

cilium assembly, GO:0060271

neural tube closure, GO:0001843
phagocytic vesicle membrane, GO:0030670
kidney development, GO:0001822
recycling endosome membrane, GO:0055038
regulation of protein localization, GO:0032880
ciliary tip, GO:0097542
axoneme, GO:0005930
liver development, GO:0001889
embryonic digit morphogenesis, GO:0042733
protein processing, GO:0016485
smoothened signaling pathway, GO:0007224
fat cell differentiation, GO:0045444
animal organ morphogenesis, GO:0009887
negative regulation of epithelial cell proliferation, GO:0050680
negative regulation of GTPase activity, GO:0034260
beta-tubulin binding, GO:0048487
RNA polymerase II repressing transcription factor binding, GO:0001103
motile cilium, GO:0031514
intracellular transport, GO:0046907
establishment of protein localization, GO:0045184
stress fiber, GO:0001725
limb development, GO:0060173
protein tyrosine/serine/threonine phosphatase activity, GO:0008138
ciliary membrane, GO:0060170
lung development, GO:0030324
branching morphogenesis of an epithelial tube, GO:0048754
coronary vasculature development, GO:0060976
palate development, GO:0060021
intraciliary transport, GO:0042073
endocytic vesicle, GO:0030139
protein localization, GO:0008104
neural tube development, GO:0021915
phagosome acidification, GO:0090383
establishment of protein localization to plasma membrane, GO:0090002
ATP-dependent microtubule motor activity, GO:0008569
regulation of exocytosis, GO:0017157
embryonic limb morphogenesis, GO:0030326
spermatid development, GO:0007286
Golgi to plasma membrane protein transport, GO:0043001
ATPase activity, GO:0042626
intraciliary transport particle B, GO:0030992
embryonic cranial skeleton morphogenesis, GO:0048701
early endosome to late endosome transport, GO:0045022
small GTPase binding, GO:0031267
embryonic forelimb morphogenesis, GO:0035115
mitotic cell cycle arrest, GO:0071850
endocytic recycling, GO:0032456
Arp2/3 complex-mediated actin nucleation, GO:0034314
protein localization to cilium, GO:0061512
regulation of cell migration, GO:0030334
negative regulation of multicellular organism growth, GO:0040015
determination of left/right symmetry, GO:0007368
alpha-tubulin binding, GO:0043014
histone acetyltransferase activity (H4-K5 specific), GO:0043995
histone acetyltransferase activity (H4-K8 specific), GO:0043996
histone acetyltransferase activity (H4-K16 specific), GO:0046972
brain morphogenesis, GO:0048854
endocrine pancreas development, GO:0031018
nucleoside diphosphate kinase activity, GO:0004550
regulation of stress fiber assembly, GO:0051492
regulation of smoothened signaling pathway, GO:0008589
regulation of fat cell differentiation, GO:0045598
vasodilation, GO:0042311
actin filament capping, GO:0051693
negative regulation of protein catabolic process, GO:0042177
lateral ventricle development, GO:0021670
nucleoside diphosphate phosphorylation, GO:0006165
positive regulation of epithelial to mesenchymal transition, GO:0010718
misfolded or incompletely synthesized protein catabolic process, GO:0006515
proton-transporting V-type ATPase, GO:0033179
intraciliary transport particle A, GO:0030991
ubiquitin-dependent protein catabolic process via the multivesicular body sorting pathway, GO:0043162
neural tube formation, GO:0001841
regulation of autophagosome assembly, GO:2000785
dorsal/ventral pattern formation, GO:0009953
left/right axis specification, GO:0070986
Arp2/3 protein complex, GO:0005885
face development, GO:0060324
negative regulation of B cell activation, GO:0050869
amyloid fibril formation, GO:1990000
BBSome, GO:0034464
negative regulation of actin filament polymerization, GO:0030837
head development, GO:0060322
cilium movement, GO:0003341
cardiovascular system development, GO:0072358
inositol-1, GO:0052659
pattern specification process, GO:0007389
axonemal dynein complex, GO:0005858
dorsal/ventral neural tube patterning, GO:0021904
clathrin complex, GO:0071439
telencephalon development, GO:0021537
apical dendrite, GO:0097440
neuronal stem cell population maintenance, GO:0097150
keratinocyte development, GO:0003334
platelet dense tubular network membrane, GO:0031095
outer dynein arm, GO:0036157
striatum development, GO:0021756
cerebellum development, GO:0021549
endoderm development, GO:0007492
positive regulation of multicellular organism growth, GO:0040018
inner ear receptor stereocilium organization, GO:0060122
hydrogen-exporting ATPase activity, GO:0008553
Golgi-associated vesicle, GO:0005798
regulation of cell-matrix adhesion, GO:0001952
epithelial cell development, GO:0002064
photoreceptor cell maintenance, GO:0045494
coenzyme binding, GO:0050662
embryonic hindlimb morphogenesis, GO:0035116
invadopodium, GO:0071437
plasma membrane tubulation, GO:0097320
branching involved in salivary gland morphogenesis, GO:0060445
cell volume homeostasis, GO:0006884
cell junction assembly, GO:0034329
cellular response to follicle-stimulating hormone stimulus, GO:0071372
negative regulation of oxidative stress-induced intrinsic apoptotic signaling pathway, GO:1902176
negative regulation of defense response to virus, GO:0050687
positive regulation of early endosome to late endosome transport, GO:2000643
embryonic camera-type eye development, GO:0031076
adult behavior, GO:0030534
hair follicle development, GO:0001942
positive regulation of smoothened signaling pathway, GO:0045880
corpus callosum development, GO:0022038
protein polyglutamylation, GO:0018095
gonad development, GO:0008406
outer dynein arm assembly, GO:0036158
establishment of planar polarity, GO:0001736
olfactory bulb development, GO:0021772
cell fate commitment, GO:0045165
epithelium development, GO:0060429
cellular response to increased oxygen levels, GO:0036295
cardiac muscle cell differentiation, GO:0055007
cerebellar cortex morphogenesis, GO:0021696
coronary artery morphogenesis, GO:0060982
sarcooplasm, GO:0016528
negative regulation of calcium ion-dependent exocytosis, GO:0045955
plus-end-directed vesicle transport along microtubule, GO:0072383
epithelial cilium movement, GO:0003351
heart looping, GO:0001947
positive regulation of neuroblast proliferation, GO:0002052
limb morphogenesis, GO:0035108
cardiac left ventricle morphogenesis, GO:0003214
keratinocyte differentiation, GO:0030216
negative regulation of anoikis, GO:2000811
1-phosphatidylinositol binding, GO:0005545
GTP biosynthetic process, GO:0006183
CTP biosynthetic process, GO:0006241
actin crosslink formation, GO:0051764
inositol-1, GO:0052658
membrane invagination, GO:0010324
collateral sprouting, GO:0048668
regulation of cilium beat frequency involved in ciliary motility, GO:0060296
ATPase-coupled anion transmembrane transporter activity, GO:0043225
regulation of receptor activity, GO:0010469
positive regulation of neuron migration, GO:2001224
hair follicle morphogenesis, GO:0031069