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Building a Knowledgebase for Precision Medicine

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Institute of Biomedical Sciences Fudan University 2018.8.30

Precision Medicine

NRC: **《Toward Precision Medicine**: Building a Knowledge Network for Biomedical Research and a New Taxonomy of Disease》 November, 2011



Toward Precision Medicine



China Precision Medicine Initiative



Linked Open Data in Biomedince





National Key R&D Plan Project:

Knowledgebase of Precision Medicine for Disease Studies

Lead Institute: Fudan University

Participants:

Lead PI: Lei Liu Duration: 2016–2020

Institute of Medical Informatics, Chinese Academy of Medicine
Chinese Military Academy of Medicine
National Center for Protein Sciences
Shanghai Institute of Life Sciences, Chinese Academy of Science
Beijing Institute of Genomics, Chinese Academy of Science
Harbin Institute of Technology
Zhejiang University
Dalian University of Technology
Shanghai Center for Bioinformation Technology

Implementation Schema





Ontologies at Different Levels

Biology

				recimology
<u>Length Metric</u> 10 ⁰		ICD10(疾病)		Population
10-1		SNOMED(疾病)		Individual
10-2	(XX)	NCBI 分类系统 SNOMED (器官)		Organ
10-3				Tissue
10-4		哺乳动物的表型	, Q	cell
10 ⁻⁵	The let	SNOMED (形态学)		subcellular
10-6	ZAC	ATCC (细胞株) Cell Ontology细胞本体(细胞类型		Virus
10-7		Gene Ontology基因本体(亚细胞)		
10 -8	States O	Gene Nomenclature 基因命名		DNA
10 -9	CONFRAME.	Quaternary code 四进制码		Bases
	10 m			

Technology

UMLS Semantic Network

- UMLS = Unified Medical Language System (NLM)
- Composed of:
 - Metathesaurus
 - Semantic Network
 - \circ Lexicon
- Contains approximately 5 million codes representing 1 million concepts derived from 100 source terminologies



HPO: human phenotype ontology



Structure between phenotype Relationship between phenotype and disease

http://www.human-phenotype-ontology.org/

DO: Disease ontology

DISEASE ONTOLOGY	
Search Ontology	Go » Advanced Search »
Navigation	1 Welcome
 Open new metadata panel disease disease by infectious agent disease of anatomical entity disease of mental health disease of mental health disease of metabolism genetic disease physical disorder syndrome 	 The Disease Ontology has been developed as a standardized ontology for human disease with the purpose of providing the biomedical community with consistent, reusable and sustainable descriptions of human disease terms, phenotype characteristics and related medical vocabulary disease concepts through collaborative efforts of researchers at Northwestern University, Center for Genetic Medicine and the University of Maryland School of Medicine, Institute for Genome Sciences. The Disease Ontology semantically integrates disease and medical vocabularies through extensive cross mapping of D0 terms to MeSH, ICD, NCI's thesaurus, SNOMED and OMIM. To get started please visit the <u>tutorial page</u>.
	 Posted on 2015-04-18 The Disease Ontology database has been updated to the latest ontology as of 2015-04-18. DO now includes two cancer slim files: DO_cancer_slim and TopNodes_DOcancerslim, published in Database. You can view it <u>hare</u>. Citation: Wu, TJ., Schriml, L.M., Chen, QR., Colbert, M., Crichton, D. J., Finney, R., Hu, Y., Kibbe, W. A., Kincaid, H., Meerzaman, D., Mitraka, E., Pan, Y., Smith, K. M., Srivastava, S., Ward, S., Yan, C. and Mazumder, R. (2015) Generating a focused view of disease ontology cancer terms for pan-cancer data integration and analysis. Database, 2015, bav032. Database Updated
	Posted on 2015-03-20
	The Disease Ontology database has been updated to the latest ontology as of 2015-03-20. DO now includes a DO_MGI_slim.
	Disease Ontology paper published in NAR
	Posted on 2014-11-20

015 - Institute for Genome Sciences - University of Maryland School of Medicine 👘 Home | Tutorial | Resources Downloads | FAQ | About | Contact Us

http://disease-ontology.org/

Gene ont	ology Human phe	notype ontol	ogy Diseas	e ontology
80		● ● H ● ● P ● ● O	D ISEASE ONTOLOGY	
Relationship	Definition			
Gene has Mutation	A mutation occurs in or near a gene, usually at a given p	position.		
Patient/Cohort has Mutation	A patient or cohort has a specific genetic variation.			
Mutation related to Disease	A mutation is associated with (or causes) a disease.			
Mutation has Size	Indicates the number or frequency of mutations.	Genomics	Phenomics	Diseasomics
Disease related to Gene	A disease is associated with a gene—that is, a gene (w causes a disease.	DNA-Sequences	И (нро) /	Stickler
Disease related to Body Part	A disease may occur in a body part, or have a body pa	Genes SNPs		Syndrome
Patient has Age	A patient has a given age	Mutagenesis	Abn. of Abn. of the	Marshall syndrome
Cohort has Age	A summary age for a cohort. Often listed as a mean o	Expression Proteins	the eye system	
Patient/Cohort has Gender	A patient or cohort is male or female.	Networks	T	
Patient/Cohort has Geographic Location	A patient or cohort has a given ethnicity or lives in a g	Drug Side-effects	Retinal detachment	Pallister-Hall syndrome
Patient/Cohort has Disease	A patient or cohort has a disease.		uaciyiy	
Cohort has Size	The size of a cohort group			

PMOV2.0—2018.05

	O Mutation	O Translocation O undetermined variant O insertion O inversion O short repeat O copy number gain O NT expansion O deletion	 O Piwi-Interacting RNA O Signal Recognition Particle RNA O MicroRNA O Transfer-Messenger RNA O Telomerase RNA Component O msdRNA 	58 ontologies, thesaurus, controlled vocabularies
O owl:Precision_Medicine_Ontology	 Chemical and Drug Anatomical Structure Disease 	O duplication O copy number loss O single nucleotide variant O indel	O Small Interfering RNA O Ribosomal RNA O Small Nucleolar RNA O Mitochondrial RNA	SNOMED CT
	O Cell O Biologic Function O Gene	O Untranslated RNA O Messenger RNA O Precursor mRNA O Protein	- O LincRNA - O Small Nuclear RNA - O Transfer RNA - O Ribozyme - D Ri D RINA	ICD-10 Version:2016
	O Phenotype O Biochemical Pathway	O Protein Fragment O Protein or Riboprotein Complex O hnRNA O Body Regions O Cell Component O Embryonic Structures O Molecular Sequence	 O Pri-miRNA O Viral Small RNA O Guide RNA O Pre-miRNA O Nucleotide Sequence O Amino Acid Sequence O Carbohydrate Sequence 	NCI thesaurus Medical Subject Headings
		 Tissues Pathologic Function Physiologic Function pseudo protein-coding snRNA snRNA 	4 567	,208 terms;
		O ncRNA O scRNA O tRNA O rRNA O Anatomical Abnormality	•	,967 concepts
		 Signs and Symptoms Cell Motility Pathway Metabolic Pathway Genetic Information Processing Pathway Regulatory Pathway DNA Repair Pathway Disease Pathway Cell Differentiation or Development Pathway Orug Pathway 		

PMO: sources and statistics



PMO

Concept types related to genetic mutations

Concept	Definition
Gene	A segment of DNA that codes for a protein
Mutation	A mutation is an alteration (deletion, insertion, substitution) of nucleotides (DNA, RNA) or amino acids (Protein)
Body part	An organ or anatomical location in a person.
Disease	An abnormal condition affecting the body of an organism.
Patient	An individual with a disease
Cohort	A group of people; specifically any group or population of people that may be assigned a disease or characteristic.
Size	A number indicating the number of people in a <i>cohort</i> , or the number/frequency of a <i>mutation</i> .
Age	A number or range indicating how old a person/group of people is.
Gender	Terms indicating whether someone is male or female
Geographical location	Terms indicating where a person/group of people comes from, either based on ethnic origin or where they live.

• Verspoor, K., A. Jimeno Yepes, L. Cavedon, T. McIntosh, A. Herten-Crabb, Z. Thomas and J. P. Plazzer (2013). "Annotating the biomedical literature for the human variome." <u>Database (Oxford)</u> 2013: bat019.

Relationship	Definition
Gene has Mutation	A mutation occurs in or near a gene, usually at a given position.
Patient/Cohort has Mutation	A patient or cohort has a specific genetic variation.
<i>Mutation related to Disease</i>	A mutation is associated with (or causes) a disease.
Mutation has Size	Indicates the number or frequency of mutations.
Disease related to Gene	A disease is associated with a gene—that is, a gene (when mutated) is linked to, or causes a disease.
Disease related to Body Part	A disease may occur in a body part, or have a body part in its name.
Patient has Age	A patient has a given age
Cohort has Age	A summary age for a cohort. Often listed as a mean or an age limit.
Patient/Cohort has Gender	A patient or cohort is male or female.
Patient/Cohort has Geographic Location	A patient or cohort has a given ethnicity or lives in a given place.
Patient/Cohort has Disease	A patient or cohort has a disease.
Cohort has Size	The size of a cohort group

Semantic Relationships in PMO

Create Delete	Display name	play role in biological proce	ess
😑 📼 physical interaction 📃 🔺	IRI	http://webprotege.stanford	d.edu/RBMJCH1rdCPrFItrlyRbYa6
- 📼 physical interaction-protein-microorganism		5	
physical interaction-protein-nucleic acid			
- C physical interaction-protein-protein	Annotations	••• rdfs:label	📰 play role in biological process
- C physical interaction-protein-small molecule			
physical interaction-RNA-RNA			Enter value
🖃 📼 play functional roles in			
– play functional roles-cellular processes in			
play functional roles-molecular processes in	Domain	Genetic Mechanisms	
- 🗖 play functional roles-organismal processes in			
- 🗔 play role in biological process		Enter class name	
- 🗖 play role in cell			
protein functions/functional domains			
- contraction -	Range	O Molecular Mechanisms	3
- 🗖 regulates		O Genetic Mechanisms	
🖃 🥅 regulating toxicology			
regulating toxicology-hepatotoxicity		Cellular Mechanisms	
regulating toxicology-nephrotoxicity			
- 📼 related disease			
- 📼 secondary to			
- Cargeted by			
🖃 🥅 targeting drug			
- 🚍 antagonized by			
binded by			
inhibited by			
- Catranslocation			
📼 transport			
- C treated by			
Treats Y			

Precision Medicine Ontology Collaborative Construction Platform

Precision Medicine Ontology Collaborative Construction Platform					pmo	
ြဲ Home ို့ Class Managem	ent 🍰 Property I	Management 😡	Version Management	名 Use	r Management	
ou are working on the 1.0.0 version of pmo_B	eta					
Search	Disease					
+	Name :	Disease				
+ Cell + Phenotype + Biochemical Pathway	Annotations :	Select •	Input Value		Select 🔻	Save
+ Biologic Function + Disease + Chemical and Drug		Select database_cross_reference Source of Example	e CCPSS:0007490		Select 🔻	Save Delete
+ Gene + Gene Product + Mutation		Synonym Annotation properties Tree Number	CHV:000004014		Select 🔻	Save Delete
		dcterms:description MRID Definition	CSP:0944-4756		Select 🔻	Save Delete
		Example dcterms:creator	ICPC2P:A99001		Select 🔻	Save Delete
		dcterms:issued dcterms:created dcterms:modified	LCH:U001423		Select 🔻	Save Delete
		MCID is_a dcterms:title	LCH:U006403		Select 🔻	Save Delete
		rdfs:label owl:versionInfo	LCH_NW:sh85038411		Select 🔻	Save Delete
		database_cross_refe ▼	LNC:LP21006-9		Select 🔻	Save Delete
		database_cross_refe *	MEDCIN:39448		Select 🔻	Save Delete



decreases (Domain>Range)

complex semantic relationships embedded in text

has	ease has ethnicity	Search * Text Entity Event Relation
	al cancers obtained from nine large regional hospitals in southeastern Finland [9].	Type - Any - 🗸 🗸
has	- has has	Trigger - Any -
7 There were 895 (87.6%) MSI- cancers and 127 (12.4%)	has cohort-patient Disorder has disease MSI+ cancers.	Catalysis DNA methylation DNA demethylation
8 The MSI+ cancers were further classified as sporadic	has	Protein_modification_process Acylation Acetylation Palmitoylation
		Methylation
disease 10 Ages at cancer can be used to estimate likely numbers of oncogenie	mutations required before transformation [3-6,11].	Glycosylation Hydroxylation Phosphorylation
has has has		Lipidation
has	has	Prenylation
has has		Protein_modification_by_small_protein_conjugation Neddylation
cohort-patient has to cohort-patie		Sumoylation
Disorder cohort-patient lisease Concepts_Ideas Disorder dis disease	has has	Ubiquitination
	were respectively 71.5, 67.5, and 50.3 years (Figure 1A).	Deacylation
relatedTo relatedTo disconort/patient disease has mutation		conort inter has conort CC patients, 250 index subjects from families
	suspected of having LS [revised Bethesda guidelines] and 411 controls).	
	16 Three well-characterized LS families that fulfilled the Amsterdam II Criteria and co variant were included to assess co-occurrence and co-segregation.	onsisted of members with the pLys618A1a
	17 A subset of colorectal tumour DNA samples from 17 patients carrying the p.Lys618	
http://www.opennicta.com.au/ho	(characteristic) microsatellite instability using five mononucleotide markers.	
me/health/variome	19 Results	
	19 103010	
	21 Twenty-seven individuals were heterozygous for the p.Lysó18Ala variant; nine had	has haracteristict afdisease sporadic CRC (2.41%), seven were suspected
	of having hereditary CRC (2.8%) and 11 were controls (2.68%).	
	22 There were no significant associations in the case-control and case-case studies.	
	23 The p.Lys618Ala variant was co-existent with pathogenic mutations in two unrelated	Isease ^{The} Cohort LS families.

Top Design of Knowledge Integration



Integration of Databases



Genomics Data Integration



gene	Protein coding	20,656
	Protein no-coding	38,943

Variation Integration



- 10,725 Diseases
- 18,022 genes

Variation



dbVar is NCBI's database of genomic struct element insertions, translocations, and cor



dbSNP

dbVar

Database of single nucleotide polymorp insertions/deletions, microsatellites, and

Mutation →38,836 Genes

Known SNP database

dbSNP

	AN AN AN	SNCBI Resources 🛛 How To 🛇	Sign into NCB
5	dbSNP	dbVar Genome Browser Ho	mo sapiens: GRCh37 (GCF_000001405.13) Chr 2 (NC_000002.11): 1.299M - 1.299M
S NCBI	Short Genetic Variations	▼ View on Genome	nesen / m sonare mis page inter us and us an
	1994 (CE		
dbVar Clir	Nar GaP PubMed Nucleotide Protein		Sc.000002.11: 1.3M1.3M (52bp) ◆ ↓
	nall variations in dbSNP or large structural variations in dbVar		A T G C T A G G G T G G T G C C G C A G G G A C T C T C G T G T G G C C A T G A G C T C T G T G G C A A
Search Entrez dbSNF			TACGATCCCACCACGGCGTCCCTGAGAGCACCACCGGTACTCGAGACACCGT Genes
Have a question about dbSNP? Try	ANNOUNCEMENT	14 15 16 17 18 19 20 21 22 X Y	Gnomon Alignments
searching the SNP FAQ Archive!			NG Alignments NG 0237071
TAQ AICIIVE:	Interested in structural variations?		A T G C T A G G G T G G T G C C G C A G G G A C T C)T C G T G T G G C C A T G A G C T C T G T G G C A A Refseq Alignments
Go	Visit NCBI dbVar Database of genomic structural variation	✓ Select Assembly	
GENERAL	10 M	GRCh37	
RSS Feed	<	Select an assembly to change view Search	
Contact Us		Q- rs9677798	
Site Map	Search by IDs on All Assemblies	Enter a location, gene name or phenotype F Name Location	
dbSNP Homepage NCBI Variation	Note: <u>rs#</u> and <u>ss#</u> must be prefixed with "rs" or "ss",	rs9677798 Chr2 1,298,915	
Resources	respectively (i.e. rs25, ss25)	▶ Your Data	
Announcements	ID: Reference cluster ID(rs#) Search Reset	Region Summary Data in view Click (-) to remove track	
dbSNP Summary FTP Download	Bearer Reser	Study ID Variant Calls	
HUMAN VARIATION	Submission Information	Data available for region Click (+) to add track Study ID Variant Calls	
SNP SUBBISSION DOCUMENTATION	• By Submitter	estd203 1 (+)	
SEARCH	• <u>New Submitted Batches</u>		
RELATED SITES	• <u>Method</u>		
	• <u>Population</u> • Publication		
	Batch		
	• Enter List		
	- <u>NCBI Assay ID(ss)</u>	dhSNP	build 141: 61,060,456
	- <u>Reference SNP ID(rs)</u> - Local SNP ID	UDOINI	
	• Upload List		
	- <u>NCBI Assav ID(ss)</u> - Reference SNP_ID(rs)		
	- Local SNP ID		
	Batch Query Help		

http://www.ncbi.nlm.nih.gov/SNP/

Known association

ClinVar

🗧 😒 NCBI 🛛 Resources 🖸	How To 🗹		<u>Sign in to NCBI</u>
ClinVar	ClinVar	 Search ClinVar for gene symbols, HGVS expressions, condit 	ior Search
		Advanced	Help
Home About 🔻	Data use and mainter	ance 🔻 Using the website 🔻 How to submit 🔻 Statistics	FTP site 🔻

ClinVar submissions

This page summarizes the number of genes and distinct variant locations currently represented in ClinVar from independent submissions. A gene is reported if a variant in ClinVar is either found within, or includes, that gene. Thus the number of genes is as high as it is because of the structural variants in the database that span many genes.

This page lists all submitters and the summary of their contributions. We acknowledge their support.

Submission overview

Category of analysis	Current total (Jun 08, 2015)
Total accessioned submissions	175033
Total genes represented	26422
Total genes, in submissions with assertions, with variants in one gene	7468
Total genes, in submissions with assertions, with variants in multiple genes	26235
Total variations represented	147215
Total variations, in submissions with assertions	120309
Total submitters	332

Submitters and their submissions

Submitter	Total submissions	Total submissions with assertions	Total Genes	Last updated
OMIM; Johns Hopkins University	25662	25659	3798	Jun 05, 2015
Precancer Genomics; Leeds Institute of Molecular Medicine	22512	22512	3477	Jun 20, 2012

http://www.ncbi.nlm.nih.gov/clinvar/

The PharmGKB Knowledge Pyramid





PharmGKB提供以下信息:

- VA: Variant Annotations
- PW: Drug-Centered Pathway
- VIP: Very Important Pharmacogene Summaries
- CA: Clinical Annotations
- DG: Pharmacogenomics-Based Drug-Dosing Guidelines
- DL: Drug Labels with Pharmacogenomic Information

文章发表情况:

Total Publications: 284

- Pathway Publications: 38
- <u>Guideline Publications</u>: 23
- <u>VIP Publications</u>: 32
- Other Publications: 191



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Downloads

In addition to the PharmGKB website, we are pleased to make PharmGKB data and knowledge available as downloads. We have found that it is often critical to check with our curators at feedback@pharmgkb.org before embarking on a large project using these data, to be sure that the files and data we make available are being interpreted correctly. PharmGKB generally does NOT need to be a co-author on such analyses; we just want to make sure that there is a correct understanding of our data before lots of resources are spent.

Examples of papers that have been written by others using PharmGKB information

Primary PharmGKB Data

Versions of external data sources used in these files

- Genes: <u>genes.zip</u> (3 MB)
- RSID mapping: <u>rsid.zip</u> (151 MB)
- Drugs: drugs.zip (456 KB)
- Diseases: diseases.zip (312 KB)
- Pathways in BioPax format: pathways-biopax.zip (484 KB)
- Pathways in tsv format: pathways-tsv.zip (67 KB)
- Dosing Guidelines in <u>JSON</u> format: <u>dosingGuidelines.json.zip</u> (414 KB)
- Drug Label summary in tsv format: drugLabels.zip (6 KB)

Variant and Clinical Annotations Data

To access PharmGKB's variant and clinical annotations data please submit a Variant and Clinical Annotations Data Request.

Variant, Gene and Drug Relationship Data

To access PharmGKB's variant, gene and drug relationship data please submit a Variant, Gene and Drug Relationship Data Request.

http://www.pharmgkb.org/

Network Integration



Network Integration

Pathway Type	Edge Type	Directionality	Edge No.
	SR: Signaling Regulation	Directed	172,765
	ER: Expression Regulation	Directed	122,786
CAI: Complex Assembly Interaction		Undirected	177,227
Signaling Pathway	TR: Transport Regulation	Directed	7,296
	TRc: Transport Regulation chemical	Directed	3,285
	ca: x chemical affects P	Directed	469,519
	RNAi: RNAinterference		317,556
TechPPI	TechPPI: Technical Protein-Protein Interaction	Undirected	316,437
	sp: metabolic reaction $\stackrel{E}{s} \stackrel{F}{\rightarrow} \stackrel{F}{p}$	Directed	14,428
Metabolic Pathway	sE: metabolic reaction $\stackrel{E}{s \rightarrow p} \stackrel{F}{\rightarrow}$	Directed	22,480
	Ep: metabolic reaction $s \xrightarrow{F} p \xrightarrow{F}$	Directed	21,334
	EE: metabolic reaction $s \xrightarrow{E} p \xrightarrow{F}$	Directed	154,975
	rw: x reacts with y	Undirected	3,912

Network

Source Database	PathPPI v1.0	PathPPI v2.0
Reactome	2012.03.14	v56
NCI PID	2012.03.17	2015.17.27
NetPath	2012.04.14	2012.04.14
INOH	2010.01.31	2011.03.22 (v4.0)
KEGG	2009.10.12	2011.07
BioCarta	2010.08.13	
SPIKE	2011.03.22	
PhosphoSitePlus		2016.03.15
HumanCyc		v19.5
PANTHER Pathway		v3.4
TRANSFAC		v7.4
miRTarBase		v4.5
DrugBank		v4.3
Recon X		v2.03
Ctd		2015.06.03
SMPD		v2.0
WikiPathways		2015.09.29
HPRD	R9	R9
IntAct	2013.10.22	2016.02.16
BioGRID	R3.2.105	R3.44.135
DIP	2013.07.07	2016.01.14
MINT	2013.03.26	
BIND		2010.12.15
CORUM		2012.02.17

26 Modification

Modification	v1. 0	v2. 0	Modification	v1. 0	v2. 0
Acetylation	•	•	ADP- ribosylation		•
Botinylation	•		Acylation		•
Decanoylation	\bullet		Alkylation		•
Dimethylation	•		Amination		•
Farnesylation	•	•	Carbamoylatio n		•
Fucosylation	•		Carboxylation		•
Galactosylation	•		Ethylation		•
Geranylgeranylati on	•		Geranoylation		•
Glucosylation	•		Glucuronidatio n		•
Glycosylation	•	•	Glutathionylati on		•
Glycylation	\bullet		Glycation		•
Hydroxylation	•	•	N-glycosylation		•
Lipoylation	•	•	O- glycosylation		•
Methylation	•	•	Nitrosation		•
Myristoylation	•		Prenylation		•
Octanoylation	•		Ribosylation		•
Palmitoylation	•		Sulfation		•
Phosphopantethei ne	•				
Phosphorylation	•	•			
Sumoylation	•	•			
Trimethylation	•				
Ubiquitination	•	•			



Number of self-loops : 0 Multi-edge node pairs : 7855 Avg. number of neighbors : 37, 013 Avg. number of neighbors : 37, 013 Avg. number of neighbors : 13, 130 Avg. numbe
--

Expression regulatory networks

Clustering coefficient Connected components Network diameter Network radius Shortest paths Characteristic path length Avg. number of neighbors	: 1 : 10 : 1 : 19916671 : 3.632	(7%)	Num Net Is Number of Nulti-edg Analysi









Knowledge Graph



Visualization of Knowledge Graph



\$ match(a)-[r:TECHPPI]->(b) return a,b limit 25

Tools for the Knowledgebase: PMap

PMap Home Retrieve Analysis Explore Help Contract Us

PMap : a Precision Medicine knowledgebAse Platform

PMap is a disease Knowledge for Precision Medicine, which includes the information from biological molecular, human disease, phenotype, drugs, etc. PMap supports functions of retrieval by various biomedical terms, workflow analyses for omics datasets and also the intelligent knowledge discovery.

PMap is supported by the Chinese Program of Precision Medicine (Construction of Precision Medicine Knowledgebase for Disease Research, 2016YFC0901905).

TP53

KB>>Pathway



Literature





Ontology

PMap-ODAS
Search Engine

PM				Q Search
GENE:EGF				
Display	Gene EGF1950			
AllNone	Description epidermal growth factor			
Function	Location Homo Sapiens (Human)4q25 ge	nome browser		
✓ Protein				
Interaction	Function			
 Drugs Disease 	GO - Molecular function Ras guanyl-nucleotide exchange factor phosphatidylinositol-4,5-bisphosphate growth factor activity calcium ion binding transmembrane receptor protein tyro protein tyrosine kinase activity epidermal growth factor receptor bind Wnt-activated receptor activity protein binding Wnt-protein binding	e 3-kinase activity sine kinase activator activity		
	GO - Biological process activation of MAPK activity activation of MAPKK activity negative regulation of epidermal grow	wth factor receptor signaling pathway		
	Proteins			
	Uniprot			
	Uniprot	Description	PDB	
	P01133	Pro-epidermal growth factor	1IVO 1JL9 1NQL 1P9	J 2KV4 3NJP

Genome browser: EGF

Available Tracks	Human Interaction Data 👻 File 🕔	'iew Help				
X filter by text	0 20,000,000 40,000,000	60,000,000	80,000,000	100,000,000	120,000,000	140,000,000
▼ Gene 1			Q 🕀 🔂	chr4 - chr4:109859	001110082800 (223	.8 Kb) 🛛 😡 🍛
🕑 Gene	109,900,000		109,950,000		110,000,000	
▼ Transcript 1	S Gene					
Transcript	ch repeat, ig-like and transmembrane domains 3					•
▼ lncRNA 1	lerived rhodopsin homolog	EGF epidermal growth factor				
🕑 lncRNA						
▼ miRNA 1	See Transcript	XM_017007845.1				•
	IM_198506.4	XM_017007846.1				
	XM_017008167.1	XM_017007850.1				•
		XM_017007847.1				
		XM_017007849.1				
		XM_017007851.1				•
		XM_017007848.1				•
		XM_005262796.2				•
		XM_017007852.1				•
		XR_001741157.1			•	
		XR_001741156.1			(, + →	
		XM_017007853.1			→	
		XM_017007855.1		(
		XM_017007854.1				

EGF Related Drugs

Drugs

- cetuximab Source:PharmGKB
- bevacizumab Source:PharmGKB
- cholecalciferol Source:PharmGKB
- gefitinib Source:PharmGKB
- oxaliplatin Source:PharmGKB
- fluorouracil Source:PharmGKB
- irinotecan Source:PharmGKB
- ethanol Source:PharmGKB
- capecitabine Source:PharmGKB
- dexamethasone Source:PharmGKB
- docetaxel Source:PharmGKB
- panitumumab Source:PharmGKB
- Fatty acid derivatives Source:PharmGKB
- Insulins And Analogues Source:PharmGKB
- estrogens Source:PharmGKB
- glucocorticoids Source:PharmGKB

Disease

OMIM

OMIM Hypomagnesemia 4, renal, 611718 (3)

COSMIC

Show 10 v entries

Display

AllNone

Function

Protein

Interaction

Drugs

Disease

Drug-Drug Interaction

DRUG:Cetuximab

AllNone

Display

Interaction

✓ Disease

Genes

Drug CetuximabDrugBank DB00002 Formular C6484H10042N1732O2023S36

UNII PQX0D8J21J

PharmGKB PA10040

Interaction

Dru	ugs
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Drug	Description
Acetyldigitoxin	Acetyldigitoxin may decrease the cardiotoxic activities of Cetuximab.
Belimumab	The risk or severity of adverse effects can be increased when Cetuximab is combined with Belimumab.
Bevacizumab	Bevacizumab may increase the cardiotoxic activities of Cetuximab.
Cabazitaxel	The risk or severity of adverse effects can be increased when Cabazitaxel is combined with Cetuximab.
Cyclophosphamide	Cyclophosphamide may increase the cardiotoxic activities of Cetuximab.
Deslanoside	Deslanoside may decrease the cardiotoxic activities of Cetuximab.
Diaitoxin	Digitoxin may decrease the cardiotoxic activities of Cetuximab.

Q Search

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Cetuximab Targets and Treatments

	Trastuzumab	Trastuzumab may increase the cardiotoxic activities of Cetuximab.
	Foods	
	Diseases	
Display		ombination with irinotecan, is indicated for the treatment of EGFR-expressing, metastatic colorectal carcinoma in patients irinotecan-based chemotherapy. Cetuximab administered as a single agent is indicated for t <a>Source:drugbank Source:TTD
All	Genes	
Disease		tor receptor Source:drugbank
Genes		lobulin gamma Fc region receptor III-B 🛛 Source:drugbank component 🗳 Source:drugbank
		component subunit A 🗳 Source:drugbank component subunit B 🗳 Source:drugbank
		component subunit C 🛛 Source:drugbank
		lobulin gamma Fc region receptor III-A 🗳 Source:drugbank component 🔗 Source:drugbank
		globulin gamma Fc receptor I 🗣 Source:drugbank
		lobulin gamma Fc region receptor II-a 🛛 Source:drugbank
		lobulin gamma Fc region receptor II-b 🗳 Source:drugbank lobulin gamma Fc region receptor II-c 🏾 Source:drugbank
		ase 2 Source:PharmGKB



Ontology Annotations

- Gene Ontology (GO)
- Disease Ontology (DO)
- Human Phenotype Ontology (HPO)

O

Network Annotation

Molecular network

- Protein network
- Transcription factor regulatory network
- Phosphorylation network
- Ubiquitination network
- O

Pathway

- KEGG analysis
- Reactome Analysis

Knowledge network

O

History

Project_20170810

📄 Sample

- Workflow Analysis
 - ✓ R:Differential gene analysis
 - + Add analysis
- Genelist1
 - 🗸 GO
 - **√**KEGG
 - + Add anotation
- Genelist2
 - √GO
 - Network
 - + Add annotation
- + Add genelist
- Project_20170814
 - 🖹 Sample
 - Workflow Anaysis
 - ✓R:Differential gene analysis
 - + Add analysis
 - + Add genelist
- + New Project

R: GeneOntology						
Basic Informatio	on					
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GO terms view:	table 🔻 🚯		Targets	>=	2	
	erms, <u>Export to tree view.</u> GO term ID	GeneRatio	BgRatio	PValue	Enriched p.adjust	Sig. Enriched
		GeneRatio	BgRatio	PValue	p.adjust	Targets
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Edit filters. GO:0005515	GO term ID	GeneRatio Edit filters. Y 372(76.23%)	BgRatio Edit filter:	PValue E dit filte Y	p.adjust Edit filt	Targets Edit filters Y
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History

Project_20170810

Sample

- Workflow Analysis
 - ✓ R:Differential gene analysis
 - + Add analysis
- Genelist1
 - **√**GO
 - **V**KEGG
 - + Add anotation
- Genelist2
 - √GO
 - "Network
 - + Add annotation
- + Add genelist
- Project_20170814
 - Sample
 - Workflow Anaysis
 - ✓R:Differential gene analysis
 - + Add analysis
 - + Add genelist
- + New Project

: GeneOntology						
Basic Information	1					
Name: 0	GOAnalysisResult 🥒		Create tin	ne: 20	170210 16:57	7
GO Version: *****版本 Update time: 20170210 17:09						
Input data: GeneList(750) Size on disk: 5 kb						
Table View	Tree View					🛓 Downl
Mapped Gene Num	ı.: 500		Sig. GO t	terms:	50	
Category Display	Display GO Full Hierachy	• 0	PValue	>= (0.05	
GO terms view:	ontology 🔻 🚯		Targets	>=	2	
	rms, <u>Export to tree view.</u>				Enriched	Sig. Enriched
G	rms, <u>Export to tree view.</u> O term ID	GeneRatio	BgRatio	PValue	p.adjust	Targets
G Edit filters.	GO term ID		BgRatio	PValue	p.adjust Edit fil(y :	Targets Edit filters Y
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G Edit filters.	GO term ID Molecular_function Transcription Factor Activity, Protein Bindin	GeneRatio Edit filters. Y 17276-238) 12(2.46%) 12(2.46%)	BgRatio Edit filter Y 10893(64.14%) 48(0.28%) 58(0.34%)	PValue Edit filte Y No Filter	p.adjust Edit filt y : 192E-06 192E-06 1.58E-05	Targets Edit filters Y 372 12 12
G Edit filters. `▲ ✔) <u>GO:0003674</u> ✔) <u>GO:0000988</u>	Molecular function Transcription Factor Activity. Protein Binding Nucleic Acid Binding	GeneRatio Edit filters. Y 12(246%) 12(246%) 11(2.25%)	BgRatio Edit filter Y 10893(64 144) 48(0 29%) 58(0.34%) 50(0.29%)	PValue Edit filte Y No Filter Equal	p.adjust Edit filly: 1.92E-06 1.58E-05 1.48E-05	Targets Edit filters Y 372 12 12 11
G Edit filters. ▲ ✔) <u>GO:0003674</u>	GO term ID Molecular_function Transcription Factor Activity, Protein Bindin	GeneRatio Edit filters. Y 12(2.46%) 12(2.46%) 11(2.25%) 6(1.23%) 71(14.55%)	BgRatio Edit filter (0893(6414) 48(0.28%) 58(0.34%) 50(0.29%) 12(0.07%) 1376(8.10%)	PValue Edit filte No Filter Equal Not Equal Less Greater	p.adjust Edit filly: 192E-06 192E-06 192E-05 1.48E-05 1.07E-05 1.00152493	Targets Edit filters Y 372 12 12 12 12 12 12 12 12 12 11 6 71
G Edit filters. `▲ ✔) <u>GO:0003674</u> ✔) <u>GO:0000988</u>	Molecular_function Transcription Factor Activity, Protein Binding Nucleic Acid Binding Transcription Factor	GeneRatio Edit filters. Y 12(2.46%) 12(2.46%) 11(2.25%) 6(1.23%) 71(14.55%) 25(5.12%)	BgRatio Edit filter ¥ 48(0.28%) 58(0.34%) 50(0.29%) 12(0.07%) 1376(8.10%) 289(1.70%)	PValue Edit filte Y No Filter Equal Not Equal Less Greater 1.03E-06	p.adjust Edit fill 92E-06 92E-06 58E-05 148E-05 1.000152493 0.000152493	Targets Edit filters Y 372 12 11 6 71 25
G Edit filters.	Molecular_function Transcription Factor Activity, Protein Binding Transcription Factor Activity DNA Binding	GeneRatio Edit filters. ✓ 12(2.46%) 12(2.46%) 11(2.25%) 6(1.23%) 71(14.55%) 25(5.12%) 21(4.30%)	BgRatio Edit filter: ✓ 10593(64,14%) 48(0,28%) 58(0,34%) 50(0,29%) 12(0,07%) 127(0,68,10%) 289(1,70%) 217(1,28%)	PValue Edit filte Y No Filter Equal Not Equal Less Greater 1.03E-06 1.26E-06	p.adjust Edit filly 1.92E-06 1.92E-06 1.58E-05 1.48E-05 1.07E-05 1.00152493 0.000152493 0.000154293	Targets Edit filters Y 372 12 11 6 71 25 21
G Edit filters. Co:0003674 Co:0003674 Co:0003677 Co:0003677 Co:0003723	Molecular_function Transcription Factor Activity, Protein Binding Transcription Factor Activity DNA Binding RNA Binding din	GeneRatio Edit filters. ✓ 12(2.46%) 12(2.46%) 12(2.26%) 6(1.23%) 71(14.55%) 25(5.12%) 21(4.30%) complete the second seco	BgRatio Edit filter ♀ 10893.64 144 48(0.28%) 58(0.34%) 50(0.29%) 12(0.07%) 1376(8.10%) 289(1.70%) 217(1.28%) 5(0.03%)	PValue Edit filte Y No Filter Equal Not Equal Less Greater 1.03t-06 1.26E-06 3.29E-06	p.adjust Edit filly 1.92E-06 1.92E-06 1.58E-05 1.48E-05 1.07E-05 1.07E-05 1.000152493 0.000152493 0.000154208 0.000356267	Targets Edit filters Y 372 12 12 12 12 12 12 12 12 12 11 6 71 25 21 4
G Edit filters. Co.0003674 Co.0003674 Co.0003674 Co.0003677 Co.0003723 Co.0003723 Co.0003723	Molecular_function Transcription Factor Activity, Protein Binding Transcription Factor Activity DNA Binding RNA Binding din MRNA Binding ing	GeneRatio Edit filters.✓ 12(2.46%) 12(2.46%) 12(2.26%) 6(1.23%) 71(14.55%) 25(5.12%) 21(4.30%) c1(4.30%)	BgRatio Edit filter: ✓ 10593(64,14%) 48(0,28%) 58(0,34%) 50(0,29%) 12(0,07%) 127(0,68,10%) 289(1,70%) 217(1,28%)	PValue Edit filte Y No Filter Equal Not Equal Creater 1.03E-06 1.26E-06 3.29E-06 3.42E-06 6.73E-06	p.adjust Edit filly 1.92E-06 1.92E-06 1.58E-05 1.48E-05 1.07E-05 1.00152493 0.000152493 0.000154293	Targets Edit filters Y 372 12 11 6 71 25 21 4 6 16
G Edit filters. Comment Com	Coterm ID Molecular_function Transcription Factor Activity, Protein Binding Transcription Factor Activity DNA Binding RNA Binding GTPase Activity	GeneRatio Edit filters. ✓ 12(2.46%) 12(2.46%) 12(2.46%) 11(2.25%) 6(1.23%) 6(1.23%) 21(4.30%) 21(4.30%) 21(4.30%) 21(4.30%) 16(3.22%) 35(7.17%)	BgRatio Edit filter: ✓ 48(0.28%) 58(0.34%) 50(0.29%) 12(0.07%) 1376(8.10%) 289(1.70%) 289(1.70%) 217(1.28%) 5(0.03%) 16(0.09%) 150(0.88%) 541(3.19%)	PValue Edit filte y No Filter Equal Not Equal Less Greater 1.03L-06 1.26E-06 3.29E-06 3.42E-06 3.42E-06 6.73E-06	p.adjust Edit filly 1.92E-06 1.92E-06 1.58E-05 1.48E-05 1.07E-05 1.00152493 0.000152493 0.000154208 0.00036267 0.000366543 0.000586543	Targets Edit filters Y 372 12 12 11 6 71 25 21 4 6 35
G Edit filters. Commonstand	Coterm ID Molecular_function Transcription Factor Activity, Protein Binding Transcription Factor Activity DNA Binding RNA Binding GTPase Activity Helicase Activity	GeneRatio Edit filters. ✓ 12(2.46%) 12(2.3%) 12(3.28%) 16(3.28%) 35(7.17%) 38(7.7%)	BgRatio Edit filter ♀ 10893.64 144 48(0.28%) 58(0.34%) 50(0.29%) 12(0.07%) 1376(8.10%) 289(1.70%) 217(1.28%) 5(0.03%) 16(0.09%) 150(0.88%) 541(3.19%) 612(3.60%)	PValue Edit filte Y No Filter Equal Not Equal L26E-06 3.29E-06 3.42E-06 6.73E-06 7.03E-06 7.32E-06	p.adjust Edit fill 1.92E-06 1.92E-06 1.92E-05 1.48E-05 1.07E-05 1.000152493 0.000154293 0.000154293 0.000154208 0.00036267 0.00036267 0.000368643 0.000586543	Targets Edit filters Y 372 12 12 12 12 12 12 12 12 12 11 6 71 25 21 4 6 16 35 38
G Edit filters. Commonstand	O term ID Molecular_function Transcription Factor Activity, Protein Binding Nucleic Acid Binding Transcription Factor Activity DNA Binding RNA Binding din MRNA Binding ing GTPase Activity Helicase Activity Nuclease Activity	GeneRatio Edit filters. Edit filters. 12(2.46%) 12(2.46%) 11(2.25%) 6(1.23%) 25(5.12%) 21(4.30%) 4(0.82%) 6(1.23%) 16(3.28%) 35(7.17%) 71(14.55%)	BgRatio Edit filter: ✓ 48(0.28%) 58(0.34%) 50(0.29%) 12(0.07%) 1376(8.10%) 289(1.70%) 289(1.70%) 217(1.28%) 5(0.03%) 16(0.09%) 150(0.88%) 541(3.19%)	PValue Edit filte y No Filter Equal Not Equal Less Greater 1.03L-06 1.26E-06 3.29E-06 3.42E-06 3.42E-06 6.73E-06	p.adjust Edit filly 1.92E-06 1.92E-06 1.58E-05 1.48E-05 1.07E-05 1.00152493 0.000152493 0.000154208 0.00036267 0.000366543 0.000586543	Targets Edit filters Y 372 12 12 12 12 12 12 12 12 12 11 6 71 25 21 4 6 16 35 38 71
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G Edit filters. Commonstand	Molecular function Transcription Factor Activity, Protein Binding Nucleic Acid Binding Transcription Factor Activity DNA Binding RNA Binding GTPase Activity Helicase Activity Nuclease Activity Signal Transducer Activ Structural Molecule	GeneRatio Edit filters. ✓ 12(2.46%) 12(2.45%) 12(2.25%) 12(2.25%) 12(2.25%) 12(2.25%) 12(2.25%) 12(2.475%)	BgRatio Edit filter ♀ 10893.64 144 48(0.28%) 58(0.34%) 50(0.29%) 12(0.07%) 1376(8.10%) 289(1.70%) 217(1.28%) 5(0.03%) 16(0.09%) 150(0.88%) 541(3.19%) 612(3.60%) 1473(8.67%) 77(0.45%) 1509(8.89%) 1520(8.95%)	PValue Edit filte Y No Filter Equal Not Equal Less Greater 1.03E-06 3.29E-06 3.29E-06 3.42E-06 3.42E-06 6.73E-06 7.03E-06 7.03E-06 1.01E-05 1.19E-05 1.22E-05 1.56E-05	p.adjust Edit filly 1.92E-06 1.92E-06 1.92E-05 1.48E-05 1.07E-05 1.000152493 0.000152493 0.000152493 0.000152493 0.000152493 0.0001526543 0.000586543 0.000586543 0.000586543 0.000586543 0.000793709 0.000793709 0.000954452	Targets Edit filters Y 372 12 12 12 12 12 12 12 12 13 6 71 25 21 4 6 16 35 38 71 11 12 72
G Edit filters.	O term ID Molecular_function Transcription Factor Activity, Protein Binding Transcription Factor Activity DNA Binding RNA Binding GTPase Activity Helicase Activity Signal Transducer Activ	GeneRatio Edit filters. Y 12(2.46%) 12(2.46%) 11(2.25%) 6(1.23%) 71(14.55%) 21(4.30%) 4(0.82%) 6(1.23%) 16(3.28%) 35(7.17%) 38(7.79%) 71(14.55%) 11(2.25%) 11(2.25%) 72(14.75%) 72(14.75%) 5(1.02%)	BgRatio	PValue Edit filte Y No Filter Equal Not Equal Creater 1.03E-06 1.26E-06 3.29E-06 3.42E-06 6.73E-06 7.03E-06 7.03E-06 7.03E-06 1.01E-05 1.19E-05 1.26E-05 2.04E-05	p.adjust Edit filly: 1.92E-06 1.92E-06 1.58E-05 1.48E-05 1.07E-05 1.00152493 0.000152493 0.000152493 0.000152493 0.000164208 0.00036267 0.00036543 0.000586543 0.000586543 0.000586543 0.000793709 0.000793709 0.000793709	Targets Edit filters Y 372 12 11 6 71 25 21 4 6 16 35 38 71 11 72 5
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G Edit filters.	Molecular_function Transcription Factor Activity. Protein Bindiny Nucleic Acid Binding Transcription Factor Activity DNA Binding RNA Binding GTPase Activity Helicase Activity Nuclease Activity Signal Transducer Activ Structural Molecule Activity Cytoskeletal Protein Binding Transcription Factor	GeneRatio Edit filters. Y 12(2.46%) 12(2.46%) 11(2.25%) 6(1.23%) 71(14.55%) 21(4.30%) 4(0.82%) 6(1.23%) 16(3.28%) 35(7.17%) 38(7.79%) 71(14.55%) 11(2.25%) 11(2.25%) 72(14.75%) 72(14.75%) 5(1.02%)	BgRatio	PValue Edit filte Y No Filter Equal Not Equal Creater 1.03E-06 1.26E-06 3.29E-06 3.42E-06 6.73E-06 7.03E-06 7.03E-06 7.03E-06 1.01E-05 1.19E-05 1.26E-05 2.04E-05	p.adjust Edit filly: 1.92E-06 1.92E-06 1.58E-05 1.48E-05 1.07E-05 1.00152493 0.000152493 0.000152493 0.000152493 0.000164208 0.00036267 0.00036543 0.000586543 0.000586543 0.000586543 0.000793709 0.000793709 0.000793709	Targets Edit filters Y 372 12 11 6 71 25 21 4 6 16 35 38 71 11 72 5
G Edit filters.	Coterm ID Molecular_function Transcription Factor Activity, Protein Binding Transcription Factor Activity DNA Binding MRNA Binding GTPase Activity Helicase Activity Nuclease Activity Signal Transducer Activ Structural Molecule Activity Cytoskeletal Protein Binding Transcription Factor Binding	GeneRatio Edit filters. Y 12(246%) 12(246%) 12(246%) 11(225%) 6(1.23%) 71(14.55%) 25(5.12%) 21(4.30%) 4(6(3.28%) 35(7.17%) 38(7.79%) 35(7.17%) 38(7.79%) 71(14.55%) 11(2.25%) 72(14.75%) 72(14.75%) 11(2.25%) 72(14.75%) 11(2.25\%) 11(2.25\%)	BgRatio	PValue Edit filte y No Filter Equal Not Equal Creater 1.03E-06 1.26E-06 3.42E-06 3.42E-06 3.42E-06 6.73E-06 7.03E-06 7.03E-06 7.03E-06 1.01E-05 1.19E-05 1.22E-05 1.56E-05 2.04E-05 2.04E-05 3.63E-05 5.69E-05	p.adjust Edit filly: 1.92E-06 1.92E-06 1.58E-05 1.07E-05 1.00152493 0.000152493 0.000152493 0.000152493 0.000152493 0.000152493 0.000365643 0.000366543 0.000586543 0.000586543 0.000783709 0.000793709 0.000793709 0.000793709 0.000793709 0.000793709 0.000793709 0.000793709 0.0001888793 0.001188507 0.001188507	Targets 372 12 12 11 6 71 25 21 4 6 16 35 38 71 11 72 5 31 100 105
G Edit filters. Commonstant	Molecular_function Transcription Factor Activity. Protein Bindiny Nucleic Acid Binding Transcription Factor Activity DNA Binding RNA Binding GTPase Activity Helicase Activity Nuclease Activity Signal Transducer Activ Structural Molecule Activity Cytoskeletal Protein Binding Transcription Factor	GeneRatio Edit filters. Y 12(2.46%) 12(2.46%) 12(2.46%) 12(2.46%) 11(2.25%) 6(1.23%) 21(4.30%) 2(4.30%) 2(4.30%) 2(4.30%) 2(4.30%) 3(6.123%) 11(2.25%) 7(1.4.55%) 11(2.25%) 7(1.4.3%) (4.30%)	BgRatio Edit filter: ✓ 10593:64.149 48(0.28%) 58(0.34%) 50(0.29%) 12(0.07%) 1376(8.10%) 239(1.70%) 239(1.70%) 217(1.28%) 5(0.03%) 16(0.09%) 150(0.88%) 541(3.19%) 612(3.60%) 1473(8.67%) 1473(8.67%) 1509(8.89%) 1509(8.89%) 1509(8.4%) 2666(15.70%) 738(4.35%) 2544(14.98%) 36(0.21%)	PValue Edit filte y No Filter Equal Not Equal Less Greater 1.03L-06 1.26E-06 3.29E-06 3.29E-06 3.29E-06 3.29E-06 6.73E-06 7.32E-06 1.01E-05 1.19E-05 1.22E-05 1.56E-05 2.04E-05 3.63E-05 3.63E-05 5.69E-05 6.28E-05	p.adjust Edit filiv 1.92E-06 1.92E-06 1.58E-05 1.48E-05 1.07E-05 1.00152493 0.000152493 0.000152493 0.00036267 0.000366543 0.000586543 0.000586543 0.000586543 0.000586543 0.000586543 0.000586543 0.000586543 0.000586543 0.000586543 0.000586543 0.000586543 0.000586543 0.00028453 0.001888793 0.002162286 0.002162286 0.002284465 0.002844517	Targets 372 12 12 11 6 71 25 21 4 6 16 35 38 71 11 72 5 31 110 41 105
G Edit filters.	O term ID Molecular_function Transcription Factor Activity, Protein Binding Transcription Factor Activity DNA Binding GTPase Activity Helicase Activity Nuclease Activity Signal Transducer Activ Structural Molecule Activity Cytoskeletal Protein Binding Transcription Factor Binding Methyltransferase	GeneRatio Edit filters. 12(2.46%) 12(2.46%) 12(2.46%) 12(2.46%) 11(2.25%) 6(1.23%) 25(5.12%) 21(4.30%) 2(4.30%) 2(4.30%) 3(0.82%) 6(1.23%) 16(3.28%) 35(7.17%) 38(7.79%) 71(14.55%) 11(2.25%) 72(14.75%) 5(1.02%) 31(6.35%) 11(0.22.54%) 41(8.40%) 10(22.54%) 41(8.40%) 10(22.54%) 41(8.40%) 10(22.54%) 41(8.40%) 10(22.54%) 41(8.40%) 10(22.54%) 41(8.40%) 10(22.54%) 41(8.40%) 10(22.54%) 21(4.33%) 93(19.06%) Complements	BgRatio Edit filter: 48(0.28%) 58(0.34%) 50(0.29%) 12(0.07%) 1376(8.10%) 289(1.70%) 217(1.28%) 5(0.03%) 16(0.09%) 150(0.88%) 541(3.19%) 150(0.88%) 150(8.89%) 1520(8.95%) 13(0.09%) 482(2.84%) 2666(15.70%) 738(4.35%) 2544(14.98%) 36(0.21%) 2203(12.97%)	PValue Edit filte y No Filter Equal Not Equal L26E - 06 3.29E - 06 1.26E - 05 1.19E - 05 1.22E - 05 1.56E - 05 2.264E - 05 3.63E - 05 2.64E - 05 3.63E - 05 5.69E - 05 6.28E - 05 5.69E - 05 6.28E - 05 5.69E - 05 6.28E - 05 5.69E - 05 6.28E - 05 7.42E - 05	P.adjust Edit filly 1.92E-06 1.92E-06 1.92E-06 1.92E-05 1.07E-05 1.07E-05 1.07E-05 1.000152493 0.000152493 0.000152493 0.000152493 0.00036267 0.000362643 0.000586543 0.000586543 0.000586543 0.000747546 0.000747546 0.000793709 0.000954452 0.001180507 0.00148643 0.00188793 0.002162266 0.002694465 0.00269445	Targets 372 12 12 12 12 12 12 12 1372 12 12 11 6 71 35 38 71 11 72 5 31 110 41 105 7 93
G Edit filters. CO:0003674 CO:0003674 CO:0003674 CO:0003723	Molecular_function Transcription Factor Activity, Protein Binding Transcription Factor Activity, Protein Binding Transcription Factor Activity DNA Binding MRNA Binding GTPase Activity Helicase Activity Signal Transducer Activ Structural Molecule Activity Cytoskeletal Protein Binding Transcription Factor Activity Inding Transcription Factor Activity Signal Transducer Activ Structural Molecule Activity Peptidase Activity Ig Peptidase Activity	GeneRatio Edit filters. Y 12(2.46%) 12(2.46%) 12(2.46%) 12(2.46%) 11(2.25%) 6(1.23%) 21(4.30%) 2(4.30%) 2(4.30%) 2(4.30%) 2(4.30%) 3(6.123%) 11(2.25%) 7(1.4.55%) 11(2.25%) 7(1.4.3%) (4.30%)	BgRatio Edit filter: ✓ 10593:64.149 48(0.28%) 58(0.34%) 50(0.29%) 12(0.07%) 1376(8.10%) 239(1.70%) 239(1.70%) 217(1.28%) 5(0.03%) 16(0.09%) 150(0.88%) 541(3.19%) 612(3.60%) 1473(8.67%) 1473(8.67%) 1509(8.89%) 1509(8.89%) 1509(8.4%) 2666(15.70%) 738(4.35%) 2544(14.98%) 36(0.21%)	PValue Edit filte y No Filter Equal Not Equal Less Greater 1.03L-06 1.26E-06 3.29E-06 3.29E-06 3.29E-06 3.29E-06 6.73E-06 7.32E-06 1.01E-05 1.19E-05 1.22E-05 1.56E-05 2.04E-05 3.63E-05 3.63E-05 5.69E-05 6.28E-05	p.adjust Edit filiv 1.92E-06 1.92E-06 1.58E-05 1.48E-05 1.07E-05 1.00152493 0.000152493 0.000152493 0.00036267 0.000366543 0.000586543 0.000586543 0.000586543 0.000586543 0.000586543 0.000586543 0.000586543 0.000586543 0.000586543 0.000586543 0.000586543 0.000586543 0.00028453 0.001888793 0.002162286 0.002162286 0.002284465 0.002844517	Targets 372 12 12 11 6 71 25 21 4 6 16 35 38 71 11 72 5 31 110 41 105

History Project_20170810

- 📄 Sample
- Workflow Analysis
 - ✓ R:Differential gene analysis
 - + Add analysis
- Genelist1
 - 🖌 GO
 - **√**KEGG
 - + Add anotation
- Genelist2
 - √GO
 - Network
 - + Add annotation
- + Add genelist
- Project_20170814
 - 📄 Sample
 - Workflow Anaysis
 - ✓R:Differential gene analysis
 - + Add analysis
 - + Add genelist
- + New Project



ProDiGy Home Data browser Query My	space 🗸 Log out Help	welcome! test@bprc.cn
History 🔣	Project_20170810	
 Project_20170810 Sample 	R: ProteinNetwork	
 Workflow Analysis 	Basic Information	▼
 ✓ R:Differential gene analysis + Add analysis 	Name: NetworkAnalysisResult 🖍 Create time: 20170210 16:5	57
▼ Genelist1	Sig. Networks: 50 Update time: 20170210 17:0	19
√ GO √KEGG	Input data: GeneList(750) Size on disk: 5 kb	
 Add anotation ✓ Genelist2 	Table View Network View	🛓 Download
✓ GO ✓ GO ✓ Network + Add annotation	Sig. Networks: 50 Score >= 20 Records per page: 10 - Targets >= 2	
+ Add genelist▼ Project_20170814	700	ault GO
Sample Workflow Anavsis	Selected 30 GO terms, Export to Network view.	
✓ R:Differential gene analysis	Network ID \bigtriangledown Molecules in Network \bigtriangledown Score \bigtriangledown	Targets 🗢
+ Add analysis + Add genelist + New Project	1 vANN, ^APOBR, ^ARPIN/C15orf38-AP3S2, ^CADM3, 40 vCHCHD10, vENPP4, ^FOXA1, ^FOXA2, ^GATA3, vITGB4, vITGB7,^RCID1, ^KLF2,vLHFP	35
	 vADAD2, ^RPI, ^APP, ^CCDC149, vTOX2, vENPP4, ^FOXA1, ^FOXA2, ^GATA3, vITGB4, vITGB7,^RCID1, ^KLF2,vLHFP 	34
	3 vCCDC149, vTOX2, vENPP4, ^FOXA1, ^FOXA2, ^GATA3, 35 vITGB4, vITGB7,^RCID1, ^KLF2,vLHFP	35
	4 ^CADM3, vCHCHD10, vENPP4, ^FOXA1,vANN, ^APOBR 34	32
	5 ^CADM3, vCHCHD10, vENPP4, ^FOXA1 30	31
	Records per page: 10 - Showing 1 to 10 of 50 rows	3 4 5 Next Last

Targets mapped to this term:

Code	GO ID	GO Description	Targeted ID	Targeted Name	Gene Description
1.4	GO:0008009	chemokine activity	3627	A3GALT2	Alpha-1,3-galactosyltransferase 2 (EC 2.4.1.87) (Isoglobotriaosylceramide synthase) (iGb3 synthase) (iGb3S) [A3GALT2P] [IGBS3S]
1.4	GO:0008009	chemokine activity	10563	AADACL3	Arylacetamide deacetylase-like 3 (EC 3.1.1)
1.4	GO:0008009	chemokine activity	6373	AADACL4	Arylacetamide deacetylase-like 4 (EC 3.1.1)
1.4	GO:0008009	chemokine activity	4283	ABCA4	Retinal-specific ATP-binding cassette transporter (ATP-binding cassette sub-family A member 4) (RIM ABC transporter) (RIM protein) (RmP) (Stargardt disease protein) [ABCR]
1.4	GO:0008009	chemokine activity	6362	ABCB10	ATP-binding cassette sub-family B member 10, mitochondrial precursor (ATP-binding cassette transporter 10) (ABC transporter 10 protein) (Mitochondrial ATP-binding cassette 2) (M-ABC2)
1.4	GO:0008009	chemokine activity	6355	ABCD3	ATP-binding cassette sub-family D member 3 (70 kDa peroxisomal membrane protein) (PMP70) [PMP70] [PXMP1]
1.4	GO:0008009	chemokine activity	2921	ABL2	Abelson tyrosine-protein kinase 2 (EC 2.7.10.2) (Abelson murine leukemia viral oncogene homolog 2) (Abelson- related gene protein) (Tyrosine-protein kinase ARG) [ABLL] [ARG]
1.4	GO:0008009	chemokine activity	6364	ACADM	Medium-chain specific acyl-CoA dehydrogenase, mitochondrial precursor (EC 1.3.8.7) (MCAD)
1.4	GO:0008009	chemokine activity	3576	ACAP3	Arf-GAP with coiled-coil, ANK repeat and PH domain-containing protein 3 (Centaurin-beta-5) (Cnt-b5) [CENTB5]
1.4	GO:0008009	chemokine activity	6352	ACBD3	Golgi resident protein GCP60 (Acyl-CoA-binding domain-containing protein 3) (Golgi complex-associated protein 1) (GOCAP1) (Golgi phosphoprotein 1) (GOLPH1) (PBR- and PKA-associated protein 7) (Peripheral benzodiazepine receptor-associated protein PAP7) [Contains: Golgi resident protein GCP60, N-terminally processed] [GCP60]
1.4	GO:0008009	chemokine activity	6347	ACBD6	Acyl-CoA-binding domain-containing protein 6
1.4	GO:0008009	chemokine activity	6351	ACKR1	Atypical chemokine receptor 1 (Duffy antigen/chemokine receptor) (Fy glycoprotein) (GpFy) (Glycoprotein D) (Plasmodium vivax receptor) (CD234 antigen) [DARC] [FY] [GPD]

History

- Project_20170810
 - Sample
 - Workflow Analysis
 - ✓ R:Differential gene analysis
 - + Add analysis
 - Genelist1
 - **√**GO
 - **V**KEGG
 - + Add anotation
 - Genelist2
 - **√**GO
 - . Network
 - + Add annotation
 - + Add genelist
- Project_20170814
 - Sample
 - Workflow Anaysis
 - ✓R:Differential gene analysis
 - + Add analysis
- + Add genelist
- + New Project





Thank You!