

- MSigDB Home
- About Collections
- Browse Gene Sets
- Search Gene Sets
- Investigate Gene Sets
- View Gene Families
- Help

Compute Overlaps for Selected Genes

Converted 116 submitted identifiers into 107 entrez genes. [click here for details.](#)

Collections	# Overlaps Shown	# Gene Sets in Collections	# Genes in Comparison (n)	# Genes in Universe (N)
BP, CP, CP:BIOCARTA, CP:KEGG, CP:REACTOME	42	2145	107	45956

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).

Save to: [Excel](#) | [GenomeSpace](#)

Gene Set Name [# Genes (K)]	Description	# Genes in Overlap (k)	k/K	p-value ?	FDR q-value ?
KEGG_TIGHT_JUNCTION [134]	Tight junction	6		7.79×10^{-7}	9.15×10^{-4}
SYSTEM_PROCESS [563]	Genes annotated by the GO term GO:0003008. A biological process, occurring at the level of an organ system pertinent to the function of the organism. An organ system is a regularly interacting or interdependent group of organs or tissues that work together to carry out a given biological process.	10		8.53×10^{-7}	9.15×10^{-4}
KEGG_HYPERTROPHIC_CARDIOMYOPATHY_HCM [85]	Hypertrophic cardiomyopathy (HCM)	5		1.76×10^{-6}	1.26×10^{-3}
KEGG_DILATED_CARDIOMYOPATHY [92]	Dilated cardiomyopathy	5		2.61×10^{-6}	1.4×10^{-3}
REACTOME_METABOLISM_OF_AMINO_ACIDS_AND_DERIVATIVES [200]	Genes involved in Metabolism of amino acids and derivatives	6		7.9×10^{-6}	3.39×10^{-3}
KEGG_VIRAL_MYOCARDITIS [73]	Viral myocarditis	4		2.67×10^{-5}	9.14×10^{-3}
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.	12		3.09×10^{-5}	9.14×10^{-3}
SYSTEM_DEVELOPMENT [861]	Genes annotated by the GO term GO:0048731. The	10		3.46×10^{-5}	9.14×10^{-3}

	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 process.				
KEGG_CARDIAC_MUSCLE_CONTRACTION [80]	Cardiac muscle contraction	4		3.83 e ⁻⁵	9.14 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 animal. 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		5.26 e ⁻⁵	1.06 e ⁻²
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.	11		6.16 e ⁻⁵	1.06 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.	11		6.88 e ⁻⁵	1.06 e ⁻²
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.	4		6.91 e ⁻⁵	1.06 e ⁻²

REGULATION_OF_TRANSLATION [93]	Genes annotated by the GO term GO:0006417. Any process that modulates the frequency, rate or extent of the chemical reactions and pathways resulting in the formation of proteins by the translation of mRNA.	4		6.91 e ⁻⁵	1.06 e ⁻²
TRANSMISSION_OF_NERVE_IMPULSE [189]	Genes annotated by the GO term GO:0019226. The sequential electrochemical polarization and depolarization that travels across the membrane of a nerve cell (neuron) in response to stimulation.	5		8.45 e ⁻⁵	1.21 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 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.	3		1.14 e ⁻⁴	1.53 e ⁻²
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 carpal, or microscopic such as an acrosome.	10		1.32 e ⁻⁴	1.67 e ⁻²
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	13		1.51 e ⁻⁴	1.79 e ⁻²

	e.g. polysaccharides and proteins.				
NUCLEOBASENUCLEOSIDENUCLEOTIDE_AND_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.	11		1.59 e ⁻⁴	1.79 e ⁻²
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).	10		1.75 e ⁻⁴	1.88 e ⁻²
KEGG_ARGININE_AND_PROLINE_METABOLISM [54]	Arginine and proline metabolism	3		2.79 e ⁻⁴	2.85 e ⁻²
PID_P53DOWNSTREAMPATHWAY [137]	Direct p53 effectors	4		3.07 e ⁻⁴	2.94 e ⁻²
REACTOME_CLASS_I_MHC_MEDIATED_ANTIGEN_EN_PROCESSING_PRESENTATION [251]	Genes involved in Class I MHC mediated antigen processing & presentation	5		3.15 e ⁻⁴	2.94 e ⁻²
REACTOME_IMMUNE_SYSTEM [933]	Genes involved in Immune System	9		3.43 e ⁻⁴	3.07 e ⁻²
INTRACELLULAR_PROTEIN_TRANSPORT [145]	Genes annotated by the GO term GO:0006886. The directed movement of proteins in a cell, including the movement of proteins between specific compartments or structures within a cell, such as organelles of a eukaryotic cell.	4		3.81 e ⁻⁴	3.25 e ⁻²
ORGAN_DEVELOPMENT [571]	Genes annotated by the GO term GO:0048513. 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.	7		3.94 e ⁻⁴	3.25 e ⁻²
REGULATION_OF_MULTICELLULAR_ORGANISMAL_PROCESS [151]	Genes annotated by the GO term GO:0051239. Any process that modulates the frequency, rate or extent of an organismal process, the	4		4.44 e ⁻⁴	3.53 e ⁻²

	processes pertinent to the function of an organism above the cellular level; includes the integrated processes of tissues and organs.				
REGULATION_OF_BIOLOGICAL_QUALITY [419]	Genes annotated by the GO term GO:0065008. Any process that modulates the frequency, rate or extent of a biological quality. A biological quality is a measurable attribute of an organism or part of an organism, such as size, mass, shape, color, etc.	6		4.61 e ⁻⁴	3.53 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		4.8 e ⁻⁴	3.55 e ⁻²
PROTEIN_TRANSPORT [157]	Genes annotated by the GO term GO:0015031. The directed movement of proteins into, out of, within or between cells.	4		5.15 e ⁻⁴	3.59 e ⁻²
INTRACELLULAR_TRANSPORT [280]	Genes annotated by the GO term GO:0046907. The directed movement of substances within a cell.	5		5.19 e ⁻⁴	3.59 e ⁻²
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.	8		5.61 e ⁻⁴	3.76 e ⁻²
REGULATION_OF_CELLULAR_PROTEIN_METABOLIC_PROCESS [162]	Genes annotated by the GO term GO:0032268. Any process that modulates the frequency, rate or extent of the chemical reactions and pathways involving a	4		5.79 e ⁻⁴	3.76 e ⁻²

	protein, occurring at the level of an individual cell.				
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.	5		6.87 e ⁻⁴	4.34 e ⁻²
REGULATION_OF_ACTION_POTENTIAL [17]	Genes annotated by the GO term GO:0001508. Any process that modulates the frequency, rate or extent of action potential creation, propagation or termination.	2		7.14 e ⁻⁴	4.38 e ⁻²
REGULATION_OF_PROTEIN_METABOLIC_PROCESS [173]	Genes annotated by the GO term GO:0051246. Any process that modulates the frequency, rate or extent of the chemical reactions and pathways involving a protein.	4		7.4 e ⁻⁴	4.38 e ⁻²
SYNAPTIC_TRANSMISSION [174]	Genes annotated by the GO term GO:0007268. The process of communication from a neuron to a target (neuron, muscle, or secretory cell) across a synapse.	4		7.56 e ⁻⁴	4.38 e ⁻²
GROWTH [77]	Genes annotated by the GO term GO:0040007. The increase in size or mass of an entire organism, a part of an organism or a cell.	3		7.92 e ⁻⁴	4.47 e ⁻²
BIOSYNTHETIC_PROCESS [470]	Genes annotated by the GO term GO:0009058. The energy-requiring part of metabolism in which simpler substances are transformed into more complex ones, as in growth and other biosynthetic processes.	6		8.39 e ⁻⁴	4.54 e ⁻²
TRANSLATION [180]	Genes annotated by the GO term GO:0006412. The chemical reactions and pathways resulting in the formation of a protein. This is a ribosome-mediated process in which the information in messenger RNA (mRNA) is used to specify the sequence of amino acids in the protein.	4		8.58 e ⁻⁴	4.54 e ⁻²
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.	6		8.67 e ⁻⁴	4.54 e ⁻²
CELLULAR_BIOSYNTHETIC_PROCESS [321]	Genes annotated by the GO term GO:0044249. The chemical reactions and	5		9.58 e ⁻⁴	4.89 e ⁻²

Entrez Gene Id										Gene Symbol										KEGG_TIGHT_JUNCTION										SYSTEM_PROCESS										KEGG_HYPERTROPHIC_CARDIOMYOPATHY_HCM										KEGG_DILATED_CARDIOMYOPATHY										REACTOME_METABOLISM_OF_AMINO_ACIDS_AND_DERIVATIVES										KEGG_VIRAL_MYOCARDITIS										PROTEIN_METABOLIC_PROCESS										SYSTEM_DEVELOPMENT										KEGG_CARDIAC_MUSCLE_CONTRACTION										SKELETAL_MUSCLE_DEVELOPMENT										CELLULAR_PROTEIN_METABOLIC_PROCESS										CELLULAR_MACROMOLECULE_METABOLIC_PROCESS										MUSCLE_DEVELOPMENT										REGULATION_OF_TRANSLATION										TRANSMISSION_OF_NERVE_IMPULSE										STRIATED_MUSCLE_DEVELOPMENT										ANATOMICAL_STRUCTURE_DEVELOPMENT										BIOPOLYMER_METABOLIC_PROCESS										NUCLEOBASENUCLEOTIDE_AND_NUCLEIC_ACID_METABOLIC_PROCESS										MULTICELLULAR_ORGANISMAL_DEVELOPMENT										KEGG_ARGININE_AND_PROLINE_METABOLISM										PID_P53DOWNSTREAMPATHWAY										REACTOME_CLASS_1_MHC_MEDIATED_ANTIGEN_PROCESSING_PRESENTATION										REACTOME_IMMUNE_SYSTEM										INTRACELLULAR_PROTEIN_TRANSPORT										ORGAN_DEVELOPMENT										REGULATION_OF_MULTICELLULAR_ORGANISMAL_PROCESS										REGULATION_OF_BIOLOGICAL_QUALITY										STRIATED_MUSCLE_CONTRACTION_GO_0006941										PROTEIN_TRANSPORT										INTRACELLULAR_TRANSPORT										TRANSPORT										REGULATION_OF_CELLULAR_PROTEIN_METABOLIC_PROCESS										CELLULAR_COMPONENT_ASSEMBLY										REGULATION_OF_ACTION_POTENTIAL										REGULATION_OF_PROTEIN_METABOLIC_PROCESS										SYNAPTIC_TRANSMISSION										GROWTH										BIOSYNTHETIC_PROCESS										TRANSLATION										ORGANELLE_ORGANIZATION_AND_BIOGENESIS
----------------	--	--	--	--	--	--	--	--	--	-------------	--	--	--	--	--	--	--	--	--	---------------------	--	--	--	--	--	--	--	--	--	----------------	--	--	--	--	--	--	--	--	--	--------------------------------------	--	--	--	--	--	--	--	--	--	-----------------------------	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	------------------------	--	--	--	--	--	--	--	--	--	---------------------------	--	--	--	--	--	--	--	--	--	--------------------	--	--	--	--	--	--	--	--	--	---------------------------------	--	--	--	--	--	--	--	--	--	-----------------------------	--	--	--	--	--	--	--	--	--	------------------------------------	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--------------------	--	--	--	--	--	--	--	--	--	---------------------------	--	--	--	--	--	--	--	--	--	-------------------------------	--	--	--	--	--	--	--	--	--	-----------------------------	--	--	--	--	--	--	--	--	--	----------------------------------	--	--	--	--	--	--	--	--	--	------------------------------	--	--	--	--	--	--	--	--	--	---	--	--	--	--	--	--	--	--	--	--------------------------------------	--	--	--	--	--	--	--	--	--	--------------------------------------	--	--	--	--	--	--	--	--	--	--------------------------	--	--	--	--	--	--	--	--	--	---	--	--	--	--	--	--	--	--	--	------------------------	--	--	--	--	--	--	--	--	--	---------------------------------	--	--	--	--	--	--	--	--	--	-------------------	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	----------------------------------	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	-------------------	--	--	--	--	--	--	--	--	--	-------------------------	--	--	--	--	--	--	--	--	--	-----------	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	-----------------------------	--	--	--	--	--	--	--	--	--	--------------------------------	--	--	--	--	--	--	--	--	--	---	--	--	--	--	--	--	--	--	--	-----------------------	--	--	--	--	--	--	--	--	--	--------	--	--	--	--	--	--	--	--	--	----------------------	--	--	--	--	--	--	--	--	--	-------------	--	--	--	--	--	--	--	--	--	---------------------------------------

http://www.broadinstitute.org/gsea/msigdb/compute_overlaps.jsp

http://www.broadinstitute.org/gsea/msigdb/compute_overlaps.jsp

http://www.broadinstitute.org/gsea/msigdb/compute_overlaps.jsp

GSEA | MSigDB | Compute Overlaps

MSigDB database v4.0 updated May 31, 2013
GSEA/MSigDB web site v4.05 released June 8, 2014