine-binding protein
- 11: 9.33 SM00062:PBpb
- 12: 9.07 IPR001638:Extracellular solute-binding protein,family 3
- 13: 12.1 IPR015683:Glutamate receptor-related
- 14: 10.37 IPR018313:Extracellular solute-binding protein,family 3,conserved site
- 15: 10.89 IPR005768:lysine-arginine-ornithine-binding periplasmic protein
- 16: 4.02 GO:0015171~amino acid transmembrane transporter activity
- 17: 3.56 GO:0005275~amine transmembrane transporter activity
- 18: 9.07 IPR004840:Amino acid permease,conserved site
- 19: 5.04 IPR002293:Amino acid/polyamine transporter I
- 20: 5.04 IPR004841:Amino acid permease-associated region
- 21: 4.51 PIRSF006060:AA transporter
- 22: 3.82 PIRSF006060:amino acid transporter
- 23: 6.72 branched-chain amino acid biosynthesis
- 24: 5.35 GO:0009082~branched chain family amino acid biosynthetic process
- 25: 4.4 GO:0009081~branched chain family amino acid metabolic process
- 26: 3.91 sec00290:Valine,leucine and isoleucine biosynthesis
- 27: 4.33 GO:0003887~DNA-directed DNA polymerase activity
- 28: 4.33 GO:0034061~DNA polymerase activity
- 29: 1.8 GO:0006260~DNA replication
- 30: 1.65 GO:0030312~external encapsulating structure
- 31: 1.62 GO:0030313~cell envelope
- 32: 1.6 GO:0031975~envelope
- 33: 3.94 GO:0009073~aromatic amino acid family biosynthetic process
- 34: 3.94 GO:0046417~chorismate metabolic process
- 35: 3.74 GO:0009072~aromatic amino acid family metabolic process
- 36: 3.71 sec00400:Phenylalanine,tyrosine and tryptophan biosynthesis
- 37: 5.02 aromatic amino acid biosynthesis
- 38: 8.07 carbon-carbon lyase
- 39: 2.81 GO:0043648~dicarboxylic acid metabolic process
- 40: 1.87 GO:0019438~aromatic compound biosynthetic process
- 41: 3.25 GO:0009067~aspartate family amino acid biosynthetic process
- 42: 2.77 GO:0009066~aspartate family amino acid metabolic process
- 43: 14.08 sek00680:Methane metabolism
- 44: 3.35 st03430:Mismatch repair
- 45: 2.89 GO:0004527~exonuclease activity
- 46: 2.97 exonuclease
- 47: 2.51 GO:0030288~outer membrane-bounded periplasmic space
- 48: 1.57 GO:0044462~external encapsulating structure part

- group 1: 4.60
- group 2: 3.89
- group 3: 2.61
- group 4: 2.42
- group 5: 1.71
- group 6: 1.32
- group 7: 1.29
- group 8: 1.20
- group 9: 1.18
- group 10: 1.11
- group 11: 1.09
- group 12: 1.02
- group 13: 1.01