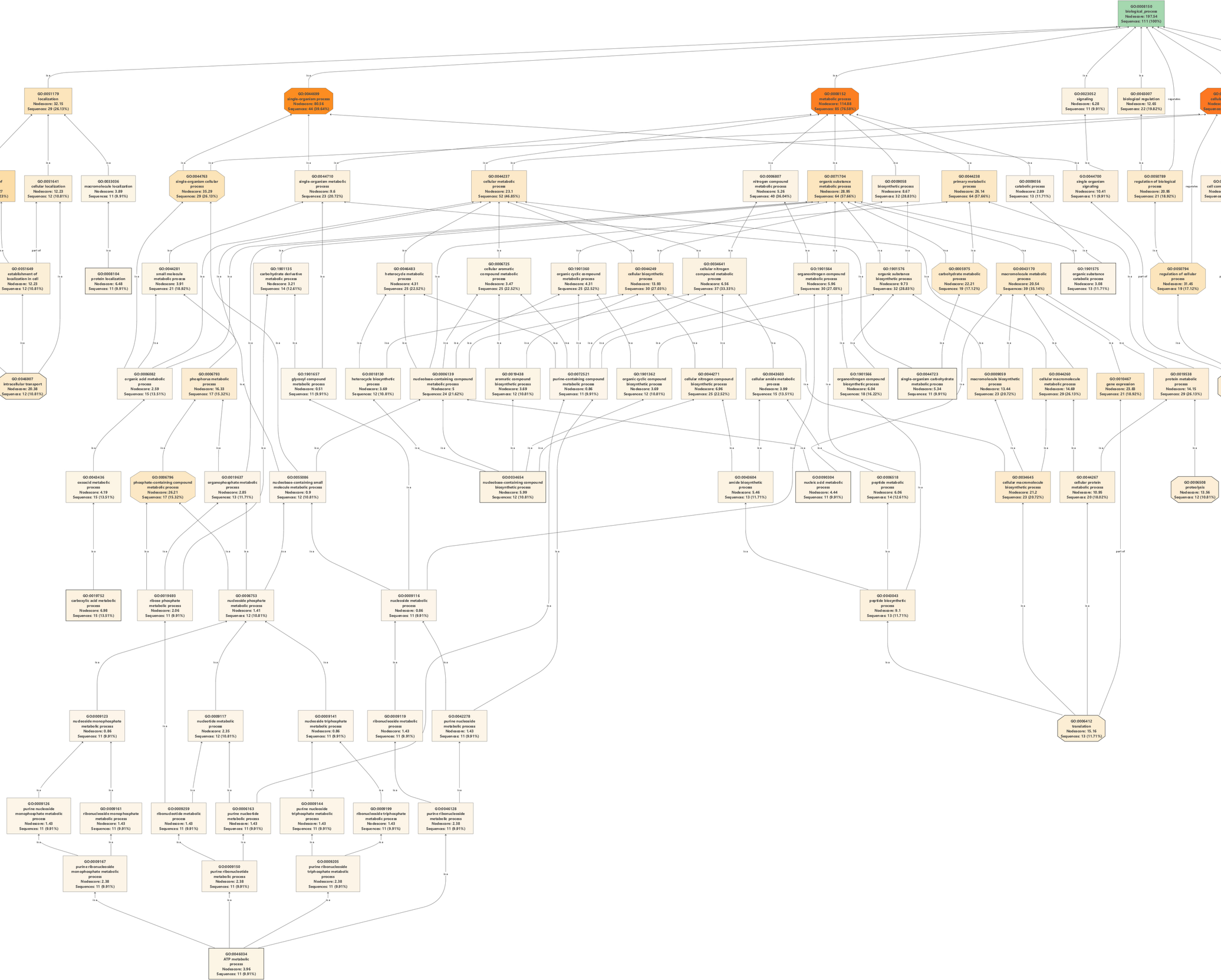
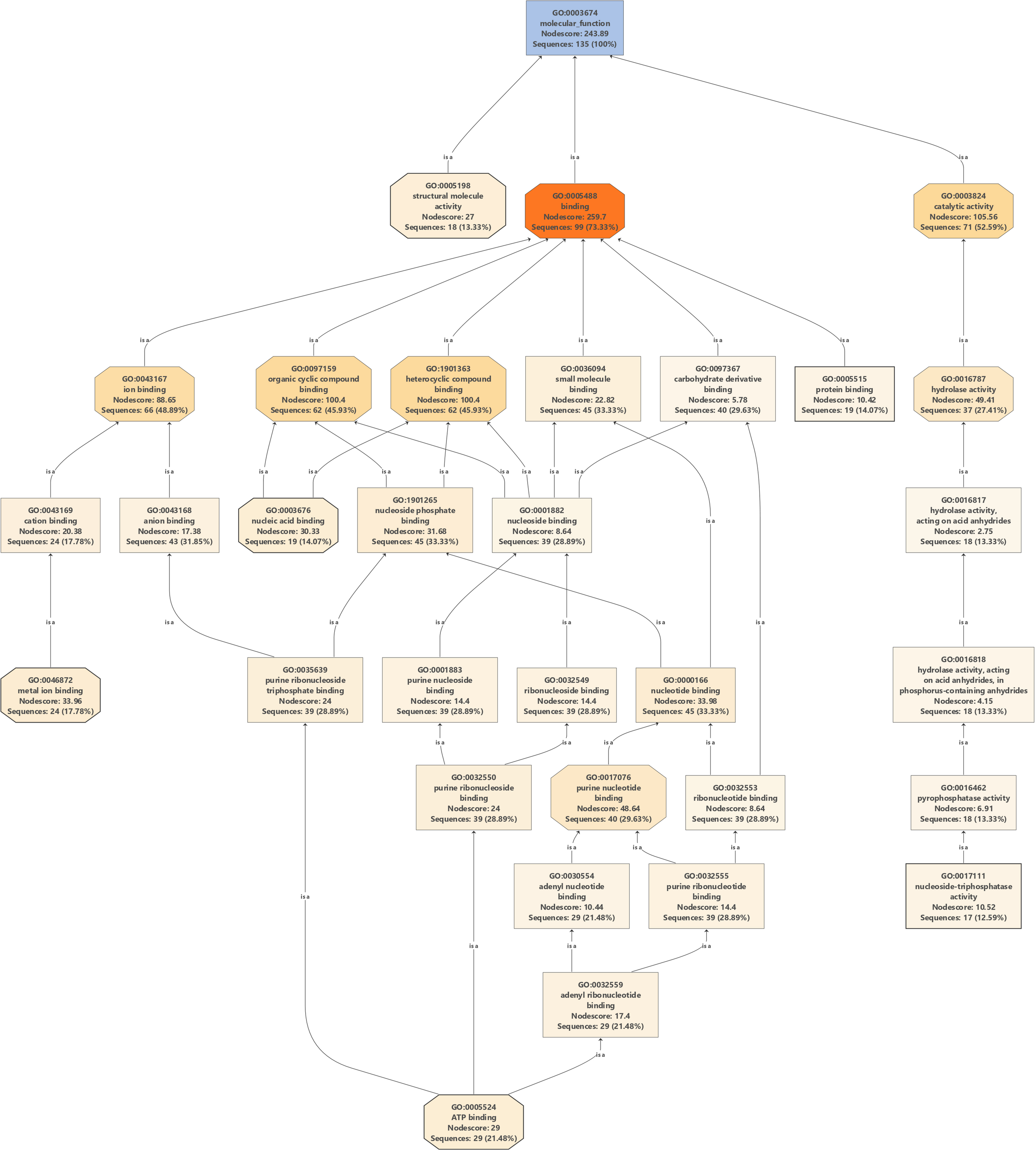
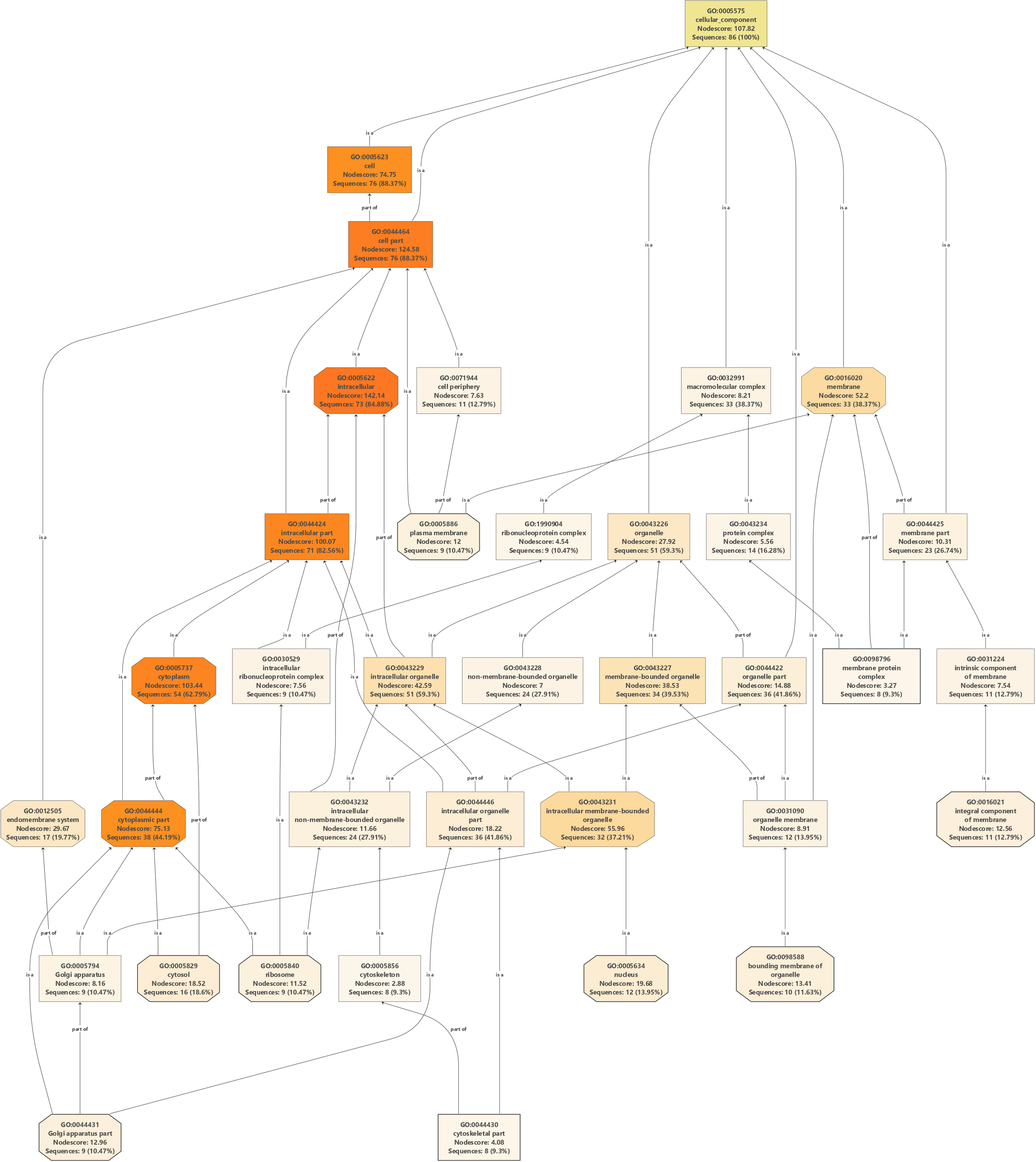

GO:0008150
biological_process
Nodescore: 197.54
Sequences: 111 (100%)
GO:0051179
localization
Nodescore: 32.15
Sequences: 29 (26.13%)
GO:0044699
single-organism process
Nodescore: 80.56
Sequences: 44 (39.64%)
GO:0008152
metabolic process
Nodescore: 114.88
Sequences: 85 (76.58%)
GO:0023052
signaling
Nodescore: 6.28
Sequences: 11 (9.91%)
GO:0065007
biological regulation
Nodescore: 12.65
Sequences: 22 (19.82%)
GO:0009987
cellular process
Nodescore: 138.23
Sequences: 77 (69.37%)
GO:0050896
response to stimulus
Nodescore: 19.7
Sequences: 13 (11.71%)
GO:0071840
cellular component organization or biogenesis
Nodescore: 3.65
Sequences: 15 (13.51%)
GO:0051234
establishment of localization
Nodescore: 45.27
Sequences: 28 (25.23%)
GO:0051641
cellular localization
Nodescore: 12.23
Sequences: 12 (10.81%)
GO:0033036
macromolecule localization
Nodescore: 3.89
Sequences: 11 (9.91%)
GO:0044763
single-organism cellular process
Nodescore: 35.29
Sequences: 29 (26.13%)
GO:0044710
single-organism metabolic process
Nodescore: 9.6
Sequences: 23 (20.72%)
GO:0044237
cellular metabolic process
Nodescore: 23.1
Sequences: 52 (46.85%)
GO:0006807
nitrogen compound metabolic process
Nodescore: 5.26
Sequences: 40 (36.04%)
GO:0071704
organic substance metabolic process
Nodescore: 28.95
Sequences: 64 (57.66%)
GO:0009058
biosynthetic process
Nodescore: 8.67
Sequences: 32 (28.83%)
GO:0044238
primary metabolic process
Nodescore: 26.14
Sequences: 64 (57.66%)
GO:0009056
catabolic process
Nodescore: 2.89
Sequences: 13 (11.71%)
GO:0044700
single organism signaling
Nodescore: 10.41
Sequences: 11 (9.91%)
GO:0050789
regulation of biological process
Nodescore: 20.95
Sequences: 21 (18.92%)
GO:0007154
cell communication
Nodescore: 10.41
Sequences: 11 (9.91%)
GO:0051716
cellular response to stimulus
Nodescore: 10.9
Sequences: 12 (10.81%)
GO:0016043
cellular component organization
Nodescore: 4.46
Sequences: 13 (11.71%)
GO:0044085
cellular component biogenesis
Nodescore: 3.56
Sequences: 13 (11.71%)
GO:0006810
transport
Nodescore: 73.05
Sequences: 28 (25.23%)
GO:0051649
establishment of localization in cell
Nodescore: 12.23
Sequences: 12 (10.81%)
GO:0008104
protein localization
Nodescore: 6.48
Sequences: 11 (9.91%)
GO:0044281
small molecule metabolic process
Nodescore: 3.91
Sequences: 21 (18.92%)
GO:1901135
carbohydrate derivative metabolic process
Nodescore: 3.21
Sequences: 14 (12.61%)
GO:0046483
heterocycle metabolic process
Nodescore: 4.31
Sequences: 25 (22.52%)
GO:0006725
cellular aromatic compound metabolic process
Nodescore: 3.47
Sequences: 25 (22.52%)
GO:1901360
organic cyclic compound metabolic process
Nodescore: 4.31
Sequences: 25 (22.52%)
GO:0044249
cellular biosynthetic process
Nodescore: 13.93
Sequences: 30 (27.03%)
GO:0034641
cellular nitrogen compound metabolic process
Nodescore: 6.56
Sequences: 37 (33.33%)
GO:1901564
organonitrogen compound metabolic process
Nodescore: 5.96
Sequences: 30 (27.03%)
GO:1901576
organic substance biosynthetic process
Nodescore: 9.73
Sequences: 32 (28.83%)
GO:0005975
carbohydrate metabolic process
Nodescore: 22.21
Sequences: 19 (17.12%)
GO:0043170
macromolecule metabolic process
Nodescore: 20.54
Sequences: 39 (35.14%)
GO:1901575
organic substance catabolic process
Nodescore: 3.08
Sequences: 13 (11.71%)
GO:0050794
regulation of cellular process
Nodescore: 31.45
Sequences: 19 (17.12%)
GO:0022607
cellular component assembly
Nodescore: 3.24
Sequences: 11 (9.91%)
GO:0016192
vesicle-mediated transport
Nodescore: 21.69
Sequences: 12 (10.81%)
GO:0046907
intracellular transport
Nodescore: 20.38
Sequences: 12 (10.81%)
GO:0006082
organic acid metabolic process
Nodescore: 2.59
Sequences: 15 (13.51%)
GO:0006793
phosphorus metabolic process
Nodescore: 16.33
Sequences: 17 (15.32%)
GO:1901657
glycosyl compound metabolic process
Nodescore: 0.51
Sequences: 11 (9.91%)
GO:0018130
heterocycle biosynthetic process
Nodescore: 3.69
Sequences: 12 (10.81%)
GO:0006139
nucleobase-containing compound metabolic process
Nodescore: 5
Sequences: 24 (21.62%)
GO:0019438
aromatic compound biosynthetic process
Nodescore: 3.69
Sequences: 12 (10.81%)
GO:0072521
purine-containing compound metabolic process
Nodescore: 0.86
Sequences: 11 (9.91%)
GO:1901362
organic cyclic compound biosynthetic process
Nodescore: 3.69
Sequences: 12 (10.81%)
GO:0044271
cellular nitrogen compound biosynthetic process
Nodescore: 6.96
Sequences: 25 (22.52%)
GO:0043603
cellular amide metabolic process
Nodescore: 3.99
Sequences: 15 (13.51%)
GO:1901566
organonitrogen compound biosynthetic process
Nodescore: 6.04
Sequences: 18 (16.22%)
GO:0044723
single-organism carbohydrate metabolic process
Nodescore: 5.34
Sequences: 11 (9.91%)
GO:0009059
macromolecule biosynthetic process
Nodescore: 13.44
Sequences: 23 (20.72%)
GO:0044260
cellular macromolecule metabolic process
Nodescore: 14.69
Sequences: 29 (26.13%)
GO:0010467
gene expression
Nodescore: 23.18
Sequences: 21 (18.92%)
GO:0019538
protein metabolic process
Nodescore: 14.15
Sequences: 29 (26.13%)
GO:0007165
signal transduction
Nodescore: 17.35
Sequences: 11 (9.91%)
GO:0043436
oxoacid metabolic process
Nodescore: 4.19
Sequences: 15 (13.51%)
GO:0006796
phosphate-containing compound metabolic process
Nodescore: 26.21
Sequences: 17 (15.32%)
GO:0019637
organophosphate metabolic process
Nodescore: 2.85
Sequences: 13 (11.71%)
GO:0055086
nucleobase-containing small molecule metabolic process
Nodescore: 0.9
Sequences: 12 (10.81%)
GO:0034654
nucleobase-containing compound biosynthetic process
Nodescore: 5.99
Sequences: 12 (10.81%)
GO:0043604
amide biosynthetic process
Nodescore: 5.46
Sequences: 13 (11.71%)
GO:0090304
nucleic acid metabolic process
Nodescore: 4.44
Sequences: 11 (9.91%)
GO:0006518
peptide metabolic process
Nodescore: 6.06
Sequences: 14 (12.61%)
GO:0034645
cellular macromolecule biosynthetic process
Nodescore: 21.2
Sequences: 23 (20.72%)
GO:0044267
cellular protein metabolic process
Nodescore: 10.95
Sequences: 20 (18.02%)
GO:0006508
proteolysis
Nodescore: 13.56
Sequences: 12 (10.81%)
GO:0019752
carboxylic acid metabolic process
Nodescore: 6.98
Sequences: 15 (13.51%)
GO:0019693
ribose phosphate metabolic process
Nodescore: 2.06
Sequences: 11 (9.91%)
GO:0006753
nucleoside phosphate metabolic process
Nodescore: 1.41
Sequences: 12 (10.81%)
GO:0009116
nucleoside metabolic process
Nodescore: 0.86
Sequences: 11 (9.91%)
GO:0043043
peptide biosynthetic process
Nodescore: 9.1
Sequences: 13 (11.71%)
GO:0006412
translation
Nodescore: 15.16
Sequences: 13 (11.71%)
GO:0009123
nucleoside monophosphate metabolic process
Nodescore: 0.86
Sequences: 11 (9.91%)
GO:0009117
nucleotide metabolic process
Nodescore: 2.35
Sequences: 12 (10.81%)
GO:0009141
nucleoside triphosphate metabolic process
Nodescore: 0.86
Sequences: 11 (9.91%)
GO:0009119
ribonucleoside metabolic process
Nodescore: 1.43
Sequences: 11 (9.91%)
GO:0042278
purine nucleoside metabolic process
Nodescore: 1.43
Sequences: 11 (9.91%)
GO:0009126
purine nucleoside monophosphate metabolic process
Nodescore: 1.43
Sequences: 11 (9.91%)
GO:0009161
ribonucleoside monophosphate metabolic process
Nodescore: 1.43
Sequences: 11 (9.91%)
GO:0009259
ribonucleotide metabolic process
Nodescore: 1.43
Sequences: 11 (9.91%)
GO:0006163
purine nucleotide metabolic process
Nodescore: 1.43
Sequences: 11 (9.91%)
GO:0009144
purine nucleoside triphosphate metabolic process
Nodescore: 1.43
Sequences: 11 (9.91%)
GO:0009199
ribonucleoside triphosphate metabolic process
Nodescore: 1.43
Sequences: 11 (9.91%)
GO:0046128
purine ribonucleoside metabolic process
Nodescore: 2.38
Sequences: 11 (9.91%)
GO:0009167
purine ribonucleoside monophosphate metabolic process
Nodescore: 2.38
Sequences: 11 (9.91%)
GO:0009150
purine ribonucleotide metabolic process
Nodescore: 2.38
Sequences: 11 (9.91%)
GO:0009205
purine ribonucleoside triphosphate metabolic process
Nodescore: 2.38
Sequences: 11 (9.91%)
GO:0046034
ATP metabolic process
Nodescore: 3.96
Sequences: 11 (9.91%)
is a
part of
regulates


GO:0003674
molecular_function
Nodescore: 243.89
Sequences: 135 (100%)
GO:0005198
structural molecule activity
Nodescore: 27
Sequences: 18 (13.33%)
GO:0005488
binding
Nodescore: 259.7
Sequences: 99 (73.33%)
GO:0003824
catalytic activity
Nodescore: 105.56
Sequences: 71 (52.59%)
GO:0043167
ion binding
Nodescore: 88.65
Sequences: 66 (48.89%)
GO:0097159
organic cyclic compound binding
Nodescore: 100.4
Sequences: 62 (45.93%)
GO:1901363
heterocyclic compound binding
Nodescore: 100.4
Sequences: 62 (45.93%)
GO:0036094
small molecule binding
Nodescore: 22.82
Sequences: 45 (33.33%)
GO:0097367
carbohydrate derivative binding
Nodescore: 5.78
Sequences: 40 (29.63%)
GO:0005515
protein binding
Nodescore: 10.42
Sequences: 19 (14.07%)
GO:0016787
hydrolase activity
Nodescore: 49.41
Sequences: 37 (27.41%)
GO:0043169
cation binding
Nodescore: 20.38
Sequences: 24 (17.78%)
GO:0043168
anion binding
Nodescore: 17.38
Sequences: 43 (31.85%)
GO:0003676
nucleic acid binding
Nodescore: 30.33
Sequences: 19 (14.07%)
GO:1901265
nucleoside phosphate binding
Nodescore: 31.68
Sequences: 45 (33.33%)
GO:0001882
nucleoside binding
Nodescore: 8.64
Sequences: 39 (28.89%)
GO:0016817
hydrolase activity, acting on acid anhydrides
Nodescore: 2.75
Sequences: 18 (13.33%)
GO:0046872
metal ion binding
Nodescore: 33.96
Sequences: 24 (17.78%)
GO:0035639
purine ribonucleoside triphosphate binding
Nodescore: 24
Sequences: 39 (28.89%)
GO:0001883
purine nucleoside binding
Nodescore: 14.4
Sequences: 39 (28.89%)
GO:0032549
ribonucleoside binding
Nodescore: 14.4
Sequences: 39 (28.89%)
GO:0000166
nucleotide binding
Nodescore: 33.98
Sequences: 45 (33.33%)
GO:0016818
hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides
Nodescore: 4.15
Sequences: 18 (13.33%)
GO:0032550
purine ribonucleoside binding
Nodescore: 24
Sequences: 39 (28.89%)
GO:0017076
purine nucleotide binding
Nodescore: 48.64
Sequences: 40 (29.63%)
GO:0032553
ribonucleotide binding
Nodescore: 8.64
Sequences: 39 (28.89%)
GO:0016462
pyrophosphatase activity
Nodescore: 6.91
Sequences: 18 (13.33%)
GO:0030554
adenyl nucleotide binding
Nodescore: 10.44
Sequences: 29 (21.48%)
GO:0032555
purine ribonucleotide binding
Nodescore: 14.4
Sequences: 39 (28.89%)
GO:0017111
nucleoside-triphosphatase activity
Nodescore: 10.52
Sequences: 17 (12.59%)
GO:0032559
adenyl ribonucleotide binding
Nodescore: 17.4
Sequences: 29 (21.48%)
GO:0005524
ATP binding
Nodescore: 29
Sequences: 29 (21.48%)
is a


GO:0005575
cellular_component
Nodescore: 107.82
Sequences: 86 (100%)
GO:0005623
cell
Nodescore: 74.75
Sequences: 76 (88.37%)
GO:0044464
cell part
Nodescore: 124.58
Sequences: 76 (88.37%)
GO:0005622
intracellular
Nodescore: 142.14
Sequences: 73 (84.88%)
GO:0071944
cell periphery
Nodescore: 7.63
Sequences: 11 (12.79%)
GO:0032991
macromolecular complex
Nodescore: 8.21
Sequences: 33 (38.37%)
GO:0016020
membrane
Nodescore: 52.2
Sequences: 33 (38.37%)
GO:0044424
intracellular part
Nodescore: 100.07
Sequences: 71 (82.56%)
GO:0005886
plasma membrane
Nodescore: 12
Sequences: 9 (10.47%)
GO:1990904
ribonucleoprotein complex
Nodescore: 4.54
Sequences: 9 (10.47%)
GO:0043226
organelle
Nodescore: 27.92
Sequences: 51 (59.3%)
GO:0043234
protein complex
Nodescore: 5.56
Sequences: 14 (16.28%)
GO:0044425
membrane part
Nodescore: 10.31
Sequences: 23 (26.74%)
GO:0005737
cytoplasm
Nodescore: 103.44
Sequences: 54 (62.79%)
GO:0030529
intracellular
ribonucleoprotein complex
Nodescore: 7.56
Sequences: 9 (10.47%)
GO:0043229
intracellular organelle
Nodescore: 42.59
Sequences: 51 (59.3%)
GO:0043228
non-membrane-bounded organelle
Nodescore: 7
Sequences: 24 (27.91%)
GO:0043227
membrane-bounded organelle
Nodescore: 38.53
Sequences: 34 (39.53%)
GO:0044422
organelle part
Nodescore: 14.88
Sequences: 36 (41.86%)
GO:0098796
membrane protein
complex
Nodescore: 3.27
Sequences: 8 (9.3%)
GO:0031224
intrinsic component
of membrane
Nodescore: 7.54
Sequences: 11 (12.79%)
GO:0012505
endomembrane system
Nodescore: 29.67
Sequences: 17 (19.77%)
GO:0044444
cytoplasmic part
Nodescore: 75.13
Sequences: 38 (44.19%)
GO:0043232
intracellular
non-membrane-bounded organelle
Nodescore: 11.66
Sequences: 24 (27.91%)
GO:0044446
intracellular organelle
part
Nodescore: 18.22
Sequences: 36 (41.86%)
GO:0043231
intracellular membrane-bounded
organelle
Nodescore: 55.96
Sequences: 32 (37.21%)
GO:0031090
organelle membrane
Nodescore: 8.91
Sequences: 12 (13.95%)
GO:0016021
integral component
of membrane
Nodescore: 12.56
Sequences: 11 (12.79%)
GO:0005794
Golgi apparatus
Nodescore: 8.16
Sequences: 9 (10.47%)
GO:0005829
cytosol
Nodescore: 18.52
Sequences: 16 (18.6%)
GO:0005840
ribosome
Nodescore: 11.52
Sequences: 9 (10.47%)
GO:0005856
cytoskeleton
Nodescore: 2.88
Sequences: 8 (9.3%)
GO:0005634
nucleus
Nodescore: 19.68
Sequences: 12 (13.95%)
GO:0098588
bounding membrane of
organelle
Nodescore: 13.41
Sequences: 10 (11.63%)
GO:0044431
Golgi apparatus part
Nodescore: 12.96
Sequences: 9 (10.47%)
GO:0044430
cytoskeletal part
Nodescore: 4.08
Sequences: 8 (9.3%)
is a
part of