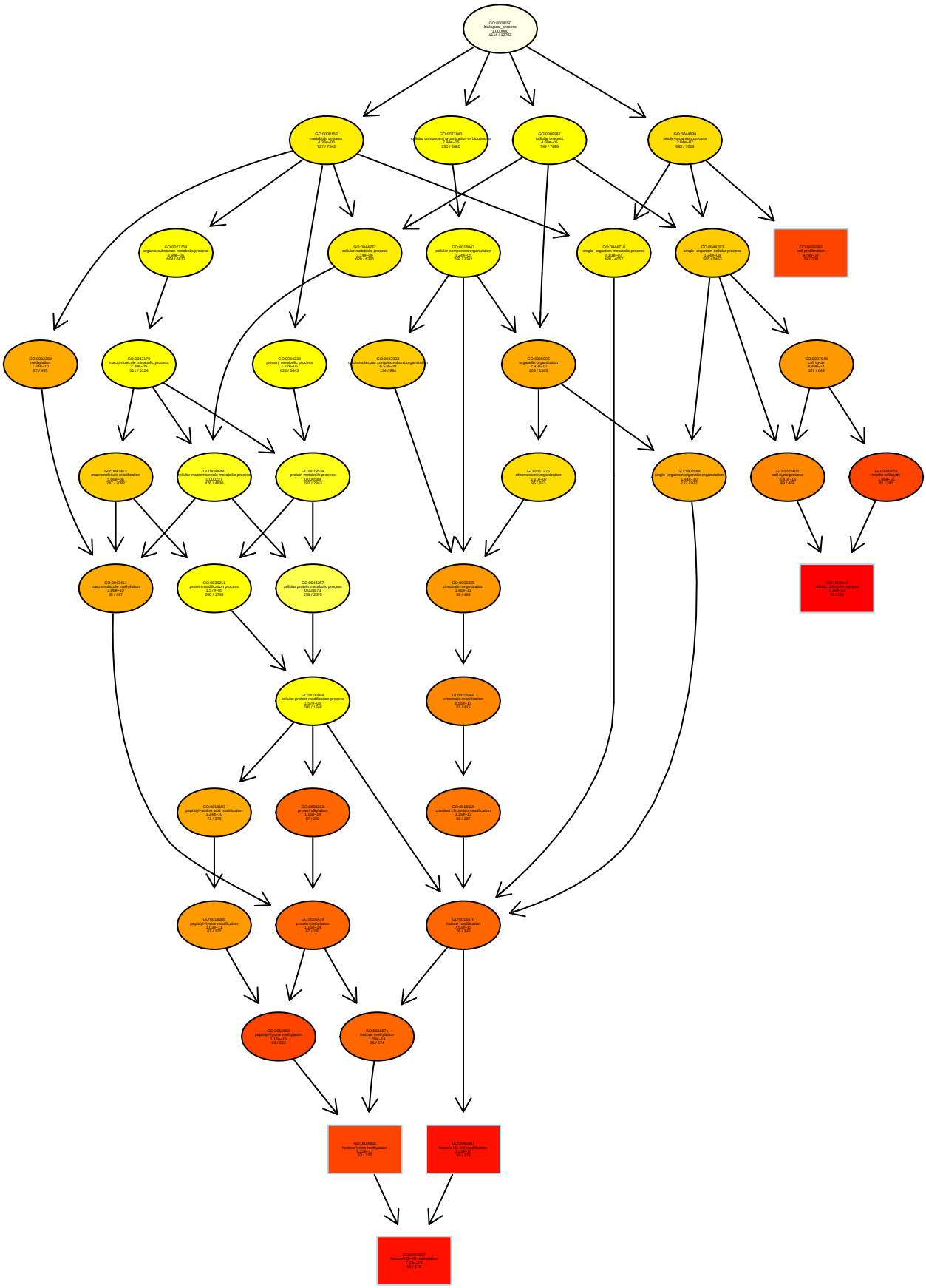
GO:0008150
biological_process
1.000000
1114 / 12782
GO:0008152
metabolic process
9.36e−06
727 / 5542
GO:0071840
cellular component organization or biogenesis
7.94e−06
260 / 2665
GO:0009987
cellular process
4.68e−05
749 / 7666
GO:0044699
single−organism process
2.56e−11
693 / 7029
GO:0071704
organic substance metabolic process
8.38e−05
664 / 6833
GO:0044237
cellular metabolic process
1.14e−05
629 / 6395
GO:0016043
cellular component organization
1.24e−05
259 / 2342
GO:0044710
single−organism metabolic process
2.81e−07
426 / 4057
GO:0044763
single−organism cellular process
1.24e−05
565 / 5463
GO:0008283
cell proliferation
1.79e−05
59 / 208
GO:0032259
methylation
1.21e−10
87 / 495
GO:0043170
macromolecule metabolic process
2.38e−05
511 / 5124
GO:0044238
primary metabolic process
1.72e−05
628 / 6443
GO:0043933
macromolecular complex subunit organization
6.53e−08
136 / 984
GO:0006996
organelle organization
2.91e−10
205 / 1563
GO:0007049
cell cycle
4.42e−11
107 / 649
GO:0043412
macromolecule modification
5.66e−05
247 / 2382
GO:0044260
cellular macromolecule metabolic process
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476 / 4830
GO:0019538
protein metabolic process
0.000581
292 / 2843
GO:0051276
chromosome organization
5.31e−07
95 / 653
GO:1902589
single−organism organelle organization
1.44e−10
127 / 922
GO:0022402
cell cycle process
6.41e−13
89 / 468
GO:0000278
mitotic cell cycle
1.99e−16
85 / 361
GO:0043414
macromolecule methylation
2.66e−10
85 / 487
GO:0036211
protein modification process
1.57e−05
266 / 1748
GO:0044267
cellular protein metabolic process
0.003873
259 / 2570
GO:0006325
chromatin organization
1.46e−11
88 / 484
GO:1903047
mitotic cell cycle process
2.30e−92
72 / 252
GO:0006464
cellular protein modification process
1.57e−05
266 / 1748
GO:0016568
chromatin modification
8.55e−13
82 / 415
GO:0018193
peptidyl−amino acid modification
5.15e−11
71 / 370
GO:0008213
protein alkylation
2.20e−12
67 / 281
GO:0018996
covalent chromatin modification
7.35e−13
80 / 387
GO:0018205
peptidyl−lysine modification
1.03e−11
67 / 322
GO:0006479
protein methylation
2.20e−12
67 / 281
GO:0016570
histone modification
7.35e−13
76 / 340
GO:0018022
peptidyl−lysine methylation
1.18e−12
63 / 232
GO:0016571
histone methylation
1.08e−14
66 / 274
GO:0034968
histone lysine methylation
4.27e−12
63 / 232
GO:0051567
histone H3−K9 methylation
1.24e−12
54 / 170
GO:0051567
histone H3−K9 methylation
1.23e−12
54 / 170