



- 1: 9.08 Porin
- 2: 8.43 GO:0046930-pore complex
- 3: 3.27 cell outer membrane
- 4: 2.58 GO:0009279-cell outer membrane
- 5: 2.46 GO:0019867-outer membrane
- 6: 2.06 GO:0044462-external encapsulating structure part
- 7: 1.7 dna-binding
- 8: 1.43 GO:0003677-DNA binding
- 9: 6.16 GO:0009982-pseudouridine synthase activity
- 10: 6.14 GO:0001522-pseudouridine synthesis
- 11: 3.11 dna recombination
- 12: 2.25 GO:0006310-DNA recombination
- 13: 2.48 ecv00240:Pyrimidine metabolism
- 14: 3.13 GO:0046377-colanic acid metabolic process
- 15: 3.13 GO:0009242-colanic acid biosynthetic process
- 16: 7.71 ecs00520:Amino sugar and nucleotide sugar metabolism
- 17: 6.05 Rotamase
- 18: 5.65 GO:0016859-cis-trans isomerase activity
- 19: 5.65 GO:0003755-peptidyl-prolyl cis-trans isomerase activity
- 20: 7.41 PIRSF003173:response regulator,OmpR type
- 21: 5.39 IPR001867:Signal transduction response regulator,C-terminal
- 22: 2.68 domain:Response regulatory
- 23: 2.54 IPR001789:Signal transduction response regulator,receiver region
- 24: 2.15 SM00448:REC
- 25: 1.8 GO:0000156-two-component response regulator activity
- 26: 1.44 two-component regulatory system
- 27: 1.25 GO:0000160-two-component signal transduction system (phosphorelay)

- group 1: 2.80
- group 2: 2.43
- group 3: 2.06
- group 4: 1.64
- group 5: 1.16
- group 6: 1.16
- group 7: 1.15
- group 8: 1.06
- group 9: 1.05
- group 10: 1.02