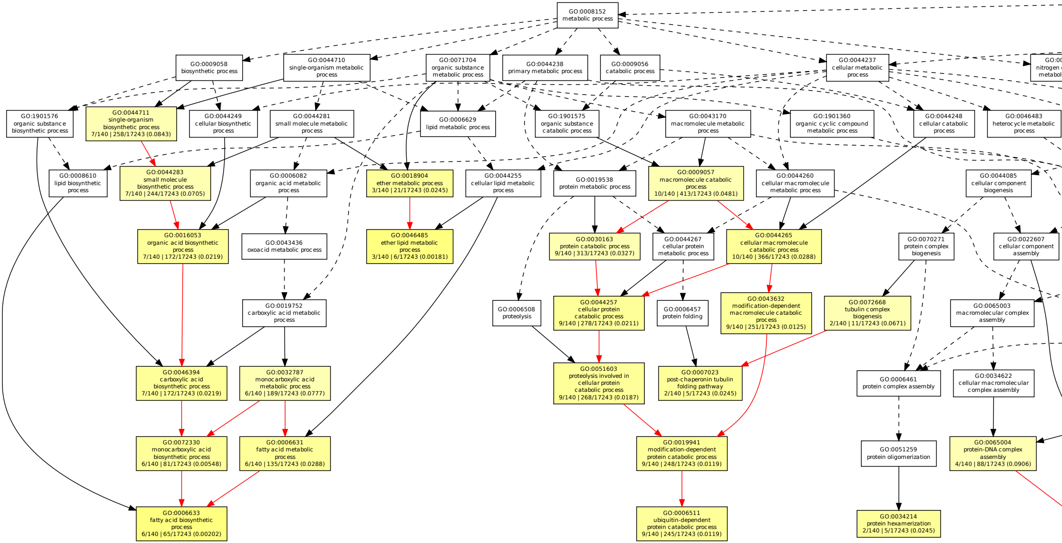
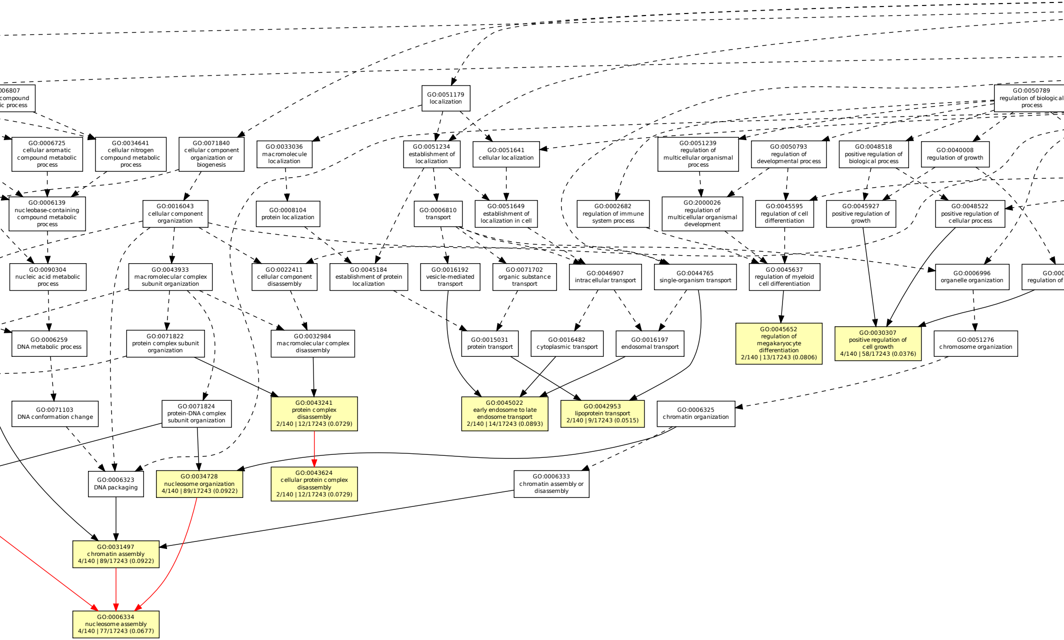
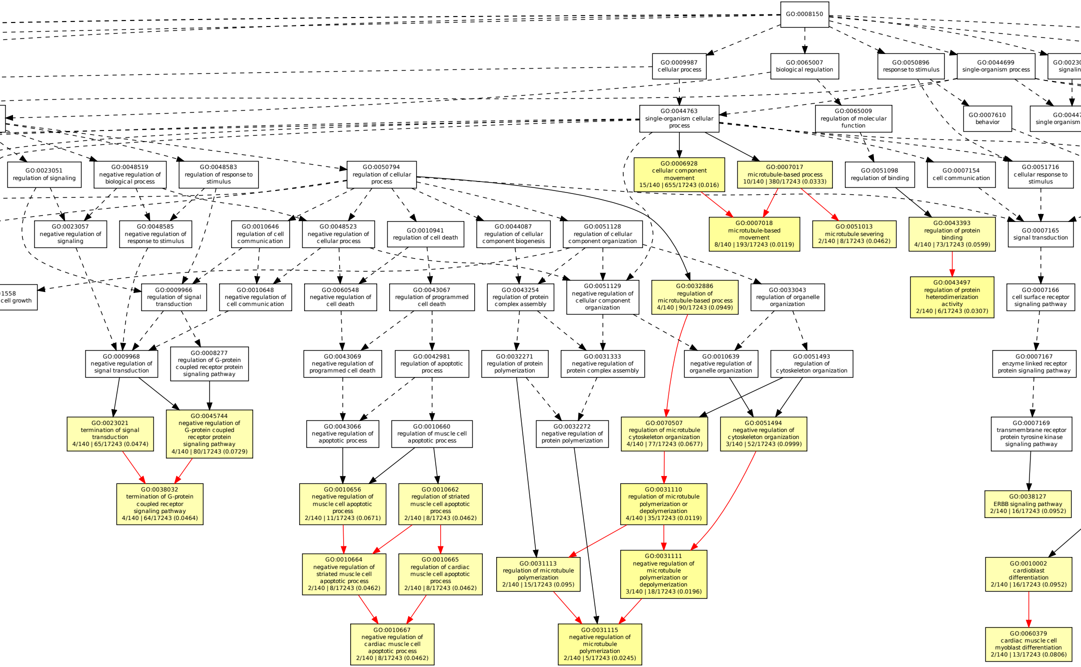
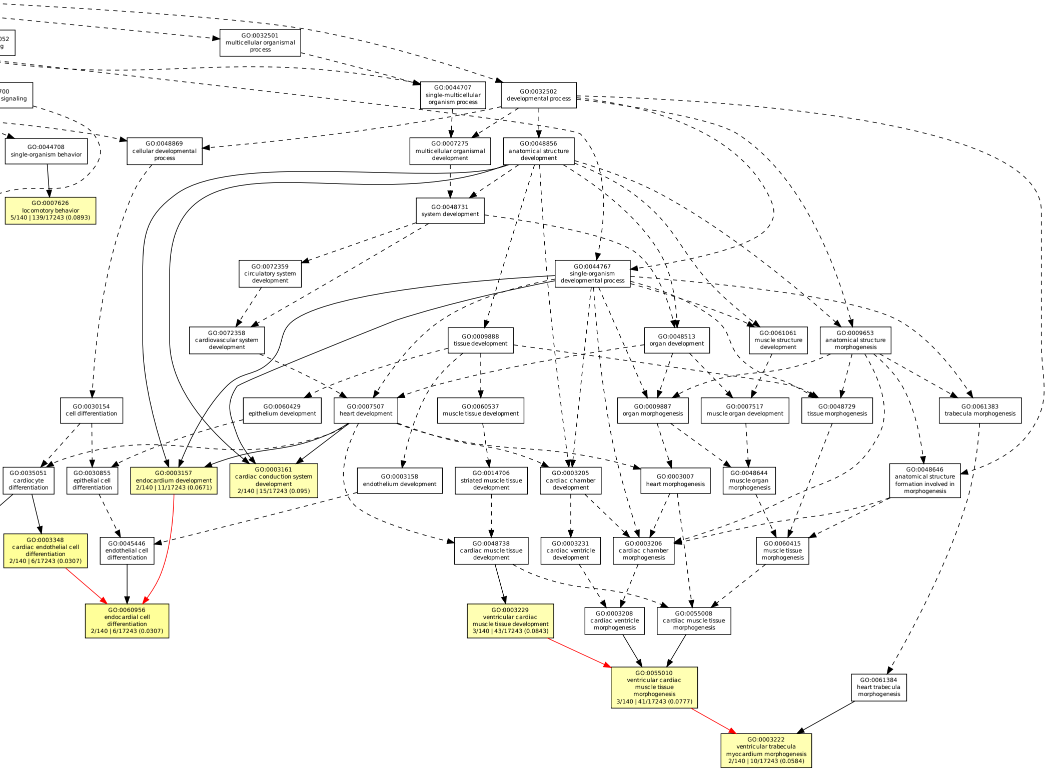

GO:0008152 metabolic process
GO:0009058 biosynthetic process
GO:0044710 single-organism metabolic process
GO:0071704 organic substance metabolic process
GO:0044238 primary metabolic process
GO:0009056 catabolic process
GO:0044237 cellular metabolic process
GO:00 nitrogen c metabol
GO:1901576 organic substance biosynthetic process
GO:0044711 single-organism biosynthetic process 7/140 | 258/17243 (0.0843)
GO:0044249 cellular biosynthetic process
GO:0044281 small molecule metabolic process
GO:0006629 lipid metabolic process
GO:1901575 organic substance catabolic process
GO:0043170 macromolecule metabolic process
GO:1901360 organic cyclic compound metabolic process
GO:0044248 cellular catabolic process
GO:0046483 heterocycle metabolic process
GO:0008610 lipid biosynthetic process
GO:0044283 small molecule biosynthetic process 7/140 | 244/17243 (0.0705)
GO:0006082 organic acid metabolic process
GO:0018904 ether metabolic process 3/140 | 21/17243 (0.0245)
GO:0044255 cellular lipid metabolic process
GO:0019538 protein metabolic process
GO:0009057 macromolecule catabolic process 10/140 | 413/17243 (0.0481)
GO:0044260 cellular macromolecule metabolic process
GO:0044085 cellular component biogenesis
GO:0016053 organic acid biosynthetic process 7/140 | 172/17243 (0.0219)
GO:0043436 oxoacid metabolic process
GO:0046485 ether lipid metabolic process 3/140 | 6/17243 (0.00181)
GO:0030163 protein catabolic process 9/140 | 313/17243 (0.0327)
GO:0044267 cellular protein metabolic process
GO:0044265 cellular macromolecule catabolic process 10/140 | 366/17243 (0.0288)
GO:0070271 protein complex biogenesis
GO:0022607 cellular component assembly
GO:0019752 carboxylic acid metabolic process
GO:0006508 proteolysis
GO:0044257 cellular protein catabolic process 9/140 | 278/17243 (0.0211)
GO:0006457 protein folding
GO:0043632 modification-dependent macromolecule catabolic process 9/140 | 251/17243 (0.0125)
GO:0072668 tubulin complex biogenesis 2/140 | 11/17243 (0.0671)
GO:0065003 macromolecular complex assembly
GO:0046394 carboxylic acid biosynthetic process 7/140 | 172/17243 (0.0219)
GO:0032787 monocarboxylic acid metabolic process 6/140 | 189/17243 (0.0777)
GO:0051603 proteolysis involved in cellular protein catabolic process 9/140 | 268/17243 (0.0187)
GO:0007023 post-chaperonin tubulin folding pathway 2/140 | 5/17243 (0.0245)
GO:0006461 protein complex assembly
GO:0034622 cellular macromolecular complex assembly
GO:0072330 monocarboxylic acid biosynthetic process 6/140 | 81/17243 (0.00548)
GO:0006631 fatty acid metabolic process 6/140 | 135/17243 (0.0288)
GO:0019941 modification-dependent protein catabolic process 9/140 | 248/17243 (0.0119)
GO:0051259 protein oligomerization
GO:0065004 protein-DNA complex assembly 4/140 | 88/17243 (0.0906)
GO:0006633 fatty acid biosynthetic process 6/140 | 65/17243 (0.00202)
GO:0006511 ubiquitin-dependent protein catabolic process 9/140 | 245/17243 (0.0119)
GO:0034214 protein hexamerization 2/140 | 5/17243 (0.0245)



006807
compound
ic process
GO:0051179
localization
GO:0050789
regulation of biological
process
GO:0006725
cellular aromatic
compound metabolic
process
GO:0034641
cellular nitrogen
compound metabolic
process
GO:0071840
cellular component
organization or
biogenesis
GO:0033036
macromolecule
localization
GO:0051234
establishment of
localization
GO:0051641
cellular localization
GO:0051239
regulation of
multicellular organismal
process
GO:0050793
regulation of
developmental process
GO:0048518
positive regulation of
biological process
GO:0040008
regulation of growth
GO:0006139
nucleobase-containing
compound metabolic
process
GO:0016043
cellular component
organization
GO:0008104
protein localization
GO:0006810
transport
GO:0051649
establishment of
localization in cell
GO:0002682
regulation of immune
system process
GO:2000026
regulation of
multicellular organismal
development
GO:0045595
regulation of cell
differentiation
GO:0045927
positive regulation of
growth
GO:0048522
positive regulation of
cellular process
GO:0090304
nucleic acid metabolic
process
GO:0043933
macromolecular complex
subunit organization
GO:0022411
cellular component
disassembly
GO:0045184
establishment of protein
localization
GO:0016192
vesicle-mediated
transport
GO:0071702
organic substance
transport
GO:0046907
intracellular transport
GO:0044765
single-organism transport
GO:0045637
regulation of myeloid
cell differentiation
GO:0006996
organelle organization
GO:00
regulation of
GO:0006259
DNA metabolic process
GO:0071822
protein complex subunit
organization
GO:0032984
macromolecular complex
disassembly
GO:0015031
protein transport
GO:0016482
cytoplasmic transport
GO:0016197
endosomal transport
GO:0045652
regulation of
megakaryocyte
differentiation
2/140 | 13/17243 (0.0806)
GO:0030307
positive regulation of
cell growth
4/140 | 58/17243 (0.0376)
GO:0051276
chromosome organization
GO:0071103
DNA conformation change
GO:0071824
protein-DNA complex
subunit organization
GO:0043241
protein complex
disassembly
2/140 | 12/17243 (0.0729)
GO:0045022
early endosome to late
endosome transport
2/140 | 14/17243 (0.0893)
GO:0042953
lipoprotein transport
2/140 | 9/17243 (0.0515)
GO:0006325
chromatin organization
GO:0006323
DNA packaging
GO:0034728
nucleosome organization
4/140 | 89/17243 (0.0922)
GO:0043624
cellular protein complex
disassembly
2/140 | 12/17243 (0.0729)
GO:0006333
chromatin assembly or
disassembly
GO:0031497
chromatin assembly
4/140 | 89/17243 (0.0922)
GO:0006334
nucleosome assembly
4/140 | 77/17243 (0.0677)


GO:0008150
GO:0009987
cellular process
GO:0065007
biological regulation
GO:0050896
response to stimulus
GO:0044699
single-organism process
GO:00230
signalin
GO:0044763
single-organism cellular process
GO:0065009
regulation of molecular function
GO:0007610
behavior
GO:00447
single organism
GO:0023051
regulation of signaling
GO:0048519
negative regulation of biological process
GO:0048583
regulation of response to stimulus
GO:0050794
regulation of cellular process
GO:0006928
cellular component movement
15/140 | 655/17243 (0.016)
GO:0007017
microtubule-based process
10/140 | 380/17243 (0.0333)
GO:0051098
regulation of binding
GO:0007154
cell communication
GO:0051716
cellular response to stimulus
GO:0023057
negative regulation of signaling
GO:0048585
negative regulation of response to stimulus
GO:0010646
regulation of cell communication
GO:0048523
negative regulation of cellular process
GO:0010941
regulation of cell death
GO:0044087
regulation of cellular component biogenesis
GO:0051128
regulation of cellular component organization
GO:0007018
microtubule-based movement
8/140 | 193/17243 (0.0119)
GO:0051013
microtubule severing
2/140 | 8/17243 (0.0462)
GO:0043393
regulation of protein binding
4/140 | 73/17243 (0.0599)
GO:0007165
signal transduction
1558
cell growth
GO:0009966
regulation of signal transduction
GO:0010648
negative regulation of cell communication
GO:0060548
negative regulation of cell death
GO:0043067
regulation of programmed cell death
GO:0043254
regulation of protein complex assembly
GO:0051129
negative regulation of cellular component organization
GO:0032886
regulation of microtubule-based process
4/140 | 90/17243 (0.0949)
GO:0033043
regulation of organelle organization
GO:0043497
regulation of protein heterodimerization activity
2/140 | 6/17243 (0.0307)
GO:0007166
cell surface receptor signaling pathway
GO:0009968
negative regulation of signal transduction
GO:0008277
regulation of G-protein coupled receptor protein signaling pathway
GO:0043069
negative regulation of programmed cell death
GO:0042981
regulation of apoptotic process
GO:0032271
regulation of protein polymerization
GO:0031333
negative regulation of protein complex assembly
GO:0010639
negative regulation of organelle organization
GO:0051493
regulation of cytoskeleton organization
GO:0007167
enzyme linked receptor protein signaling pathway
GO:0023021
termination of signal transduction
4/140 | 65/17243 (0.0474)
GO:0045744
negative regulation of G-protein coupled receptor protein signaling pathway
4/140 | 80/17243 (0.0729)
GO:0043066
negative regulation of apoptotic process
GO:0010660
regulation of muscle cell apoptotic process
GO:0032272
negative regulation of protein polymerization
GO:0070507
regulation of microtubule cytoskeleton organization
4/140 | 77/17243 (0.0677)
GO:0051494
negative regulation of cytoskeleton organization
3/140 | 52/17243 (0.0999)
GO:0007169
transmembrane receptor protein tyrosine kinase signaling pathway
GO:0038032
termination of G-protein coupled receptor signaling pathway
4/140 | 64/17243 (0.0464)
GO:0010656
negative regulation of muscle cell apoptotic process
2/140 | 11/17243 (0.0671)
GO:0010662
regulation of striated muscle cell apoptotic process
2/140 | 8/17243 (0.0462)
GO:0031110
regulation of microtubule polymerization or depolymerization
4/140 | 35/17243 (0.0119)
GO:0038127
ERBB signaling pathway
2/140 | 16/17243 (0.0952)
GO:0010664
negative regulation of striated muscle cell apoptotic process
2/140 | 8/17243 (0.0462)
GO:0010665
regulation of cardiac muscle cell apoptotic process
2/140 | 8/17243 (0.0462)
GO:0031113
regulation of microtubule polymerization
2/140 | 15/17243 (0.095)
GO:0031111
negative regulation of microtubule polymerization or depolymerization
3/140 | 18/17243 (0.0196)
GO:0010002
cardioblast differentiation
2/140 | 16/17243 (0.0952)
GO:0010667
negative regulation of cardiac muscle cell apoptotic process
2/140 | 8/17243 (0.0462)
GO:0031115
negative regulation of microtubule polymerization
2/140 | 5/17243 (0.0245)
GO:0060379
cardiac muscle cell myoblast differentiation
2/140 | 13/17243 (0.0806)


052
g
GO:0032501
multicellular organismal process
700
signaling
GO:0044707
single-multicellular organism process
GO:0032502
developmental process
GO:0044708
single-organism behavior
GO:0048869
cellular developmental process
GO:0007275
multicellular organismal development
GO:0048856
anatomical structure development
GO:0007626
locomotory behavior
5/140 | 139/17243 (0.0893)
GO:0048731
system development
GO:0072359
circulatory system development
GO:0044767
single-organism developmental process
GO:0072358
cardiovascular system development
GO:0009888
tissue development
GO:0048513
organ development
GO:0061061
muscle structure development
GO:0009653
anatomical structure morphogenesis
GO:0030154
cell differentiation
GO:0060429
epithelium development
GO:0007507
heart development
GO:0060537
muscle tissue development
GO:0009887
organ morphogenesis
GO:0007517
muscle organ development
GO:0048729
tissue morphogenesis
GO:0061383
trabecula morphogenesis
GO:0035051
cardiocyte differentiation
GO:0030855
epithelial cell differentiation
GO:0003157
endocardium development
2/140 | 11/17243 (0.0671)
GO:0003161
cardiac conduction system development
2/140 | 15/17243 (0.095)
GO:0003158
endothelium development
GO:0014706
striated muscle tissue development
GO:0003205
cardiac chamber development
GO:0003007
heart morphogenesis
GO:0048644
muscle organ morphogenesis
GO:0048646
anatomical structure formation involved in morphogenesis
GO:0003348
cardiac endothelial cell differentiation
2/140 | 6/17243 (0.0307)
GO:0045446
endothelial cell differentiation
GO:0048738
cardiac muscle tissue development
GO:0003231
cardiac ventricle development
GO:0003206
cardiac chamber morphogenesis
GO:0060415
muscle tissue morphogenesis
GO:0060956
endocardial cell differentiation
2/140 | 6/17243 (0.0307)
GO:0003229
ventricular cardiac muscle tissue development
3/140 | 43/17243 (0.0843)
GO:0003208
cardiac ventricle morphogenesis
GO:0055008
cardiac muscle tissue morphogenesis
GO:0055010
ventricular cardiac muscle tissue morphogenesis
3/140 | 41/17243 (0.0777)
GO:0061384
heart trabecula morphogenesis
GO:0003222
ventricular trabecula myocardium morphogenesis
2/140 | 10/17243 (0.0584)