

Bioconductor Affymetrix Probe Listing

| Probe | Symbol | Description | Chromosome | Chromosome Location | GenBank | Gene | Cytoband | PubMed | Gene Ontology | Pathway |
|-------------------------|--------|--------------------------------|------------|--|------------------------|-----------------------|----------------------|---------------------|---|---------|
| 1134_at | TNK2 | tyrosine kinase non receptor 2 | 3 | -195863363, -195863363, -195863363, -195863363, -195863363 | L13738 | 10188 | 3q29 | 140 | nucleotide binding protein kinase activity protein serine/threonine kinase activity protein serine/threonine/tyrosine kinase activity protein serine/threonine/tyrosine kinase activity protein tyrosine kinase activity protein tyrosine kinase activity protein tyrosine kinase activity non-membrane spanning protein tyrosine kinase activity non-membrane spanning protein tyrosine kinase activity GTPase inhibitor activity epidermal growth factor receptor binding protein binding ATP binding nucleus nucleus cytoplasm cytoplasm endosome endosome cytosol cytosol plasma membrane plasma membrane plasma membrane clathrin-coated pit clathrin-coated pit adherens junction endocytosis signal transduction cell surface receptor signaling pathway small GTPase-mediated signal transduction membrane membrane kinase activity phosphorylation transferase activity clathrin-coated vesicle clathrin-coated vesicle cytoplasmic vesicle membrane cytoplasmic vesicle ubiquitin protein ligase binding identical protein binding metal ion binding perinuclear region of cytoplasm WW domain binding positive regulation of peptidyl-tyrosine phosphorylation | |

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|---------------------------|--------|------------------------------------|---|--|------------------------|----------------------|------------------------|---------------------|---|--|
| | | | | | | | | | anchoring junction Grb2-EGFR complex cytoophidium protein serine kinase activity regulation of clathrin-dependent endocytosis | |
| 1202_g_at | RAB33A | RAB33A, member RAS oncogene family | X | 130171961 | D14889 | 9363 | Xq26.1 | 22 | autophagosome assembly Golgi membrane nucleotide binding GTPase activity GTPase activity GTPase activity protein binding GTP binding GTP binding endosome Golgi apparatus Golgi apparatus plasma membrane membrane hydrolase activity antigen processing and presentation Rab protein signal transduction metal ion binding | |
| 1213_at | SRPK2 | SRSF protein kinase 2 | 7 | -105116373, -105116373, -105116373, -105116373, -105116373 | U88666 | 6733 | 7q22.3 | 138 | nucleotide binding spliceosomal complex assembly spliceosomal complex assembly spliceosomal complex assembly magnesium ion binding magnesium ion binding chromatin angiogenesis RNA binding protein kinase activity protein serine/threonine kinase activity protein serine/threonine kinase activity protein serine/threonine kinase activity protein serine/threonine kinase activity protein binding ATP binding ATP binding nucleus nucleus nucleus nucleoplasm nucleoplasm chromosome nucleolus cytoplasm cytoplasm cytosol cytosol mRNA processing protein phosphorylation positive regulation of cell population proliferation positive regulation of cell population proliferation RNA splicing RNA splicing | |

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|---------------------------|-----|-----------------|----|------------------------------------|------------------------|----------------------|-------------------------|---------------------|---|--|--|
| | | | | | | | | | | regulation of gene expression positive regulation of gene expression kinase activity nuclear speck nuclear speck transferase activity peptidyl-serine phosphorylation cell differentiation nuclear speck organization intracellular signal transduction intracellular signal transduction intracellular signal transduction phosphatidylinositol 3-kinase/protein kinase B signal transduction positive regulation of neuron apoptotic process positive regulation of viral genome replication negative regulation of viral genome replication innate immune response positive regulation of cell cycle regulation of mRNA splicing, via spliceosome regulation of mRNA processing R-loop processing 14-3-3 protein binding presynapse protein serine kinase activity | |
| 1236 s at | NF1 | neurofibromin 1 | 17 | 31094926, 31094976, 31094976 | M89914 | 4763 | 17q11.2 | 639 | MAPK cascade MAPK cascade angiogenesis osteoblast differentiation osteoblast differentiation metanephros development metanephros development response to hypoxia response to hypoxia liver development liver development endothelial cell proliferation negative regulation of endothelial cell proliferation negative regulation of endothelial cell proliferation positive regulation of endothelial cell proliferation regulation of cell-matrix adhesion regulation of cell-matrix adhesion negative regulation of cell-matrix adhesion negative regulation of leukocyte migration GTPase activator activity | 04010 | |

[GTPase activator activity](#)
[GTPase activator activity](#)
[protein binding](#)
[nucleus](#)
[nucleus](#)
[nucleoplasm](#)
[nucleolus](#)
[cytoplasm](#)
[cytoplasm](#)
[cytosol](#)
[plasma membrane](#)
[plasma membrane](#)
[protein import into nucleus](#)
[apoptotic process](#)
[cell communication](#)
[cell communication](#)
[Ras protein signal transduction](#)
[Ras protein signal transduction](#)
[neurotransmitter secretion](#)
[neuroblast proliferation](#)
[negative regulation of neuroblast proliferation](#)
[negative regulation of neuroblast proliferation](#)
[brain development](#)
[brain development](#)
[peripheral nervous system development](#)
[peripheral nervous system development](#)
[heart development](#)
[heart development](#)
[skeletal muscle tissue development](#)
[cell population proliferation](#)
[negative regulation of cell population proliferation](#)
[lipid binding](#)
[phosphatidylethanolamine binding](#)
[visual learning](#)
[visual learning](#)
[extrinsic apoptotic signaling pathway via death domain receptors](#)
[regulation of gene expression](#)
[negative regulation of Schwann cell proliferation](#)
[glial cell proliferation](#)
[Schwann cell proliferation](#)
[Schwann cell development](#)
[membrane](#)
[membrane](#)
[cell migration](#)
[negative regulation of angiogenesis](#)
[Rac protein signal transduction](#)
[spinal cord development](#)
[spinal cord development](#)
[amygdala development](#)
[forebrain astrocyte development](#)

[forebrain astrocyte development](#)
[neural tube development](#)
[cerebral cortex development](#)
[cerebral cortex development](#)
[myelination in peripheral nervous system](#)
[myelination in peripheral nervous system](#)
[actin cytoskeleton organization](#)
[actin cytoskeleton organization](#)
[extracellular matrix organization](#)
[extracellular matrix organization](#)
[collagen fibril organization](#)
[collagen fibril organization](#)
[osteoclast differentiation](#)
[adrenal gland development](#)
[adrenal gland development](#)
[negative regulation of cell migration](#)
[axon](#)
[dendrite](#)
[phosphatidylcholine binding](#)
[regulation of synaptic transmission](#)
[GABAergic](#)
[mast cell apoptotic process](#)
[positive regulation of mast cell apoptotic process](#)
[myeloid cell apoptotic process](#)
[positive regulation of myeloid cell apoptotic process](#)
[cellular response to heat](#)
[negative regulation of Rac protein signal transduction](#)
[Schwann cell migration](#)
[wound healing](#)
[wound healing](#)
[regulation of cell population proliferation](#)
[negative regulation of protein import into nucleus](#)
[positive regulation of apoptotic process](#)
[positive regulation of apoptotic process](#)
[regulation of MAPK cascade](#)
[negative regulation of MAPK cascade](#)
[negative regulation of MAPK cascade](#)
[negative regulation of MAPK cascade](#)
[pigmentation](#)
[pigmentation](#)

[phosphatidylinositol 3-kinase/protein kinase B signal transduction](#)
[phosphatidylinositol 3-kinase/protein kinase B signal transduction](#)
[positive regulation of neuron apoptotic process](#)
[positive regulation of neuron apoptotic process](#)
[regulation of blood vessel endothelial cell migration](#)
[positive regulation of GTPase activity](#)
[positive regulation of GTPase activity](#)
[regulation of bone resorption](#)
[regulation of bone resorption](#)
[negative regulation of osteoclast differentiation](#)
[regulation of glial cell differentiation](#)
[regulation of glial cell differentiation](#)
[regulation of angiogenesis](#)
[regulation of angiogenesis](#)
[negative regulation of Ras protein signal transduction](#)
[negative regulation of neurotransmitter secretion](#)
[fibroblast proliferation](#)
[negative regulation of fibroblast proliferation](#)
[negative regulation of fibroblast proliferation](#)
[regulation of long-term neuronal synaptic plasticity](#)
[sympathetic nervous system development](#)
[sympathetic nervous system development](#)
[camera-type eye morphogenesis](#)
[camera-type eye morphogenesis](#)
[astrocyte differentiation](#)
[oligodendrocyte differentiation](#)
[negative regulation of astrocyte differentiation](#)
[negative regulation of oligodendrocyte differentiation](#)
[negative regulation of oligodendrocyte differentiation](#)
[smooth muscle tissue development](#)
[smooth muscle tissue development](#)
[hair follicle maturation](#)
[artery morphogenesis](#)
[artery morphogenesis](#)
[forebrain morphogenesis](#)
[forebrain morphogenesis](#)

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|---------------------------|-------|-----------|---|-------------------------|------------------------|---------------------|----------------------|-----|--|--|
| | | | | | | | | | regulation of developmental process cognition neuron apoptotic process negative regulation of glial cell proliferation long-term synaptic potentiation gamma-aminobutyric acid secretion , neurotransmission glutamate secretion , neurotransmission regulation of ERK1 and ERK2 cascade mast cell proliferation negative regulation of mast cell proliferation leukocyte apoptotic process stem cell proliferation extrinsic apoptotic signaling pathway in absence of ligand myeloid leukocyte migration observational learning presynapse glutamatergic synapse regulation of postsynapse organization negative regulation of Schwann cell migration regulation of long-term synaptic potentiation regulation of intracellular signal transduction positive regulation of vascular associated smooth muscle cell proliferation vascular associated smooth muscle cell migration negative regulation of vascular associated smooth muscle cell migration vascular associated smooth muscle cell proliferation positive regulation of leukocyte apoptotic process negative regulation of stem cell proliferation positive regulation of extrinsic apoptotic signaling pathway in absence of ligand | |
| 1239_s_at | CASP2 | caspase 2 | 7 | 143289587, 143288350 | U13021 | 835 | 7q34 | 198 | luteolysis neural retina development cysteine-type endopeptidase activity cysteine-type endopeptidase activity cysteine-type endopeptidase activity cysteine-type endopeptidase activity protein binding nucleus nucleus | |

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|-------------------------|--------|--------------------------------|---|----------|------------------------|----------------------|------------------------|--------------------|---|--|
| | | | | | | | | | nucleolus cytoplasm cytoplasm cytosol proteolysis apoptotic process apoptotic process apoptotic process <u>DNA damage response</u> peptidase activity <u>cysteine-type peptidase activity</u> <u>intrinsic apoptotic signaling pathway in response to DNA damage</u> <u>intrinsic apoptotic signaling pathway in response to DNA damage</u> protein processing hydrolase activity enzyme binding protein domain specific binding <u>DNA damage response, signal transduction by p53 class mediator</u> <u>ectopic germ cell programmed cell death</u> <u>identical protein binding</u> <u>regulation of apoptotic process</u> <u>positive regulation of apoptotic process</u> <u>positive regulation of apoptotic process</u> <u>positive regulation of apoptotic process</u> <u>negative regulation of apoptotic process</u> <u>positive regulation of neuron apoptotic process</u> <u>positive regulation of neuron apoptotic process</u> protein maturation cellular response to mechanical stimulus apoptotic signaling pathway apoptotic signaling pathway <u>extrinsic apoptotic signaling pathway in absence of ligand</u> <u>extrinsic apoptotic signaling pathway in absence of ligand</u> <u>execution phase of apoptosis</u> endopeptidase complex positive regulation of apoptotic signaling pathway | |
| 1254_at | GUCA1A | guanylate cyclase activator 1A | 6 | 42173363 | L36861 | 2978 | 6p21.1 | 59 | photoreceptor outer segment photoreceptor inner segment photoreceptor inner segment | 04740 04744 |

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|-------------------------|-------|-------------------------------|---|----------------------|------------------------|----------------------|------------------------|---------------------|---|--|--|
| | | | | | | | | | | photoreceptor inner segment calcium ion binding calcium ion binding calcium ion binding protein binding signal transduction visual perception visual perception visual perception phototransduction calcium sensitive guanylate cyclase activator activity regulation of signal transduction positive regulation of cGMP-mediated signaling membrane guanylate cyclase regulator activity guanylate cyclase regulator activity guanylate cyclase regulator activity guanylate cyclase regulator activity positive regulation of guanylate cyclase activity cell projection metal ion binding cellular response to calcium ion photoreceptor disc membrane photoreceptor disc membrane cone photoreceptor outer segment cone photoreceptor outer segment cone photoreceptor outer segment | |
| 1310_at | PSMB2 | proteasome 20S subunit beta 2 | 1 | -35599540, -35599540 | D26599 | 5690 | 1p34.3 | 198 | proteasome complex proteasome complex proteasome complex proteasome complex protein binding nucleus nucleus nucleus nucleus nucleoplasm nucleoplasm cytoplasm cytoplasm cytosol cytosol proteasome core complex proteasome core complex proteasome core complex proteasomal protein catabolic process | 03050 | |

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|---------------------------|-------|--------------------------------|---|----------|------------------------|----------------------|------------------------|----------------------|--|--|
| | | | | | | | | | membrane proteasome core complex , beta-subunit complex proteasome core complex , beta-subunit complex proteasome-mediated ubiquitin-dependent protein catabolic process proteasome-mediated ubiquitin-dependent protein catabolic process proteolysis involved in protein catabolic process extracellular exosome | |
| 1369 s at | CXCL8 | C-X-C motif chemokine ligand 8 | 4 | 73740568 | M28130 | 3576 | 4q13.3 | 2500 | angiogenesis response to molecule of bacterial origin cytokine activity interleukin-8 receptor binding protein binding extracellular region extracellular region extracellular space extracellular space extracellular space chemotaxis chemotaxis defense response inflammatory response inflammatory response inflammatory response immune response signal transduction G protein-coupled receptor signaling pathway chemokine activity chemokine activity chemokine activity heparin binding negative regulation of cell population proliferation positive regulation of gene expression negative regulation of gene expression calcium-mediated signaling regulation of cell adhesion neutrophil chemotaxis neutrophil chemotaxis neutrophil chemotaxis receptor internalization killing of cells of another organism response to endoplasmic reticulum stress intracellular signal transduction neutrophil activation neutrophil activation cellular response to fibroblast growth factor stimulus regulation of single stranded viral RNA replication via double stranded DNA intermediate | 04060 04062 04620 04621 04622 05120 05131 05142 05144 05146 05160 05200 05219 05323 |

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|-------------------------|-------|----------------------------------|---|-------------------------|------------------------|----------------------|----------------------|---|--|---|
| | | | | | | | | CXCR chemokine receptor binding negative regulation of G protein-coupled receptor signaling pathway positive regulation of angiogenesis embryonic digestive tract development induction of positive chemotaxis negative regulation of cell adhesion molecule production antimicrobial humoral immune response mediated by antimicrobial peptide antimicrobial humoral immune response mediated by antimicrobial peptide cellular response to lipopolysaccharide cellular response to lipopolysaccharide cellular response to interleukin-1 cellular response to tumor necrosis factor positive regulation of neutrophil chemotaxis regulation of entry of bacterium into host cell | | |
| 1377 at | NFKB1 | nuclear factor kappa B subunit 1 | 4 | 102501358, 102501933 | M58603 | 4790 | 4q24 | 3390 | negative regulation of transcription by RNA polymerase II negative regulation of transcription by RNA polymerase II MAPK cascade MAPK cascade chromatin chromatin chromatin transcription cis-regulatory region binding RNA polymerase II transcription regulatory region sequence-specific DNA binding RNA polymerase II cis-regulatory region sequence-specific DNA binding RNA polymerase II cis-regulatory region sequence-specific DNA binding RNA polymerase II cis-regulatory region sequence-specific DNA binding DNA-binding transcription factor activity, RNA polymerase II-specific DNA-binding transcription factor | 04010 04062 04210 04380 04620 04621 04622 04623 04660 04662 04722 04920 05120 05131 05140 05142 05145 05146 05160 05200 05212 05215 05220 05221 05222 |

activity, RNA
polymerase II-specific
DNA-binding
transcription factor
activity, RNA
polymerase II-specific
DNA-binding
transcription factor
activity, RNA
polymerase II-specific
transcription coactivator
binding
DNA-binding
transcription repressor
activity, RNA
polymerase II-specific
DNA-binding
transcription activator
activity, RNA
polymerase II-specific
DNA-binding
transcription activator
activity, RNA
polymerase II-specific
negative regulation of
cytokine production
immune system process
DNA binding
chromatin binding
DNA-binding
transcription factor
activity
DNA-binding
transcription factor
activity
transcription coregulator
activity
protein binding
extracellular region
nucleus
nucleus
nucleus
nucleoplasm
nucleoplasm
transcription regulator
complex
cytoplasm
cytoplasm
cytoplasm
cytoplasm
mitochondrion
cytosol
cytosol
cytosol
regulation of DNA-
templated transcription
regulation of transcription
by RNA polymerase II
transcription by RNA
polymerase II
apoptotic process
inflammatory response
inflammatory response
signal transduction
canonical NF-kappaB
signal transduction
JNK cascade
gene expression
regulation of gene
expression
positive regulation of
macromolecule

[biosynthetic process](#)
[negative regulation of gene expression](#)
[positive regulation of macrophage derived foam cell differentiation](#)
[positive regulation of cholesterol efflux](#)
[positive regulation of lipid storage](#)
[negative regulation of vitamin D biosynthetic process](#)
[signal transduction](#)
[involved in regulation of gene expression](#)
[negative regulation of interleukin-12 production](#)
[tumor necrosis factor-mediated signaling pathway](#)
[I-kappaB/NF-kappaB complex](#)
[I-kappaB/NF-kappaB complex](#)
[secretory granule lumen](#)
[NF-kappaB p50/p65 complex](#)
[NF-kappaB p50/p65 complex](#)
[specific granule lumen](#)
[response to muscle stretch](#)
[non-canonical NF-kappaB signal transduction](#)
[identical protein binding](#)
[identical protein binding](#)
[actinin binding](#)
[negative regulation of apoptotic process](#)
[sequence-specific DNA binding](#)
[negative regulation of DNA-templated transcription](#)
[positive regulation of transcription by RNA polymerase II](#)
[positive regulation of transcription by RNA polymerase II](#)
[positive regulation of transcription by RNA polymerase II](#)
[negative regulation of inflammatory response](#)
[negative regulation of inflammatory response](#)
[positive regulation of inflammatory response](#)

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|-------------------------|-------|---|---|-----------|------------------------|----------------------|------------------------|---------------------|---|
| | | | | | | | | | B cell receptor signaling pathway mammary gland involution positive regulation of transcription initiation by RNA polymerase II cellular response to lipopolysaccharide cellular response to lipopolysaccharide cellular response to mechanical stimulus cellular response to nicotine cellular response to cytokine stimulus cellular response to interleukin-6 cellular response to tumor necrosis factor cellular response to dsRNA positive regulation of canonical Wnt signaling pathway cellular response to interleukin-17 cellular response to virus protein sequestering activity antibacterial innate immune response negative regulation of cytokine production involved in inflammatory response positive regulation of hyaluronan biosynthetic process cellular response to angiotensin positive regulation of miRNA metabolic process |
| 1385 at | TGFBI | transforming growth factor beta induced | 5 | 136028987 | M77349 | 7045 | 5q31.1 | 319 | angiogenesis chondrocyte differentiation integrin binding extracellular matrix structural constituent extracellular matrix structural constituent protein binding collagen binding extracellular region extracellular region extracellular region basement membrane extracellular space extracellular space extracellular space extracellular space trans-Golgi network trans-Golgi network plasma membrane cell adhesion cell adhesion negative regulation of cell adhesion visual perception visual perception |

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|--------------------------|------|------------------------------|----|--|------------------------|----------------------|--------------------------|---------------------|--|
| | | | | | | | | | cell population proliferation extracellular matrix organization extracellular matrix organization extracellular matrix extracellular matrix extracellular matrix extracellular matrix identical protein binding cell adhesion molecule binding extracellular matrix binding extracellular exosome cell periphery |
| 145 s at | TBX5 | T-box transcription factor 5 | 12 | -114353929, -114353929, -114353910 | U80987 | 6910 | 12q24.21 | 161 | chromatin chromatin RNA polymerase II transcription regulatory region sequence-specific DNA binding RNA polymerase II cis-regulatory region sequence-specific DNA binding RNA polymerase II cis-regulatory region sequence-specific DNA binding RNA polymerase II cis-regulatory region sequence-specific DNA binding DNA-binding transcription factor activity, RNA polymerase II-specific DNA-binding transcription factor activity, RNA polymerase II-specific DNA-binding transcription factor activity, RNA polymerase II-specific DNA-binding transcription activator activity, RNA polymerase II-specific DNA-binding transcription activator activity, RNA polymerase II-specific cell fate specification morphogenesis of an epithelium sinoatrial node development sinoatrial node development bundle of His development bundle of His development atrioventricular bundle cell differentiation |

[atrioventricular bundle](#)
[cell differentiation](#)
[atrioventricular valve](#)
[morphogenesis](#)
[endocardial cushion](#)
[development](#)
[cardiac left ventricle](#)
[formation](#)
[cardiac left ventricle](#)
[formation](#)
[cardiac left ventricle](#)
[formation](#)
[ventricular cardiac muscle](#)
[tissue development](#)
[ventricular septum](#)
[development](#)
[ventricular septum](#)
[development](#)
[atrial septum](#)
[development](#)
[DNA binding](#)
[DNA binding](#)
[DNA-binding](#)
[transcription factor](#)
[activity](#)
[DNA-binding](#)
[transcription factor](#)
[activity](#)
[DNA-binding](#)
[transcription factor](#)
[activity](#)
[protein binding](#)
[nucleus](#)
[nucleus](#)
[nucleus](#)
[nucleoplasm](#)
[transcription regulator](#)
[complex](#)
[cytoplasm](#)
[cytoplasm](#)
[cytoplasm](#)
[regulation of DNA-](#)
[templated transcription](#)
[regulation of transcription](#)
[by RNA polymerase II](#)
[transcription by RNA](#)
[polymerase II](#)
[cell-cell signaling](#)
[cell-cell signaling](#)
[cell-cell signaling](#)
[pattern specification](#)
[process](#)
[pattern specification](#)
[process](#)
[heart development](#)
[heart development](#)
[heart development](#)
[negative regulation of cell](#)
[population proliferation](#)
[negative regulation of](#)
[epithelial to](#)
[mesenchymal transition](#)
[lung development](#)
[embryonic limb](#)
[morphogenesis](#)
[embryonic limb](#)
[morphogenesis](#)
[negative regulation of cell](#)
[migration](#)
[protein-containing](#)
[complex](#)
[protein-DNA complex](#)

[embryonic forelimb morphogenesis](#)
[embryonic forelimb morphogenesis](#)
[forelimb morphogenesis](#)
[forelimb morphogenesis](#)
[sequence-specific DNA binding](#)
[positive regulation of DNA-templated transcription](#)
[positive regulation of DNA-templated transcription](#)
[positive regulation of transcription by RNA polymerase II](#)
[positive regulation of cardioblast differentiation](#)
[cardiac muscle cell differentiation](#)
[cardiac muscle cell proliferation](#)
[pericardium development](#)
[negative regulation of cardiac muscle cell proliferation](#)
[positive regulation of cardiac muscle cell proliferation](#)
[regulation of atrial cardiac muscle cell membrane depolarization](#)
[regulation of atrial cardiac muscle cell membrane depolarization](#)
[atrial septum morphogenesis](#)
[atrioventricular node cell development](#)
[atrioventricular node cell development](#)
[atrioventricular node cell fate commitment](#)
[atrioventricular node cell fate commitment](#)
[cell migration involved in coronary vasculogenesis](#)
[RNA polymerase II-specific DNA-binding transcription factor binding](#)
[positive regulation of secondary heart field cardioblast proliferation](#)
[bundle of His cell to Purkinje myocyte communication by electrical coupling](#)
[bundle of His cell to Purkinje myocyte](#)

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|---------------------------|-----|--|---|-----------|------------------------|----------------------|------------------------|--|--|--|
| | | | | | | | | communication by electrical coupling positive regulation of cell communication by electrical coupling involved in cardiac conduction positive regulation of gap junction assembly positive regulation of gap junction assembly positive regulation of cardiac conduction positive regulation of cardiac conduction | | |
| 1473_s_at | MYB | MYB proto-oncogene, transcription factor | 6 | 135181307 | U22376 | 4602 | 6q23.3 | 367 | G1/S transition of mitotic cell cycle negative regulation of transcription by RNA polymerase II mitotic cell cycle RNA polymerase II cis-regulatory region sequence-specific DNA binding RNA polymerase II cis-regulatory region sequence-specific DNA binding RNA polymerase II cis-regulatory region sequence-specific DNA binding DNA-binding transcription factor activity, RNA polymerase II-specific DNA-binding transcription activator activity, RNA polymerase II-specific DNA-binding transcription activator activity, RNA polymerase II-specific response to hypoxia in utero embryonic development response to ischemia DNA binding DNA-binding transcription factor activity protein binding nucleus nucleus nucleus nucleoplasm nucleoplasm cytosol cytosol regulation of DNA-templated transcription regulation of DNA-templated transcription calcium ion transport regulation of gene expression skeletal muscle cell proliferation nuclear matrix stem cell division | |

myeloid cell differentiation
B cell differentiation
erythrocyte differentiation
positive regulation of collagen biosynthetic process
positive regulation of neuron apoptotic process
T-helper 2 cell differentiation
negative regulation of megakaryocyte differentiation
negative regulation of DNA-templated transcription
positive regulation of DNA-templated transcription
positive regulation of DNA-templated transcription
positive regulation of transcription by RNA polymerase II
spleen development
thymus development
embryonic digestive tract development
positive regulation of smooth muscle cell proliferation
homeostasis of number of cells
positive regulation of glial cell proliferation
myeloid cell development
cellular response to hydrogen peroxide
cellular response to retinoic acid
cellular response to interleukin-6
positive regulation of transforming growth factor beta production
WD40-repeat domain binding
RNA polymerase II transcription regulator complex
negative regulation of hematopoietic progenitor cell differentiation
positive regulation of miRNA transcription
positive regulation of hepatic stellate cell proliferation

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|---------------------------|------|--|----|--|------------------------|----------------------|-------------------------|---|--|
| | | | | | | | | cellular response to leukemia inhibitory factor positive regulation of hepatic stellate cell activation positive regulation of testosterone secretion | |
| 1545_g_at | FLT1 | fms related receptor tyrosine kinase 1 | 13 | -28368091, -28300345, -28399043, -28385548 | S77812 | 2321 | 13q12.3 | 831 | nucleotide binding angiogenesis sprouting angiogenesis monocyte chemotaxis protein kinase activity protein tyrosine kinase activity transmembrane receptor protein tyrosine kinase activity vascular endothelial growth factor receptor activity protein binding ATP binding extracellular region extracellular space extracellular space cytoplasm endosome cytosol plasma membrane plasma membrane plasma membrane plasma membrane focal adhesion chemotaxis cell surface receptor protein tyrosine kinase signaling pathway cell surface receptor protein tyrosine kinase signaling pathway positive regulation of cell population proliferation positive regulation of cell population proliferation actin cytoskeleton membrane kinase activity cell migration cell migration transferase activity peptidyl-tyrosine phosphorylation growth factor binding growth factor binding cell differentiation positive regulation of cell migration |

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|-------------------------|-------|-----------------------------------|----|-----------------------|------------------------|----------------------|-------------------------|---------------------|--|---|--|
| | | | | | | | | | | positive regulation of cell migration cellular response to vascular endothelial growth factor stimulus vascular endothelial growth factor receptor-1 signaling pathway placental growth factor receptor activity vascular endothelial growth factor signaling pathway regulation of cell population proliferation receptor complex receptor complex positive regulation of MAP kinase activity positive regulation of MAPK cascade positive regulation of MAPK cascade positive regulation of MAPK cascade positive regulation of angiogenesis protein autophosphorylation vascular endothelial growth factor receptor signaling pathway blood vessel morphogenesis embryonic morphogenesis positive regulation of developmental process positive regulation of phosphatidylinositol 3-kinase/protein kinase B signal transduction negative regulation of vascular endothelial cell proliferation hyaloid vascular plexus regression | |
| 1585_at | ERBB3 | erb-b2 receptor tyrosine kinase 3 | 12 | 56080107, 56080164 | M34309 | 2065 | 12q13.2 | 574 | nucleotide binding endocardial cushion development protein kinase activity transmembrane signaling receptor activity transmembrane signaling receptor activity protein binding ATP binding extracellular region extracellular space plasma membrane plasma membrane plasma membrane negative regulation of cell adhesion | 04012 04020 04144 | |

[signal transduction](#)
[cell surface receptor](#)
[protein tyrosine kinase](#)
[signaling pathway](#)
[cell surface receptor](#)
[protein tyrosine kinase](#)
[signaling pathway](#)
[cell surface receptor](#)
[protein tyrosine kinase](#)
[signaling pathway](#)
[epidermal growth factor](#)
[receptor signaling](#)
[pathway](#)
[peripheral nervous system](#)
[development](#)
[peripheral nervous system](#)
[development](#)
[heart development](#)
[basal plasma membrane](#)
[negative regulation of](#)
[signal transduction](#)
[positive regulation of](#)
[gene expression](#)
[Schwann cell](#)
[differentiation](#)
[Schwann cell](#)
[differentiation](#)
[Schwann cell](#)
[development](#)
[membrane](#)
[kinase activity](#)
[basolateral plasma](#)
[membrane](#)
[basolateral plasma](#)
[membrane](#)
[apical plasma membrane](#)
[lateral plasma membrane](#)
[transferase activity](#)
[growth factor binding](#)
[growth factor binding](#)
[cranial nerve](#)
[development](#)
[cranial nerve](#)
[development](#)
[neuron differentiation](#)
[protein tyrosine kinase](#)
[activator activity](#)
[ubiquitin protein ligase](#)
[binding](#)
[signaling receptor activity](#)
[neuregulin receptor](#)
[activity](#)
[neuregulin receptor](#)
[activity](#)
[neuregulin binding](#)
[neuregulin binding](#)
[ERBB2-ERBB3 signaling](#)
[pathway](#)
[ERBB3:ERBB2 complex](#)
[wound healing](#)
[regulation of cell](#)
[population proliferation](#)
[myelination](#)
[identical protein binding](#)
[negative regulation of](#)
[apoptotic process](#)
[ErbB-3 class receptor](#)
[binding](#)
[receptor complex](#)
[receptor complex](#)
[receptor complex](#)
[receptor complex](#)

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|-------------------------|------|----------------------------|---|-------------------------|------------------------|----------------------|------------------------|-----|---|----------------------------------|
| | | | | | | | | | positive regulation of MAPK cascade phosphatidylinositol 3-kinase/protein kinase B signal transduction negative regulation of neuron apoptotic process negative regulation of neuron apoptotic process protein heterodimerization activity positive regulation of epithelial cell proliferation negative regulation of secretion neuron apoptotic process neuron apoptotic process positive regulation of phosphatidylinositol 3-kinase/protein kinase B signal transduction positive regulation of cardiac muscle tissue development positive regulation of calcineurin-NFAT signaling cascade motor neuron apoptotic process extrinsic apoptotic signaling pathway in absence of ligand negative regulation of motor neuron apoptotic process | |
| 1593 at | FGF2 | fibroblast growth factor 2 | 4 | 122826707, 122826830 | J04513 | 2247 | 4q28.1 | 878 | angiogenesis osteoblast differentiation branching involved in ureric bud morphogenesis branching involved in ureric bud morphogenesis organ induction endothelial cell proliferation positive regulation of endothelial cell proliferation positive regulation of endothelial cell proliferation positive regulation of endothelial cell proliferation cell migration involved in sprouting angiogenesis cell migration involved in sprouting angiogenesis positive regulation of neuroblast proliferation fibroblast growth factor receptor binding fibroblast growth factor receptor binding fibroblast growth factor receptor binding cytokine activity integrin binding | 04010 04810 05200 05218 |

[protein binding](#)
[extracellular region](#)
[extracellular region](#)
[extracellular space](#)
[extracellular space](#)
[extracellular space](#)
[extracellular space](#)
[nucleus](#)
[nucleus](#)
[cytoplasm](#)
[chromatin organization](#)
[transcription by RNA polymerase II](#)
[chemotaxis](#)
[signal transduction](#)
[Ras protein signal transduction](#)
[nervous system development](#)
[neuroblast proliferation](#)
[growth factor activity](#)
[growth factor activity](#)
[growth factor activity](#)
[heparin binding](#)
[cell population proliferation](#)
[positive regulation of cell population proliferation](#)
[negative regulation of cell population proliferation](#)
[fibroblast growth factor receptor signaling pathway](#)
[embryo development ending in birth or egg hatching](#)
[animal organ morphogenesis](#)
[glial cell differentiation](#)
[positive regulation of endothelial cell migration](#)
[positive regulation of endothelial cell migration](#)
[positive regulation of gene expression](#)
[negative regulation of gene expression](#)
[negative regulation of fibroblast migration](#)
[growth factor dependent regulation of skeletal](#)

[muscle satellite cell proliferation](#)
[chemokine binding](#)
[substantia nigra development](#)
[cerebellar granule cell precursor proliferation](#)
[positive regulation of cerebellar granule cell precursor proliferation](#)
[neurogenesis](#)
[cell differentiation](#)
[hyaluronan catabolic process](#)
[lung development](#)
[regulation of cell migration](#)
[paracrine signaling](#)
[paracrine signaling](#)
[negative regulation of fibroblast growth factor receptor signaling pathway](#)
[chemoattractant activity](#)
[wound healing](#)
[wound healing](#)
[inner ear auditory receptor cell differentiation](#)
[positive regulation of cell fate specification](#)
[identical protein binding](#)
[positive regulation of MAP kinase activity](#)
[positive regulation of MAPK cascade](#)
[positive regulation of MAPK cascade](#)
[positive regulation of MAPK cascade](#)
[phosphatidylinositol 3-kinase/protein kinase B signal transduction](#)
[positive regulation of blood vessel endothelial cell migration](#)
[positive regulation of blood vessel endothelial cell migration](#)
[negative regulation of blood vessel endothelial cell migration](#)
[endothelial cell migration](#)
[response to ethanol](#)
[positive regulation of inner ear auditory receptor cell differentiation](#)
[positive regulation of osteoblast differentiation](#)
[regulation of angiogenesis](#)
[positive regulation of angiogenesis](#)
[positive regulation of angiogenesis](#)
[positive regulation of angiogenesis](#)
[positive regulation of transcription by RNA polymerase II](#)
[positive regulation of transcription by RNA polymerase II](#)

[regulation of retinal cell programmed cell death](#)
[behavioral response to ethanol](#)
[embryonic morphogenesis](#)
[positive regulation of smooth muscle cell proliferation](#)
[response to axon injury](#)
[stem cell differentiation](#)
[stem cell development](#)
[epithelial cell proliferation](#)
[positive regulation of epithelial cell proliferation](#)
[positive chemotaxis](#)
[release of sequestered calcium ion into cytosol](#)
[regulation of cell cycle](#)
[positive regulation of cell division](#)
[positive regulation of phosphatidylinositol 3-kinase/protein kinase B signal transduction](#)
[positive regulation of phosphatidylinositol 3-kinase/protein kinase B signal transduction](#)
[positive regulation of phosphatidylinositol 3-kinase/protein kinase B signal transduction](#)
[positive regulation of cardiac muscle cell proliferation](#)
[positive regulation of cardiac muscle cell proliferation](#)
[canonical Wnt signaling pathway](#)
[corticotropin hormone secreting cell differentiation](#)
[thyroid-stimulating hormone-secreting cell differentiation](#)
[neuroepithelial cell differentiation](#)
[chondroblast differentiation](#)
[mammary gland epithelial cell differentiation](#)
[angiogenesis involved in coronary vascular morphogenesis](#)
[negative regulation of wound healing](#)
[histone H3K9me2/3 reader activity](#)
[ERK1 and ERK2 cascade](#)
[positive regulation of ERK1 and ERK2 cascade](#)
[positive regulation of ERK1 and ERK2 cascade](#)
[cellular response to mechanical stimulus](#)
[stem cell proliferation](#)
[stem cell proliferation](#)

[regulation of cell migration involved in sprouting angiogenesis](#)
[positive regulation of cell migration involved in sprouting angiogenesis](#)
[positive regulation of canonical Wnt signaling pathway](#)
[receptor-receptor interaction](#)
[positive regulation of lens fiber cell differentiation](#)
[positive regulation of miRNA transcription](#)
[positive regulation of neuroepithelial cell differentiation](#)
[negative regulation of oxidative stress-induced neuron intrinsic apoptotic signaling pathway](#)
[regulation of blood vessel endothelial cell proliferation involved in sprouting angiogenesis](#)
[positive regulation of sprouting angiogenesis](#)
[positive regulation of sprouting angiogenesis](#)
[positive regulation of sprouting angiogenesis](#)
[response to wortmannin](#)
[positive regulation of vascular associated smooth muscle cell proliferation](#)
[lymphatic endothelial cell migration](#)
[positive regulation of epithelial tube formation](#)
[regulation of morphogenesis of an epithelium](#)
[positive regulation of blood vessel branching](#)
[positive regulation of vascular endothelial cell proliferation](#)
[regulation of endothelial cell chemotaxis to fibroblast growth factor](#)
[regulation of endothelial cell chemotaxis to fibroblast growth factor](#)
[regulation of endothelial cell chemotaxis to fibroblast growth factor](#)
[positive regulation of endothelial cell chemotaxis to fibroblast growth factor](#)
[positive regulation of DNA biosynthetic process](#)
[positive regulation of DNA biosynthetic process](#)
[negative regulation of stem cell proliferation](#)
[positive regulation of stem cell proliferation](#)

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|-------------------------|------|--------------------------|----|-------------------------|------------------------|-----------------------|--------------------------|-----|---|--|--|
| | | | | | | | | | | positive regulation of stem cell differentiation | |
| 1700 at | BBC3 | BCL2 binding component 3 | 19 | -47220823, -47220823 | U82987 | 27113 | 19q13.32 | 238 | release of cytochrome c from mitochondria release of cytochrome c from mitochondria protein binding mitochondrion mitochondrion mitochondrion mitochondrion mitochondrion mitochondrial outer membrane lysosome cytosol apoptotic process apoptotic process DNA damage response DNA damage response determination of adult lifespan determination of adult lifespan positive regulation of protein-containing complex assembly response to endoplasmic reticulum stress response to endoplasmic reticulum stress intrinsic apoptotic signaling pathway in response to DNA damage by p53 class mediator positive regulation of apoptotic process positive regulation of neuron apoptotic process positive regulation of neuron apoptotic process fibroblast apoptotic process ATPase binding intrinsic apoptotic signaling pathway in response to endoplasmic reticulum stress intrinsic apoptotic signaling pathway in response to endoplasmic reticulum stress intrinsic apoptotic signaling pathway in response to endoplasmic reticulum stress intrinsic apoptotic signaling pathway in response to endoplasmic reticulum stress lymphocyte apoptotic process positive regulation of lymphocyte apoptotic process T cell apoptotic process | 04115 05016 | |

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|-------------------------|-------|-----------|---|---------------------------------------|------------------------|---------------------|------------------------|---------------------|--|--|--|
| | | | | | | | | | | positive regulation of T cell apoptotic process positive regulation of thymocyte apoptotic process positive regulation of thymocyte apoptotic process cellular response to hypoxia cellular response to ionizing radiation positive regulation of release of cytochrome c from mitochondria positive regulation of release of cytochrome c from mitochondria positive regulation of release of cytochrome c from mitochondria apoptotic signaling pathway intrinsic apoptotic signaling pathway intrinsic apoptotic signaling pathway execution phase of apoptosis execution phase of apoptosis positive regulation of endoplasmic reticulum stress-induced intrinsic apoptotic signaling pathway positive regulation of establishment of protein localization to mitochondrion positive regulation of IRE1-mediated unfolded protein response positive regulation of fibroblast apoptotic process positive regulation of intrinsic apoptotic signaling pathway positive regulation of intrinsic apoptotic signaling pathway | |
| 1794 at | CCND3 | cyclin D3 | 6 | -41934932, -41934932, -41934953 | M92287 | 896 | 6p21.1 | 223 | G1/S transition of mitotic cell cycle G1/S transition of mitotic cell cycle G1/S transition of mitotic cell cycle negative regulation of transcription by RNA polymerase II cyclin-dependent protein kinase holoenzyme complex cyclin-dependent protein kinase holoenzyme complex cyclin-dependent protein kinase holoenzyme complex cyclin-dependent protein serine/threonine kinase | 04110 04115 04310 04510 04630 | |

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|-------------------------|------|----------------------------|----|-----------|------------------------|----------------------|-------------------------|--------------------|--|--|
| | | | | | | | | | activity protein binding nucleus nucleus nucleoplasm nucleoplasm cytoplasm cytoplasm microtubule organizing center cytosol signal transduction cyclin-dependent protein serine/threonine kinase regulator activity protein kinase binding protein kinase binding T cell proliferation regulation of cell population proliferation protein serine/threonine kinase activator activity cell division regulation of cell cycle cyclin-dependent protein serine/threonine kinase activator activity cyclin-dependent protein serine/threonine kinase activator activity cyclin-dependent protein serine/threonine kinase activator activity cyclin D3-CDK4 complex cyclin D3-CDK6 complex positive regulation of G1/S transition of mitotic cell cycle | |
| 1855_at | FGF3 | fibroblast growth factor 3 | 11 | -69809967 | X14445 | 2248 | 11q13.3 | 54 | fibroblast growth factor receptor binding protein binding extracellular region extracellular region extracellular space cytoplasm signal transduction cell-cell signaling growth factor activity growth factor activity growth factor activity positive regulation of cell population proliferation positive regulation of cell population proliferation positive regulation of cell population proliferation fibroblast growth factor receptor signaling pathway fibroblast growth factor receptor signaling pathway fibroblast growth factor receptor signaling pathway anatomical structure morphogenesis anatomical structure morphogenesis neurogenesis cell differentiation regulation of cell migration | 04010 04810 05200 05218 |

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|-------------------------|-----|---|---|-----------|------------------------|----------------------|------------------------|--|---|
| | | | | | | | | positive regulation of MAPK cascade | |
| | | | | | | | | regulation of developmental process | |
| | | | | | | | | regulation of multicellular organismal process | |
| | | | | | | | | positive regulation of cell division | |
| | | | | | | | | negative regulation of cardiac muscle tissue development | |
| 1895 at | JUN | Jun proto-oncogene, AP-1 transcription factor subunit | 1 | -58780790 | J04111 | 3725 | 1p32.1 | 1324 | negative regulation of transcription by RNA polymerase II |
| | | | | | | | | negative regulation of transcription by RNA polymerase II | |
| | | | | | | | | nuclear chromosome | |
| | | | | | | | | chromatin | |
| | | | | | | | | chromatin | |
| | | | | | | | | euchromatin | |
| | | | | | | | | transcription cis-regulatory region | |
| | | | | | | | | binding | |
| | | | | | | | | transcription cis-regulatory region | |
| | | | | | | | | binding | |
| | | | | | | | | RNA polymerase II cis-regulatory region | |
| | | | | | | | | sequence-specific DNA binding | |
| | | | | | | | | RNA polymerase II cis-regulatory region | |
| | | | | | | | | sequence-specific DNA binding | |
| | | | | | | | | DNA-binding | |
| | | | | | | | | transcription factor activity, RNA polymerase II-specific | |
| | | | | | | | | DNA-binding | |
| | | | | | | | | transcription factor activity, RNA polymerase II-specific | |
| | | | | | | | | DNA-binding | |
| | | | | | | | | transcription factor activity, RNA polymerase II-specific | |
| | | | | | | | | DNA-binding | |
| | | | | | | | | transcription activator activity, RNA polymerase II-specific | |
| | | | | | | | | DNA-binding | |
| | | | | | | | | transcription activator activity, RNA polymerase II-specific | |
| | | | | | | | | angiogenesis | |
| | | | | | | | | microglial cell activation | |
| | | | | | | | | liver development | |
| | | | | | | | | positive regulation of endothelial cell proliferation | |
| | | | | | | | | outflow tract morphogenesis | |
| | | | | | | | | DNA binding | |
| | | | | | | | | DNA binding | |
| | | | | | | | | chromatin binding | |

[double-stranded DNA binding](#)
[DNA-binding transcription factor activity](#)
[DNA-binding transcription factor activity](#)
[RNA binding](#)
[GTPase activator activity](#)
[protein binding](#)
[nucleus](#)
[nucleus](#)
[nucleus](#)
[nucleoplasm](#)
[nucleoplasm](#)
[transcription regulator complex](#)
[transcription regulator complex](#)
[regulation of DNA-templated transcription](#)
[regulation of transcription by RNA polymerase II](#)
[regulation of transcription by RNA polymerase II](#)
[apoptotic process](#)
[transforming growth factor beta receptor signaling pathway](#)
[JNK cascade](#)
[JNK cascade](#)
[cell population proliferation](#)
[negative regulation of cell population proliferation](#)
[response to xenobiotic stimulus](#)
[positive regulation of epithelial cell migration](#)
[transcription repressor complex](#)
[release from viral latency](#)
[enzyme binding](#)
[monocyte differentiation](#)
[axon regeneration](#)
[ubiquitin protein ligase binding](#)
[response to endoplasmic reticulum stress](#)
[leading edge cell differentiation](#)
[cAMP response element binding](#)
[transcription factor AP-1 complex](#)
[transcription factor AP-1 complex](#)
[transcription factor AP-1 complex](#)
[transcription factor AP-1 complex](#)
[response to muscle stretch](#)
[regulation of cell population proliferation](#)
[identical protein binding](#)
[positive regulation of apoptotic process](#)
[negative regulation of apoptotic process](#)
[negative regulation of DNA binding](#)

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| | | | | | | | | | | |
| 1918_at | SKI | SKI proto-oncogene | 1 | 2228318 | X15218 | 6497 | 1p36.33-p36.32 | 167 | negative regulation of neuron apoptotic process host-mediated suppression of viral transcription host-mediated activation of viral transcription ubiquitin-like protein ligase binding negative regulation of DNA-templated transcription positive regulation of DNA-templated transcription positive regulation of transcription by RNA polymerase II positive regulation of fibroblast proliferation response to steroid hormone regulation of cell cycle regulation of cell cycle SMAD protein signal transduction eyelid development in camera-type eye RNA polymerase II-specific DNA-binding transcription factor binding positive regulation of ERK1 and ERK2 cascade R-SMAD binding cellular response to calcium ion cellular response to anisomycin RNA polymerase II transcription regulator complex general transcription initiation factor binding integrated stress response signaling positive regulation of miRNA transcription positive regulation of miRNA transcription positive regulation of vascular associated smooth muscle cell proliferation sequence-specific double-stranded DNA binding positive regulation of DNA-templated transcription initiation | |

[negative regulation of transcription by RNA polymerase II](#)
[negative regulation of transcription by RNA polymerase II](#)
[RNA polymerase II cis-regulatory region](#)
[sequence-specific DNA binding](#)
[DNA-binding transcription factor activity, RNA polymerase II-specific](#)
[DNA-binding transcription repressor activity, RNA polymerase II-specific](#)
[DNA-binding transcription repressor activity, RNA polymerase II-specific](#)
[neural tube closure](#)
[lens morphogenesis in camera-type eye](#)
[protein binding](#)
[nucleus](#)
[nucleus](#)
[nucleoplasm](#)
[nucleoplasm](#)
[transcription regulator complex](#)
[transcription regulator complex](#)
[cytoplasm](#)
[cytoplasm](#)
[centrosome](#)
[transforming growth factor beta receptor signaling pathway](#)
[zinc ion binding](#)
[negative regulation of cell population proliferation](#)
[anterior/posterior axis specification](#)
[negative regulation of Schwann cell proliferation](#)
[myotube differentiation](#)
[nuclear body](#)
[PML body](#)
[PML body](#)
[transcription repressor complex](#)
[protein kinase binding](#)
[protein domain specific binding](#)
[olfactory bulb development](#)
[myelination in peripheral nervous system](#)
[positive regulation of Wnt signaling pathway](#)
[embryonic limb morphogenesis](#)
[negative regulation of transforming growth factor beta receptor signaling pathway](#)
[negative regulation of transforming growth factor beta receptor signaling pathway](#)

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|-------------------------|-------|-----------|---|-----------------------|------------------------|---------------------|------------------------|---------------------|--|--|
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| 1945_at | CCNB1 | cyclin B1 | 5 | 69167009, 69167149 | M25753 | 891 | 5q13.2 | 596 | negative regulation of transforming growth factor beta receptor signaling pathway negative regulation of transforming growth factor beta receptor signaling pathway negative regulation of transforming growth factor beta receptor signaling pathway negative regulation of BMP signaling pathway negative regulation of BMP signaling pathway negative regulation of BMP signaling pathway ubiquitin protein ligase binding negative regulation of activin receptor signaling pathway protein-containing complex somatic stem cell population maintenance identical protein binding camera-type eye development positive regulation of DNA binding nose morphogenesis negative regulation of osteoblast differentiation positive regulation of transcription by RNA polymerase II SMAD binding SMAD binding SMAD binding histone deacetylase inhibitor activity negative regulation of fibroblast proliferation camera-type eye morphogenesis skeletal muscle fiber development cell motility regulation of neurogenesis roof of mouth development cardiac muscle cell proliferation retina development in camera-type eye face morphogenesis bone morphogenesis negative regulation of SMAD protein signal transduction muscle structure development DNA-binding transcription factor binding | 04110 04114 04115 04914 |

[spindle pole](#)
[outer kinetochore](#)
[oocyte maturation](#)
[in utero embryonic development](#)
[patched binding](#)
[protein binding](#)
[nucleus](#)
[nucleus](#)
[nucleus](#)
[nucleoplasm](#)
[cytoplasm](#)
[cytoplasm](#)
[cytoplasm](#)
[mitochondrial matrix](#)
[mitochondrial matrix](#)
[mitochondrial matrix](#)
[centrosome](#)
[centrosome](#)
[microtubule organizing center](#)
[cytosol](#)
[cytosol](#)
[cytosol](#)
[cytoskeleton](#)
[mitotic spindle organization](#)
[mitotic metaphase chromosome alignment](#)
[mitotic metaphase chromosome alignment spermatogenesis](#)
[response to xenobiotic stimulus](#)
[response to mechanical stimulus](#)
[response to toxic substance](#)
[negative regulation of gene expression](#)
[positive regulation of G2/M transition of mitotic cell cycle membrane](#)
[cyclin-dependent protein serine/threonine kinase regulator activity](#)
[cyclin-dependent protein serine/threonine kinase regulator activity protein kinase binding](#)
[protein kinase binding positive regulation of mRNA 3'-end processing](#)
[tissue regeneration ubiquitin-like protein ligase binding](#)
[mitotic cell cycle phase transition](#)
[positive regulation of cell cycle](#)
[positive regulation of mitotic cell cycle](#)
[response to DDT](#)
[positive regulation of fibroblast proliferation digestive tract development](#)
[cell division](#)
[positive regulation of attachment of spindle](#)

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|-----------|------|----------------|---|------------------------------------|------------------------|----------------------|------------------------|---|--|-------------------------|
| | | | | | | | | microtubules to kinetochore ventricular cardiac muscle cell development positive regulation of cardiac muscle cell proliferation regulation of chromosome condensation cyclin-dependent protein serine/threonine kinase activator activity protein-containing complex assembly cellular response to iron(III) ion cellular response to fatty acid cellular response to hypoxia regulation of mitotic cell cycle spindle assembly checkpoint cyclin B1-CDK1 complex cyclin B1-CDK1 complex cyclin B1-CDK1 complex positive regulation of mitochondrial ATP synthesis coupled electron transport | | |
| 2003_s_at | MSH6 | mutS homolog 6 | 2 | 47783081, 47783954, 47783144 | U28946 | 2956 | 2p16.3 | 533 | nucleotide binding magnesium ion binding four-way junction DNA binding meiotic mismatch repair chromatin DNA binding chromatin binding damaged DNA binding double-stranded DNA binding protein binding ATP binding ATP binding nucleus nucleus nucleus nucleoplasm nucleoplasm chromosome Golgi apparatus cytosol DNA repair DNA repair mismatch repair mismatch repair mismatch repair mismatch repair mismatch repair chromatin organization DNA damage response spermatogenesis ATP-dependent activity, acting on DNA determination of adult lifespan determination of adult lifespan intrinsic apoptotic signaling pathway in response to DNA damage | 03430 05200 05210 |

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|---------------------------|-------|--|---|-----------|------------------------|----------------------|-------------------------|---------------------|---|--|
| | | | | | | | | | | intrinsic apoptotic signaling pathway in response to DNA damage response to UV response to UV somatic hypermutation of immunoglobulin genes somatic hypermutation of immunoglobulin genes somatic recombination of immunoglobulin gene segments somatic recombination of immunoglobulin gene segments enzyme binding mismatched DNA binding mismatched DNA binding mismatched DNA binding guanine/thymine mispair binding guanine/thymine mispair binding single guanine insertion binding single thymine insertion binding MutSα complex MutSα complex MutSα complex MutSα complex oxidized purine DNA binding MutLα complex binding ADP binding isotype switching isotype switching negative regulation of DNA recombination negative regulation of DNA recombination intrinsic apoptotic signaling pathway intrinsic apoptotic signaling pathway histone H3K36me3 reader activity ATP-dependent DNA damage sensor activity |
| 2012 s at | PRKDC | protein kinase, DNA-activated, catalytic subunit | 8 | -47773112 | U34994 | 5591 | 8q11.21 | 902 | nucleotide binding maturation of 5.8S rRNA telomere maintenance telomere maintenance double-strand break repair via homologous recombination chromosome, telomeric region chromatin somitogenesis negative regulation of protein phosphorylation activation of innate immune response B cell lineage commitment immature B cell differentiation pro-B cell differentiation T cell lineage commitment | 03450 04110 |

[immune system process](#)
[DNA binding](#)
[double-stranded DNA binding](#)
[double-stranded DNA binding](#)
[RNA binding](#)
[protein kinase activity](#)
[protein kinase activity](#)
[protein kinase activity](#)
[protein serine/threonine kinase activity](#)
[protein serine/threonine kinase activity](#)
[protein serine/threonine kinase activity](#)
[protein serine/threonine kinase activity](#)
[DNA-dependent protein kinase activity](#)
[DNA-dependent protein kinase activity](#)
[protein binding](#)
[ATP binding](#)
[nucleus](#)
[nucleus](#)
[nucleus](#)
[nucleoplasm](#)
[nucleoplasm](#)
[transcription regulator complex](#)
[nucleolus](#)
[nucleolus](#)
[cytoplasm](#)
[cytosol](#)
[cytosol](#)
[DNA-dependent protein kinase-DNA ligase 4 complex](#)
[DNA repair](#)
[DNA repair](#)
[double-strand break repair](#)
[double-strand break repair](#)
[double-strand break repair](#)
[double-strand break repair via nonhomologous end joining](#)
[double-strand break repair via nonhomologous end joining](#)
[double-strand break repair via nonhomologous end joining](#)
[DNA recombination](#)
[protein phosphorylation](#)
[protein phosphorylation](#)
[DNA damage response](#)
[DNA damage response](#)
[brain development](#)
[heart development](#)
[intrinsic apoptotic signaling pathway in response to DNA damage](#)
[intrinsic apoptotic signaling pathway in response to DNA damage](#)
[response to ionizing radiation](#)
[response to gamma radiation](#)
[membrane](#)

[telomere capping](#)
[kinase activity](#)
[transferase activity](#)
[peptidyl-serine phosphorylation](#)
[peptidyl-threonine phosphorylation](#)
[enzyme binding](#)
[protein domain specific binding](#)
[lymphocyte differentiation](#)
[replication fork processing](#)
[mitotic G1 DNA damage](#)
[checkpoint signaling](#)
[protein destabilization](#)
[small-subunit processome](#)
[cellular response to insulin stimulus](#)
[protein-containing complex](#)
[protein-DNA complex](#)
[T cell differentiation in thymus](#)
[V\(D\)J recombination](#)
[immunoglobulin V\(D\)J recombination](#)
[immunoglobulin V\(D\)J recombination](#)
[T cell receptor V\(D\)J recombination](#)
[small-subunit processome assembly](#)
[U3 snoRNA binding](#)
[ectopic germ cell programmed cell death](#)
[histone H2AXS139 kinase activity](#)
[protein modification process](#)
[ribosome biogenesis](#)
[regulation of circadian rhythm](#)
[regulation of circadian rhythm](#)
[positive regulation of apoptotic process](#)
[negative regulation of apoptotic process](#)
[innate immune response](#)
[positive regulation of lymphocyte differentiation](#)
[positive regulation of lymphocyte differentiation](#)
[positive regulation of erythrocyte differentiation](#)
[positive regulation of translation](#)
[positive regulation of translation](#)
[positive regulation of transcription by RNA polymerase II](#)
[rhythmic process](#)
[regulation of smooth muscle cell proliferation](#)

[regulation of epithelial cell proliferation](#)
[RNA polymerase II-specific DNA-binding transcription factor binding](#)
[DNA-dependent protein kinase complex](#)
[nonhomologous end joining complex](#)
[protein localization to chromatin](#)
[regulation of cellular response to stress](#)
[double-strand break repair via alternative nonhomologous end joining](#)
[protein serine kinase activity](#)
[DNA repair-dependent chromatin remodeling](#)
[cGAS/STING signaling pathway](#)
[negative regulation of cGAS/STING signaling pathway](#)
[regulation of hematopoietic stem cell differentiation](#)
[regulation of hematopoietic stem cell differentiation](#)
[positive regulation of platelet formation](#)
[positive regulation of platelet formation](#)
[positive regulation of double-strand break repair via nonhomologous end joining](#)

[2015 s at](#)

[U14658](#)

[nucleotide binding](#)
[DNA binding](#)
[DNA binding](#)
[single-stranded DNA binding](#)
[nuclease activity](#)
[endonuclease activity](#)
[endonuclease activity](#)
[protein binding](#)
[ATP binding](#)
[nucleus](#)
[nucleus](#)
[nucleus](#)
[nucleoplasm](#)
[nucleoplasm](#)
[cytosol](#)
[DNA repair](#)
[mismatch repair](#)
[mismatch repair](#)
[mismatch repair](#)
[mismatch repair](#)
[mismatch repair](#)
[DNA damage response](#)
[response to xenobiotic stimulus](#)
[somatic hypermutation of immunoglobulin genes](#)
[somatic hypermutation of immunoglobulin genes](#)
[somatic recombination of immunoglobulin gene](#)

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|---------------------------|------|------------------------------------|----|---|------------------------|----------------------|--------------------------|--|--|--|
| | | | | | | | | segments hydrolase activity ATP hydrolysis activity ATP hydrolysis activity mismatched DNA binding single base insertion or deletion binding mismatch repair complex MutLalpha complex MutLalpha complex MutSalpha complex binding positive regulation of isotype switching to IgA isotypes positive regulation of isotype switching to IgG isotypes ATP-dependent DNA damage sensor activity | | |
| 2084_s_at | ETV4 | ETS variant transcription factor 4 | 17 | -43527845, -43527845, -43527845 | D12765 | 2118 | 17q21.31 | 141 | chromatin RNA polymerase II cis-regulatory region sequence-specific DNA binding DNA-binding transcription factor activity, RNA polymerase II-specific DNA-binding transcription factor activity, RNA polymerase II-specific DNA-binding transcription activator activity, RNA polymerase II-specific DNA-binding transcription activator activity, RNA polymerase II-specific DNA binding DNA-binding transcription factor activity protein binding nucleus nucleus nucleoplasm chromosome nucleolus regulation of DNA-templated transcription regulation of transcription by RNA polymerase II regulation of transcription by RNA polymerase II cell differentiation sequence-specific DNA binding positive regulation of keratinocyte differentiation positive regulation of transcription by RNA polymerase II sequence-specific double-stranded DNA binding | |
| 219_i_at | MAP2 | microtubule associated protein 2 | 2 | 209579606, 209424046, 209579331, 209661495, 209424046 | S76756 | 4133 | 2q34 | 157 | microtubule cytoskeleton organization microtubule cytoskeleton organization dystroglycan binding | |

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|------------------------|------|--|----|-----------|-----------------------------|----------------------|-------------------------|--------------------|--|---|
| | | | | | | | | | structural molecule activity protein binding calmodulin binding cytoplasm cytoplasm cytosol cytosol cytoskeleton microtubule microtubule associated complex plasma membrane cilium microtubule binding microtubule binding microtubule binding tubulin binding dendrite development central nervous system neuron development dendrite dendrite negative regulation of axon extension regulation of microtubule polymerization negative regulation of microtubule polymerization neuron projection development neuron projection development dendrite cytoplasm regulation of protein localization cell projection neuron projection neuron projection neuronal cell body axon initial segment dendritic shaft axon hillock dendritic growth cone dendritic branch tau protein binding dendrite morphogenesis basal dendrite primary dendrite distal dendrite apical distal dendrite positive regulation of anterograde dense core granule transport regulation of organelle transport along microtubule dendritic filopodium positive regulation of anterograde synaptic vesicle transport proximal dendrite proximal neuron projection | |
| 304 at | SOS2 | SOS Ras/Rho guanine nucleotide exchange factor 2 | 14 | -50117131 | HG961-HT961 | 6655 | 14q21.3 | 64 | B cell homeostasis lymphocyte homeostasis guanyl-nucleotide exchange factor activity guanyl-nucleotide exchange factor activity protein binding | 04010 04012 04062 04320 04510 04540 04630 |

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|--------------------------|-------|--|----|-----------|--------------------------|----------------------|-------------------------|--|---|----------------|
| | | | | | | | | cytosol cytosol plasma membrane small GTPase-mediated signal transduction Ras protein signal transduction insulin receptor signaling pathway regulation of T cell differentiation in thymus regulation of T cell proliferation protein heterodimerization activity regulation of pro-B cell differentiation | 04650 04660 04662 04664 04722 04810 04910 04912 05160 05200 05211 05213 05214 05215 05220 05221 05223 | |
| 31337 at | GNRH2 | gonadotropin releasing hormone 2 | 20 | 3043621 | AF036329 | 2797 | 20p13 | 62 | hormone activity hormone activity gonadotropin hormone-releasing hormone activity extracellular region extracellular region extracellular space extracellular space signal transduction gonadotropin-releasing hormone receptor binding | 04912 |
| 31380 at | ERN1 | endoplasmic reticulum to nucleus signaling 1 | 17 | -64039141 | AF059198 | 2081 | 17q23.3 | 325 | nucleotide binding magnesium ion binding magnesium ion binding endothelial cell proliferation catalytic activity endonuclease activity RNA endonuclease activity RNA endonuclease activity RNA endonuclease activity RNA nuclelease activity protein kinase activity protein serine/threonine kinase activity protein serine/threonine kinase activity protein serine/threonine kinase activity platelet-derived growth factor receptor binding protein binding ATP binding ATP binding nuclear inner membrane cytoplasm mitochondrion endoplasmic reticulum endoplasmic reticulum endoplasmic reticulum endoplasmic reticulum membrane endoplasmic reticulum membrane endoplasmic reticulum membrane mRNA processing RNA catabolic process mRNA catabolic process | 04141 05010 |

[protein phosphorylation](#)
[apoptotic process](#)
[response to unfolded protein](#)
[negative regulation of gene expression](#)
[membrane](#)
[regulation of macroautophagy](#)
[kinase activity](#)
[transferase activity](#)
[hydrolase activity](#)
[enzyme binding](#)
[Hsp70 protein binding](#)
[endoplasmic reticulum](#)
[unfolded protein response](#)
[endoplasmic reticulum](#)
[unfolded protein response](#)
[protein-containing complex](#)
[positive regulation of RNA splicing](#)
[positive regulation of RNA splicing](#)
[cellular response to unfolded protein](#)
[cellular response to unfolded protein](#)
[response to endoplasmic reticulum stress](#)
[cellular response to vascular endothelial growth factor stimulus](#)
[IRE1-mediated unfolded protein response](#)
[identical protein binding](#)
[protein homodimerization activity](#)
[protein homodimerization activity](#)
[protein homodimerization activity](#)
[ADP binding](#)
[positive regulation of JNK cascade](#)
[positive regulation of JNK cascade](#)
[metal ion binding](#)
[unfolded protein binding](#)
[Hsp90 protein binding](#)
[mRNA splicing, via endonucleolytic cleavage and ligation](#)
[mRNA splicing, via endonucleolytic cleavage and ligation](#)
[mRNA splicing, via endonucleolytic cleavage and ligation](#)
[intrinsic apoptotic signaling pathway in](#)

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|----------------------------|-----|---|----|-----------|------------------------|----------------------|-------------------------|--|---|
| | | | | | | | | response to endoplasmic reticulum stress intrinsic apoptotic signaling pathway in response to endoplasmic reticulum stress intrinsic apoptotic signaling pathway in response to endoplasmic reticulum stress cellular response to hydrogen peroxide cellular response to glucose stimulus cellular response to glucose stimulus protein serine kinase activity positive regulation of endoplasmic unfolded protein response insulin metabolic process positive regulation of vascular associated smooth muscle cell proliferation positive regulation of response to endoplasmic reticulum stress Ire1 complex AP1-IRE1 complex IRE1-TRAF2-ASK1 complex IRE1-TRAF2-ASK1 complex IRE1-RACK1-PP2A complex | |
| 31486_s_at | MN1 | MN1 proto-oncogene, transcriptional regulator | 22 | -27748276 | Z70218 | 4330 | 22q12.1 | 65 | intramembranous ossification protein binding nucleus nucleus regulation of DNA-templated transcription negative regulation of osteoblast proliferation positive regulation of vitamin D receptor signaling pathway regulation of cell cycle G1/S phase transition |
| 31493_s_at | | | | | J03071 | | | | growth hormone receptor binding growth hormone receptor binding hormone activity hormone activity hormone activity protein binding extracellular region extracellular region extracellular space extracellular space cytoplasm endoplasmic reticulum growth factor activity endomembrane system response to nutrient levels endosome lumen vesicle vesicle |

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|--------------------------|----------|------------------------------------|---|---|------------------------|-----------------------|-------------------------|---|
| | | | | | | | | positive regulation of receptor signaling pathway via JAK-STAT metal ion binding animal organ development growth hormone receptor signaling pathway |
| 315_at | PRDM2 | PR/SET domain 2 | 1 | 13749414, 13704854, 13704854, 13700187 | D45132 | 7799 | 1p36.21 | 100 negative regulation of transcription by RNA polymerase II RNA polymerase II transcription regulatory region sequence-specific DNA binding DNA-binding transcription factor activity, RNA polymerase II-specific DNA-binding transcription repressor activity, RNA polymerase II-specific DNA-binding transcription activator activity, RNA polymerase II-specific DNA-binding transcription activator activity, RNA polymerase II-specific DNA binding DNA-binding transcription factor activity protein binding nucleus nucleus nucleus nucleus nucleoplasm Golgi apparatus chromatin remodeling regulation of DNA-templated transcription regulation of transcription by RNA polymerase II methyltransferase activity zinc ion binding zinc ion binding determination of adult lifespan transferase activity methylation histone methyltransferase activity sequence-specific DNA binding positive regulation of transcription by RNA polymerase II metal ion binding histone H3K9 trimethyltransferase activity |
| 31501_at | | | | | W27645 | | | |
| 31512_at | IGKV1-13 | immunoglobulin kappa variable 1-13 | 2 | | Z00010 | 28939 | 2p11.2 | 3 adaptive immune response immune system process extracellular region plasma membrane immune response |

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|----------------------------|--------|----------------------------------|----|------------|--------------------------|-----------------------|------------------------|--|---|--|
| | | | | | | | | membrane immunoglobulin complex immunoglobulin complex | | |
| 31542_at | FLG | filaggrin | 1 | -152302164 | M60502 | 2312 | 1q21.3 | 459 | cornified envelope cornified envelope structural molecule activity calcium ion binding protein binding nucleus cytosol peptide cross-linking keratinocyte differentiation structural constituent of skin epidermis extracellular matrix keratohyalin granule keratohyalin granule cytoplasmic ribonucleoprotein granule metal ion binding transition metal ion binding establishment of skin barrier establishment of skin barrier | |
| 31563_at | TRBV16 | T cell receptor beta variable 16 | 7 | | U03115 | 28571 | 7q34 | 9 | adaptive immune response immune system process plasma membrane plasma membrane cell surface receptor signaling pathway membrane T cell receptor complex | |
| 31623_f_at | MT1A | metallothionein 1A | 16 | 56638665 | K01383 | 4489 | 16q13 | 89 | protein binding nucleus nucleus cytoplasm cytoplasm cytosol intracellular zinc ion homeostasis zinc ion binding detoxification of copper ion negative regulation of growth metal ion binding metal ion binding cellular response to cadmium ion cellular response to cadmium ion cellular response to copper ion cellular response to zinc ion cellular response to zinc ion | |
| 31631_f_at | PTTG2 | pituitary tumor-transforming 2 | 4 | 37960397 | AF095288 | 10744 | 4p14 | 12 | protein binding nucleus nucleus cytoplasm SH3 domain binding homologous chromosome segregation chromosome organization | 04110 04114 |

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|----------------------------|-------|-------------------------|----|---------------------------|------------------------|----------------------|-------------------------|-----|--|---|
| 31687_f_at | HBB | hemoglobin subunit beta | 11 | -5225463 | M25079 | 3043 | 11p15.4 | 871 | peroxidase activity oxygen carrier activity oxygen carrier activity oxygen carrier activity protein binding extracellular region extracellular space cytosol hemoglobin complex inflammatory response regulation of blood pressure carbon dioxide transport oxygen binding oxygen binding heme binding heme binding nitric oxide transport nitric oxide transport hemoglobin binding haptoglobin binding hemoglobin alpha binding haptoglobin-hemoglobin complex haptoglobin-hemoglobin complex response to hydrogen peroxide hydrogen peroxide catabolic process positive regulation of nitric oxide biosynthetic process metal ion binding erythrocyte development extracellular exosome renal absorption platelet aggregation endocytic vesicle lumen blood microparticle blood vessel diameter maintenance cellular oxidant detoxification tertiary granule lumen ficolin-1-rich granule lumen | 05143 05144 |
| 31715_at | TEX28 | testis expressed 28 | X | -154271264, -154271264 | U93720 | 1527 | Xq28 | 12 | protein binding endomembrane system membrane | |
| 31719_at | FN1 | fibronectin 1 | 2 | -215360864, -215414655 | X02761 | 2335 | 2q35 | 872 | angiogenesis regulation of protein phosphorylation protease binding protease binding signaling receptor binding signaling receptor binding integrin binding integrin binding integrin binding | 04510 04512 04810 05100 05146 05200 05222 |

[integrin binding](#)
[extracellular matrix](#)
[structural constituent](#)
[extracellular matrix](#)
[structural constituent](#)
[extracellular matrix](#)
[structural constituent](#)
[protein binding](#)
[collagen binding](#)
[extracellular region](#)
[extracellular region](#)
[extracellular region](#)
[fibrinogen complex](#)
[fibrinogen complex](#)
[basement membrane](#)
[extracellular space](#)
[extracellular space](#)
[extracellular space](#)
[endoplasmic reticulum](#)
[lumen](#)
[endoplasmic reticulum-](#)
[Golgi intermediate](#)
[compartment](#)
[plasma membrane](#)
[acute-phase response](#)
[cell-substrate junction](#)
[assembly](#)
[cell-substrate junction](#)
[assembly](#)
[cell adhesion](#)
[cell adhesion](#)
[cell-matrix adhesion](#)
[cell-matrix adhesion](#)
[calcium-independent cell-](#)
[matrix adhesion](#)
[integrin-mediated](#)
[signaling pathway](#)
[nervous system](#)
[development](#)
[heart development](#)
[heparin binding](#)
[heparin binding](#)
[positive regulation of cell](#)
[population proliferation](#)
[regulation of cell shape](#)
[response to wounding](#)
[positive regulation of](#)
[gene expression](#)
[response to muscle](#)
[activity](#)
[apical plasma membrane](#)
[peptidase activator](#)
[activity](#)
[extracellular matrix](#)
[extracellular matrix](#)
[extracellular matrix](#)
[extracellular matrix](#)
[platelet alpha granule](#)
[lumen](#)
[integrin activation](#)
[substrate adhesions-](#)
[dependent cell spreading](#)
[substrate adhesions-](#)
[dependent cell spreading](#)
[endodermal cell](#)
[differentiation](#)
[wound healing](#)
[identical protein binding](#)
[proteoglycan binding](#)
[proteoglycan binding](#)
[endothelial cell migration](#)

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|--------------------------|-------|---------------------------|----|----------|------------------------|----------------------|-------------------------|--------------------|--|--|
| | | | | | | | | | positive regulation of axon extension receptor ligand activity positive regulation of fibroblast proliferation biological process involved in interaction with symbiont positive regulation of phosphatidylinositol 3-kinase/protein kinase B signal transduction extracellular exosome extracellular exosome regulation of ERK1 and ERK2 cascade negative regulation of transforming growth factor beta production blood coagulation, fibrin clot formation blood microparticle negative regulation of monocyte activation negative regulation of monocyte activation neural crest cell migration involved in autonomic nervous system development positive regulation of substrate-dependent cell migration, cell attachment to substrate | |
| 31733_at | P2RX3 | purinergic receptor P2X 3 | 11 | 57338351 | Y07683 | 5024 | 11q12.1 | 67 | nucleotide binding purinergic nucleotide receptor activity purinergic nucleotide receptor activity purinergic nucleotide receptor activity response to hypoxia extracellularly ATP-gated monoatomic cation channel activity monoatomic ion channel activity ATP binding ATP binding ATP binding plasma membrane plasma membrane plasma membrane plasma membrane monoatomic ion transport monoatomic cation transport signal transduction chemical synaptic transmission | 04020 04080 |

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|--------------------------|-------|--------------------------------|---|------------|------------------------|--------------------|-------------------------|---|--|
| | | | | | | | | neuromuscular synaptic transmission response to temperature stimulus response to heat response to cold response to mechanical stimulus response to carbohydrate positive regulation of calcium ion transport into cytosol urinary bladder smooth muscle contraction membrane axon peristalsis response to ATP monoatomic ion transmembrane transport purinergic nucleotide receptor signaling pathway neuron projection receptor complex metal ion binding regulation of synaptic plasticity behavioral response to pain modulation of chemical synaptic transmission positive regulation of calcium-mediated signaling sensory perception of taste establishment of localization in cell excitatory postsynaptic potential protein homotrimerization calcium ion transmembrane transport calcium ion transmembrane transport cellular response to ATP monoatomic cation transmembrane transport inorganic cation transmembrane transport Schaffer collateral - CA1 synapse hippocampal mossy fiber to CA3 synapse postsynapse | |
| 31737 at | ACTA1 | actin alpha 1, skeletal muscle | 1 | -229431245 | M20543 | 58 | 1q42.13 | 454 | nucleotide binding stress fiber stress fiber structural constituent of cytoskeleton protein binding ATP binding ATP binding extracellular space cytoplasm cytosol cytoskeleton |

| | | | | | | | | | |
|--------------------------|-------|-------------------------------|----|-----------------------|------------------------|------------------------|-------------------------|---------------------|---|
| | | | | | | | | | striated muscle thin filament striated muscle thin filament actin filament actin filament muscle contraction positive regulation of gene expression actin cytoskeleton actin cytoskeleton hydrolase activity myosin binding sarcomere lamellipodium filopodium skeletal muscle thin filament assembly skeletal muscle thin filament assembly ADP binding cell body skeletal muscle fiber development skeletal muscle fiber development extracellular exosome blood microparticle mesenchyme migration |
| 31770_at | | | | | W27119 | | | | |
| 31771_at | TEX41 | testis expressed 41 | 2 | 144667966 | U80770 | 401014 | 2q22.3 | 6 | |
| 31792_at | ANXA3 | annexin A3 | 4 | 78551769 | M20560 | 306 | 4q21.21 | 105 | phosphatidylserine binding phospholipase inhibitor activity calcium ion binding calcium-dependent phospholipid binding calcium-dependent phospholipid binding calcium-dependent phospholipid binding nucleus cytoplasm cytoplasm plasma membrane plasma membrane phagocytosis positive regulation of endothelial cell migration vesicle membrane membrane phospholipase A2 inhibitor activity phagocytic vesicle membrane specific granule defense response to bacterium neutrophil degranulation positive regulation of angiogenesis calcium-dependent protein binding positive regulation of DNA-binding transcription factor activity extracellular exosome |
| 31872_at | SS18 | SS18 subunit of BAF chromatin | 18 | -26016252, -26016252, | X79201 | 6760 | 18q11.2 | 105 | microtubule cytoskeleton organization |

| | | | | | | | | | | |
|----------|--------|---------------------------------------|-----------|-----------|--------|-----|---------|-----|---|----------------|
| | | remodeling complex | -26016252 | | | | | | chromatin cell morphogenesis transcription coactivator activity transcription coactivator activity protein binding nucleus nucleus nucleoplasm nucleoplasm chromatin remodeling regulation of transcription by RNA polymerase II cytoskeleton organization positive regulation of cell population proliferation response to xenobiotic stimulus microtubule cytoskeleton SWI/SNF complex SWI/SNF complex intracellular signal transduction negative regulation of cell differentiation positive regulation of transcription by RNA polymerase II positive regulation of transcription by RNA polymerase II ephrin receptor signaling pathway npBAF complex neuronal stem cell population maintenance GBAF complex positive regulation of stem cell population maintenance | |
| 31934_at | ADAM10 | ADAM metallopeptidase domain 10 | 15 | -58588808 | Z48614 | 102 | 15q21.3 | 419 | Golgi membrane in utero embryonic development in utero embryonic development endopeptidase activity endopeptidase activity endopeptidase activity metalloendopeptidase activity metalloendopeptidase activity metalloendopeptidase activity metalloendopeptidase activity metalloendopeptidase activity integrin binding protein binding nucleus cytoplasm endoplasmic reticulum lumen Golgi apparatus Golgi apparatus Golgi-associated vesicle plasma membrane | 05010 05120 |

[plasma membrane](#)
[plasma membrane](#)
[plasma membrane](#)
[plasma membrane](#)
[adherens junction](#)
[focal adhesion](#)
[proteolysis](#)
[membrane protein](#)
[ectodomain proteolysis](#)
[membrane protein](#)
[ectodomain proteolysis](#)
[membrane protein](#)
[ectodomain proteolysis](#)
[membrane protein](#)
[ectodomain proteolysis](#)
[negative regulation of cell adhesion](#)
[negative regulation of cell adhesion](#)
[Notch signaling pathway](#)
[Notch signaling pathway](#)
[Notch signaling pathway](#)
[integrin-mediated signaling pathway](#)
[cell-cell signaling](#)
[peptidase activity](#)
[metallopeptidase activity](#)
[metallopeptidase activity](#)
[metallopeptidase activity](#)
[positive regulation of cell population proliferation](#)
[regulation of Notch signaling pathway](#)
[cell surface](#)
[cell surface](#)
[negative regulation of gene expression](#)
[positive regulation of T cell chemotaxis](#)
[postsynaptic density](#)
[membrane](#)
[membrane](#)
[membrane](#)
[protein processing](#)
[protein processing](#)
[hydrolase activity](#)
[SH3 domain binding](#)
[protein kinase binding](#)
[extracellular matrix disassembly](#)
[clathrin-coated vesicle](#)
[positive regulation of cell growth](#)
[positive regulation of cell migration](#)
[axon](#)
[dendrite](#)
[cytoplasmic vesicle](#)
[positive regulation of tumor necrosis factor production](#)
[adherens junction organization](#)
[response to tumor necrosis factor](#)
[specific granule membrane](#)
[epidermal growth factor receptor ligand maturation](#)
[monocyte activation](#)
[protein homodimerization activity](#)

| | | | | | | | | | |
|--------------------------|-------|---|---|------------------------|--------------------------|-----------------------|------------------------|--|---|
| | | | | | | | | protein homodimerization activity amyloid precursor protein catabolic process amyloid precursor protein catabolic process cell projection metal ion binding pore complex pore complex pore complex assembly pore complex assembly constitutive protein ectodomain proteolysis extracellular exosome anchoring junction metallodipeptidase activity tertiary granule membrane cochlea development perinuclear endoplasmic reticulum synaptic membrane synaptic membrane synaptic membrane tetraspanin-enriched microdomain regulation of neurotransmitter receptor localization to postsynaptic specialization membrane glutamatergic synapse postsynapse organization regulation of postsynapse organization protein catabolic process at postsynapse signaling receptor ligand precursor processing regulation of vasculature development metalloendopeptidase activity involved in amyloid precursor protein catabolic process metalloendopeptidase activity involved in amyloid precursor protein catabolic process metalloendopeptidase activity involved in amyloid precursor protein catabolic process positive regulation of tumor necrosis factor-mediated signaling pathway | |
| 31986_at | REPS1 | RALBP1 associated Eps domain containing 1 | 6 | -138904014, -138903494 | AL049259 | 85021 | 6q24.1 | 66 | calcium ion binding protein binding nucleoplasm cytoplasm cytosol cytosol plasma membrane plasma membrane clathrin-coated pit clathrin-coated pit endocytosis membrane |

| | | | | | | | | | |
|----------------------------|--------|--|---|--|--------------------------|-----------------------|-------------------------|--|--|
| | | | | | | | | endosomal transport SH3 domain binding protein-macromolecule adaptor activity metal ion binding | |
| 32049_f_at | ELOA | elongin A | 1 | 23743365 | AF070554 | 6924 | 1p36.11 | 126 | protein binding extracellular space nucleus nucleoplasm nucleoplasm regulation of DNA-templated transcription regulation of transcription by RNA polymerase II transcription by RNA polymerase II transcription initiation at RNA polymerase II promoter transcription elongation by RNA polymerase II elongin complex elongin complex site of DNA damage |
| 32119_at | ZBTB20 | zinc finger and BTB domain containing 20 | 3 | -114314499, -114314499, -114314499, -114314515, -114314515, -114314515, -114314515, -114314499, -114314499 | AL049423 | 26137 | 3q13.31 | 73 | negative regulation of transcription by RNA polymerase II negative regulation of transcription by RNA polymerase II transcription cis-regulatory region binding transcription cis-regulatory region binding RNA polymerase II cis-regulatory region sequence-specific DNA binding DNA-binding transcription repressor activity, RNA polymerase II-specific DNA-binding transcription repressor activity, RNA polymerase II-specific regulation of cytokine production regulation of immune system process DNA binding nucleus nucleus nucleoplasm nucleoplasm cytoplasm cytoplasm zinc ion binding negative regulation of gene expression nuclear body positive regulation of interferon-beta production positive regulation of interleukin-6 production positive regulation of tumor necrosis factor production positive regulation of glycolytic process |

| | | | | | | | | | | |
|--------------------------|--------|--|---|---------------------------|------------------------|----------------------|-------------------------|-----|---|---|
| | | | | | | | | | positive regulation of glycolytic process negative regulation of DNA-templated transcription metal ion binding positive regulation of lipid biosynthetic process positive regulation of lipid biosynthetic process lipid homeostasis lipid homeostasis cellular response to glucose stimulus cellular response to glucose stimulus sequence-specific double-stranded DNA binding sequence-specific double-stranded DNA binding | |
| 32121_at | PIK3CD | phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit delta | 1 | 9691466, 9651730, 9689543 | U86453 | 5293 | 1p36.22 | 231 | nucleotide binding natural killer cell differentiation positive regulation of cytokine production positive regulation of endothelial cell proliferation adaptive immune response adaptive immune response immune system process leukocyte mediated immunity mast cell chemotaxis respiratory burst involved in defense response protein binding ATP binding cytoplasm cytoplasm cytosol cytosol plasma membrane plasma membrane phosphatidylinositol 3-kinase complex phosphatidylinositol 3-kinase complex phosphatidylinositol 3-kinase complex, class IA phosphatidylinositol 3-kinase complex, class IA phosphatidylinositol 3-kinase complex, class IA protein phosphorylation lipid metabolic process chemotaxis inflammatory response inflammatory response immune response signal transduction cell surface receptor signaling pathway positive regulation of endothelial cell migration | 00562 04012 04062 04070 04150 04210 04370 04380 04510 04620 04630 04650 04660 04662 04664 04666 04670 04722 04810 04910 04914 04930 04960 04973 05100 05142 05145 05146 05160 05200 05210 05211 05212 05213 05214 05215 05218 05220 05221 05222 05223 |

[positive regulation of endothelial cell migration](#)
[positive regulation of gene expression](#)
[positive regulation of gene expression](#)
[T cell chemotaxis](#)
[kinase activity](#)
[1-phosphatidylinositol-3-kinase activity](#)
[1-phosphatidylinositol-3-kinase activity](#)
[1-phosphatidylinositol-3-kinase activity](#)
[1-phosphatidylinositol-3-kinase activity](#)
[cell migration](#)
[transferase activity](#)
[regulation of anatomical structure morphogenesis](#)
[natural killer cell activation](#)
[cell differentiation](#)
[B cell differentiation](#)
[T cell differentiation](#)
[T cell differentiation](#)
[positive regulation of cell migration](#)
[neutrophil chemotaxis](#)
[T cell costimulation](#)
[positive regulation of neutrophil apoptotic process](#)
[positive regulation of neutrophil apoptotic process](#)
[1-phosphatidylinositol-4-phosphate 3-kinase activity](#)
[natural killer cell chemotaxis](#)
[B cell chemotaxis](#)
[phosphatidylinositol-3-phosphate biosynthetic process](#)
[vascular endothelial growth factor signaling pathway](#)
[T cell activation](#)
[B cell activation](#)
[B cell activation](#)
[mast cell degranulation](#)
[phosphatidylinositol 3-kinase/protein kinase B signal transduction](#)
[innate immune response](#)
[innate immune response](#)
[positive regulation of angiogenesis](#)

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|----------------------------|--------|-----------------------------------|----|--------------------|--------------------------|-----------------------|-------------------------------|-----|---|-------|
| | | | | | | | | | phosphatidylinositol phosphate biosynthetic process 1-phosphatidylinositol-4,5-bisphosphate 3-kinase activity 1-phosphatidylinositol-4,5-bisphosphate 3-kinase activity phosphatidylinositol-mediated signaling T cell receptor signaling pathway B cell receptor signaling pathway positive regulation of developmental process positive regulation of multicellular organismal process mast cell differentiation neutrophil extravasation positive regulation of epithelial tube formation regulation of multicellular organismal development | |
| 32170_g_at | FBXO21 | F-box protein 21 | 12 | -117141990 | AB020682 | 23014 | 12q24.22 | 55 | ubiquitin ligase complex DNA binding ubiquitin-protein transferase activity protein binding cytosol ubiquitin-dependent protein catabolic process apoptotic process cytokine-mediated signaling pathway hematopoietic stem cell differentiation hematopoietic stem cell homeostasis ERK1 and ERK2 cascade | |
| 32179_s_at | SNAP23 | synaptosome associated protein 23 | 15 | 42495305, 42495633 | Y09568 | 8773 | 15q15.1-q15.2 | 191 | histamine secretion by mast cell SNAP receptor activity protein binding nucleoplasm cytoplasm mitochondrion plasma membrane plasma membrane plasma membrane plasma membrane adherens junction focal adhesion cilium exocytosis exocytosis post-Golgi vesicle-mediated transport vesicle targeting protein transport membrane synaptic vesicle priming syntaxin binding syntaxin binding phagocytic vesicle membrane SNARE complex SNARE complex SNARE complex cytoplasmic vesicle | 04130 |

| | | | | | | | | |
|----------------------------|-------|-----------------------------------|---|----------|--------------------------|----------------------|-------------------------|---|
| | | | | | | | | synaptic vesicle fusion to presynaptic active zone membrane specific granule membrane specific granule membrane azurophil granule neuron projection synapse membrane fusion extracellular exosome tertiary granule membrane tertiary granule membrane presynapse |
| 32257 f at | TERF1 | telomeric repeat binding factor 1 | 8 | 73008863 | AF003001 | 7013 | 8q21.11 | 232 telomere maintenance telomere maintenance chromosome, telomeric region chromosome, telomeric region chromosome, telomeric region nuclear telomere cap complex nuclear telomere cap complex nuclear telomere cap complex nuclear telomere cap complex fibrillar center DNA binding DNA binding double-stranded telomeric DNA binding double-stranded telomeric DNA binding telomerase activity telomerase activity protein binding nucleus nucleus nucleus nucleoplasm nucleoplasm chromosome nucleolus cytoplasm spindle spindle cytoskeleton telomere maintenance via telomerase telomere maintenance via telomerase telomere maintenance via telomerase microtubule binding negative regulation of DNA replication DNA binding, bending response to xenobiotic stimulus telomere capping nuclear body positive regulation of telomere maintenance |

| | | | | | | | | | | |
|--------------------------|-------|-------------|---|---|------------------------|----------------------|------------------------|--------------------|--|--|
| | | | | | | | | | | negative regulation of telomere maintenance via telomerase negative regulation of telomere maintenance via telomerase negative regulation of telomere maintenance via telomerase negative regulation of telomere maintenance via semi-conservative replication telomeric DNA binding telomeric DNA binding identical protein binding protein homodimerization activity protein homodimerization activity meiotic telomere clustering cell division telomeric D-loop disassembly telomeric D-loop disassembly shelterin complex shelterin complex shelterin complex shelterin complex shelterin complex ankyrin repeat binding t-circle formation G-rich strand telomeric DNA binding G-rich strand telomeric DNA binding negative regulation of telomere maintenance via telomere lengthening positive regulation of shelterin complex assembly negative regulation of establishment of protein localization to telomere negative regulation of establishment of RNA localization to telomere negative regulation of establishment of protein-containing complex localization to telomere negative regulation of telomeric D-loop disassembly negative regulation of telomeric D-loop disassembly negative regulation of telomeric D-loop disassembly |
| 32266_at | CDH12 | cadherin 12 | 5 | -21750865, -21750865, -21750865, -21750675, -21750865 | L33477 | 1010 | 5p14.3 | 30 | cell morphogenesis calcium ion binding plasma membrane plasma membrane adherens junction cell-cell junction assembly cell adhesion homophilic cell adhesion via plasma membrane | |

| | | | | | | | | | |
|--------------------------|-------|---|----|-------------------------|--------------------------|-----------------------|--------------------------|---|--|
| | | | | | | | | adhesion molecules beta-catenin binding membrane calcium-dependent cell-cell adhesion via plasma membrane cell adhesion molecules catenin complex cell migration adherens junction organization cell-cell adhesion mediated by cadherin cadherin binding metal ion binding cell-cell adhesion | |
| 32281_at | | | | | AF070549 | | | | |
| 32339_at | PPY | pancreatic polypeptide | 17 | -43940803, -43940801 | AA844998 | 5539 | 17q21.31 | 49 | G protein-coupled receptor binding G protein-coupled receptor binding hormone activity hormone activity neuropeptide hormone activity protein binding extracellular region extracellular region extracellular space extracellular space cytoplasm neuropeptide signaling pathway feeding behavior protein secretion neuropeptide Y receptor binding |
| 32354_at | NPAS3 | neuronal PAS domain protein 3 | 14 | 32938878 | AL079281 | 64067 | 14q13.1 | 48 | chromatin RNA polymerase II transcription regulatory region sequence-specific DNA binding DNA-binding transcription factor activity, RNA polymerase II-specific DNA-binding transcription factor activity, RNA polymerase II-specific DNA binding protein binding nucleus nucleus nucleoplasm regulation of DNA-templated transcription regulation of transcription by RNA polymerase II positive regulation of DNA-templated transcription protein heterodimerization activity protein dimerization activity |
| 32359_at | CCN4 | cellular communication network factor 4 | 8 | 133191038 | AF100779 | 8840 | 8q24.22 | 136 | osteoblast differentiation regulation of cytokine production integrin binding protein binding |

[extracellular region](#)
[extracellular space](#)
[extracellular space](#)
[extracellular space](#)
[cytoplasm](#)
[cytosol](#)
[cell adhesion](#)
[cell adhesion](#)
[signal transduction](#)
[signal transduction](#)
[signal transduction](#)
[cell-cell signaling](#)
[heparin binding](#)
[positive regulation of smooth muscle cell migration](#)
[Wnt signaling pathway](#)
[positive regulation of Wnt signaling pathway](#)
[osteoclast differentiation](#)
[extracellular matrix](#)
[negative regulation of chondrocyte differentiation](#)
[glucose homeostasis](#)
[regulation of cell differentiation](#)
[positive regulation of cell differentiation](#)
[negative regulation of fat cell differentiation](#)
[positive regulation of osteoblast differentiation](#)
[positive regulation of smooth muscle cell proliferation](#)
[positive regulation of inflammatory response](#)
[regulation of multicellular organismal process](#)
[bone development](#)
[positive regulation of wound healing](#)

[32452_at](#)

[X66357](#)

[G1/S transition of mitotic cell cycle](#)
[G1/S transition of mitotic cell cycle](#)
[nucleotide binding](#)
[cyclin-dependent protein kinase holoenzyme complex](#)
[cyclin-dependent protein kinase holoenzyme complex](#)
[cyclin-dependent protein kinase holoenzyme complex](#)
[protein kinase activity](#)
[protein serine/threonine kinase activity](#)
[cyclin-dependent protein serine/threonine kinase activity](#)
[cyclin-dependent protein serine/threonine kinase activity](#)
[cyclin-dependent protein serine/threonine kinase activity](#)
[protein binding](#)
[ATP binding](#)
[nucleus](#)

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|----------------------------|-----------|--|----|---|--------------------------|----------------------|--------------------------|---|--|---|
| | | | | | | | | cytoplasm DNA damage response signal transduction cell population proliferation regulation of G2/M transition transition of mitotic cell cycle regulation of gene expression kinase activity transferase activity cyclin binding G0 to G1 transition G0 to G1 transition negative regulation of Notch signaling pathway cell division protein serine kinase activity | | |
| 32457_f_at | PRB4 | proline rich protein BstNI subfamily 4 | 12 | -502039, -11307076, -502043, -11307080 | K03207 | 5545 | 12p13.2 | 23 | extracellular region extracellular region | |
| 32479_at | TNFRSF11A | TNF receptor superfamily member 11a | 18 | 62325309, 62325286 | AF018253 | 8792 | 18q21.33 | 292 | ossification ossification adaptive immune response immune system process monocyte chemotaxis transmembrane signaling receptor activity transmembrane signaling receptor activity tumor necrosis factor receptor activity protein binding cytosol plasma membrane plasma membrane plasma membrane signal transduction cell-cell signaling positive regulation of cell population proliferation response to mechanical stimulus external side of plasma membrane external side of plasma membrane cell surface membrane cytokine binding cytokine binding osteoclast differentiation osteoclast differentiation response to lipopolysaccharide response to lipopolysaccharide response to insulin tumor necrosis factor-mediated signaling pathway tumor necrosis factor-mediated signaling | 04060 04380 05323 |

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|----------|-------|-----------|---|----------|------------------------|-----------------------|------------------------|--------------------|--|--|
| | | | | | | | | | | |
| 32516_at | CAPN7 | calpain 7 | 3 | 15206245 | W28621 | 23473 | 3p25.1 | 34 | pathway tumor necrosis factor-mediated signaling pathway tumor necrosis factor-mediated signaling pathway tumor necrosis factor-mediated signaling pathway cellular response to zinc ion starvation response to tumor necrosis factor response to tumor necrosis factor signaling receptor activity positive regulation of canonical NF-kappaB signal transduction membrane raft membrane raft response to ethanol positive regulation of osteoclast differentiation positive regulation of osteoclast differentiation positive regulation of bone resorption positive regulation of bone resorption positive regulation of JNK cascade metal ion binding lymph node development lymph node development circadian temperature homeostasis circadian temperature homeostasis mammary gland alveolus development positive regulation of ERK1 and ERK2 cascade response to interleukin-1 response to interleukin-1 positive regulation of fever generation by positive regulation of prostaglandin secretion positive regulation of fever generation by positive regulation of prostaglandin secretion multinuclear osteoclast differentiation multinuclear osteoclast differentiation positive regulation of non-canonical NF-kappaB signal transduction | |

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|----------|--|--|--|--------|--|--|---|
| | | | | | | | proteolysis proteolysis peptidase activity cysteine-type peptidase activity positive regulation of epithelial cell migration hydrolase activity extracellular exosome MIT domain binding self proteolysis |
| 32520_at | | | | M24900 | | | negative regulation of transcription by RNA polymerase II negative regulation of transcription by RNA polymerase II negative regulation of transcription by RNA polymerase II chromatin chromatin transcription cis-regulatory region binding transcription cis-regulatory region binding RNA polymerase II transcription regulatory region sequence-specific DNA binding RNA polymerase II cis-regulatory region sequence-specific DNA binding RNA polymerase II cis-regulatory region sequence-specific DNA binding RNA polymerase II cis-regulatory region sequence-specific DNA binding DNA-binding transcription factor activity, RNA polymerase II-specific DNA-binding transcription factor activity, RNA polymerase II-specific transcription corepressor binding transcription corepressor binding DNA-binding transcription repressor activity, RNA polymerase II-specific cartilage condensation ossification intracellular glucose homeostasis thyroid hormone receptor signaling pathway regulation of thyroid hormone receptor signaling pathway positive regulation of thyroid hormone receptor signaling pathway |

[positive regulation of thyroid hormone receptor signaling pathway](#)
[DNA binding](#)
[DNA-binding transcription factor activity](#)
[DNA-binding transcription factor activity](#)
[nuclear steroid receptor activity](#)
[nuclear receptor activity](#)
[nuclear receptor activity](#)
[nuclear receptor activity](#)
[protein binding](#)
[nucleus](#)
[nucleus](#)
[nucleus](#)
[nucleus](#)
[nucleus](#)
[nucleoplasm](#)
[nucleoplasm](#)
[cytoplasm](#)
[cytoplasm](#)
[cytosol](#)
[glycogen biosynthetic process](#)
[glycogen biosynthetic process](#)
[regulation of DNA-templated transcription](#)
[regulation of transcription by RNA polymerase II](#)
[transcription by RNA polymerase II](#)
[learning or memory](#)
[circadian rhythm](#)
[regulation of heart contraction](#)
[female courtship behavior](#)
[zinc ion binding](#)
[response to cold](#)
[hormone-mediated signaling pathway](#)
[hormone-mediated signaling pathway](#)
[animal organ morphogenesis](#)
[proteasomal protein catabolic process](#)
[proteasomal protein catabolic process](#)
[nuclear body](#)
[TBP-class protein binding](#)
[negative regulation of RNA polymerase II transcription](#)
[preinitiation complex assembly](#)
[regulation of lipid metabolic process](#)
[regulation of lipid metabolic process](#)
[protein domain specific binding](#)
[heme binding](#)
[cell differentiation](#)
[cell differentiation](#)
[erythrocyte differentiation](#)
[dendrite](#)

[dendrite](#)
[nuclear receptor-mediated steroid hormone signaling pathway](#)
[intracellular receptor signaling pathway](#)
[thyroid gland development](#)
[chromatin DNA binding](#)
[protein destabilization](#)
[protein destabilization](#)
[circadian regulation of gene expression](#)
[circadian regulation of gene expression](#)
[regulation of myeloid cell apoptotic process](#)
[negative regulation of toll-like receptor 4 signaling pathway](#)
[cholesterol homeostasis](#)
[regulation of circadian sleep/wake cycle](#)
[regulation of circadian sleep/wake cycle](#)
[regulation of circadian rhythm](#)
[regulation of circadian rhythm](#)
[mRNA transcription by RNA polymerase II](#)
[mRNA transcription by RNA polymerase II](#)
[cell projection](#)
[negative regulation of canonical NF-kappaB signal transduction](#)
[negative regulation of canonical NF-kappaB signal transduction](#)
[dendritic spine](#)
[dendritic spine](#)
[sequence-specific DNA binding](#)
[response to leptin](#)
[response to leptin](#)
[response to leptin](#)
[protein-containing complex binding](#)
[synapse](#)
[regulation of fat cell differentiation](#)
[regulation of fat cell differentiation](#)
[negative regulation of DNA-templated transcription](#)
[negative regulation of DNA-templated transcription](#)
[negative regulation of DNA-templated transcription](#)
[positive regulation of DNA-templated transcription](#)
[positive regulation of DNA-templated transcription](#)
[positive regulation of female receptivity](#)
[positive regulation of transcription by RNA](#)

[polymerase II](#)
[positive regulation of transcription by RNA polymerase II](#)
[positive regulation of transcription by RNA polymerase II](#)
[metal ion binding](#)
[retinoic acid receptor signaling pathway](#)
[rhythmic process](#)
[negative regulation of inflammatory response](#)
[negative regulation of inflammatory response](#)
[regulation of lipid catabolic process](#)
[circadian temperature homeostasis](#)
[circadian temperature homeostasis](#)
[type I pneumocyte differentiation](#)
[regulation of insulin secretion involved in cellular response to glucose stimulus](#)
[regulation of insulin secretion involved in cellular response to glucose stimulus](#)
[regulation of type B pancreatic cell proliferation](#)
[regulation of type B pancreatic cell proliferation](#)
[negative regulation of astrocyte activation](#)
[negative regulation of astrocyte activation](#)
[thyroid hormone binding](#)
[thyroid hormone binding](#)
[positive regulation of bile acid biosynthetic process](#)
[positive regulation of bile acid biosynthetic process](#)
[E-box binding](#)
[cellular response to lipopolysaccharide](#)
[cellular response to interleukin-1](#)
[cellular response to interleukin-1](#)
[cellular response to tumor necrosis factor](#)
[cellular response to tumor necrosis factor](#)
[RNA polymerase II transcription regulator complex](#)
[RNA polymerase II transcription regulator complex](#)
[positive regulation of cold-induced thermogenesis](#)
[positive regulation of cold-induced thermogenesis](#)
[negative regulation of cold-induced](#)

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|--------------------------|---------|---|----|---------------------------------------|------------------------|-----------------------|-------------------------|----|--|----------------------------------|
| | | | | | | | | | thermogenesis negative regulation of cold-induced thermogenesis general transcription initiation factor binding negative regulation of neuroinflammatory response negative regulation of neuroinflammatory response negative regulation of microglial cell activation negative regulation of microglial cell activation sequence-specific double-stranded DNA binding negative regulation of DNA-templated transcription initiation | |
| 32651_at | TAGLN3 | transgelin 3 | 3 | 111998738, 111999159, 111998921 | W28770 | 29114 | 3q13.2 | 19 | negative regulation of transcription by RNA polymerase II protein binding nucleus actin filament organization central nervous system development actin cytoskeleton synapse actin filament binding | |
| 32676_at | ALDH6A1 | aldehyde dehydrogenase 6 family member A1 | 14 | -74056846 | M93405 | 4329 | 14q24.3 | 51 | RNA binding methylmalonate-semialdehyde dehydrogenase (acylating, NAD) activity nucleoplasm mitochondrion mitochondrion mitochondrion mitochondrion mitochondrion mitochondrial matrix thymine catabolic process thymine catabolic process valine metabolic process L-valine catabolic process L-valine catabolic process | 00280 00562 00640 01100 |

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|----------------------------|-------|-----------------------------------|----|------------------------------------|--------------------------|----------------------|--------------------------|---|---|-----------------------|
| | | | | | | | | branched-chain amino acid catabolic process oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor malonate-semialdehyde dehydrogenase (acetylating) activity thymine metabolic process brown fat cell differentiation | | |
| 32679_at | MTFR1 | mitochondrial fission regulator 1 | 8 | 65669872, 65644733, 65644652 | D13634 | 9650 | 8q13.1 | 49 | mitochondrial fission mitochondrial fission protein binding mitochondrion mitochondrion mitochondrion mitochondrion mitochondrion mitochondrion cytosol plasma membrane mitochondrion organization aerobic respiration aerobic respiration aerobic respiration | |
| 32756_at | ECH1 | enoyl-CoA hydratase 1 | 19 | -225093, -38815421 | AF030249 | 1891 | 19q13.2 | 100 | catalytic activity protein binding cytoplasm mitochondrion mitochondrion mitochondrion mitochondrial matrix peroxisome peroxisome peroxisomal matrix cytosol lipid metabolic process fatty acid metabolic process fatty acid beta-oxidation membrane isomerase activity delta(3,5)-delta(2,4)-dienoyl-CoA isomerase activity extracellular exosome | 04146 |
| 32758_g_at | RAE1 | ribonucleic acid export 1 | 20 | 57351561, 57351254 | U84720 | 8480 | 20q13.31 | 182 | spindle pole transcription-dependent tethering of RNA polymerase II gene DNA at nuclear periphery fibrillar center RNA binding RNA binding protein binding nucleus nucleus nuclear envelope nuclear envelope nuclear envelope nuclear pore nuclear pore nuclear pore nuclear pore nucleoplasm | 03013 |

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|--------------------------|----------|--|---|----------|--------------------------|----------------------|-------------------------|--|--|---|
| | | | | | | | | cytoplasm cytoplasm cytoskeleton RNA export from nucleus mRNA export from nucleus nucleocytoplasmic transport microtubule binding ubiquitin binding cell division regulation of mitotic spindle organization mitotic spindle pole | | |
| 32759_at | | | | | U85943 | | | | | |
| 32773_at | HLA-DQA1 | major histocompatibility complex, class II, DQ alpha 1 | 6 | 32637405 | AA868382 | 3117 | 6p21.32 | 838 | Golgi membrane adaptive immune response immune system process peptide antigen assembly with MHC class II protein complex antigen processing and presentation of peptide or polysaccharide antigen via MHC class II protein binding lysosome lysosomal membrane lysosomal membrane endosome endoplasmic reticulum endoplasmic reticulum membrane Golgi apparatus plasma membrane plasma membrane plasma membrane immune response immune response endosome membrane ER to Golgi transport vesicle membrane membrane membrane antigen processing and presentation antigen processing and presentation of exogenous peptide antigen via MHC class II MHC class II protein complex binding transport vesicle membrane endocytic vesicle membrane clathrin-coated endocytic vesicle membrane late endosome membrane MHC class II receptor activity MHC class II receptor activity trans-Golgi network membrane peptide antigen binding peptide antigen binding | 04145 04514 04612 04672 04940 05140 05145 05150 05310 05320 05322 05323 05330 05332 05416 |

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|----------------------------|------|-----------------|---|---------------------------|--------------------------|-----------------------|------------------------|--|--|---|
| | | | | | | | | MHC class II protein complex MHC class II protein complex MHC class II protein complex positive regulation of immune response positive regulation of T cell activation luminal side of endoplasmic reticulum membrane | | |
| 32896_at | | | | | AL080072 | | | | | |
| 32905_s_at | | | | | M30038 | | | serine-type endopeptidase activity serine-type endopeptidase activity serine-type endopeptidase activity protein binding extracellular region extracellular region extracellular region extracellular space extracellular space proteolysis proteolysis defense response peptidase activity serine-type peptidase activity serine-type peptidase activity hydrolase activity extracellular matrix disassembly extracellular matrix identical protein binding | | |
| 32934_i_at | | | | | F08219 | | | | | |
| 32973_s_at | NOX1 | NADPH oxidase 1 | X | -100843323, -100843323 | AI821410 | 27035 | Xq22.1 | 226 | MAPK cascade angiogenesis regulation of systemic arterial blood pressure by renin-angiotensin protein binding cytoplasm endosome early endosome plasma membrane plasma membrane plasma membrane plasma membrane NADP+ metabolic process defense response inflammatory response signal transduction JNK cascade regulation of blood pressure positive regulation of cell population proliferation intrinsic apoptotic signaling pathway in response to oxidative stress positive regulation of vascular endothelial growth factor production membrane | 04145 04380 04670 |

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|--------------------------|--------|-----------------------|----|---------------------------------------|--------------------------|------|---------|-----|---|--|--|
| | | | | | | | | | | NAD(P)H oxidase H2O2-forming activity superoxide-generating NAD(P)H oxidase activity cell migration oxidoreductase activity extracellular matrix organization small GTPase binding superoxide anion generation superoxide anion generation superoxide anion generation superoxide anion generation hydrogen peroxide metabolic process cell projection NADPH oxidase complex NADPH oxidase complex positive regulation of MAPK cascade positive regulation of integrin biosynthetic process respiratory burst positive regulation of JNK cascade metal ion binding positive regulation of smooth muscle cell proliferation NADP binding oxidoreductase activity, acting on NAD(P)H, oxygen as acceptor anchoring junction cellular response to hyperoxia oxygen metabolic process superoxide-generating NADPH oxidase activity positive regulation of oxidative stress-induced intrinsic apoptotic signaling pathway | |
| 33144_at | CSNK1D | casein kinase 1 delta | 17 | -82242660, -82239018, -82242666 | AA129777 | 1453 | 17q25.3 | 194 | nucleotide binding protein kinase activity protein serine/threonine kinase activity | 04340 04540 04710 | |

[protein serine/threonine kinase activity](#)
[protein serine/threonine kinase activity](#)
[protein serine/threonine kinase activity](#)
[protein binding](#)
[ATP binding](#)
[nucleus](#)
[nucleus](#)
[nucleoplasm](#)
[nucleoplasm](#)
[cytoplasm](#)
[cytoplasm](#)
[Golgi apparatus](#)
[Golgi apparatus](#)
[centrosome](#)
[centrosome](#)
[spindle](#)
[spindle](#)
[cytosol](#)
[cytosol](#)
[cytoskeleton](#)
[spindle microtubule](#)
[spindle microtubule](#)
[plasma membrane](#)
[plasma membrane](#)
[cilium](#)
[protein phosphorylation](#)
[endocytosis](#)
[microtubule nucleation](#)
[Golgi organization](#)
[signal transduction](#)
[actin cytoskeleton](#)
[membrane](#)
[Wnt signaling pathway](#)
[kinase activity](#)
[transferase activity](#)
[regulation of Wnt signaling pathway](#)
[positive regulation of proteasomal ubiquitin-dependent protein catabolic process](#)
[positive regulation of proteasomal ubiquitin-dependent protein catabolic process](#)
[circadian regulation of gene expression](#)
[endoplasmic reticulum-Golgi intermediate compartment membrane](#)
[protein localization to Golgi apparatus](#)
[ciliary basal body](#)
[regulation of circadian rhythm](#)
[regulation of circadian rhythm](#)
[cadherin binding](#)
[COPII vesicle coating](#)
[perinuclear region of cytoplasm](#)
[perinuclear region of cytoplasm](#)
[rhythmic process](#)
[tau-protein kinase activity](#)
[spindle assembly](#)
[spindle assembly](#)
[protein localization to cilium](#)

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|--------------------------|------|-------------------------------|---|-----------|--------------------------|------|-------------------------|--|--|--|
| | | | | | | | | protein localization to centrosome positive regulation of canonical Wnt signaling pathway positive regulation of canonical Wnt signaling pathway protein serine kinase activity protein serine kinase activity protein serine kinase activity midbrain dopaminergic neuron differentiation non-motile cilium assembly non-motile cilium assembly positive regulation of non-canonical Wnt signaling pathway | | |
| 33275_at | ELK1 | ETS transcription factor ELK1 | X | -47635519 | AB016194 | 2002 | Xp11.23 | 239 | chromatin transcription cis-regulatory region binding RNA polymerase II cis-regulatory region sequence-specific DNA binding RNA polymerase II cis-regulatory region sequence-specific DNA binding DNA-binding transcription factor activity, RNA polymerase II-specific DNA-binding transcription factor activity, RNA polymerase II-specific DNA-binding transcription factor activity, RNA polymerase II-specific DNA-binding transcription activator activity, RNA polymerase II-specific DNA-binding transcription activator activity, RNA polymerase II-specific liver development DNA binding chromatin binding double-stranded DNA binding DNA-binding transcription factor activity DNA-binding transcription factor activity protein binding nucleus nucleus nucleus nucleoplasm nucleoplasm | 04010 04012 04510 04910 04912 05020 05140 05213 |

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|--------------------------|-------|---------------------|---|-----------------------|------------------------|---------------------|------------------------|--------------------|--|--|
| | | | | | | | | | regulation of DNA-templated transcription regulation of transcription by RNA polymerase II regulation of transcription by RNA polymerase II response to light stimulus gene expression cell differentiation lung development dendrite mitochondrial membrane mediator complex binding neuronal cell body sequence-specific DNA binding axon terminus response to ethanol positive regulation of DNA-templated transcription positive regulation of DNA-templated transcription positive regulation of DNA-templated transcription positive regulation of transcription by RNA polymerase II positive regulation of transcription by RNA polymerase II positive regulation of transcription by RNA polymerase II RNA polymerase II-specific DNA-binding transcription factor binding cellular response to testosterone stimulus cellular response to lipid cellular response to gamma radiation response to fibroblast growth factor response to fibroblast growth factor hippocampal neuron apoptotic process transcription regulator inhibitor activity transcription regulator activator activity sequence-specific double-stranded DNA binding | |
| 33353_at | ADCY1 | adenylate cyclase 1 | 7 | 45574139, 45574367 | W26466 | 107 | 7p12.3 | 54 | nucleotide binding adenylate cyclase activity adenylate cyclase activity calmodulin binding ATP binding cytoplasm cytoplasm plasma membrane plasma membrane plasma membrane plasma membrane plasma membrane cAMP biosynthetic process cAMP biosynthetic process | 00230 04020 04062 04114 04270 04540 04720 04912 04914 04916 04970 04971 04972 04976 05142 05146 |

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|--------------------------|------|-----------------------------------|----|----------|--------------------------|-----------------------|-------------------------|--------------------|--|-----------------------|
| | | | | | | | | | cAMP biosynthetic process adenylate cyclase-activating G protein-coupled receptor signaling pathway adenylate cyclase-activating G protein-coupled receptor signaling pathway axonogenesis long-term memory calcium- and calmodulin-responsive adenylate cyclase activity calcium- and calmodulin-responsive adenylate cyclase activity cyclic nucleotide biosynthetic process postsynaptic density membrane lyase activity phosphorus-oxygen lyase activity positive regulation of CREB transcription factor activity intracellular signal transduction regulation of circadian rhythm regulation of circadian rhythm membrane raft metal ion binding rhythmic process modulation of chemical synaptic transmission extracellular exosome cellular response to calcium ion Schaffer collateral - CA1 synapse hippocampal mossy fiber to CA3 synapse presynapse postsynaptic density membrane glutamatergic synapse presynaptic modulation of chemical synaptic transmission neuroinflammatory response neuroinflammatory response positive regulation of long-term synaptic potentiation positive regulation of long-term synaptic potentiation cellular response to forskolin | 05414 |
| 33406_at | CBY1 | chibby 1, beta catenin antagonist | 22 | 38656652 | AL050345 | 25776 | 22q13.1 | 59 | protein binding nucleus nucleus nucleus nucleoplasm nucleoplasm nucleolus cytoplasm | |

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|--------------------------|------|----------------------------------|----|---------------------------------|------------------------|--------------------|-------------------------|--------------------|---|--|
| | | | | | | | | | Golgi apparatus trans-Golgi network centrosome centriole centriole cytosol cytoskeleton cilium beta-catenin binding beta-catenin binding intracellular protein localization nuclear speck cell projection organization cell differentiation negative regulation of Wnt signaling pathway negative regulation of Wnt signaling pathway motile cilium floor plate development ciliary basal body sperm flagellum sperm flagellum identical protein binding protein homodimerization activity cell projection fat cell differentiation fat cell differentiation negative regulation of DNA-templated transcription protein homotetramerization cardiac muscle cell differentiation cardiac muscle cell differentiation canonical Wnt signaling pathway cilium assembly negative regulation of canonical Wnt signaling pathway | |
| 33446_at | ABAT | 4-aminobutyrate aminotransferase | 16 | 8720712, 8712968, 8674616 | W26407 | 18 | 16p13.2 | 58 | response to hypoxia mitochondrion mitochondrion mitochondrion mitochondrion mitochondrion mitochondrial matrix mitochondrial matrix copulation locomotory behavior transaminase activity response to xenobiotic stimulus gamma-aminobutyric acid metabolic process gamma-aminobutyric acid metabolic process gamma-aminobutyric acid biosynthetic process gamma-aminobutyric acid catabolic process response to iron ion negative regulation of gamma-aminobutyric acid secretion transferase activity | 00250 00280 00410 00640 00650 01100 |

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|--------------------------|-------|---|----|-----------|--------------------------|----------------------|--------------------------|---------------------|---|--|
| | | | | | | | | | cerebellum development pyridoxal phosphate binding pyridoxal phosphate binding pyridoxal phosphate binding positive regulation of heat generation positive regulation of insulin secretion 4-aminobutyrate transaminase complex succinate-semialdehyde dehydrogenase binding negative regulation of dopamine secretion 4-aminobutyrate:2-oxoglutarate transaminase activity 4-aminobutyrate:2-oxoglutarate transaminase activity response to nicotine exploration behavior response to cocaine identical protein binding response to ethanol negative regulation of blood pressure positive regulation of dopamine metabolic process metal ion binding (S)-3-amino-2-methylpropionate transaminase activity nervous system process nervous system process iron-sulfur cluster binding positive regulation of uterine smooth muscle contraction positive regulation of inhibitory postsynaptic potential positive regulation of prolactin secretion positive regulation of aspartate secretion | |
| 33704_at | URB1 | URB1 ribosome biogenesis factor | 21 | -32311017 | AB011111 | 9875 | 21q22.11 | 71 | maturation of LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA) maturation of 5.8S rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA) fibrillar center RNA binding nucleus nucleolus nucleolus nucleolus nucleolus | |
| 33721_at | ABCC2 | ATP binding cassette subfamily C member 2 | 10 | 99782639 | U49248 | 1244 | 10q24.2 | 361 | nucleotide binding protein binding ATP binding plasma membrane plasma membrane | 02010 04976 |

[plasma membrane](#)
[xenobiotic metabolic process](#)
[xenobiotic metabolic process](#)
[xenobiotic transmembrane transport](#)
[lipid transport](#)
[organic anion transmembrane transporter activity](#)
[ABC-type xenobiotic transporter activity](#)
[cell surface](#)
[cell surface](#)
[negative regulation of gene expression](#)
[bilirubin transmembrane transporter activity](#)
[bilirubin transmembrane transporter activity](#)
[ABC-type glutathione S-conjugate transporter activity](#)
[ABC-type glutathione S-conjugate transporter activity](#)
[bile acid and bile salt transport](#)
[bilirubin transport membrane](#)
[apical plasma membrane](#)
[apical plasma membrane](#)
[apical plasma membrane](#)
[ATP hydrolysis activity transmembrane transporter activity](#)
[heme catabolic process](#)
[ATPase-coupled transmembrane transporter activity](#)
[ATPase-coupled transmembrane transporter activity](#)
[xenobiotic transmembrane transporter activity](#)
[xenobiotic transmembrane transporter activity](#)
[ATPase-coupled inorganic anion transmembrane transporter activity](#)
[ATPase-coupled inorganic anion transmembrane transporter activity](#)
[intercellular canaliculus](#)
[xenobiotic export from cell](#)
[carboxylic acid transport](#)
[transmembrane transport](#)
[transmembrane transport](#)
[transmembrane transport](#)
[transepithelial transport](#)
[leukotriene transport](#)

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|----------------------------|--------|-----------------------------------|----|------------|--------------------------|----------------------|--------------------------|---|--|---|
| | | | | | | | | monoatomic anion transmembrane transport ABC-type transporter activity ABC-type transporter activity transport across blood-brain barrier xenobiotic transport across blood-brain barrier | | |
| | | | | | | | | | | |
| 33726_at | POLR2D | RNA polymerase II subunit D | 2 | -127843552 | U89387 | 5433 | 2q14.3 | 151 | nucleotide binding DNA-directed RNA polymerase complex protein binding nucleus nucleus nucleoplasm nucleoplasm nucleoplasm RNA polymerase II, core complex RNA polymerase II, core complex cytosol DNA-templated transcription initiation transcription by RNA polymerase II transcription by RNA polymerase II transcription initiation at RNA polymerase II promoter nuclear speck RNA polymerase complex translation initiation factor binding | 00230 00240 01100 03020 05016 |
| 33782_r_at | UBE2M | ubiquitin conjugating enzyme E2 M | 19 | -58555711 | AA587372 | 9040 | 19q13.43 | 183 | nucleotide binding ubiquitin-protein transferase activity ubiquitin-protein transferase activity protein binding ATP binding nucleus nucleoplasm cytosol cytosol transferase activity ubiquitin-like protein transferase activity NEDD8 transferase activity NEDD8 transferase activity NEDD8 transferase activity protein modification by small protein conjugation protein modification process protein modification process post-translational protein modification protein neddylation protein neddylation protein neddylation | 04120 |

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|--------------------------|---------|--|----|--|--------------------------|-----------------------|-------------------------|--------------------|---|--|
| | | | | | | | | | NEDD8 conjugating enzyme activity presynapse postsynapse glutamatergic synapse regulation of postsynapse assembly | |
| 33826_at | CIZ1 | CDKN1A interacting zinc finger protein 1 | 9 | -128166064, -128166064, -128166064 | AL120500 | 25792 | 9q34.11 | 65 | nucleic acid binding protein binding nucleus nucleus nucleus nucleus nucleoplasm plasma membrane zinc ion binding zinc ion binding cyclin binding positive regulation of DNA-templated DNA replication initiation metal ion binding maintenance of protein location in nucleus random inactivation of X chromosome | |
| 33865_at | ZMYND11 | zinc finger MYND-type containing 11 | 10 | 134799, 179993, 135454, 134483, 134799, 135808, 135264, 135454, 130087, 134292, 135597 | AI926555 | 10771 | 10p15.3 | 69 | DNA binding double-stranded DNA binding transcription corepressor activity transcription corepressor activity protein binding nucleus nucleus nucleus nucleoplasm chromosome chromatin organization zinc ion binding zinc ion binding zinc ion binding regulation of signal transduction regulation of transcription elongation by RNA polymerase II regulation of transcription elongation by RNA polymerase II regulation of transcription elongation by RNA polymerase II negative regulation of canonical NF-kappaB signal transduction negative regulation of DNA-templated transcription negative regulation of DNA-templated transcription negative regulation of JNK cascade metal ion binding defense response to virus histone H3K36me3 reader activity histone H3K36me3 reader activity | |

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|--------------------------|----------|-----------------------------|---|----------|------------------------|-----------------------|------------------------|-----|---|--|
| | | | | | | | | | | histone H3K36me3 reader activity negative regulation of extrinsic apoptotic signaling pathway |
| 33912_at | ZMPSTE24 | zinc metallopeptidase STE24 | 1 | 40258235 | Y13834 | 10269 | 1p34.2 | 123 | liver development hair follicle development heart morphogenesis ventricular cardiac muscle tissue development cardiac ventricle development growth plate cartilage development double-stranded DNA binding endopeptidase activity endopeptidase activity metalloendopeptidase activity metalloendopeptidase activity protein binding nucleus nuclear envelope nuclear inner membrane endosome endoplasmic reticulum endoplasmic reticulum membrane endoplasmic reticulum membrane DNA repair chromatin organization regulation of DNA-templated transcription proteolysis proteolysis lipid metabolic process inflammatory cell apoptotic process DNA damage response nucleus organization nuclear envelope organization nuclear envelope organization regulation of mitotic cell cycle adult walking behavior regulation of heart contraction peptidase activity metalloexopeptidase activity metallopeptidase activity determination of adult lifespan regulation of cell shape epidermis development regulation of autophagy positive regulation of gene expression negative regulation of gene expression regulation of glucose metabolic process membrane membrane protein processing hydrolase activity | |

[regulation of lipid metabolic process](#)
[bone mineralization](#)
[prenylated protein catabolic process](#)
[regulation of bone mineralization](#)
[early endosome membrane](#)
[late endosome membrane](#)
[regulation of TOR signaling](#)
[regulation of hormone metabolic process](#)
[protein-containing complex](#)
[multicellular organism growth](#)
[regulation of multicellular organism growth](#)
[epigenetic regulation of gene expression](#)
[maintenance of rDNA](#)
[regulation of DNA damage response, signal transduction by p53 class mediator](#)
[positive regulation of gene expression via chromosomal CpG island demethylation](#)
[metal ion binding](#)
[regulation of fibroblast proliferation](#)
[thymus development](#)
[regulation of defense response to virus](#)
[regulation of defense response to virus](#)
[neuromuscular process](#)
[chromosome organization](#)
[protein maturation](#)
[protein maturation](#)
[cardiac muscle cell development](#)
[regulation of ventricular cardiac muscle cell membrane repolarization](#)
[kidney morphogenesis](#)
[cardiac conduction](#)
[CAMKK-AMPK signaling cascade](#)
[extracellular exosome](#)
[regulation of stress-activated protein kinase signaling cascade](#)
[cellular response to gamma radiation](#)
[CAAX-box protein processing](#)
[CAAX-box protein processing](#)
[response to DNA damage](#)
[checkpoint signaling](#)
[regulation of mitotic cell cycle DNA replication](#)
[regulation of blood circulation](#)
[negative regulation of miRNA processing](#)
[calcium ion import into sarcoplasmic reticulum](#)

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|--------------------------|-------|--|----|----------------------|------------------------|----------------------|-------------------------|--|---|
| | | | | | | | | regulation of termination of RNA polymerase I transcription regulation of cellular senescence | |
| 34152_at | SAG | S-antigen visual arrestin | 2 | 233307815, 253153 | W28071 | 6295 | 2q37.1 | 52 | G protein-coupled receptor binding photoreceptor outer segment photoreceptor outer segment photoreceptor outer segment photoreceptor inner segment photoreceptor inner segment G protein-coupled receptor internalization opsin binding protein phosphatase inhibitor activity protein binding cytosol signal transduction cell surface receptor signaling pathway sensory perception membrane G protein-coupled opsin signaling pathway spectrin binding cell projection phosphoprotein binding |
| 34311_at | GLRX | glutaredoxin | 5 | -95813848, -95813848 | X76648 | 2745 | 5q15 | 112 | protein binding nucleus cytoplasm cytosol disulfide oxidoreductase activity glutathione disulfide oxidoreductase activity glutathione disulfide oxidoreductase activity glutathione disulfide oxidoreductase activity nucleobase-containing small molecule interconversion sodium channel regulator activity positive regulation of membrane potential extracellular exosome |
| 34370_at | ARCN1 | archain 1 coat protein complex I subunit delta | 11 | 118572386, 118572408 | X81198 | 372 | 11q23.3 | 188 | Golgi membrane Golgi membrane RNA binding protein binding cytoplasm endoplasmic reticulum endoplasmic reticulum membrane Golgi apparatus cytosol intracellular protein transport endoplasmic reticulum to Golgi vesicle-mediated transport retrograde vesicle-mediated transport , |

[Golgi to endoplasmic reticulum](#)
[retrograde vesicle-mediated transport](#),
[Golgi to endoplasmic reticulum](#)
adult locomotory behavior
protein transport membrane
membrane vesicle-mediated transport
cerebellar Purkinje cell layer maturation
COPI vesicle coat
COPI vesicle coat
COPI vesicle coat
transport vesicle
COPI-coated vesicle
COPI-coated vesicle membrane
cytoplasmic vesicle pigmentation
[Golgi vesicle transport](#)
[Golgi localization](#)
establishment of localization in cell

91 Genes