| | positive regulation tumor necrosis fact | er membrane, GO:0005741 of NF-kappaB transcription factor activity, GO:0051092 tor-mediated signaling pathway, GO:0033209 mplex, GO:0000151 |
|---|--|--|
| | ubiquitin binding, I-kappaB kinase/N | • |
| | activation of cystein response to hypoxi | |
| | interferon-gamma- protein autoubiqui | lysaccharide, GO:0032496 -mediated signaling pathway, GO:0060333 itination, GO:0051865 o lipopolysaccharide, GO:0071222 |
| | activation of protei execution phase of | peptidase activity, GO:0004197 in kinase activity, GO:0032147 apoptosis, GO:0097194 n of viral genome replication, GO:0045071 |
| | positive regulation protein oligomeriza | of JNK cascade, GO:0046330 |
| | type I interferon sig | o mechanical stimulus, GO:0071260 gnaling pathway, GO:0060337 GO:0009615 l ubiquitination, GO:0070534 |
| | cytokine-mediated NF-kappaB binding | signaling pathway, GO:0019221 |
| | positive regulation negative regulation | n of NF-kappaB transcription factor activity, GO:0032088 n of B cell activation, GO:0050871 n of tumor necrosis factor production, GO:0032720 orticoid, GO:0051384 |
| | positive regulation toll-like receptor sig | of protein catabolic process, GO:0045732 gnaling pathway, GO:0002224 signaling pathway, GO:0097191 |
| | cytoplasmic side of cytokine production | chondrial membrane potential, GO:0051881 f plasma membrane, GO:0009898 on, GO:0001816 a of MAPK cascade, GO:0043410 |
| | T cell activation, G | e-mediated signaling pathway, GO:0031663 O:0042110 |
| | extrinsic apoptotic SMAD binding, GC | iquitin binding, GO:0070530 signaling pathway via death domain receptors, GO:0008625 O:0046332 se activity, GO:0016409 |
| | negative regulation positive regulation | of B cell proliferation, GO:0030890 n of extrinsic apoptotic signaling pathway, GO:2001237 n of release of cytochrome c from mitochondria, GO:0090200 n of inflammatory response, GO:0050729 |
| | positive regulation RAGE receptor bin positive regulation | of interferon-gamma production, GO:0032729 ading, GO:0050786 of T cell proliferation, GO:0042102 |
| | cullin family protei protein-cysteine S- ₁ | tor receptor binding, GO:0005164 in binding, GO:0097602 palmitoyltransferase activity, GO:0019706 vator activity, GO:0001205 |
| | activation of JUN k cellular response to positive regulation | kinase activity, GO:0007257 o organic substance, GO:0071310 of cell-matrix adhesion, GO:0001954 |
| | actin cytoskeleton i positive regulation | signaling pathway in response to endoplasmic reticulum stress, GO:0070059 reorganization, GO:0031532 of transcription factor import into nucleus, GO:0042993 of JNK cascade, GO:0046329 |
| | positive regulation positive regulation establishment of pr | of extrinsic apoptotic signaling pathway, GO:2001238 of protein complex assembly, GO:0031334 rotein localization to plasma membrane, GO:0090002 |
| | MAP kinase kinase response to bacteri | of phosphatidylinositol 3-kinase signaling, GO:0014068 e kinase activity, GO:0004709 ium, GO:0009617 ive oxygen species metabolic process, GO:2000377 |
| | ossification, GO:000 metal ion transport | |
| | positive regulation | of defense response to virus by host, GO:0002230 n of extrinsic apoptotic signaling pathway in absence of ligand, GO:2001240 |
| | negative regulation cysteine-type endo | igase activity involved in ERAD pathway, GO:1904264 on of growth of symbiont in host, GO:0044130 opeptidase activator activity involved in apoptotic process, GO:0008656 protein kinase kinase kinase binding, GO:0031435 |
| | regulation of innate integral componen negative regulation | e immune response, GO:0045088 It of mitochondrial outer membrane, GO:0031307 In of reactive oxygen species metabolic process, GO:2000378 |
| | negative regulation | ly, GO:0005771 mmatory response, GO:0050727 n of apoptotic signaling pathway, GO:2001234 n of interleukin-6 production, GO:0032755 |
| | positive regulation defense response, C epithelial to mesen | of interleukin-6 secretion, GO:2000778 GO:0006952 achymal transition, GO:0001837 |
| | negative regulation positive regulation | re morphogenesis, GO:0009653 n of insulin receptor signaling pathway, GO:0046627 n of endothelial cell proliferation, GO:0001938 n homeostasis, GO:0006874 |
| | regulation of cytok negative regulation protein kinase B sig | tine secretion, GO:0050707 n of inflammatory response, GO:0050728 gnaling, GO:0043491 |
| | regulation of extrin | intracellular domain proteolysis, GO:0031293 nsic apoptotic signaling pathway via death domain receptors, GO:1902041 mbrane with host plasma membrane, GO:0019064 mber of cells, GO:0048872 |
| | toll-like receptor 9 | , GO:0007034 o virus, GO:0098586 signaling pathway, GO:0034162 n of T cell proliferation, GO:0042130 |
| | positive regulation negative regulation intrinsic apoptotic | of cell division, GO:0051781 n of MAP kinase activity, GO:0043407 signaling pathway by p53 class mediator, GO:0072332 nation, GO:1990000 |
| | negative regulation positive regulation positive regulation | n of fat cell differentiation, GO:0045599 n of interleukin-17 production, GO:0032740 n of interleukin-10 production, GO:0032733 |
| | // regulation of mitoc // T cell proliferation, | n of extrinsic apoptotic signaling pathway via death domain receptors, GO:1902042 chondrion organization, GO:0010821 , GO:0042098 ron-beta, GO:0035456 |
| positive regulation of I-kappaB kinase/NF-kappaB signaling, GO:0043123 | positive regulation | nediated immune response, GO:0016064 a of interleukin-2 production, GO:0032743 a of stress-activated MAPK cascade, GO:0032874 |
| positive regulation of 1-kappab kinase/141-kappab signaling, GO:0043123 | \ \ 1 | • |
| | positive regulation positive regulation cellular response to | of interleukin-1 beta secretion, GO:0050718 of Rho protein signal transduction, GO:0035025 o exogenous dsRNA, GO:0071360 |
| | monocyte chemota calcium-dependent | secretion, GO:0050702 exis, GO:0002548 t cell-cell adhesion via plasma membrane cell adhesion molecules, GO:0016339 signaling pathway in absence of ligand, GO:0097192 |
| | | |
| | negative regulation mitochondrion loca | of interleukin-8 production, GO:0032757 n of endothelial cell proliferation, GO:0001937 alization, GO:0051646 n of mitochondrial fission, GO:0090141 |
| | activation of NF-ka positive regulation cysteine-type endo | appaB-inducing kinase activity, GO:0007250 of NF-kappaB import into nucleus, GO:0042346 opeptidase activity involved in execution phase of apoptosis, GO:0097200 |
| | positive regulation response to muram | vation, GO:0001774 of interleukin-2 biosynthetic process, GO:0045086 nyl dipeptide, GO:0032495 nous dsRNA, GO:0043330 |
| | positive regulation | GO:0032009 a of osteoclast differentiation, GO:0045672 a of ubiquitin-protein transferase activity, GO:0051443 ared signaling pathway, GO:0070098 |
| | intrinsic component positive regulation ectopic germ cell pr | nt of plasma membrane, GO:0031226 a of nitric-oxide synthase biosynthetic process, GO:0051770 programmed cell death, GO:0035234 |
| | positive regulation ion transmembrane | of neutrophil chemotaxis, GO:0090023 of interferon-gamma biosynthetic process, GO:0045078 e transporter activity, GO:0015075 cell selection, GO:0045060 |
| | death-inducing sign | |
| | | gration, C ₁ O:0043542 |
| | I-kappaB phosphorcell activation, GO: | |
| | I-kappaB phosphorcell activation, GO: protein kinase C aclipopolysaccharide positive regulation T-helper 1 type improved the control of the c | of reactive oxygen species metabolic process, GO:2000379 rylation, GO:0007252 :0001775 ctivity, GO:0004697 e binding, GO:0001530 of superoxide anion generation, GO:0032930 mune response, GO:0042088 |
| | I-kappaB phosphorcell activation, GO: protein kinase C aclipopolysaccharide positive regulation T-helper 1 type immunitochondrial oute CARD domain bind negative regulation | of reactive oxygen species metabolic process, GO:2000379 rylation, GO:0007252 :0001775 ctivity, GO:0004697 e binding, GO:0001530 a of superoxide anion generation, GO:0032930 mune response, GO:0042088 er membrane translocase complex, GO:0005742 |
| | I-kappaB phosphorcell activation, GO: protein kinase C aclipopolysaccharide positive regulation T-helper 1 type immunitochondrial oute CARD domain bind negative regulation toll-like receptor 3 ripoptosome, GO:0 negative regulation negative regulation negative regulation | of reactive oxygen species metabolic process, GO:2000379 rylation, GO:0007252 :0001775 :tivity, GO:0004697 :binding, GO:0001530 of superoxide anion generation, GO:0032930 mune response, GO:0042088 er membrane translocase complex, GO:0005742 ding, GO:0050700 of interleukin-8 secretion, GO:2000483 signaling pathway, GO:0034138 0097342 of by host of viral genome replication, GO:0044828 of of tumor necrosis factor-mediated signaling pathway, GO:0010804 |
| | I-kappaB phosphorcell activation, GO: protein kinase C activation, GO: protein kinase C actipopolysaccharide positive regulation. T-helper 1 type immediate the compositive regulation are regulation toll-like receptor 3 ripoptosome, GO:0 negative regulation negative regulation response to tumor thistone ubiquitinat negative regulation positive regulation positive regulation | of reactive oxygen species metabolic process, GO:2000379 rylation, GO:0007252 :0001775 :tivity, GO:0004697 :binding, GO:0001530 of superoxide anion generation, GO:0032930 mune response, GO:0042088 :r membrane translocase complex, GO:005742 ding, GO:0050700 of interleukin-8 secretion, GO:2000483 signaling pathway, GO:0034138 0097342 of by host of viral genome replication, GO:0044828 of tumor necrosis factor-mediated signaling pathway, GO:0010804 necrosis factor, GO:0034612 tion, GO:0016574 of of seeclast differentiation, GO:0045671 of chemokine production, GO:0032722 |
| | I-kappaB phosphorcell activation, GO: protein kinase C acclipopolysaccharide positive regulation. T-helper 1 type immunitochondrial outer CARD domain bind negative regulation toll-like receptor 3 ripoptosome, GO:0 negative regulation negative regulation response to tumor histone ubiquitinat negative regulation death-inducing sign positive regulation regulation of immunity in the second positive regulation regulation of immunity regulation regulation of immunity regulation of immunity regulation regulation regulation regulation of immunity regulation re | of reactive oxygen species metabolic process, GO:2000379 rylation, GO:0007252 ::0001775 ::tivity, GO:0004697 :: binding, GO:0001530 :: of superoxide anion generation, GO:0032930 :: mune response, GO:0042088 :: membrane translocase complex, GO:0005742 :: ding, GO:0050700 :: of interleukin-8 secretion, GO:2000483 :: signaling pathway, GO:0034138 :: op yhost of viral genome replication, GO:0044828 :: of tumor necrosis factor-mediated signaling pathway, GO:0010804 :: necrosis factor, GO:0034612 :: tion, GO:0016574 :: of osteoclast differentiation, GO:0045671 |
| | I-kappaB phosphorcell activation, GO: protein kinase C acclipopolysaccharide positive regulation. T-helper 1 type immitochondrial outer CARD domain bind negative regulation toll-like receptor 3 ripoptosome, GO:0 negative regulation negative regulation response to tumor histone ubiquitinat negative regulation death-inducing sign positive regulation regulation of immurpositive regulation magnesium ion transpositive regulation activation of cystein | of reactive oxygen species metabolic process, GO:2000379 rylation, GO:0007252 :0001775 :tivity, GO:0004697 :b binding, GO:0001530 of superoxide anion generation, GO:0032930 mune response, GO:0042088 er membrane translocase complex, GO:0005742 ding, GO:0050700 of interleukin-8 secretion, GO:2000483 signaling pathway, GO:0034138 0097342 |
| | I-kappaB phosphor cell activation, GO: protein kinase C actipopolysaccharide positive regulation T-helper 1 type immediate the compositive regulation toll-like receptor 3 ripoptosome, GO:0 negative regulation response to tumor response to tumor histone ubiquitinat negative regulation death-inducing sign positive regulation regulation of immer positive regulation magnesium ion transpositive regulation activation of cystein positive regulation negative regulation negative regulation regulation for cystein positive regulation negative regulation regulation regulation regulation regulation of Cystein positive regulation negative regulation regulation regulation of T cell | of reactive oxygen species metabolic process, GO:2000379 rylation, GO:0007252 r0001775 ricivity, GO:0004697 ricivity, GO:0001530 rof superoxide anion generation, GO:0032930 mune response, GO:0042088 remembrane translocase complex, GO:0005742 rofinerleukin-8 secretion, GO:2000483 signaling pathway, CO:0034138 rof student necrosis factor-mediated signaling pathway, GO:0010804 recrosis factor, GO:0034612 rion, GO:0016574 rof osteoclast differentiation, GO:0045671 rof of chemokine production, GO:0032722 ranaling complex, GO:0031264 rof interleukin-8 secretion, GO:2000484 rof interleukin-8 secretion, GO:0005095 rof tumor necrosis factor-mediated signaling pathway, GO:1903265 ranaling complex, GO:0031264 rof of tumor necrosis factor-mediated signaling pathway, GO:1903265 ranaling complex, GO:00505083 rof tumor necrosis factor-mediated signaling pathway, GO:1903265 response of pasmAPK cascade, GO:1900745 rof tumor necrosis factor-mediated signaling pathway, GO:1903265 response of pasmAPK cascade, GO:1900745 rof rotein ubiquitination involved in ubiquitin-dependent protein catabolic process, GO:2000060 rof viral entry into host cell, GO:0046597 rof toll-like receptor 4 signaling pathway, GO:0034145 racivation, GO:0050863 |
| | I-kappaB phosphorcell activation, GO: protein kinase C actipopolysaccharide positive regulation T-helper 1 type immitochondrial outer CARD domain bind negative regulation toll-like receptor 3 ripoptosome, GO:0 negative regulation negative regulation response to tumor thistone ubiquitinat negative regulation death-inducing sign positive regulation death-inducing sign positive regulation regulation of immurpositive regulation activation of cystein positive regulation negative regulation regulation for cystein positive regulation negative regulation regulation of T cell positive regulation positive reg | of reactive oxygen species metabolic process, GO:2000379 rylation, GO:0007252 rivity, GO:0004697 rivity, GO:0004697 rivity, GO:0001530 rof superoxide amion generation, GO:0032930 mune response, GO:0042088 re membrane translocase complex, GO:0005742 ding, GO:0050700 rof interleukin-8 secretion, GO:2000483 signaling pathway, GO:0034138 rof superoxide amion replication, GO:0044828 rof tumor necrosis factor-mediated signaling pathway, GO:0010804 recrosis factor, GO:0034612 rof osteoclast differentiation, GO:0032722 rabin of chemokine production, GO:0032722 rading complex, GO:0031264 rof interleukin-8 secretion, GO:2000484 ranglobulin secretion, GO:0001023 rof tumor necrosis factor-mediated signaling pathway, GO:1903265 romsmembrane transporter activity, GO:0015095 rof p38MAPK cascade, GO:1900745 rof viral entry into host cells, GO:0046597 rof foll-like receptor 4 signaling pathway, GO:004145 rof viral entry into host cells, GO:0046597 rof foll-like receptor 4 signaling pathway, GO:004469 rof interferon-beta biosynthetic process, GO:00405359 rof fumor necrosis factor secretion, GO:1900741 rof endothelial cell apoptotic process, GO:2000053 |
| | I-kappaB phosphorcell activation, GO: protein kinase C actipopolysaccharide positive regulation. T-helper 1 type immitochondrial outer CARD domain bind negative regulation toll-like receptor 3 ripoptosome, GO:0 negative regulation response to tumor histone ubiquitinat negative regulation death-inducing sign positive regulation regulation of immurpositive regulation magnesium ion transpositive regulation activation of cystein positive regulation negative regulation regulation of cystein positive regulation negative regulation positive regula | of reactive oxygen species metabolic process, GO:2000379 rylation, GO:0007252 |
| | I-kappaB phosphor cell activation, GO: protein kinase C actipopolysaccharide positive regulation T-helper 1 type immitochondrial oute CARD domain bind negative regulation toll-like receptor 3 ripoptosome, GO:0 negative regulation response to tumor histone ubiquitinat negative regulation death-inducing sign positive regulation regulation of immurpositive regulation magnesium ion trapositive regulation activation of cystein positive regulation negative regulation regulation for the regulation of T cell positive regulation | of reactive oxygen species metabolic process, GO:2000379 rylation, GO:0007252 rivity, CO:0004697 rivity, CO:0004697 rivity, CO:0004697 rivity, CO:0004697 rivity, CO:0004698 runner response, GO:0042088 runner response, GO:00483 signaling pathway, GO:0034138 signaling pathway, GO:0034138 signaling pathway, GO:0034138 signaling pathway, GO:0034138 signaling pathway, GO:0034612 sinch recrosis factor-mediated signaling pathway, CO:0010804 recrosis factor, GO:0034612 sinch, GO:0016574 run of oxteoclast differentiation, GO:0045671 sof chemokine production, GO:0032722 runling complex, CO:0031264 sof interleukin-8 secretion, GO:0032722 runling complex, GO:0031264 sof interleukin-8 secretion, GO:00501023 sof tumor necrosis factor-mediated signaling pathway, GO:1903265 susmembrane transporter activity, GO:0015095 sof p38MAPK Go:acsac, GC:01900745 sun-type endopeptidase activity, GO:0097202 sof protein ubiquifination involved in ubiquifina-dependent protein catabolic process, GO:2000060 sof viral entry into host cell, CO:00465897 sof toll-like receptor 4 signaling pathway, GO:0034145 activation, GO:0050863 sof tumor necrosis factor secretion, GO:1904469 sof interferon-alpha secretion, GO:1902741 sof endothelial cell apoptotic process, GO:2000353 evelopment, GO:0020038 sof interleukin-1 beta secretion, GO:0050713 susmembrane transport, GO:1903830 sof cytokine secretion, GO:0032897 |
| | I-kappaB phosphor cell activation, GO: protein kinase C ac lipopolysaccharide positive regulation T-helper 1 type immitochondrial oute CARD domain bind negative regulation toll-like receptor 3 ripoptosome, GO:0 negative regulation response to tumor histone ubiquitinat negative regulation positive regulation regulation of immurpositive regulation regulation of cystein positive regulation activation of cystein positive regulation negative regulation regulation of T cell positive regulation positive regu | of reactive oxygen species metabolic process, GO:2000379 rylation, GO:0007252 stivity, GO:0004697 stivity, GO:0004697 stivity, GO:0004697 stivity, GO:0004697 stivity, GO:0004697 stivity, GO:0004698 st membrane translocase complex, GO:0003742 ding, GO:0005700 or of interleukin-8 secretion, GO:2000483 signaling pathway, GO:0034188 s097342 or by host of viral genome replication, GO:0044828 or of tumor necrosis factor-mediated signaling pathway, CO:0010804 necrosis factor, GO:0034612 tion, GO:0016574 or of ostoclast differentiation, GO:0045671 or of ostoclast differentiation, GO:0032722 naling complex, GO:0031264 or of interleukin-8 secretion, GO:003484 unoglobulin secretion, CO:0051023 of tumor necrosis factor-mediated signaling pathway, GO:1903265 nsmembrane transporter activity, GO:0015095 or for standard secretion, GO:0004697 or of viral entry into host cell, GO:004697 or of viral entry into host cell, GO:0046597 or of viral entry into host cell, GO:0046691 or of viral entry into host cell, GO:00 |
| | I-kappaB phosphor cell activation, GO: protein kinase C ac lipopolysaccharide positive regulation T-helper 1 type immultochondrial outer CARD domain bind negative regulation toll-like receptor 3 ripoptosome, GO:0 negative regulation negative regulation response to tumor histone ubiquitinat negative regulation positive regulation death-inducing signositive regulation regulation of immultopistive regulation activation of cystein positive regulation negative regulation negative regulation positive regulation regulation of protein regulation of protein positive regulation positive re | of reactive oxygen species metabolic process, GO:2000379 mylation, GO:0007232 mylation, GO:0007232 mylation, GO:000735 mylation, GO:000735 more response, GO:0002088 mune response, GO:0002088 mune response, GO:0002088 more response, GO:0002088 mile response, GO:0000700 more interleukin-8 secretion, GO:2000833 signaling pathway, GO:0004138 mylation pathway, GO:0004138 mylation pathway, GO:0014138 mylation pathway, GO:0014138 mylation pathway, GO:0014828 more future received factor-mediated signaling pathway, GO:0010804 mecrosis factor-mediated signaling pathway, GO:0010804 mecrosis factor-mediated signaling pathway, GO:0010804 mecrosis factor, GO:0034612 more formal mylation good mylation, GO:0016374 more formal mylation good good good good good good good go |
| | I-kappaB phosphoricell activation, GO: protein kinase C actipopolysaccharide positive regulation T-helper 1 type immitochondrial outer CARD domain bind negative regulation regulation response to tumor histone ubiquitinat negative regulation response to tumor positive regulation regulation of immit positive regulation regulation of cystein positive regulation activation of cystein positive regulation negative regulation regulation of T cell positive regulation regulation of T cell positive regulation positive regulation positive regulation regulation of T cell positive regulation regulation positive regulation positive regulation positive regulation positive regulation regulation positive regulation positive regulation positive regulation positive regulation regulation of protein regulation of pr | cort reactive oxygen species metabolic process, GO:2000379 rylation, CO:000075 tivity, CO:00004697 tivity, CO:00001630 tof supcrovide anion generation, CO:00032930 minure response, GO:0001808 tor supcrovide anion generation, CO:0003742 ding, CO:0050700 do interleukin-8 secretion, GO:2000483 signaling pathway, CO:00034138 897342 signaling pathway, GO:0034138 897342 tof tumor necrosis factor-mediated signaling pathway, CO:0010804 mercosis factor, CO:0034612 tion, CO:0016574 tof chemokine production, GO:0045671 of chemokine production, GO:0037222 panling complex, GO:0031264 tof interleukin 8 secretion, GO:0034084 unoglobulin secretion, GO:0031264 tof interleukin 8 secretion, GO:0031265 tof ps80AAPK cascade, GO:1900745 tof ps80AAPK cascade, GO:1900745 tof ps80AAPK cascade, GO:1900745 tof ps80AAPK cascade, GO:1900745 tof protein ubiquitination involved in ubiquitin-dependent protein catabolic process, GO:2000060 tof viral entry into host cell, GO:0046597 tof tof lell-like receiptor 4 signaling pathway, CO:003139 of tumor necrosis factor secretion, GO:1902741 tof tof lell-like receiptor 4 signaling pathway, CO:003139 of tumor mercosis factor secretion, GO:1904469 tof viral entry into host cell, GO:0046597 tof tof li-like receiptor 4 signaling pathway, CO:0030339 of tumor mercosis factor secretion, GO:1904469 tof interferon-beha biosynthetic process, GO:0005033 evolopment, GO:0050863 tof of of-dothellal cell apoptitic process, GO:0005073 nest of-mothellal cell process, GO:0005073 tof cold of-mothellal cell chemotaxis, GO:0005073 tof cold of-mothellal cell chemotaxis, GO:0005073 tof endothellal cell chemotaxis, GO:0005073 tof endothellal c |
| | I-kappaB phosphoricell activation, GO: protein kinase C actipopolysaccharide positive regulation T-helper 1 type immitochondrial outer CARD domain binate negative regulation regulation response to tumor histone ubiquitinate negative regulation response to tumor histone ubiquitinate negative regulation regulation of immurpositive regulation regulation of immurpositive regulation regulation of cystein positive regulation activation of cystein positive regulation negative regulation regulation of T cell positive regulation regulation of protein regulation regulation of protein regulation of protein regulation regulation of protein regulation regulation regulation regulation regulati | indirective oxygen species metabolic process, CO-2000379 pythation, CO-000752 2000773 |
| | I-kappaB phosphor cell activation, GO: protein kinase C actipopolysaccharide positive regulation T-helper 1 type immitochondrial oute CARD domain bind negative regulation toll-like receptor 3 ripoptosome, GO:0 negative regulation response to tumor histone ubiquitinat negative regulation death-inducing signositive regulation regulation of immupositive regulation activation of cystein positive regulation negative regulation activation of cystein positive regulation positive regulation regulation of T cell positive regulation regulation of magnesium ion trapositive regulation positive regulation positive regulation regulation of protein regulation of protein transport, of tissue development regulation re | in fractive oxygen species metabolic process, GO:2000379 plation, CO:0000252 20001773 1ct ity, CO:00004897 1binding, CO:00001590 of superoxide amion generation, GO:0082981 mune response, GO:00002688 2ct membrane translocase complex, CO:0005742 ding, GO:0000700 of interleukin-8 secretion, GO:2000488 3signaling pathway, CO:0004188 1097312 1097312 1097312 1097313 1097313 1097313 1097314 109 |
| | I-kappaB phosphor cell activation, GO: protein kinase C actipopolysaccharide positive regulation T-helper 1 type immitochondrial oute CARD domain bind negative regulation toll-like receptor 3 ripoptosome, GO:0 negative regulation response to tumor histone ubiquitinat negative regulation death-inducing sigpositive regulation regulation of immupositive regulation activation of cystein positive regulation negative regulation negative regulation regulation of T cell positive regulation regulation of protein reg | of reactive exygen species metabolic process, GO.2000379 plation, CO.0007252 dx001773 tvity, GO.0004097 binding, GO.0001580 of superoxide arting generation, GO.0002990 mune response, GO.00012088 r membrane translecase complex, GO.0005742 ding, GC.00031700 of interleckikin-8 secretion, GO.2000483 signaling pathway, GO.0034138 097342 typ host of viral genome replication, GO.00044828 of anturleckikin-8 secretion, GO.00044828 of the translecase complex, GO.00044828 of the control of viral genome replication, GO.00044828 of the control of viral genome replication, GO.00044828 of the control of viral genome replication, GO.000467 of chemokine production, GO.0003272 rapiding complex, GO.0003285 replication recrosis factor secretion, GO.0004649 replication of viral entry into host call, GO.0004697 replication of viral entry into host call, GO.0004697 replication, GO.0005083 replication, GO.0005083 replication, GO.00000083 replication, GO.0000000000000000000000000000000000 |
| | I-kappaB phosphor cell activation, GO: protein kinase C actipopolysaccharide positive regulation T-helper 1 type immitochondrial oute CARD domain bind negative regulation toll-like receptor 3 ripoptosome, GO:0 negative regulation negative regulation response to tumor histone ubiquitinat negative regulation death-inducing signositive regulation regulation of immurpositive regulation activation of cystein positive regulation activation of cystein positive regulation negative regulation regulation of T cell positive regulation regulation of protein re | informatics covigon species metabolic process, CO-2000379 pylakon, CO-2000-2729 20001775 2000 |
| | I-kappaB phosphor cell activation, GO: protein kinase C actipopolysaccharide positive regulation T-helper 1 type immitochondrial outer CARD domain bind negative regulation toll-like receptor 3 ripoptosome, GO:0 negative regulation negative regulation response to tumor histone ubiquitinat negative regulation positive regulation regulation of immurpositive regulation regulation of cystein positive regulation activation of cystein positive regulation negative regulation regulation of T cell positive regulation regulation of protein trimerization of myelowound healing, GO Toll-like receptor be regulation of protein trimerization of protein trimerizatio | informative coxygen species metabolic process, CO-2000379 pulption, CO-000752 5000775 |
| | I-kappaB phosphor cell activation, GO: protein kinase C actipopolysaccharide positive regulation T-helper 1 type immitochondrial oute CARD domain bind negative regulation toll-like receptor 3 ripoptosome, GO:0 negative regulation response to tumor histone ubiquitinat negative regulation death-inducing signositive regulation regulation of immurpositive regulation activation of cystein positive regulation regulation for cystein positive regulation negative regulation regulation of T cell positive regulation regulation of protein regulation of protein positive regulation positive regulation of protein regulation of protein regulation of protein regulation of protein trimerization atrial cardiac music toll-like receptor be regulation of protein trimerization of pro | inforective crygen species metabolic process, CO:200079 pultion CO:000797 pultion CO |
| | I-kappaB phosphor cell activation, GO: protein kinase C actipopolysaccharide positive regulation T-helper 1 type immultiochondrial outer CARD domain bine negative regulation toll-like receptor 3 ripoptosome, GO:0 negative regulation regative regulation regative regulation regative regulation positive regulation positive regulation regulation of immultipositive regulation positive regulation activation of cystein positive regulation positive regulation positive regulation negative regulation regulation of T cell positive regulation regulation of protein trapositive regulation positive regulation positive regulation regulation of protein trapositive regulation regulation regulation of protein trapositive regulation | of reactive extygen species metabolic process, GO-200379 yindrion, CO-000752 2001775 1-binding, GO-0001390 1-of supervoked confine generation, GO-0007380 1-of supervoked confine generation, GO-0007482 1-of supervoked scalar mediated of signaling pathway, GO-0007481 1-of confine generation, GO-000747 1-of confine generation, GO-000747 1-of confine generation, GO-000772 1-of supervoked generation, GO-000773 1-of supervoked generation generation, GO-000773 1-of supervoked generation generation, GO-0 |