

protein complex assembly, GO:0006461

- positive regulation of NF-kappaB transcription factor activity, GO:0051092
- positive regulation of apoptotic signaling pathway, GO:2001235
- cytoplasmic side of plasma membrane, GO:0009898
- regulation of nucleic acid-templated transcription, GO:1903506
- positive regulation of smooth muscle cell proliferation, GO:0048661
- antiporter activity, GO:0015297
- amino acid transmembrane transporter activity, GO:0015171
- amino acid transport, GO:0006865
- interleukin-1-mediated signaling pathway, GO:0070498
- cytokine receptor activity, GO:0004896
- tumor necrosis factor receptor binding, GO:0005164
- protein tetramerization, GO:0051262
- positive regulation of extrinsic apoptotic signaling pathway, GO:2001238
- negative regulation of cell cycle, GO:0045786
- cellular response to retinoic acid, GO:0071300
- cartilage development, GO:0051216
- B cell activation, GO:0042113
- positive regulation of reactive oxygen species metabolic process, GO:2000379
- tumor necrosis factor-activated receptor activity, GO:0005031
- epithelial to mesenchymal transition, GO:0001837
- DNA damage response, GO:0030330
- microvillus, GO:0005902
- gamete generation, GO:0007276
- negative regulation of fibroblast proliferation, GO:0048147
- amino acid transmembrane transport, GO:0003333
- response to bacterium, GO:0009617
- mitogen-activated protein kinase kinase kinase binding, GO:0031435
- BMP signaling pathway, GO:0030509
- entrainment of circadian clock by photoperiod, GO:0043153
- actin filament polymerization, GO:0030041
- toll-like receptor signaling pathway, GO:0002224
- regulation of extrinsic apoptotic signaling pathway via death domain receptors, GO:1902041
- GTPase regulator activity, GO:0030695
- small molecule metabolic process, GO:0044281
- positive regulation of cell adhesion mediated by integrin, GO:0033630
- maintenance of protein location in nucleus, GO:0051457
- positive regulation of histone acetylation, GO:0035066
- response to activity, GO:0014823
- positive regulation of interleukin-2 production, GO:0032743
- positive regulation of extrinsic apoptotic signaling pathway in absence of ligand, GO:2001241
- definitive hemopoiesis, GO:0060216
- transcription coactivator binding, GO:0001223
- positive regulation of synapse assembly, GO:0051965
- positive regulation of pri-miRNA transcription from RNA polymerase II promoter, GO:1902895
- molybdopterin cofactor biosynthetic process, GO:0032324
- actin polymerization or depolymerization, GO:0008154
- syntaxin-1 binding, GO:0017075
- interphase microtubule nucleation by interphase microtubule organizing center, GO:0051415
- equatorial microtubule organizing center, GO:0000923
- activation of NF-kappaB-inducing kinase activity, GO:0007250
- positive regulation of Notch signaling pathway, GO:0045747
- positive regulation of B cell proliferation, GO:0030890
- bicellular tight junction assembly, GO:0070830
- cytokine-mediated signaling pathway, GO:0019221
- ventricular septum morphogenesis, GO:0060412
- cellular response to hepatocyte growth factor stimulus, GO:0035729
- retinoic acid receptor signaling pathway, GO:0048384
- positive regulation of tyrosine phosphorylation of STAT protein, GO:0042531
- positive regulation of transcription regulatory region DNA binding, GO:2000679
- erythrocyte development, GO:0048821
- cardiac muscle hypertrophy, GO:0003300
- structural constituent of muscle, GO:0008307
- prenyltransferase activity, GO:0004659
- Mo-molybdopterin cofactor biosynthetic process, GO:0006777
- cardiac muscle hypertrophy in response to stress, GO:0014898
- positive regulation of interleukin-2 biosynthetic process, GO:0045086
- maintenance of epithelial cell apical/basal polarity, GO:0045199
- positive regulation of BMP signaling pathway, GO:0030513
- neuromuscular process controlling posture, GO:0050884
- hormone biosynthetic process, GO:0042446
- CD40 receptor complex, GO:0035631
- negative regulation of chromatin silencing, GO:0031936
- embryonic heart tube morphogenesis, GO:0003143
- glucose transmembrane transporter activity, GO:0005355
- glucose transmembrane transport, GO:1904659
- positive regulation of heart rate, GO:0010460
- heart trabecula formation, GO:0060347
- regulation of myeloid cell differentiation, GO:0045637
- vascular smooth muscle cell development, GO:0097084
- negative regulation of ossification, GO:0030279
- defense response to protozoan, GO:0042832
- transcription factor activity, GO:0003705
- sarcomere organization, GO:0045214
- leukocyte tethering or rolling, GO:0050901
- extracellular matrix structural constituent, GO:0005201
- positive regulation of T cell cytokine production, GO:0002726
- neutral amino acid transmembrane transporter activity, GO:0015175
- regulation of timing of cell differentiation, GO:0048505
- protein geranylgeranylation, GO:0018344
- peptide transport, GO:0015833
- transcription factor activity, GO:0000983
- myeloid dendritic cell differentiation, GO:0043011