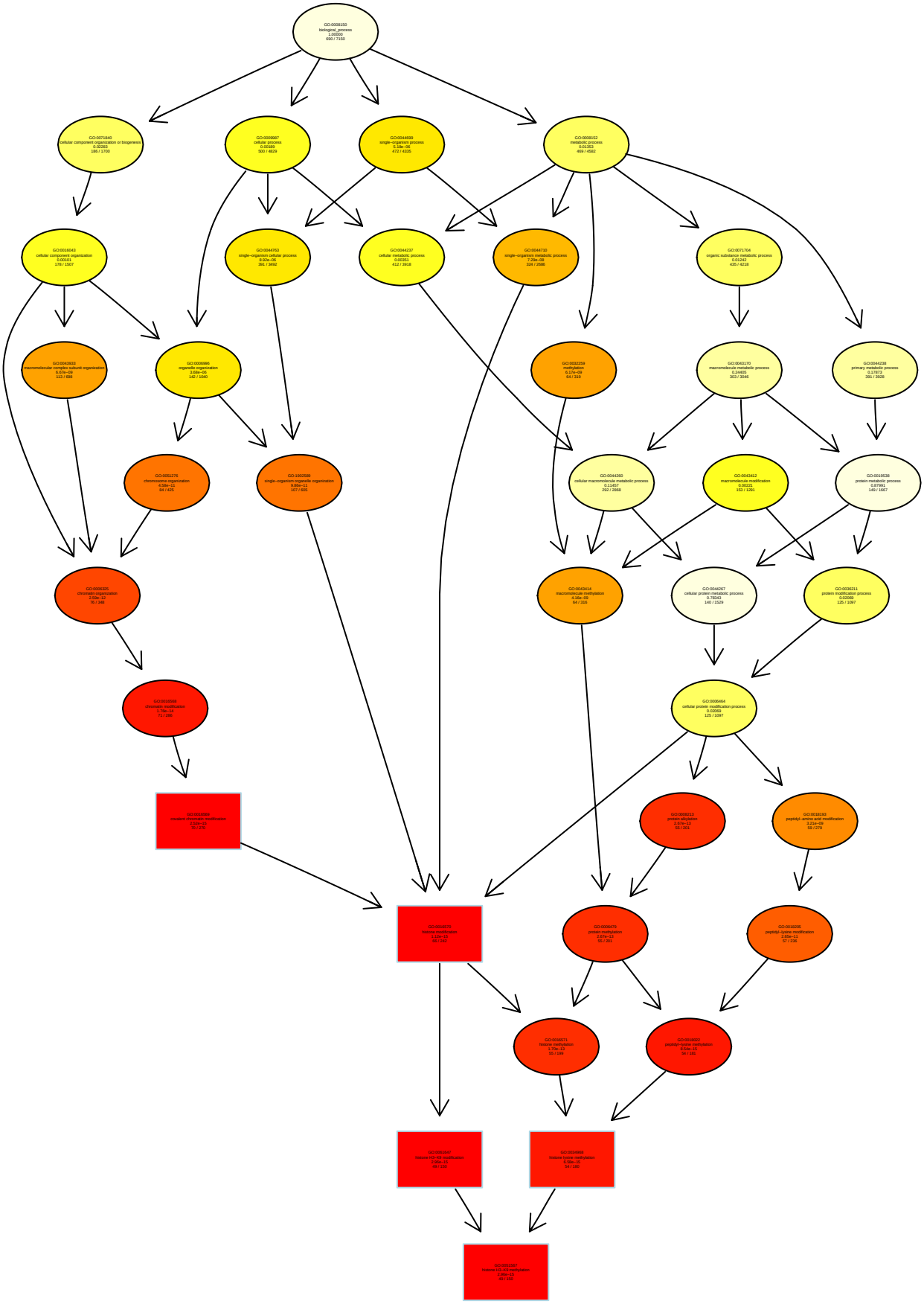
GO:0008150
biological_process
1.00000
690 / 7150
GO:0071840
cellular component organization or biogenesis
0.02283
188 / 3700
GO:0009987
cellular process
0.00189
520 / 4029
GO:0044699
single-organism process
5.18e-06
473 / 4155
GO:0008152
metabolic process
0.01353
469 / 4582
GO:0016043
cellular component organization
0.00101
178 / 1507
GO:0044763
single-organism cellular process
8.93e-06
391 / 3492
GO:0044237
cellular metabolic process
0.00251
412 / 3918
GO:0044710
single-organism metabolic process
7.29e-08
324 / 2686
GO:0071704
organic substance metabolic process
0.01243
435 / 4218
GO:0043933
macromolecular complex subunit organization
6.43e-09
113 / 898
GO:0006996
organelle organization
3.68e-05
142 / 1040
GO:0032259
methylation
6.17e-09
64 / 319
GO:0043170
macromolecule metabolic process
0.24455
303 / 3046
GO:0044238
primary metabolic process
0.17873
391 / 3928
GO:0051276
chromosome organization
4.58e-11
84 / 425
GO:1902589
single-organism organelle organization
9.56e-11
107 / 605
GO:0044260
cellular macromolecule metabolic process
0.11457
292 / 2868
GO:0043412
macromolecule modification
0.00221
153 / 1291
GO:0019538
protein metabolic process
0.87061
149 / 1667
GO:0006325
chromatin organization
2.59e-12
76 / 348
GO:0043414
macromolecule methylation
4.16e-09
64 / 316
GO:0044267
cellular protein metabolic process
0.78243
140 / 1529
GO:0036211
protein modification process
0.02069
125 / 1097
GO:0016568
chromatin modification
1.76e-14
71 / 286
GO:0006464
cellular protein modification process
0.02069
125 / 1097
GO:0016569
covalent chromatin modification
2.53e-10
70 / 270
GO:0018212
peptidyl-tyrosine modification
2.63e-12
55 / 201
GO:0018193
peptidyl-amino acid modification
1.21e-09
59 / 279
GO:0016570
histone modification
1.12e-15
66 / 242
GO:0006479
protein methylation
2.67e-12
55 / 201
GO:0018205
peptidyl-lysine modification
2.65e-11
57 / 236
GO:0016571
histone methylation
1.76e-13
55 / 199
GO:0018022
peptidyl-lysine methylation
8.54e-15
54 / 193
GO:0061647
histone H3-K9 modification
2.66e-15
49 / 180
GO:0034968
histone lysine methylation
6.58e-15
54 / 180
GO:0051567
histone H3-K9 methylation
2.66e-15
49 / 180