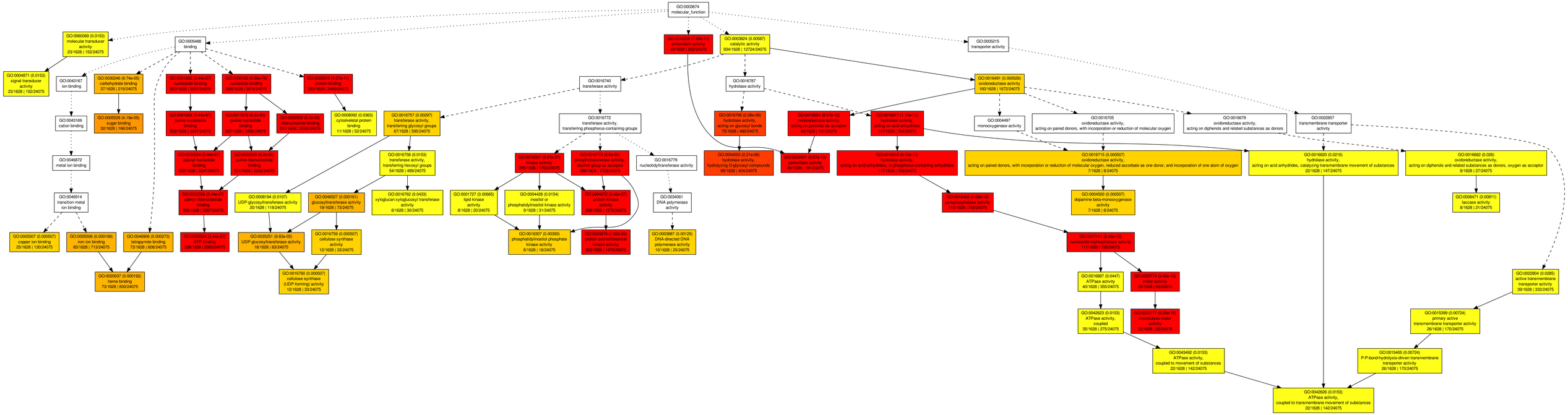
GO:0003674
molecular_function
GO:0060089 (0.0153)
molecular transducer activity
23/1628 | 152/24075
GO:0005488
binding
GO:0018209 (7.99e-11)
antioxidant activity
49/1628 | 203/24075
GO:0003824 (0.00587)
catalytic activity
934/1628 | 12724/24075
GO:0005215
transporter activity
GO:0004871 (0.0153)
signal transducer activity
23/1628 | 152/24075
GO:0043167
ion binding
GO:0030246 (9.74e-05)
carbohydrate binding
37/1628 | 219/24075
GO:0001882 (3.44e-87)
nucleoside binding
553/1628 | 3257/24075
GO:0000166 (4.96e-76)
nucleotide binding
566/1628 | 3374/24075
GO:0005515 (4.27e-11)
protein binding
263/1628 | 2460/24075
GO:0016740
transferase activity
GO:0016787
hydrolase activity
GO:0016491 (0.000526)
oxidoreductase activity
160/1628 | 1672/24075
GO:0043169
cation binding
GO:0005529 (4.19e-05)
sugar binding
32/1628 | 166/24075
GO:0001883 (3.44e-87)
purine nucleoside binding
552/1628 | 3247/24075
GO:0017076 (6.9e-85)
purine nucleotide binding
567/1628 | 3456/24075
GO:0032553 (6.2e-85)
ribonucleotide binding
551/1628 | 3232/24075
GO:0008092 (0.0363)
cytoskeletal protein binding
11/1628 | 52/24075
GO:0016757 (0.00297)
transferase activity, transferring glycosyl groups
67/1628 | 595/24075
GO:0016772
transferase activity, transferring phosphorus-containing groups
GO:0016798 (0.08e-06)
hydrolase activity, acting on glycosyl bonds
75/1628 | 460/24075
GO:0016684 (8.07e-12)
oxidoreductase activity, acting on peroxide as acceptor
49/1628 | 181/24075
GO:0016817 (1.15e-12)
hydrolase activity, acting on acid anhydrides
117/1628 | 764/24075
GO:0004497
monooxygenase activity
GO:0016705
oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen
GO:0016679
oxidoreductase activity, acting on diphenols and related substances as donors
GO:0022857
transmembrane transporter activity
GO:0046872
metal ion binding
GO:0032554 (3.44e-87)
adenyl nucleotide binding
552/1628 | 3247/24075
GO:0032555 (6.2e-85)
purine ribonucleotide binding
551/1628 | 3232/24075
GO:0016758 (0.0153)
transferase activity, transferring hexosyl groups
54/1628 | 489/24075
GO:0016301 (3.02e-37)
kinase activity
265/1628 | 1759/24075
GO:0016773 (2.6e-36)
phosphotransferase activity, alcohol group as acceptor
280/1628 | 1726/24075
GO:0016779
nucleotidyltransferase activity
GO:0004553 (2.21e-08)
hydrolase activity, hydrolyzing O-glycosyl compounds
69/1628 | 424/24075
GO:0004601 (8.07e-12)
peroxidase activity
49/1628 | 181/24075
GO:0016818 (8.13e-13)
hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides
157/1628 | 750/24075
GO:0016705
oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, reduced ascorbate as one donor, and incorporation of one atom of oxygen
7/1628 | 8/24075
GO:0016820 (0.0216)
hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances
22/1628 | 147/24075
GO:0016682 (0.026)
oxidoreductase activity, acting on diphenols and related substances as donors, oxygen as acceptor
8/1628 | 27/24075
GO:0046914
transition metal ion binding
GO:0032559 (3.44e-87)
adenyl ribonucleotide binding
556/1628 | 3087/24075
GO:0008194 (0.0107)
UDP-glycosyltransferase activity
20/1628 | 118/24075
GO:0046527 (0.000161)
glucosyltransferase activity
19/1628 | 73/24075
GO:0016762 (0.0433)
xyloglucan:xyloglucosyl transferase activity
8/1628 | 30/24075
GO:0001727 (0.00665)
lipid kinase activity
8/1628 | 20/24075
GO:0004428 (0.0154)
inositol or phosphatidylinositol kinase activity
9/1628 | 31/24075
GO:0004672 (6.42e-37)
protein kinase activity
266/1628 | 1575/24075
GO:0034061
DNA polymerase activity
GO:0016491 (0.000526)
oxidoreductase activity
160/1628 | 1672/24075
GO:0016462 (4.68e-12)
pyrophosphatase activity
113/1628 | 743/24075
GO:0004500 (0.000507)
dopamine beta-monooxygenase activity
7/1628 | 8/24075
GO:0008471 (0.00811)
laccase activity
8/1628 | 21/24075
GO:0005507 (0.000507)
copper ion binding
25/1628 | 130/24075
GO:0005506 (0.000199)
iron ion binding
63/1628 | 713/24075
GO:0046906 (0.000273)
tetrapyrrole binding
73/1628 | 608/24075
GO:0035639 (9.44e-87)
ATP binding
339/1628 | 3085/24075
GO:0035251 (9.83e-05)
UDP-glucosyltransferase activity
18/1628 | 63/24075
GO:0016759 (0.000507)
cellulose synthase activity
12/1628 | 33/24075
GO:0016301 (3.02e-37)
kinase activity
265/1628 | 1759/24075
GO:0016307 (0.00393)
phosphatidylinositol phosphate kinase activity
8/1628 | 18/24075
GO:0004674 (1.30e-39)
protein serine/threonine kinase activity
262/1628 | 1479/24075
GO:0003887 (0.00125)
DNA-directed DNA polymerase activity
10/1628 | 25/24075
GO:0020037 (0.000192)
heme binding
73/1628 | 600/24075
GO:0016760 (0.000507)
cellulose synthase (UDP-forming) activity
12/1628 | 33/24075
GO:0017111 (5.46e-12)
nucleoside-triphosphatase activity
111/1628 | 726/24075
GO:0016887 (0.0447)
ATPase activity
40/1628 | 355/24075
GO:0000774 (9.46e-16)
motor activity
36/1628 | 69/24075
GO:0022804 (0.0285)
active transmembrane transporter activity
39/1628 | 333/24075
GO:0042623 (0.0153)
ATPase activity, coupled
35/1628 | 275/24075
GO:0003777 (5.29e-15)
microtubule motor activity
32/1628 | 55/24075
GO:0015399 (0.00724)
primary active transmembrane transporter activity
26/1628 | 170/24075
GO:0043492 (0.0153)
ATPase activity, coupled to movement of substances
22/1628 | 142/24075
GO:0015405 (0.00724)
P-P-bond-hydrolysis-driven transmembrane transporter activity
26/1628 | 170/24075
GO:0042626 (0.0153)
ATPase activity, coupled to transmembrane movement of substances
22/1628 | 142/24075