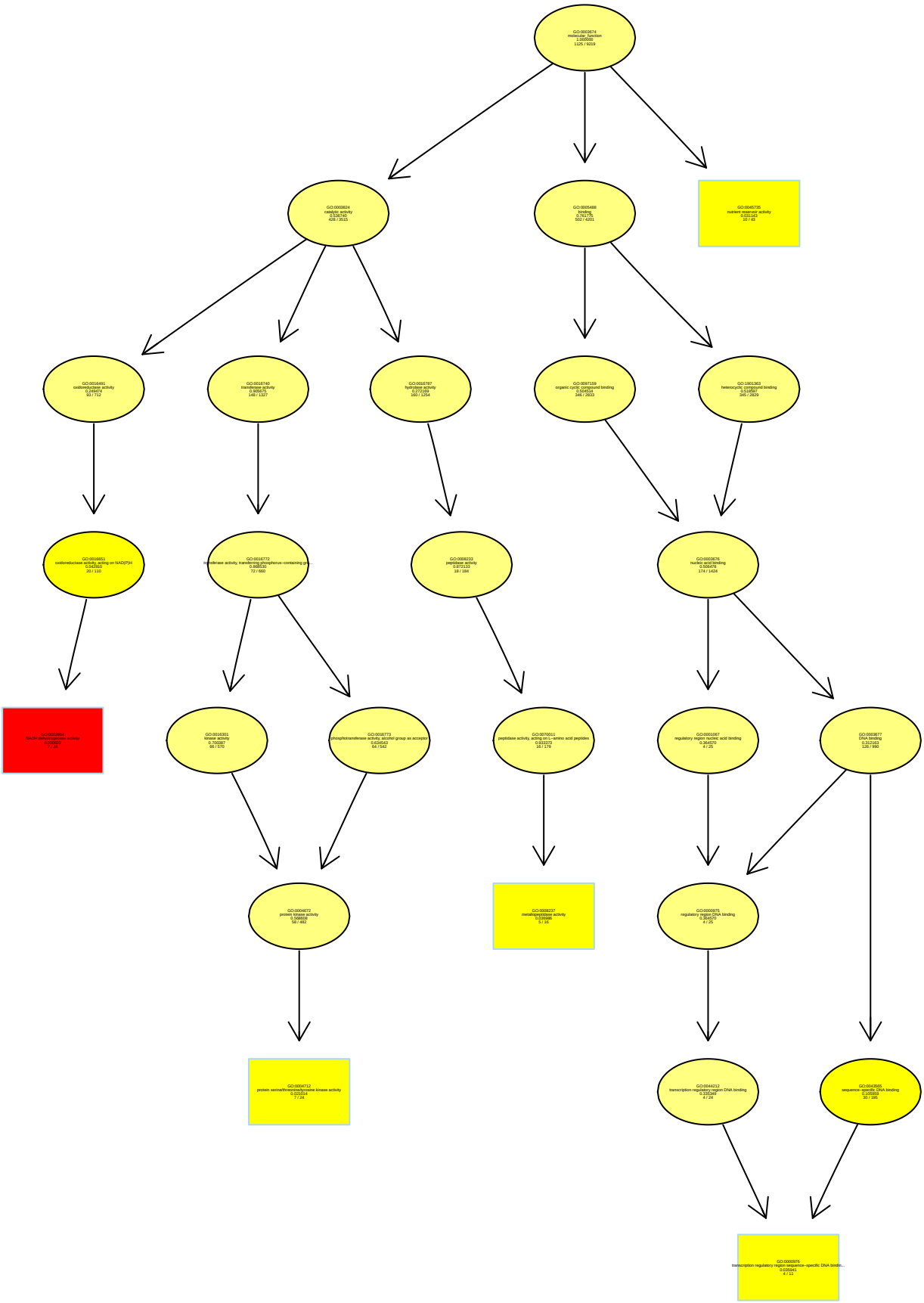
GO:0003674
molecular_function
1.000000
1125 / 9219
GO:0003824
catalytic activity
0.536745
428 / 3515
GO:0005488
binding
0.761775
502 / 4201
GO:0045735
nutrient reservoir activity
0.031143
10 / 43
GO:0016491
oxidoreductase activity
0.249674
93 / 712
GO:0016740
transferase activity
0.118956
148 / 1327
GO:0008787
hydrolase activity
0.127149
160 / 1254
GO:0097159
organic cyclic compound binding
0.104521
346 / 2833
GO:1901363
heterocyclic compound binding
0.101657
345 / 2829
GO:0016651
oxidoreductase activity, acting on NAD(P)H
0.084211
26 / 116
GO:0016772
transferase activity, transferring phosphorus-containing gro
0.054480
72 / 665
GO:0008233
peptidase activity
0.064151
18 / 184
GO:0003676
nucleic acid binding
0.137401
174 / 1424
GO:0003954
NADH dehydrogenase activity
0.000622
7 / 14
GO:0016301
kinase activity
0.706287
66 / 570
GO:0016773
phosphotransferase activity, alcohol group as acceptor
0.634543
64 / 542
GO:0070011
peptidase activity, acting on L-amino acid peptides
0.932373
16 / 179
GO:0001067
regulatory region nucleic acid binding
0.364570
4 / 25
GO:0003677
DNA binding
0.321563
126 / 960
GO:0004672
protein kinase activity
0.558828
58 / 482
GO:0008237
metallopeptidase activity
0.156986
5 / 16
GO:0000975
regulatory region DNA binding
0.364570
4 / 25
GO:0004712
protein serine/threonine/tyrosine kinase activity
0.320214
7 / 24
GO:0044212
transcription regulatory region DNA binding
0.335349
4 / 24
GO:0043565
sequence-specific DNA binding
0.105959
30 / 185
GO:0000976
transcription regulatory region sequence-specific DNA bindin...
0.335349
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