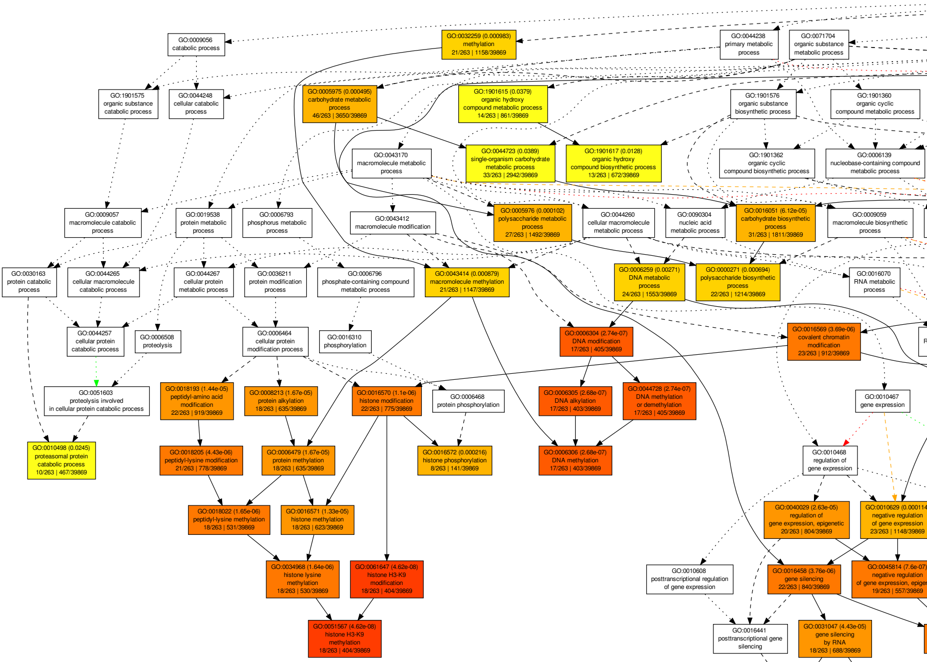
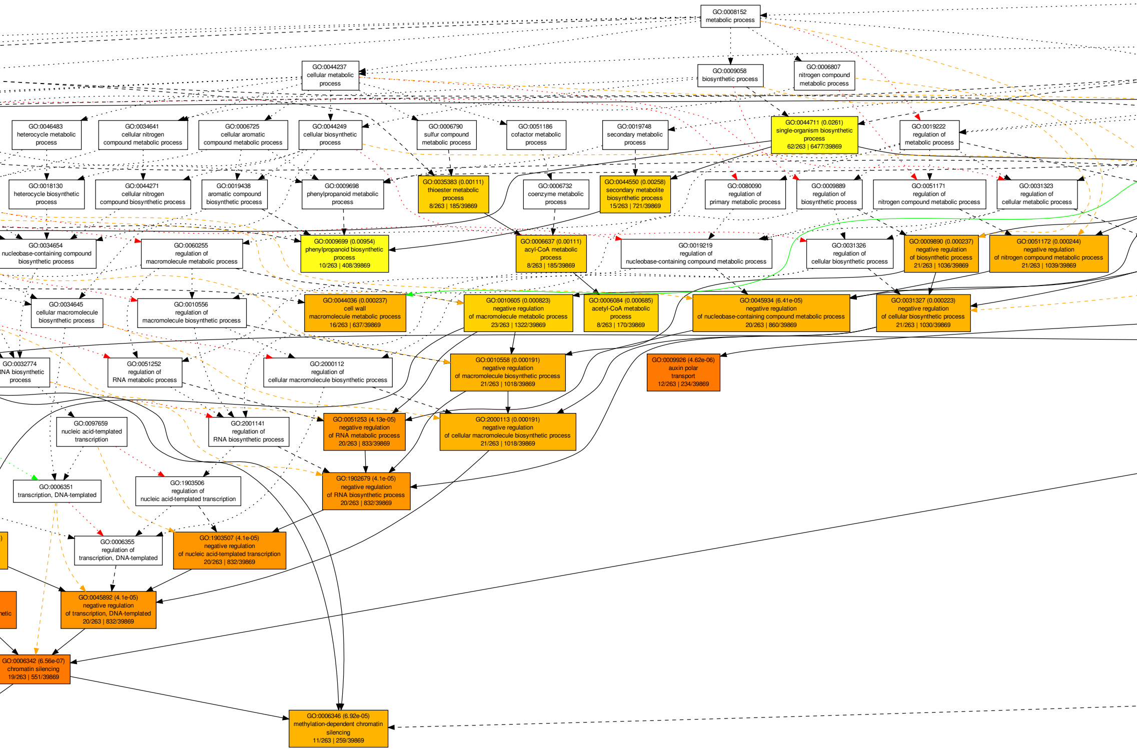
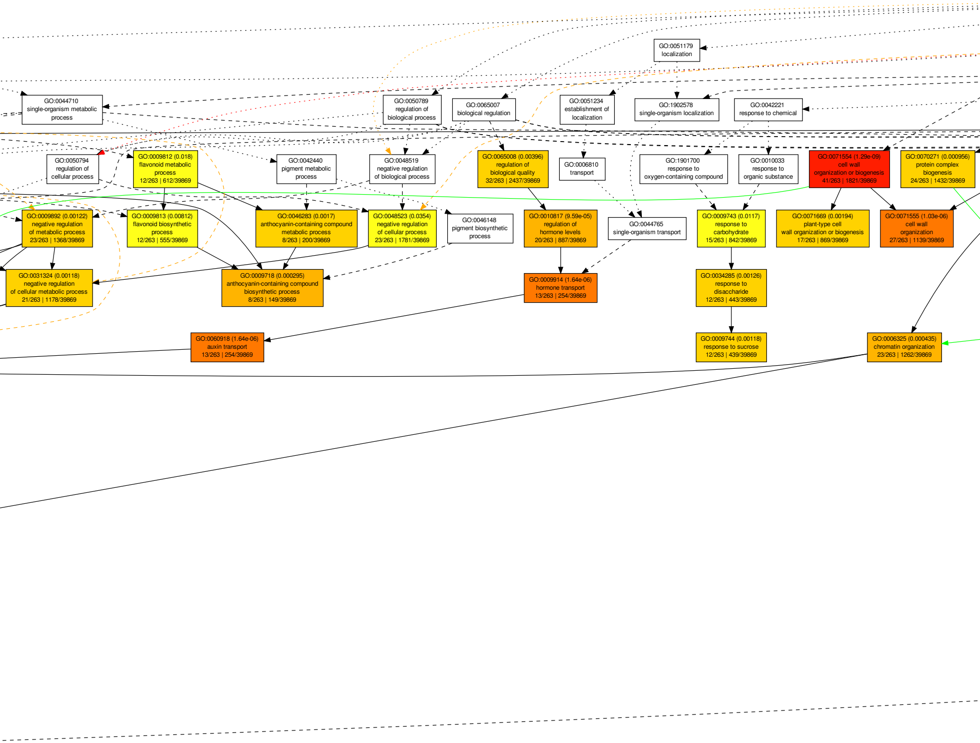
6d v 10d Upregulated


GO:0009056
catabolic process
GO:0032259 (0.000983)
methylation
21/263 | 1158/39869
GO:0044238
primary metabolic
process
GO:0071704
organic substance
metabolic process
GO:1901575
organic substance
catabolic process
GO:0044248
cellular catabolic
process
GO:0005975 (0.000495)
carbohydrate metabolic
process
46/263 | 3650/39869
GO:1901615 (0.0379)
organic hydroxy
compound metabolic process
14/263 | 861/39869
GO:1901576
organic substance
biosynthetic process
GO:1901360
organic cyclic
compound metabolic process
GO:0043170
macromolecule metabolic
process
GO:0044723 (0.0389)
single-organism carbohydrate
metabolic process
33/263 | 2942/39869
GO:1901617 (0.0128)
organic hydroxy
compound biosynthetic process
13/263 | 672/39869
GO:1901362
organic cyclic
compound biosynthetic process
GO:0006139
nucleobase-containing compound
metabolic process
GO:0009057
macromolecule catabolic
process
GO:0019538
protein metabolic
process
GO:0006793
phosphorus metabolic
process
GO:0043412
macromolecule modification
GO:0005976 (0.000102)
polysaccharide metabolic
process
27/263 | 1492/39869
GO:0044260
cellular macromolecule
metabolic process
GO:0090304
nucleic acid
metabolic process
GO:0016051 (6.12e-05)
carbohydrate biosynthetic
process
31/263 | 1811/39869
GO:0009059
macromolecule biosynthetic
process
GO:0030163
protein catabolic
process
GO:0044265
cellular macromolecule
catabolic process
GO:0044267
cellular protein
metabolic process
GO:0036211
protein modification
process
GO:0006796
phosphate-containing compound
metabolic process
GO:0043414 (0.000879)
macromolecule methylation
21/263 | 1147/39869
GO:0006259 (0.00271)
DNA metabolic
process
24/263 | 1553/39869
GO:0000271 (0.000694)
polysaccharide biosynthetic
process
22/263 | 1214/39869
GO:0016070
RNA metabolic
process
GO:0044257
cellular protein
catabolic process
GO:0006508
proteolysis
GO:0006464
cellular protein
modification process
GO:0016310
phosphorylation
GO:0006304 (2.74e-07)
DNA modification
17/263 | 405/39869
GO:0016569 (3.69e-06)
covalent chromatin
modification
23/263 | 912/39869
R
GO:0051603
proteolysis involved
in cellular protein catabolic process
GO:0018193 (1.44e-05)
peptidyl-amino acid
modification
22/263 | 919/39869
GO:0008213 (1.67e-05)
protein alkylation
18/263 | 635/39869
GO:0016570 (1.1e-06)
histone modification
22/263 | 775/39869
GO:0006468
protein phosphorylation
GO:0006305 (2.68e-07)
DNA alkylation
17/263 | 403/39869
GO:0044728 (2.74e-07)
DNA methylation
or demethylation
17/263 | 405/39869
GO:0010467
gene expression
GO:0010498 (0.0245)
proteasomal protein
catabolic process
10/263 | 467/39869
GO:0018205 (4.43e-06)
peptidyl-lysine modification
21/263 | 778/39869
GO:0006479 (1.67e-05)
protein methylation
18/263 | 635/39869
GO:0016572 (0.000216)
histone phosphorylation
8/263 | 141/39869
GO:0006306 (2.68e-07)
DNA methylation
17/263 | 403/39869
GO:0010468
regulation of
gene expression
GO:0018022 (1.65e-06)
peptidyl-lysine methylation
18/263 | 531/39869
GO:0016571 (1.33e-05)
histone methylation
18/263 | 623/39869
GO:0040029 (2.63e-05)
regulation of
gene expression, epigenetic
20/263 | 804/39869
GO:0010629 (0.00011
negative regulation
of gene expression
23/263 | 1148/39869
GO:0034968 (1.64e-06)
histone lysine
methylation
18/263 | 530/39869
GO:0061647 (4.62e-08)
histone H3-K9
modification
18/263 | 404/39869
GO:0010608
posttranscriptional regulation
of gene expression
GO:0016458 (3.76e-06)
gene silencing
22/263 | 840/39869
GO:0045814 (7.6e-07)
negative regulation
of gene expression, epiger
19/263 | 557/39869
GO:0051567 (4.62e-08)
histone H3-K9
methylation
18/263 | 404/39869
GO:0016441
posttranscriptional gene
silencing
GO:0031047 (4.43e-05)
gene silencing
by RNA
18/263 | 688/39869
GO:0035194 (0.0389)
posttranscriptional gene
silencing by RNA
9/263 | 417/39869
GO:0031048 (0.00667)
chromatin silencing
by small RNA
8/263 | 250/39869


GO:0008152 metabolic process
GO:0044237 cellular metabolic process
GO:0009058 biosynthetic process
GO:0006807 nitrogen compound metabolic process
GO:0046483 heterocycle metabolic process
GO:0034641 cellular nitrogen compound metabolic process
GO:0006725 cellular aromatic compound metabolic process
GO:0044249 cellular biosynthetic process
GO:0006790 sulfur compound metabolic process
GO:0051186 cofactor metabolic process
GO:0019748 secondary metabolic process
GO:0044711 (0.0261) single-organism biosynthetic process 62/263 | 6477/39869
GO:0019222 regulation of metabolic process
GO:0018130 heterocycle biosynthetic process
GO:0044271 cellular nitrogen compound biosynthetic process
GO:0019438 aromatic compound biosynthetic process
GO:0009698 phenylpropanoid metabolic process
GO:0035383 (0.00111) thioester metabolic process 8/263 | 185/39869
GO:0006732 coenzyme metabolic process
GO:0044550 (0.00258) secondary metabolite biosynthetic process 15/263 | 721/39869
GO:0080090 regulation of primary metabolic process
GO:0009889 regulation of biosynthetic process
GO:0051171 regulation of nitrogen compound metabolic process
GO:0031323 regulation of cellular metabolic process
GO:0034654 nucleobase-containing compound biosynthetic process
GO:0060255 regulation of macromolecule metabolic process
GO:0009699 (0.00954) phenylpropanoid biosynthetic process 10/263 | 408/39869
GO:0006637 (0.00111) acyl-CoA metabolic process 8/263 | 185/39869
GO:0019219 regulation of nucleobase-containing compound metabolic process
GO:0031326 regulation of cellular biosynthetic process
GO:0009890 (0.000237) negative regulation of biosynthetic process 21/263 | 1036/39869
GO:0051172 (0.000244) negative regulation of nitrogen compound metabolic process 21/263 | 1039/39869
GO:0034645 cellular macromolecule biosynthetic process
GO:0010556 regulation of macromolecule biosynthetic process
GO:0044036 (0.000237) cell wall macromolecule metabolic process 16/263 | 637/39869
GO:0010605 (0.000823) negative regulation of macromolecule metabolic process 23/263 | 1322/39869
GO:0006084 (0.000685) acetyl-CoA metabolic process 8/263 | 170/39869
GO:0045934 (6.41e-05) negative regulation of nucleobase-containing compound metabolic process 20/263 | 860/39869
GO:0031327 (0.000223) negative regulation of cellular biosynthetic process 21/263 | 1030/39869
GO:0032774 NA biosynthetic process
GO:0051252 regulation of RNA metabolic process
GO:2000112 regulation of cellular macromolecule biosynthetic process
GO:0010558 (0.000191) negative regulation of macromolecule biosynthetic process 21/263 | 1018/39869
GO:0009926 (4.62e-06) auxin polar transport 12/263 | 234/39869
GO:0097659 nucleic acid-templated transcription
GO:2001141 regulation of RNA biosynthetic process
GO:0051253 (4.13e-05) negative regulation of RNA metabolic process 20/263 | 833/39869
GO:2000113 (0.000191) negative regulation of cellular macromolecule biosynthetic process 21/263 | 1018/39869
GO:0006351 transcription, DNA-templated
GO:1903506 regulation of nucleic acid-templated transcription
GO:1902679 (4.1e-05) negative regulation of RNA biosynthetic process 20/263 | 832/39869
GO:0006355 regulation of transcription, DNA-templated
GO:1903507 (4.1e-05) negative regulation of nucleic acid-templated transcription 20/263 | 832/39869
GO:0045892 (4.1e-05) negative regulation of transcription, DNA-templated 20/263 | 832/39869
netic
GO:0006342 (6.56e-07) chromatin silencing 19/263 | 551/39869
GO:0006346 (6.92e-05) methylation-dependent chromatin silencing 11/263 | 259/39869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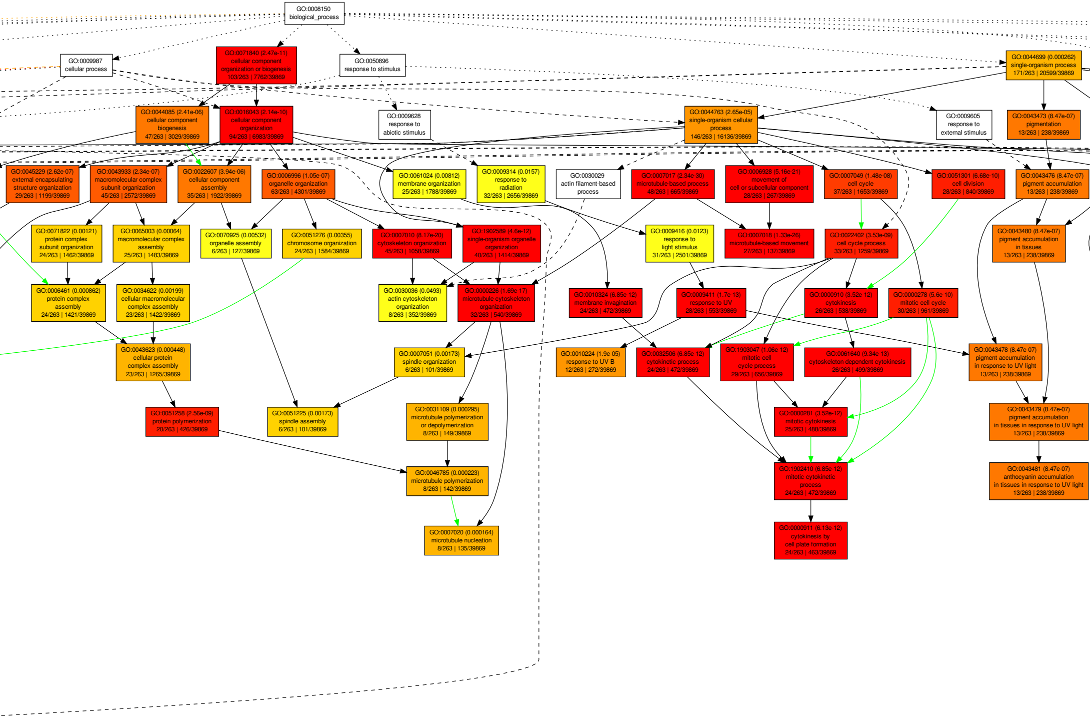
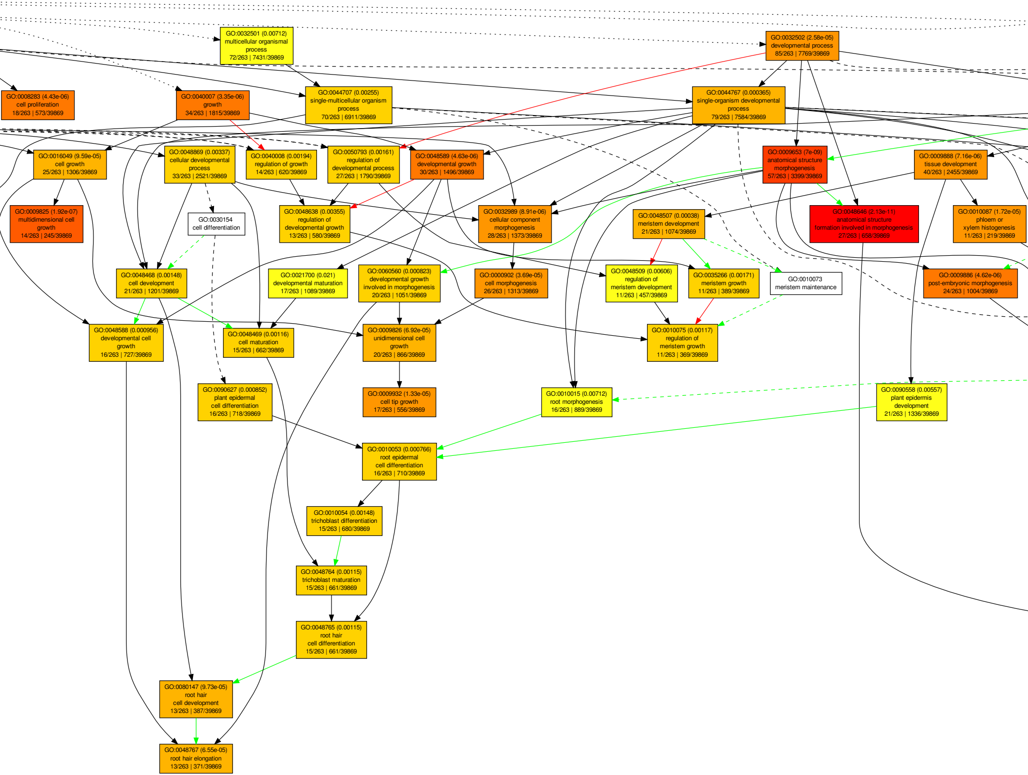
localization
GO:0044710
single-organism metabolic
process
GO:0050789
regulation of
biological process
GO:0065007
biological regulation
GO:0051234
establishment of
localization
GO:1902578
single-organism localization
GO:0042221
response to chemical
GO:0050794
regulation of
cellular process
GO:0009812 (0.018)
flavonoid metabolic
process
12/263 | 612/39869
GO:0042440
pigment metabolic
process
GO:0048519
negative regulation
of biological process
GO:0065008 (0.00396)
regulation of
biological quality
32/263 | 2437/39869
GO:0006810
transport
GO:1901700
response to
oxygen-containing compound
GO:0010033
response to
organic substance
GO:0071554 (1.29e-09)
cell wall
organization or biogenesis
41/263 | 1821/39869
GO:0070271 (0.000956)
protein complex
biogenesis
24/263 | 1432/39869
GO:0009892 (0.00122)
negative regulation
of metabolic process
23/263 | 1368/39869
GO:0009813 (0.00812)
flavonoid biosynthetic
process
12/263 | 555/39869
GO:0046283 (0.0017)
anthocyanin-containing compound
metabolic process
8/263 | 200/39869
GO:0048523 (0.0354)
negative regulation
of cellular process
23/263 | 1781/39869
GO:0046148
pigment biosynthetic
process
GO:0010817 (9.59e-05)
regulation of
hormone levels
20/263 | 887/39869
GO:0044765
single-organism transport
GO:0009743 (0.0117)
response to
carbohydrate
15/263 | 842/39869
GO:0071669 (0.00194)
plant-type cell
wall organization or biogenesis
17/263 | 869/39869
GO:0071555 (1.03e-06)
cell wall
organization
27/263 | 1139/39869
GO:0031324 (0.00118)
negative regulation
of cellular metabolic process
21/263 | 1178/39869
GO:0009718 (0.000295)
anthocyanin-containing compound
biosynthetic process
8/263 | 149/39869
GO:0009914 (1.64e-06)
hormone transport
13/263 | 254/39869
GO:0034285 (0.00126)
response to
disaccharide
12/263 | 443/39869
GO:0060918 (1.64e-06)
auxin transport
13/263 | 254/39869
GO:0009744 (0.00118)
response to sucrose
12/263 | 439/39869
GO:0006325 (0.000435)
chromatin organization
23/263 | 1262/39869


GO:0008150 biological_process
GO:0009987 cellular process
GO:0071840 (2.47e-11) cellular component organization or biogenesis 103/263 | 7762/39869
GO:0050896 response to stimulus
GO:0044699 (0.000262) single-organism process 171/263 | 20599/39869
GO:0044085 (2.41e-06) cellular component biogenesis 47/263 | 3029/39869
GO:0016043 (2.14e-10) cellular component organization 94/263 | 6983/39869
GO:0009628 response to abiotic stimulus
GO:0044763 (2.65e-05) single-organism cellular process 146/263 | 16136/39869
GO:0009605 response to external stimulus
GO:0043473 (8.47e-07) pigmentation 13/263 | 238/39869
GO:0045229 (2.62e-07) external encapsulating structure organization 29/263 | 1199/39869
GO:0043933 (2.34e-07) macromolecular complex subunit organization 45/263 | 2572/39869
GO:0022607 (3.94e-06) cellular component assembly 35/263 | 1922/39869
GO:0006996 (1.05e-07) organelle organization 63/263 | 4301/39869
GO:0061024 (0.00812) membrane organization 25/263 | 1788/39869
GO:0009314 (0.0157) response to radiation 32/263 | 2656/39869
GO:0030029 actin filament-based process
GO:0007017 (2.34e-30) microtubule-based process 48/263 | 665/39869
GO:0006928 (5.16e-21) movement of cell or subcellular component 28/263 | 267/39869
GO:0007049 (1.48e-08) cell cycle 37/263 | 1653/39869
GO:0051301 (6.68e-10) cell division 28/263 | 840/39869
GO:0043476 (8.47e-07) pigment accumulation 13/263 | 238/39869
GO:0071822 (0.00121) protein complex subunit organization 24/263 | 1462/39869
GO:0065003 (0.00064) macromolecular complex assembly 25/263 | 1483/39869
GO:0070925 (0.00532) organelle assembly 6/263 | 127/39869
GO:0051276 (0.00355) chromosome organization 24/263 | 1584/39869
GO:0007010 (8.17e-20) cytoskeleton organization 45/263 | 1058/39869
GO:1902589 (4.6e-12) single-organism organelle organization 40/263 | 1414/39869
GO:0009416 (0.0123) response to light stimulus 31/263 | 2501/39869
GO:0007018 (1.33e-26) microtubule-based movement 27/263 | 137/39869
GO:0022402 (3.53e-09) cell cycle process 33/263 | 1259/39869
GO:0043480 (8.47e-07) pigment accumulation in tissues 13/263 | 238/39869
GO:0006461 (0.000862) protein complex assembly 24/263 | 1421/39869
GO:0034622 (0.00199) cellular macromolecular complex assembly 23/263 | 1422/39869
GO:0030036 (0.0493) actin cytoskeleton organization 8/263 | 352/39869
GO:0000226 (1.69e-17) microtubule cytoskeleton organization 32/263 | 540/39869
GO:0010324 (6.85e-12) membrane invagination 24/263 | 472/39869
GO:0009411 (1.7e-13) response to UV 28/263 | 553/39869
GO:0000910 (3.52e-12) cytokinesis 26/263 | 538/39869
GO:0000278 (5.6e-10) mitotic cell cycle 30/263 | 961/39869
GO:0043623 (0.000448) cellular protein complex assembly 23/263 | 1265/39869
GO:0007051 (0.00173) spindle organization 6/263 | 101/39869
GO:0010224 (1.9e-05) response to UV-B 12/263 | 272/39869
GO:0032506 (6.85e-12) cytokinetic process 24/263 | 472/39869
GO:1903047 (1.06e-12) mitotic cell cycle process 29/263 | 656/39869
GO:0061640 (9.34e-13) cytoskeleton-dependent cytokinesis 26/263 | 499/39869
GO:0043478 (8.47e-07) pigment accumulation in response to UV light 13/263 | 238/39869
GO:0051258 (2.56e-09) protein polymerization 20/263 | 426/39869
GO:0051225 (0.00173) spindle assembly 6/263 | 101/39869
GO:0031109 (0.000295) microtubule polymerization or depolymerization 8/263 | 149/39869
GO:0000281 (3.52e-12) mitotic cytokinesis 25/263 | 488/39869
GO:0043479 (8.47e-07) pigment accumulation in tissues in response to UV light 13/263 | 238/39869
GO:0046785 (0.000223) microtubule polymerization 8/263 | 142/39869
GO:1902410 (6.85e-12) mitotic cytokinetic process 24/263 | 472/39869
GO:0043481 (8.47e-07) anthocyanin accumulation in tissues in response to UV light 13/263 | 238/39869
GO:0007020 (0.000164) microtubule nucleation 8/263 | 135/39869
GO:0000911 (6.13e-12) cytokinesis by cell plate formation 24/263 | 463/39869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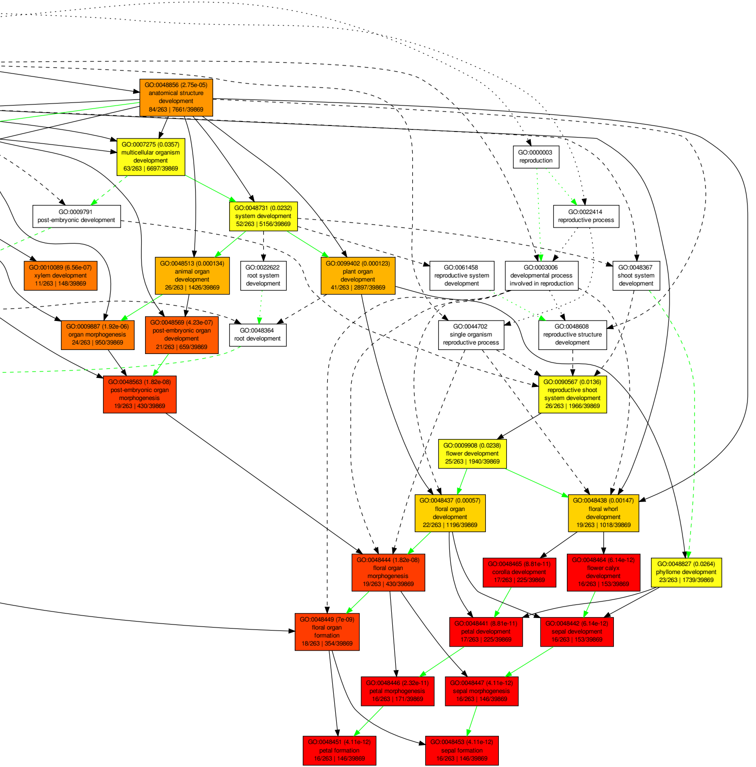
multicellular organismal process
72/263 | 7431/39869
GO:0032502 (2.58e-05)
developmental process
85/263 | 7769/39869
GO:0008283 (4.43e-06)
cell proliferation
18/263 | 573/39869
GO:0040007 (3.35e-06)
growth
34/263 | 1815/39869
GO:0044707 (0.00255)
single-multicellular organism process
70/263 | 6911/39869
GO:0044767 (0.000365)
single-organism developmental process
79/263 | 7584/39869
GO:0016049 (9.59e-05)
cell growth
25/263 | 1306/39869
GO:0048869 (0.00337)
cellular developmental process
33/263 | 2521/39869
GO:0040008 (0.00194)
regulation of growth
14/263 | 620/39869
GO:0050793 (0.00161)
regulation of developmental process
27/263 | 1790/39869
GO:0048589 (4.63e-06)
developmental growth
30/263 | 1496/39869
GO:0009653 (7e-09)
anatomical structure morphogenesis
57/263 | 3399/39869
GO:0009888 (7.16e-06)
tissue development
40/263 | 2455/39869
GO:0009825 (1.92e-07)
multidimensional cell growth
14/263 | 245/39869
GO:0030154
cell differentiation
GO:0048638 (0.00355)
regulation of developmental growth
13/263 | 580/39869
GO:0032989 (8.91e-06)
cellular component morphogenesis
28/263 | 1373/39869
GO:0048507 (0.00038)
meristem development
21/263 | 1074/39869
GO:0048646 (2.13e-11)
anatomical structure formation involved in morphogenesis
27/263 | 658/39869
GO:0010087 (1.72e-05)
phloem or xylem histogenesis
11/263 | 219/39869
GO:0048468 (0.00148)
cell development
21/263 | 1201/39869
GO:0021700 (0.021)
developmental maturation
17/263 | 1089/39869
GO:0060560 (0.000823)
developmental growth involved in morphogenesis
20/263 | 1051/39869
GO:0000902 (3.69e-05)
cell morphogenesis
26/263 | 1313/39869
GO:0048509 (0.00606)
regulation of meristem development
11/263 | 457/39869
GO:0035266 (0.00171)
meristem growth
11/263 | 389/39869
GO:0010073
meristem maintenance
GO:0009886 (4.62e-06)
post-embryonic morphogenesis
24/263 | 1004/39869
GO:0048588 (0.000956)
developmental cell growth
16/263 | 727/39869
GO:0048469 (0.00116)
cell maturation
15/263 | 662/39869
GO:0009826 (6.92e-05)
unidimensional cell growth
20/263 | 866/39869
GO:0010075 (0.00117)
regulation of meristem growth
11/263 | 369/39869
GO:0009932 (1.33e-05)
cell tip growth
17/263 | 556/39869
GO:0090627 (0.000852)
plant epidermal cell differentiation
16/263 | 718/39869
GO:0010015 (0.00712)
root morphogenesis
16/263 | 889/39869
GO:0090558 (0.00557)
plant epidermis development
21/263 | 1336/39869
GO:0010053 (0.000766)
root epidermal cell differentiation
16/263 | 710/39869
GO:0010054 (0.00148)
trichoblast differentiation
15/263 | 680/39869
GO:0048764 (0.00115)
trichoblast maturation
15/263 | 661/39869
GO:0048765 (0.00115)
root hair cell differentiation
15/263 | 661/39869
GO:0080147 (9.73e-05)
root hair cell development
13/263 | 387/39869
GO:0048767 (6.55e-05)
root hair elongation
13/263 | 371/39869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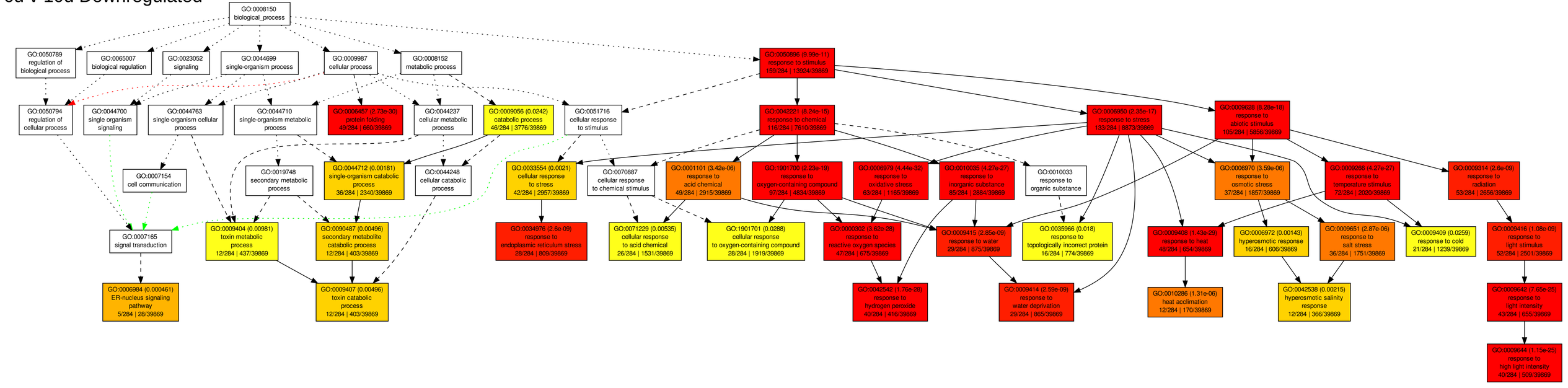
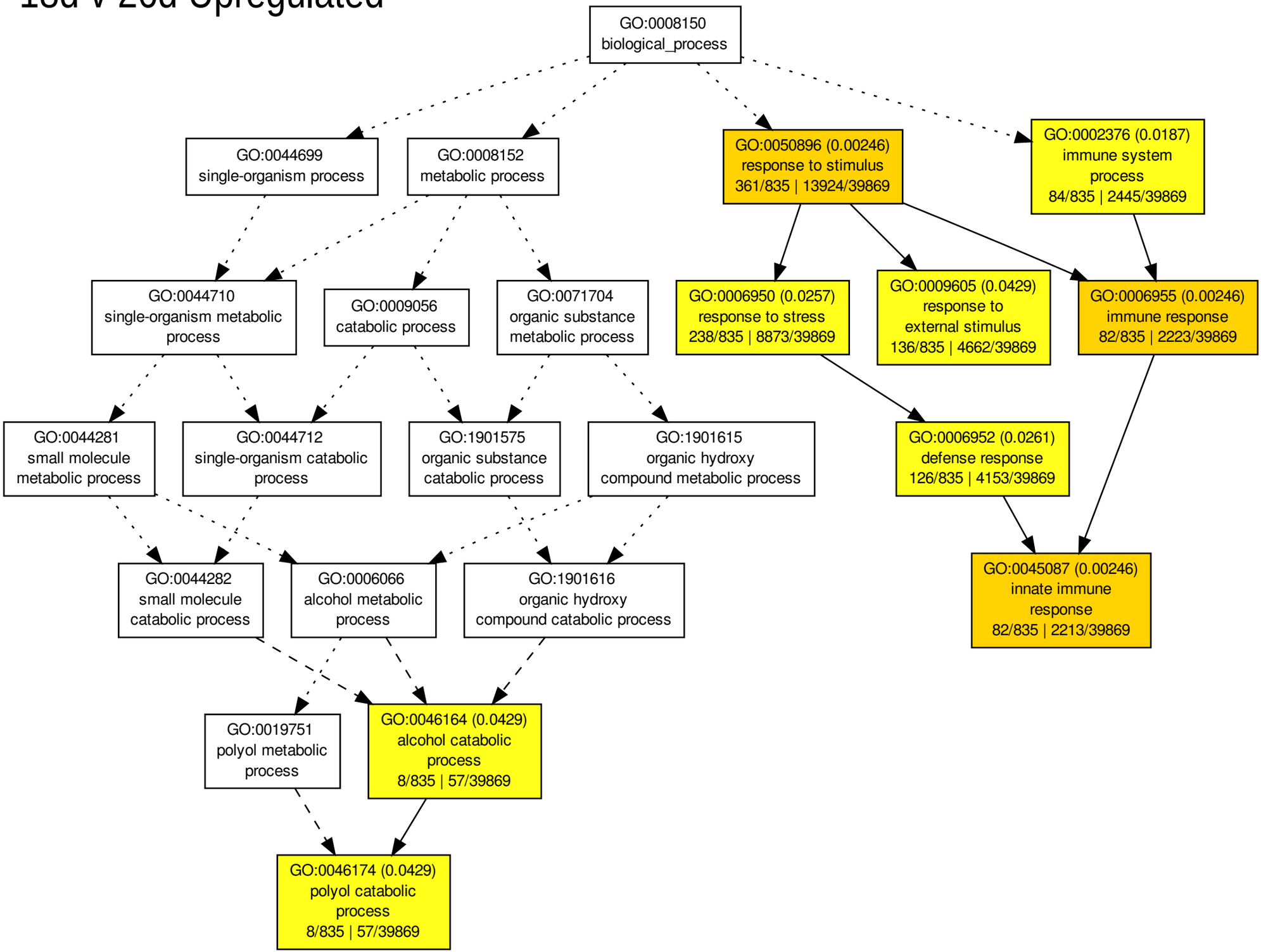
anatomical structure
development
84/263 | 7661/39869
GO:0007275 (0.0357)
multicellular organism
development
63/263 | 6697/39869
GO:0000003
reproduction
GO:0009791
post-embryonic development
GO:0048731 (0.0232)
system development
52/263 | 5156/39869
GO:0022414
reproductive process
GO:0010089 (6.56e-07)
xylem development
11/263 | 148/39869
GO:0048513 (0.000134)
animal organ
development
26/263 | 1426/39869
GO:0022622
root system
development
GO:0099402 (0.000123)
plant organ
development
41/263 | 2897/39869
GO:0061458
reproductive system
development
GO:0003006
developmental process
involved in reproduction
GO:0048367
shoot system
development
GO:0009887 (1.92e-06)
organ morphogenesis
24/263 | 950/39869
GO:0048569 (4.23e-07)
post-embryonic organ
development
21/263 | 659/39869
GO:0048364
root development
GO:0044702
single organism
reproductive process
GO:0048608
reproductive structure
development
GO:0048563 (1.82e-08)
post-embryonic organ
morphogenesis
19/263 | 430/39869
GO:0090567 (0.0136)
reproductive shoot
system development
26/263 | 1966/39869
GO:0009908 (0.0238)
flower development
25/263 | 1940/39869
GO:0048437 (0.00057)
floral organ
development
22/263 | 1196/39869
GO:0048438 (0.00147)
floral whorl
development
19/263 | 1018/39869
GO:0048444 (1.82e-08)
floral organ
morphogenesis
19/263 | 430/39869
GO:0048465 (8.81e-11)
corolla development
17/263 | 225/39869
GO:0048464 (6.14e-12)
flower calyx
development
16/263 | 153/39869
GO:0048827 (0.0264)
phyllome development
23/263 | 1739/39869
GO:0048449 (7e-09)
floral organ
formation
18/263 | 354/39869
GO:0048441 (8.81e-11)
petal development
17/263 | 225/39869
GO:0048442 (6.14e-12)
sepal development
16/263 | 153/39869
GO:0048446 (2.32e-11)
petal morphogenesis
16/263 | 171/39869
GO:0048447 (4.11e-12)
sepal morphogenesis
16/263 | 146/39869
GO:0048451 (4.11e-12)
petal formation
16/263 | 146/39869
GO:0048453 (4.11e-12)
sepal formation
16/263 | 146/39869

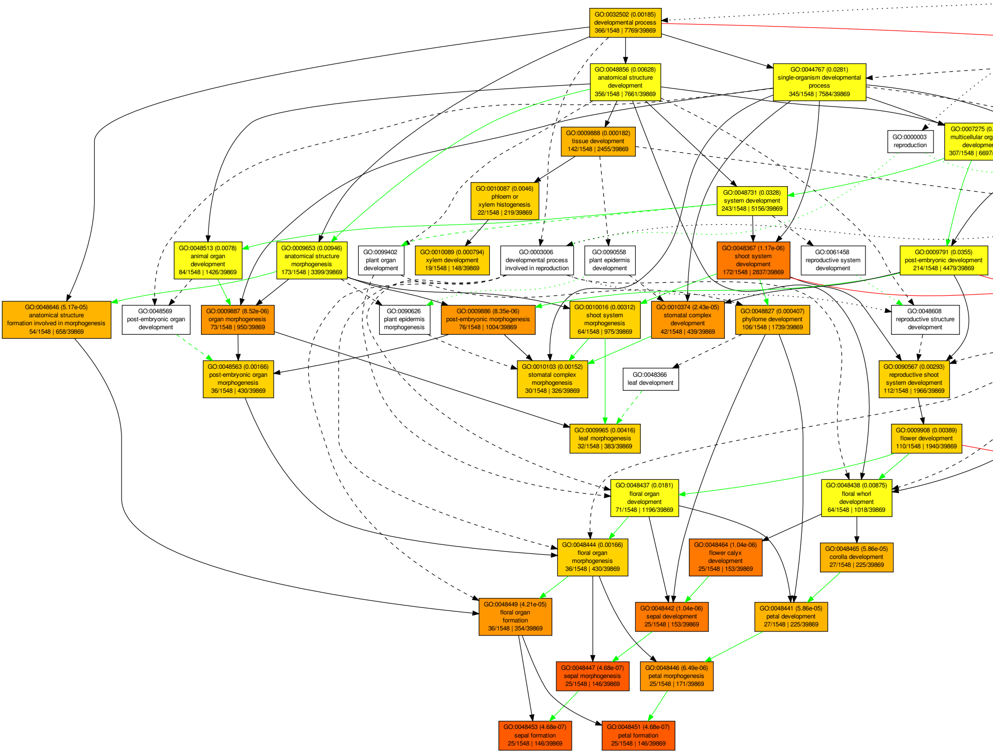
6d v 10d Downregulated



18d v 26d Upregulated



18d v 26d Downregulated


GO:0032502 (0.00185) developmental process 366/1548 | 7769/39869
GO:0048856 (0.00628) anatomical structure development 356/1548 | 7661/39869
GO:0044767 (0.0281) single-organism developmental process 345/1548 | 7584/39869
GO:0007275 (0. multicellular org developmen 307/1548 | 6697/
GO:0000003 reproduction
GO:0009888 (0.000182) tissue development 142/1548 | 2455/39869
GO:0010087 (0.0046) phloem or xylem histogenesis 22/1548 | 219/39869
GO:0048731 (0.0328) system development 243/1548 | 5156/39869
GO:0048513 (0.0078) animal organ development 84/1548 | 1426/39869
GO:0009653 (0.00946) anatomical structure morphogenesis 173/1548 | 3399/39869
GO:0099402 plant organ development
GO:0010089 (0.000794) xylem development 19/1548 | 148/39869
GO:0003006 developmental process involved in reproduction
GO:0090558 plant epidermis development
GO:0048367 (1.17e-06) shoot system development 172/1548 | 2837/39869
GO:0061458 reproductive system development
GO:0009791 (0.0355) post-embryonic development 214/1548 | 4479/39869
GO:0048646 (5.17e-05) anatomical structure formation involved in morphogenesis 54/1548 | 658/39869
GO:0048569 post-embryonic organ development
GO:0009887 (8.52e-06) organ morphogenesis 73/1548 | 950/39869
GO:0090626 plant epidermis morphogenesis
GO:0009886 (8.35e-06) post-embryonic morphogenesis 76/1548 | 1004/39869
GO:0010016 (0.00312) shoot system morphogenesis 64/1548 | 975/39869
GO:0010374 (2.43e-05) stomatal complex development 42/1548 | 439/39869
GO:0048827 (0.000407) phyllome development 106/1548 | 1739/39869
GO:0048608 reproductive structure development
GO:0048563 (0.00166) post-embryonic organ morphogenesis 36/1548 | 430/39869
GO:0010103 (0.00152) stomatal complex morphogenesis 30/1548 | 326/39869
GO:0048366 leaf development
GO:0090567 (0.00293) reproductive shoot system development 112/1548 | 1966/39869
GO:0009965 (0.00416) leaf morphogenesis 32/1548 | 383/39869
GO:0009908 (0.00389) flower development 110/1548 | 1940/39869
GO:0048437 (0.0181) floral organ development 71/1548 | 1196/39869
GO:0048438 (0.00875) floral whorl development 64/1548 | 1018/39869
GO:0048444 (0.00166) floral organ morphogenesis 36/1548 | 430/39869
GO:0048464 (1.04e-06) flower calyx development 25/1548 | 153/39869
GO:0048465 (5.86e-05) corolla development 27/1548 | 225/39869
GO:0048449 (4.21e-05) floral organ formation 36/1548 | 354/39869
GO:0048442 (1.04e-06) sepal development 25/1548 | 153/39869
GO:0048441 (5.86e-05) petal development 27/1548 | 225/39869
GO:0048447 (4.68e-07) sepal morphogenesis 25/1548 | 146/39869
GO:0048446 (6.49e-06) petal morphogenesis 25/1548 | 171/39869
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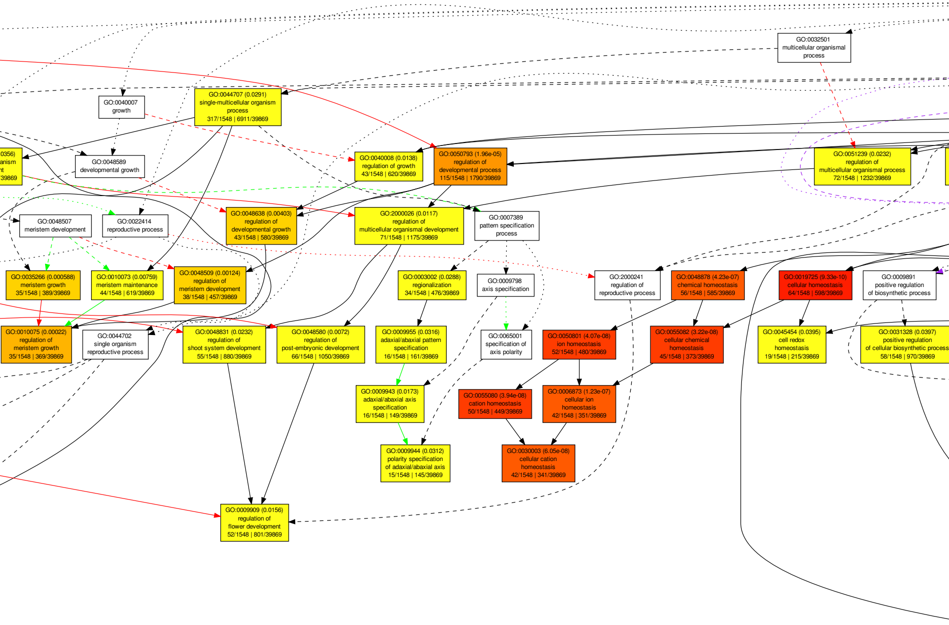
GO:0048451 (4.68e-07) petal formation 25/1548 | 146/39869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GO:0040007 growth
GO:0044707 (0.0291) single-multicellular organism process 317/1548 | 6911/39869
0356) anism nt 39869
GO:0048589 developmental growth
GO:0040008 (0.0138) regulation of growth 43/1548 | 620/39869
GO:0050793 (1.96e-05) regulation of developmental process 115/1548 | 1790/39869
GO:0051239 (0.0232) regulation of multicellular organismal process 72/1548 | 1232/39869
GO:0048507 meristem development
GO:0022414 reproductive process
GO:0048638 (0.00403) regulation of developmental growth 43/1548 | 580/39869
GO:2000026 (0.0117) regulation of multicellular organismal development 71/1548 | 1175/39869
GO:0007389 pattern specification process
GO:0035266 (0.000588) meristem growth 35/1548 | 389/39869
GO:0010073 (0.00759) meristem maintenance 44/1548 | 619/39869
GO:0048509 (0.00124) regulation of meristem development 38/1548 | 457/39869
GO:0003002 (0.0288) regionalization 34/1548 | 476/39869
GO:0009798 axis specification
GO:2000241 regulation of reproductive process
GO:0048878 (4.23e-07) chemical homeostasis 56/1548 | 585/39869
GO:0019725 (9.33e-10) cellular homeostasis 64/1548 | 598/39869
GO:0009891 positive regulation of biosynthetic process
GO:0010075 (0.00022) regulation of meristem growth 35/1548 | 369/39869
GO:0044702 single organism reproductive process
GO:0048831 (0.0232) regulation of shoot system development 55/1548 | 880/39869
GO:0048580 (0.0072) regulation of post-embryonic development 66/1548 | 1050/39869
GO:0009955 (0.0316) adaxial/abaxial pattern specification 16/1548 | 161/39869
GO:0065001 specification of axis polarity
GO:0050801 (4.07e-08) ion homeostasis 52/1548 | 480/39869
GO:0055082 (3.22e-08) cellular chemical homeostasis 45/1548 | 373/39869
GO:0045454 (0.0395) cell redox homeostasis 19/1548 | 215/39869
GO:0031328 (0.0397) positive regulation of cellular biosynthetic process 58/1548 | 970/39869
GO:0009943 (0.0173) adaxial/abaxial axis specification 16/1548 | 149/39869
GO:0055080 (3.94e-08) cation homeostasis 50/1548 | 449/39869
GO:0006873 (1.23e-07) cellular ion homeostasis 42/1548 | 351/39869
GO:0009944 (0.0312) polarity specification of adaxial/abaxial axis 15/1548 | 145/39869
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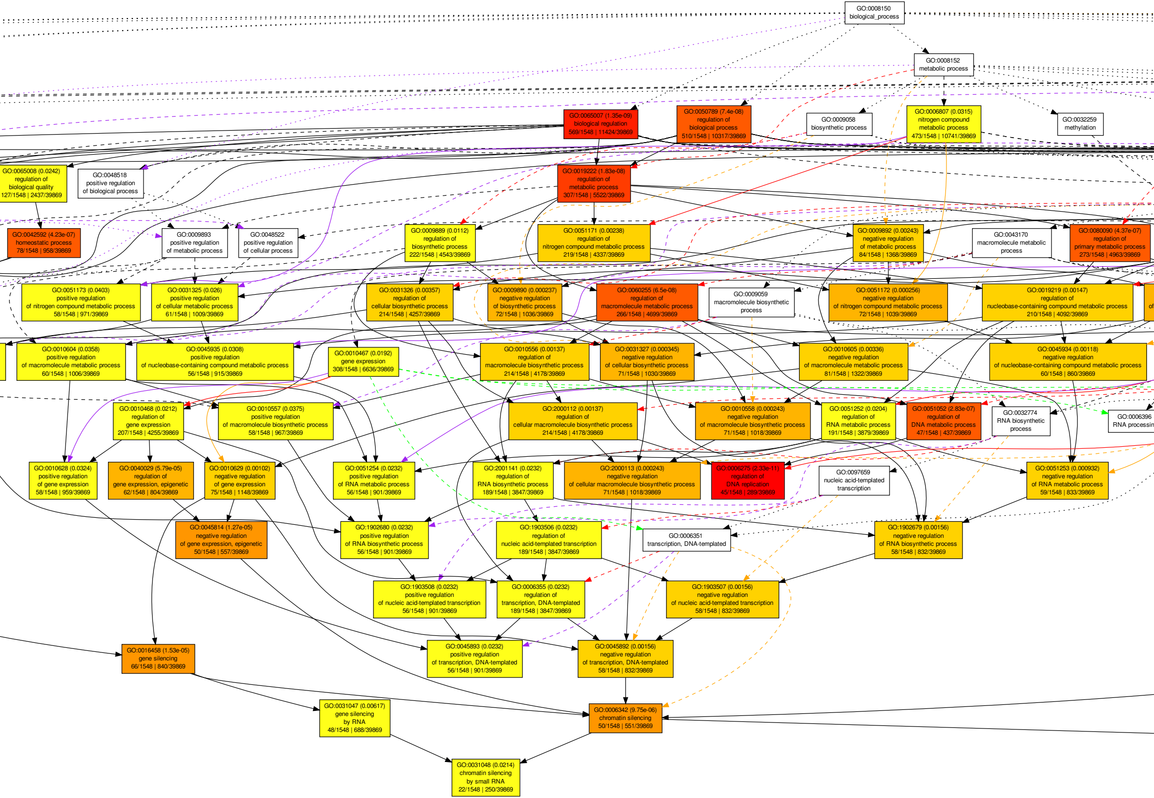
GO:0009909 (0.0156) regulation of flower development 52/1548 | 801/39869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GO:0008152 metabolic process
GO:0065007 (1.35e-09) biological regulation 569/1548 | 11424/39869
GO:0050789 (7.4e-08) regulation of biological process 510/1548 | 10317/39869
GO:0009058 biosynthetic process
GO:0006807 (0.0315) nitrogen compound metabolic process 473/1548 | 10741/39869
GO:0032259 methylation
GO:0065008 (0.0242) regulation of biological quality 127/1548 | 2437/39869
GO:0048518 positive regulation of biological process
GO:0019222 (1.83e-08) regulation of metabolic process 307/1548 | 5522/39869
GO:0042592 (4.23e-07) homeostatic process 78/1548 | 958/39869
GO:0009893 positive regulation of metabolic process
GO:0048522 positive regulation of cellular process
GO:0009889 (0.0112) regulation of biosynthetic process 222/1548 | 4543/39869
GO:0051171 (0.00238) regulation of nitrogen compound metabolic process 219/1548 | 4337/39869
GO:0009892 (0.00243) negative regulation of metabolic process 84/1548 | 1368/39869
GO:0043170 macromolecule metabolic process
GO:0080090 (4.37e-07) regulation of primary metabolic process 273/1548 | 4963/39869
GO:0051173 (0.0403) positive regulation of nitrogen compound metabolic process 58/1548 | 971/39869
GO:0031325 (0.026) positive regulation of cellular metabolic process 61/1548 | 1009/39869
GO:0031326 (0.00357) regulation of cellular biosynthetic process 214/1548 | 4257/39869
GO:0009890 (0.000237) negative regulation of biosynthetic process 72/1548 | 1036/39869
GO:0060255 (6.5e-08) regulation of macromolecule metabolic process 266/1548 | 4699/39869
GO:0009059 macromolecule biosynthetic process
GO:0051172 (0.000256) negative regulation of nitrogen compound metabolic process 72/1548 | 1039/39869
GO:0019219 (0.00147) regulation of nucleobase-containing compound metabolic process 210/1548 | 4092/39869
GO:0010604 (0.0358) positive regulation of macromolecule metabolic process 60/1548 | 1006/39869
GO:0045935 (0.0308) positive regulation of nucleobase-containing compound metabolic process 56/1548 | 915/39869
GO:0010467 (0.0192) gene expression 308/1548 | 6636/39869
GO:0010556 (0.00137) regulation of macromolecule biosynthetic process 214/1548 | 4178/39869
GO:0031327 (0.000345) negative regulation of cellular biosynthetic process 71/1548 | 1030/39869
GO:0010605 (0.00336) negative regulation of macromolecule metabolic process 81/1548 | 1322/39869
GO:0045934 (0.00118) negative regulation of nucleobase-containing compound metabolic process 60/1548 | 860/39869
GO:0010468 (0.0212) regulation of gene expression 207/1548 | 4255/39869
GO:0010557 (0.0375) positive regulation of macromolecule biosynthetic process 58/1548 | 967/39869
GO:2000112 (0.00137) regulation of cellular macromolecule biosynthetic process 214/1548 | 4178/39869
GO:0010558 (0.000243) negative regulation of macromolecule biosynthetic process 71/1548 | 1018/39869
GO:0051252 (0.0204) regulation of RNA metabolic process 191/1548 | 3879/39869
GO:0051052 (2.83e-07) regulation of DNA metabolic process 47/1548 | 437/39869
GO:0032774 RNA biosynthetic process
GO:0006396 RNA processin
GO:0010628 (0.0324) positive regulation of gene expression 58/1548 | 959/39869
GO:0040029 (5.79e-05) regulation of gene expression, epigenetic 62/1548 | 804/39869
GO:0010629 (0.00102) negative regulation of gene expression 75/1548 | 1148/39869
GO:0051254 (0.0232) positive regulation of RNA metabolic process 56/1548 | 901/39869
GO:2001141 (0.0232) regulation of RNA biosynthetic process 189/1548 | 3847/39869
GO:2000113 (0.000243) negative regulation of cellular macromolecule biosynthetic process 71/1548 | 1018/39869
GO:0006275 (2.33e-11) regulation of DNA replication 45/1548 | 289/39869
GO:0097659 nucleic acid-templated transcription
GO:0051253 (0.000932) negative regulation of RNA metabolic process 59/1548 | 833/39869
GO:0045814 (1.27e-05) negative regulation of gene expression, epigenetic 50/1548 | 557/39869
GO:1902680 (0.0232) positive regulation of RNA biosynthetic process 56/1548 | 901/39869
GO:1903506 (0.0232) regulation of nucleic acid-templated transcription 189/1548 | 3847/39869
GO:0006351 transcription, DNA-templated
GO:1902679 (0.00156) negative regulation of RNA biosynthetic process 58/1548 | 832/39869
GO:1903508 (0.0232) positive regulation of nucleic acid-templated transcription 56/1548 | 901/39869
GO:0006355 (0.0232) regulation of transcription, DNA-templated 189/1548 | 3847/39869
GO:1903507 (0.00156) negative regulation of nucleic acid-templated transcription 58/1548 | 832/39869
GO:0016458 (1.53e-05) gene silencing 66/1548 | 840/39869
GO:0045893 (0.0232) positive regulation of transcription, DNA-templated 56/1548 | 901/39869
GO:0045892 (0.00156) negative regulation of transcription, DNA-templated 58/1548 | 832/39869
GO:0031047 (0.00617) gene silencing by RNA 48/1548 | 688/39869
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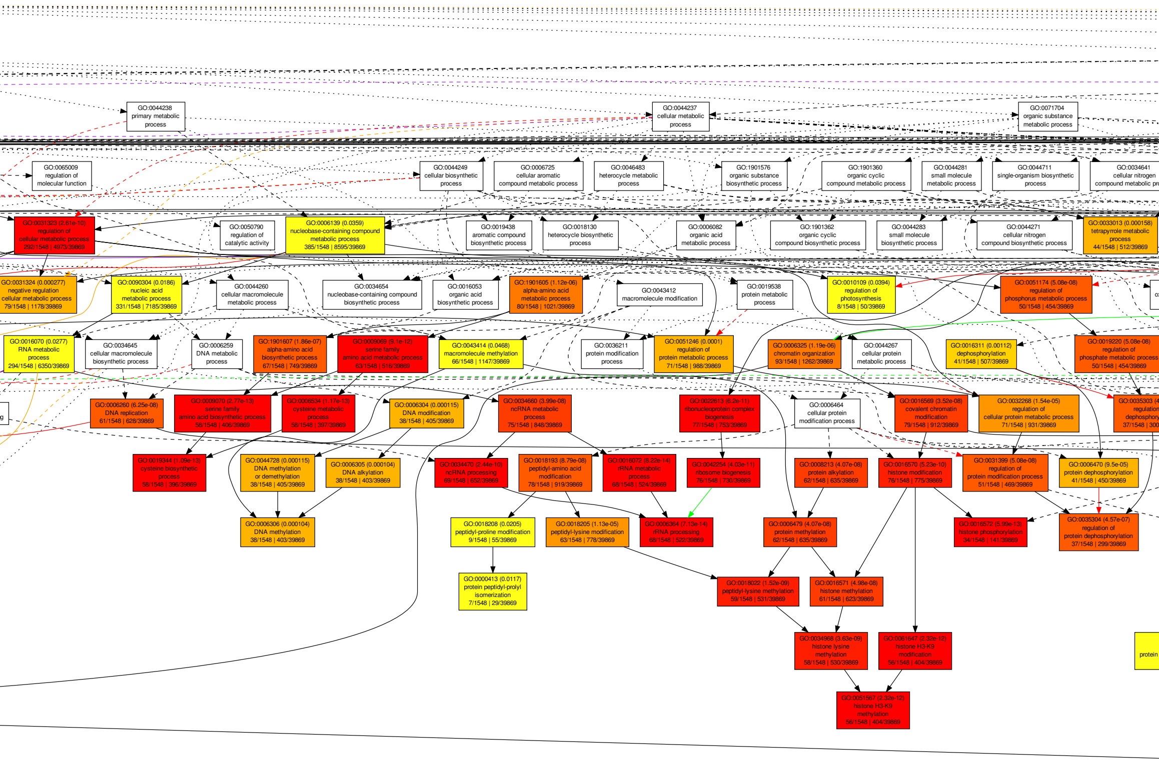
GO:0031048 (0.0214) chromatin silencing by small RNA 22/1548 | 250/39869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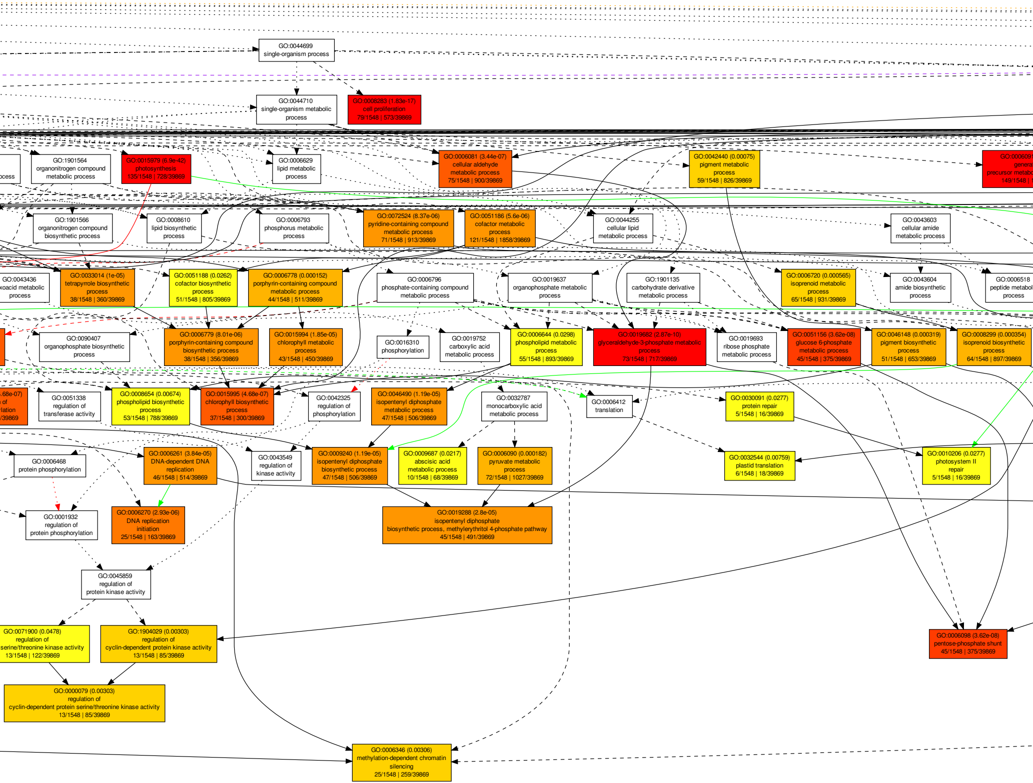
primary metabolic
process
GO:0044237
cellular metabolic
process
GO:0071704
organic substance
metabolic process
GO:0065009
regulation of
molecular function
GO:0044249
cellular biosynthetic
process
GO:0006725
cellular aromatic
compound metabolic process
GO:0046483
heterocycle metabolic
process
GO:1901576
organic substance
biosynthetic process
GO:1901360
organic cyclic
compound metabolic process
GO:0044281
small molecule
metabolic process
GO:0044711
single-organism biosynthetic
process
GO:0034641
cellular nitrogen
compound metabolic pr
GO:0031323 (2.61e-10)
regulation of
cellular metabolic process
292/1548 | 4973/39869
GO:0050790
regulation of
catalytic activity
GO:0006139 (0.0359)
nucleobase-containing compound
metabolic process
385/1548 | 8595/39869
GO:0019438
aromatic compound
biosynthetic process
GO:0018130
heterocycle biosynthetic
process
GO:0006082
organic acid
metabolic process
GO:1901362
organic cyclic
compound biosynthetic process
GO:0044283
small molecule
biosynthetic process
GO:0044271
cellular nitrogen
compound biosynthetic process
GO:0033013 (0.000158)
tetrapyrrole metabolic
process
44/1548 | 512/39869
GO:0031324 (0.000277)
negative regulation
cellular metabolic process
79/1548 | 1178/39869
GO:0090304 (0.0186)
nucleic acid
metabolic process
331/1548 | 7185/39869
GO:0044260
cellular macromolecule
metabolic process
GO:0034654
nucleobase-containing compound
biosynthetic process
GO:0016053
organic acid
biosynthetic process
GO:1901605 (1.12e-06)
alpha-amino acid
metabolic process
80/1548 | 1021/39869
GO:0043412
macromolecule modification
GO:0019538
protein metabolic
process
GO:0010109 (0.0394)
regulation of
photosynthesis
8/1548 | 50/39869
GO:0051174 (5.08e-08)
regulation of
phosphorus metabolic process
50/1548 | 454/39869
GO:0016070 (0.0277)
RNA metabolic
process
294/1548 | 6350/39869
GO:0034645
cellular macromolecule
biosynthetic process
GO:0006259
DNA metabolic
process
GO:1901607 (1.86e-07)
alpha-amino acid
biosynthetic process
67/1548 | 749/39869
GO:0009069 (9.1e-12)
serine family
amino acid metabolic process
63/1548 | 516/39869
GO:0043414 (0.0468)
macromolecule methylation
66/1548 | 1147/39869
GO:0036211
protein modification
process
GO:0051246 (0.0001)
regulation of
protein metabolic process
71/1548 | 988/39869
GO:0006325 (1.19e-06)
chromatin organization
93/1548 | 1262/39869
GO:0044267
cellular protein
metabolic process
GO:0016311 (0.00112)
dephosphorylation
41/1548 | 507/39869
GO:0019220 (5.08e-08)
regulation of
phosphate metabolic process
50/1548 | 454/39869
GO:0006260 (6.25e-08)
DNA replication
61/1548 | 628/39869
GO:0009070 (2.77e-13)
serine family
amino acid biosynthetic process
58/1548 | 406/39869
GO:0006534 (1.17e-13)
cysteine metabolic
process
58/1548 | 397/39869
GO:0006304 (0.000115)
DNA modification
38/1548 | 405/39869
GO:0034660 (3.99e-08)
ncRNA metabolic
process
75/1548 | 848/39869
GO:0022613 (6.2e-11)
ribonucleoprotein complex
biogenesis
77/1548 | 753/39869
GO:0006464
cellular protein
modification process
GO:0016569 (3.52e-08)
covalent chromatin
modification
79/1548 | 912/39869
GO:0032268 (1.54e-05)
regulation of
cellular protein metabolic process
71/1548 | 931/39869
GO:0035303 (4
regulation
dephosphory
37/1548 | 300
GO:0019344 (1.09e-13)
cysteine biosynthetic
process
58/1548 | 396/39869
GO:0044728 (0.000115)
DNA methylation
or demethylation
38/1548 | 405/39869
GO:0006305 (0.000104)
DNA alkylation
38/1548 | 403/39869
GO:0034470 (2.44e-10)
ncRNA processing
69/1548 | 652/39869
GO:0018193 (8.79e-08)
peptidyl-amino acid
modification
78/1548 | 919/39869
GO:0016072 (8.22e-14)
rRNA metabolic
process
68/1548 | 524/39869
GO:0042254 (4.03e-11)
ribosome biogenesis
76/1548 | 730/39869
GO:0008213 (4.07e-08)
protein alkylation
62/1548 | 635/39869
GO:0016570 (5.23e-10)
histone modification
76/1548 | 775/39869
GO:0031399 (5.08e-08)
regulation of
protein modification process
51/1548 | 469/39869
GO:0006470 (9.5e-05)
protein dephosphorylation
41/1548 | 450/39869
GO:0006306 (0.000104)
DNA methylation
38/1548 | 403/39869
GO:0018208 (0.0205)
peptidyl-proline modification
9/1548 | 55/39869
GO:0018205 (1.13e-05)
peptidyl-lysine modification
63/1548 | 778/39869
GO:0006364 (7.13e-14)
rRNA processing
68/1548 | 522/39869
GO:0006479 (4.07e-08)
protein methylation
62/1548 | 635/39869
GO:0016572 (5.99e-13)
histone phosphorylation
34/1548 | 141/39869
GO:0035304 (4.57e-07)
regulation of
protein dephosphorylation
37/1548 | 299/39869
GO:0000413 (0.0117)
protein peptidyl-prolyl
isomerization
7/1548 | 29/39869
GO:0018022 (1.52e-09)
peptidyl-lysine methylation
59/1548 | 531/39869
GO:0016571 (4.98e-08)
histone methylation
61/1548 | 623/39869
GO:0034968 (3.63e-09)
histone lysine
methylation
58/1548 | 530/39869
GO:0061647 (2.32e-12)
histone H3-K9
modification
56/1548 | 404/39869
protein
GO:0051567 (2.32e-12)
histone H3-K9
methylation
56/1548 | 404/39869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single-organism process
GO:0044710
single-organism metabolic process
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cell proliferation
79/1548 | 573/39869
GO:1901564
organonitrogen compound metabolic process
GO:0015979 (6.9e-42)
photosynthesis
135/1548 | 728/39869
GO:0006629
lipid metabolic process
GO:0006081 (3.44e-07)
cellular aldehyde metabolic process
75/1548 | 900/39869
GO:0042440 (0.00075)
pigment metabolic process
59/1548 | 826/39869
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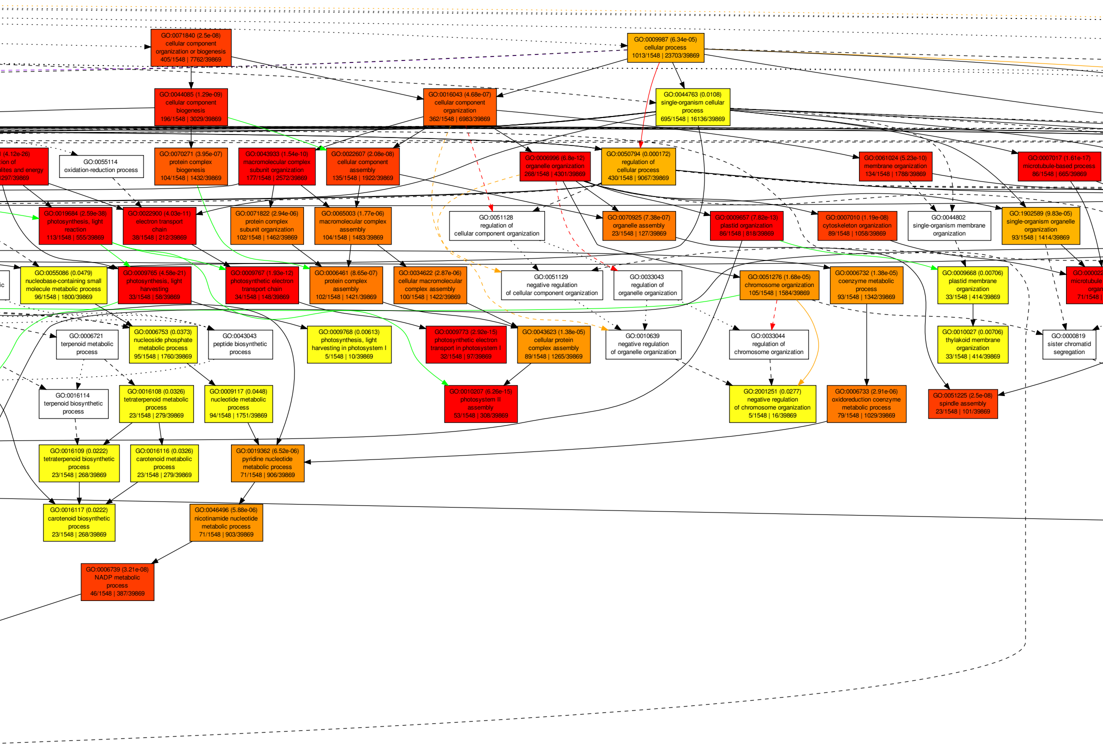
organonitrogen compound biosynthetic process
GO:0008610
lipid biosynthetic process
GO:0006793
phosphorus metabolic process
GO:0072524 (8.37e-06)
pyridine-containing compound metabolic process
71/1548 | 913/39869
GO:0051186 (5.6e-06)
cofactor metabolic process
121/1548 | 1858/39869
GO:0044255
cellular lipid metabolic process
GO:0043603
cellular amide metabolic process
GO:0043436
GO:0033014 (1e-05)
tetrapyrrole biosynthetic process
38/1548 | 360/39869
GO:0051188 (0.0262)
cofactor biosynthetic process
51/1548 | 805/39869
GO:0006778 (0.000152)
porphyrin-containing compound metabolic process
44/1548 | 511/39869
GO:0006796
phosphate-containing compound metabolic process
GO:0019637
organophosphate metabolic process
GO:1901135
carbohydrate derivative metabolic process
GO:0006720 (0.000565)
isoprenoid metabolic process
65/1548 | 931/39869
GO:0043604
amide biosynthetic process
GO:0006518
GO:0090407
organophosphate biosynthetic process
GO:0006779 (8.01e-06)
porphyrin-containing compound biosynthetic process
38/1548 | 356/39869
GO:0015994 (1.85e-05)
chlorophyll metabolic process
43/1548 | 450/39869
GO:0016310
phosphorylation
GO:0019752
carboxylic acid metabolic process
GO:0006644 (0.0298)
phospholipid metabolic process
55/1548 | 893/39869
GO:0019682 (2.87e-10)
glyceraldehyde-3-phosphate metabolic process
73/1548 | 717/39869
GO:0019693
ribose phosphate metabolic process
GO:0051156 (3.62e-08)
glucose 6-phosphate metabolic process
45/1548 | 375/39869
GO:0046148 (0.000319)
pigment biosynthetic process
51/1548 | 653/39869
GO:0008299 (0.000354)
isoprenoid biosynthetic process
64/1548 | 897/39869
GO:0051338
regulation of transferase activity
GO:0008654 (0.00674)
phospholipid biosynthetic process
53/1548 | 788/39869
GO:0015995 (4.68e-07)
chlorophyll biosynthetic process
37/1548 | 300/39869
GO:0042325
regulation of phosphorylation
GO:0046490 (1.19e-05)
isopentenyl diphosphate metabolic process
47/1548 | 506/39869
GO:0032787
monocarboxylic acid metabolic process
GO:0006412
translation
GO:0030091 (0.0277)
protein repair
5/1548 | 16/39869
GO:0006468
protein phosphorylation
GO:0006261 (3.84e-05)
DNA-dependent DNA replication
46/1548 | 514/39869
GO:0043549
regulation of kinase activity
GO:0009240 (1.19e-05)
isopentenyl diphosphate biosynthetic process
47/1548 | 506/39869
GO:0009687 (0.0217)
abscisic acid metabolic process
10/1548 | 68/39869
GO:0006090 (0.000182)
pyruvate metabolic process
72/1548 | 1027/39869
GO:0032544 (0.00759)
plastid translation
6/1548 | 18/39869
GO:0010206 (0.0277)
photosystem II repair
5/1548 | 16/39869
GO:0001932
regulation of protein phosphorylation
GO:0006270 (2.93e-06)
DNA replication initiation
25/1548 | 163/39869
GO:0019288 (2.8e-05)
isopentenyl diphosphate biosynthetic process, methylerythritol 4-phosphate pathway
45/1548 | 491/39869
GO:0045859
regulation of protein kinase activity
GO:0071900 (0.0478)
regulation of serine/threonine kinase activity
13/1548 | 122/39869
GO:1904029 (0.00303)
regulation of cyclin-dependent protein kinase activity
13/1548 | 85/39869
GO:0006098 (3.62e-08)
pentose-phosphate shunt
45/1548 | 375/39869
GO:0000079 (0.00303)
regulation of cyclin-dependent protein serine/threonine kinase activity
13/1548 | 85/39869
GO:0006346 (0.00306)
methylation-dependent chromatin silencing
25/1548 | 259/39869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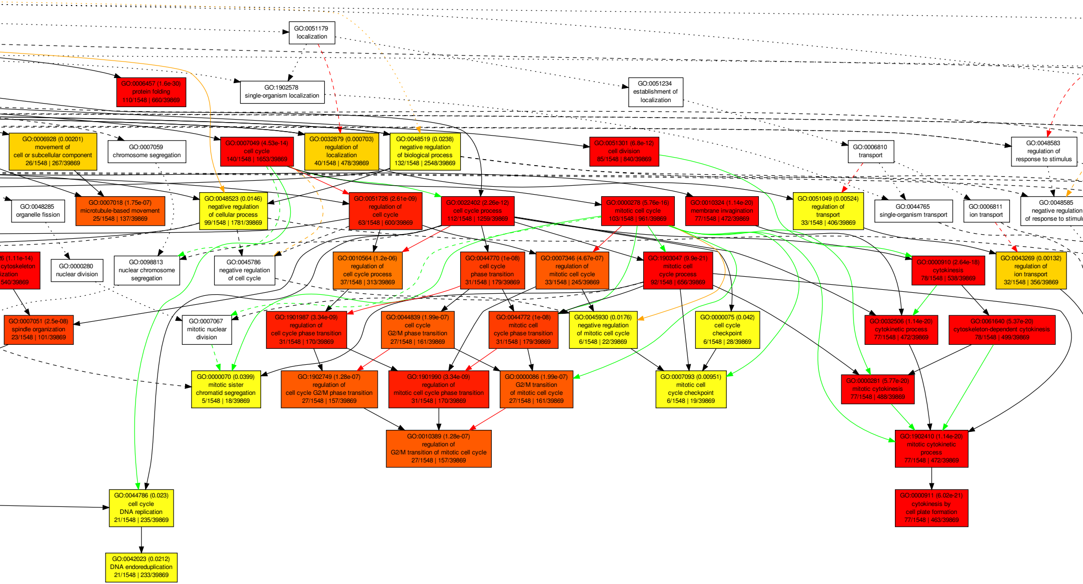
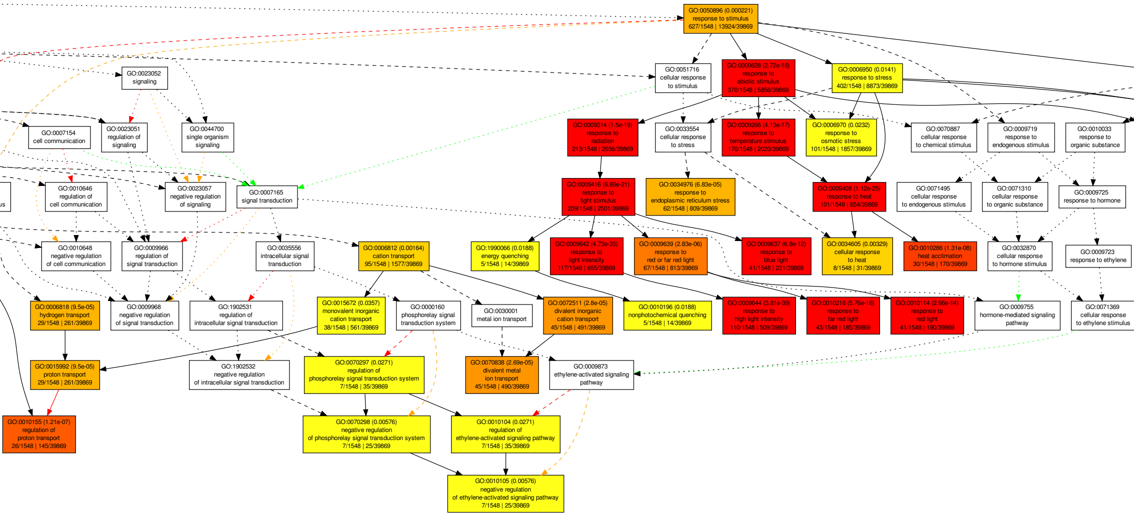
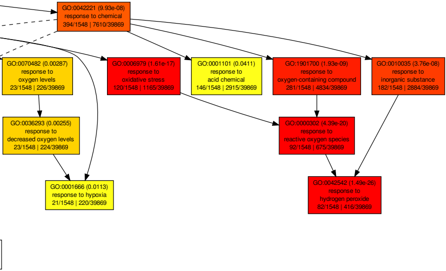
GO:0009987 (6.34e-05) cellular process 1013/1548 | 23703/39869
GO:0044085 (1.29e-09) cellular component biogenesis 196/1548 | 3029/39869
GO:0016043 (4.68e-07) cellular component organization 362/1548 | 6983/39869
GO:0044763 (0.0108) single-organism cellular process 695/1548 | 16136/39869
) (4.12e-26) tion of lites and energy 297/39869
GO:0055114 oxidation-reduction process
GO:0070271 (3.95e-07) protein complex biogenesis 104/1548 | 1432/39869
GO:0043933 (1.54e-10) macromolecular complex subunit organization 177/1548 | 2572/39869
GO:0022607 (2.08e-08) cellular component assembly 135/1548 | 1922/39869
GO:0006996 (6.8e-12) organelle organization 268/1548 | 4301/39869
GO:0050794 (0.000172) regulation of cellular process 430/1548 | 9067/39869
GO:0061024 (5.23e-10) membrane organization 134/1548 | 1788/39869
GO:0007017 (1.61e-17) microtubule-based process 86/1548 | 665/39869
GO:0019684 (2.59e-38) photosynthesis, light reaction 113/1548 | 555/39869
GO:0022900 (4.03e-11) electron transport chain 38/1548 | 212/39869
GO:0071822 (2.94e-06) protein complex subunit organization 102/1548 | 1462/39869
GO:0065003 (1.77e-06) macromolecular complex assembly 104/1548 | 1483/39869
GO:0051128 regulation of cellular component organization
GO:0070925 (7.38e-07) organelle assembly 23/1548 | 127/39869
GO:0009657 (7.82e-13) plastid organization 86/1548 | 818/39869
GO:0007010 (1.19e-08) cytoskeleton organization 89/1548 | 1058/39869
GO:0044802 single-organism membrane organization
GO:1902589 (9.83e-05) single-organism organelle organization 93/1548 | 1414/39869
ic
GO:0055086 (0.0479) nucleobase-containing small molecule metabolic process 96/1548 | 1800/39869
GO:0009765 (4.58e-21) photosynthesis, light harvesting 33/1548 | 58/39869
GO:0009767 (1.93e-12) photosynthetic electron transport chain 34/1548 | 148/39869
GO:0006461 (8.65e-07) protein complex assembly 102/1548 | 1421/39869
GO:0034622 (2.87e-06) cellular macromolecular complex assembly 100/1548 | 1422/39869
GO:0051129 negative regulation of cellular component organization
GO:0033043 regulation of organelle organization
GO:0051276 (1.68e-05) chromosome organization 105/1548 | 1584/39869
GO:0006732 (1.38e-05) coenzyme metabolic process 93/1548 | 1342/39869
GO:0009668 (0.00706) plastid membrane organization 33/1548 | 414/39869
GO:00002 microtubule organ 71/1548
GO:0006721 terpenoid metabolic process
GO:0006753 (0.0373) nucleoside phosphate metabolic process 95/1548 | 1760/39869
GO:0043043 peptide biosynthetic process
GO:0009768 (0.00613) photosynthesis, light harvesting in photosystem I 5/1548 | 10/39869
GO:0009773 (2.92e-15) photosynthetic electron transport in photosystem I 32/1548 | 97/39869
GO:0043623 (1.38e-05) cellular protein complex assembly 89/1548 | 1265/39869
GO:0010639 negative regulation of organelle organization
GO:0033044 regulation of chromosome organization
GO:0010027 (0.00706) thylakoid membrane organization 33/1548 | 414/39869
GO:0000819 sister chromatid segregation
GO:0016114 terpenoid biosynthetic process
GO:0016108 (0.0326) tetraterpenoid metabolic process 23/1548 | 279/39869
GO:0009117 (0.0448) nucleotide metabolic process 94/1548 | 1751/39869
GO:0010207 (6.26e-15) photosystem II assembly 53/1548 | 308/39869
GO:2001251 (0.0277) negative regulation of chromosome organization 5/1548 | 16/39869
GO:0006733 (2.91e-06) oxidoreduction coenzyme metabolic process 79/1548 | 1029/39869
GO:0051225 (2.5e-08) spindle assembly 23/1548 | 101/39869
GO:0016109 (0.0222) tetraterpenoid biosynthetic process 23/1548 | 268/39869
GO:0016116 (0.0326) carotenoid metabolic process 23/1548 | 279/39869
GO:0019362 (6.52e-06) pyridine nucleotide metabolic process 71/1548 | 906/39869
GO:0016117 (0.0222) carotenoid biosynthetic process 23/1548 | 268/39869
GO:0046496 (5.88e-06) nicotinamide nucleotide metabolic process 71/1548 | 903/39869
GO:0006739 (3.21e-08) NADP metabolic process 46/1548 | 387/39869


GO:0051179
localization
GO:0006457 (1.6e-30)
protein folding
110/1548 | 660/39869
GO:1902578
single-organism localization
GO:0051234
establishment of
localization
GO:0006928 (0.00201)
movement of
cell or subcellular component
26/1548 | 267/39869
GO:0007059
chromosome segregation
GO:0007049 (4.53e-14)
cell cycle
140/1548 | 1653/39869
GO:0032879 (0.000703)
regulation of
localization
40/1548 | 478/39869
GO:0048519 (0.0238)
negative regulation
of biological process
132/1548 | 2548/39869
GO:0051301 (6.8e-12)
cell division
85/1548 | 840/39869
GO:0006810
transport
GO:0048583
regulation of
response to stimulus
GO:0048285
organelle fission
GO:0007018 (1.75e-07)
microtubule-based movement
25/1548 | 137/39869
GO:0048523 (0.0146)
negative regulation
of cellular process
99/1548 | 1781/39869
GO:0051726 (2.61e-09)
regulation of
cell cycle
63/1548 | 600/39869
GO:0022402 (2.26e-12)
cell cycle process
112/1548 | 1259/39869
GO:0000278 (5.76e-16)
mitotic cell cycle
103/1548 | 961/39869
GO:0010324 (1.14e-20)
membrane invagination
77/1548 | 472/39869
GO:0051049 (0.00524)
regulation of
transport
33/1548 | 406/39869
GO:0044765
single-organism transport
GO:0006811
ion transport
GO:0048585
negative regulation
of response to stimul
6 (1.11e-14)
cytoskeleton
ization
540/39869
GO:0000280
nuclear division
GO:0098813
nuclear chromosome
segregation
GO:0045786
negative regulation
of cell cycle
GO:0010564 (1.2e-06)
regulation of
cell cycle process
37/1548 | 313/39869
GO:0044770 (1e-08)
cell cycle
phase transition
31/1548 | 179/39869
GO:0007346 (4.67e-07)
regulation of
mitotic cell cycle
33/1548 | 245/39869
GO:1903047 (9.9e-21)
mitotic cell
cycle process
92/1548 | 656/39869
GO:0000910 (2.64e-18)
cytokinesis
78/1548 | 538/39869
GO:0043269 (0.00132)
regulation of
ion transport
32/1548 | 356/39869
GO:0007051 (2.5e-08)
spindle organization
23/1548 | 101/39869
GO:0007067
mitotic nuclear
division
GO:1901987 (3.34e-09)
regulation of
cell cycle phase transition
31/1548 | 170/39869
GO:0044839 (1.99e-07)
cell cycle
G2/M phase transition
27/1548 | 161/39869
GO:0044772 (1e-08)
mitotic cell
cycle phase transition
31/1548 | 179/39869
GO:0045930 (0.0176)
negative regulation
of mitotic cell cycle
6/1548 | 22/39869
GO:0000075 (0.042)
cell cycle
checkpoint
6/1548 | 28/39869
GO:0032506 (1.14e-20)
cytokinetic process
77/1548 | 472/39869
GO:0061640 (5.37e-20)
cytoskeleton-dependent cytokinesis
78/1548 | 499/39869
GO:0000070 (0.0399)
mitotic sister
chromatid segregation
5/1548 | 18/39869
GO:1902749 (1.28e-07)
regulation of
cell cycle G2/M phase transition
27/1548 | 157/39869
GO:1901990 (3.34e-09)
regulation of
mitotic cell cycle phase transition
31/1548 | 170/39869
GO:0000086 (1.99e-07)
G2/M transition
of mitotic cell cycle
27/1548 | 161/39869
GO:0007093 (0.00951)
mitotic cell
cycle checkpoint
6/1548 | 19/39869
GO:0000281 (5.77e-20)
mitotic cytokinesis
77/1548 | 488/39869
GO:0010389 (1.28e-07)
regulation of
G2/M transition of mitotic cell cycle
27/1548 | 157/39869
GO:1902410 (1.14e-20)
mitotic cytokinetic
process
77/1548 | 472/39869
GO:0044786 (0.023)
cell cycle
DNA replication
21/1548 | 235/39869
GO:0000911 (6.02e-21)
cytokinesis by
cell plate formation
77/1548 | 463/39869
GO:0042023 (0.0212)
DNA endoreduplication
21/1548 | 233/39869


GO:0050896 (0.000221) response to stimulus 627/1548 | 13924/39869
GO:0023052 signaling
GO:0051716 cellular response to stimulus
GO:0009628 (2.72e-18) response to abiotic stimulus 370/1548 | 5856/39869
GO:0006950 (0.0141) response to stress 402/1548 | 8873/39869
GO:0007154 cell communication
GO:0023051 regulation of signaling
GO:0044700 single organism signaling
GO:0009314 (1.5e-19) response to radiation 213/1548 | 2656/39869
GO:0033554 cellular response to stress
GO:0009266 (4.13e-17) response to temperature stimulus 170/1548 | 2020/39869
GO:0006970 (0.0232) response to osmotic stress 101/1548 | 1857/39869
GO:0070887 cellular response to chemical stimulus
GO:0009719 response to endogenous stimulus
GO:0010033 response to organic substance
us
GO:0010646 regulation of cell communication
GO:0023057 negative regulation of signaling
GO:0007165 signal transduction
GO:0009416 (6.89e-21) response to light stimulus 209/1548 | 2501/39869
GO:0034976 (6.83e-05) response to endoplasmic reticulum stress 62/1548 | 809/39869
GO:0009408 (1.12e-25) response to heat 101/1548 | 654/39869
GO:0071495 cellular response to endogenous stimulus
GO:0071310 cellular response to organic substance
GO:0009725 response to hormone
GO:0010648 negative regulation of cell communication
GO:0009966 regulation of signal transduction
GO:0035556 intracellular signal transduction
GO:0006812 (0.00164) cation transport 95/1548 | 1577/39869
GO:1990066 (0.0188) energy quenching 5/1548 | 14/39869
GO:0009642 (4.73e-35) response to light intensity 117/1548 | 655/39869
GO:0009639 (2.83e-06) response to red or far red light 67/1548 | 813/39869
GO:0009637 (6.8e-12) response to blue light 41/1548 | 231/39869
GO:0034605 (0.00329) cellular response to heat 8/1548 | 31/39869
GO:0010286 (1.31e-08) heat acclimation 30/1548 | 170/39869
GO:0032870 cellular response to hormone stimulus
GO:0009723 response to ethylene
GO:0006818 (9.5e-05) hydrogen transport 29/1548 | 261/39869
GO:0009968 negative regulation of signal transduction
GO:1902531 regulation of intracellular signal transduction
GO:0015672 (0.0357) monovalent inorganic cation transport 38/1548 | 561/39869
GO:0000160 phosphorelay signal transduction system
GO:0030001 metal ion transport
GO:0072511 (2.8e-05) divalent inorganic cation transport 45/1548 | 491/39869
GO:0010196 (0.0188) nonphotochemical quenching 5/1548 | 14/39869
GO:0009644 (3.81e-39) response to high light intensity 110/1548 | 509/39869
GO:0010218 (5.76e-16) response to far red light 43/1548 | 185/39869
GO:0010114 (2.96e-14) response to red light 41/1548 | 190/39869
GO:0009755 hormone-mediated signaling pathway
GO:0071369 cellular response to ethylene stimulus
GO:0015992 (9.5e-05) proton transport 29/1548 | 261/39869
GO:1902532 negative regulation of intracellular signal transduction
GO:0070297 (0.0271) regulation of phosphorelay signal transduction system 7/1548 | 35/39869
GO:0070838 (2.69e-05) divalent metal ion transport 45/1548 | 490/39869
GO:0009873 ethylene-activated signaling pathway
GO:0010155 (1.21e-07) regulation of proton transport 26/1548 | 145/39869
GO:0070298 (0.00576) negative regulation of phosphorelay signal transduction system 7/1548 | 25/39869
GO:0010104 (0.0271) regulation of ethylene-activated signaling pathway 7/1548 | 35/39869
GO:0010105 (0.00576) negative regulation of ethylene-activated signaling pathway 7/1548 | 25/39869


GO:0042221 (9.93e-08)
response to chemical
394/1548 | 7610/39869
GO:0070482 (0.00287)
response to
oxygen levels
23/1548 | 226/39869
GO:0006979 (1.61e-17)
response to
oxidative stress
120/1548 | 1165/39869
GO:0001101 (0.0411)
response to
acid chemical
146/1548 | 2915/39869
GO:1901700 (1.93e-09)
response to
oxygen-containing compound
281/1548 | 4834/39869
GO:0010035 (3.76e-08)
response to
inorganic substance
182/1548 | 2884/39869
GO:0036293 (0.00255)
response to
decreased oxygen levels
23/1548 | 224/39869
GO:0000302 (4.39e-20)
response to
reactive oxygen species
92/1548 | 675/39869
GO:0001666 (0.0113)
response to hypoxia
21/1548 | 220/39869
GO:0042542 (1.49e-26)
response to
hydrogen peroxide
82/1548 | 416/39869