

Gene Ontology

Дано: набор белков или генов

Дано: набор белков или генов

Откуда их взять?

Экспрессия

Дифференциальная экспрессия

Масспектрометрия

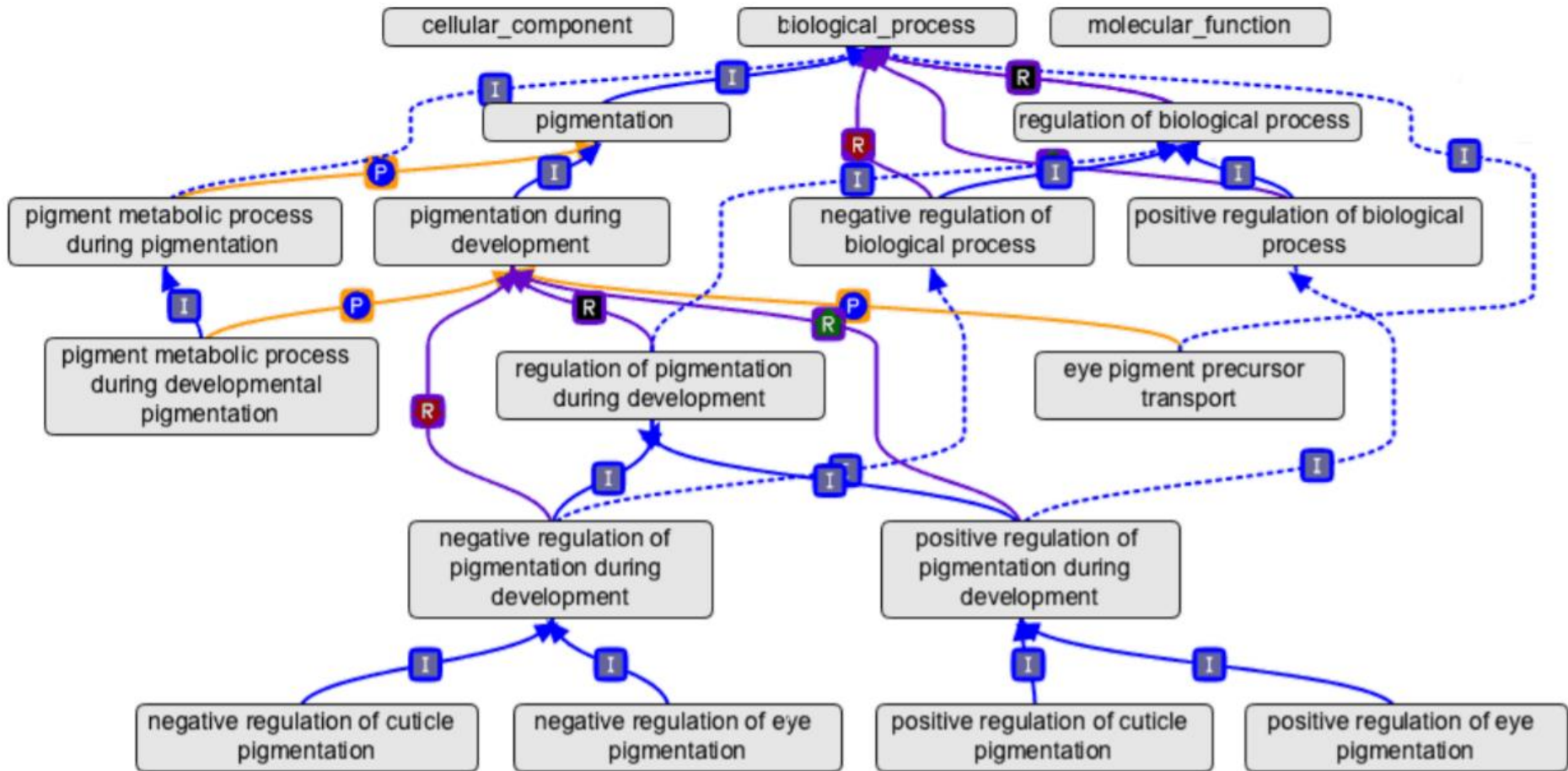
Любимый набор

...

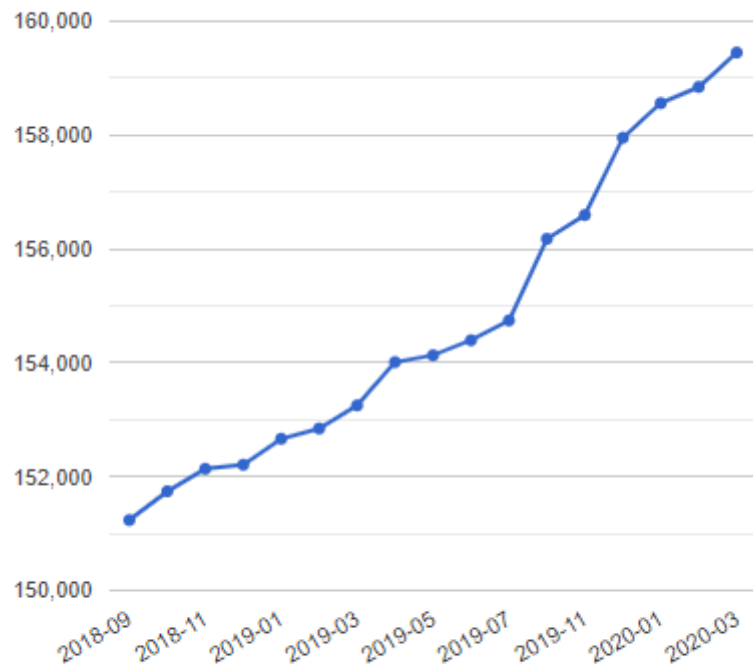
Что дальше делать?

Gene Ontology – GO
<http://geneontology.org/>

База данных GO представляет собой граф биологических терминов, соединенных различными отношениями



Growth of annotated scientific publications over time



Ontology

Property	Value
Valid terms	44531 ($\Delta = -48$)
Obsoleted terms	2895 ($\Delta = 40$)
Merged terms	1967 ($\Delta = 35$)
Biological process terms	29225
Molecular function terms	11124
Cellular component terms	4182

Annotations

Property	Value
Number of annotations	7,524,022
Annotations for biological process	2,927,597
Annotations for molecular function	2,325,747
Annotations for cellular component	2,270,678
Annotations for evidence PHYLO	3,610,054
Annotations for evidence IEA	2,041,235
Annotations for evidence OTHER	832,336
Annotations for evidence EXP	757,235
Annotations for evidence ND	242,830
Annotations for evidence HTP	40,332
Number of annotated scientific publications	159,450

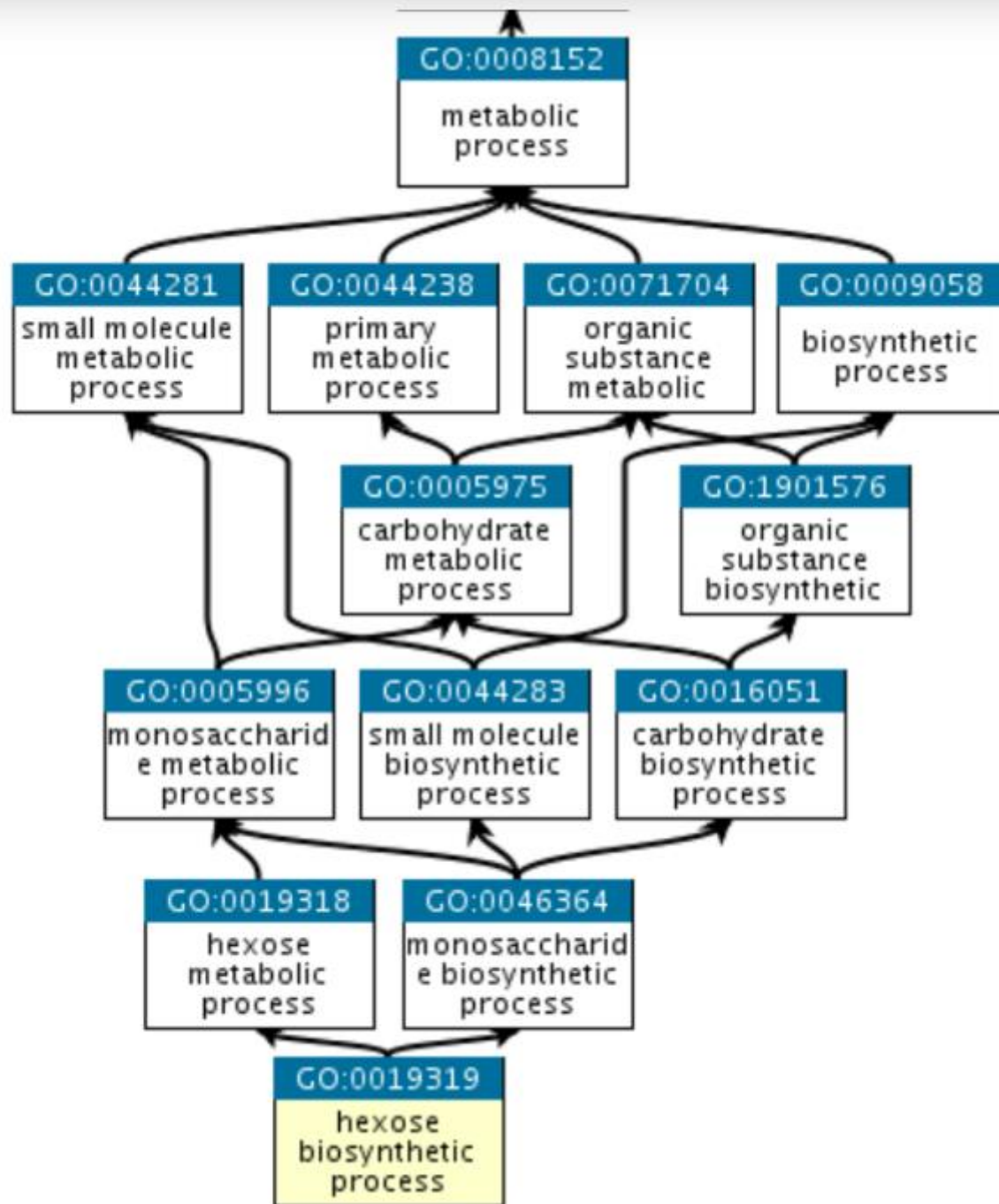
Gene products and species

Property	Value
Annotated gene products	1,405,061
Annotated species	4,593
Annotated species with over 1,000 annotations	195

Молекулярные функции (англ. molecular function) — специфическая активность генного продукта на молекулярном уровне, например, связывание углеводов или АТФ-азная активность.

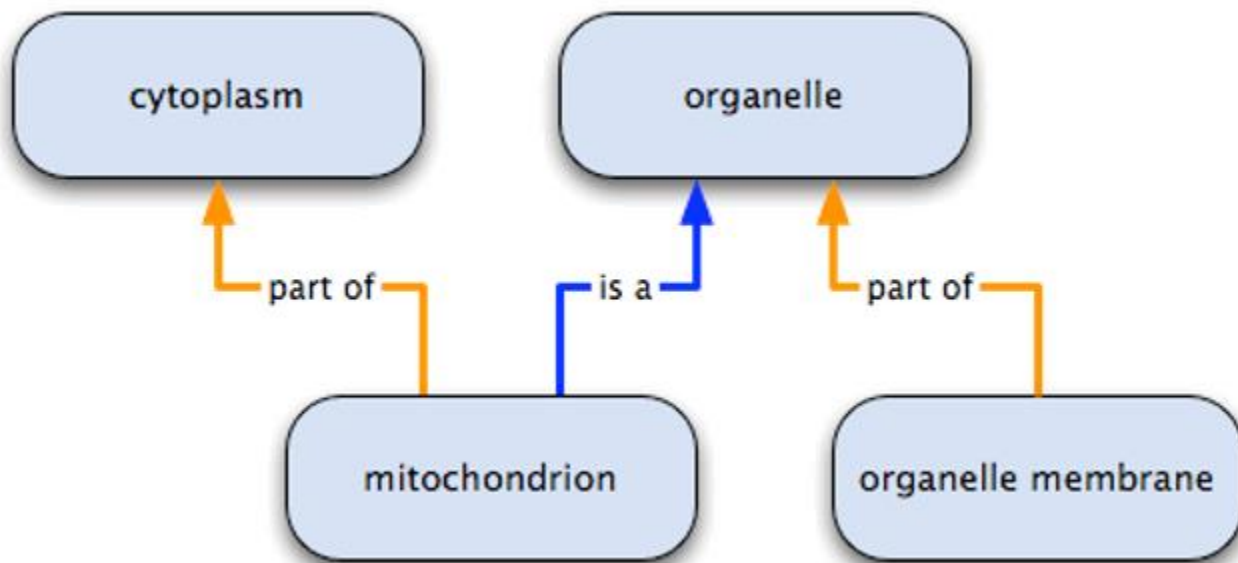
Биологические процессы (англ. biological process) — сложные явления, необходимые для жизнедеятельности организмов и происходящие благодаря осуществлению последовательности молекулярных функций, например, митоз или биосинтез пуринов.

Клеточные компоненты (англ. cellular component) — части клетки или внеклеточного пространства, где осуществляется функция генного продукта, например, ядро или рибосома.



Термин GO (GO term) – узел графа – может иметь любое количество связей с любыми другими узлами

Отношения между узлами – ребра графа бывают разного типа



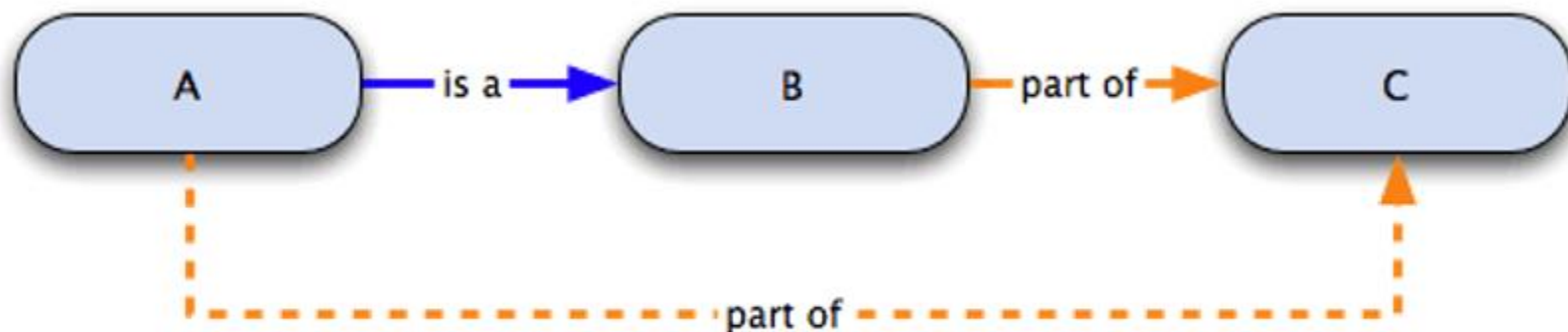
A *is a* B

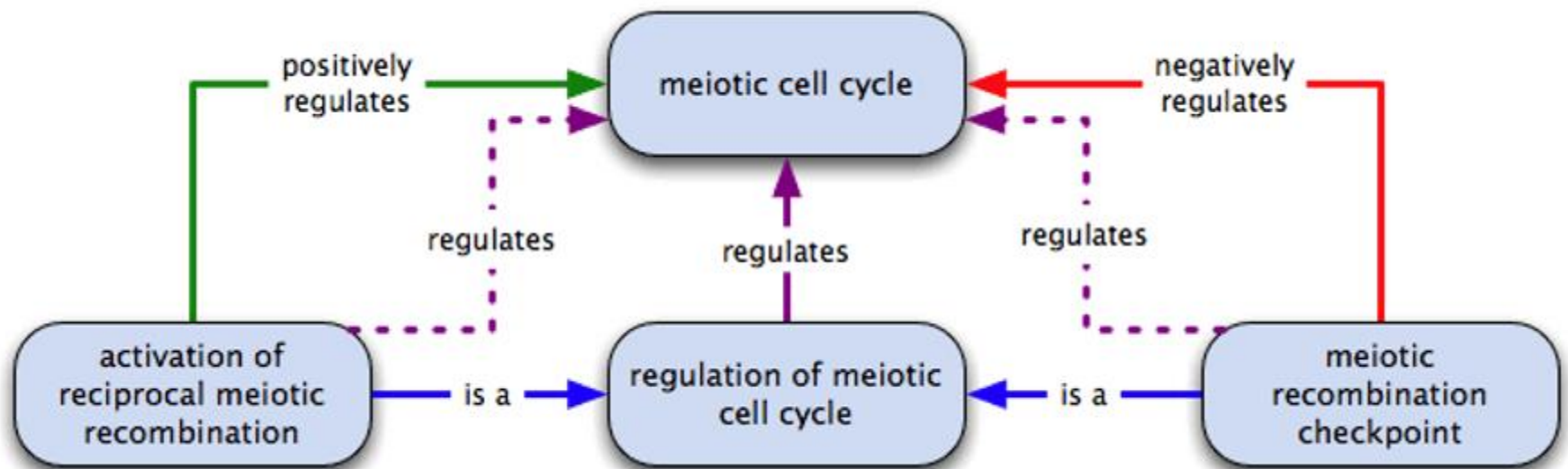
B *part of* C

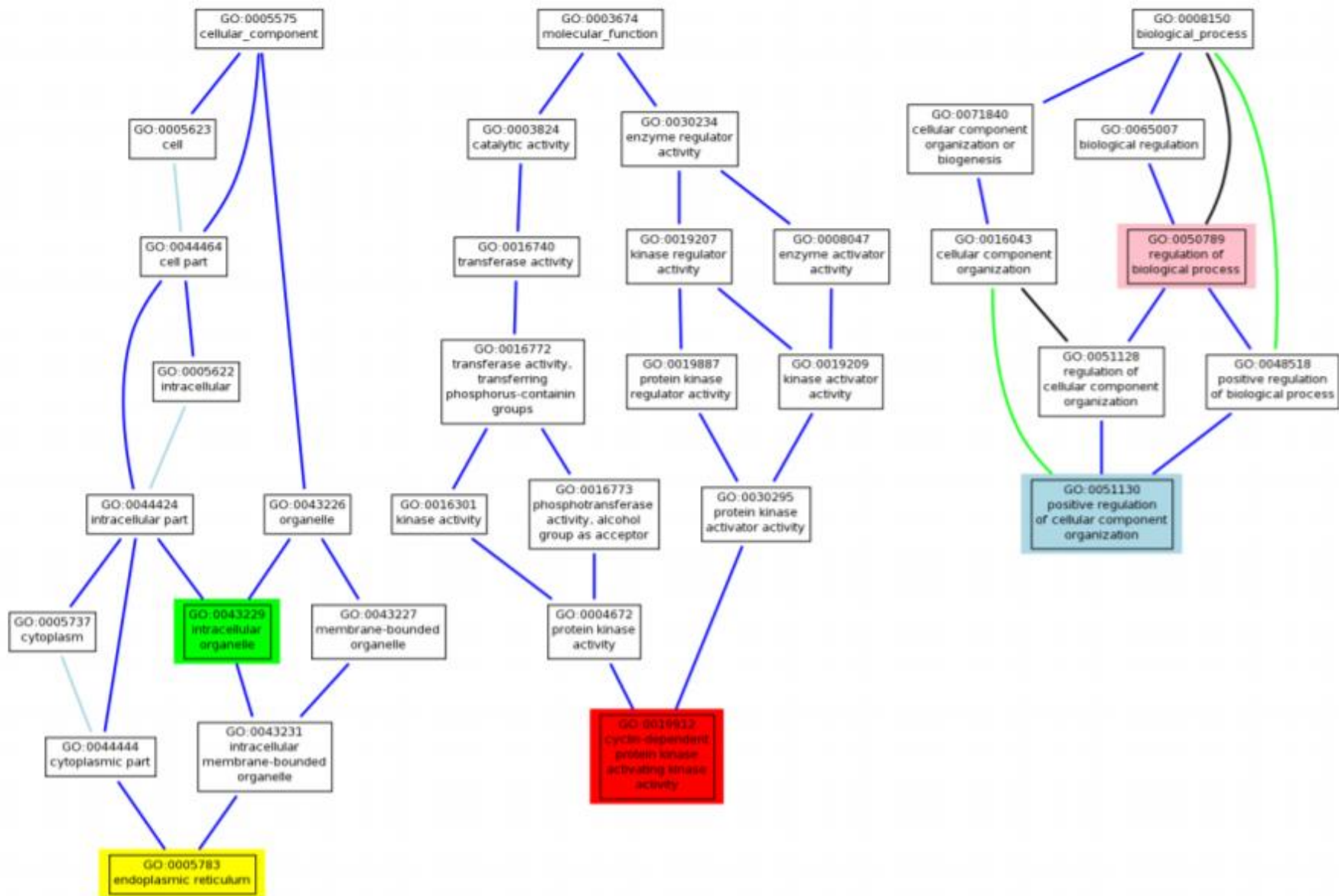
Значит, A *part of* C

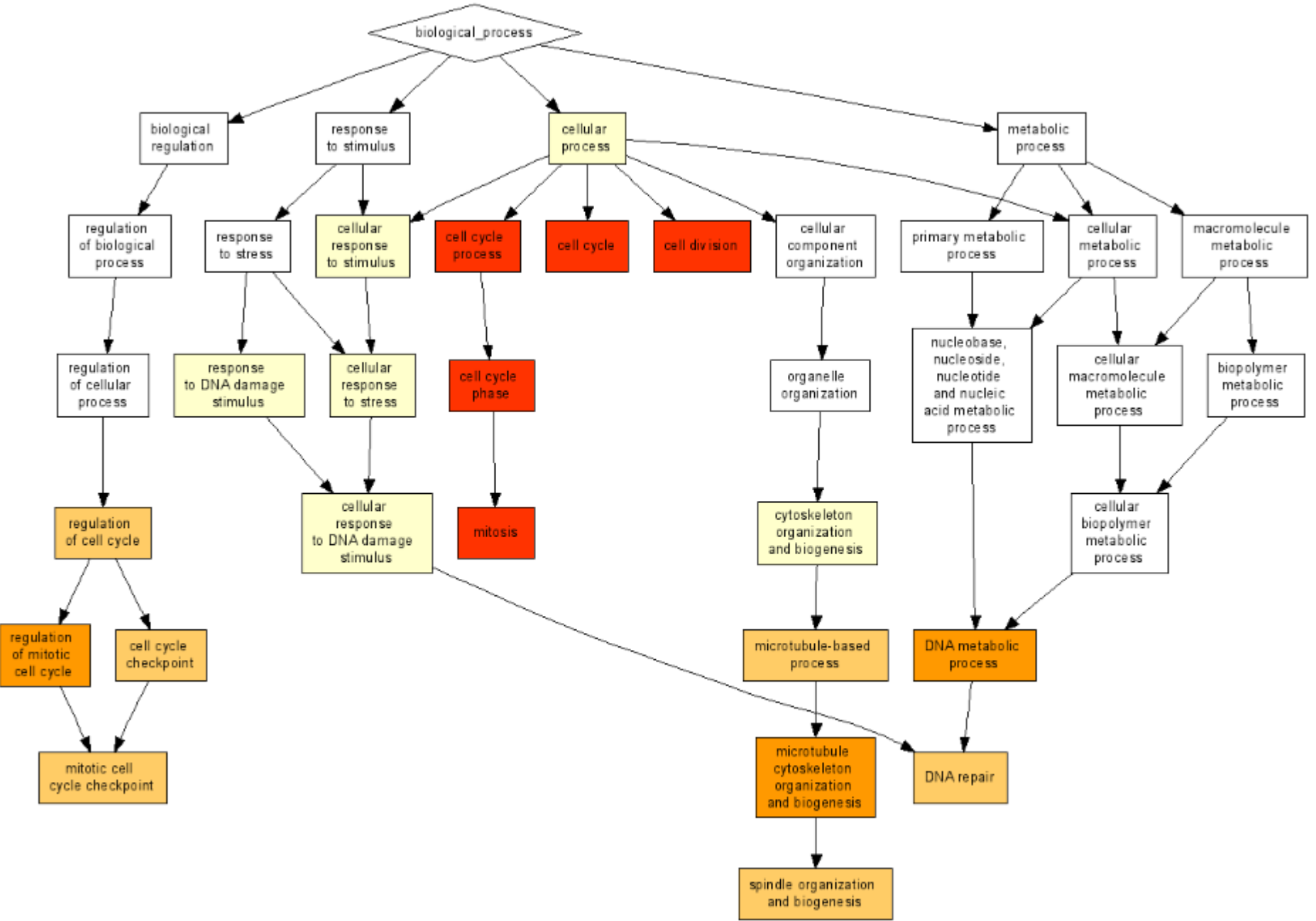
→ Указанные
→ непосредственно

- - - - -> Логически вытекающее









Типы достоверности

Inferred from Electronic Annotation (**IEA**) →

Inferred from Sequence or structural Similarity (**ISS**)

- Inferred from Sequence Orthology (**ISO**)
- Inferred from Sequence Alignment (**ISA**)
- Inferred from Sequence Model (**ISM**)

Inferred from Experiment (**EXP**)

- Inferred from Direct Assay (**IDA**)
- Inferred from Physical Interaction (**IPI**)
- Inferred from Mutant Phenotype (**IMP**)
- Inferred from Genetic Interaction (**IGI**)
- Inferred from Expression Pattern (**IEP**)

Traceable Author Statement (**TAS**)

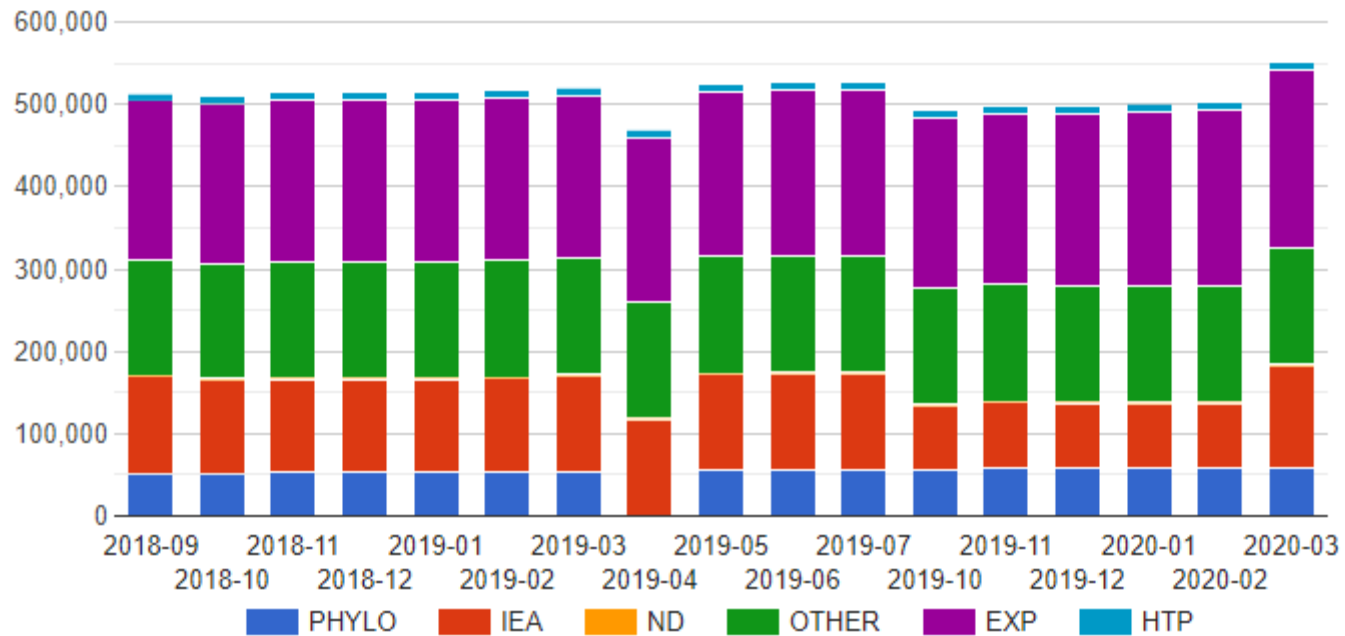
Non-traceable Author Statement (**NAS**)



<input type="checkbox"/> Gene/product	Gene/product name	Annotation qualifier	GO class (direct)	Annotation extension	Contributor	Organism	Evidence	Evidence with	PANTHER family	Type	Isoform
<input type="checkbox"/> Fcεr1g	Fc fragment of IgE receptor Ig		positive regulation of type IIa hypersensitivity		RGD	Rattus norvegicus	ISO	RGD:10572	high affinity immunoglobulin epsilon receptor gamma-subunit pthr16803	gene	
<input type="checkbox"/> Fcεr1g	Fc fragment of IgE receptor Ig		positive regulation of type IIa hypersensitivity		RGD	Rattus norvegicus	ISO	RGD:10572	high affinity immunoglobulin epsilon receptor gamma-subunit pthr16803	gene	
<input type="checkbox"/> Fcεr1g	Fc fragment of IgE receptor Ig		positive regulation of type IIa hypersensitivity		RGD	Rattus norvegicus	ISO	RGD:10572	high affinity immunoglobulin epsilon receptor gamma-subunit pthr16803	gene	
<input type="checkbox"/> Fcγr2a	Fc fragment of IgG receptor IIa		positive regulation of type IIa hypersensitivity		RGD	Rattus norvegicus	ISO	RGD:736451	immunoglobulin fc receptor pthr11481	gene	
<input type="checkbox"/> Fcγr2a	Fc fragment of IgG receptor IIa		positive regulation of type IIa hypersensitivity		RGD	Rattus norvegicus	ISO	RGD:736451	immunoglobulin fc receptor pthr11481	gene	
<input type="checkbox"/> Fcγr2a	Fc fragment of IgG receptor		regulation of antibody-		RGD	Rattus norvegicus	IMP		immunoglobulin fc receptor pthr11481	gene	

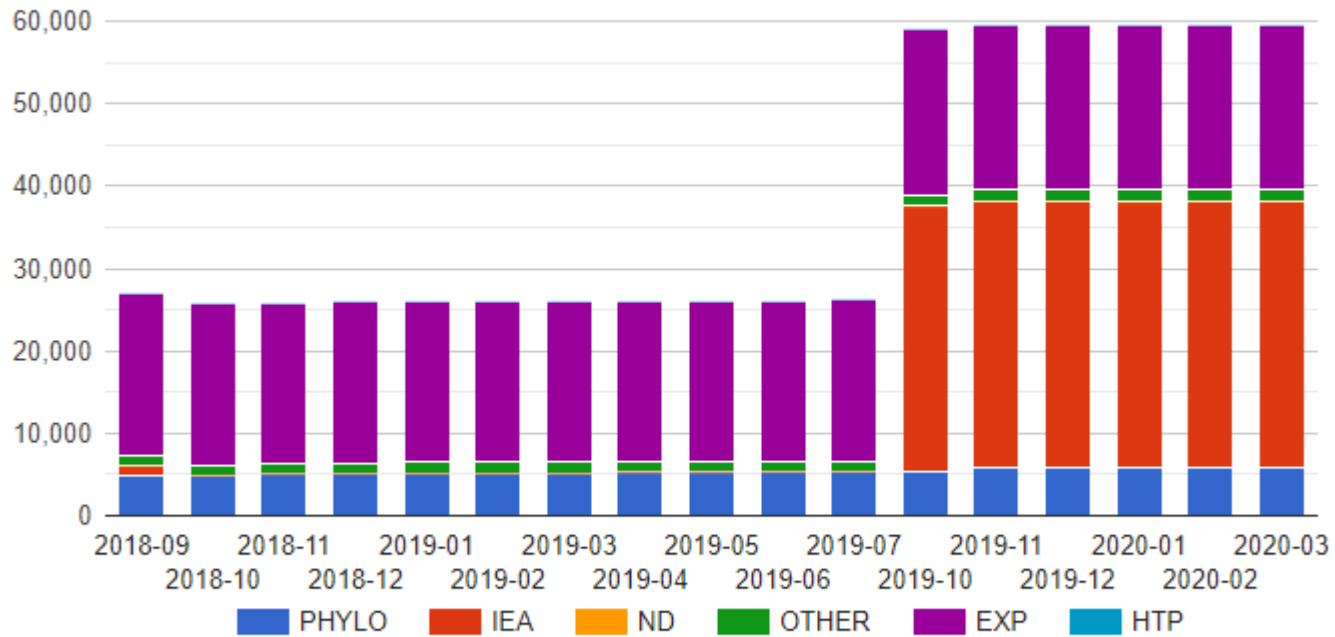
Number of annotations by evidence

Species filter:



Number of annotations by evidence

Species filter:



GO Enrichment Analysis ?

Powered by PANTHER

APOH
APP
CND2
COL3A1
COL5A2
CXCL6
FOXP4

biological process

Homo sapiens

Examples

Launch >

Gene set example: genes up-regulated during formation of blood vessels/angiogenesis (source: msigdb)

Selection Summary:

Analysis Type: PANTHER Overrepresentation Test (Released 20200407)


Annotation Version and Release Date: GO Ontology database Released 2020-02-21

Analyzed List: upload_1 (Homo sapiens)

[Change](#)

Reference List: Homo sapiens (all genes in database)

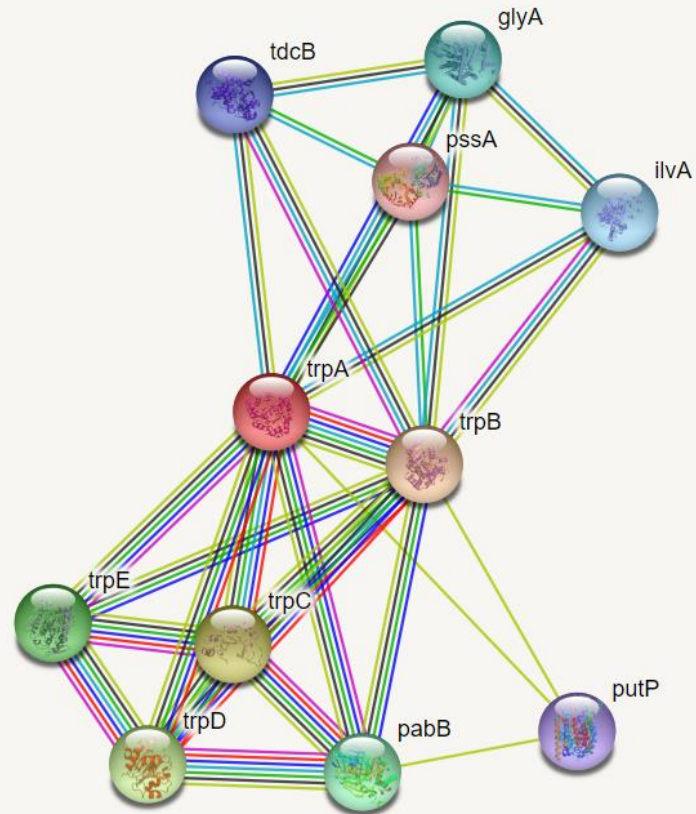
[Change](#)

Annotation Data Set: 

Test Type: Fisher's Exact Binomial

Correction: Calculate False Discovery Rate Use the Bonferroni correction for multiple testing  No correction

[Launch analysis](#)



<https://string-db.org/>

Node Color



colored nodes:
query proteins and first shell of interactors



white nodes:
second shell of interactors

Node Content



empty nodes:
proteins of unknown 3D structure



filled nodes:
some 3D structure is known or predicted

Known Interactions

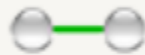


from curated databases



experimentally determined

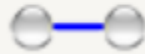
Predicted Interactions



gene neighborhood



gene fusions



gene co-occurrence

Others



textmining



co-expression



protein homology

Protein by name >

Protein by sequence >

Multiple proteins >

Multiple sequences >

Proteins with Values/Ranks ^{New} >

Organisms >

Protein families ("COGs") >

Examples >

Random entry >

SEARCH

Multiple Proteins by Names / Identifiers

List Of Names: (one per line; examples: #1 #2 #3)

COQ6
CUBN
CYP24A1
CYP27A1
CYP27B1
CYP2E1

... or, upload a file:

Browse ...

Organism:

Homo sapiens

SEARCH

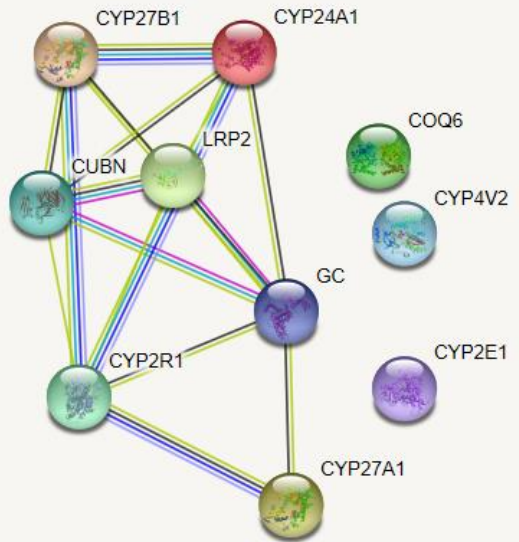
'COQ6':

- COQ6** - Ubiquinone biosynthesis monooxygenase **COQ6**, mitochondrial; FAD-dependent monooxygenase required for the C5-ring hydroxylation during ubiquinone biosynthesis. Catalyzes the hydroxylation of 3-polyprenyl-4-hydroxybenzoic acid to 3- polyprenyl-4,5-dihydroxybenzoic acid. The electrons required for the hydroxylation reaction may be funneled indirectly from NADPH via a ferredoxin/ferredoxin reductase system to **COQ6**

'CUBN':

- CUBN** - Cubilin; Cotransporter which plays a role in lipoprotein, vitamin and iron metabolism, by facilitating their uptake. Binds to ALB, MB, Kappa and lambda-light chains, TF, hemoglobin, GC, SCGB1A1, APOA1, high density lipoprotein, and the GIF-cobalamin complex. The binding of all ligands requires calcium. Serves as important transporter in several absorptive epithelia, including intestine, renal proximal tubules and embryonic yolk sac. Interaction with LRP2 mediates its trafficking throughout vesicles and facilitates the uptake of specific ligands like GC, hemoglobin, ALB, TF and SCGB1A1. [...]
- GIF - Gastric intrinsic factor; Promotes absorption of the essential vitamin cobalamin (Cbl) in the ileum. After interaction with **CUBN**, the GIF-cobalamin complex is internalized via receptor-mediated endocytosis [a.k.a. *IFMH, ENST00000533847, CCDS7977*]
- LRP2 - Low-density lipoprotein receptor-related protein 2; Multiligand endocytic receptor (By similarity). Acts together with **CUBN** to mediate endocytosis of high-density lipoproteins (By similarity). Mediates receptor-mediated uptake of polybasic drugs such as aprotinin, aminoglycosides and polymyxin B (By similarity). In the kidney, mediates the tubular uptake and clearance of leptin (By similarity). Also mediates transport of leptin across the blood-brain barrier through endocytosis at the choroid plexus epithelium (By similarity). Endocytosis of leptin in neuronal cells is required for hyp [...] [a.k.a. *HPA005980, GP330, NP_004516.2*]
- AMN - Protein amnionless; Necessary for efficient absorption of vitamin B12. Required for normal **CUBN**- mediated protein transport in the kidney. May direct the production of trunk mesoderm during development by modulating a bone morphogenetic protein (BMP) signaling pathway in the underlying visceral endoderm (By similarity) [a.k.a. *UNQ513/PRO1028, NP_112205.2, OTTHUMT00000415706*]

'CYP24A1':



- Viewers >
- Legend >
- Settings** v
- Analysis >
- Exports >
- Clusters >
- More +
- Less -

Basic Settings

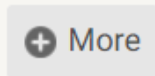
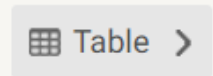
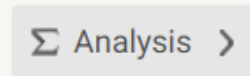
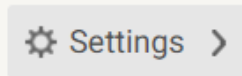
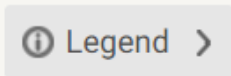
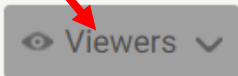
meaning of network edges:

- evidence (line color indicates the type of interaction evidence)
- confidence (line thickness indicates the strength of data support)
- molecular action (line shape indicates the predicted mode of action)

active interaction sources:

- Textmining
- Experiments
- Databases
- Co-expression
- Neighborhood
- Gene Fusion
- Co-occurrence

UPDATE



Network

Summary view: shows current interactions. Nodes can be moved; popups provide information on nodes & edges.



Cooccurrence

Gene families whose occurrence patterns across genomes show similarities.



Experiments

Co-purification, co-crystallization, Yeast2Hybrid, Genetic Interactions, etc ... as imported from primary sources.



Coexpression

Proteins whose genes are observed to be correlated in expression, across a large number of experiments.



Databases

Known metabolic pathways, protein complexes, signal transduction pathways, etc ... from curated databases.



Neighborhood

Groups of genes that are frequently observed in each other's genomic neighborhood.



Textmining

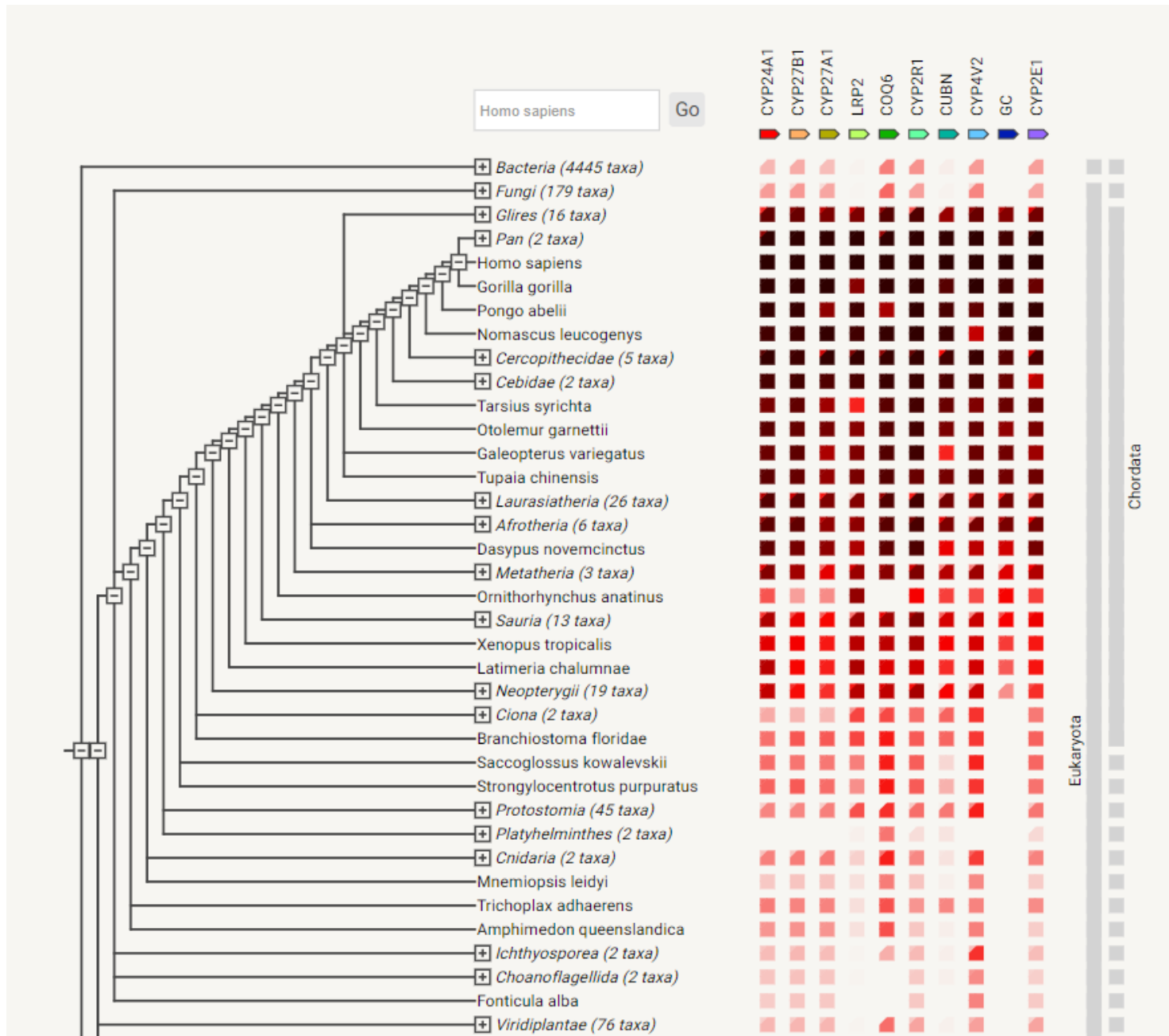
Automated, unsupervised textmining - searching for proteins that are frequently mentioned together.

currently showing

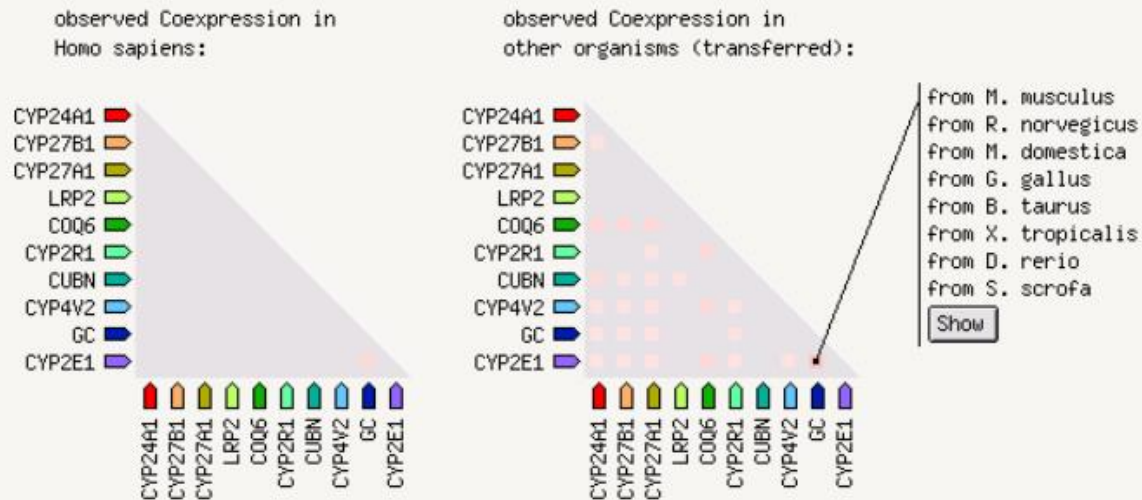


Fusion

Genes that are sometimes fused into single open reading frames.



GENE COEXPRESSION



Coexpression scores based on RNA expression patterns and protein co-regulation provided by [ProteomeHD](#)
 [click on the heatmap elements for details]

Network
 Summary view: shows current interactions. Nodes can be moved; popups provide information on nodes & edges.

Cooccurrence
 Gene families whose occurrence patterns across genomes show similarities.

Experiments
 Co-purification, co-crystallization, Yeast2Hybrid, Genetic Interactions, etc ... as imported from primary sources.

Coexpression currently showing
 Proteins whose genes are observed to be correlated in expression, across a large number of experiments.



GORILLA



Gene Ontology enRIchment anaLysis and visuaLizAtion tool

Step 1: [Choose organism](#)

Homo sapiens ▼

Step 2: [Choose running mode](#)

- Single ranked list of genes Two unranked lists of genes (target and background lists)

Step 3: [Paste a ranked list of gene/protein names](#)

Names should be separated by an <ENTER>. The preferred format is gene symbol. Other supported formats are: gene and protein RefSeq, Uniprot, Unigene and Ensembl.

Or upload a file: Файл не выбран

Step 4: [Choose an ontology](#)

- Process Function Component All



DAVID Bioinformatics Resources 6.8
Laboratory of Human Retrovirology and Immunoinformatics (LHRI)

Home Start Analysis Shortcut to DAVID Tools Technical Center Downloads & APIs Term of Service Why DAVID? About Us

*** Welcome to DAVID 6.8 ***

*** If you are looking for [DAVID 6.7](#), please visit our [development site](#). ***

Recommending: A [paper](#) published in *Nature Protocols* describes step-by-step procedure to use DAVID!

Shortcut to DAVID Tools

▶ Functional Annotation

Gene-annotation enrichment analysis, functional annotation clustering, BioCarta & KEGG pathway mapping, gene-disease association, homologue match, ID translation, literature match and [more](#)

▶ Gene Functional Classification

Provide a rapid means to reduce large lists of genes into functionally related groups of genes to help unravel the biological content captured by high throughput technologies. [More](#)

▶ Gene ID Conversion

Convert list of gene ID/accessions to others of your choice with the most comprehensive gene ID mapping repository. The ambiguous accessions in the list can also be determined semi-automatically. [More](#)

▶ Gene Name Batch Viewer

Welcome to DAVID 6.8

2003 - 2020

The Database for Annotation, Visualization and Integrated Discovery (DAVID) v6.8 [comprises a full Knowledgebase update to the sixth version](#) of our original web-accessible programs. DAVID now provides a comprehensive set of functional annotation tools for investigators to understand biological meaning behind large list of genes. For any given gene list, DAVID tools are able to:

➔ What's Important in DAVID?

- [Cite DAVID](#)
- [IDs of Affy Exon and Gene arrays supported](#)
- [Novel Classification Algorithms](#)
- [Pre-built Affymetrix and Illumina backgrounds](#)
- [User's customized gene background](#)
- [Enhanced calculating speed](#)

➔ Statistics of DAVID

<https://www.proteinatlas.org/>

THE HUMAN PROTEIN ATLAS

≡ MENU HELP NEWS

SEARCH¹

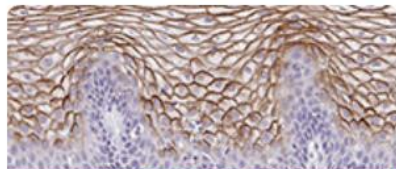
Search

Fields »

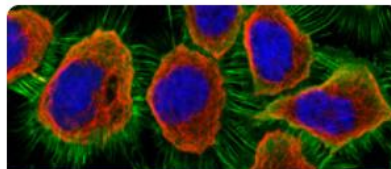
e.g. RBM3, insulin, CD36



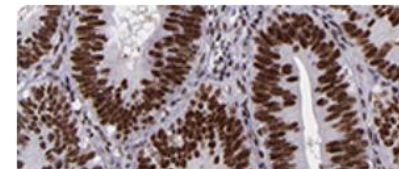
SARS-CoV-2 relevant proteins



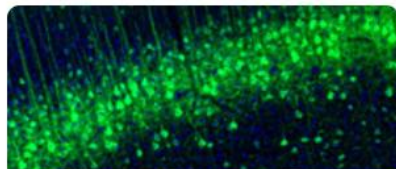
TISSUE ATLAS



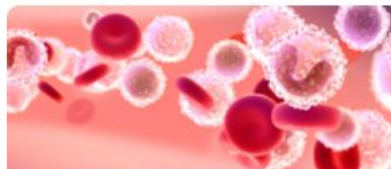
CELL ATLAS



PATHOLOGY ATLAS



BRAIN ATLAS



BLOOD ATLAS



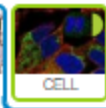
METABOLIC ATLAS

LRP2

Search

Fields »

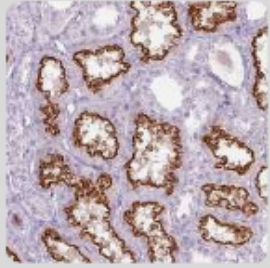
LRP2



HUMAN PROTEIN ATLAS SUMMARY ⁱ	
Protein	Apolipoprotein B
Gene name ⁱ	APOB
Tissue specificity ⁱ	Group enriched (intestine, liver)
Extracellular location ⁱ	Secreted to blood
Subcellular location ⁱ	Vesicles, Cytosol
Cancer prognostic summary	Gene product is not prognostic
Brain specificity ⁱ	Not detected in human brain
Blood specificity ⁱ	Not detected in immune cells
Predicted location ⁱ	Secreted
Protein function (UniProt) ⁱ	Apolipoprotein B is a major protein constituent of chylomicrons (apo B-48), LDL (apo B-100) and VLDL (apo B-100). Apo B-100 functions as a recognition signal for the cellular binding and internalization of LDL particles by the apoB/E receptor. show less
Molecular function (UniProt) ⁱ	Heparin-binding
Biological process (UniProt) ⁱ	Cholesterol metabolism, Lipid metabolism, Lipid transport, Steroid metabolism, Sterol metabolism, Transport
Disease involvement ⁱ	Atherosclerosis, Disease mutation
Gene summary (Entrez) ⁱ	This gene product is the main apolipoprotein of chylomicrons and low density lipoproteins. It occurs in plasma as two main isoforms, apoB-48 and apoB-100: the former is synthesized exclusively in the gut and the latter in the liver. The intestinal and the hepatic forms of apoB are encoded by a single gene from a single, very long mRNA. The two isoforms share a common N-terminal sequence. The shorter apoB-48 protein is produced after RNA editing of the apoB-100 transcript at residue 2180 (CAA->UAA), resulting in the creation of a stop codon, and early translation termination. Mutations in this gene or its regulatory region cause hypobetalipoproteinemia, normotriglyceridemic hypobetalipoproteinemia, and hypercholesterolemia due to ligand-defective apoB, diseases affecting plasma cholesterol and apoB levels. [provided by RefSeq, Jul 2008] show less

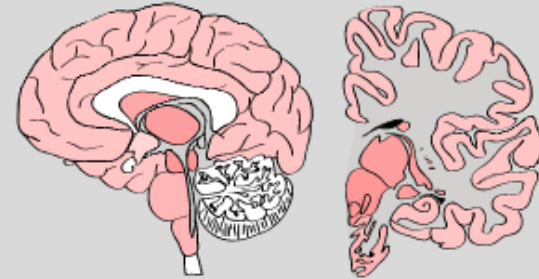


TISSUE ATLASⁱ



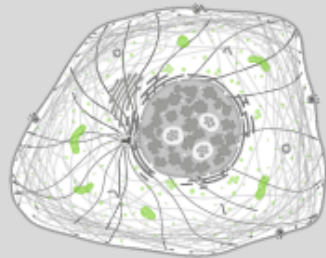
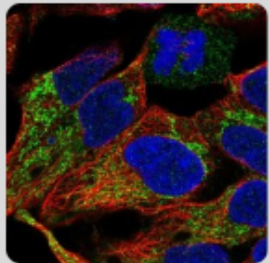
Tissue specificity (RNA) ⁱ	Tissue enhanced (kidney, parathyroid gland)
Tissue distribution (RNA) ⁱ	Detected in some
Protein expression ⁱ	Membranous expression mainly in renal tubules and parathyroid gland.

BRAIN ATLASⁱ



Human regional specificity ⁱ	Low region specificity
Pig regional specificity ⁱ	Low region specificity
Mouse regional specificity ⁱ	Not detected

CELL ATLASⁱ



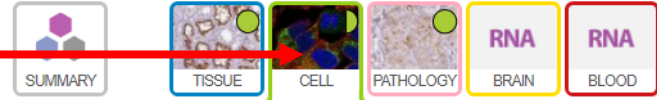
Main location ⁱ	Localized to the Vesicles, Mitochondria
Cell line specificity ⁱ	Group enriched (AF22, CACO-2)

BLOOD ATLASⁱ

	Granulocytes	Monocytes	Dendritic Cells	NK-cells	B-cells	T-cells
Immune cell specificity ⁱ	Not detected					
Detected in blood by immunoassay ⁱ	No (not applicable)					
Detected in blood by mass spectrometry ⁱ	No					

Ваш ID может быть специфичен для какой-либо ткани, может присутствовать везде или нигде не быть детектирован

LRP2



CELL ATLAS

RNA EXPRESSION

HUMAN CELLS

GENE/PROTEIN

ANTIBODIES
AND
VALIDATION



Dictionary

Mitochondria

Vesicles

Human cell

Mitochondria

Vesicles

GENERAL INFORMATION¹

Gene name ¹	LRP2
Gene description	LDL receptor related protein 2
Protein class ¹	Disease related genes Plasma proteins Potential drug targets Transporters
Predicted location ¹	Intracellular, Membrane
Number of transcripts ¹	2

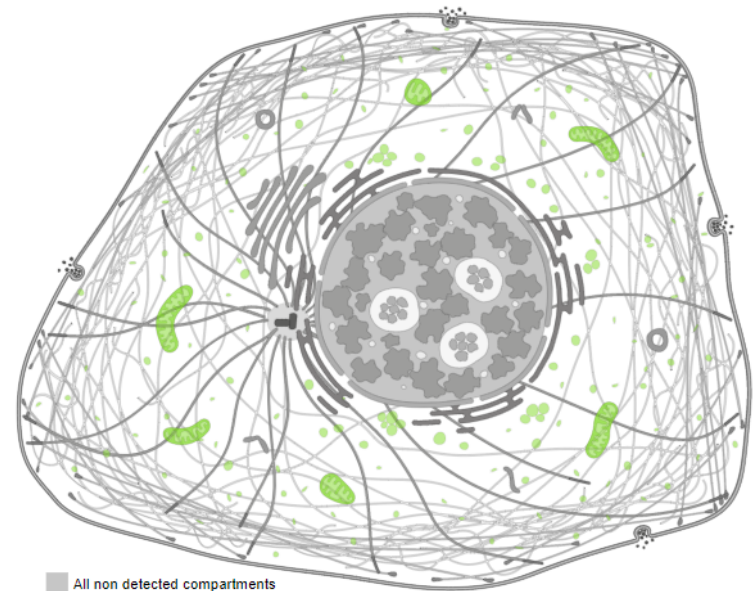
HUMAN PROTEIN ATLAS INFORMATION¹

Summary ¹	Localized to the mitochondria & vesicles.
RNA cell specificity ¹	Group enriched (AF22, CACO-2)
RNA cell distribution ¹	Detected in some
Protein evidence ¹	Evidence at protein level
Main location ¹	Localized to the Vesicles (approved), Mitochondria (approved)
Single-cell variation ¹	Single-cell variation in protein expression observed.

DATA RELIABILITY¹

Reliability score ¹	Approved
Antibodies ¹	HPA064792

[SHOW MORE](#)



■ All non detected compartments
■ LRP2 detected in Vesicles and Mitochondria

LRP2



TISSUE ATLAS

PRIMARY DATA

GENE/PROTEIN

ANTIBODIES AND VALIDATION



Dictionary



Tissue proteome



GENERAL INFORMATION¹

Gene name ¹	LRP2
Gene description	LDL receptor related protein 2
Protein class ¹	Disease related genes Plasma proteins Potential drug targets Transporters
Predicted location ¹	Intracellular,Membrane
Number of transcripts ¹	2

HUMAN PROTEIN ATLAS INFORMATION¹

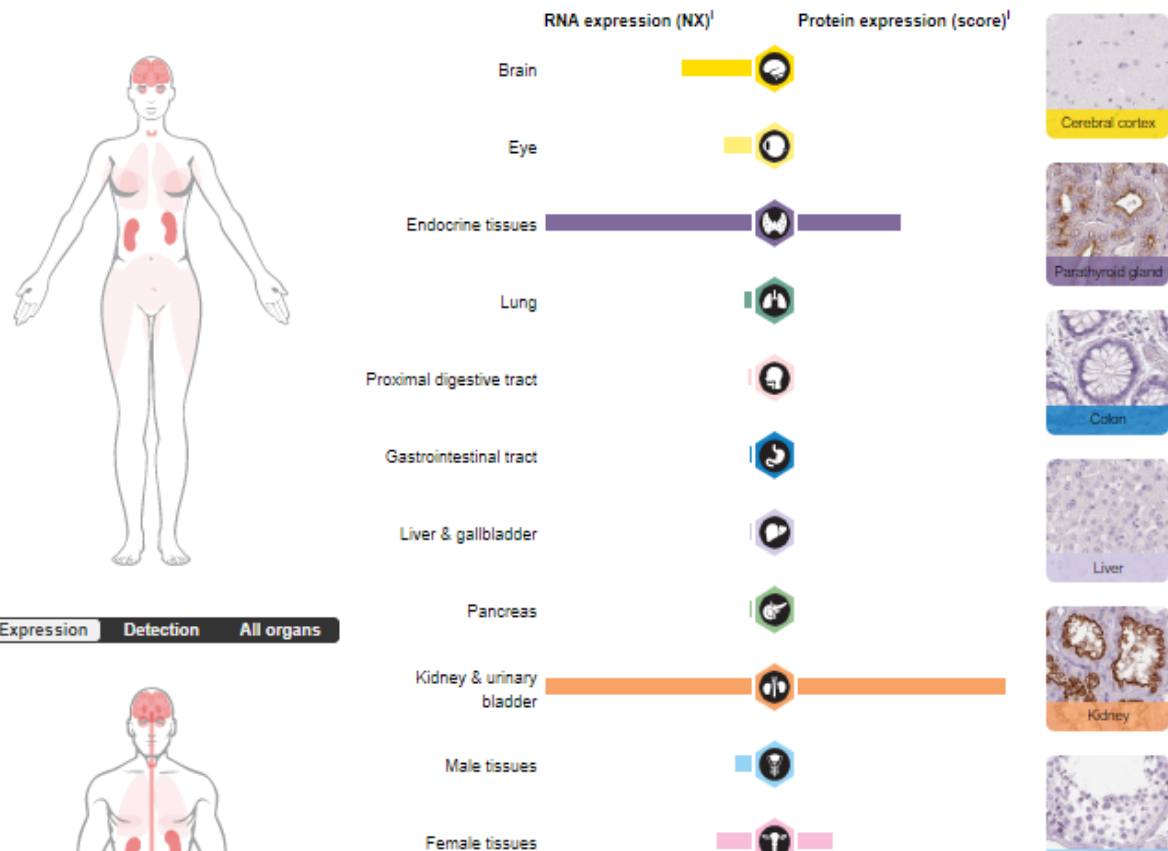
RNA tissue specificity ¹	Tissue enhanced (kidney, parathyroid gland)
RNA tissue distribution ¹	Detected in some
Protein evidence ¹	Evidence at protein level
Protein expression ¹	Membranous expression mainly in renal tubules and parathyroid gland.

IMMUNOHISTOCHEMISTRY DATA RELIABILITY

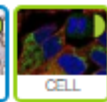
Data reliability description ¹	Antibody staining consistent with RNA expression data.
Reliability score ¹	Enhanced
Antibodies ¹	HPA005980, HPA064792

[SHOW MORE](#)

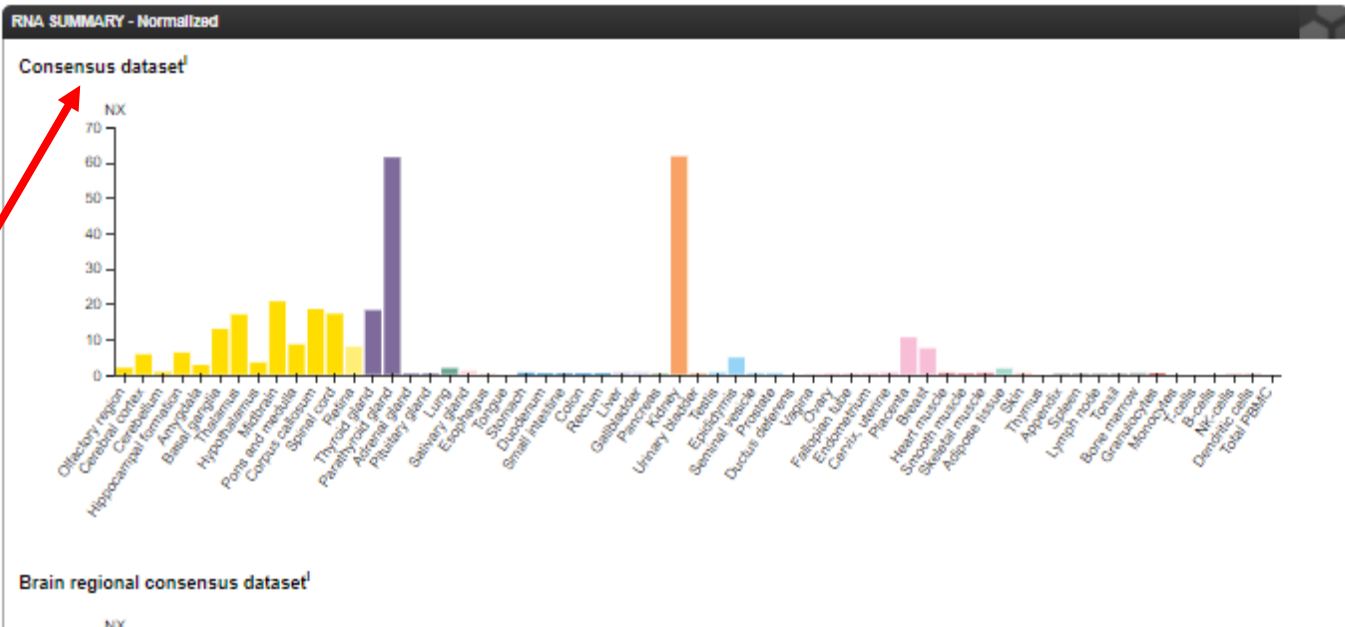
RNA AND PROTEIN EXPRESSION SUMMARY¹



LRP2



- PROTEIN SUMMARY
- RNA DATA
- GENE/PROTEIN
- ANTIBODIES AND VALIDATION



Метаболические пути

KEGG



KEGG ▼

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KEGG Database

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KEGG: Kyoto Encyclopedia of Genes and Genomes

KEGG is a database resource for understanding high-level functions and utilities of the biological system, such as the cell, the organism and the ecosystem, from molecular-level information, especially large-scale molecular datasets generated by genome sequencing and other high-throughput experimental technologies. See [Release notes](#) (April 1, 2020) for new and updated features.

Main entry point to the KEGG web service

KEGG2 [KEGG Table of Contents](#) [[Update notes](#) | [Release history](#)]

Data-oriented entry points

KEGG PATHWAY [KEGG pathway maps](#)
KEGG BRITE [BRITE hierarchies and tables](#)
KEGG MODULE [KEGG modules](#)
KEGG ORTHOLOGY [KO functional orthologs](#) [[Annotation](#)]
KEGG GENOME [Genomes](#) [[Pathogen](#) | [Virus](#) | [Plant](#)]
KEGG GENES [Genes and proteins](#) [[SeqData](#)]
KEGG COMPOUND [Small molecules](#)
KEGG GLYCAN [Glycans](#)
KEGG REACTION [Biochemical reactions](#) [[RModule](#)]
KEGG ENZYME [Enzyme nomenclature](#)
KEGG NETWORK [Disease-related network elements](#)
KEGG DISEASE [Human diseases](#) [[Cancer](#)]
KEGG DRUG [Drugs](#) [[New drug approvals](#)]

KEGG MEDICUS [Health information resource](#) [[Drug labels search](#)]

Organism-specific entry points

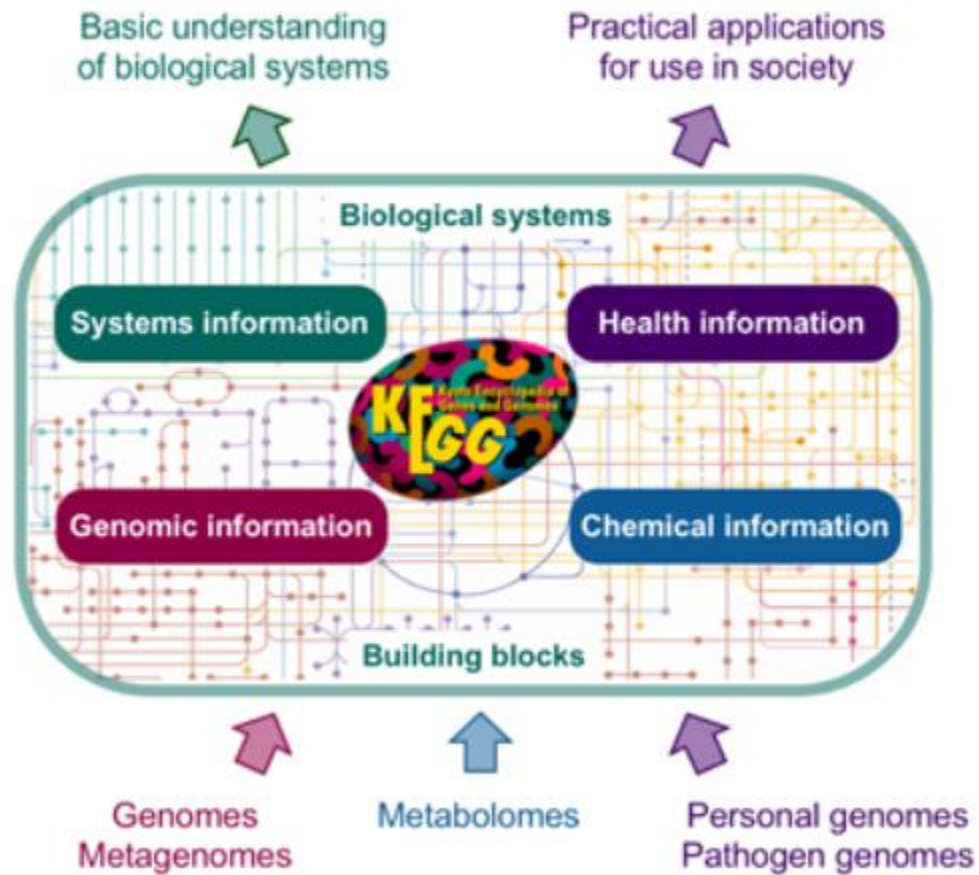
KEGG Organisms Enter org code(s) [hsa](#) [hsa eco](#)

Analysis tools

KEGG Mapper [KEGG PATHWAY/BRITE/MODULE mapping tools](#)
BlastKOALA [BLAST-based KO annotation and KEGG mapping](#)
GhostKOALA [GHOSTX-based KO annotation and KEGG mapping](#)
KofamKOALA [HMM profile-based KO annotation and KEGG mapping](#)
BLAST/FASTA [Sequence similarity search](#)
SIMCOMP [Chemical structure similarity search](#)

Classification

[Pathway](#)
[Brite](#)
[Brite table](#)
[Module](#)
[KO \(Function\)](#)
[Organism](#)
[Compound](#)
[Network](#)
[Disease \(ICD\)](#)
[Drug \(ATC\)](#)
[Drug \(Target\)](#)



Current Statistics

KEGG Database as of 2020/4/29

Systems information

KEGG PATHWAY	Pathway maps, reference (total)	537 (705,156)
KEGG BRITE	Functional hierarchies, reference (total)	200 (247,573)
KEGG MODULE	KEGG modules	394
	Reaction modules	41

Genomic information

KEGG ORTHOLOGY	KEGG Orthology (KO) groups	23,354
KEGG GENOME	KEGG organisms (540 eukaryotes, 5659 bacteria, 318 archaea)	6,517
	KEGG selected viruses	341
KEGG GENES	Genes in KEGG organisms and other categories (including 4,057 addendum, 372,625 viral) (see annotation statistics)	31,487,727
KEGG SSDB	Best hit relations within GENES	375,636,238,942
	Bi-directional best hit relations within GENES	18,772,924,969

Chemical information





KEGG COMPOUND	Metabolites and other small molecules	18,700
KEGG GLYCAN	Glycans	11,040
KEGG REACTION	Biochemical reactions	11,415
	Reaction class	3,165
KEGG ENZYME	Enzyme nomenclature	7,736

Health information

KEGG NETWORK	Disease-related network elements	1,011
	Network variation maps	114
KEGG VARIANT	Human gene variants	416
KEGG DISEASE	Human diseases	2,420
KEGG DRUG	Drugs	11,255
	Drug groups	2,276
KEGG ENVIRON	Crude drugs and health-related substances	864

Drug labels

KEGG MEDICUS	Japanese prescription drug labels from JAPIC	14,076
	Japanese OTC drug labels from JAPIC	11,011
KEGG MEDICUS	FDA prescription drug labels linked to DailyMed	27,668
	FDA OTC drug labels linked to DailyMed	36,506

Category	Database	Content	Color
Systems information	KEGG PATHWAY	KEGG pathway maps	
	KEGG BRITE	BRITE hierarchies and tables	
	KEGG MODULE	KEGG modules	
Genomic information	KEGG ORTHOLOGY (KO)	Functional orthologs	
	KEGG GENOME	KEGG organisms (complete genomes)	
	KEGG GENES	Genes and proteins	
	KEGG SSDB	GENES sequence similarity	
Chemical information	KEGG COMPOUND	Small molecules	
	KEGG GLYCAN	Glycans	
	KEGG REACTION	Biochemical reactions	
	KEGG RCLASS	Reaction class	
	KEGG ENZYME	Enzyme nomenclature	
Health information	KEGG NETWORK	Disease-related network elements	
	KEGG VARIANT	Human gene variants	
	KEGG DISEASE	Human diseases	
	KEGG DRUG	Drugs	
	KEGG DGROUP	Drug groups	
	KEGG ENVIRON	Health-related substances	

Chemical information category is collectively called **KEGG LIGAND**

Health information category integrated with drug labels is called **KEGG MEDICUS**

Pathway Maps

KEGG PATHWAY is a collection of manually drawn [pathway maps](#) representing our knowledge on the molecular interaction, reaction and relation networks for:

1. Metabolism

Global/overview Carbohydrate Energy Lipid Nucleotide Amino acid Other amino Glycan
Cofactor/vitamin Terpenoid/PK Other secondary metabolite Xenobiotics Chemical structure

2. Genetic Information Processing

3. Environmental Information Processing

4. Cellular Processes

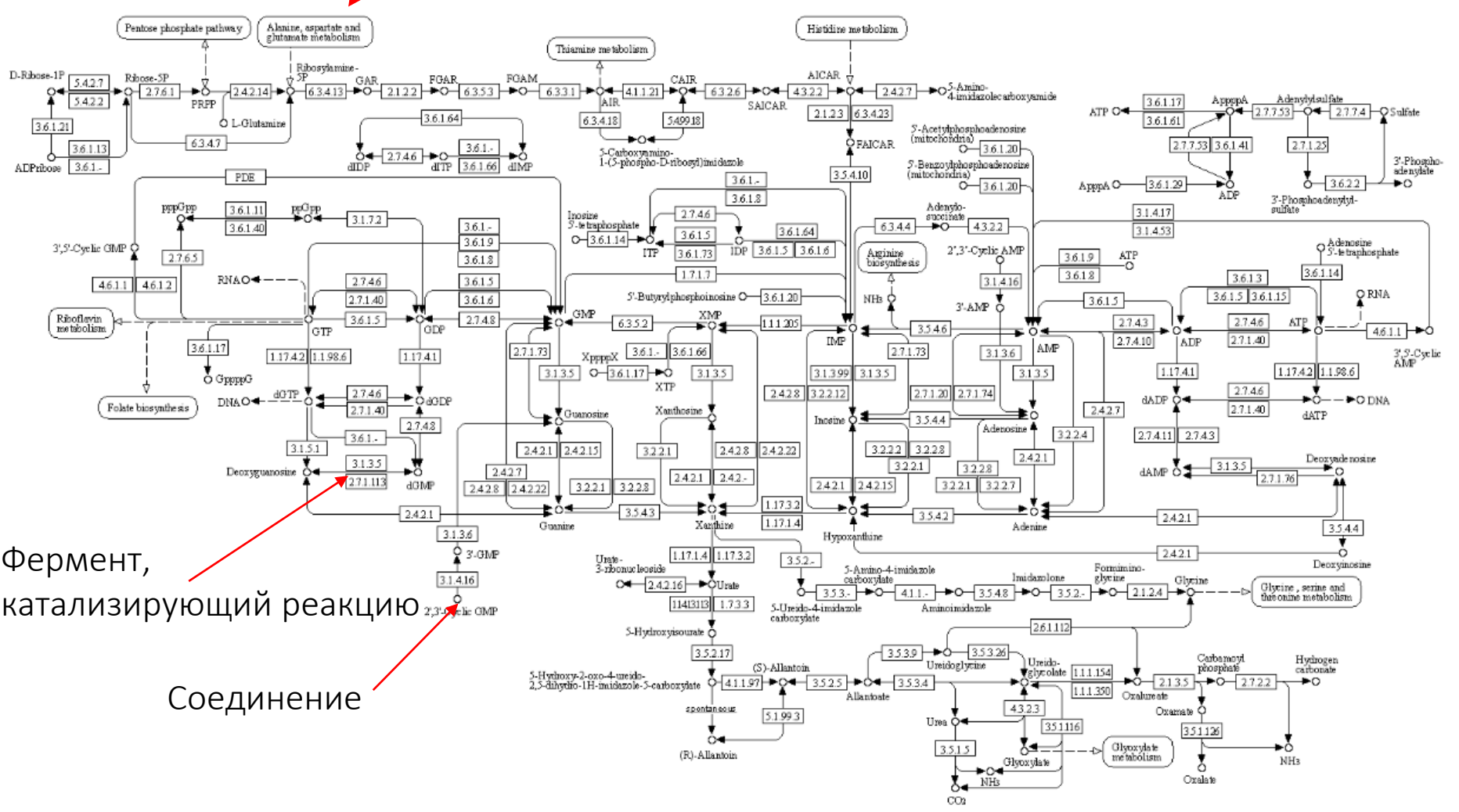
5. Organismal Systems

6. Human Diseases

7. Drug Development

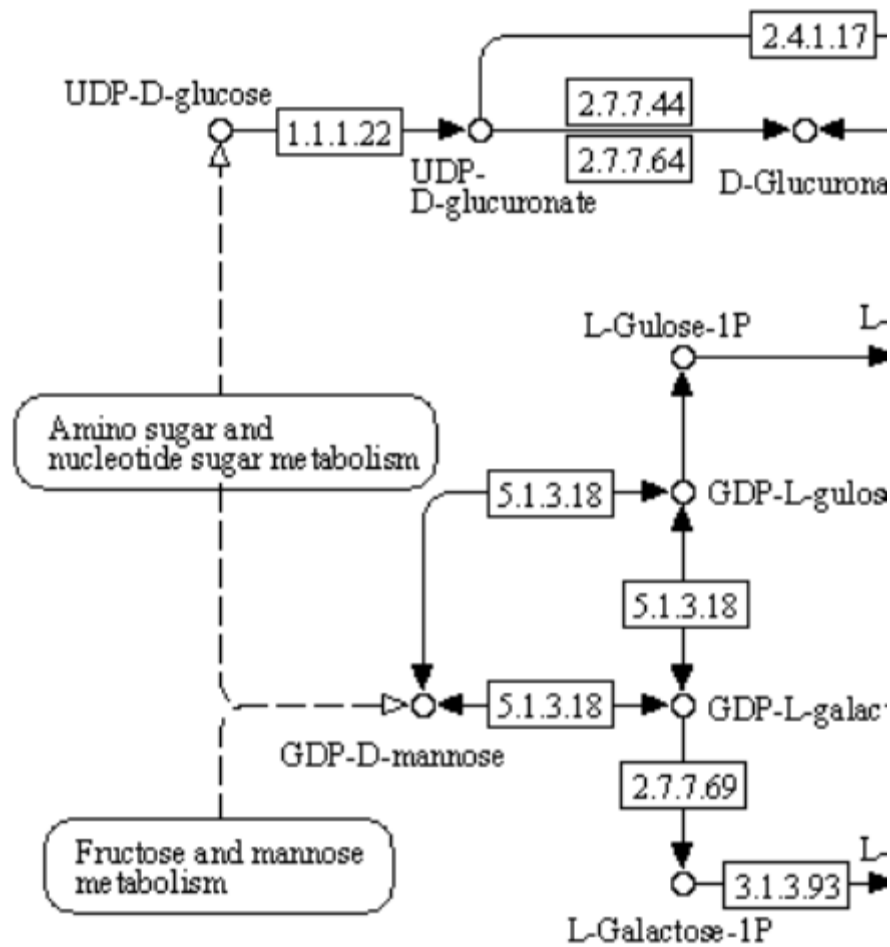
Другой метаболический путь

PURINE METABOLISM



Фермент, катализирующий реакцию

Соединение



Entry	EC 2.7.7.4 Enzyme
Name	sulfate adenylyltransferase; ATP-sulfurylase; adenosine-5'-triphosphate sulfurylase; adenosinetriphosphate sulfurylase; adenylylsulfate pyrophosphorylase; ATP sulfurylase; ATP-sulfurylase; sulfurylase
Class	Transferases; Transferring phosphorus-containing groups; Nucleotidyltransferases BRITE hierarchy
Sysname	ATP:sulfate adenylyltransferase
Reaction(IUBMB)	ATP + sulfate = diphosphate + adenylyl sulfate [RN:R00529]
Reaction(KEGG)	R00529; (other) R04929 Reaction
Substrate	ATP [CPD:C00002]; sulfate [CPD:C00059]
Product	diphosphate [CPD:C00013]; adenylyl sulfate [CPD:C00224]
Comment	The human phosphoadenosine-phosphosulfate synthase (PAPS) system is a bifunctional enzyme (fusion product of two catalytic activities). In a first step, sulfate adenylyltransferase catalyses the formation of adenosine 5'-phosphosulfate (APS) from ATP and inorganic sulfate. The second step is catalysed by the adenylylsulfate kinase portion of 3'-phosphoadenosine 5'-phosphosulfate (PAPS) synthase, which involves the formation of PAPS from enzyme-bound APS and ATP. In contrast, in bacteria, yeast, fungi and plants, the formation of PAPS is carried out by two individual polypeptides, sulfate adenylyltransferase (EC 2.7.7.4) and adenylyl-sulfate kinase (EC 2.7.1.25).

All links

[Pathway \(16\)](#)
 [KEGG PATHWAY \(14\)](#)
 [KEGG MODULE \(2\)](#)
[Chemical substance \(6\)](#)
 [KEGG COMPOUND \(6\)](#)
[Chemical reaction \(4\)](#)
 [KEGG REACTION \(2\)](#)
 [KEGG RCLASS \(2\)](#)
[Gene \(106612\)](#)
 [KEGG ORTHOLOGY \(5\)](#)
 [KEGG GENES \(8508\)](#)
 [KEGG MGENES \(61373\)](#)
 [RefGene \(36726\)](#)
[Protein sequence \(77269\)](#)
 [UniProt \(40770\)](#)
 [SWISS-PROT \(457\)](#)
 [RefSeq\(pep\) \(35969\)](#)
 [PDBSTR \(54\)](#)
 [PMD \(19\)](#)
[DNA sequence \(141864\)](#)
 [RefSeq\(nuc\) \(127520\)](#)
 [GenBank \(7103\)](#)
 [EMBL \(7241\)](#)
[3D Structure \(24\)](#)
 [PDB \(24\)](#)
[Protein domain \(9\)](#)
 [InterPro \(8\)](#)
 [Pfam \(1\)](#)
[All databases \(325804\)](#)

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Код фермента

Класс – код первого уровня: 1-7. Номер одного из семи главных классов ферментов

Подкласс – код второго уровня. Номер характеризует основные виды субстратов, участвующих в данном виде химических реакций.

Под-подкласс – код третьего уровня. Номер определяет более частные подгруппы, отличающиеся природой химических соединений доноров или акцепторов, участвующих в данной подгруппе реакций.

Код четвертого уровня – все ферменты, относящиеся к данному под-подклассу получают свои порядковые номера.

Пример: глюкозооксидаза – 1.1.3.4

КФ 1 — Оксидоредуктазы

КФ 1.1 — Алкогольоксидоредуктазы

КФ 1.1.3 — Оксидоредуктазы, окисляющие группу СН-ОН и восстанавливающие кислород.

КФ 1.1.3.4 — Оксидоредуктазы, окисляющие глюкозу в присутствии кислорода. Всего известно 3 глюкозооксидазы из разных организмов.

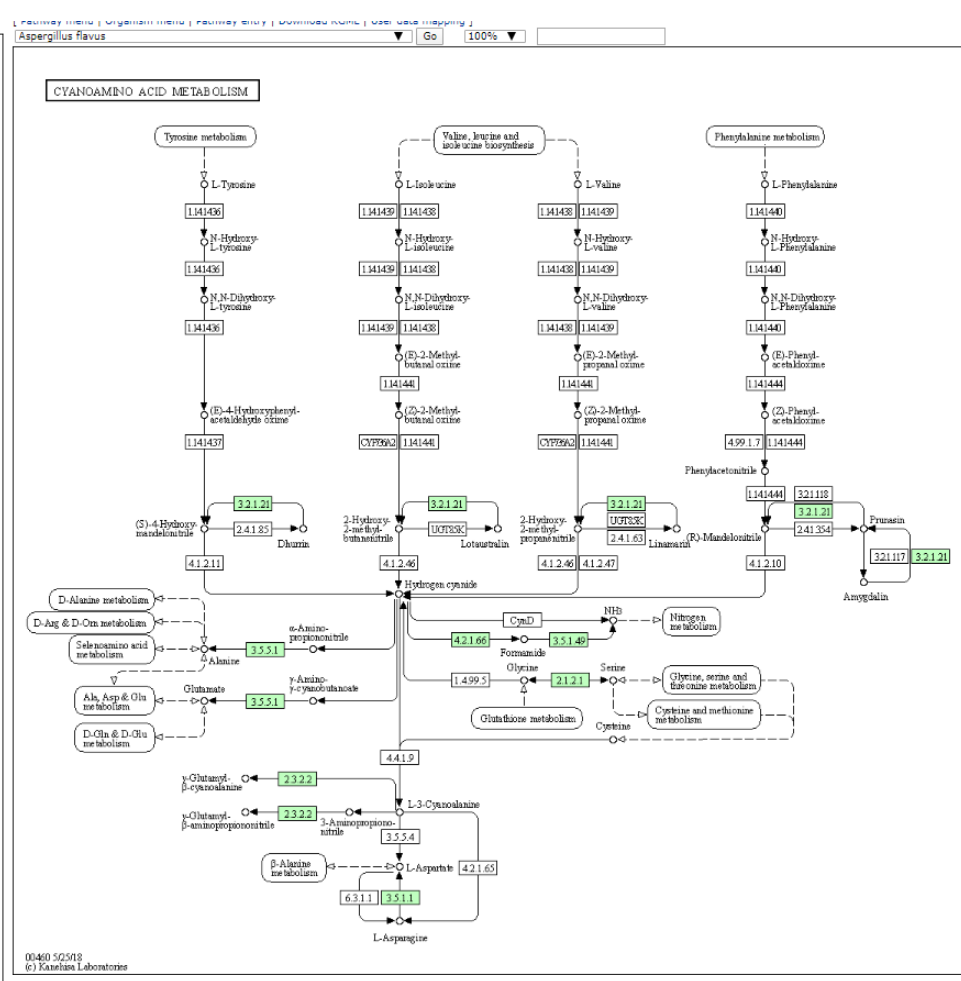
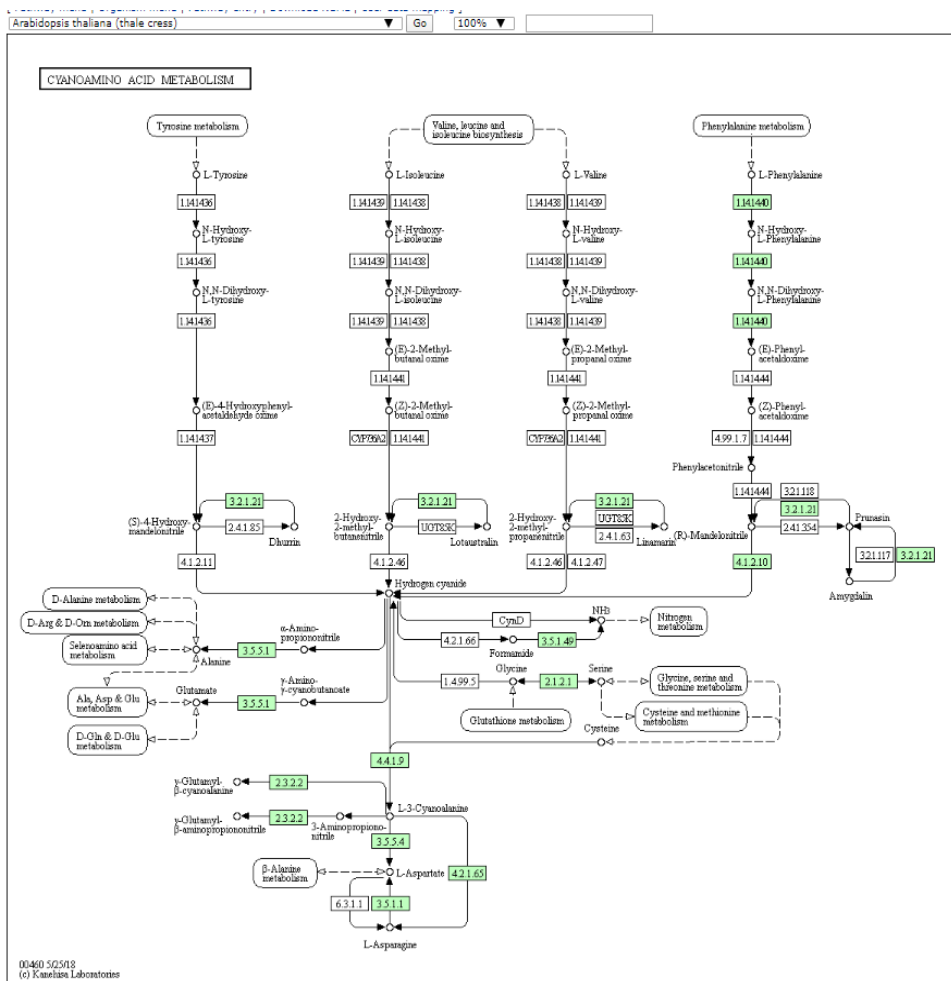
https://ru.wikipedia.org/wiki/%D0%A8%D0%B8%D1%84%D1%80_%D0%9A%D0%A4

Основные классы ферментов

Коды первого уровня

Класс	Катализируемая реакция	Тип реакции	Важнейшие подклассы
КФ 1 <i>Оксидоредуктазы</i>	Окислительно-восстановительные реакции. Перенос атомов Н и О или электронов от одного субстрата на другой	$AH + B \rightarrow A + BH$ (восстановленный) $A + O \rightarrow AO$ (окисленный)	дегидрогеназа, оксидаза, пероксидаза, редуктаза, монооксидаза, диоксигеназа
КФ 2 <i>Трансферазы</i>	Перенос функциональной группы от одного субстрата на другой. Это может быть метильная, ацильная, фосфатная группа или аминогруппа.	$AB + C \rightarrow A + BC$	аминотрансфераза, фосфотрансфераза, С1-трансфераза, гликозилтрансфераза
КФ 3 <i>Гидролазы</i>	Образование двух продуктов из одного субстрата в результате гидролиза.	$AB + H_2O \rightarrow AOH + BH$	эстераза, гликозил-гидролаза, пептидаза, амидаза
КФ 4 <i>Лиазы (синтазы)</i>	Негидролитическое добавление или удаление группы к или от субстрата. Образование С-С, С-Н, С-О или С-С связи.	$RCO_2COOH \rightarrow RCOH + CO_2$	С-О-лиаза, С-S-лиаза, С-N-лиаза, С-С-лиаза
КФ 5 <i>Изомеразы</i>	Внутримолекулярная перестановка, то есть изомеризация молекулы субстрата.	$AB \rightarrow BA$	эпимераза, цис-транс-изомераза, внутримолекулярная оксидоредуктаза и др.
КФ 6 <i>Лигазы (синтазы)</i>	Соединение двух молекул в результате синтеза новой С-О, С-S, С-N или С-С связи, сопряженное с одновременным гидролизом АТФ.	$X + Y + ATP \rightarrow XY + ADP + P_i$	С-О-лигаза, С-S-лигаза, С-N-лигаза, С-С-лигаза
КФ 7 <i>Транслоказы</i>	Перенос ионов или молекул через мембраны или их разделение в мембранах.	$AB + C_{[side\ 1]} \rightarrow AB^* + C_{[side\ 2]}$	ЕС 7.1 - транслокация H ⁺ ; ЕС 7.2 - транслокация неорганических катионов и их хелатов; ЕС 7.3 - транслокация неорганических анионов; ЕС 7.4 - транслокация аминокислот и пептидов; ЕС 7.5 - транслокация углеводов и их производных; ЕС 7.6 - транслокация других соединений. ^[2]

Сравнительная геномика



Можно искать от организма



Search for

Database: KEGG - Search term: neurospora crassa

KEGG GENES

cmi:CMM_2688

no KO assigned | (GenBank) unnamed protein product; putative acetyl xylan esterase (XP_330314.1) hypothetical protein [Neurospora crassa]; AAC39371.1| acetyl xylan esterase II precursor [Penicillium purpurogenum]), pfam01083, Cutinase, Cutinase.; Conserved hypothetical protein

vg:1449901

no KO assigned | (RefSeq) MSV087, MseVgp087; Melanoplus sanguinipes entomopoxvirus; ORF MSV087 putative thioredoxin, similar to Neurospora crassa GB:D45892

vg:1449935

no KO assigned | (RefSeq) MSV144, MseVgp144; Melanoplus sanguinipes entomopoxvirus; ORF MSV144 putative ubiquitin, similar to Neurospora crassa GB:U01220

KEGG GENOME

→ T01034

ncr, 367110; Neurospora crassa OR74A

KEGG MGENES

T30455:18971

similarity to hypothetical protein CAD21257.1 - neurospora crassa

T30456:15058

similarity to hypothetical protein CAD21257.1 - neurospora crassa

T30579:1733

similarity to hypothetical protein CAD21257.1 - neurospora crassa

KEGG ENZYME

3.1.30.1

Aspergillus nuclease S1; endonuclease S1 (Aspergillus); single-stranded-nucleate endonuclease; deoxyribonuclease S1; deoxyribonuclease S1; nuclease S1; Neurospora crassa single-strand specific endonuclease; S1 nuclease; single-strand endodeoxyribonu •••



GENOME: *Neurospora crassa*

[Help](#)

Entry	T01034	Complete Genome
Name	ncr, 367110	
Definition	Neurospora crassa OR74A	
Category	Reference genome	
Annotation	yes Show organism	
Taxonomy	TAX:367110	
Lineage	Eukaryota; Fungi; Dikarya; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetidae; Sordariales; Sordariaceae; Neurospora Taxonomy	
Data source	RefSeq (Assembly:GCF_000182925.2) BioProject:132	
Original DB	Broad	
Statistics	Number of protein genes:	9758
	Number of RNA genes:	416
Created	2007	
Reference	PMID:12712197	
Authors	Galagan JE, Calvo SE, Borkovich KA, Selker EU, Read ND, Jaffe D, FitzHugh W, Ma LJ, Smirnov S, Purcell S, et al.	
Title	The genome sequence of the filamentous fungus <i>Neurospora crassa</i> .	
Journal	Nature 422:859-68 (2003) DOI:10.1038/nature01554	

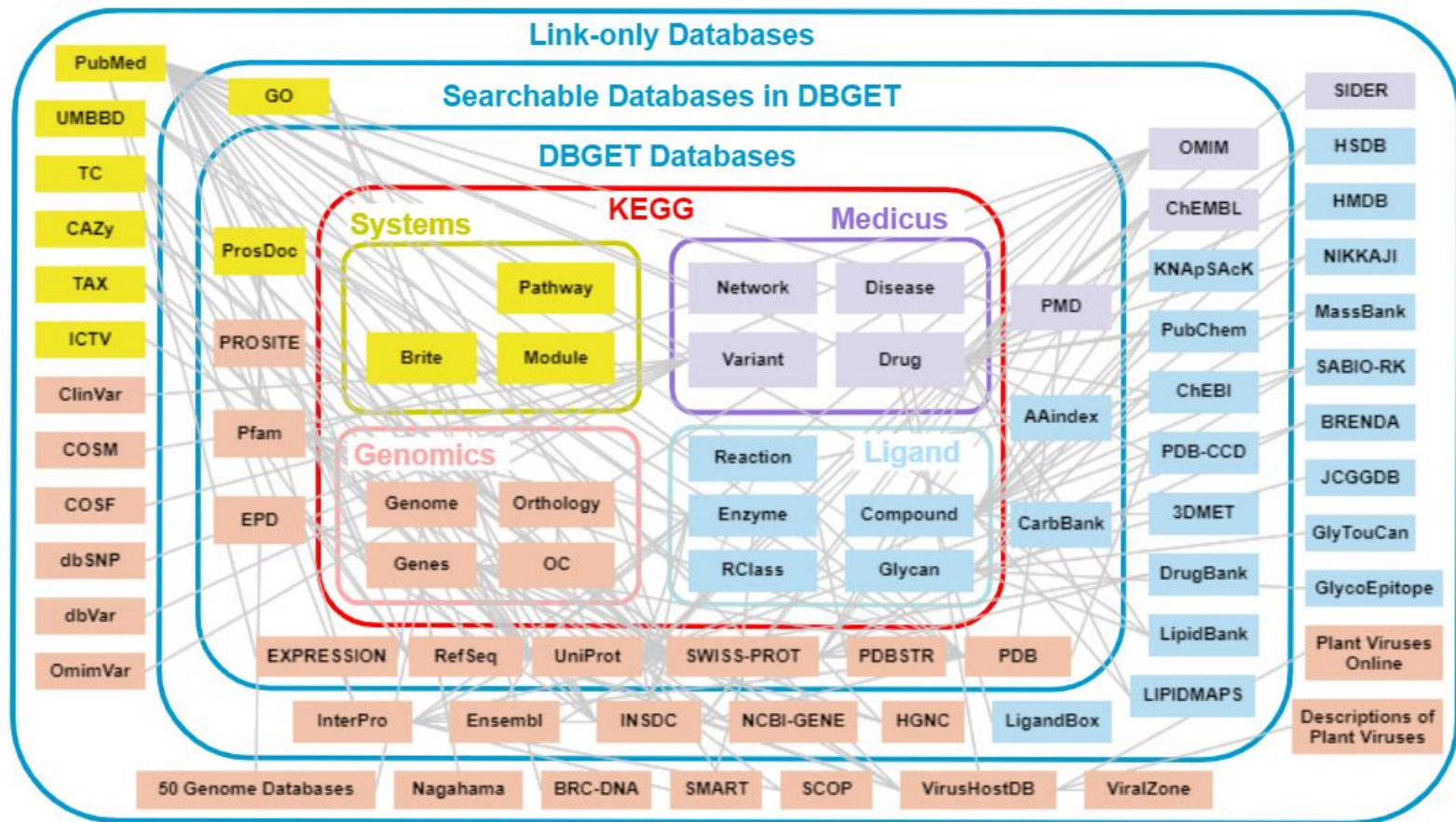
All links

[Ontology \(43\)](#)
[KEGG BRITE \(43\)](#)
[Pathway \(297\)](#)
[KEGG PATHWAY \(119\)](#)
[KEGG MODULE \(178\)](#)
[Genome \(1\)](#)
[ASSEMBLY \(1\)](#)
[Gene \(15422\)](#)
[KEGG GENES \(10174\)](#)
[KEGG MGENES \(613\)](#)
[RefGene \(4635\)](#)
[Literature \(1\)](#)
[PubMed \(1\)](#)
[Taxonomy \(1\)](#)
[TAX \(1\)](#)
[All databases \(15765\)](#)

[Download RDF](#)

<https://www.kegg.jp/kegg/rest/keggapi.html>

<https://www.genome.jp/linkdb/>



<https://reactome.org/>

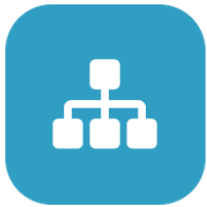


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Find Reactions, Proteins and Pathways

e.g. O95631, NTN1, signaling by EGFR, glucose

Go!



Pathway Browser

Visualize and interact with Reactome biological pathways



Analysis Tools

Merges pathway identifier mapping, over-representation, and expression analysis



ReactomeFIViz

Designed to find pathways and network patterns related to cancer and other types of diseases



Documentation

Information to browse the database and use its principal tools for data analysis



Analyse gene list



Analyse gene expression



Species Comparison



Your data

Options

Analysis

Step 1: Select a file from your computer or paste your own data and click on the corresponding "Continue" button.

Select data file for analysis: Файл не выбран

Continue

Paste your data to analyse or try example data sets:

```
LOC100047604  
D730039F16Rik  
Scyl1  
1700023B02Rik  
1700034H14Rik  
Fbxo8  
Paip1  
Tmem186  
Atpaf1  
LOC100046254  
LOC100047604  
Coq10a  
Fn3k  
Sipa111  
Slc25a16  
Slc25a40  
Rps6ka5  
Trim37
```

Clear

Continue

Some examples:

UniProt accession list

Gene name list

Gene NCBI / Entrez list

Small molecules (ChEBI)

Small molecules (KEGG)

Microarray data

Metabolomics data

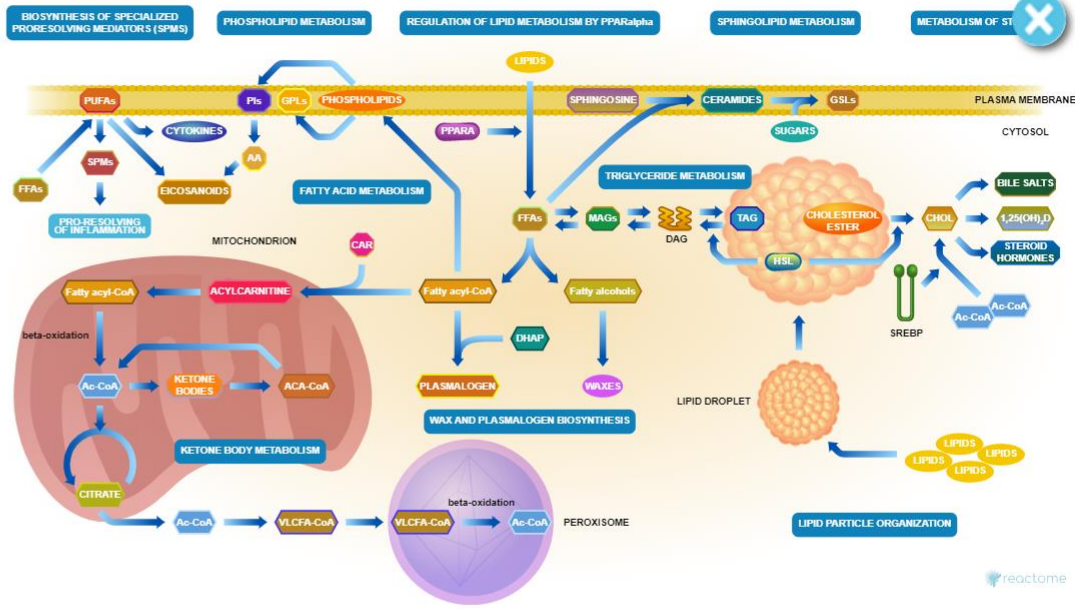
Cancer Gene Census (COSMIC)

Tissue Specific Expression (HPA)



Event Hierarchy:

- Metabolism (77/3,634) FDR: 9.99E-1
 - Metabolism of carbohydrates (10/456) FDR: 8.38E-1
 - Inositol phosphate metabolism (1/90) FDR: 9.24E-1
 - Metabolism of lipids (21/1,437) FDR: 10E-1**
 - Integration of energy metabolism (3/145) FDR: 7.82E-1
 - Regulation of insulin secretion (3/106) FDR: 6.62E-1
 - Glucagon signaling in metabolic regulation (2/40) FDR: 6.62E-1
 - PKA-mediated phosphorylation of key metabolic factors (2/7) FDR: 6.62E-1
 - Insulin effects increased synthesis of Xylulose-5-Phosphate
 - Activation of PP2A by Xylulose-5-phosphate
 - AMPK inhibits chREBP transcriptional activation activity
 - PP2A-mediated dephosphorylation of key metabolic factors
 - ChREBP activates metabolic gene expression
 - Metabolism of nitric oxide: NOS3 activation and regulation (1/41) FDR: 6.9E-1
 - The citric acid (TCA) cycle and respiratory electron transport (11/235) FDR: 6.62E-1
 - Metabolism of nucleotides (3/253) FDR: 9.76E-1
 - Metabolism of vitamins and cofactors (9/377) FDR: 7.48E-1
 - Metabolism of amino acids and derivatives (15/661) FDR: 8.48E-1
 - Metabolism of porphyrins (2/74) FDR: 6.62E-1
 - Biological oxidations (9/545) FDR: 9.74E-1



Enrichr



Input data

Посмотреть огромный
список доступных
аннотации

Choose an input file to upload. Either in BED format or a list of genes.

Try an example [BED file](#).

Выберите файл Файл не выбран

Здесь загрузить файл со
списком генов

Paste a list of valid Entrez gene symbols on each row in the text-box below. [Try a gene set example](#).

или скопировать гены сюда

! Нужны символьные названия
генов !

0 gene(s) entered

In order to enable others to search your list please enter a brief description of it.

Contribute your list so it can be searched by others

Submit



Input data

Choose an input file to upload. Either in BED format or a list of genes.

Try an example [BED file](#).

Файл не выбран

Paste a list of valid Entrez gene symbols on each row in the text-box below. [Try a gene set example](#).

```
Nsun3
Polrmt
Nlrp1
Sfxn5
Zc3h12c
Slc25a39
Arsg
Defb29
Ndufb6
Zfand1
```

375 gene(s) entered

Sample gene list

Contribute your list so it can be searched by others

2. Жмякнули кнопку

1. Задали список интересных генов:



Enrichr

[Login](#) | [Register](#)

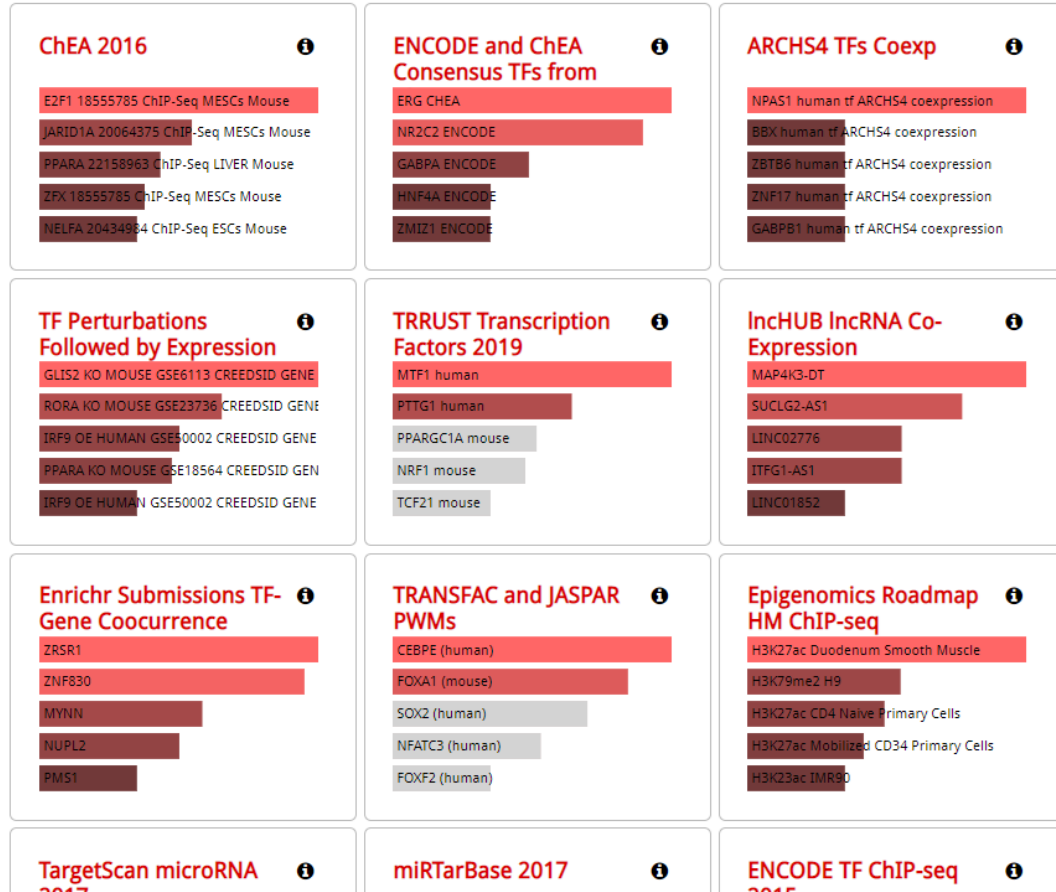
Группы аннотаций

Transcription Pathways Ontologies Diseases/Drugs Cell Types Misc Legacy Crowd

Description Sample gene list (375 genes)

Получили результат - радуемся!

Еще больше результатов по разным аннотациям





Выбрали группу аннотаций

Изучили результаты
по нужным аннотациям!

Description Sample gene list (375 genes)



COVID-19 Related Gene Sets

Bar Graph

Table

Clustergram

Appyter



Click the bars to sort. Now sorted by p-value ranking.

SVG PNG JPG

Down-regulated by MHV-A59 in murine liver 5d from GSE146074

Down-regulated by SARS-CoV-2 infection in Vero E6 from GSE153940

COVID19-Nsp13 protein host PPI from Krogan

COVID19-All 332 protein host PPI from Krogan

Down-regulated by SARS-CoV-2 in A549-ACE2 treated with Terfenadine from GSE15461

Up-regulated by SARS-CoV-2 in ferret trachea from GSE147507

SARS Perturbation Down Genes Mouse Lung from GSE19137:GPL1261:5

SARS-CoV perturbation Down Genes bronchial epithelial 2B4 from GSE17400:GPL570:5

COVID19-Orf9c protein host PPI from Krogan

Down-regulated by MHV-A59 in murine liver 3d from GSE146074

Обогащенные
категории



Выбрали вид
как представлены результаты

MSigDB

- ▶ [MSigDB Home](#)
- ▶ [About Collections](#)
- ▶ [Browse Gene Sets](#)
- ▶ [Search Gene Sets](#)
- ▶ [Investigate Gene Sets](#)
- ▶ [View Gene Families](#)
- ▶ [Help](#)

MSigDB Collections

The 32284 gene sets in the Molecular Signatures Database (MSigDB) are divided into 9 major collections, and several sub-collections. See the table below for a brief description of each, and the [MSigDB Collections: Details and Acknowledgments](#) page for more detailed descriptions. See also the [MSigDB Statistics](#) and the [MSigDB Release Notes](#).

Click on the "browse gene sets" links in the table below to view the gene sets in a collection. Or download the gene sets in a collection by clicking on the links below the "Download GMT Files" headings. For a description of the [GMT file format](#) see the [Data Formats](#) in the [Documentation](#) section. The gene sets can be downloaded as NCBI (Entrez) Gene Identifiers or HUGO (HGNC) Gene Symbols. An XML file containing all the MSigDB gene sets is available on the [Downloads](#) page.

<p>H: hallmark gene sets (browse 50 gene sets)</p>	<p>Hallmark gene sets summarize and represent specific well-defined biological states or processes and display coherent expression. These gene sets were generated by a computational methodology based on identifying overlaps between gene sets in other MSigDB collections and retaining genes that display coordinate expression. details</p>	<p>Download GMT Files Gene Symbols NCBI (Entrez) Gene IDs</p>
<p>C1: positional gene sets (browse 278 gene sets)</p>	<p>Gene sets corresponding to each human chromosome and each cytogenetic band. details</p>	<p>Download GMT Files Gene Symbols NCBI (Entrez) Gene IDs</p>
<p>C2: curated gene sets (browse 6290 gene sets)</p>	<p>Gene sets in this collection are curated from various sources, including online pathway databases and the biomedical literature. Many sets are also contributed by individual domain experts. The gene set page for each gene set lists its source. The C2 collection is divided into the following two sub-collections: Chemical and genetic perturbations (CGP) and Canonical pathways (CP). details</p>	<p>Download GMT Files Gene Symbols NCBI (Entrez) Gene IDs</p>

Аннотации сгруппированы по 9 коллекциям.

Можно скачать все сразу, либо отдельные коллекции или аннотации внутри коллекций.

Коллекции включают в себя и широко известные GO, KEGG,

Reactome...

так и более

специализированные

коллекции:

- связанные с иммунной

Есть и маркеры клеточных

типов, собранные по

нескольким scRNA-seq

публикациям.

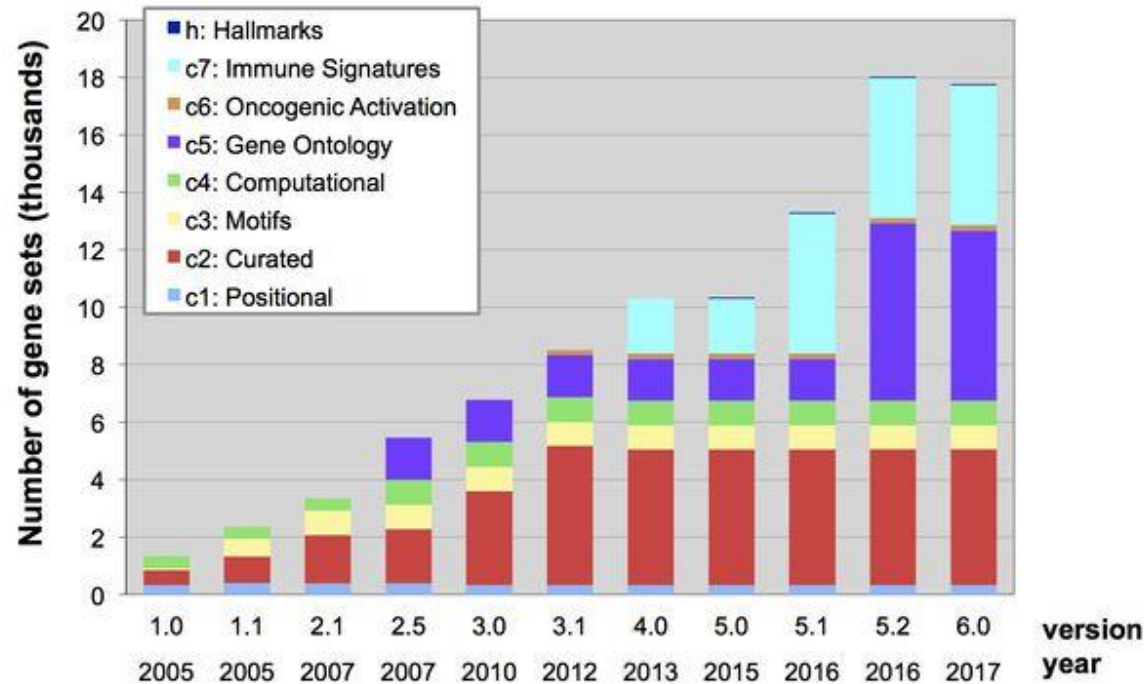
На этом же сайте можно скачать

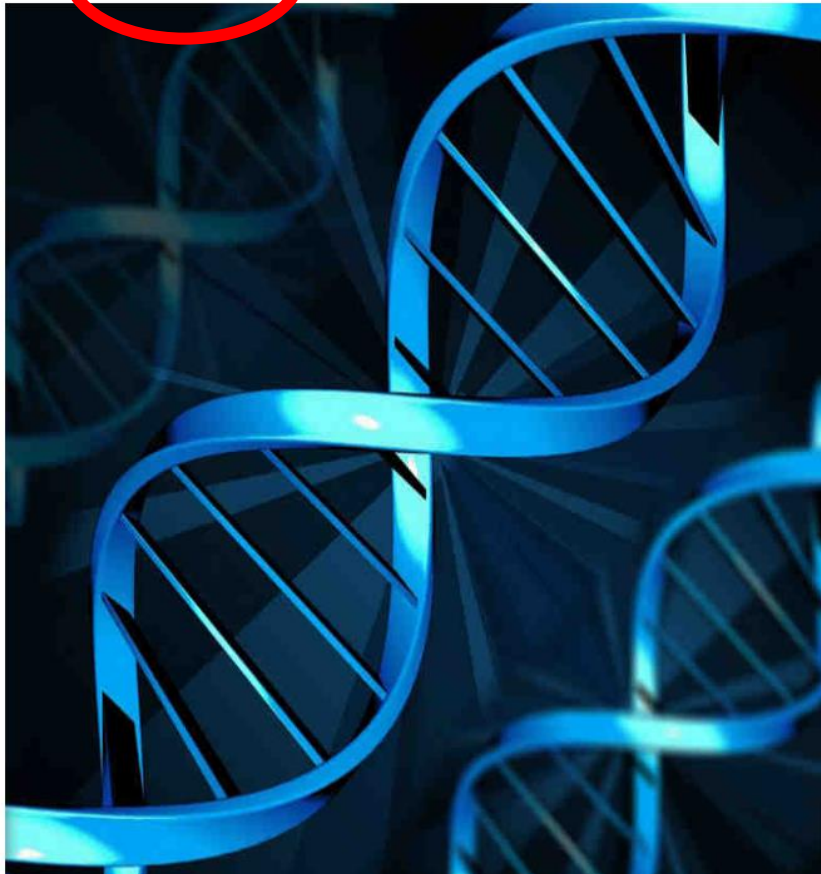
ПО для GSEA анализа.

Так же можно использовать

веб-сервис

<https://www.genepattern.org/>





Our tools

- **Genome Browser**
interactively visualize genomic data
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rapidly align sequences to the genome
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rapidly align PCR primer pairs to the genome
- **LiftOver**
convert genome coordinates between assemblies
- **Track Hubs**
import and view external data tracks
- **REST API**
returns data in JSON format

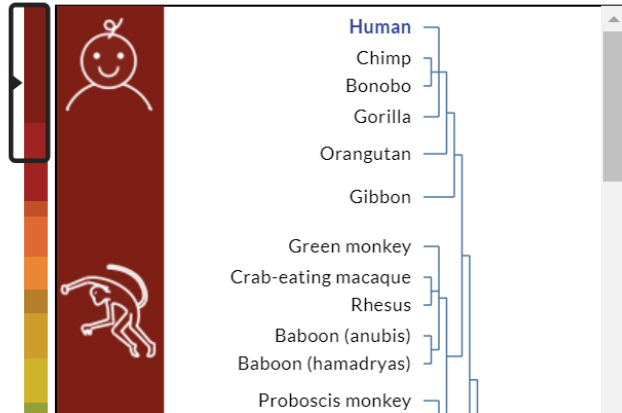
Browse/Select Species

POPULAR SPECIES



Enter species or common name

REPRESENTED SPECIES



Find Position

Human Assembly

Dec. 2013 (GRCh38/hg38)

GO

Position/Search Term

Enter position, gene symbol or search terms

Current position: chrX:15,560,138-15,602,945

Human Genome Browser - hg38 assembly

[view sequences](#)

UCSC Genome Browser assembly ID: hg38
Sequencing/Assembly provider ID: Genome Reference Consortium Human GRCh38.p12 (GCA_000001405.27)
Assembly date: Dec. 2013 initial release; Dec. 2017 patch release 12
Assembly accession: [GCA_000001405.27](#)
NCBI Genome ID: 51 (Homo sapiens (human))
NCBI Assembly ID: [5800238](#) (GRCh38.p12, GCA_000001405.27)
BioProject ID: [PRJNA31257](#)



Homo sapiens
(Graphic courtesy of CBSE)

Search the assembly:

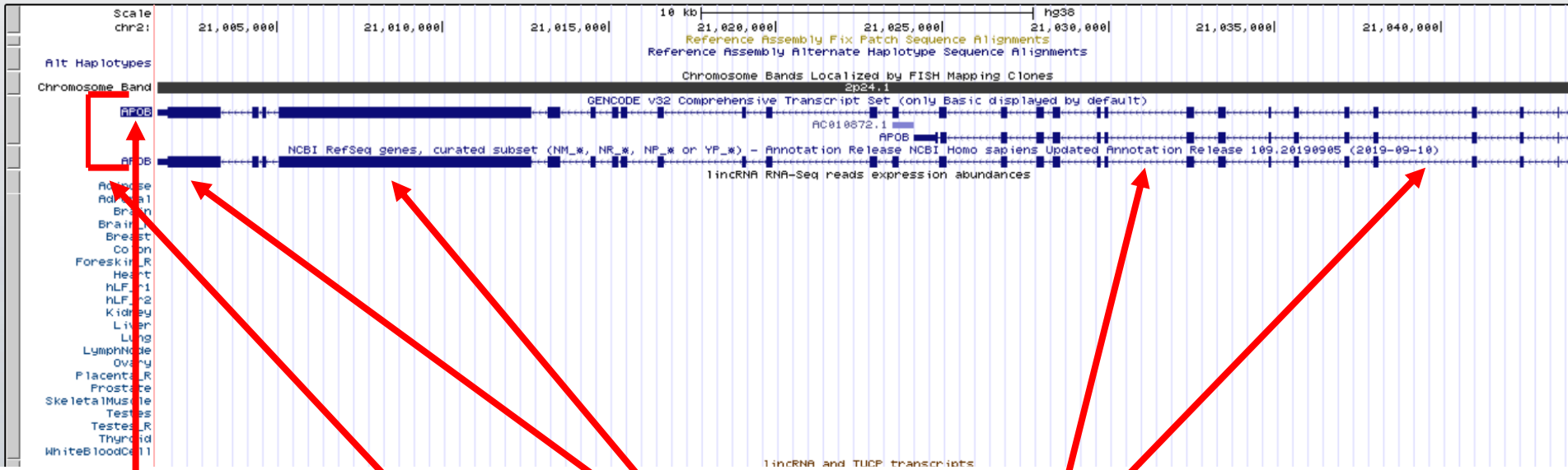
- 1) Выбираем человека – Human
- 2) Версия генома человека – GRCh38/hg38
- 3) В раздел Position/Search Term вводим название своего гена или координаты локуса



UCSC Genome Browser on Human Dec. 2013 (GRCh38/hg38) Assembly

move <<< << < > >> >>> zoom in 1.5x 3x 10x base zoom out 1.5x 3x 10x 100x

chr2:21,001,429-21,044,073 42,645 bp. enter position, gene symbol, HGVS or search terms go



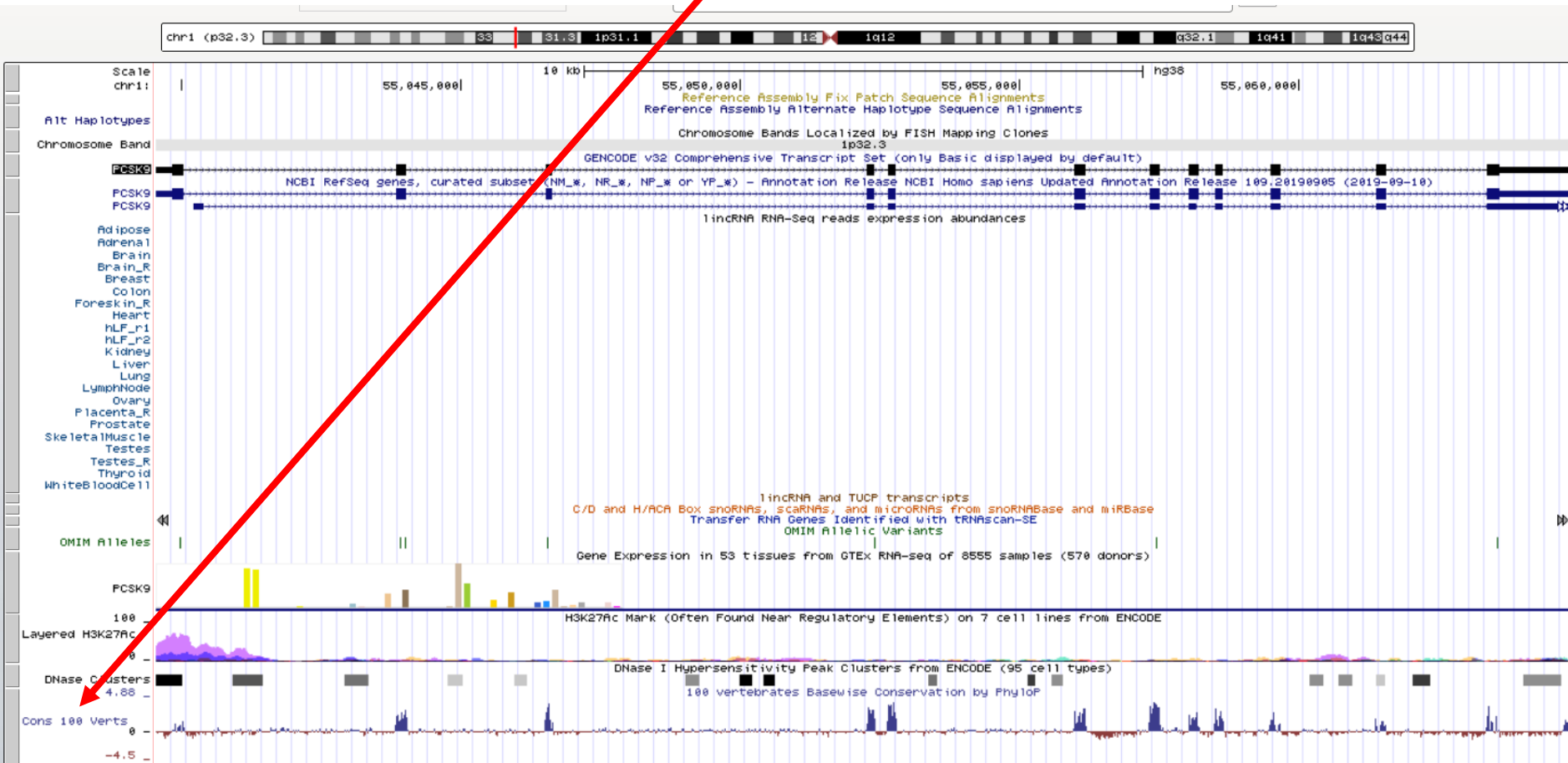
Ген

Экзоны

Интроны

Нажимаем на название гена и попадаем на страницу его подробного описания

Обратите внимание на трек консервативности



Можно спрятать все треки

UCSC Genome Browser on Human Dec. 2013 (GRCh38/hg38) Assembly

chr1:55,039,548-55,064,852 25,305 bp. enter position, gene symbol, HGVS or search terms go

chr1 (p32.3) hg38

Scale chr1: 55,045,000 10 kb 55,050,000 55,055,000 55,060,000

move start < 2.0 > move end < 2.0 >

track search default tracks default order **hide all** add custom tracks track hubs configure multi-region reverse resize refresh

collapse all Use drop down controls below and press refresh to alter tracks displayed. expand all

Tracks with lots of items will automatically be displayed in more compact modes.

Mapping and Sequencing refresh

Открыть только некоторые

Genes and Gene Predictions refresh

P12 [GENCODE v32](#) [RefSeq](#) [Other RefSeq](#) [Updated All GENCODE...](#) [AUGUSTUS](#) [CCDS](#)

hide ▼ **full** ▼ hide ▼ hide ▼ hide ▼ hide ▼

P12 [Genscan](#) [IKMC Genes](#)

Repeats refresh

P12 [RepeatMasker](#) [Interrupted Rpts](#) [RepeatMasker Viz.](#) [Microsatellite](#) [Segmental Dups](#) [Self Chain](#)

full ▼ hide ▼ hide ▼ hide ▼ hide ▼

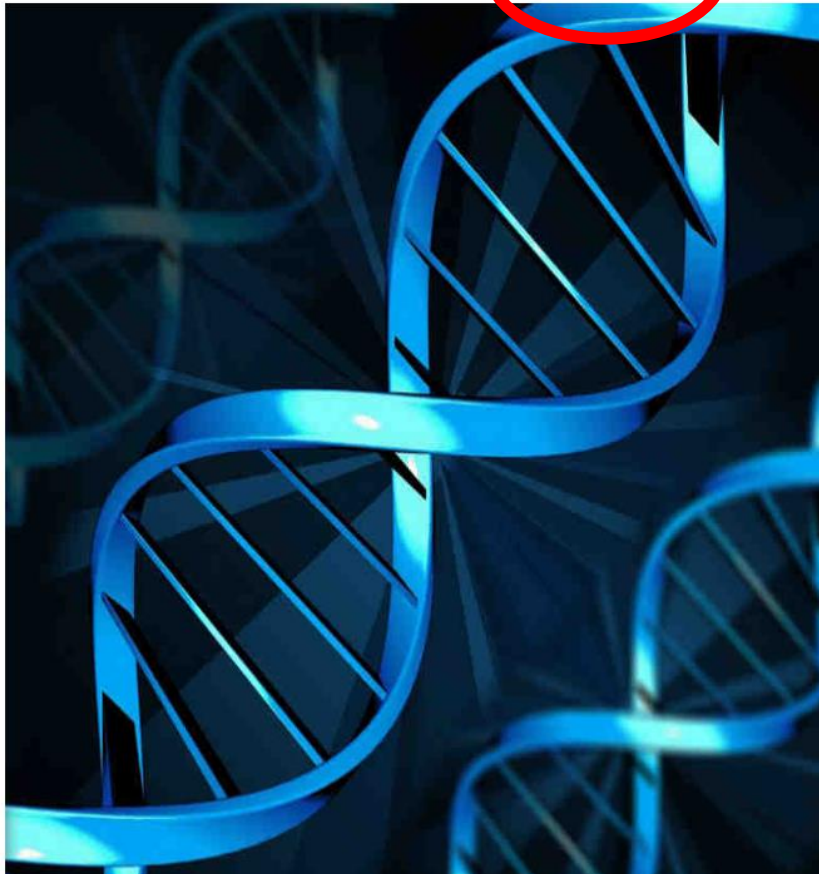
P12 [Simple Repeats](#) [WM + SDust](#)

hide ▼ hide ▼



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Table Browser

Use this program to retrieve the data associated with a track in text format, to calculate intersections between tracks, and to retrieve DNA sequence covered by a track. For help in using this application see [Using the Table Browser](#) for a description of the controls in this form, and the [User's Guide](#) for general information and sample queries. For more complex queries, you may want to use [Galaxy](#) or our [public MySQL server](#). To examine the biological function of your set through annotation enrichments, send the data to [GREAT](#). Refer to the [Credits](#) page for the list of contributors and usage restrictions associated with these data. All tables can be downloaded in their entirety from the [Sequence and Annotation Downloads](#) page.

clade: **genome:** **assembly:**

group: **track:**

table:

region: genome position

filter:

subtrack merge:

intersection:

correlation:

output format: Send output to [Galaxy](#) [GREAT](#)

output file: (leave blank to keep output in browser)

file type returned: plain text gzip compressed

Note: to return more than 100,000 lines, change the filter setting (above). The entire data set may be available for download as a very large file that contains the original data values (not compressed into the wiggle format) -- see the Downloads page.

To reset **all** user cart settings (including custom tracks), [click here](#).

GeneCards®: The Human Gene Database

GeneCards is a searchable, integrative database that provides comprehensive, user-friendly information on all annotated and predicted human genes. The knowledgebase automatically integrates gene-centric data from ~150 web sources, including genomic, transcriptomic, proteomic, genetic, clinical and functional information.



Explore a Gene

IL6 [GO](#)

Jump to section for this gene:

- | | | | | | | | | |
|--------------------------|---------------------------|--------------------------|--------------------------|------------------------------|--------------------------|---------------------------|------------------------------|---------------------------|
| Aliases | Disorders | Domains | Drugs | Expression | Function | Genomics | Localization | Orthologs |
| Paralogs | Pathways | Products | Proteins | Publications | Sources | Summaries | Transcripts | Variants |

GeneCardsSuite

NGS Analysis



Affiliated Databases



Analysis Tools



IL6 Gene (Protein Coding) ★

Interleukin 6

GCID: GC07P022725 [?]

GIFTS: 50 [?]



Genes
Participants

Jump to section	Aliases	Disorders	Domains	Drugs	Expression	Function	Genomics	Localization	Orthologs
	Paralogs	Pathways	Products	Proteins	Publications	Sources	Summaries	Transcripts	Variants
Research Products	Antibodies Cell Lines	Assays Clones	Proteins Primers	Inhib. RNA Genotyping	CRISPR	Exp. Assays	miRNA	Drugs	Animal Models

	Proteins Primary Antibodies ELISAs Antibody Arrays Activity Assays		Proteins Antibodies Assays Genes shRNA Primers CRISPR Lentiviral Particles		Antibodies Proteins Lysates Elisa Kits		Gene Synthesis ORF clones Peptide Service Peptide Library CRISPR
--	--	--	--	--	---	--	--

Aliases for IL6 Gene [?]

Aliases for IL6 Gene

- | | |
|--|---|
| Interleukin 6 ^{2 3 5} | IFNB2 ^{3 4} |
| IL-6 ^{2 3 4} | BSF2 ^{2 3} |
| B-Cell Stimulatory Factor 2 ^{3 4} | CDF ^{3 4} |
| CTL Differentiation Factor ^{3 4} | HGF ^{2 3} |
| Hybridoma Growth Factor ^{3 4} | HSF ^{2 3} |
| Interferon Beta-2 ^{3 4} | Interleukin 6 (Interferon, Beta 2) ² |
| Interleukin-6 ^{3 4} | B-Cell Differentiation Factor ³ |
| IFN-Beta-2 ^{3 4} | Interferon, Beta 2 ² |
| BSF-2 ^{3 4} | Interleukin BSF-2 ³ |
| | IL6 ⁵ |

GeneCards for AI/ML ✕

Access comprehensive integrated data from >190 biomedical sources in machine-readable formats

JSON
XML
CSV
API
...

AI >



The mission of UniProt is to provide the scientific community with a comprehensive, high-quality and freely accessible resource of protein sequence and functional information.

UniProtKB
UniProt Knowledgebase

Swiss-Prot
(564,638)

Manually annotated and reviewed.

Records with information extracted from literature and curator-evaluated computational analysis.

TrEMBL
(214,406,399)

Automatically annotated and not

UniRef

Sequence clusters

UniParc

Sequence archive

Proteomes

Proteome sets

Supporting data

Literature citations 	Taxonomy 	Subcellular locations
Cross-ref. databases 	Diseases 	Keywords

New UniProt portal for the latest SARS-CoV-2 coronavirus protein entries and receptors, updated independent of the general UniProt release cycle.

View SARS-CoV-2 Proteins and Receptors

News

Forthcoming changes
Planned changes for UniProt

UniProt release 2021_02
With a little help from my friend | SwissBioPics subcellular location visualization | Change of evidence codes for combinatorial evidence

UniProt release 2021_01
(Almost) all about that CBASS | Cross-references to

Retrieve/ID mapping

How to use Retrieve/ID mapping tool

Enter or upload a list of identifiers to do one of the following:

Retrieve the corresponding UniProt entries to download them or work with them on this website.

Convert identifiers which are of a different type to UniProt identifiers or vice versa and download the identifier lists.

1. Enter identifiers, separated by spaces or new lines, into the form field, for example:
P31946 P62258
ALBU_HUMAN
EFTU_ECOLI
2. If you need to convert to another identifier type, select the source and target type from the dropdown menus.
3. Click the *Submit* button.


[? Help](#)[▶ Help video](#)[▶ Other tutorials and videos](#)[↓ Downloads](#)

1. Provide your identifiers

e.g. P31946 P62258 ALBU_HUMAN EFTU_ECOLI

Results

1 out of 1 identifier from UniProtKB AC/ID was successfully mapped to 1 Gene name ID.

 Download

1 to 1 of 1

From	To
P31946	YWHAB

1 to 1 of 1

<http://www.pantherdb.org/>

1. Enter ids and or select file for batch upload. Else enter ids or select file or list from workspace for comparing to a reference list.

Enter IDs:
[Supported IDs](#)
 separate IDs by a space or comma

Upload IDs: Файл не выбран

[File format](#)

Please [login](#) to be able to select lists from your workspace.

Select List Type: ID List
 Previously exported text search results
 Workspace list
 PANTHER Generic Mapping
 ID's from Reference Proteome Genome
Organism for id list
 VCF File Flanking region Search Enhancer Data

2. Select organism.

Mus musculus
Rattus norvegicus
Gallus gallus
Danio rerio

3. Select Analysis.

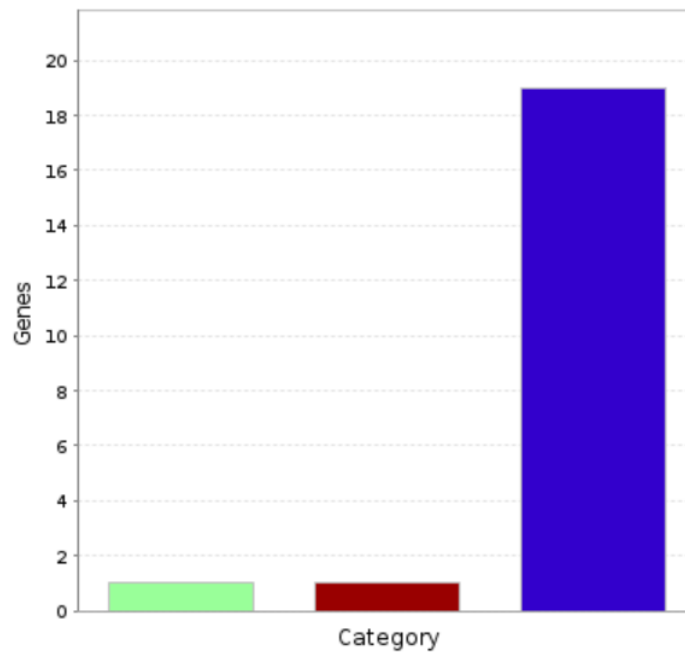
Functional classification viewed in gene list
 Functional classification viewed in graphic charts Bar chart Pie chart

<http://www.pantherdb.org/>

Select Ontology: View:


PANTHER Protein Class

Total # Genes: 22 Total # protein class hits: 21



Click to get gene list for a category:

- [RNA metabolism protein \(PC00031\)](#)
- [protein-binding activity modulator \(PC00095\)](#)
- [translational protein \(PC00263\)](#)

Color picker powered by  Web Colors by VistiBone