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Compute Overlaps for Selected Genes

Converted 115 submitted identifiers into 104 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	93	2155	104	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).

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Gene Set Name [# Genes (K)]	Description	# Genes in Overlap (k)	k/K	p-value ?	FDR q-value ?
KEGG_RIBOSOME [88]	Ribosome	20		4.83 e ⁻³⁵	1.04 e ⁻³¹
REACTOME_3_UTR_MEDIATED_TRANSLATIONAL_AL_REGULATION [176]	Genes involved in 3' - UTR-mediated translational regulation	21		2 e ⁻³⁰	2.15 e ⁻²⁷
REACTOME_TRANSLATION [222]	Genes involved in Translation	22		5.24 e ⁻³⁰	3.77 e ⁻²⁷
REACTOME_PEPTIDE_CHAIN_ELONGATION [153]	Genes involved in Peptide chain elongation	20		7.77 e ⁻³⁰	4.19 e ⁻²⁷
REACTOME_INFLUENZA_VIRAL_RNA_TRANSCRIPTION_AND_REPLICATION [169]	Genes involved in Influenza Viral RNA Transcription and Replication	20		6.28 e ⁻²⁹	2.71 e ⁻²⁶
REACTOME_NONSENSE_MEDIATED_DECAY_ENHANCED_BY_THE_EXON_JUNCTION_COMPLEX [176]	Genes involved in Nonsense Mediated Decay Enhanced by the Exon Junction Complex	20		1.47 e ⁻²⁸	5.26 e ⁻²⁶
REACTOME_SRP_DEPENDENT_COTRANSLATIONAL_PROTEIN_TARGETING_TO_MEMBRANE [179]	Genes involved in SRP-dependent cotranslational protein targeting to membrane	20		2.08 e ⁻²⁸	6.42 e ⁻²⁶
REACTOME_INFLUENZA_LIFE_CYCLE [203]	Genes involved in Influenza Life Cycle	20		2.83 e ⁻²⁷	7.63 e ⁻²⁵
REACTOME_METABOLISM_OF_MRNA [284]	Genes involved in Metabolism of mRNA	21		6.22 e ⁻²⁶	1.49 e ⁻²³
REACTOME_METABOLISM_OF_RNA [330]	Genes involved in Metabolism of RNA	21		1.5 e ⁻²⁴	3.23 e ⁻²²
REACTOME_METABOLISM_OF_PROTEINS [518]	Genes involved in Metabolism of proteins	23		2.85 e ⁻²³	5.58 e ⁻²¹
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.	14		7 e ⁻¹⁸	1.26 e ⁻¹⁵
CELLULAR_BIOSYNTHETIC_PROCESS [321]	Genes annotated by the GO term GO:0044249. The chemical reactions and pathways resulting in the formation of substances, carried out by individual cells.	16		3.37 e ⁻¹⁷	5.58 e ⁻¹⁵
BIOSYNTHETIC_PROCESS [470]	Genes annotated by the GO term GO:0009058. The energy-requiring	16		1.29 e ⁻¹⁴	1.99 e ⁻¹²



	part of metabolism in which simpler substances are transformed into more complex ones, as in growth and other biosynthetic processes.				
MACROMOLECULE_BIOSYNTHETIC_PROCESS [321]	Genes annotated by the GO term GO:0009059. The chemical reactions and pathways resulting in the formation of macromolecules, large molecules including proteins, nucleic acids and carbohydrates.	14		2.24 e ⁻¹⁴	3.22 e ⁻¹²
REACTOME_FORMATION_OF_THE_TERNARY_COMPLEX_AND_SUBSEQUENTLY_THE_43S_COMPLEX [74]	Genes involved in Formation of the ternary complex, and subsequently, the 43S complex	8		6.96 e ⁻¹²	9.38 e ⁻¹⁰
REACTOME_ACTIVATION_OF_THE_MRNA_UPON_BINDING_OF_THE_CAP_BINDING_COMPLEX_AND_EIFs_AND_SUBSEQUENT_BINDING_TO_43S [84]	Genes involved in Activation of the mRNA upon binding of the cap-binding complex and eIFs, and subsequent binding to 43S	8		1.98 e ⁻¹¹	2.51 e ⁻⁹
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.	18		7.11 e ⁻¹¹	8.52 e ⁻⁹
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.	18		8.69 e ⁻¹¹	9.86 e ⁻⁹
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.	18		3.37 e ⁻¹⁰	3.63 e ⁻⁸
KEGG_ALZHEIMERS_DISEASE [169]	Alzheimer's disease	7		1.26 e ⁻⁷	1.3 e ⁻⁵
REACTOME_GLYCOLYSIS [29]	Genes involved in Glycolysis	4		5.63 e ⁻⁷	5.51 e ⁻⁵
REACTOME_GLUONEOGENESIS [34]	Genes involved in Gluconeogenesis	4		1.09 e ⁻⁶	1.02 e ⁻⁴
BIOCARTA_GLYCOLYSIS_PATHWAY [10]	Glycolysis Pathway	3		1.34 e ⁻⁶	1.2 e ⁻⁴
REACTOME_RESPIRATORY_ELECTRON_TRANSPORT_ATP_SYNTHESIS_BY_CHEMIOSMOTIC_COUPLING_AND_HEAT_PRODUCTION_BY_UNCOUPLING_PROTEINS_ [98]	Genes involved in Respiratory electron transport, ATP synthesis by chemiosmotic coupling, and heat production by uncoupling proteins.	5		3.09 e ⁻⁶	2.67 e ⁻⁴
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	3		4.02 e ⁻⁶	3.34 e ⁻⁴

	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.				
BIOCARTA_MTA3_PATHWAY [19]	Downregulated of MTA-3 in ER-negative Breast Tumors	3		1.06 e ⁻⁵	8.18 e ⁻⁴
REGULATION_OF_MUSCLE_CONTRACTION [19]	Genes annotated by the GO term GO:0006937. Any process that modulates the frequency, rate or extent of muscle contraction.	3		1.06 e ⁻⁵	8.18 e ⁻⁴
KEGG_GLYCOLYSIS_GLUONEOGENESIS [62]	Glycolysis / Gluconeogenesis	4		1.25 e ⁻⁵	9.27 e ⁻⁴
KEGG_PARKINSONS_DISEASE [133]	Parkinson's disease	5		1.38 e ⁻⁵	9.88 e ⁻⁴
KEGG_OXIDATIVE_PHOSPHORYLATION [135]	Oxidative phosphorylation	5		1.48 e ⁻⁵	1.03 e ⁻³
REACTOME_TCA_CYCLE_AND_RESPIRATORY_ELE ELECTRON_TRANSPORT [141]	Genes involved in The citric acid (TCA) cycle and respiratory electron transport	5		1.82 e ⁻⁵	1.21 e ⁻³
KEGG_COMPLEMENT_AND_COAGULATION_CASCAD CADES [69]	Complement and coagulation cascades	4		1.91 e ⁻⁵	1.21 e ⁻³
REACTOME_GLUCOSE_METABOLISM [69]	Genes involved in Glucose metabolism	4		1.91 e ⁻⁵	1.21 e ⁻³
REACTOME_METABOLISM_OF_NUCLEOTIDES [72]	Genes involved in Metabolism of nucleotides	4		2.26 e ⁻⁵	1.39 e ⁻³
REACTOME_STRIATED_MUSCLE_CONTRACTION [27]	Genes involved in Striated Muscle Contraction	3		3.17 e ⁻⁵	1.89 e ⁻³
PID_MYC_ACTIVPATHWAY [79]	Validated targets of C-MYC transcriptional activation	4		3.26 e ⁻⁵	1.9 e ⁻³
KEGG_CARDIAC_MUSCLE_CONTRACTION [80]	Cardiac muscle contraction	4		3.43 e ⁻⁵	1.94 e ⁻³
REACTOME_LIPOPROTEIN_METABOLISM [28]	Genes involved in Lipoprotein metabolism	3		3.54 e ⁻⁵	1.96 e ⁻³
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.	8		4.44 e ⁻⁵	2.39 e ⁻³
KEGG_FRUCTOSE_AND_MANNOSE_METABOLISM [34]	Fructose and mannose metabolism	3		6.4 e ⁻⁵	3.36 e ⁻³
KEGG_HUNTINGTONS_DISEASE [185]	Huntington's disease	5		6.67 e ⁻⁵	3.42 e ⁻³
REACTOME_HEMOSTASIS [466]	Genes involved in Hemostasis	7		9.61 e ⁻⁵	4.81 e ⁻³
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	10		1.04 e ⁻⁴	5.11 e ⁻³

	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.				
NEGATIVE_REGULATION_OF_CELLULAR_PROCESSES [646]	Genes annotated by the GO term GO:0048523. Any process that stops, prevents or reduces 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.	8		1.15 e-4	5.51 e-3
PID_HNF3APATHWAY [44]	FOXA1 transcription factor network	3		1.39 e-4	6.53 e-3
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 process.	9		1.54 e-4	7 e-3
NEGATIVE_REGULATION_OF_BIOLOGICAL_PROCESS [677]	Genes annotated by the GO term GO:0048519. Any process that stops, prevents or reduces 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.	8		1.59 e-4	7 e-3
REACTOME_LIPID_DIGESTION_MOBILIZATION_ON_AND_TRANSPORT [46]	Genes involved in Lipid digestion, mobilization, and transport	3		1.59 e-4	7 e-3
REACTOME_MUSCLE_CONTRACTION [48]	Genes involved in Muscle contraction	3		1.81 e-4	7.79 e-3
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		2.26 e-4	9.53 e-3
KEGG_ARGININE_AND_PROLINE_METABOLISM [54]	Arginine and proline metabolism	3		2.57 e-4	1.06 e-2
GLUCOSE_CATABOLIC_PROCESS [11]	Genes annotated by the GO term GO:0006007. The chemical reactions and pathways resulting in the breakdown of glucose, the aldohexose gluco-hexose.	2		2.75 e-4	1.12 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	7		3.31 e-4	1.32 e-2

	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.				
REACTOME_APOPTOSIS [148]	Genes involved in Apoptosis	4		3.7 e ⁻⁴	1.45 e ⁻²
BIOCARTA_AHSP_PATHWAY [13]	Hemoglobin's Chaperone	2		3.89 e ⁻⁴	1.47 e ⁻²
REACTOME_PURINE_SALVAGE [13]	Genes involved in Purine salvage	2		3.89 e ⁻⁴	1.47 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 processes pertinent to the function of an organism above the cellular level; includes the integrated processes of tissues and organs.	4		3.99 e ⁻⁴	1.48 e ⁻²
PID_ERA_GENOMIC_PATHWAY [65]	Validated nuclear estrogen receptor alpha network	3		4.44 e ⁻⁴	1.58 e ⁻²
NEGATIVE_REGULATION_OF_CELL_PROLIFERATION [156]	Genes annotated by the GO term GO:0008285. Any process that stops, prevents or reduces the rate or extent of cell proliferation.	4		4.51 e ⁻⁴	1.58 e ⁻²
NEGATIVE_REGULATION_OF_HYDROLASE_ACTIVITY [14]	Genes annotated by the GO term GO:0051346. Any process that stops or reduces the rate of hydrolase activity, the catalysis of the hydrolysis of various bonds.	2		4.53 e ⁻⁴	1.58 e ⁻²
REACTOME_REGULATION_OF_COMPLEMENT_CASCADE [14]	Genes involved in Regulation of Complement cascade	2		4.53 e ⁻⁴	1.58 e ⁻²
KEGG_PURINE_METABOLISM [159]	Purine metabolism	4		4.85 e ⁻⁴	1.66 e ⁻²
NABA_MATRISOME [807]	Ensemble of genes encoding extracellular matrix and extracellular matrix-associated proteins	8		5.12 e ⁻⁴	1.72 e ⁻²
PID_THROMBIN_PAR4_PATHWAY [15]	PAR4-mediated thrombin signaling events	2		5.22 e ⁻⁴	1.73 e ⁻²
KEGG_PPAR_SIGNALING_PATHWAY [69]	PPAR signaling pathway	3		5.29 e ⁻⁴	1.73 e ⁻²
PID_CDC42_PATHWAY [70]	CDC42 signaling events	3		5.52 e ⁻⁴	1.75 e ⁻²
REACTOME_IMMUNOREGULATORY_INTERACTIONS_BETWEEN_A_LYMPHOID_AND_A_NON_LYMPHOID_CELL [70]	Genes involved in Immunoregulatory interactions between a Lymphoid and a non-Lymphoid cell	3		5.52 e ⁻⁴	1.75 e ⁻²
EPIDERMIS_DEVELOPMENT [71]	Genes annotated by the GO term GO:0008544. The process whose specific outcome is the progression of the epidermis over time, from its formation to the mature structure. The epidermis is the outer epithelial layer of a plant or animal, it may be a single layer that produces an extracellular material (e.g. the cuticle of arthropods) or a	3		5.75 e ⁻⁴	1.78 e ⁻²

	complex stratified squamous epithelium, as in the case of many vertebrate species.				
REACTOME_CHYLOMICRON_MEDIATED_LIPID_TRANSPORT [16]	Genes involved in Chylomicron-mediated lipid transport	2		5.96 e ⁻⁴	1.78 e ⁻²
REACTOME_FORMATION_OF_ATP_BY_CHEMIOSMOTIC_COUPLING [16]	Genes involved in Formation of ATP by chemiosmotic coupling	2		5.96 e ⁻⁴	1.78 e ⁻²
RIBONUCLEOTIDE_METABOLIC_PROCESS [16]	Genes annotated by the GO term GO:0009259. The chemical reactions and pathways involving a ribonucleotide, a compound consisting of ribonucleoside (a base linked to a ribose sugar) esterified with a phosphate moiety at either the 3' or 5'-hydroxyl group of its glycosyl moiety.	2		5.96 e ⁻⁴	1.78 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).	9		6.45 e ⁻⁴	1.9 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		7.47 e ⁻⁴	2.18 e ⁻²
REACTOME_RESPIRATORY_ELECTRON_TRANSPORT [79]	Genes involved in Respiratory electron transport	3		7.86 e ⁻⁴	2.24 e ⁻²
REACTOME_METABOLISM_OF_LIPIDS_AND_LIPOPROTEINS [478]	Genes involved in Metabolism of lipids and lipoproteins	6		7.89 e ⁻⁴	2.24 e ⁻²
ECTODERM_DEVELOPMENT [80]	Genes annotated by the GO term GO:0007398. The process whose specific outcome is the progression of the ectoderm over time, from its formation to the mature structure. In animal embryos, the ectoderm is the outer germ layer of the embryo, formed during gastrulation.	3		8.15 e ⁻⁴	2.28 e ⁻²
REACTOME_SYNTHESIS_AND_INTERCONVERSION_OF_NUCLEOTIDE_DI_AND_TRIPHOSPHATES [19]	Genes involved in Synthesis and interconversion of nucleotide di- and triphosphates	2		8.46 e ⁻⁴	2.34 e ⁻²
KEGG_HYPERTROPHIC_CARDIOMYOPATHY_HCM [85]	Hypertrophic cardiomyopathy (HCM)	3		9.72 e ⁻⁴	2.65 e ⁻²
BIOCARTA_NDKDYNAMIN_PATHWAY [21]	Endocytotic role of NDK, Phosphins and Dynamin	2		1.04 e ⁻³	2.79 e ⁻²
REACTOME_RESPONSE_TO_ELEVATED_PLATELET_CYTOSOLIC_CA2_ [89]	Genes involved in Response to elevated platelet cytosolic Ca2+	3		1.11 e ⁻³	2.95 e ⁻²
REACTOME_METABOLISM_OF_AMINO_ACIDS_AND_DERIVATIVES [200]	Genes involved in Metabolism of amino acids and derivatives	4		1.14 e ⁻³	3 e ⁻²
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	7		1.18 e ⁻³	3.06 e ⁻²

	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.				
KEGG_DILATED_CARDIOMYOPATHY [92]	Dilated cardiomyopathy	3		1.22 e ⁻³	3.13 e ⁻²
CELLULAR_CARBOHYDRATE_CATABOLIC_PROCESS [23]	Genes annotated by the GO term GO:0044275. The chemical reactions and pathways resulting in the breakdown of carbohydrates, any of a group of organic compounds based of the general formula Cx(H2O)y, as carried out by individual cells.	2		1.24 e ⁻³	3.15 e ⁻²
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.	4		1.32 e ⁻³	3.26 e ⁻²
REACTOME_PLATELET_ACTIVATION_SIGNALING_AND_AGGREGATION [208]	Genes involved in Platelet activation, signaling and aggregation	4		1.32 e ⁻³	3.26 e ⁻²
CARBOHYDRATE_CATABOLIC_PROCESS [24]	Genes annotated by the GO term GO:0016052. The chemical reactions and pathways resulting in the breakdown of carbohydrates, any of a group of organic compounds based of the general formula Cx(H2O)y.	2		1.36 e ⁻³	3.32 e ⁻²
POSITIVE_REGULATION_OF_CELL_DIFFERENTIATION [25]	Genes annotated by the GO term GO:0045597. Any process that activates or increases the frequency, rate or extent of cell differentiation.	2		1.47 e ⁻³	3.52 e ⁻²
REGULATION_OF_HEART_CONTRACTION [25]	Genes annotated by the GO term GO:0008016. Any process that modulates the frequency, rate or extent of heart contraction. Heart contraction is the process by which the heart decreases in volume in a characteristic way to propel blood through the body.	2		1.47 e ⁻³	3.52 e ⁻²
KEGG_PENTOSE_PHOSPHATE_PATHWAY [27]	Pentose phosphate pathway	2		1.72 e ⁻³	4.06 e ⁻²
GLUCOSE_METABOLIC_PROCESS [28]	Genes annotated by the GO term GO:0006006. The chemical reactions and pathways involving glucose, the aldohexose gluco-hexose. D-glucose is dextrorotatory and is sometimes known as dextrose; it is an important source of energy for living organisms and is found free as well as combined in homo- and hetero-oligosaccharides and polysaccharides.	2		1.85 e ⁻³	4.32 e ⁻²
PID_INTEGRIN2_PATHWAY [29]	Beta2 integrin cell	2			

	surface interactions			1.98 e ⁻³	4.59 e ⁻²
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Gene/geneset overlap matrix

Entrez Gene Id	Gene Symbol
	KEGG_RIBOSOME
	REACTOME_3_UTR_MEDIATED_TRANSLATIONAL_REGULATION
	REACTOME_TRANSLATION
	REACTOME_PEPTIDE_CHAIN_ELONGATION
	REACTOME_INFLUENZA_VIRAL_RNA_TRANSCRIPTION_AND_REPLICATION
	REACTOME_NONSENSE_MEDIATED_DECAY_ENHANCED_BY_THE_EXON_JUNCTION_COMPLEX
	REACTOME_SRP_DEPENDENT_COTRANSLATIONAL_PROTEIN_TARGETING_TO_MEMBRANE
	REACTOME_INFLUENZA_LIFE_CYCLE
	REACTOME_METABOLISM_OF_MRNA
	REACTOME_METABOLISM_OF_RNA
	REACTOME_METABOLISM_OF_PROTEINS
	TRANSLATION
	CELLULAR_BIOSYNTHETIC_PROCESS
	BIOSYNTHETIC_PROCESS
	MACROMOLECULE_BIOSYNTHETIC_PROCESS
	REACTOME_FORMATION_OF_THE_TERNARY_COMPLEX_AND_SUBSEQUENTLY_THE_43S_COMPLEX
	REACTOME_ACTIVATION_OF_THE_MRNA_UPON_BINDING_OF_THE_CAP_BINDING_COMPLEX_AND_EIF5_AND_SUBSEQUENT_BINDING_TO_43S
	CELLULAR_PROTEIN_METABOLIC_PROCESS
	CELLULAR_MACROMOLECULE_METABOLIC_PROCESS
	PROTEIN_METABOLIC_PROCESS
	KEGG_ALZHEIMERS_DISEASE
	REACTOME_GLYCOLYSIS
	REACTOME_GLUconeogenesis
	BIOCARTA_GLYCOLYSIS_PATHWAY
	REACTOME_RESPIRATORY_ELECTRON_TRANSPORT_ATP_SYNTHESIS_BY_CHEMIOSMOTIC_COUPLING_AND_HEAT_PRODUCTION_BY_UNCOUPLING_PROTEINS
	STRIATED_MUSCLE_CONTRACTION_G0_0006941
	BIOCARTA_MTA3_PATHWAY
	REGULATION_OF_MUSCLE_CONTRACTION
	KEGG_GLYCOLYSIS_GLUconeogenesis
	KEGG_PARKINSONS_DISEASE
	KEGG_OXIDATIVE_PHOSPHORYLATION
	REACTOME_TCA_CYCLE_AND_RESPIRATORY_ELECTRON_TRANSPORT
	KEGG_COMPLEMENT_AND_COAGULATION_CASCADES
	REACTOME_GLUCOSE_METABOLISM
	REACTOME_METABOLISM_OF_NUCLEOTIDES
	REACTOME_STRIATED_MUSCLE_CONTRACTION
	PID_MYC_ACTIVPATHWAY
	KEGG_CARDIAC_MUSCLE_CONTRACTION
	REACTOME_LIPOPROTEIN_METABOLISM
	SYSTEM_PROCESS
	KEGG_FRUCTOSE_AND_MANNOSE_METABOLISM
	KEGG_HUNTINGTONS_DISEASE
	REACTOME_HEMOSTASIS
	ANATOMICAL_STRUCTURE_DEVELOPMENT
	NEGATIVE_REGULATION_OF_CELLULAR_PROCESS
	PID_HNF3APATHWAY
	SYSTEM_DEVELOPMENT
	NEGATIVE_REGULATION_OF_BIOLOGICAL_PROCESS
	REACTOME_LIPID_DIGESTION_MOBILIZATION_AND_TRANSPORT
	REACTOME_MUSCLE_CONTRACTION
	POSITIVE_REGULATION_OF_EPITHELIAL_CELL_PROLIFERATION
	KEGG_ARGININE_AND_PROLINE_METABOLISM
	GLUCOSE_CATABOLIC_PROCESS
	ORGAN_DEVELOPMENT
	REACTOME_APOPTOSIS
	BIOCARTA_AHSP_PATHWAY
	REACTOME_PURINE_SALVAGE
	REGULATION_OF_MULTICELLULAR_ORGANISMAL_PROCESS
	PID_ERA_GENOMIC_PATHWAY
	NEGATIVE_REGULATION_OF_CELL_PROLIFERATION
	NEGATIVE_REGULATION_OF_HYDROLASE_ACTIVITY
	REACTOME_REGULATION_OF_COMPLEMENT_CASCADE
	KEGG_PURINE_METABOLISM
	NABA_MATRISOME
	PID_THROMBIN_PAR4_PATHWAY
	KEGG_PPAR_SIGNALING_PATHWAY
	PID_CDC42_PATHWAY
	REACTOME_IMMUNOREGULATORY_INTERACTIONS_BETWEEN_A_LYMPHOID_AND_A_NON_LYMPHOID_CELL
	EPIDERMIS_DEVELOPMENT
	REACTOME_CHYLOMICRON_MEDIATED_LIPID_TRANSPORT
	REACTOME_FORMATION_OF_ATP_BY_CHEMIOSMOTIC_COUPLING
	RIBONUCLEOTIDE_METABOLIC_PROCESS
	MULTICELLULAR_ORGANISMAL_DEVELOPMENT
	ORGANELLE_ORGANIZATION_AND_BIOGENESIS
	REACTOME_RESPIRATORY_ELECTRON_TRANSPORT
	REACTOME_METABOLISM_OF_LIPIDS_AND_LIPOPROTEINS
	ECTODERM_DEVELOPMENT
	REACTOME_SYNTHESIS_AND_INTERCONVERSION_OF_NUCLEOTIDE_DL_AND_TRIPHOSPHATES
	KEGG_HYPERTROPHIC_CARDIOMYOPATHY_HCM
	BIOCARTA_NDKDYNAMIN_PATHWAY
	REACTOME_RESPONSE_TO_ELEVATED_PLATELET_CYTOSOLIC_CA2
	REACTOME_METABOLISM_OF_AMINO_ACIDS_AND_DERIVATIVES
	POSITIVE_REGULATION_OF_BIOLOGICAL_PROCESS
	KEGG_DILATED_CARDIOMYOPATHY
	CELLULAR_CARBOHYDRATE_CATABOLIC_PROCESS
	CYTOSKELETON_ORGANIZATION_AND_BIOGENESIS





