



- 1: 1.38 oxidoreductase
- 2: 1.32 GO:0055114~oxidation reduction
- 3: 3.93 IPR017909:Twin arginine translocation signal,Tat
- 4: 3.73 IPR006311:Twin-arginine translocation pathway signal
- 5: 3.3 ecx00910:Nitrogen metabolism
- 6: 4.41 SM00490:HELIcC
- 7: 4.39 IPR014021:Helicase,superfamily 1 and 2,ATP-binding
- 8: 4.17 SM00487:DEXDc
- 9: 4.16 domain:Helicase C-terminal
- 10: 4.15 IPR001650:DNA/RNA helicase,C-terminal
- 11: 3.94 domain:Helicase ATP-binding
- 12: 3.93 IPR014001:DEAD-like helicase,N-terminal
- 13: 3.62 GO:0008026~ATP-dependent helicase activity
- 14: 3.62 GO:0070035~purine NTP-dependent helicase activity
- 15: 4.66 IPR011545:DNA/RNA helicase,DEAD/DEAH box type,N-terminal
- 16: 2.68 helicase
- 17: 2.37 GO:0004386~helicase activity
- 18: 3.75 copper
- 19: 3.62 GO:0005507~copper ion binding
- 20: 13.88 PIRSF000420:ribosomal protein serine N-acetyltransferase
- 21: 3.73 IPR016181:Acyl-CoA N-acyltransferase
- 22: 5.66 Translation,ribosomal structure and biogenesis
- 23: 3.26 domain:N-acetyltransferase
- 24: 3.24 IPR000182:GCN5-related N-acetyltransferase
- 25: 2.75 GO:0008080~N-acetyltransferase activity
- 26: 2.46 GO:0016410~N-acyltransferase activity
- 27: 2.34 FAD
- 28: 1.68 Flavoprotein

- group 1: 1.13 ■
- group 2: 1.09 ■
- group 3: 1.08 ■
- group 4: 1.05 ■
- group 5: 1.05 ■
- group 6: 1.03 ■
- group 7: 1.00 ■