



- 1: 2.68 GO:0030203-glycosaminoglycan metabolic process
- 2: 2.68 GO:0000270-peptidoglycan metabolic process
- 3: 2.64 GO:0006022-aminoglycan metabolic process
- 4: 4.57 ecm00770:Pantothenate and CoA biosynthesis
- 5: 2.82 cell cycle
- 6: 2.62 cell division
- 7: 2.36 GO:0051301-cell division
- 8: 2.28 GO:0007049-cell cycle
- 9: 2.55 GO:0044038-cell wall macromolecule biosynthetic process
- 10: 2.55 GO:0070580-cellular component macromolecule biosynthetic process
- 11: 2.55 GO:0009273-peptidoglycan-based cell wall biogenesis
- 12: 2.55 GO:0042546-cell wall biogenesis
- 13: 2.55 GO:0006023-aminoglycan biosynthetic process
- 14: 2.55 GO:0006024-glycosaminoglycan biosynthetic process
- 15: 2.55 GO:0009252-peptidoglycan biosynthetic process
- 16: 2.5 GO:0010382-cellular cell wall macromolecule metabolic process
- 17: 1.92 GO:0044036-cell wall macromolecule metabolic process
- 18: 7.61 IPR018211:Alcohol dehydrogenase,iron-type,conserved site
- 19: 7.61 IPR001670:Alcohol dehydrogenase,iron-type
- 20: 1.77 GO:0006732-coenzyme metabolic process
- 21: 1.57 GO:0051186-cofactor metabolic process
- 22: 5.09 GO:0010629-negative regulation of gene expression
- 23: 5.09 GO:0016481-negative regulation of transcription
- 24: 4.14 GO:0045934-negative regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process
- 25: 4.14 GO:0010605-negative regulation of macromolecule metabolic process
- 26: 4.14 GO:0051172-negative regulation of nitrogen compound metabolic process
- 27: 4.14 GO:0010558-negative regulation of macromolecule biosynthetic process
- 28: 3.89 GO:0031327-negative regulation of cellular biosynthetic process
- 29: 3.89 GO:0009890-negative regulation of biosynthetic process
- 30: 3.31 GO:0009082-branched chain family amino acid biosynthetic process
- 31: 4.14 GO:0009098-leucine biosynthetic process
- 32: 4.14 GO:0006551-leucine metabolic process
- 33: 3.06 GO:0009081-branched chain family amino acid metabolic process
- 34: 7.76 ecp00770:Pantothenate and CoA biosynthesis
- 35: 1.95 GO:0009108-coenzyme biosynthetic process
- 36: 1.6 GO:0051188-cofactor biosynthetic process
- 37: 2.85 GO:0042559-pteridine and derivative biosynthetic process
- 38: 2.85 GO:0042558-pteridine and derivative metabolic process
- 39: 2.37 amino-acid transport
- 40: 2.07 GO:0006865-amino acid transport
- 41: 1.88 GO:0015837-amine transport
- 42: 1.65 GO:0015849-organic acid transport
- 43: 1.65 GO:0046942-carboxylic acid transport
- 44: 1.3 signal
- 45: 1.3 signal peptide

- group 1: 2.17
- group 2: 1.55
- group 3: 1.44
- group 4: 1.41
- group 5: 1.26
- group 6: 1.25
- group 7: 1.22
- group 8: 1.18
- group 9: 1.10
- group 10: 1.05
- group 11: 1.03
- group 12: 1.01
- group 13: 1.00