

protein autophosphorylation, GO:0046777

cell-cell junction, GO:0005911
positive regulation of l-kappaB kinase/NF-kappaB signaling, GO:0043123
response to lipopolysaccharide, GO:003296
calmodulin binding, GO:0005516
peptidyl-tyrosine phosphorylation, GO:0018108
protein-tyrosine kinase activity, GO:0004713
positive regulation of NF-kappaB transcription factor activity, GO:0051092
positive regulation of protein phosphorylation, GO:0001934
platelet activation, GO:0030168
positive regulation of cell migration, GO:0030335
hemopoiesis, GO:0030097
integrin binding, GO:0005178
response to virus, GO:0009615
aging, GO:0007568
regulation of mitotic cell cycle, GO:0007346
response to oxidative stress, GO:0006979
transmembrane receptor protein tyrosine kinase signaling pathway, GO:0007169
cellular response to oxidative stress, GO:0034599
response to organic substance, GO:0010033
T cell costimulation, GO:0031295
apoptotic signaling pathway, GO:0097190
positive regulation of angiogenesis, GO:0045766
protein phosphatase binding, GO:0019903
negative regulation of neuron apoptotic process, GO:0043524
interferon-gamma-mediated signaling pathway, GO:0060333
regulation of autophagy, GO:0010506
integrin-mediated signaling pathway, GO:0007229
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negative regulation of protein phosphorylation, GO:0001933
regulation of protein phosphorylation, GO:0001932
negative regulation of protein kinase activity, GO:0006469
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receptor complex, GO:0043235
chemotaxis, GO:0006935
positive regulation of neuron projection development, GO:0010976
phosphatidylinositol-mediated signaling, GO:0048015
cellular response to insulin stimulus, GO:0032869
interleukin-7-mediated signaling pathway, GO:0038111
response to hormone, GO:0009725
positive regulation of endothelial cell proliferation, GO:0001938
non-membrane spanning protein tyrosine kinase activity, GO:0004715
negative regulation of ERK1 and ERK2 cascade, GO:0070373
substrate adhesion-dependent cell spreading, GO:0034446
negative regulation of cell migration, GO:0030336
activation of JUN kinase activity, GO:0007257
positive regulation of cell growth, GO:0030307
regulation of inflammatory response, GO:0050727
positive regulation of JNK cascade, GO:0046330
actin cytoskeleton reorganization, GO:0031532
positive regulation of synapse assembly, GO:0051965
post-embryonic development, GO:0009791
phosphatidylinositol phosphorylation, GO:0046854
epidermal growth factor receptor signaling pathway, GO:0007173
cellular response to amino acid starvation, GO:0034198
positive regulation of autophagy, GO:0010508
cellular response to transforming growth factor beta stimulus, GO:0071560
extrinsic apoptotic signaling pathway, GO:0097191
regulation of actin cytoskeleton organization, GO:0032956
positive regulation of sequence-specific DNA binding transcription factor activity, GO:0051091
response to hydrogen peroxide, GO:0042542
positive regulation of peptidyl-tyrosine phosphorylation, GO:0050731
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sphingolipid biosynthetic process, GO:0030148
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axonogenesis, GO:0007409
execution phase of apoptosis, GO:0097194
central nervous system development, GO:0007417
glucose homeostasis, GO:0042593
positive regulation of MAPK cascade, GO:0043410
phosphotyrosine residue binding, GO:0001784
sarcoplasmic reticulum, GO:0016529
focal adhesion assembly, GO:0048041
neuron differentiation, GO:0030182
positive regulation of phosphatidylinositol 3-kinase signaling, GO:0014068
microvillus, GO:0005902
canonical Wnt signaling pathway, GO:0060070
negative regulation of cysteine-type endopeptidase activity involved in apoptotic process, GO:0043154
wound healing, GO:0042060
peptidyl-tyrosine autophosphorylation, GO:0038083
insulin receptor signaling pathway, GO:0008286
regulation of phosphatidylinositol 3-kinase signaling, GO:0014066
male meiotic nuclear division, GO:0007140
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positive regulation of endothelial cell migration, GO:0010595
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14-3-3 protein binding, GO:0071889
activation of protein kinase activity, GO:0032147
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platelet-derived growth factor receptor signaling pathway, GO:0048008
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positive regulation of smooth muscle cell proliferation, GO:0048661
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signal transduction by protein phosphorylation, GO:0023014
positive regulation of extrinsic apoptotic signaling pathway, GO:2001238
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positive regulation of axonogenesis, GO:0050772
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transmembrane receptor protein tyrosine kinase activity, GO:0004714
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cell periphery, GO:0071944
protein kinase C binding, GO:0005080
positive regulation of reactive oxygen species metabolic process, GO:2000379
nuclear euchromatin, GO:0005719
positive regulation of cytosolic calcium ion concentration, GO:0007204
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positive regulation of neuron apoptotic process, GO:0043525
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positive regulation of MAP kinase activity, GO:0043406
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negative regulation of MAP kinase activity, GO:0043407
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1-phosphatidylinositol-3-kinase activity, GO:0016303
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toll-like receptor signaling pathway, GO:0022224
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regulation of actin cytoskeleton reorganization, GO:2000249
intrinsic apoptotic signaling pathway in response to oxidative stress, GO:0008631
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negative regulation of macroautophagy, GO:0016242
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positive regulation of cell death, GO:0010942
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positive regulation of calcium ion transport, GO:0051928
positive regulation of dendritic spine development, GO:0060999
activation of phospholipase C activity, GO:0007202
B cell activation, GO:0042113
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regulation of JNK cascade, GO:0046328
T cell receptor complex, GO:0042101
phosphatidylinositol 3-kinase binding, GO:0043548
positive regulation of interleukin-8 production, GO:0032757
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positive regulation of smooth muscle cell migration, GO:0014911
negative regulation of endocytosis, GO:0045806
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pre-autophagosomal structure membrane, GO:0034045
skeletal system morphogenesis, GO:0048705
heme binding, GO:0020037
transcription corepressor binding, GO:0001222
regulation of focal adhesion assembly, GO:0051893
retina vasculature development in camera-type eye, GO:0061298
signal complex assembly, GO:0007172
positive regulation of fibroblast migration, GO:0010763
positive regulation of protein targeting to membrane, GO:0090314
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positive regulation of protein tyrosine kinase activity, GO:0061098
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negative regulation of axonogenesis, GO:0050771
regulation of calcium ion transport, GO:0051924
positive regulation of synapse maturation, GO:0090129
negative regulation of anoikis, GO:2000811
embryonic digestive tract morphogenesis, GO:0048557
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lymph vessel development, GO:0001945
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positive regulation of glial cell proliferation, GO:0060252
regulation of cellular senescence, GO:2000772
negative regulation of viral release from host cell, GO:1902187
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positive regulation of glucose metabolic process, GO:0010907
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response to hydrogen peroxide, GO:0033194
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positive regulation of DNA biosynthetic process, GO:2000573
positive regulation of B cell differentiation, GO:0045579
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positive regulation of actin cytoskeleton reorganization, GO:2000251
positive regulation of phosphorylation, GO:0042327
positive regulation of vascular endothelial growth factor receptor signaling pathway, GO:0030949
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negative regulation of B cell proliferation, GO:0030889
regulation of developmental pigmentation, GO:0048070
AP-2 adaptor complex binding, GO:0035612
calcium-dependent protein serine/threonine kinase activity, GO:0009931
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oligodendrocyte differentiation, GO:0048709
positive regulation of glucose import, GO:0046326
inner ear development, GO:0048839
leukotriene biosynthetic process, GO:0019370
peripheral nervous system neuron development, GO:0048935
regulation of sodium ion transport, GO:0002028
MAP kinase activity, GO:0004707
regulation of myelination, GO:0031641
positive regulation of calcium-mediated signaling, GO:0050850
positive regulation of chemokine secretion, GO:0090197
positive regulation of mitochondrial depolarization, GO:0051901
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regulation of clathrin-dependent endocytosis, GO:2000369
negative regulation of extrinsic apoptotic signaling pathway in absence of ligand, GO:2001240
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positive regulation of vascular endothelial growth factor production, GO:0010575
negative regulation of interleukin-6 production, GO:0032715
positive regulation of mesenchymal cell proliferation, GO:0002053
somatic stem cell division, GO:0048103
corpus callosum development, GO:0022038
UTP biosynthetic process, GO:0006228
nitric oxide biosynthetic process, GO:0006809
uterus development, GO:0060065
insulin receptor substrate binding, GO:0043560
positive regulation of mast cell degranulation, GO:0043306
positive regulation of fat cell differentiation, GO:0045600
regulation of protein kinase A signaling, GO:0010738
positive regulation of phospholipase C activity, GO:0010863
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positive regulation of mitochondrial outer membrane permeabilization involved in apoptotic signaling pathway, GO:1901030
B cell differentiation, GO:0030183
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branching involved in salivary gland morphogenesis, GO:0060445
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positive regulation of macrophage differentiation, GO:0045651
activin receptor signaling pathway, GO:0032924
thymic T cell selection, GO:0045061
maintenance of protein location in mitochondrion, GO:0072656
T cell migration, GO:0072678
regulation of locomotion, GO:0040012
cAMP response element binding protein binding, GO:0008140
lens fiber cell differentiation, GO:0070306
sprouting angiogenesis, GO:0002040
ureteric bud development, GO:0001657
NMDA selective glutamate receptor complex, GO:0017146
negative regulation of organ growth, GO:0046621
positive regulation of alpha-beta T cell differentiation, GO:0046638
regulation of energy homeostasis, GO:2000505
response to immobilization stress, GO:0035902
signal transducer, GO:0004702
positive regulation of lipid biosynthetic process, GO:0046889
establishment or maintenance of epithelial cell apical/basal polarity, GO:0045197
myeloid progenitor cell differentiation, GO:0002318
regulation of smooth muscle cell differentiation, GO:0051150
hepatocyte growth factor receptor signaling pathway, GO:0048012
regulation of cell adhesion mediated by integrin, GO:0033628
MAP kinase kinase kinase kinase activity, GO:0008349
calcium-transporting ATPase activity, GO:0005388
positive regulation of cardiac muscle cell apoptotic process, GO:0010666
positive regulation of cytokine secretion, GO:0050715
learning or memory, GO:0007611
regulation of mitochondrial fission, GO:0090140
death-inducing signaling complex assembly, GO:0071550