

response to hypoxia, GO:0001666

cellular response to organic cyclic compound, GO:0071407
cellular response to lipopolysaccharide, GO:0071222
protein homotetramerization, GO:0051289
dioxigenase activity, GO:0051213
heparin binding, GO:0008201
electron carrier activity, GO:0009055
Z disc, GO:0030018
response to mechanical stimulus, GO:0009612
T cell activation, GO:0042110
NAD binding, GO:0051287
cellular response to mechanical stimulus, GO:0071260
calcium ion transmembrane transport, GO:0070588
skeletal system development, GO:0001501
ligand-dependent nuclear receptor transcription coactivator activity, GO:0030374
kidney development, GO:0001822
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SMAD binding, GO:0046332
cholesterol metabolic process, GO:0008203
RNA polymerase II transcription factor activity, GO:0000981
transcriptional activator activity, GO:0001228
positive regulation of protein dephosphorylation, GO:0035307
negative regulation of inflammatory response, GO:0050728
palate development, GO:0060021
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ADP binding, GO:0043531
stress fiber, GO:0001725
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negative regulation of signal transduction, GO:0009968
hematopoietic progenitor cell differentiation, GO:0002244
regulation of lipid metabolic process, GO:0019216
BMP signaling pathway, GO:0030509
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intracellular receptor signaling pathway, GO:0030522
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chromatin DNA binding, GO:0031490
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positive regulation of Wnt signaling pathway, GO:0030177
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amyloid-beta binding, GO:0001540
locomotory behavior, GO:0007626
response to progesterone, GO:0032570
copper ion binding, GO:0005507
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secretory granule, GO:0030141
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cell adhesion mediated by integrin, GO:0033627
negative regulation of cell cycle, GO:0045786
regulation of nucleic acid-templated transcription, GO:1903506
response to muscle stretch, GO:0035994
developmental growth, GO:0048589
cartilage development, GO:0051216
peripheral nervous system development, GO:0007422
transforming growth factor beta binding, GO:0050431
positive regulation of bone mineralization, GO:0030501
regulation of insulin secretion, GO:0050796
activation of adenylate cyclase activity, GO:0007190
coreceptor activity, GO:0015026
response to metal ion, GO:0010038
artery morphogenesis, GO:0048844
positive regulation of apoptotic signaling pathway, GO:2001235
embryonic digestive tract development, GO:0048566
positive regulation of protein import into nucleus, GO:0042307
negative regulation of endothelial cell proliferation, GO:0001937
heterophilic cell-cell adhesion via plasma membrane cell adhesion molecules, GO:0007157
female pregnancy, GO:0007565
positive regulation of collagen biosynthetic process, GO:0032967
positive regulation of inflammatory response, GO:0050729
blood circulation, GO:0008015
peroxidase activity, GO:0004601
startle response, GO:0001964
negative regulation of smooth muscle cell proliferation, GO:0048662
positive regulation of protein complex assembly, GO:0031334
cellular response to estradiol stimulus, GO:0071392
calcium ion transport into cytosol, GO:0060402
modulation of synaptic transmission, GO:0050804
activin binding, GO:0048185
negative regulation of blood pressure, GO:0045776
response to amphetamine, GO:0001975
camera-type eye morphogenesis, GO:0048593
endodermal cell differentiation, GO:0035987
cholesterol binding, GO:0015485
cellular response to interleukin-4, GO:0071353
mammary gland development, GO:0030879
face morphogenesis, GO:0060325
negative regulation of angiogenesis, GO:0016525
L-ascorbic acid binding, GO:0031418
cell fate commitment, GO:0045165
glycolytic process, GO:0006096
positive regulation of extrinsic apoptotic signaling pathway via death domain receptors, GO:1902043
RNA polymerase II transcription factor complex, GO:0090575
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cell communication by electrical coupling involved in cardiac conduction, GO:0086064
embryonic camera-type eye morphogenesis, GO:0048596
positive regulation of BMP signaling pathway, GO:0030513
membrane depolarization, GO:0051899
cellular response to interleukin-1, GO:0071347
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action potential, GO:0001508
lipid homeostasis, GO:0055088
superoxide metabolic process, GO:0006801
cysteine-type endopeptidase activator activity involved in apoptotic process, GO:0008656
negative regulation of Ras protein signal transduction, GO:0046580
negative regulation of DNA biosynthetic process, GO:2000279
positive regulation of filopodium assembly, GO:0051491
excitatory postsynaptic potential, GO:0060079
NADP binding, GO:0050661
response to iron ion, GO:0010039
positive regulation of interleukin-6 production, GO:0032755
positive regulation of neuron differentiation, GO:0045666
negative regulation of tumor necrosis factor production, GO:0032720
extracellular ligand-gated ion channel activity, GO:0005230
membrane protein ectodomain proteolysis, GO:0006509
acetyltransferase activity, GO:0016407
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chemokine-mediated signaling pathway, GO:0070098
cAMP biosynthetic process, GO:0006171
response to activity, GO:0014823
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positive regulation of cell division, GO:0051781
positive regulation of smooth muscle contraction, GO:0045987
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negative regulation of ossification, GO:0030279
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positive regulation of erythrocyte differentiation, GO:0045648
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positive regulation of interleukin-12 production, GO:0032735
SMAD protein signal transduction, GO:0060395
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positive regulation of blood vessel diameter, GO:0097755
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death receptor binding, GO:0005123
membrane protein intracellular domain proteolysis, GO:0031293
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negative regulation of bone mineralization, GO:0030502
positive regulation of B cell proliferation, GO:0030890
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positive regulation of cell-cell adhesion, GO:0022409
positive regulation of macrophage chemotaxis, GO:0010759
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FMN binding, GO:0010181
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D-glucose transmembrane transporter activity, GO:0055056
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positive regulation of histone acetylation, GO:0035066
negative regulation of vascular associated smooth muscle cell migration, GO:1904753
negative regulation of glycolytic process, GO:0045820
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odontogenesis of dentin-containing tooth, GO:0042475
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negative regulation of glucose import, GO:0046325
negative regulation of vascular smooth muscle cell proliferation, GO:1904706
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response to muscle activity, GO:0014850
positive regulation of branching involved in ureteric bud morphogenesis, GO:0090190
pulmonary valve morphogenesis, GO:0003184
fibroblast migration, GO:0010761
negative regulation of interleukin-1 beta secretion, GO:0050713
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cation transmembrane transport, GO:0098655
proteoglycan binding, GO:0043394
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positive regulation of activated T cell proliferation, GO:0042104
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positive regulation of p38MAPK cascade, GO:1900745
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response to dietary excess, GO:0002021
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acetylcholine-gated cation-selective channel activity, GO:0022848
positive regulation of synaptic transmission, GO:0032224
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positive regulation of blood pressure, GO:0045777
cysteine-type endopeptidase activity involved in apoptotic process, GO:0097153
positive regulation of heart rate, GO:0010460
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lymphatic endothelial cell differentiation, GO:0060836
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acetylcholine receptor signaling pathway, GO:0095500
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acellular tight junction assembly, GO:0070830
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