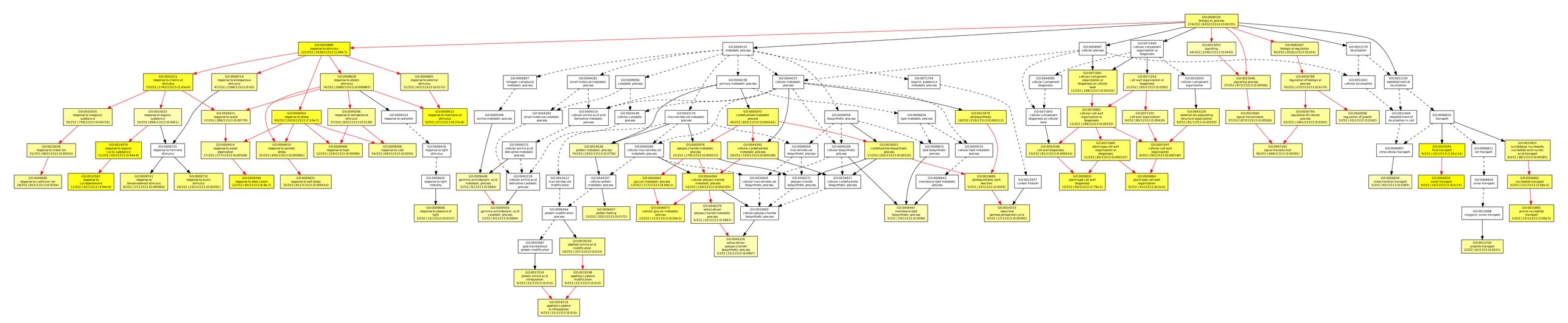
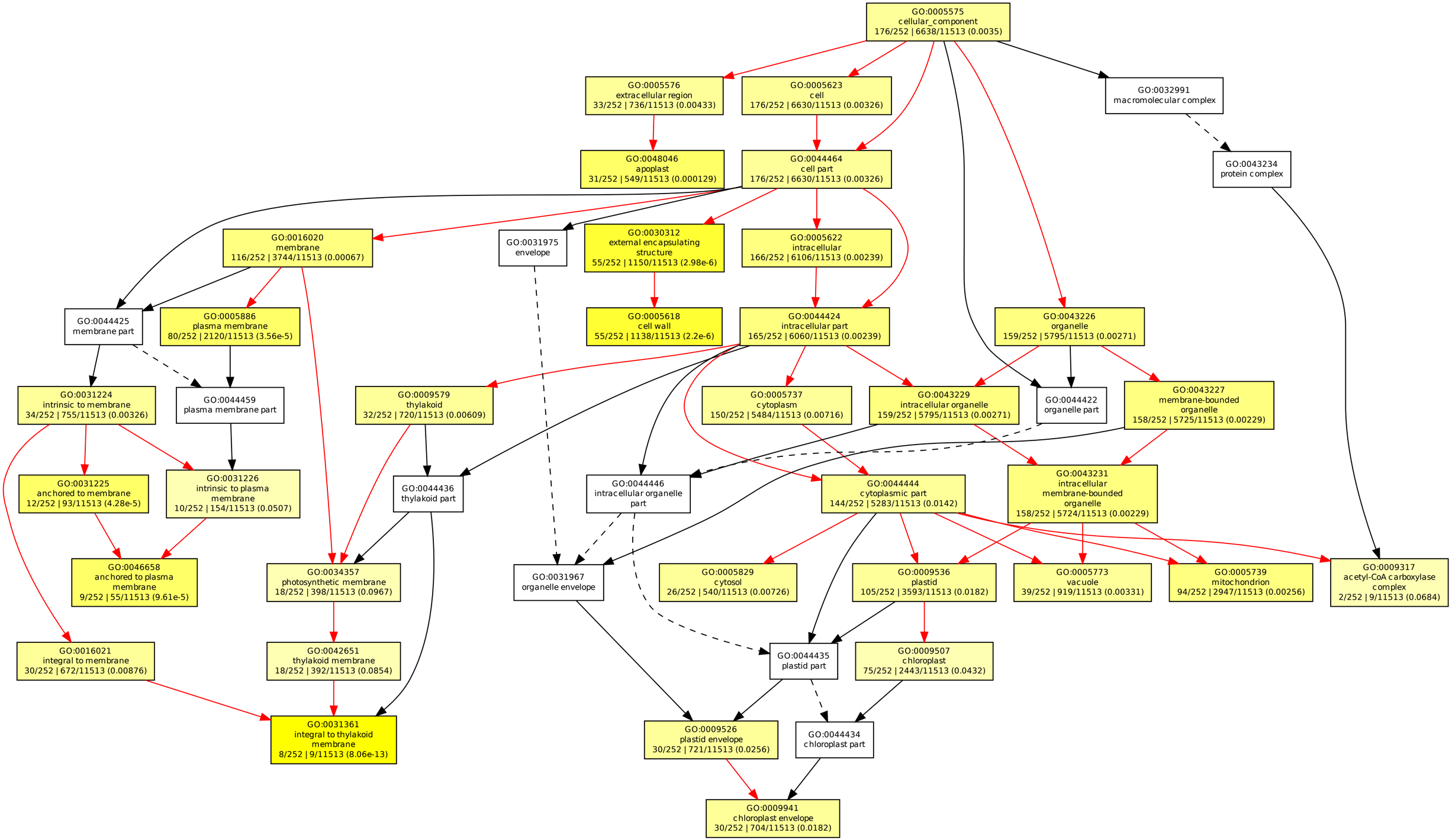
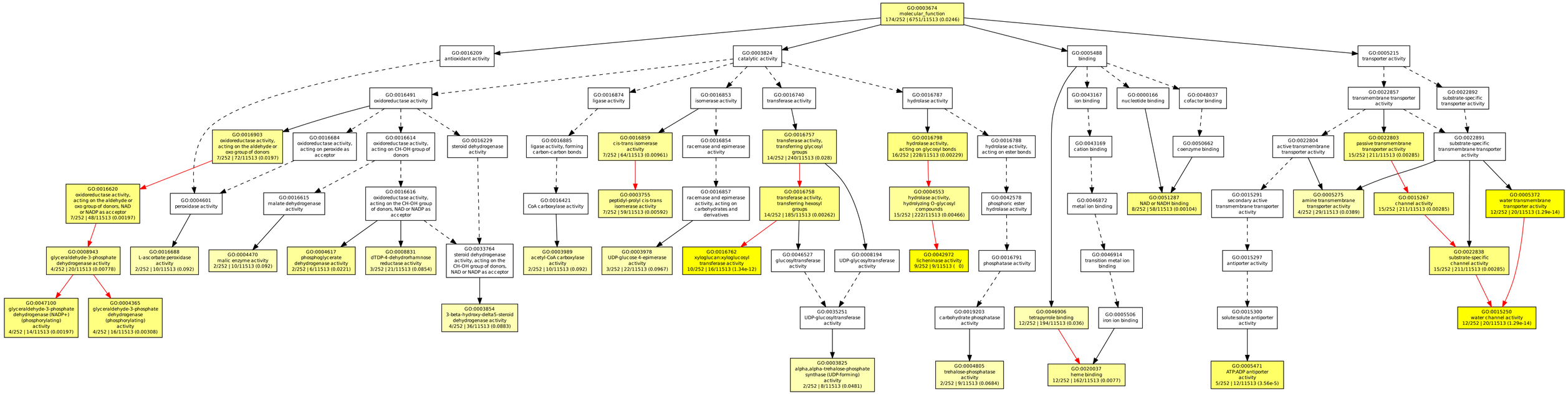

GO:0008150
biological_process
174/252 | 6432/11513 (0.00135)
GO:0050896
response to stimulus
121/252 | 3438/11513 (1.99e-7)
GO:0008152
metabolic process
GO:0009987
cellular process
GO:0071840
cellular component organization or biogenesis
GO:0023052
signaling
44/252 | 1240/11513 (0.0432)
GO:0065007
biological regulation
82/252 | 2616/11513 (0.014)
GO:0051179
localization
GO:0043221
response to chemical stimulus
73/252 | 1742/11513 (2.43e-6)
GO:0009719
response to endogenous stimulus
47/252 | 1298/11513 (0.02)
GO:0009628
response to abiotic stimulus
74/252 | 2080/11513 (0.00087)
GO:0009605
response to external stimulus
21/252 | 421/11513 (0.0172)
GO:0009612
response to mechanical stimulus
9/252 | 27/11513 (8.74e-8)
GO:0010035
response to inorganic substance
33/252 | 759/11513 (0.00716)
GO:0010033
response to organic substance
33/252 | 890/11513 (0.0951)
GO:0009415
response to water
17/252 | 286/11513 (0.00778)
GO:0009950
response to stress
93/252 | 2410/11513 (7.12e-7)
GO:0009266
response to temperature stimulus
37/252 | 922/11513 (0.0138)
GO:0009314
response to radiation
GO:0010038
response to metal ion
31/252 | 683/11513 (0.00555)
GO:0014070
response to organic cyclic substance
11/252 | 42/11513 (3.94e-8)
GO:0009725
response to hormone stimulus
GO:0009414
response to water deprivation
17/252 | 277/11513 (0.00588)
GO:0006970
response to osmotic stress
32/252 | 640/11513 (0.000982)
GO:0009408
response to heat
12/252 | 324/11513 (0.0088)
GO:0009409
response to cold
34/252 | 843/11513 (0.0204)
GO:0009416
response to light stimulus
GO:0046688
response to cadmium ion
28/252 | 653/11513 (0.0244)
GO:0010583
response to cyclopentenone
11/252 | 42/11513 (3.94e-8)
GO:0009741
response to brassinosteroid stimulus
8/252 | 57/11513 (0.000964)
GO:0009733
response to auxin stimulus
16/252 | 232/11513 (0.00262)
GO:0009269
response to desiccation
12/252 | 305/11513 (8.9e-7)
GO:0009651
response to salt stress
32/252 | 811/11513 (0.000414)
GO:0009646
response to absence of light
3/252 | 12/11513 (0.0127)
GO:0006807
nitrogen compound metabolic process
GO:0044281
small molecule metabolic process
GO:0009056
catabolic process
GO:0044238
primary metabolic process
GO:0044237
cellular metabolic process
GO:0071704
organic substance metabolic process
GO:0044085
cellular component biogenesis
GO:0071841
cellular component organization or biogenesis at cellular level
11/252 | 108/11513 (0.00102)
GO:0071354
cell wall organization or biogenesis
11/252 | 165/11513 (0.0293)
GO:0016043
cellular component organization
GO:0023046
signaling process
37/252 | 873/11513 (0.00506)
GO:0051641
cellular localization
GO:0051234
establishment of localization
GO:0009308
amine metabolic process
GO:0044282
small molecule catabolic process
GO:0006519
cellular amino acid and derivative metabolic process
GO:0044248
cellular catabolic process
GO:0043170
macromolecule metabolic process
GO:0005975
carbohydrate metabolic process
40/252 | 822/11513 (0.000165)
GO:0009058
biosynthetic process
GO:0006629
lipid metabolic process
GO:0015979
photosynthesis
18/252 | 219/11513 (0.000113)
GO:0071843
cellular component biogenesis at cellular level
GO:0070887
cellular cell wall organization or biogenesis
11/252 | 108/11513 (0.00102)
GO:0071555
cell wall organization
9/252 | 90/11513 (0.00418)
GO:0045229
external encapsulating structure organization
9/252 | 81/11513 (0.00229)
GO:0023060
signal transmission
37/252 | 873/11513 (0.00506)
GO:0050789
regulation of biological process
70/252 | 2157/11513 (0.0174)
GO:0040008
regulation of growth
5/252 | 43/11513 (0.0342)
GO:0051649
establishment of localization in cell
GO:0006810
transport
GO:0006807
nitrogen compound metabolic process
GO:0006575
cellular amino acid derivative metabolic process
GO:0019538
protein metabolic process
74/252 | 2452/11513 (0.0758)
GO:0044260
cellular macromolecule metabolic process
GO:0005976
polysaccharide metabolic process
15/252 | 178/11513 (0.00015)
GO:0044262
cellular carbohydrate metabolic process
29/252 | 520/11513 (0.000348)
GO:0009059
macromolecule biosynthetic process
GO:0044249
cellular biosynthetic process
GO:0016051
carbohydrate biosynthetic process
17/252 | 262/11513 (0.00316)
GO:0008610
lipid biosynthetic process
GO:0044255
cellular lipid metabolic process
GO:0042546
cell wall biogenesis
10/252 | 81/11513 (0.000414)
GO:0071669
plant-type cell wall organization or biogenesis
11/252 | 95/11513 (0.000107)
GO:0007047
cellular cell wall organization
9/252 | 58/11513 (0.000146)
GO:0007165
signal transduction
36/252 | 848/11513 (0.00592)
GO:0046907
intracellular transport
GO:0042044
fluid transport
9/252 | 10/11513 (1.81e-14)
GO:0006811
ion transport
GO:0015931
nucleobase, nucleoside, nucleotide and nucleic acid transport
6/252 | 38/11513 (0.00285)
GO:0009642
response to light intensity
GO:0009446
gamma-aminobutyric acid metabolic process
2/252 | 9/11513 (0.0684)
GO:0042219
cellular amino acid derivative catabolic process
GO:0043412
macromolecule modification
GO:0044267
cellular protein metabolic process
GO:0044047
glucan metabolic process
13/252 | 117/11513 (9.49e-5)
GO:0044264
cellular polysaccharide metabolic process
14/252 | 144/11513 (0.000183)
GO:0036463
cellular macromolecule biosynthetic process
GO:0034637
cellular carbohydrate biosynthetic process
GO:0000271
polysaccharide biosynthetic process
GO:0009450
gamma-aminobutyric acid catabolic process
2/252 | 9/11513 (0.0684)
GO:0006464
protein modification process
GO:0006457
protein folding
13/252 | 202/11513 (0.0172)
GO:0006073
cellular glucan metabolic process
13/252 | 113/11513 (9.29e-5)
GO:0046379
extracellular polysaccharide metabolic process
3/252 | 22/11513 (0.0967)
GO:0033692
cellular polysaccharide biosynthetic process
GO:0045226
extracellular polysaccharide biosynthetic process
3/252 | 22/11513 (0.0967)
GO:0043687
post-translational protein modification
GO:0018193
peptidyl-amino acid modification
19/252 | 357/11513 (0.014)
GO:0017014
protein amino acid nitrosylation
6/252 | 51/11513 (0.014)
GO:0018198
peptidyl-cysteine modification
6/252 | 51/11513 (0.014)
GO:0018119
peptidyl-cysteine S-nitrosylation
6/252 | 51/11513 (0.014)
GO:0006644
membrane lipid metabolic process
GO:0046467
membrane lipid biosynthetic process
3/252 | 19/11513 (0.0396)
GO:0015977
carbon fixation
GO:0019685
photosynthesis, dark reaction
5/252 | 25/11513 (0.0026)
GO:0019253
reductive pentose-phosphate cycle
4/252 | 17/11513 (0.00392)
GO:0006839
mitochondrial transport
5/252 | 44/11513 (0.0383)
GO:0006833
water transport
9/252 | 10/11513 (1.81e-14)
GO:0006820
anion transport
GO:0006862
nucleotide transport
5/252 | 12/11513 (5.56e-5)
GO:0015698
inorganic anion transport
GO:0015700
arsenite transport
2/252 | 6/11513 (0.0221)
GO:0015865
purine nucleotide transport
5/252 | 12/11513 (5.56e-5)


GO:0005575
cellular_component
176/252 | 6638/11513 (0.0035)
GO:0005576
extracellular region
33/252 | 736/11513 (0.00433)
GO:0005623
cell
176/252 | 6630/11513 (0.00326)
GO:0032991
macromolecular complex
GO:0048046
apoplast
31/252 | 549/11513 (0.000129)
GO:0044464
cell part
176/252 | 6630/11513 (0.00326)
GO:0043234
protein complex
GO:0016020
membrane
116/252 | 3744/11513 (0.00067)
GO:0031975
envelope
GO:0030312
external encapsulating structure
55/252 | 1150/11513 (2.98e-6)
GO:0005622
intracellular
166/252 | 6106/11513 (0.00239)
GO:0044425
membrane part
GO:0005886
plasma membrane
80/252 | 2120/11513 (3.56e-5)
GO:0005618
cell wall
55/252 | 1138/11513 (2.2e-6)
GO:0044424
intracellular part
165/252 | 6060/11513 (0.00239)
GO:0043226
organelle
159/252 | 5795/11513 (0.00271)
GO:0031224
intrinsic to membrane
34/252 | 755/11513 (0.00326)
GO:0044459
plasma membrane part
GO:0009579
thylakoid
32/252 | 720/11513 (0.00609)
GO:0005737
cytoplasm
150/252 | 5484/11513 (0.00716)
GO:0043229
intracellular organelle
159/252 | 5795/11513 (0.00271)
GO:0044422
organelle part
GO:0043227
membrane-bounded organelle
158/252 | 5725/11513 (0.00229)
GO:0031225
anchored to membrane
12/252 | 93/11513 (4.28e-5)
GO:0031226
intrinsic to plasma membrane
10/252 | 154/11513 (0.0507)
GO:0044436
thylakoid part
GO:0044446
intracellular organelle part
GO:0044444
cytoplasmic part
144/252 | 5283/11513 (0.0142)
GO:0043231
intracellular membrane-bounded organelle
158/252 | 5724/11513 (0.00229)
GO:0046658
anchored to plasma membrane
9/252 | 55/11513 (9.61e-5)
GO:0034357
photosynthetic membrane
18/252 | 398/11513 (0.0967)
GO:0031967
organelle envelope
GO:0005829
cytosol
26/252 | 540/11513 (0.00726)
GO:0009536
plastid
105/252 | 3593/11513 (0.0182)
GO:0005773
vacuole
39/252 | 919/11513 (0.00331)
GO:0005739
mitochondrion
94/252 | 2947/11513 (0.00256)
GO:0009317
acetyl-CoA carboxylase complex
2/252 | 9/11513 (0.0684)
GO:0016021
integral to membrane
30/252 | 672/11513 (0.00876)
GO:0042651
thylakoid membrane
18/252 | 392/11513 (0.0854)
GO:0044435
plastid part
GO:0009507
chloroplast
75/252 | 2443/11513 (0.0432)
GO:0031361
integral to thylakoid membrane
8/252 | 9/11513 (8.06e-13)
GO:0009526
plastid envelope
30/252 | 721/11513 (0.0256)
GO:0044434
chloroplast part
GO:0009941
chloroplast envelope
30/252 | 704/11513 (0.0182)


GO:0003674
molecular_function
174/252 | 6751/11513 (0.0246)
GO:0016209
antioxidant activity
GO:0003824
catalytic activity
GO:0005488
binding
GO:0005215
transporter activity
GO:0016491
oxidoreductase activity
GO:0016874
ligase activity
GO:0016853
isomerase activity
GO:0016740
transferase activity
GO:0016787
hydrolase activity
GO:0043167
ion binding
GO:0000166
nucleotide binding
GO:0048037
cofactor binding
GO:0022857
transmembrane transporter activity
GO:0022892
substrate-specific transporter activity
GO:0016903
oxidoreductase activity, acting on the aldehyde or oxo group of donors
7/252 | 72/11513 (0.0197)
GO:0016684
oxidoreductase activity, acting on peroxide as acceptor
GO:0016614
oxidoreductase activity, acting on CH-OH group of donors
GO:0016229
steroid dehydrogenase activity
GO:0016885
ligase activity, forming carbon-carbon bonds
GO:0016859
cis-trans isomerase activity
7/252 | 64/11513 (0.00961)
GO:0016854
racemase and epimerase activity
GO:0016757
transferase activity, transferring glycosyl groups
14/252 | 240/11513 (0.028)
GO:0016798
hydrolase activity, acting on glycosyl bonds
16/252 | 228/11513 (0.00229)
GO:0016788
hydrolase activity, acting on ester bonds
GO:0043169
cation binding
GO:0050662
coenzyme binding
GO:0022804
active transmembrane transporter activity
GO:0022803
passive transmembrane transporter activity
15/252 | 211/11513 (0.00285)
GO:0022891
substrate-specific transmembrane transporter activity
GO:0016620
oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor
7/252 | 48/11513 (0.00197)
GO:0004601
peroxidase activity
GO:0016615
malate dehydrogenase activity
GO:0016616
oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor
GO:0016421
CoA carboxylase activity
GO:0003755
peptidyl-prolyl cis-trans isomerase activity
7/252 | 59/11513 (0.00592)
GO:0016857
racemase and epimerase activity, acting on carbohydrates and derivatives
GO:0016758
transferase activity, transferring hexosyl groups
14/252 | 185/11513 (0.00262)
GO:0004553
hydrolase activity, hydrolyzing O-glycosyl compounds
15/252 | 222/11513 (0.00466)
GO:0042578
phosphoric ester hydrolase activity
GO:0046872
metal ion binding
GO:0051287
NAD or NADH binding
8/252 | 58/11513 (0.00104)
GO:0015291
secondary active transmembrane transporter activity
GO:0005275
amine transmembrane transporter activity
4/252 | 29/11513 (0.0389)
GO:0015267
channel activity
15/252 | 211/11513 (0.00285)
GO:0005372
water transmembrane transporter activity
12/252 | 20/11513 (1.29e-14)
GO:0008943
glyceraldehyde-3-phosphate dehydrogenase activity
4/252 | 20/11513 (0.00778)
GO:0016688
L-ascorbate peroxidase activity
2/252 | 10/11513 (0.092)
GO:0004470
malic enzyme activity
2/252 | 10/11513 (0.092)
GO:0004617
phosphoglycerate dehydrogenase activity
2/252 | 6/11513 (0.0221)
GO:0008831
dTDP-4-dehydrorhamnose reductase activity
3/252 | 21/11513 (0.0854)
GO:0033764
steroid dehydrogenase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor
GO:0003989
acetyl-CoA carboxylase activity
2/252 | 10/11513 (0.092)
GO:0003978
UDP-glucose 4-epimerase activity
3/252 | 22/11513 (0.0967)
GO:0016762
xyloglucan:xyloglucosyl transferase activity
10/252 | 16/11513 (1.34e-12)
GO:0046527
glucosyltransferase activity
GO:0008194
UDP-glycosyltransferase activity
GO:0042972
lichenase activity
9/252 | 9/11513 (0)
GO:0016791
phosphatase activity
GO:0046914
transition metal ion binding
GO:0015297
antiporter activity
GO:0022838
substrate-specific channel activity
15/252 | 211/11513 (0.00285)
GO:0015250
water channel activity
12/252 | 20/11513 (1.29e-14)
GO:0047100
glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) activity
4/252 | 14/11513 (0.00197)
GO:0004365
glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) activity
4/252 | 16/11513 (0.00308)
GO:0003854
3-beta-hydroxy-delta5-steroid dehydrogenase activity
4/252 | 36/11513 (0.0883)
GO:0035251
UDP-glucosyltransferase activity
GO:0003825
alpha,alpha-trehalose-phosphate synthase (UDP-forming) activity
2/252 | 8/11513 (0.0481)
GO:0019203
carbohydrate phosphatase activity
GO:0004805
trehalose-phosphatase activity
2/252 | 9/11513 (0.0684)
GO:0046906
tetrapyrrole binding
12/252 | 194/11513 (0.036)
GO:0005506
iron ion binding
GO:0020037
heme binding
12/252 | 162/11513 (0.0077)
GO:0015300
solute:solute antiporter activity
GO:0005471
ATP,ADP antiporter activity
5/252 | 12/11513 (3.56e-5)