**Enriched GO Terms** GO:0016236~macroautophagy GO:0008654~phospholipid biosynthetic process GO:0046474~glycerophospholipid biosynthetic process GO:0061919~process utilizing autophagic mechanism GO:0006914~autophagy GO:0045017~glycerolipid biosynthetic process GO:0006650~glycerophospholipid metabolic process GO:0006977~DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest GO:1902400~intracellular signal transduction involved in G1 DNA damage checkpoint GO:0072431~signal transduction involved in mitotic G1 DNA damage checkpoint GO:1902115~regulation of organelle assembly GO:0009791~post-embryonic development GO:1902403~signal transduction involved in mitotic DNA integrity checkpoint GO:1902402~signal transduction involved in mitotic DNA damage checkpoint GO:0072413~signal transduction involved in mitotic cell cycle checkpoint GO:0071156~regulation of cell cycle arrest GO:0007033~vacuole organization GO:0072331~signal transduction by p53 class mediator GO:0044819~mitotic G1/S transition checkpoint GO:0031571~mitotic G1 DNA damage checkpoint GO:0006354~DNA-templated transcription, elongation GO:0044783~G1 DNA damage checkpoint GO:0032784~regulation of DNA-templated transcription, elongation GO:1905037~autophagosome organization GO:0046486~glycerolipid metabolic process GO:0071158~positive regulation of cell cycle arrest GO:0006661~phosphatidylinositol biosynthetic process GO:0007050~cell cycle arrest GO:0034199~activation of protein kinase A activity GO:0006644~phospholipid metabolic process GO:2000134~negative regulation of G1/S transition of mitotic cell cycle GO:0072422~signal transduction involved in DNA damage checkpoint GO:0072401~signal transduction involved in DNA integrity checkpoint GO:0072395~signal transduction involved in cell cycle checkpoint GO:0030104~water homeostasis GO:0048193~Golgi vesicle transport — GO:0000045~autophagosome assembly GO:1902807~negative regulation of cell cycle G1/S phase transition GO:0046058~cAMP metabolic process GO:0046488~phosphatidylinositol metabolic process GO:0044773~mitotic DNA damage checkpoint GO:0016197~endosomal transport GO:0099518~vesicle cytoskeletal trafficking GO:0050891~multicellular organismal water homeostasis GO:2000045~regulation of G1/S transition of mitotic cell cycle GO:0000077~DNA damage checkpoint GO:0044774~mitotic DNA integrity checkpoint GO:0000082~G1/S transition of mitotic cell cycle GO:0030330~DNA damage response, signal transduction by p53 class mediator GO:0034330~cell junction organization GO:0031570~DNA integrity checkpoint GO:0034243~regulation of transcription elongation from RNA polymerase II promoter GO:0006470~protein dephosphorylation GO:1902806~regulation of cell cycle G1/S phase transition GO:0044843~cell cycle G1/S phase transition GO:0016050~vesicle organization GO:1990182~exosomal secretion GO:0045815~positive regulation of gene expression, epigenetic GO:0035335~peptidyl-tyrosine dephosphorylation GO:0007093~mitotic cell cycle checkpoint GO:0097734~extracellular exosome biogenesis GO:0032147~activation of protein kinase activity -GO:0048284~organelle fusion GO:0010948~negative regulation of cell cycle process — GO:0006171~cAMP biosynthetic process GO:0000075~cell cycle checkpoint GO:0007041~lysosomal transport GO:0032801~receptor catabolic process GO:0034329~cell junction assembly GO:0016241~regulation of macroautophagy GO:0045921~positive regulation of exocytosis GO:0140112~extracellular vesicle biogenesis GO:0033762~response to glucagon GO:1902373~negative regulation of mRNA catabolic process GO:0016311~dephosphorylation — GO:1902222~erythrose 4-phosphate/phosphoenolpyruvate family amino acid catabolic process GO:1902221~erythrose 4–phosphate/phosphoenolpyruvate family amino acid metabolic process GO:0006559~L-phenylalanine catabolic process GO:0006558~L-phenylalanine metabolic process GO:0000185~activation of MAPKKK activity GO:0000289~nuclear-transcribed mRNA poly(A) tail shortening GO:0042770~signal transduction in response to DNA damage GO:1903894~regulation of IRE1-mediated unfolded protein response GO:0090161~Golgi ribbon formation GO:0006906~vesicle fusion GO:1902117~positive regulation of organelle assembly GO:0009187~cyclic nucleotide metabolic process GO:0051310~metaphase plate congression GO:0046856~phosphatidylinositol dephosphorylation GO:0035563~positive regulation of chromatin binding GO:0030948~negative regulation of vascular endothelial growth factor receptor signaling pathway GO:1902882~regulation of response to oxidative stress GO:0051403~stress–activated MAPK cascade — GO:0071377~cellular response to glucagon stimulus GO:0033561~regulation of water loss via skin GO:0009411~response to UV GO:1902369~negative regulation of RNA catabolic process GO:0008333~endosome to lysosome transport GO:0007034~vacuolar transport GO:0007030~Golgi organization GO:0009416~response to light stimulus GO:0031098~stress-activated protein kinase signaling cascade GO:0120193~tight junction organization GO:0007254~JNK cascade GO:0051650~establishment of vesicle localization GO:0090174~organelle membrane fusion GO:0033169~histone H3–K9 demethylation GO:0007080~mitotic metaphase plate congression GO:0031929~TOR signaling GO:1903543~positive regulation of exosomal secretion GO:0042559~pteridine-containing compound biosynthetic process GO:0019471~4-hydroxyproline metabolic process GO:0006892~post-Golgi vesicle-mediated transport GO:0090068~positive regulation of cell cycle process GO:0006368~transcription elongation from RNA polymerase II promoter GO:1901991~negative regulation of mitotic cell cycle phase transition GO:1903541~regulation of exosomal secretion GO:0048012~hepatocyte growth factor receptor signaling pathway GO:0035372~protein localization to microtubule GO:1903580~positive regulation of ATP metabolic process GO:0034404~nucleobase–containing small molecule biosynthetic process GO:0051648~vesicle localization GO:1900407~regulation of cellular response to oxidative stress GO:0043506~regulation of JUN kinase activity GO:0045216~cell-cell junction organization GO:0048535~lymph node development GO:0018904~ether metabolic process GO:0016254~preassembly of GPI anchor in ER membrane GO:0006402~mRNA catabolic process — GO:0009166~nucleotide catabolic process GO:0043467~regulation of generation of precursor metabolites and energy GO:0033059~cellular pigmentation GO:0009896~positive regulation of catabolic process GO:0048814~regulation of dendrite morphogenesis GO:0046328~regulation of JNK cascade GO:0042558~pteridine-containing compound metabolic process GO:0006903~vesicle targeting GO:0051169~nuclear transport — GO:0002532~production of molecular mediator involved in inflammatory response GO:1901292~nucleoside phosphate catabolic process GO:0061154~endothelial tube morphogenesis GO:0035493~SNARE complex assembly GO:0034312~diol biosynthetic process GO:0034063~stress granule assembly GO:0003159~morphogenesis of an endothelium GO:1901988~negative regulation of cell cycle phase transition — GO:2000785~regulation of autophagosome assembly GO:0018209~peptidyl-serine modification GO:0070085~glycosylation GO:1900076~regulation of cellular response to insulin stimulus GO:0043507~positive regulation of JUN kinase activity GO:2001169~regulation of ATP biosynthetic process GO:0032886~regulation of microtubule–based process GO:0090313~regulation of protein targeting to membrane GO:0030947~regulation of vascular endothelial growth factor receptor signaling pathway GO:0003091~renal water homeostasis GO:0010256~endomembrane system organization — GO:1903201~regulation of oxidative stress-induced cell death GO:0051303~establishment of chromosome localization GO:0050658~RNA transport GO:0050657~nucleic acid transport GO:1901673~regulation of mitotic spindle assembly GO:0031936~negative regulation of chromatin silencing GO:0018105~peptidyl-serine phosphorylation— GO:0046390~ribose phosphate biosynthetic process — GO:0050000~chromosome localization GO:0001824~blastocyst development GO:1901653~cellular response to peptide — GO:0060236~regulation of mitotic spindle organization GO:0046839~phospholipid dephosphorylation GO:0006623~protein targeting to vacuole GO:0051236~establishment of RNA localization — GO:1903578~regulation of ATP metabolic process GO:0000288~nuclear-transcribed mRNA catabolic process, deadenylation-dependent decay GO:1901990~regulation of mitotic cell cycle phase transition — GO:1900016~negative regulation of cytokine production involved in inflammatory response GO:0006622~protein targeting to lysosome GO:1900544~positive regulation of purine nucleotide metabolic process GO:0045981~positive regulation of nucleotide metabolic process GO:0006487~protein N-linked glycosylation GO:0097352~autophagosome maturation GO:0045022~early endosome to late endosome transport GO:0006656~phosphatidylcholine biosynthetic process GO:0031331~positive regulation of cellular catabolic process GO:0051592~response to calcium ion GO:0007043~cell-cell junction assembly GO:0009314~response to radiation — GO:1990542~mitochondrial transmembrane transport GO:1903312~negative regulation of mRNA metabolic process GO:0006110~regulation of glycolytic process GO:0030522~intracellular receptor signaling pathway — GO:0052652~cyclic purine nucleotide metabolic process GO:0042094~interleukin–2 biosynthetic process GO:0034311~diol metabolic process GO:0009190~cyclic nucleotide biosynthetic process GO:0007289~spermatid nucleus differentiation GO:0002088~lens development in camera-type eye GO:0032386~regulation of intracellular transport — GO:0044264~cellular polysaccharide metabolic process GO:0016579~protein deubiquitination -GO:0016570~histone modification — GO:0030811~regulation of nucleotide catabolic process GO:0006403~RNA localization GO:0046822~regulation of nucleocytoplasmic transport GO:0006401~RNA catabolic process — GO:1903320~regulation of protein modification by small protein conjugation or removal — GO:0061436~establishment of skin barrier GO:0045821~positive regulation of glycolytic process GO:0035561~regulation of chromatin binding GO:0016338~calcium-independent cell-cell adhesion via plasma membrane cell-adhesion molecules GO:0006359~regulation of transcription by RNA polymerase III GO:0034644~cellular response to UV GO:0061025~membrane fusion GO:0006913~nucleocytoplasmic transport — GO:0098927~vesicle-mediated transport between endosomal compartments GO:0090224~regulation of spindle organization GO:0070317~negative regulation of G0 to G1 transition GO:1903902~positive regulation of viral life cycle GO:0080171~lytic vacuole organization GO:0007040~lysosome organization GO:0048145~regulation of fibroblast proliferation GO:0046470~phosphatidylcholine metabolic process GO:0007052~mitotic spindle organization GO:0009108~coenzyme biosynthetic process — GO:0051898~negative regulation of protein kinase B signaling GO:0032623~interleukin-2 production GO:0009124~nucleoside monophosphate biosynthetic process — GO:0048144~fibroblast proliferation GO:1903421~regulation of synaptic vesicle recycling GO:1902410~mitotic cytokinetic process GO:0018126~protein hydroxylation GO:0010288~response to lead ion GO:0009110~vitamin biosynthetic process GO:1901031~regulation of response to reactive oxygen species GO:0044088~regulation of vacuole organization GO:0061136~regulation of proteasomal protein catabolic process — GO:0051225~spindle assembly GO:0031330~negative regulation of cellular catabolic process — GO:0043122~regulation of I–kappaB kinase/NF–kappaB signaling — GO:0032872~regulation of stress–activated MAPK cascade — GO:0016482~cytosolic transport — GO:0009132~nucleoside diphosphate metabolic process — GO:0071375~cellular response to peptide hormone stimulus — GO:0009260~ribonucleotide biosynthetic process — GO:0060612~adipose tissue development GO:0030258~lipid modification — GO:2000644~regulation of receptor catabolic process GO:1904903~ESCRT III complex disassembly GO:1904896~ESCRT complex disassembly GO:1903862~positive regulation of oxidative phosphorylation GO:0048757~pigment granule maturation GO:0046485~ether lipid metabolic process GO:0043485~endosome to pigment granule transport GO:0035646~endosome to melanosome transport GO:0034378~chylomicron assembly GO:1902275~regulation of chromatin organization — GO:0006766~vitamin metabolic process GO:0006165~nucleoside diphosphate phosphorylation GO:1900101~regulation of endoplasmic reticulum unfolded protein response GO:0051197~positive regulation of coenzyme metabolic process GO:0033522~histone H2A ubiquitination GO:0032438~melanosome organization GO:0030813~positive regulation of nucleotide catabolic process GO:0043297~apical junction assembly GO:0036498~IRE1-mediated unfolded protein response GO:0070302~regulation of stress–activated protein kinase signaling cascade — GO:0006888~ER to Golgi vesicle–mediated transport — GO:0006664~glycolipid metabolic process GO:0070507~regulation of microtubule cytoskeleton organization — GO:1903509~liposaccharide metabolic process GO:0038093~Fc receptor signaling pathway — GO:0015931~nucleobase–containing compound transport — GO:0072665~protein localization to vacuole GO:1903050~regulation of proteolysis involved in cellular protein catabolic process — GO:0007249~I-kappaB kinase/NF-kappaB signaling — GO:0046939~nucleotide phosphorylation — GO:0051188~cofactor biosynthetic process — Raw p-value GO:0043470~regulation of carbohydrate catabolic process 0.04 GO:0042147~retrograde transport, endosome to Golgi 0.03 GO:1904754~positive regulation of vascular associated smooth muscle cell migration 0.02 GO:0097066~response to thyroid hormone Term 0.01 GO:0071684~organism emergence from protective structure GO:0048753~pigment granule organization Num. Genes GO:0035188~hatching • 10 GO:0001835~blastocyst hatching **2**0 GO:0010506~regulation of autophagy — GO:0070646~protein modification by small protein removal — GO:1901617~organic hydroxy compound biosynthetic process — GO:0016569~covalent chromatin modification — GO:0032869~cellular response to insulin stimulus — GO:0070316~regulation of G0 to G1 transition GO:0042771~intrinsic apoptotic signaling pathway in response to DNA damage by p53 class mediator GO:0044282~small molecule catabolic process — GO:0006497~protein lipidation GO:0002223~stimulatory C–type lectin receptor signaling pathway GO:0032868~response to insulin GO:0030048~actin filament-based movement GO:0009179~purine ribonucleoside diphosphate metabolic process GO:0009135~purine nucleoside diphosphate metabolic process GO:0008584~male gonad development GO:1905146~lysosomal protein catabolic process GO:0090042~tubulin deacetylation GO:0072537~fibroblast activation GO:0035404~histone-serine phosphorylation GO:0006853~carnitine shuttle GO:0006048~UDP-N-acetylglucosamine biosynthetic process GO:0001821~histamine secretion GO:0005976~polysaccharide metabolic process GO:0046546~development of primary male sexual characteristics GO:0045787~positive regulation of cell cycle — GO:0090169~regulation of spindle assembly GO:0046885~regulation of hormone biosynthetic process GO:0009651~response to salt stress GO:0002021~response to dietary excess GO:1901136~carbohydrate derivative catabolic process — GO:0009185~ribonucleoside diphosphate metabolic process GO:0006096~glycolytic process GO:1901987~regulation of cell cycle phase transition — GO:0070231~T cell apoptotic process GO:0048066~developmental pigmentation GO:0047496~vesicle transport along microtubule GO:0045023~G0 to G1 transition GO:0006757~ATP generation from ADP GO:0002220~innate immune response activating cell surface receptor signaling pathway GO:1900542~regulation of purine nucleotide metabolic process GO:0070076~histone lysine demethylation GO:0036296~response to increased oxygen levels GO:0033598~mammary gland epithelial cell proliferation GO:0009074~aromatic amino acid family catabolic process GO:0009065~glutamine family amino acid catabolic process GO:0001702~gastrulation with mouth forming second GO:1900371~regulation of purine nucleotide biosynthetic process -GO:0010639~negative regulation of organelle organization — GO:0036473~cell death in response to oxidative stress GO:0048871~multicellular organismal homeostasis GO:0072666~establishment of protein localization to vacuole GO:0008542~visual learning GO:1902337~regulation of apoptotic process involved in morphogenesis GO:0099640~axo-dendritic protein transport GO:0051608~histamine transport GO:0043482~cellular pigment accumulation GO:0043476~pigment accumulation GO:0035751~regulation of lysosomal lumen pH GO:0034497~protein localization to phagophore assembly site GO:0034244~negative regulation of transcription elongation from RNA polymerase II promoter GO:0010960~magnesium ion homeostasis GO:0006662~glycerol ether metabolic process GO:0006527~arginine catabolic process GO:0002024~diet induced thermogenesis GO:0030808~regulation of nucleotide biosynthetic process GO:0097191~extrinsic apoptotic signaling pathway — GO:0007051~spindle organization — GO:0045930~negative regulation of mitotic cell cycle — GO:0009156~ribonucleoside monophosphate biosynthetic process — GO:0042158~lipoprotein biosynthetic process GO:0033157~regulation of intracellular protein transport — GO:0000209~protein polyubiquitination — GO:0051193~regulation of cofactor metabolic process — • GO:0042866~pyruvate biosynthetic process GO:0070229~negative regulation of lymphocyte apoptotic process GO:0042219~cellular modified amino acid catabolic process GO:0031116~positive regulation of microtubule polymerization GO:0016577~histone demethylation GO:0010390~histone monoubiquitination GO:0051196~regulation of coenzyme metabolic process GO:0061013~regulation of mRNA catabolic process— GO:0016052~carbohydrate catabolic process — GO:0006140~regulation of nucleotide metabolic process — GO:0033044~regulation of chromosome organization — GO:0048010~vascular endothelial growth factor receptor signaling pathway GO:0030968~endoplasmic reticulum unfolded protein response GO:0072698~protein localization to microtubule cytoskeleton GO:0001701~in utero embryonic development — GO:1903205~regulation of hydrogen peroxide-induced cell death GO:0097421~liver regeneration GO:0090314~positive regulation of protein targeting to membrane GO:0048147~negative regulation of fibroblast proliferation GO:0032743~positive regulation of interleukin–2 production GO:0006362~transcription elongation from RNA polymerase I promoter GO:0001782~B cell homeostasis GO:1902902~negative regulation of autophagosome assembly GO:1900103~positive regulation of endoplasmic reticulum unfolded protein response GO:0051315~attachment of mitotic spindle microtubules to kinetochore GO:0050746~regulation of lipoprotein metabolic process GO:0046349~amino sugar biosynthetic process GO:0030656~regulation of vitamin metabolic process GO:0019511~peptidyl-proline hydroxylation GO:0010642~negative regulation of platelet–derived growth factor receptor signaling pathway GO:0009650~UV protection GO:0031100~animal organ regeneration GO:0043413~macromolecule glycosylation — GO:0006486~protein glycosylation — GO:0046165~alcohol biosynthetic process — GO:0032007~negative regulation of TOR signaling GO:2001056~positive regulation of cysteine–type endopeptidase activity — GO:0051092~positive regulation of NF-kappaB transcription factor activity — GO:0050773~regulation of dendrite development — GO:0009267~cellular response to starvation — GO:0043434~response to peptide hormone — GO:0043473~pigmentation GO:0005977~glycogen metabolic process GO:0072659~protein localization to plasma membrane — GO:0031396~regulation of protein ubiquitination — GO:0046471~phosphatidylglycerol metabolic process GO:0032786~positive regulation of DNA-templated transcription, elongation GO:0008214~protein dealkylation GO:0006506~GPI anchor biosynthetic process GO:0006482~protein demethylation GO:0006363~termination of RNA polymerase I transcription GO:0002082~regulation of oxidative phosphorylation GO:0010008~endosome membrane GO:0061695~transferase complex, transferring phosphorus-containing groups GO:1902911~protein kinase complex GO:0001726~ruffle GO:0031252~cell leading edge GO:1902554~serine/threonine protein kinase complex GO:0031519~PcG protein complex GO:0030014~CCR4-NOT complex GO:0005635~nuclear envelope — GO:0043296~apical junction complex GO:0000407~phagophore assembly site GO:0005923~bicellular tight junction GO:0030175~filopodium GO:0030027~lamellipodium GO:0005793~endoplasmic reticulum–Golgi intermediate compartment GO:0016461~unconventional myosin complex GO:0070160~tight junction GO:0005819~spindle GO:0072686~mitotic spindle GO:0000421~autophagosome membrane GO:0005776~autophagosome GO:0032587~ruffle membrane GO:0005802~trans–Golgi network GO:0000307~cyclin-dependent protein kinase holoenzyme complex GO:0031588~nucleotide-activated protein kinase complex GO:0005774~vacuolar membrane — GO:0017053~transcriptional repressor complex GO:0000932~P-body GO:0031083~BLOC-1 complex GO:0055029~nuclear DNA-directed RNA polymerase complex GO:0000428~DNA-directed RNA polymerase complex GO:0016607~nuclear speck — GO:0005884~actin filament GO:0030880~RNA polymerase complex GO:0045178~basal part of cell GO:0005769~early endosome — GO:0000922~spindle pole GO:0044232~organelle membrane contact site GO:0031082~BLOC complex GO:0030496~midbody — GO:0031463~Cul3-RING ubiquitin ligase complex GO:0031901~early endosome membrane -GO:0000118~histone deacetylase complex GO:0005798~Golgi-associated vesicle GO:0005876~spindle microtubule GO:0031227~intrinsic component of endoplasmic reticulum membrane — GO:0036464~cytoplasmic ribonucleoprotein granule GO:0031902~late endosome membrane GO:0031301~integral component of organelle membrane GO:0000776~kinetochore GO:0090575~RNA polymerase II transcription factor complex GO:0016459~myosin complex GO:0005643~nuclear pore GO:0099023~tethering complex GO:0000775~chromosome, centromeric region GO:0035770~ribonucleoprotein granule GO:1990907~beta-catenin-TCF complex GO:0031932~TORC2 complex GO:0032588~trans-Golgi network membrane GO:0090543~Flemming body GO:0005770~late endosome -GO:0044798~nuclear transcription factor complex — GO:0030008~TRAPP complex GO:0055037~recycling endosome — GO:0005795~Golgi stack — GO:0030176~integral component of endoplasmic reticulum membrane — GO:0043292~contractile fiber GO:0044233~Mitochondria-associated ER Membrane GO:0016580~Sin3 complex GO:0016605~PML body -GO:0019898~extrinsic component of membrane — GO:0098858~actin-based cell projection — GO:0031300~intrinsic component of organelle membrane — GO:1902555~endoribonuclease complex GO:1905348~endonuclease complex GO:0038201~TOR complex GO:0010369~chromocenter GO:0004674~protein serine/threonine kinase activity GO:0042393~histone binding GO:0004693~cyclin-dependent protein serine/threonine kinase activity GO:0097472~cyclin-dependent protein kinase activity GO:0016780~phosphotransferase activity, for other substituted phosphate groups GO:0016646~oxidoreductase activity, acting on the CH-NH group of donors, NAD or NADP as acceptor GO:0004725~protein tyrosine phosphatase activity GO:0070513~death domain binding GO:0004016~adenylate cyclase activity GO:0034593~phosphatidylinositol bisphosphate phosphatase activity GO:0017110~nucleoside-diphosphatase activity GO:0004438~phosphatidylinositol-3-phosphatase activity GO:0003713~transcription coactivator activity — GO:0052744~phosphatidylinositol monophosphate phosphatase activity GO:0032454~histone demethylase activity (H3–K9 specific) GO:0019887~protein kinase regulator activity GO:0004721~phosphoprotein phosphatase activity GO:0003899~DNA-directed 5'-3' RNA polymerase activity GO:0030371~translation repressor activity GO:0019207~kinase regulator activity -GO:0052866~phosphatidylinositol phosphate phosphatase activity GO:0016645~oxidoreductase activity, acting on the CH–NH group of donors GO:0097747~RNA polymerase activity GO:0034062~5'-3' RNA polymerase activity GO:0016706~oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors GO:0016758~transferase activity, transferring hexosyl groups — GO:0070402~NADPH binding GO:0050700~CARD domain binding GO:0017016~Ras GTPase binding — GO:0047485~protein N-terminus binding GO:0031267~small GTPase binding — GO:0016705~oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen — • GO:0016779~nucleotidyltransferase activity GO:0042578~phosphoric ester hydrolase activity — GO:0001091~RNA polymerase II basal transcription factor binding GO:0019208~phosphatase regulator activity GO:0070530~K63-linked polyubiquitin modification-dependent protein binding GO:0070063~RNA polymerase binding GO:0003779~actin binding — GO:0140030~modification-dependent protein binding -GO:0016791~phosphatase activity GO:0035091~phosphatidylinositol binding — GO:0016849~phosphorus-oxygen lyase activity GO:0009975~cyclase activity GO:0005158~insulin receptor binding GO:0000146~microfilament motor activity GO:0016627~oxidoreductase activity, acting on the CH-CH group of donors GO:0045182~translation regulator activity GO:0017137~Rab GTPase binding GO:0016757~transferase activity, transferring glycosyl groups— GO:0051400~BH domain binding GO:0004860~protein kinase inhibitor activity GO:0004712~protein serine/threonine/tyrosine kinase activity GO:0019209~kinase activator activity GO:0051019~mitogen-activated protein kinase binding GO:0016628~oxidoreductase activity, acting on the CH-CH group of donors, NAD or NADP as acceptor GO:0140034~methylation-dependent protein binding GO:0035064~methylated histone binding GO:0016813~hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in linear amidines GO:0005225~volume-sensitive anion channel activity GO:0004865~protein serine/threonine phosphatase inhibitor activity GO:0032452~histone demethylase activity GO:0019210~kinase inhibitor activity GO:0080025~phosphatidylinositol-3,5-bisphosphate binding GO:0004114~3',5'-cyclic-nucleotide phosphodiesterase activity GO:0042975~peroxisome proliferator activated receptor binding GO:0031543~peptidyl-proline dioxygenase activity GO:0030898~actin-dependent ATPase activity GO:0004115~3',5'-cyclic-AMP phosphodiesterase activity GO:0051213~dioxygenase activity GO:0046966~thyroid hormone receptor binding GO:0033764~steroid dehydrogenase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor GO:0004112~cyclic–nucleotide phosphodiesterase activity GO:0016538~cyclin-dependent protein serine/threonine kinase regulator activity 3 12 Fold Enrichment

Homo sapiens, Sourced: 2019-Jul10