

Click the gene set name to see the gene set page. Click the number of genes [in brackets] to download the list of genes.

Color bar shading from light green to black, where lighter colors indicate more significant FDR q-values (< 0.05) and black indicates less significant FDR q-values (≥ 0.05).

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Gene Set Name [# Genes (K)]	Description	# Genes in Overlap (k)	k/K	p-value 	FDR q-value 
BIOPOLYMER_METABOLIC_PROCESS [1684]	Genes annotated by the GO term GO:0043283. The chemical reactions and pathways involving biopolymers, long, repeating chains of monomers found in nature e.g. polysaccharides and proteins.	26		5.27 e ⁻¹¹	1.14 e ⁻⁷
NUCLEOBASENUCLEOSIDENUCLEOTIDE_AND_NUC NUCLEIC_ACID_METABOLIC_PROCESS [1244]	Genes annotated by the GO term GO:0006139. The chemical reactions and pathways involving nucleobases, nucleosides, nucleotides and nucleic acids.	20		5.6 e ⁻⁹	6.04 e ⁻⁶
RNA_METABOLIC_PROCESS [841]	Genes annotated by the GO term GO:0016070. The chemical reactions and pathways involving RNA, ribonucleic acid, one of the two main type of nucleic acid, consisting of a long, unbranched macromolecule formed from ribonucleotides joined in 3',5'-phosphodiester linkage.	16		2.12 e ⁻⁸	1.53 e ⁻⁵
PID_INTEGRIN4_PATHWAY [11]	Alpha6 beta4 integrin-ligand interactions	4		3.63 e ⁻⁸	1.96 e ⁻⁵
ANATOMICAL_STRUCTURE_DEVELOPMENT [1013]	Genes annotated by the GO term GO:0048856. The biological process whose specific outcome is the progression of an anatomical structure from an initial condition to its mature state. This process begins with the formation of the structure and ends with the mature structure, whatever form that may be including its natural destruction. An anatomical structure is any biological entity that occupies space and is distinguished from its surroundings. Anatomical structures can be macroscopic such as a carpel, or microscopic such as an acrosome.	17		4.61 e ⁻⁸	1.99 e ⁻⁵
ORGAN_DEVELOPMENT [571]	Genes annotated by the GO term GO:0048513.	13		6.17 e ⁻⁸	2.22 e ⁻⁵

	Development of a tissue or tissues that work together to perform a specific function or functions. Development pertains to the process whose specific outcome is the progression of a structure over time, from its formation to the mature structure. Organs are commonly observed as visibly distinct structures, but may also exist as loosely associated clusters of cells that work together to perform a specific function or functions.				
NABA_BASEMENT_MEMBRANES [40]	Genes encoding structural components of basement membranes	5		2.15 e ⁻⁷	6.62 e ⁻⁵
KEGG_ECM_RECEPTOR_INTERACTION [84]	ECM-receptor interaction	6		3.75 e ⁻⁷	8.89 e ⁻⁵
REGULATION_OF_CELLULAR_METABOLIC_PROCESS [787]	Genes annotated by the GO term GO:0031323. Any process that modulates the frequency, rate or extent of the chemical reactions and pathways by which individual cells transform chemical substances.	14		3.79 e ⁻⁷	8.89 e ⁻⁵
REGULATION_OF_TRANSCRIPTION [566]	Genes annotated by the GO term GO:0045449. Any process that modulates the frequency, rate or extent of the synthesis of either RNA on a template of DNA or DNA on a template of RNA.	12		4.31 e ⁻⁷	8.89 e ⁻⁵
REGULATION_OF_METABOLIC_PROCESS [799]	Genes annotated by the GO term GO:0019222. Any process that modulates the frequency, rate or extent of the chemical reactions and pathways within a cell or an organism.	14		4.54 e ⁻⁷	8.89 e ⁻⁵
MUSCLE_DEVELOPMENT [93]	Genes annotated by the GO term GO:0007517. The process whose specific outcome is the progression of the muscle over time, from its formation to the mature structure. The muscle is an organ consisting of a tissue made up of various elongated cells that are specialized to contract and thus to produce movement and mechanical work.	6		6.86 e ⁻⁷	1.23 e ⁻⁴
REGULATION_OF_NUCLEOBASENUCLEOSIDENUCLEOTIDE_AND_NUCLEIC_ACID_METABOLIC_PATHWAY [618]	Genes annotated by the GO term GO:0019219. Any process that modulates the frequency, rate or extent of the chemical reactions and pathways involving nucleobases, nucleosides, nucleotides and nucleic acids.	12		1.08 e ⁻⁶	1.68 e ⁻⁴
SYSTEM_DEVELOPMENT [861]	Genes annotated by the GO term GO:0048731. The process whose specific outcome is the progression of an organismal system over time, from its formation to the mature structure. A system is a regularly interacting or interdependent group of organs or tissues that work together to carry out a given biological	14		1.09 e ⁻⁶	1.68 e ⁻⁴

	process.				
TRANSCRIPTION [753]	Genes annotated by the GO term GO:0006350. The synthesis of either RNA on a template of DNA or DNA on a template of RNA.	13		1.4 e-6	1.91 e-4
TRANSCRIPTION_DNA_DEPENDENT [636]	Genes annotated by the GO term GO:0006351. The synthesis of RNA on a template of DNA.	12		1.45 e-6	1.91 e-4
RNA_BIOSYNTHETIC_PROCESS [638]	Genes annotated by the GO term GO:0032774. The chemical reactions and pathways resulting in the formation of RNA, ribonucleic acid, one of the two main type of nucleic acid, consisting of a long, unbranched macromolecule formed from ribonucleotides joined in 3',5'-phosphodiester linkage. Includes polymerization of ribonucleotide monomers.	12		1.5 e-6	1.91 e-4
MULTICELLULAR_ORGANISMAL_DEVELOPMENT [1049]	Genes annotated by the GO term GO:0007275. The biological process whose specific outcome is the progression of an organism over time from an initial condition (e.g. a zygote or a young adult) to a later condition (e.g. a multicellular animal or an aged adult).	15		2.17 e-6	2.6 e-4
TRANSPORT [795]	Genes annotated by the GO term GO:0006810. The directed movement of substances (such as macromolecules, small molecules, ions) into, out of, within or between cells.	13		2.53 e-6	2.8 e-4
REGULATION_OF_GENE_EXPRESSION [673]	Genes annotated by the GO term GO:0010468. Any process that modulates the frequency, rate or extent of gene expression. Gene expression is the process in which a gene's coding sequence is converted into a mature gene product or products (proteins or RNA). This includes the production of an RNA transcript as well as any processing to produce a mature RNA product or an mRNA (for protein-coding genes) and the translation of that mRNA into protein. Some protein processing events may be included when they are required to form an active form of a product from an inactive precursor form.	12		2.6 e-6	2.8 e-4
PID_INTEGRIN1_PATHWAY [66]	Beta1 integrin cell surface interactions	5		2.72 e-6	2.8 e-4
PROTEIN_METABOLIC_PROCESS [1231]	Genes annotated by the GO term GO:0019538. The chemical reactions and pathways involving a specific protein, rather than of proteins in general. Includes protein modification.	16		3.32 e-6	3.12 e-4
REGULATION_OF_TRANSCRIPTIONDNA_DEPENDENT [461]	Genes annotated by the GO term GO:0006355. Any process that modulates the frequency, rate or extent of DNA-dependent transcription.	10		3.33 e-6	3.12 e-4

REGULATION_OF_RNA_METABOLIC_PROCESS [471]	Genes annotated by the GO term GO:0051252. Any process that modulates the frequency, rate or extent of the chemical reactions and pathways involving RNA.	10		4.02 e ⁻⁶	3.61 e ⁻⁴
KEGG_FOCAL_ADHESION [201]	Focal adhesion	7		5 e ⁻⁶	4.31 e ⁻⁴
PID_ARF6_PATHWAY [35]	Arf6 signaling events	4		5.42 e ⁻⁶	4.49 e ⁻⁴
REACTOME_INTEGRIN_CELL_SURFACE_INTERACTIONS [79]	Genes involved in Integrin cell surface interactions	5		6.64 e ⁻⁶	5.15 e ⁻⁴
ESTABLISHMENT_OF_LOCALIZATION [870]	Genes annotated by the GO term GO:0051234. The directed movement of a cell, substance or cellular entity, such as a protein complex or organelle, to a specific location.	13		6.69 e ⁻⁶	5.15 e ⁻⁴
CELLULAR_COMPONENT_ASSEMBLY [298]	Genes annotated by the GO term GO:0022607. A cellular process that results in the assembly of a part of the cell.	8		7.09 e ⁻⁶	5.27 e ⁻⁴
KEGG_SMALL_CELL_LUNG_CANCER [84]	Small cell lung cancer	5		8.97 e ⁻⁶	6.45 e ⁻⁴
POSITIVE_REGULATION_OF_CELLULAR_PROCESSES [668]	Genes annotated by the GO term GO:0048522. Any process that activates or increases the frequency, rate or extent of cellular processes, those that are carried out at the cellular level, but are not necessarily restricted to a single cell. For example, cell communication occurs among more than one cell, but occurs at the cellular level.	11		1.44 e ⁻⁵	1 e ⁻³
PID_A6B1_A6B4_INTEGRIN_PATHWAY [46]	a6b1 and a6b4 Integrin signaling	4		1.64 e ⁻⁵	1.11 e ⁻³
POSITIVE_REGULATION_OF_BIOLOGICAL_PROCESS [709]	Genes annotated by the GO term GO:0048518. Any process that activates or increases the frequency, rate or extent of a biological process. Biological processes are regulated by many means; examples include the control of gene expression, protein modification or interaction with a protein or substrate molecule.	11		2.49 e ⁻⁵	1.63 e ⁻³
PID_NFAT_3PATHWAY [54]	Role of Calcineurin-dependent NFAT signaling in lymphocytes	4		3.12 e ⁻⁵	1.98 e ⁻³
NABA_CORE_MATRISOME [275]	Ensemble of genes encoding core extracellular matrix including ECM glycoproteins, collagens and proteoglycans	7		3.77 e ⁻⁵	2.32 e ⁻³
MACROMOLECULAR_COMPLEX_ASSEMBLY [280]	Genes annotated by the GO term GO:0065003. The aggregation, arrangement and bonding together of a set of macromolecules to form a complex.	7		4.22 e ⁻⁵	2.53 e ⁻³
CYTOSKELETON_ORGANIZATION_AND_BIOGENESIS [208]	Genes annotated by the GO term GO:0007010. A process that is carried out at the cellular level which results in the formation, arrangement of constituent parts, or disassembly of cytoskeletal structures.	6		6.9 e ⁻⁵	4.02 e ⁻³
KEGG_VIRAL_MYOCARDITIS [73]	Viral myocarditis	4		1.02 e ⁻⁴	5.8 e ⁻³
KEGG_PATHWAYS_IN_CANCER [328]	Pathways in cancer	7		1.13 e ⁻⁴	6.27 e ⁻³

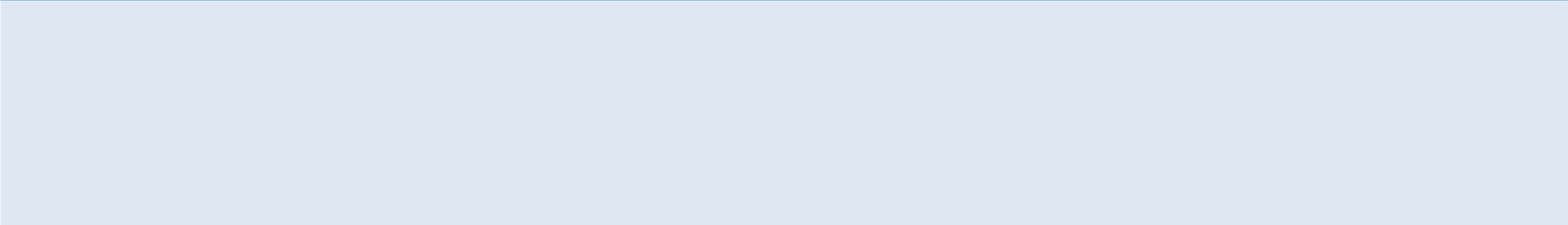
PID_TCRCALCIUMPATHWAY [29]	Calcium signaling in the CD4+ TCR pathway	3		1.19 e-4	6.28 e-3
POSITIVE_REGULATION_OF_TRANSCRIPTION [144]	Genes annotated by the GO term GO:0045941. Any process that activates or increases the frequency, rate or extent of transcription.	5		1.19 e-4	6.28 e-3
REACTOME_APOPTOSIS [148]	Genes involved in Apoptosis	5		1.36 e-4	6.97 e-3
TRANSCRIPTION_FROM_RNA_POLYMERASE_II_P I_PROMOTER [457]	Genes annotated by the GO term GO:0006366. The synthesis of RNA from a DNA template by RNA polymerase II (Pol II), originating at a Pol II-specific promoter. Includes transcription of messenger RNA (mRNA) and certain small nuclear RNAs (snRNAs).	8		1.45 e-4	7.16 e-3
SKELETAL_MUSCLE_DEVELOPMENT [31]	Genes annotated by the GO term GO:0007519. The developmental sequence of events leading to the formation of adult muscle that occurs in the anima. In vertebrate skeletal muscle the main events are: the fusion of myoblasts to form myotubes that increase in size by further fusion to them of myoblasts, the formation of myofibrils within their cytoplasm and the establishment of functional neuromuscular junctions with motor neurons. At this stage they can be regarded as mature muscle fibers.	3		1.46 e-4	7.16 e-3
POSITIVE_REGULATION_OF_NUCLEOBASENUCLE CLEOSIDENUCLEOTIDE_AND_NUCLEIC_ACID_ME _METABOLIC_PROCESS [154]	Genes annotated by the GO term GO:0045935. Any process that activates or increases the frequency, rate or extent of the chemical reactions and pathways involving nucleobases, nucleosides, nucleotides and nucleic acids.	5		1.63 e-4	7.83 e-3
ORGANELLE_ORGANIZATION_AND_BIOGENESIS [473]	Genes annotated by the GO term GO:0006996. A process that is carried out at the cellular level which results in the formation, arrangement of constituent parts, or disassembly of any organelle within a cell.	8		1.83 e-4	8.46 e-3
KEGG_HYPERTROPHIC_CARDIOMYOPATHY_HCM [85]	Hypertrophic cardiomyopathy (HCM)	4		1.84 e-4	8.46 e-3
BIOCARTA_AGR_PATHWAY [36]	Agrin in Postsynaptic Differentiation	3		2.29 e-4	1.03 e-2
PROTEIN_COMPLEX_ASSEMBLY [167]	Genes annotated by the GO term GO:0006461. The aggregation, arrangement and bonding together of a set of components to form a protein complex.	5		2.38 e-4	1.05 e-2
KEGG_DILATED_CARDIOMYOPATHY [92]	Dilated cardiomyopathy	4		2.5 e-4	1.08 e-2
REACTOME_APOPTOTIC_CLEAVAGE_OF_CELLULA ULAR_PROTEINS [40]	Genes involved in Apoptotic cleavage of cellular proteins	3		3.14 e-4	1.3 e-2
STRIATED_MUSCLE_DEVELOPMENT [40]	Genes annotated by the GO term GO:0014706. The process whose specific outcome is the progression of a striated muscle over time, from its formation to the mature structure. Striated muscle contain fibers that	3		3.14 e-4	1.3 e-2

	are divided by transverse bands into striations, and cardiac and skeletal muscle are types of striated muscle. Skeletal muscle myoblasts fuse to form myotubes and eventually multinucleated muscle fibers. The fusion of cardiac cells is very rare and can only form binucleate cells.				
CELLULAR_PROTEIN_METABOLIC_PROCESS [1117]	Genes annotated by the GO term GO:0044267. The chemical reactions and pathways involving a specific protein, rather than of proteins in general, occurring at the level of an individual cell. Includes protein modification.	12		3.42 e ⁻⁴	1.39 e ⁻²
ION_TRANSPORT [185]	Genes annotated by the GO term GO:0006811. The directed movement of charged atoms or small charged molecules into, out of, within or between cells.	5		3.81 e ⁻⁴	1.5 e ⁻²
CELLULAR_MACROMOLECULE_METABOLIC_PROCESS [1131]	Genes annotated by the GO term GO:0044260. The chemical reactions and pathways involving macromolecules, large molecules including proteins, nucleic acids and carbohydrates, as carried out by individual cells.	12		3.82 e ⁻⁴	1.5 e ⁻²
PID_INTEGRIN3_PATHWAY [43]	Beta3 integrin cell surface interactions	3		3.9 e ⁻⁴	1.5 e ⁻²
ACTIN_CYTOSKELETON_ORGANIZATION_AND_BIOGENESIS [105]	Genes annotated by the GO term GO:0030036. A process that is carried out at the cellular level which results in the formation, arrangement of constituent parts, or disassembly of cytoskeletal structures comprising actin filaments and their associated proteins.	4		4.14 e ⁻⁴	1.56 e ⁻²
POSITIVE_REGULATION_OF_EPITHELIAL_CELL_PROLIFERATION [10]	Genes annotated by the GO term GO:0050679. Any process that activates or increases the rate or extent of epithelial cell proliferation.	2		4.74 e ⁻⁴	1.73 e ⁻²
REACTOME_SYNTHESIS_OF_PIPS_AT_THE_LATE_ENDOSOME_MEMBRANE [10]	Genes involved in Synthesis of PIPs at the late endosome membrane	2		4.74 e ⁻⁴	1.73 e ⁻²
REACTOME_MUSCLE_CONTRACTION [48]	Genes involved in Muscle contraction	3		5.4 e ⁻⁴	1.94 e ⁻²
ACTIN_FILAMENT_BASED_PROCESS [115]	Genes annotated by the GO term GO:0030029. Any cellular process that depends upon or alters the actin cytoskeleton, that part of the cytoskeleton comprising actin filaments and their associated proteins.	4		5.83 e ⁻⁴	2.06 e ⁻²
METAL_ION_TRANSPORT [117]	Genes annotated by the GO term GO:0030001. The directed movement of metal ions, any metal ion with an electric charge, into, out of, within or between cells.	4		6.22 e ⁻⁴	2.16 e ⁻²
REACTOME_SYNTHESIS_OF_PIPS_AT_THE_EARLY_ENDOSOME_MEMBRANE [12]	Genes involved in Synthesis of PIPs at the early endosome membrane	2		6.93 e ⁻⁴	2.37 e ⁻²
REACTOME_APOPTOTIC_EXECUTION_PHASE [54]	Genes involved in Apoptotic execution phase	3		7.63 e ⁻⁴	2.57 e ⁻²

REACTOME_CASPASE_MEDIATED_CLEAVAGE_OF_OF_CYTOSKELETAL_PROTEINS [13]	Genes involved in Caspase-mediated cleavage of cytoskeletal proteins	2		8.17 e ⁻⁴	2.71 e ⁻²
STRIATED_MUSCLE_CONTRACTION_GO_0006941 [14]	Genes annotated by the GO term GO:0006941. A process whereby force is generated within striated muscle tissue, resulting in a change in muscle geometry. Force generation involves a chemo-mechanical energy conversion step. The chemo-mechanical energy conversion step is carried out by the actin/myosin complex activity, which generates force through ATP hydrolysis. Striated muscle is a type of muscle in which the repeating units (sarcomeres) of the contractile myofibrils are arranged in registry throughout the cell, resulting in transverse or oblique striations observable at the level of the light microscope.	2		9.51 e ⁻⁴	3.11 e ⁻²
POSITIVE_REGULATION_OF_CELLULAR_METABOLIC_PROCESS [229]	Genes annotated by the GO term GO:0031325. Any process that activates or increases the frequency, rate or extent of the chemical reactions and pathways by which individual cells transform chemical substances.	5		9.98 e ⁻⁴	3.21 e ⁻²
POST_TRANSLATIONAL_PROTEIN_MODIFICATION [476]	Genes annotated by the GO term GO:0043687. The covalent alteration of one or more amino acids occurring in a protein after the protein has been completely translated and released from the ribosome.	7		1.05 e ⁻³	3.33 e ⁻²
PID_AR_PATHWAY [61]	Coregulation of Androgen receptor activity	3		1.09 e ⁻³	3.37 e ⁻²
CYTOPLASM_ORGANIZATION_AND_BIOGENESIS [15]	Genes annotated by the GO term GO:0007028. A process that is carried out at the cellular level which results in the formation, arrangement of constituent parts, or disassembly of the cytoplasm and its components.	2		1.09 e ⁻³	3.37 e ⁻²
POSITIVE_REGULATION_OF_METABOLIC_PROCESS [236]	Genes annotated by the GO term GO:0009893. Any process that activates or increases the frequency, rate or extent of the chemical reactions and pathways within a cell or an organism.	5		1.14 e ⁻³	3.45 e ⁻²
KEGG_UBIQUITIN_MEDIATED_PROTEOLYSIS [138]	Ubiquitin mediated proteolysis	4		1.15 e ⁻³	3.45 e ⁻²
PROTEIN_MODIFICATION_PROCESS [631]	Genes annotated by the GO term GO:0006464. The covalent alteration of one or more amino acids occurring in proteins, peptides and nascent polypeptides (co-translational, post-translational modifications). Includes the modification of charged tRNAs that are destined to occur in a protein (pre-translation modification).	8		1.21 e ⁻³	3.56 e ⁻²
CELL_MATURATION [16]	Genes annotated by the	2		1.25 e ⁻³	3.64 e ⁻²

	GO term GO:0048469. A developmental process, independent of morphogenetic (shape) change, that is required for a cell to attain its fully functional state.				
MYOBLAST_DIFFERENTIATION [17]	Genes annotated by the GO term GO:0045445. The process whereby a relatively unspecialized cell acquires specialized features of a myoblast. A myoblast is a mononucleate cell type that, by fusion with other myoblasts, gives rise to the myotubes that eventually develop into skeletal muscle fibers.	2		1.41 e ⁻³	4.06 e ⁻²
CATION_TRANSPORT [147]	Genes annotated by the GO term GO:0006812. The directed movement of cations, atoms or small molecules with a net positive charge, into, out of, within or between cells.	4		1.45 e ⁻³	4.07 e ⁻²
BIOPOLYMER_MODIFICATION [650]	Genes annotated by the GO term GO:0043412. The covalent alteration of one or more monomeric units in a polypeptide, polynucleotide, polysaccharide, or other biological polymer, resulting in a change in its properties.	8		1.45 e ⁻³	4.07 e ⁻²
REACTOME_AXON_GUIDANCE [251]	Genes involved in Axon guidance	5		1.5 e ⁻³	4.13 e ⁻²
DEVELOPMENTAL_MATURATION [18]	Genes annotated by the GO term GO:0021700. A developmental process, independent of morphogenetic (shape) change, that is required for an anatomical structure, cell or cellular component to attain its fully functional state.	2		1.59 e ⁻³	4.28 e ⁻²
ANATOMICAL_STRUCTURE_MORPHOGENESIS [376]	Genes annotated by the GO term GO:0009653. The process by which anatomical structures are generated and organized. Morphogenesis pertains to the creation of form.	6		1.59 e ⁻³	4.28 e ⁻²
INTRACELLULAR_SIGNALING_CASCADE [667]	Genes annotated by the GO term GO:0007242. A series of reactions within the cell that occur as a result of a single trigger reaction or compound.	8		1.71 e ⁻³	4.55 e ⁻²

Gene/geneset overlap matrix



Entrez Gene Id	Gene Symbol	BIOPOLYMER_METABOLIC_PROCESS	NUCLEOBASENUCLEOSIDENUCLEOTIDE_AND_NUCLEIC_ACID_METABOLIC_PROCESS	RNA_METABOLIC_PROCESS	PID_INTEGRIN4_PATHWAY	ANATOMICAL_STRUCTURE_DEVELOPMENT	ORGAN_DEVELOPMENT	NABA_BASEMENT_MEMBRANES	KEGG_ECM_RECEPTOR_INTERACTION	REGULATION_OF_CELLULAR_METABOLIC_PROCESS	REGULATION_OF_TRANSCRIPTION	REGULATION_OF_METABOLIC_PROCESS	MUSCLE_DEVELOPMENT	REGULATION_OF_NUCLEOBASENUCLEOSIDENUCLEOTIDE_AND_NUCLEIC_ACID_METABOLIC_PROCESS	SYSTEM_DEVELOPMENT	TRANSCRIPTION	TRANSCRIPTION_DNA_DEPENDENT	RNA_BIOSYNTHETIC_PROCESS	MULTICELLULAR_ORGANISMAL_DEVELOPMENT	TRANSPORT	REGULATION_OF_GENE_EXPRESSION	PID_INTEGRIN1_PATHWAY	PROTEIN_METABOLIC_PROCESS	REGULATION_OF_TRANSCRIPTIONDNA_DEPENDENT	REGULATION_OF_RNA_METABOLIC_PROCESS	KEGG_FOCAL_ADHESION	PID_ARF6_PATHWAY	REACTOME_INTEGRIN_CELL_SURFACE_INTERACTIONS	ESTABLISHMENT_OF_LOCALIZATION	CELLULAR_COMPONENT_ASSEMBLY	KEGG_SMALL_CELL_LUNG_CANCER	POSITIVE_REGULATION_OF_CELLULAR_PROCESS	PID_A6B1_A6B4_INTEGRIN_PATHWAY	POSITIVE_REGULATION_OF_BIOLOGICAL_PROCESS	PID_NFAT_3PATHWAY	NABA_CORE_MATRISOME	MACROMOLECULAR_COMPLEX_ASSEMBLY	CYTOSKELETON_ORGANIZATION_AND_BIOGENESIS	KEGG_VIRAL_MYOCARDITIS	KEGG_PATHWAYS_IN_CANCER	PID_TCRCALCIUMPATHWAY	POSITIVE_REGULATION_OF_TRANSCRIPTION	REACTOME_APOPTOSIS	TRANSCRIPTION_FROM_RNA_POLYMERASE_IL_PROMOTER	SKELETAL_MUSCLE_DEVELOPMENT	POSITIVE_REGULATION_OF_NUCLEOBASENUCLEOSIDENUCLEOTIDE_AND_NUCLEIC_ACID_METABOLIC_PROCESS	ORGANELLE_ORGANIZATION_AND_BIOGENESIS	KEGG_HYPERTROPHIC_CARDIOMYOPATHY_HCM	BIOCARTA_AGR_PATHWAY	PROTEIN_COMPLEX_ASSEMBLY	KEGG_DILATED_CARDIOMYOPATHY	REACTOME_APOPTOTIC_CLEAVAGE_OF_CELLULAR_PROTEINS	STRIATED_MUSCLE_DEVELOPMENT	CELLULAR_PROTEIN_METABOLIC_PROCESS	ION_TRANSPORT	CELLULAR_MACROMOLECULE_METABOLIC_PROCESS	PID_INTEGRIN3_PATHWAY	ACTIN_CYTOSKELETON_ORGANIZATION_AND_BIOGENESIS	POSITIVE_REGULATION_OF_EPITHELIAL_CELL_PROLIFERATION	REACTOME_SYNTHESIS_OF_PIP3_AT_THE_LATE_ENDOSOME_MEMBRANE	REACTOME_MUSCLE_CONTRACTION	ACTIN_FILAMENT_BASED_PROCESS	METAL_ION_TRANSPORT	REACTOME_SYNTHESIS_OF_PIP3_AT_THE_EARLY_ENDOSOME_MEMBRANE	REACTOME_APOPTOTIC_EXECUTION_PHASE	REACTOME_CASPASE_MEDIATED_CLEAVAGE_OF_CYTOSKELETAL_PROTEINS	STRIATED_MUSCLE_CONTRACTION_GO_0006941	POSITIVE_REGULATION_OF_CELLULAR_METABOLIC_PROCESS	POST_TRANSLATIONAL_PROTEIN_MODIFICATION	PID_AR_PATHWAY	CYTOPLASM_ORGANIZATION_AND_BIOGENESIS	POSITIVE_REGULATION_OF_METABOLIC_PROCESS	KEGG_UBIQUITIN_MEDIATED_PROTEOLYSIS	PROTEIN_MODIFICATION_PROCESS	CELL_MATURATION	MYOBLAST_DIFFERENTIATION	CATION_TRANSPORT	BIOPOLYMER_MODIFICATION	REACTOME_AXON_GUIDANCE	DEVELOPMENTAL_MATURATION	ANATOMICAL_STRUCTURE_MORPHOGENESIS	INTRACELLULAR_SIGNALING_CASCADE
Entrez	Source	Gene	Description																																																																															
6096	RORB		S RAR-related orphan receptor B																																																																															
4853	NOTCH2		S notch 2																																																																															
6939	TCF15		S transcription factor 15 (basic helix-loop-helix)																																																																															
4297	MLL		S myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila)																																																																															
6239	RREB1		S ras responsive element binding protein 1																																																																															
22906	TRAK1		S trafficking protein, kinesin binding 1																																																																															
9149	DYRK1B		S dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1B																																																																															
9969	MED13		S mediator complex subunit 13																																																																															
4775	NFATC3		S nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 3																																																																															
10847	SRCAP		S Snf2-related CREBBP activator protein																																																																															
1112	FOXN3		S forkhead box N3																																																																															
5927	KDM5A		S lysine (K)-specific demethylase 5A																																																																															
23381	SMG5		S smg-5 homolog, nonsense mediated mRNA decay factor (C. elegans)																																																																															
7536	SF1		S splicing factor 1																																																																															
6421	SFPQ		S splicing factor proline/glutamine-rich																																																																															
6625	SNRNP70		S small nuclear ribonucleoprotein 70kDa (U1)																																																																															
4595	MUTYH		S mutY homolog (E.																																																																															

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