actin filament binding, GO:0051015 transcription initiation from RNA polymerase II promoter, GO:0006367 rhythmic process, GO:0048511 protein N-terminus binding, GO:0047485 peroxisome, GO:0005777 protein complex assembly, GO:0006461 transcription factor complex, GO:0005667 kinase binding, GO:0019900 peptidyl-tyrosine phosphorylation, GO:0018108 cell-cell junction, GO:0005911 response to oxidative stress, GO:0006979 positive regulation of type I interferon production, GO:0032481 protein tyrosine kinase activity, GO:0004713 response to organic cyclic compound, GO:0014070 histone deacetylase binding, GO:0042826 positive regulation of cell migration, GO:0030335 transcription cofactor activity, GO:0003712 bicellular tight junction, GO:0005923 transcription factor TFIID complex, GO:0005669 cytoskeletal protein binding, GO:0008092 actin filament organization, GO:0007015 hemopoiesis, GO:0030097 protein phosphatase binding, GO:0019903 cellular response to hypoxia, GO:0071456 peroxisomal 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homeostasis, GO:0042593 cellular response to glucose starvation, GO:0042149 embryonic organ development, GO:0048568 positive regulation of cysteine-type endopeptidase activity involved in apoptotic process, GO:0043280 protein self-association, GO:0043621 actin filament, GO:0005884 cortical actin cytoskeleton, GO:0030864 non-membrane spanning protein tyrosine kinase activity, GO:0004715 response to estrogen, GO:0043627 post-embryonic development, GO:0009791 peptidyl-tyrosine autophosphorylation, GO:0038083 regulation of molecular function, GO:0065009 T-tubule, GO:0030315 learning, GO:0007612 regulation of protein localization, GO:0032880 telomeric DNA binding, GO:0042162 T cell costimulation, GO:0031295 ciliary tip, GO:0097542 wound healing, GO:0042060 histone H4 acetylation, GO:0043967 sarcolemma, GO:0042383 estrogen receptor binding, GO:0030331 potassium ion transport, GO:0006813 protein kinase C binding, GO:0005080 repressing transcription factor binding, GO:0070491 fat cell differentiation, GO:0045444 substrate adhesion-dependent cell spreading, GO:0034446 cell-matrix adhesion, GO:0007160 core promoter sequence-specific DNA binding, GO:0001046 response to wounding, GO:0009611 immunological synapse, GO:0001772 response to antibiotic, GO:0046677 positive regulation of actin filament polymerization, GO:0030838 nuclear euchromatin, GO:0005719 cellular response to growth factor stimulus, GO:0071363 adherens junction organization, GO:0034332 viral budding via host ESCRT complex, GO:0039702 extracellular vesicle, GO:1903561 dendrite development, GO:0016358 negative regulation of ERK1 and ERK2 cascade, GO:0070373 sensory perception of sound, GO:0007605 response to hydrogen peroxide, GO:0042542 regulation of cardiac conduction, GO:1903779 dorsal/ventral pattern formation, GO:0009953 neuron differentiation, GO:0030182 response to interferon-gamma, GO:0034341 negative regulation of DNA binding, GO:0043392 protease binding, GO:0002020 platelet formation, GO:0030220 intracellular steroid hormone receptor signaling pathway, GO:0030518 response to interleukin-1, GO:0070555 regulation of cell motility, GO:2000145 nucleus organization, GO:0006997 T cell differentiation in thymus, GO:0033077 protein phosphatase 1 binding, GO:0008157 response to cAMP, GO:0051591 cellular response to epidermal growth factor stimulus, GO:0071364 cell separation after cytokinesis, GO:0000920 positive regulation of cell death, GO:0010942 ubiquitin-dependent protein catabolic process via the multivesicular body sorting pathway, GO:0043162 negative regulation of sequence-specific DNA binding transcription factor activity, GO:0043433 cellular senescence, GO:0090398 JAK-STAT cascade, GO:0007259 positive regulation of phosphorylation, GO:0042327 beta-catenin destruction complex, GO:0030877 RNA polymerase II transcription factor binding, GO:0001085 regulation of exocytosis, GO:0017157 intraciliary transport particle B, GO:0030992 response to retinoic acid, GO:0032526 S100 protein 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transcription from RNA polymerase II promoter in response to endoplasmic reticulum stress, GO:1990440 apicolateral plasma membrane, GO:0016327 small protein activating enzyme activity, GO:0008641 cellular response to fluid shear stress, GO:0071498 regulation of stress-activated MAPK cascade, GO:0032872 phosphatidylinositol 3-kinase binding, GO:0043548 oogenesis, GO:0048477 positive regulation of nitric-oxide synthase activity, GO:0051000 embryonic viscerocranium morphogenesis, GO:0048703 negative regulation of macrophage derived foam cell differentiation, GO:0010745 positive regulation of transforming growth factor beta receptor signaling pathway, GO:0030511 dendritic spine membrane, GO:0032591 vocalization behavior, GO:0071625 microvillus membrane, GO:0031528 positive regulation of synaptic transmission, GO:0051968 embryonic hindlimb morphogenesis, GO:0035116 regulation of heart contraction, GO:0008016 establishment of planar polarity, GO:0001736 cellular sodium ion homeostasis, GO:0006883 negative regulation of phagocytosis, GO:0050765 negative regulation of oxidative stress-induced neuron death, GO:1903204 negative regulation of endothelial cell apoptotic process, GO:2000352 placenta blood vessel development, GO:0060674 negative regulation of receptor internalization, GO:0002091 spinal cord development, GO:0021510 cellular response to interferon-gamma, GO:0071346 respiratory burst, GO:0045730 SUMO transferase activity, GO:0019789 B cell differentiation, GO:0030183 regulation of calcium ion transport, GO:0051924 MMXD complex, GO:0071817 somatic recombination of immunoglobulin gene segments, GO:0016447 response to hydroperoxide, GO:0033194 cAMP response element binding protein binding, GO:0008140 core TFIIH complex, GO:0000439 positive regulation of lipopolysaccharide-mediated signaling pathway, GO:0031666 ubiquitin-protein transferase activator activity, GO:0097027 erythrocyte maturation, GO:0043249 cytoskeletal anchoring at plasma membrane, GO:0007016 positive regulation of axonogenesis, GO:0050772 nucleotide-activated protein kinase complex, GO:0031588 armadillo repeat domain binding, GO:0070016 long-term synaptic potentiation, GO:0060291 AMP-activated protein kinase activity, GO:0004679 relaxation of cardiac muscle, GO:0055119 viral budding, GO:0046755 positive regulation of interleukin-8 biosynthetic process, GO:0045416 negative regulation of osteoblast differentiation, GO:0045668 calcium channel regulator activity, GO:0005246 fibronectin binding, GO:0001968 alpha-actinin binding, GO:0051393 potassium ion import, GO:0010107 mesoderm development, GO:0007498 DNA N-glycosylase activity, GO:0019104 cell fate determination, GO:0001709 HMG box domain binding, GO:0071837 plasma membrane organization, GO:0007009 synaptic vesicle exocytosis, GO:0016079 carnitine shuttle, GO:0006853 membrane repolarization, GO:0086009 regulation of receptor activity, GO:0010469 branching involved in ureteric bud morphogenesis, GO:0001658 regulation of myelination, GO:0031641 sympathetic ganglion development, GO:0061549 nuclear telomere cap complex, GO:0000783 telomere maintenance via telomere lengthening, GO:0010833 transcription cofactor binding, GO:0001221 co-SMAD binding, GO:0070410 mammary gland alveolus development, GO:0060749 arachidonic acid binding, GO:0050544 thioredoxin peroxidase activity, GO:0008379 small protein activating enzyme binding, GO:0044388 positive regulation of regulated secretory pathway, GO:1903307 positive regulation of phagocytosis, GO:0060100 spectrin-associated cytoskeleton, GO:0014731 peroxiredoxin activity, GO:0051920 depyrimidination, GO:0045008 protein tag, GO:0031386 actin monomer binding, GO:0003785 blood vessel endothelial cell migration, GO:0043534 positive regulation of potassium ion transport, GO:0043268 regulation of energy homeostasis, GO:2000505 response to molecule of bacterial origin, GO:0002237 postsynaptic density membrane, GO:0098839 chondrocyte proliferation, GO:0035988 positive regulation of G-protein coupled receptor protein signaling pathway, GO:0045745 LBD domain binding, GO:0050693 establishment of protein localization to telomere, GO:0070200 trachea formation, GO:0060440 negative regulation of cholesterol storage, GO:0010887 proteolysis in other organism, GO:0035897 response to sucrose, GO:0009744 cytoskeletal adaptor activity, GO:0008093 I-SMAD binding, GO:0070411 IkappaB kinase complex, GO:0008385 tissue homeostasis, GO:0001894 transcriptional activator activity, GO:0001190 DNA binding, GO:0008301 peroxisome proliferator activated receptor signaling pathway, GO:0035357 filamin binding, GO:0031005 protein polymerization, GO:0051258