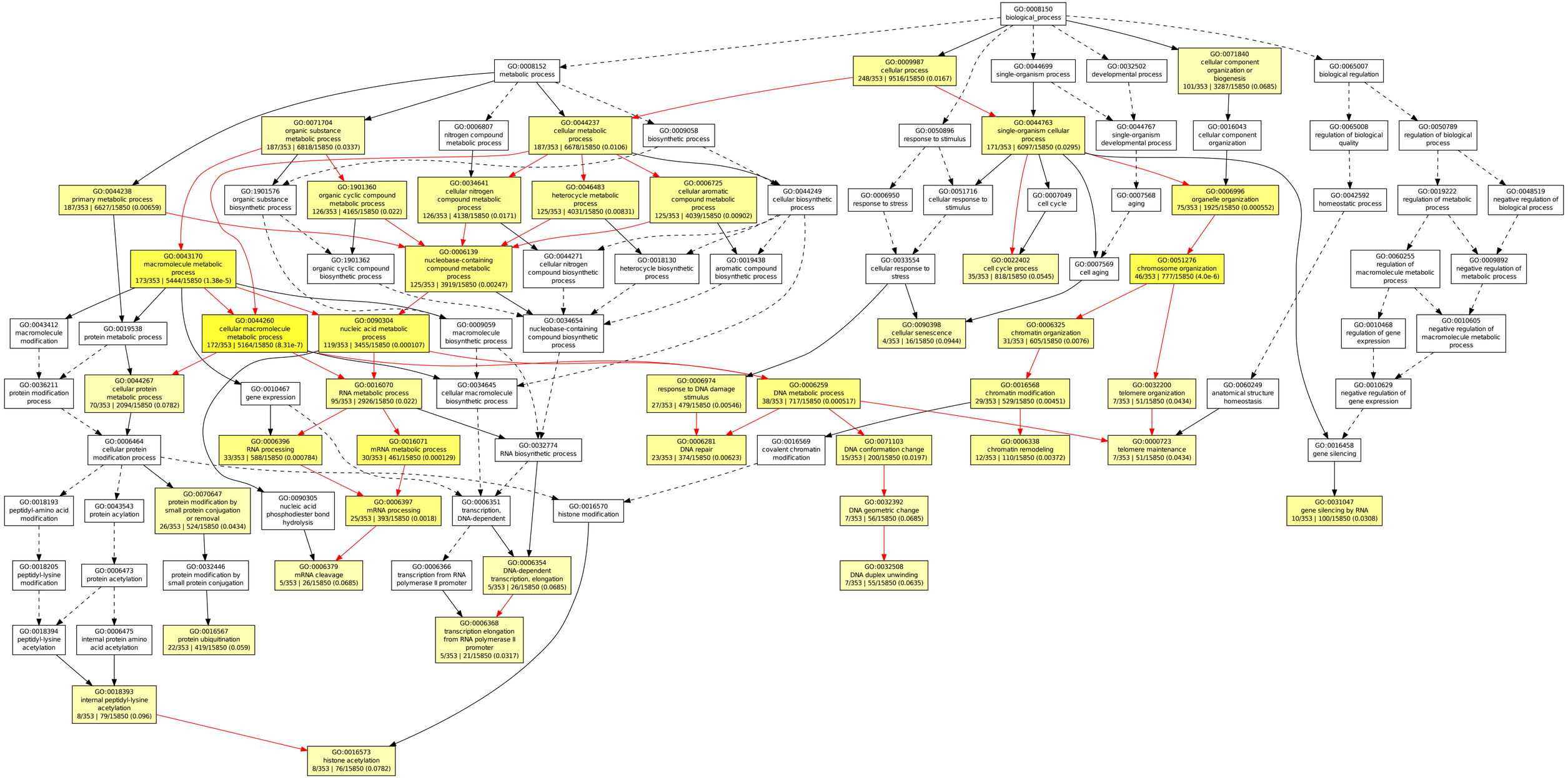
GO:0008150
biological_process
GO:0008152
metabolic process
GO:0009987
cellular process
248/353 | 9516/15850 (0.0167)
GO:0044699
single-organism process
GO:0032502
developmental process
GO:0071840
cellular component organization or biogenesis
101/353 | 3287/15850 (0.0685)
GO:0065007
biological regulation
GO:0071704
organic substance metabolic process
187/353 | 6818/15850 (0.0337)
GO:0006807
nitrogen compound metabolic process
GO:0044237
cellular metabolic process
187/353 | 6678/15850 (0.0106)
GO:0009058
biosynthetic process
GO:0050896
response to stimulus
GO:0044763
single-organism cellular process
171/353 | 6097/15850 (0.0295)
GO:0044767
single-organism developmental process
GO:0016043
cellular component organization
GO:0065008
regulation of biological quality
GO:0050789
regulation of biological process
GO:0044238
primary metabolic process
187/353 | 6627/15850 (0.00659)
GO:1901576
organic substance biosynthetic process
GO:1901360
organic cyclic compound metabolic process
126/353 | 4165/15850 (0.022)
GO:0034641
cellular nitrogen compound metabolic process
126/353 | 4138/15850 (0.0171)
GO:0046483
heterocycle metabolic process
125/353 | 4031/15850 (0.00831)
GO:0006725
cellular aromatic compound metabolic process
125/353 | 4039/15850 (0.00902)
GO:0044249
cellular biosynthetic process
GO:0006950
response to stress
GO:0051716
cellular response to stimulus
GO:0007049
cell cycle
GO:0007568
aging
GO:0006996
organelle organization
75/353 | 1925/15850 (0.000552)
GO:0042592
homeostatic process
GO:0019222
regulation of metabolic process
GO:0048519
negative regulation of biological process
GO:0043170
macromolecule metabolic process
173/353 | 5444/15850 (1.38e-5)
GO:1901362
organic cyclic compound biosynthetic process
GO:0006139
nucleobase-containing compound metabolic process
125/353 | 3919/15850 (0.00247)
GO:0044271
cellular nitrogen compound biosynthetic process
GO:0018130
heterocycle biosynthetic process
GO:0019438
aromatic compound biosynthetic process
GO:0033554
cellular response to stress
GO:0022402
cell cycle process
35/353 | 818/15850 (0.0545)
GO:0007569
cell aging
GO:0051276
chromosome organization
46/353 | 777/15850 (4.0e-6)
GO:0060255
regulation of macromolecule metabolic process
GO:0009892
negative regulation of metabolic process
GO:0043412
macromolecule modification
GO:0019538
protein metabolic process
GO:0044260
cellular macromolecule metabolic process
172/353 | 5164/15850 (8.31e-7)
GO:0090304
nucleic acid metabolic process
119/353 | 3455/15850 (0.000107)
GO:0009059
macromolecule biosynthetic process
GO:0034654
nucleobase-containing compound biosynthetic process
GO:0090398
cellular senescence
4/353 | 16/15850 (0.0944)
GO:0006325
chromatin organization
31/353 | 605/15850 (0.0076)
GO:0010468
regulation of gene expression
GO:0010605
negative regulation of macromolecule metabolic process
GO:0036211
protein modification process
GO:0044267
cellular protein metabolic process
70/353 | 2094/15850 (0.0782)
GO:0010467
gene expression
GO:0016070
RNA metabolic process
95/353 | 2926/15850 (0.022)
GO:0034645
cellular macromolecule biosynthetic process
GO:0006974
response to DNA damage stimulus
27/353 | 479/15850 (0.00546)
GO:0006259
DNA metabolic process
38/353 | 717/15850 (0.000517)
GO:0016568
chromatin modification
29/353 | 529/15850 (0.00451)
GO:0032200
telomere organization
7/353 | 51/15850 (0.0434)
GO:0060249
anatomical structure homeostasis
GO:0010629
negative regulation of gene expression
GO:0006464
cellular protein modification process
GO:0006396
RNA processing
33/353 | 588/15850 (0.000784)
GO:0016071
mRNA metabolic process
30/353 | 461/15850 (0.000129)
GO:0032774
RNA biosynthetic process
GO:0006281
DNA repair
23/353 | 374/15850 (0.00623)
GO:0016569
covalent chromatin modification
GO:0071103
DNA conformation change
15/353 | 200/15850 (0.0197)
GO:0006338
chromatin remodeling
12/353 | 110/15850 (0.00372)
GO:0000723
telomere maintenance
7/353 | 51/15850 (0.0434)
GO:0016458
gene silencing
GO:0018193
peptidyl-amino acid modification
GO:0043543
protein acylation
GO:0070647
protein modification by small protein conjugation or removal
26/353 | 524/15850 (0.0434)
GO:0090305
nucleic acid phosphodiester bond hydrolysis
GO:0006397
mRNA processing
25/353 | 393/15850 (0.0018)
GO:0006351
transcription, DNA-dependent
GO:0016570
histone modification
GO:0032392
DNA geometric change
7/353 | 56/15850 (0.0685)
GO:0031047
gene silencing by RNA
10/353 | 100/15850 (0.0308)
GO:0018205
peptidyl-lysine modification
GO:0006473
protein acetylation
GO:0032446
protein modification by small protein conjugation
GO:0006379
mRNA cleavage
5/353 | 26/15850 (0.0685)
GO:0006366
transcription from RNA polymerase II promoter
GO:0006354
DNA-dependent transcription, elongation
5/353 | 26/15850 (0.0685)
GO:0032508
DNA duplex unwinding
7/353 | 55/15850 (0.0635)
GO:0018394
peptidyl-lysine acetylation
GO:0006475
internal protein amino acid acetylation
GO:0016567
protein ubiquitination
22/353 | 419/15850 (0.059)
GO:0006368
transcription elongation from RNA polymerase II promoter
5/353 | 21/15850 (0.0317)
GO:0018393
internal peptidyl-lysine acetylation
8/353 | 79/15850 (0.096)
GO:0016573
histone acetylation
8/353 | 76/15850 (0.0782)