



- 1: 1.5 transmembrane
- 2: 1.5 transmembrane region
- 3: 1.36 membrane
- 4: 1.17 cell membrane
- 5: 1.15 GO:0016021-integral to membrane
- 6: 1.1 GO:0031224-intoxic to membrane
- 7: 1.06 GO:0005886-plasma membrane
- 8: 1.8 GO:0005581-photosynthesis
- 9: 3.81 GO:0008111-peptidase activity
- 10: 2.54 GO:0070011-peptidase activity,acting on L-amino acid peptides
- 11: 1.14 protease
- 12: 1.81 GO:0030435-sporulation resulting in formation of a cellular spore
- 13: 1.81 GO:0043934-sporulation
- 14: 1.67 sporulation
- 15: 24.88 PR0500193-pyruvate 5-carboxylase reductase
- 16: 24.89 PR0500193-pyruvate 5-carboxylate reductase
- 17: 21.84 GO:0004725-pyruvate 5-carboxylate reductase activity
- 18: 18.57 PR0004455-NADP oxidoreductase,coenzyme F420-dependent
- 19: 18.57 PR0003504-delta 3-pyruvate 5-carboxylate reductase
- 20: 8.74 GO:0016646-oxidoreductase activity,acting on the CH-NH group of donors,NAD or NADP as acceptor
- 21: 8.29 GO:0006561-proline biosynthetic process
- 22: 7.94 GO:0016645-oxidoreductase activity,acting on the CH-NH group of donors
- 23: 1.53 GO:0006560-proline metabolic process
- 24: 3.19 GO:0009084-glutamine family amino acid biosynthetic process
- 25: 2.3 GO:0006644-glutamine family amino acid metabolic process
- 26: 2.6 bsu03130 Arginine and proline metabolism
- 27: 8.89 GO:0018130-heterocycle biosynthetic process
- 28: 6.07 GO:0044252-serine-type endopeptidase activity
- 29: 4.29 Serine protease
- 30: 3.28 GO:0018111-serine hydrolase activity
- 31: 3.52 GO:0008236-serine-type peptidase activity
- 32: 4.54 S080315-HTH\_CTR1
- 33: 4.6 PR000524-Bacterial regulatory protein GntR,HTH
- 34: 4.38 domain HTH\_gntR-type
- 35: 7.34 Secreted
- 36: 1.77 GO:0005776-extracellular region
- 37: 8.39 PR013500-Peptidase S8\_sustilisin-related
- 38: 8.39 PR000020-Peptidase S8 and S23\_sustilisin\_kexin\_sedolisin
- 39: 3.7 zymogen

- group 1: 2.29
- group 2: 2.08
- group 3: 1.85
- group 4: 1.64
- group 5: 1.59
- group 6: 1.28
- group 7: 1.23
- group 8: 1.13