



1: 1.47 cell membrane
 2: 1.63 membrane
 3: 1.09 GO:0008955-pannicle membrane
 4: 1.03 GO:0011224-intrinsic to membrane
 5: 1.2 signal
 6: 1.5 signal peptide
 7: 1.38 topological domain Cytoplasmic
 8: 1.38 topological domain Periplasmic
 9: 1.17 Transmembrane region
 10: 1.27 transmembrane
 11: 1.03 GO:0030214-intrinsic to membrane
 12: 1.04 GO:0005774-membrane
 13: 1.06 GO:0000771-polyaccharide biosynthetic process
 14: 1.26 GO:0005976-polyaccharide metabolic process
 15: 1.26 GO:0016951-carbohydrate biosynthetic process
 16: 6.9 GO:0016042-lipid catabolic process
 17: 9 lipids degradation
 18: 3.38 lipid metabolism
 19: 3.47 ecg00950-Butanolate metabolism
 20: 1.26 nucleotide phosphate binding region
 21: 1.43 GO:0009881-branched chain family amino acid metabolic process
 22: 2.87 GO:0009882-branched chain family amino acid biosynthetic process

group 1: 2, 36
 group 2: 1, 94
 group 3: 1, 63
 group 4: 1, 33
 group 5: 1, 32
 group 6: 1, 24
 group 7: 1, 05
 group 8: 1, 04