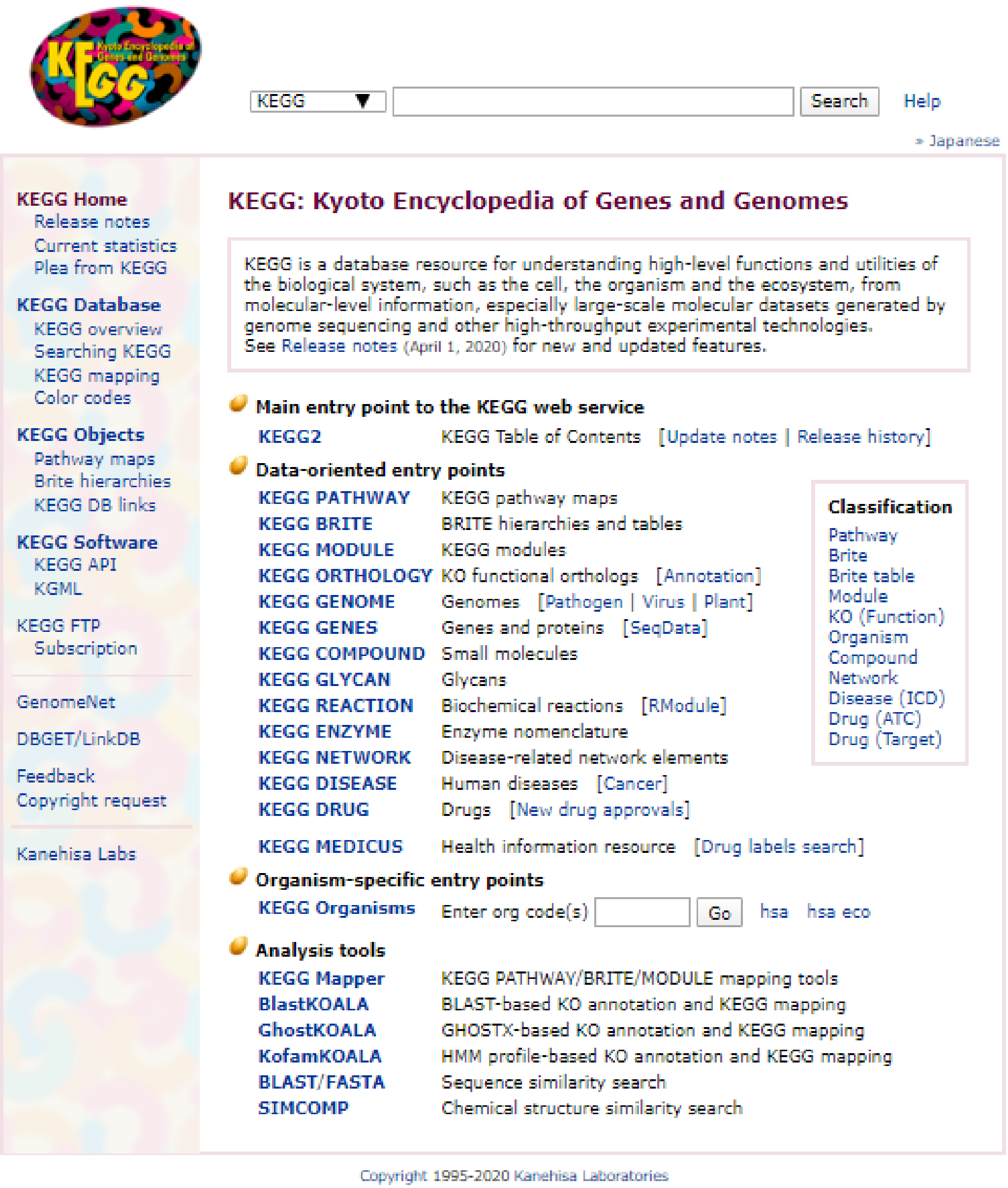
Метаболические пути

KEGG

https://www.genome.jp/kegg/



KEGG Home
- Release notes
- Current statistics
- Plea from KEGG

KEGG Database
- KEGG overview
- Searching KEGG
- KEGG mapping
- Color codes

KEGG Objects
- Pathway maps
- Brite hierarchies
- KEGG DB links

KEGG Software
- KEGG API
- KGML

KEGG FTP
- Subscription

GenomeNet

DBGET/LinkDB

Feedback
Copyright request

Kanehisa Labs

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]

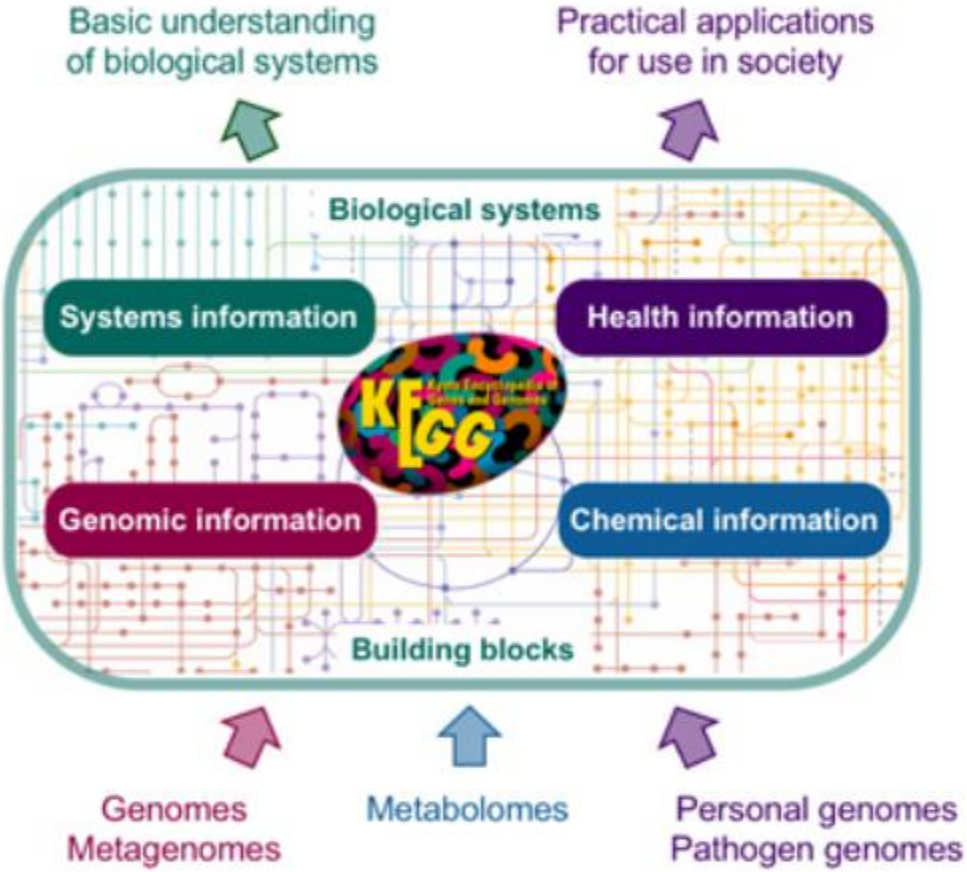
Classification
- Pathway
- Brite
- Brite table
- Module
- KO (Function)
- Organism
- Compound
- Network
- Disease (ICD)
- Drug (ATC)
- Drug (Target)

Organism-specific entry points

KEGG Organisms Enter org code(s) [ ] Go 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



Basic understanding of biological systems

Practical applications for use in society

Biological systems

Systems information

Health information

Genomic information

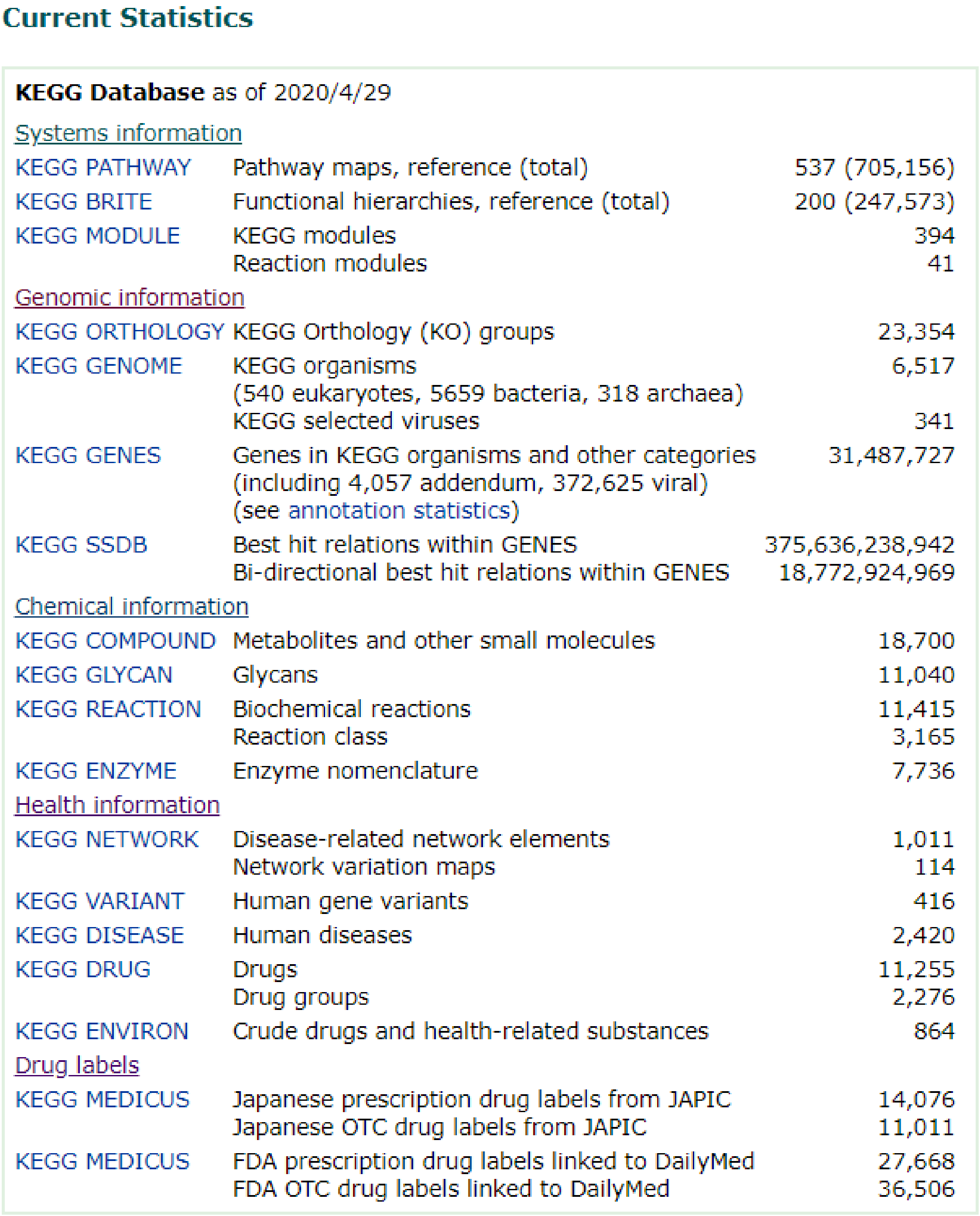
Chemical information

Building blocks

Genomes
Metagenomes

Metabolomes

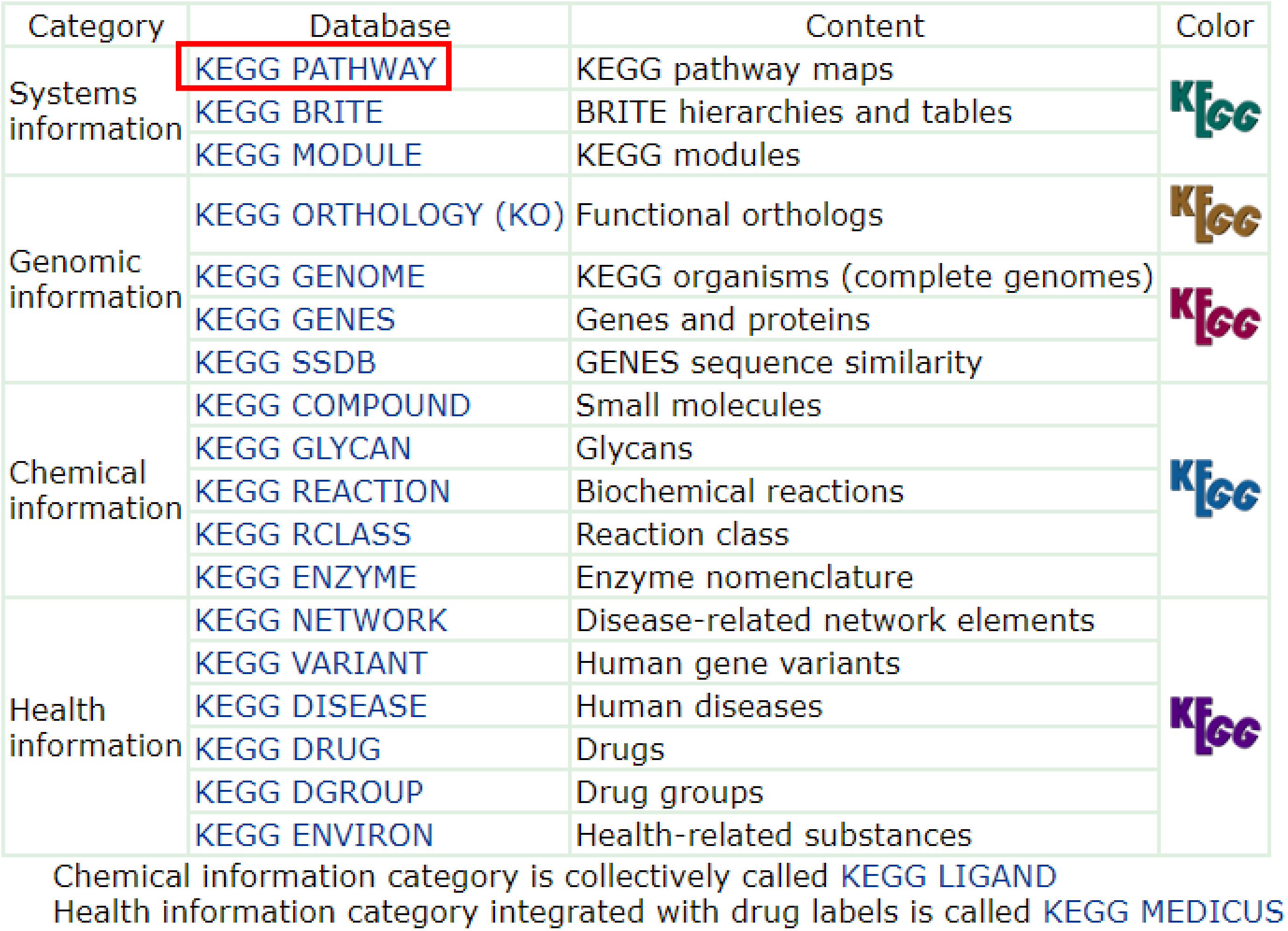
Personal genomes
Pathogen genomes



Current Statistics

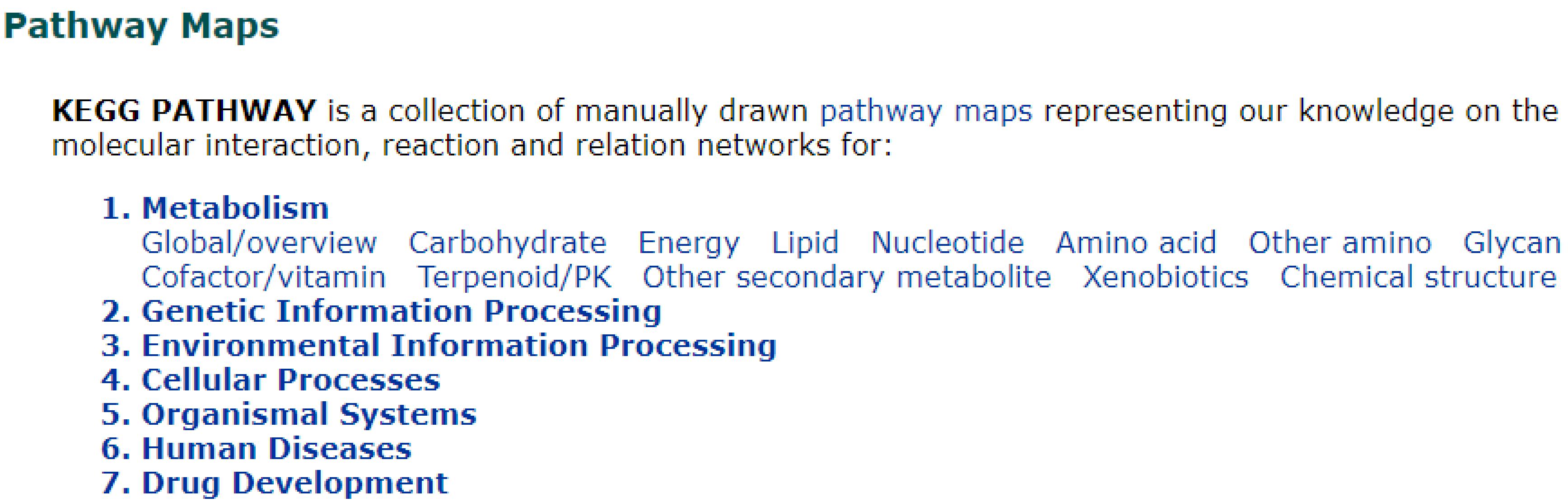
KEGG Database as of 2020/4/29

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
	KEGG BRITE	BRITE hierarchies and tables	
	KEGG MODULE	KEGG modules	
Genomic information	KEGG ORTHOLOGY (KO)	Functional orthologs	KEGG
	KEGG GENOME	KEGG organisms (complete genomes)	KEGG
	KEGG GENES	Genes and proteins	
	KEGG SSDB	GENES sequence similarity	
Chemical information	KEGG COMPOUND	Small molecules	KEGG
	KEGG GLYCAN	Glycans	
	KEGG REACTION	Biochemical reactions	
	KEGG RCLASS	Reaction class	
	KEGG ENZYME	Enzyme nomenclature	
Health information	KEGG NETWORK	Disease-related network elements	KEGG
	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

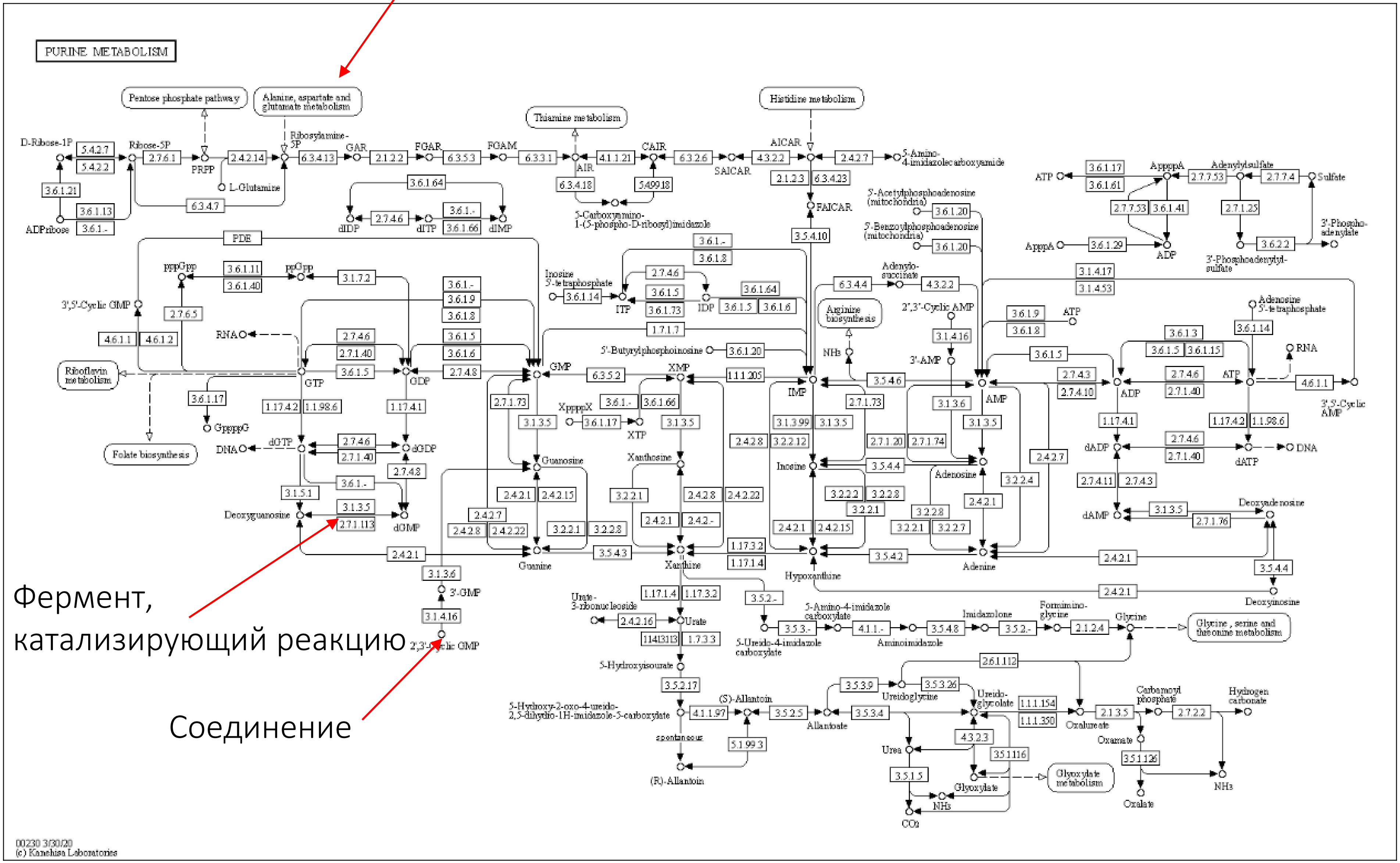


Pathway Maps

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

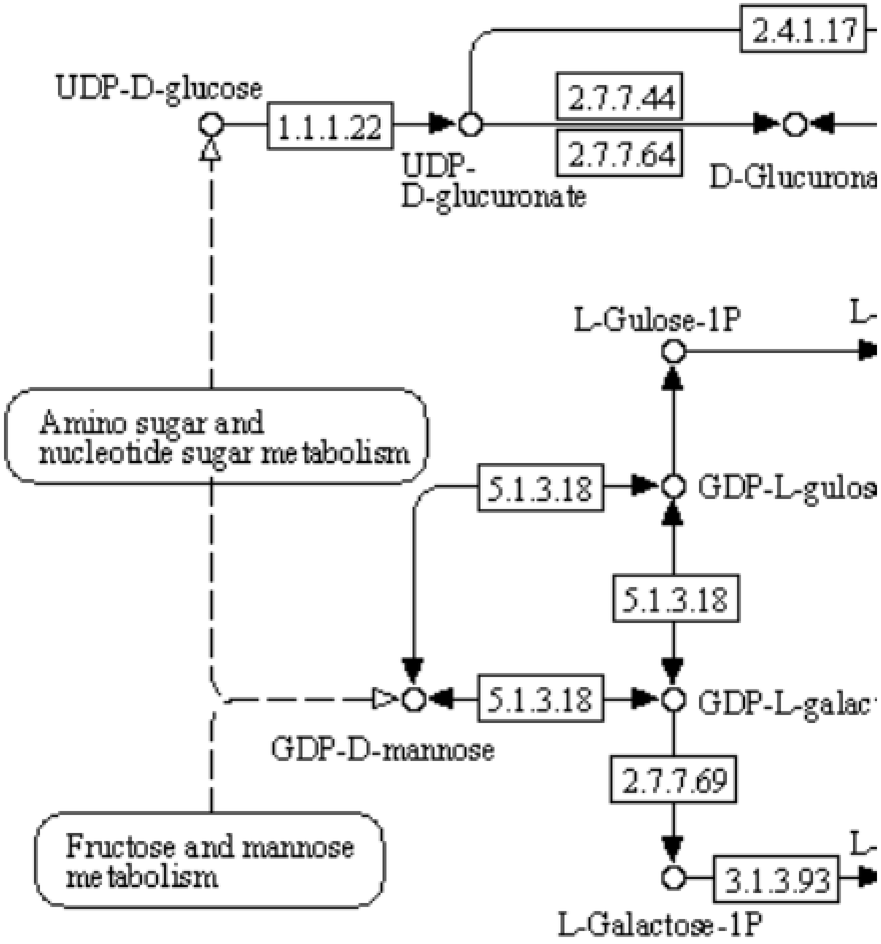
1. **Metabolism**
   Global/overview Carbohydrate Energy Lipid Nucleotide Amino acid Other amino Glycan
   Cofactor/vitamin Terpenoid/PK Other secondary metabolite Xenobiotics Chemical structure
2. **Genetic Information Processing**
3. **Environmental Information Processing**
4. **Cellular Processes**
5. **Organismal Systems**
6. **Human Diseases**
7. **Drug Development**

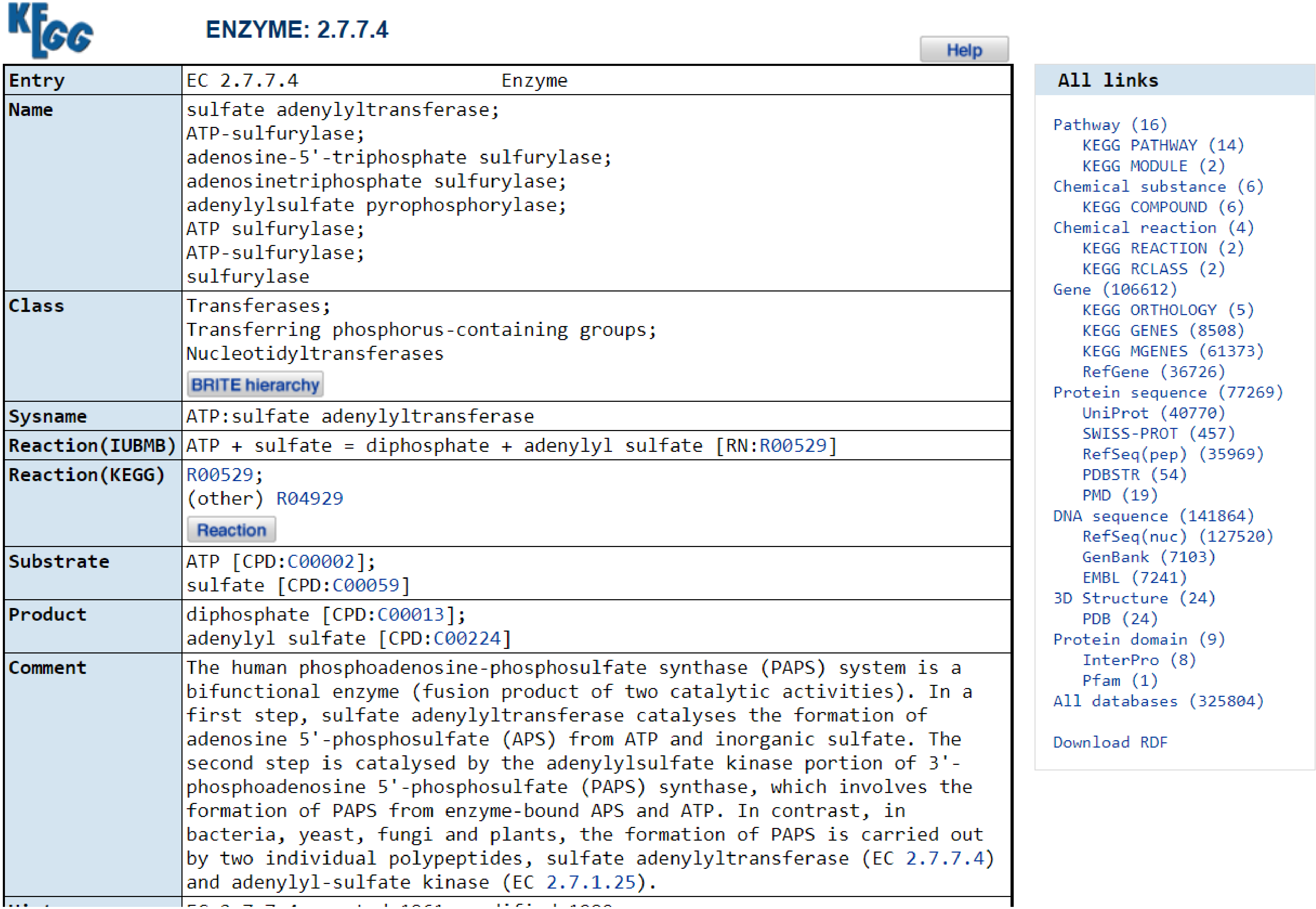
Другой метаболический путь



Фермент, катализирующий реакцию

Соединение


2.4.1.17
UDP-D-glucose
1.1.1.22
2.7.7.44
2.7.7.64
UDP-
D-glucuronate
D-Glucurona
L-Gulose-1P
L-
Amino sugar and
nucleotide sugar metabolism
5.1.3.18
GDP-L-gulos
5.1.3.18
5.1.3.18
GDP-L-galac
GDP-D-mannose
2.7.7.69
Fructose and mannose
metabolism
L-
3.1.3.93
L-Galactose-1P



KEGG

ENZYME: 2.7.7.4

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)

Download RDF

Код фермента

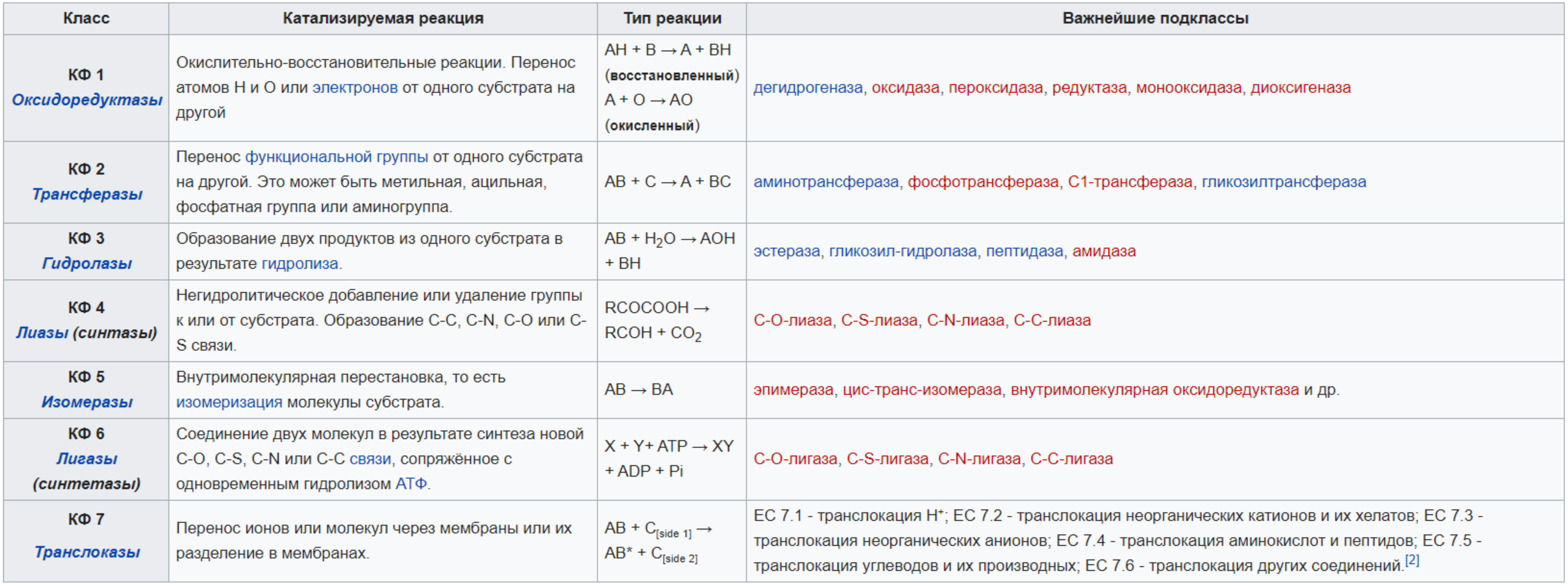
Класс – код первого уровня: 1-7. Номер одного из семи главных классов ферментов
Подкласс – код второго уровня. Номер характеризует основные виды субстратов, участвующих в данном виде химических реакций.
Под-подкласс – код третьего уровня. Номер определяет более частные подгруппы, отличающиеся природой 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: глюкозоксидаза – 1.1.3.4

КФ 1 — Оксидоредуктазы
КФ 1.1 — Алкогольоксидоредуктазы
КФ 1.1.3 — Оксидоредуктазы, окисляющие группу CH-OH и восстанавливающие кислород.
КФ 1.1.3.4 — Оксидоредуктазы, окисляющие глюкозу в присутствии кислорода. Всего известно 3 глюкозоксидазы из разных организмов.

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

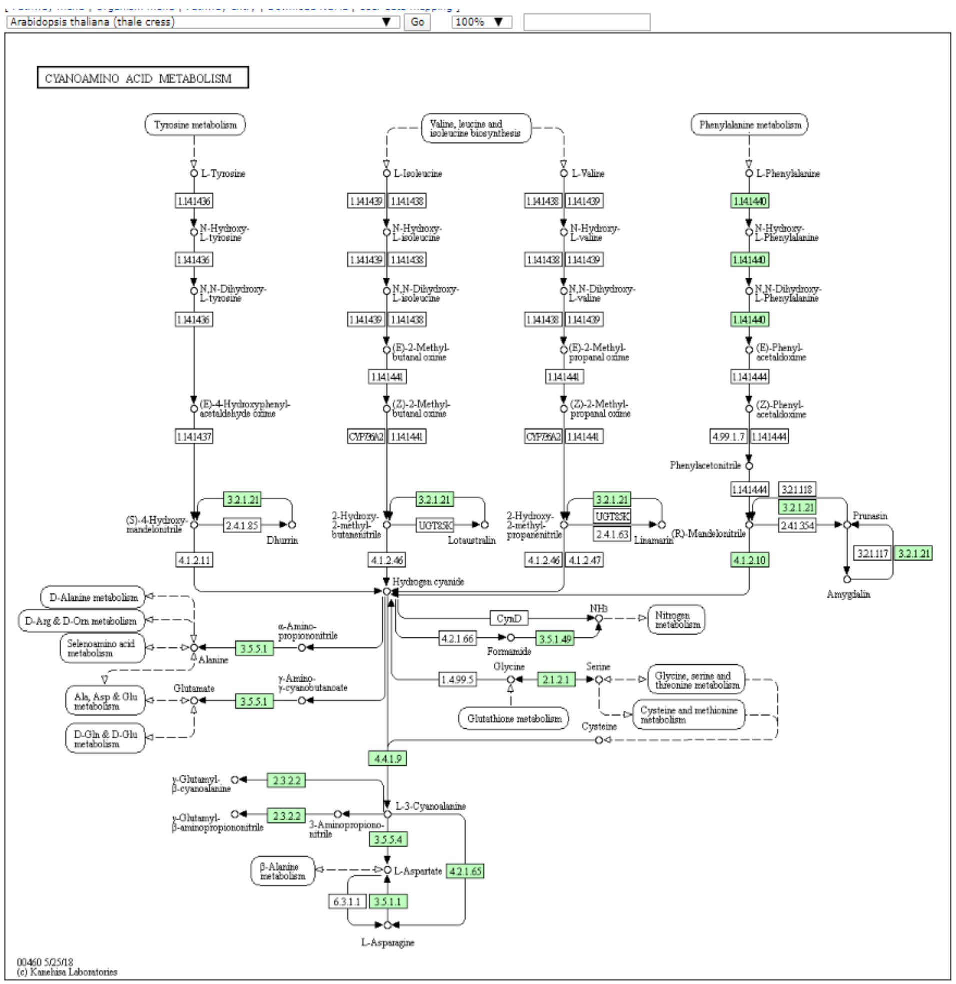
Основные классы ферментов
Коды первого уровня



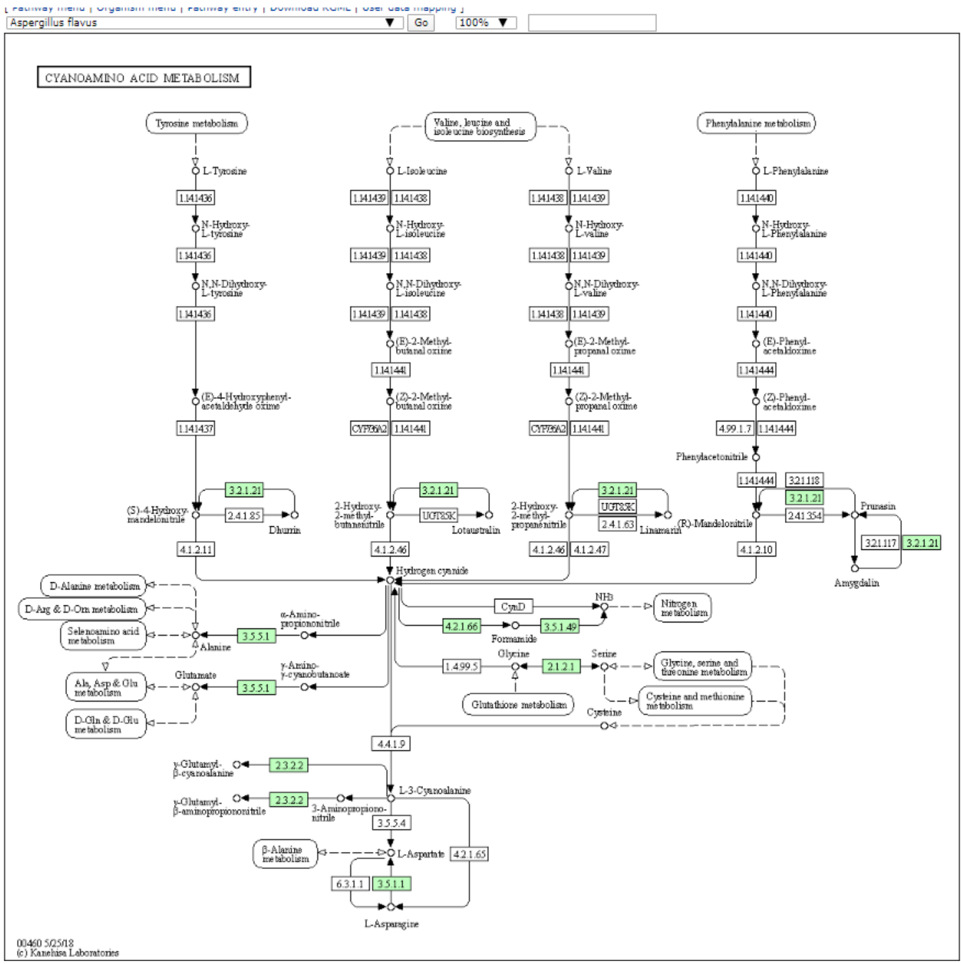
Класс	Катализируемая реакция	Тип реакции	Важнейшие подклассы
КФ 1 ***Оксидоредуктазы***	Окислительно-восстановительные реакции. Перенос атомов H и O или электронов от одного субстрата на другой	AH + B → A + BH **(восстановленный)** A + O → AO **(окисленный)**	дегидрогеназа, оксидаза, пероксидаза, редуктаза, монооксидаза, диоксигеназа
КФ 2 ***Трансферазы***	Перенос функциональной группы от одного субстрата на другой. Это может быть метильная, ацильная, фосфатная группа или аминогруппа.	AB + C → A + BC	аминотрансфераза, фосфотрансфераза, C1-трансфераза, гликозилтрансфераза
КФ 3 ***Гидролазы***	Образование двух продуктов из одного субстрата в результате гидролиза.	AB + H_2O → AOH + BH	эстераза, гликозил-гидролаза, пептидаза, амидаза
КФ 4 ***Лиазы (синтазы)***	Негидролитическое добавление или удаление группы к или от субстрата. Образование C-C, C-N, C-O или C-S связи.	RCOCOOH → RCOH + CO_2	C-O-лиаза, C-S-лиаза, C-N-лиаза, C-C-лиаза
КФ 5 ***Изомеразы***	Внутримолекулярная перестановка, то есть изомеризация молекулы субстрата.	AB → BA	эпимераза, цис-транс-изомераза, внутримолекулярная оксидоредуктаза и др.
КФ 6 ***Лигазы (синтетазы)***	Соединение двух молекул в результате синтеза новой C-O, C-S, C-N или C-C связи, сопряжённое с одновременным гидролизом АТФ.	X + Y+ ATP → XY + ADP + Pi	C-O-лигаза, C-S-лигаза, C-N-лигаза, C-C-лигаза
КФ 7 ***Транслоказы***	Перенос ионов или молекул через мембраны или их разделение в мембранах.	AB + $C_{[side\ 1]}$ → AB* + $C_{[side\ 2]}$	EC 7.1 - транслокация H^+; EC 7.2 - транслокация неорганических катионов и их хелатов; EC 7.3 - транслокация неорганических анионов; EC 7.4 - транслокация аминокислот и пептидов; EC 7.5 - транслокация углеводов и их производных; EC 7.6 - транслокация других соединений.[2]

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

Сравнительная геномика

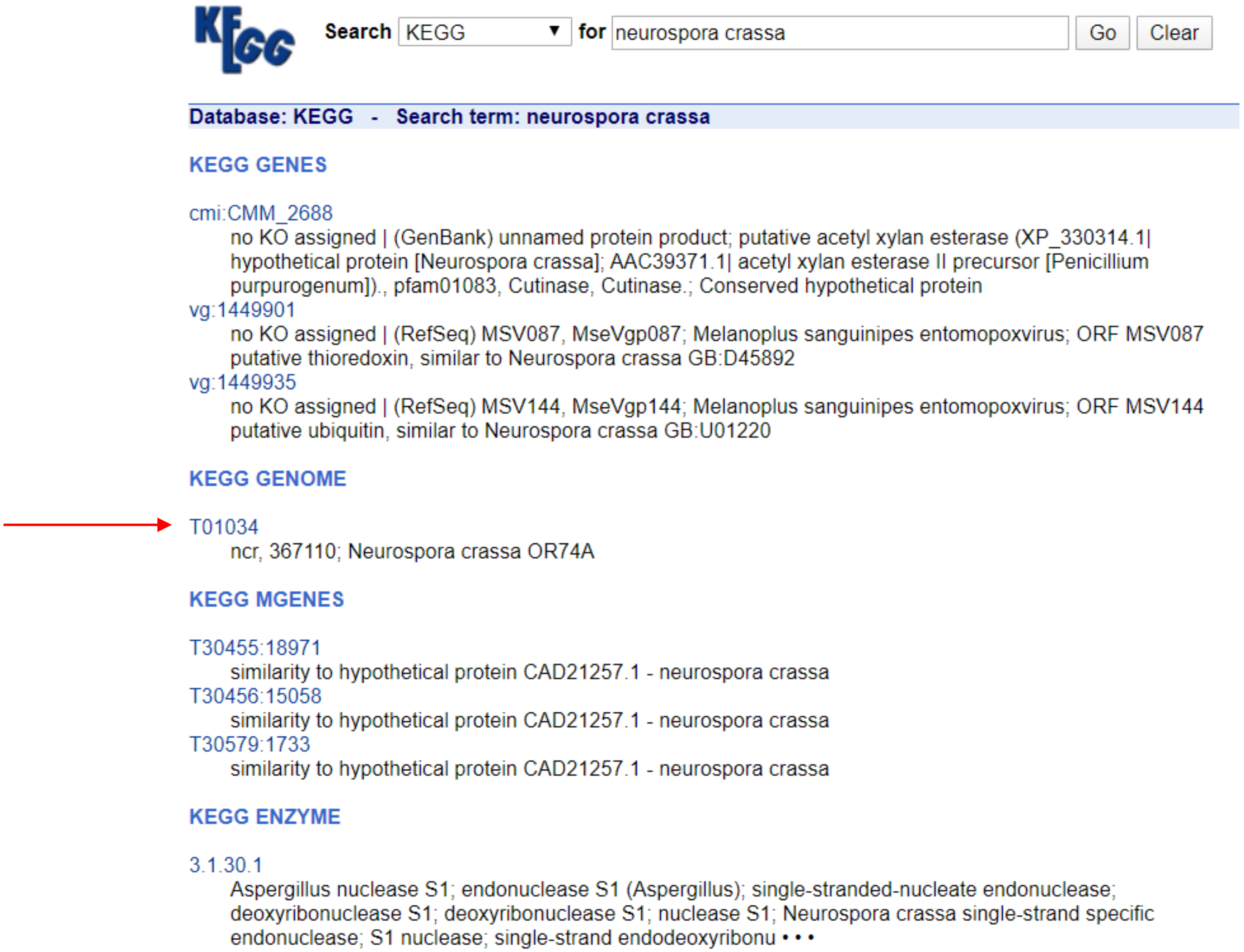


Arabidopsis thaliana (thale cress) ▼ Go 100% ▼



Aspergillus flavus ▼ Go 100% ▼

Можно искать от организма



Search KEGG **for** neurospora crassa

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

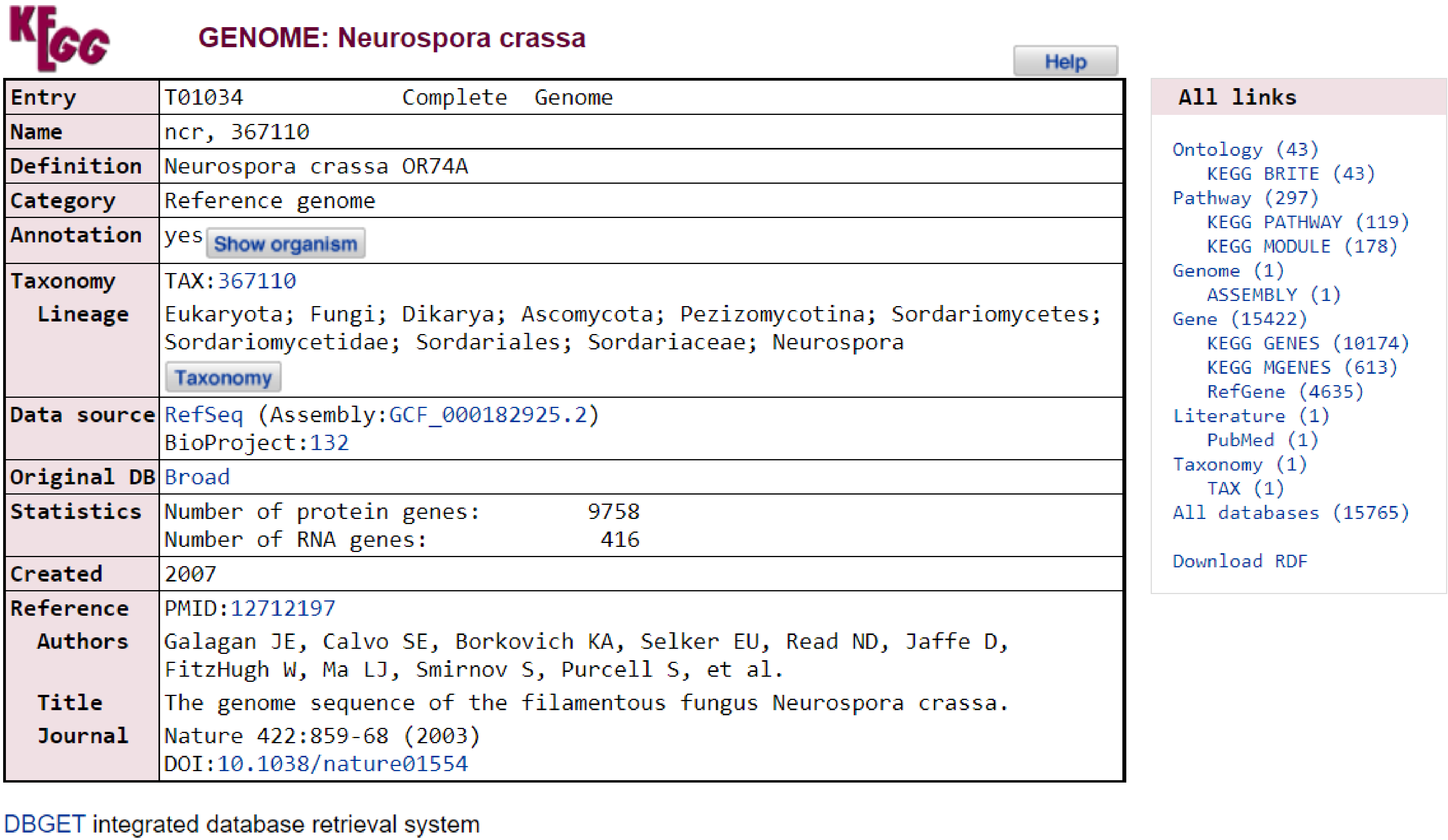
T30455:18971
similarity to hypothetical protein CAD21257.1 - neurospora crassa

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

Entry	T01034 Complete Genome
Name	ncr, 367110
Definition	Neurospora crassa OR74A
Category	Reference genome
Annotation	yes
Taxonomy	TAX:367110
Lineage	Eukaryota; Fungi; Dikarya; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetidae; Sordariales; Sordariaceae; Neurospora
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 Neurospora crassa.
Journal	Nature 422:859-68 (2003) DOI:10.1038/nature01554

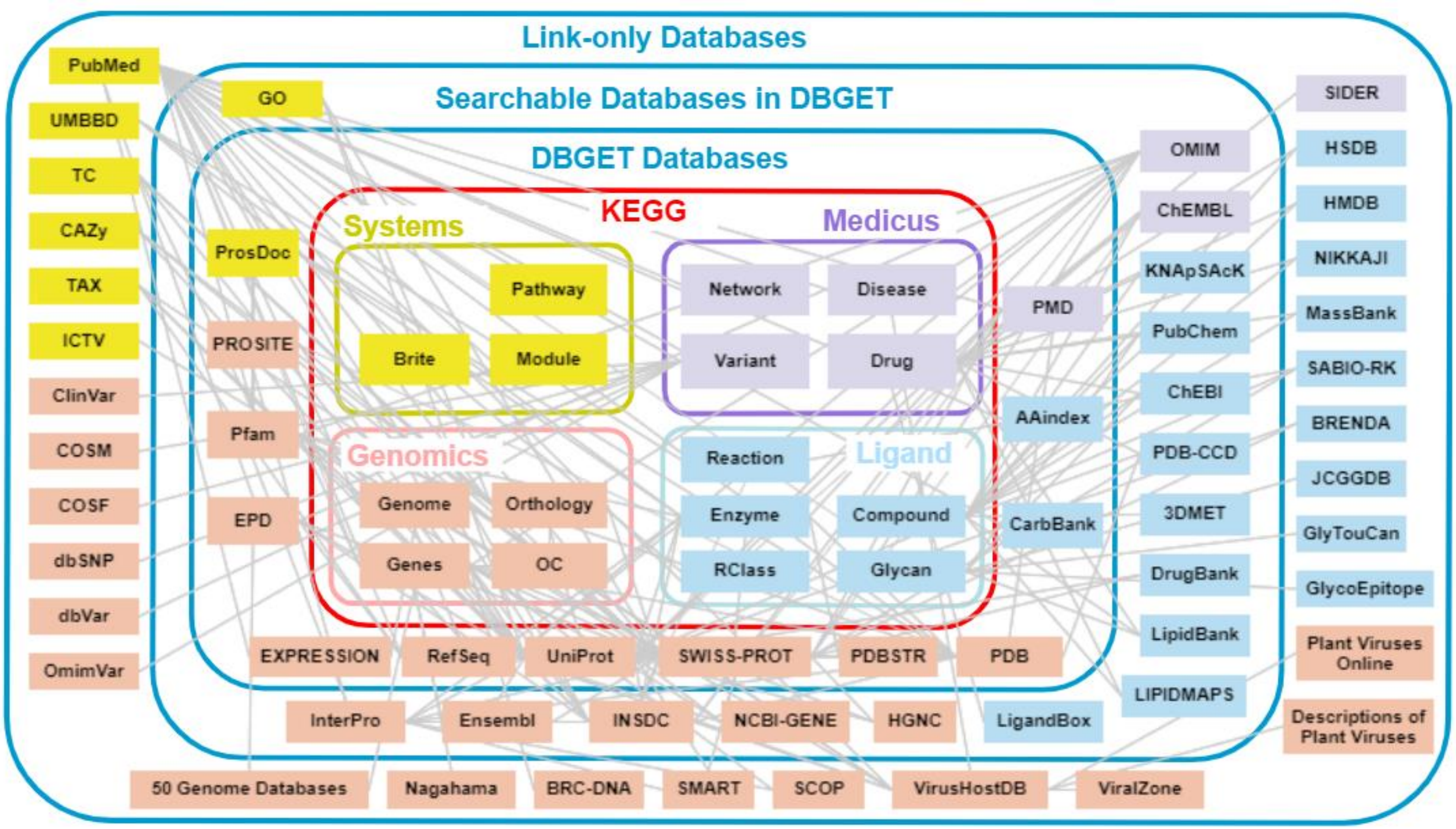
All links

- 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)

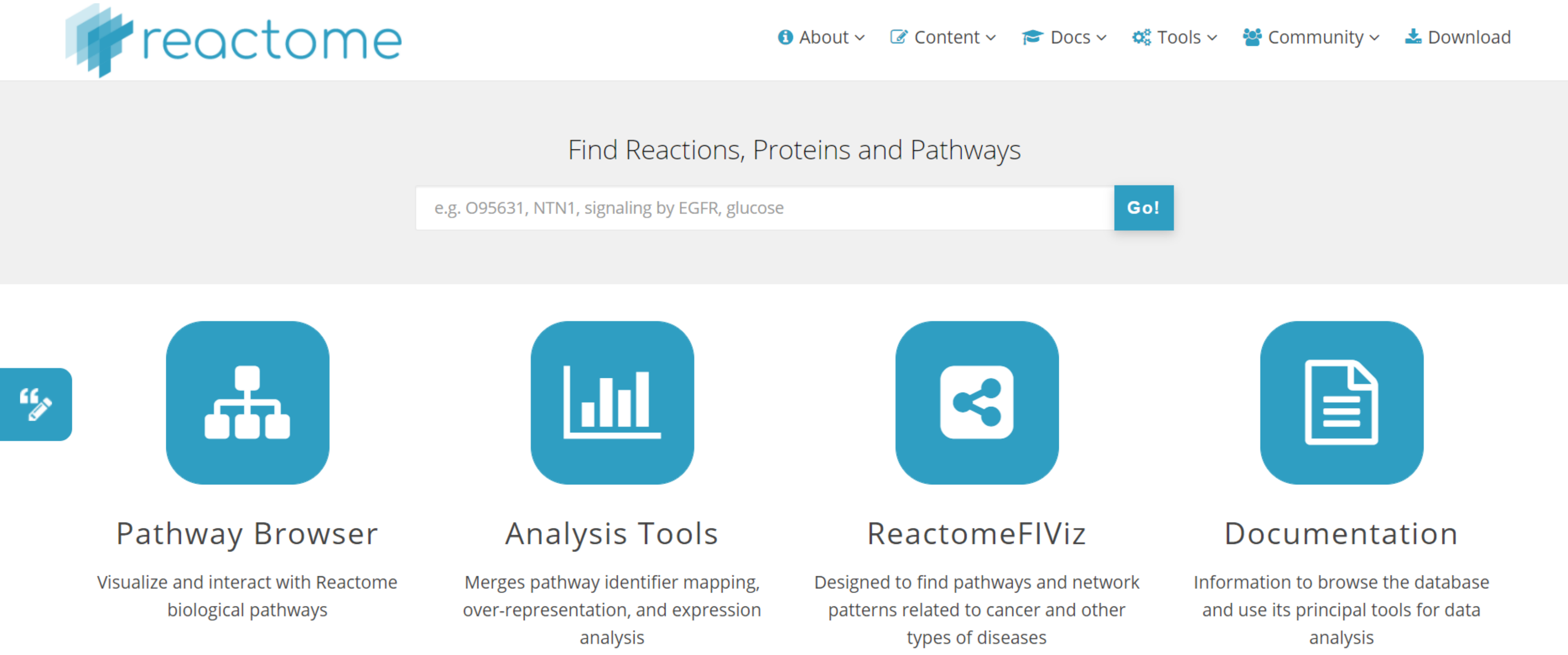
Download RDF

DBGET integrated database retrieval system https://www.kegg.jp/kegg/rest/keggapi.html

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



https://reactome.org/



Find Reactions, Proteins and Pathways

Pathway Browser

Visualize and interact with Reactome biological pathways

Analysis Tools

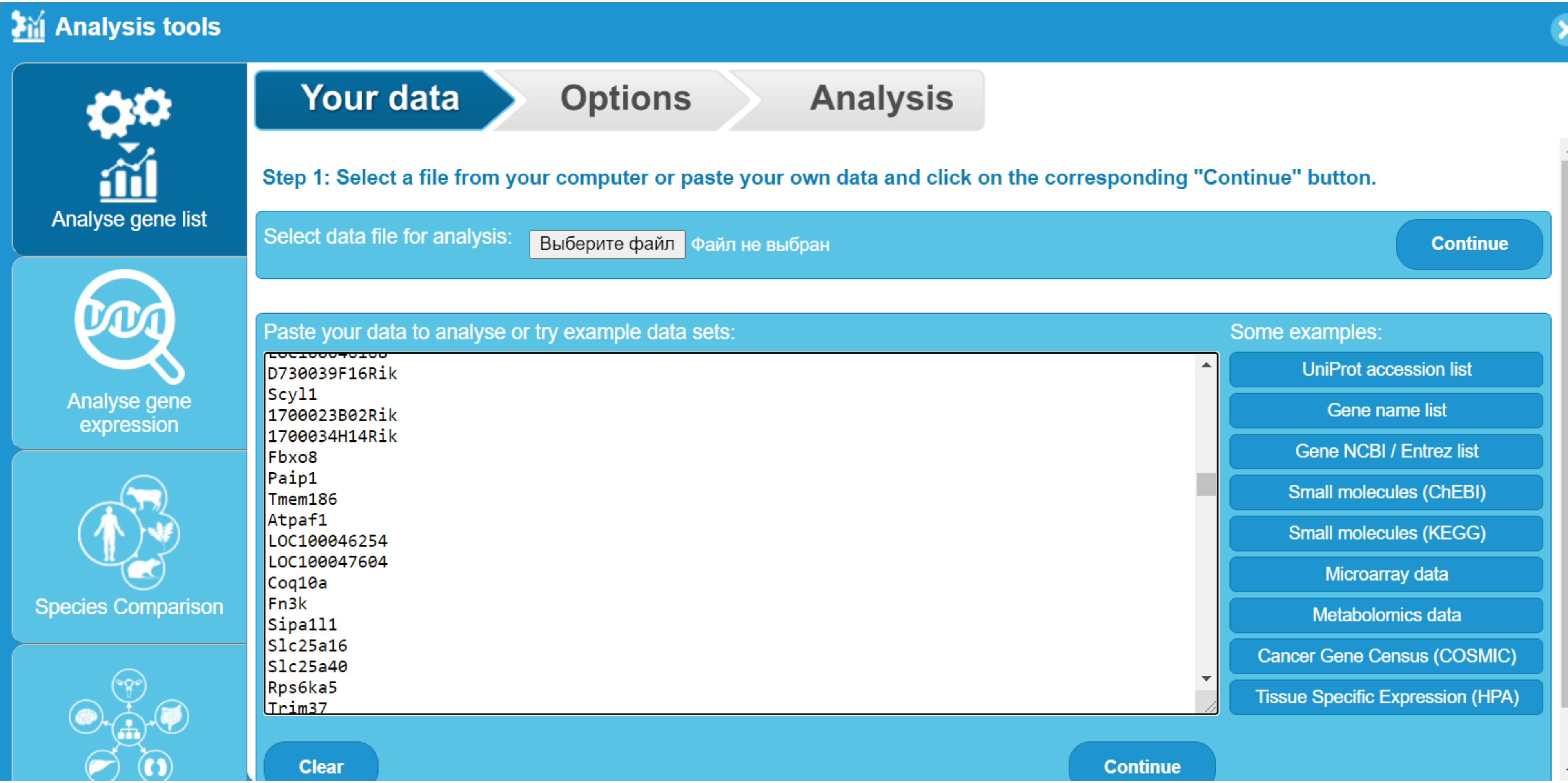
Merges pathway identifier mapping, over-representation, and expression analysis

ReactomeFIViz

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

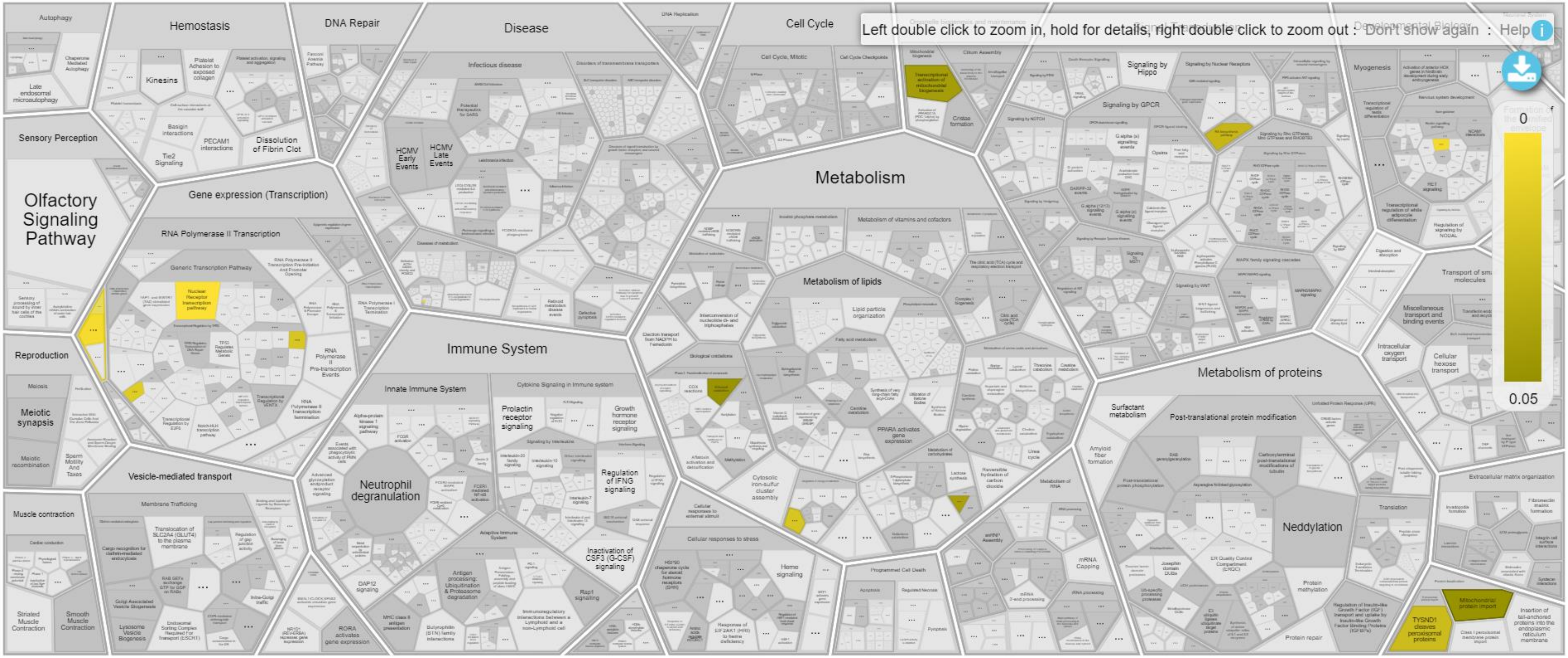
Documentation

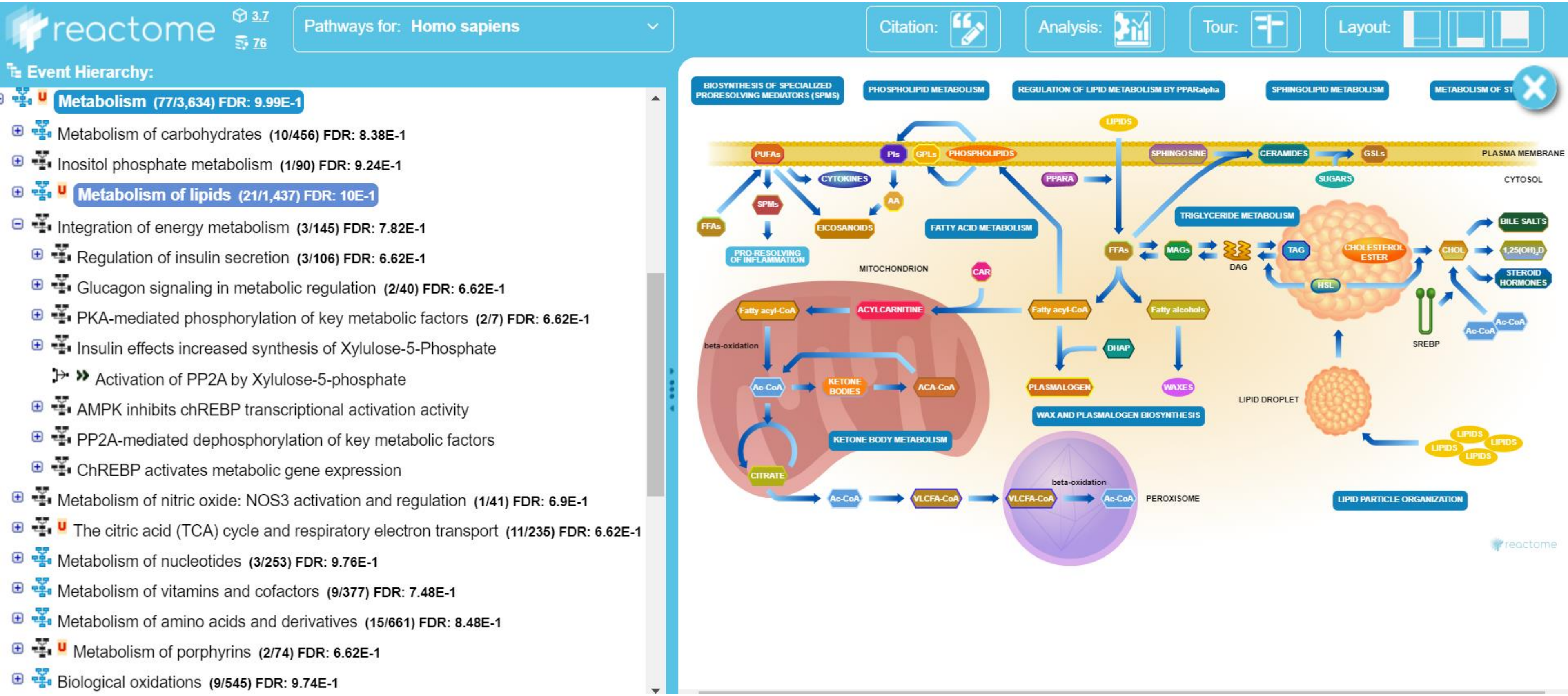
Information to browse the database and use its principal tools for data analysis



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

```
D730039F16Rik
Scyl1
1700023B02Rik
1700034H14Rik
Fbxo8
Paip1
Tmem186
Atpaf1
LOC100046254
LOC100047604
Coq10a
Fn3k
Sipa1l1
Slc25a16
Slc25a40
Rps6ka5
Trim37
```

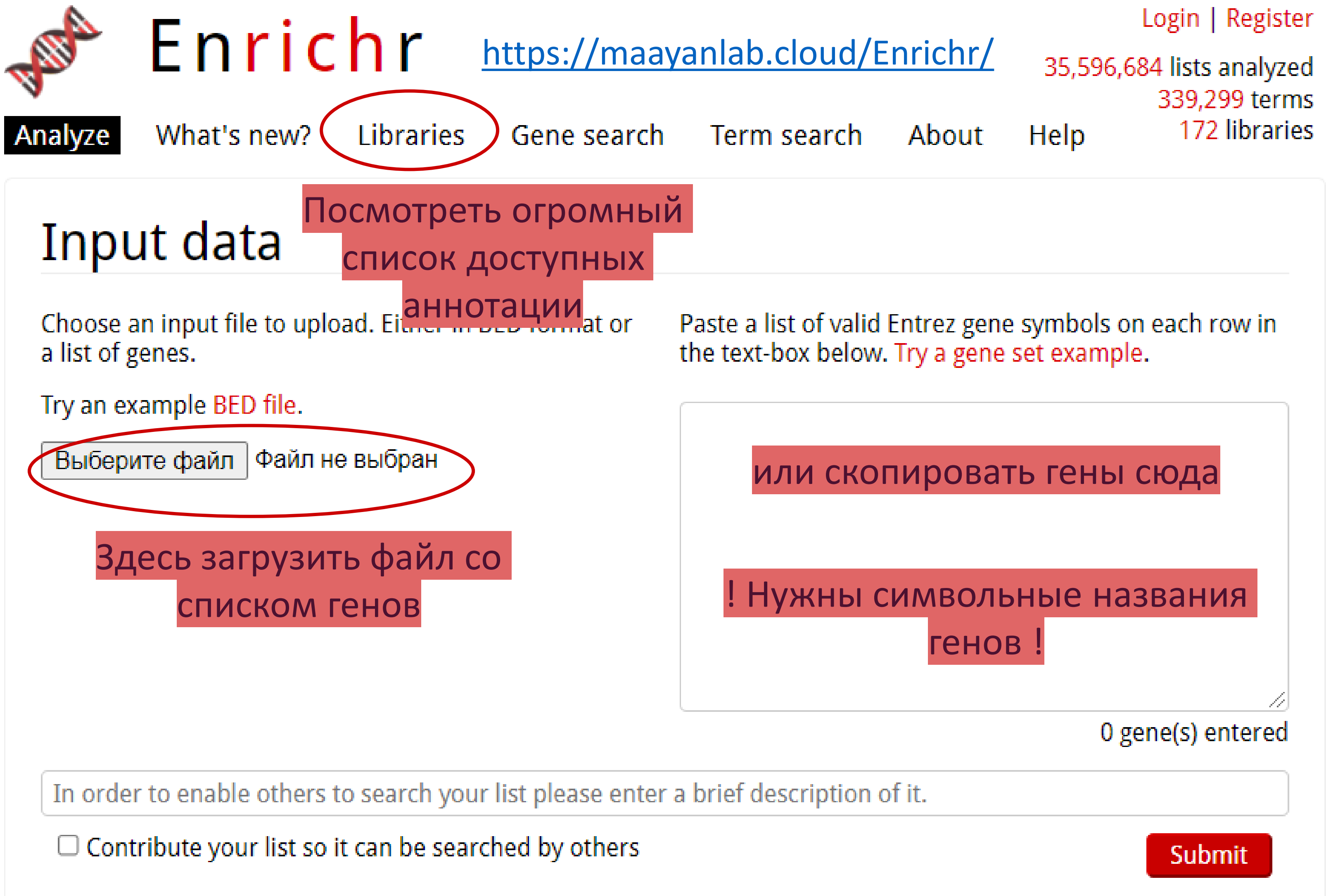

Left double click to zoom in, hold for details, right double click to zoom out : Don't show again : Help
0
0.05
Autophagy
Hemostasis
DNA Repair
Disease
DNA Replication
Cell Cycle
Developmental Biology
Late endosomal microautophagy
Kinesins
Platelet Adhesion to exposed collagen
Sensory Perception
Basigin interactions
Tie2 Signaling
PECAM1 interactions
Dissolution of Fibrin Clot
Infectious disease
HCMV Early Events
HCMV Late Events
Cell Cycle, Mitotic
Cell Cycle Checkpoints
Transcriptional activation of mitochondrial biogenesis
Cristae formation
Signaling by Hippo
Signaling by GPCR
Myogenesis
Olfactory Signaling Pathway
Gene expression (Transcription)
RNA Polymerase II Transcription
Generic Transcription Pathway
Nuclear Receptor transcription pathway
RNA Polymerase II Pre-transcription Events
Metabolism
Metabolism of lipids
Metabolism of vitamins and cofactors
Lipid particle organization
PPARA activates gene expression
Reproduction
Meiosis
Meiotic synapsis
Meiotic recombination
Sperm Motility And Taxes
Immune System
Innate Immune System
Cytokine Signaling in Immune system
Prolactin receptor signaling
Growth hormone receptor signaling
Neutrophil degranulation
Regulation of IFNG signaling
Adaptive Immune System
Antigen processing: Ubiquitination & Proteasome degradation
Inactivation of CSF3 (G-CSF) signaling
Rap1 signaling
DAP12 signaling
Butyrophilin (BTN) family interactions
MHC class II antigen presentation
Vesicle-mediated transport
Membrane Trafficking
Translocation of SLC2A4 (GLUT4) to the plasma membrane
Cargo recognition for clathrin-mediated endocytosis
Golgi Associated Vesicle Biogenesis
Lysosome Vesicle Biogenesis
Endosomal Sorting Complex Required For Transport (ESCRT)
Intra-Golgi traffic
RORA activates gene expression
Muscle contraction
Striated Muscle Contraction
Smooth Muscle Contraction
Electron transport from NADPH to Ferredoxin
Biological oxidations
COX reactions
Cytosolic iron-sulfur cluster assembly
Cellular responses to external stimuli
Cellular responses to stress
HSP90 chaperone cycle for steroid hormone receptors (SHR)
Heme signaling
Response of EIF2AK1 (HRI) to heme deficiency
Programmed Cell Death
Apoptosis
Regulated Necrosis
Pyroptosis
Metabolism of RNA
mRNA Capping
mRNA 3'-end processing
Metabolism of proteins
Surfactant metabolism
Post-translational protein modification
Amyloid fiber formation
Neddylation
Protein methylation
Protein repair
Translation
Mitochondrial protein import
TYSND1 cleaves peroxisomal proteins
Insertion of tail-anchored proteins into the endoplasmic reticulum membrane
Extracellular matrix organization
Transport of small molecules
Miscellaneous transport and binding events
Intracellular oxygen transport
Cellular hexose transport
Signaling by NOTCH
Signaling by WNT
MAPK family signaling cascades
Signaling by Nuclear Receptors
Signaling by Rho GTPases, Miro GTPases and RHOBTB3
RET signaling
Regulation of signaling by NODAL



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



Enrichr https://maayanlab.cloud/Enrichr/

35,596,684 lists analyzed
339,299 terms
172 libraries

Посмотреть огромный список доступных аннотации

Input data

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

Try an example BED file.

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.

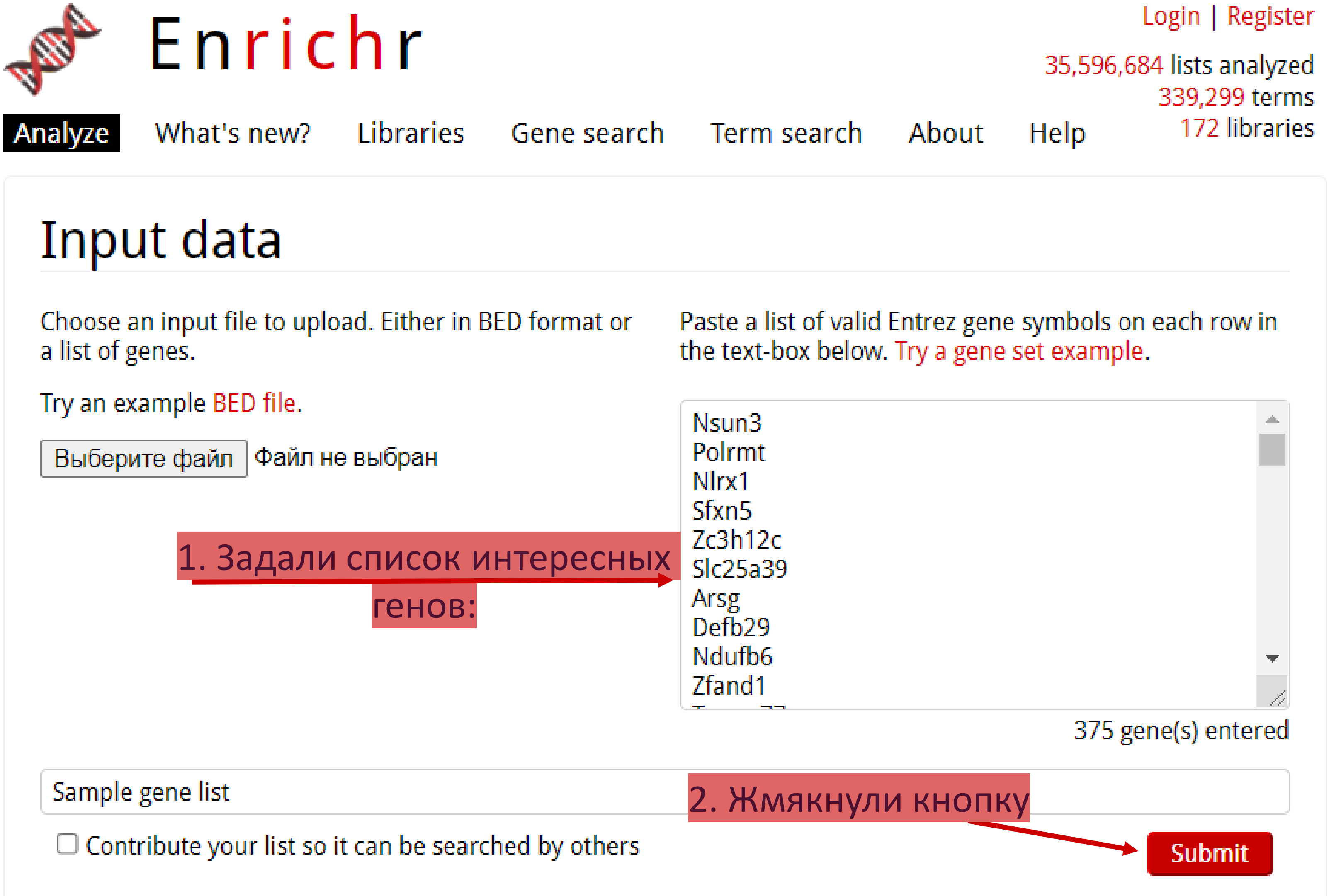
или скопировать гены сюда

! 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



35,596,684 lists analyzed
339,299 terms
172 libraries

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
Nlrx1
Sfxn5
Zc3h12c
Slc25a39
Arsg
Defb29
Ndufb6
Zfand1

375 gene(s) entered

Sample gene list

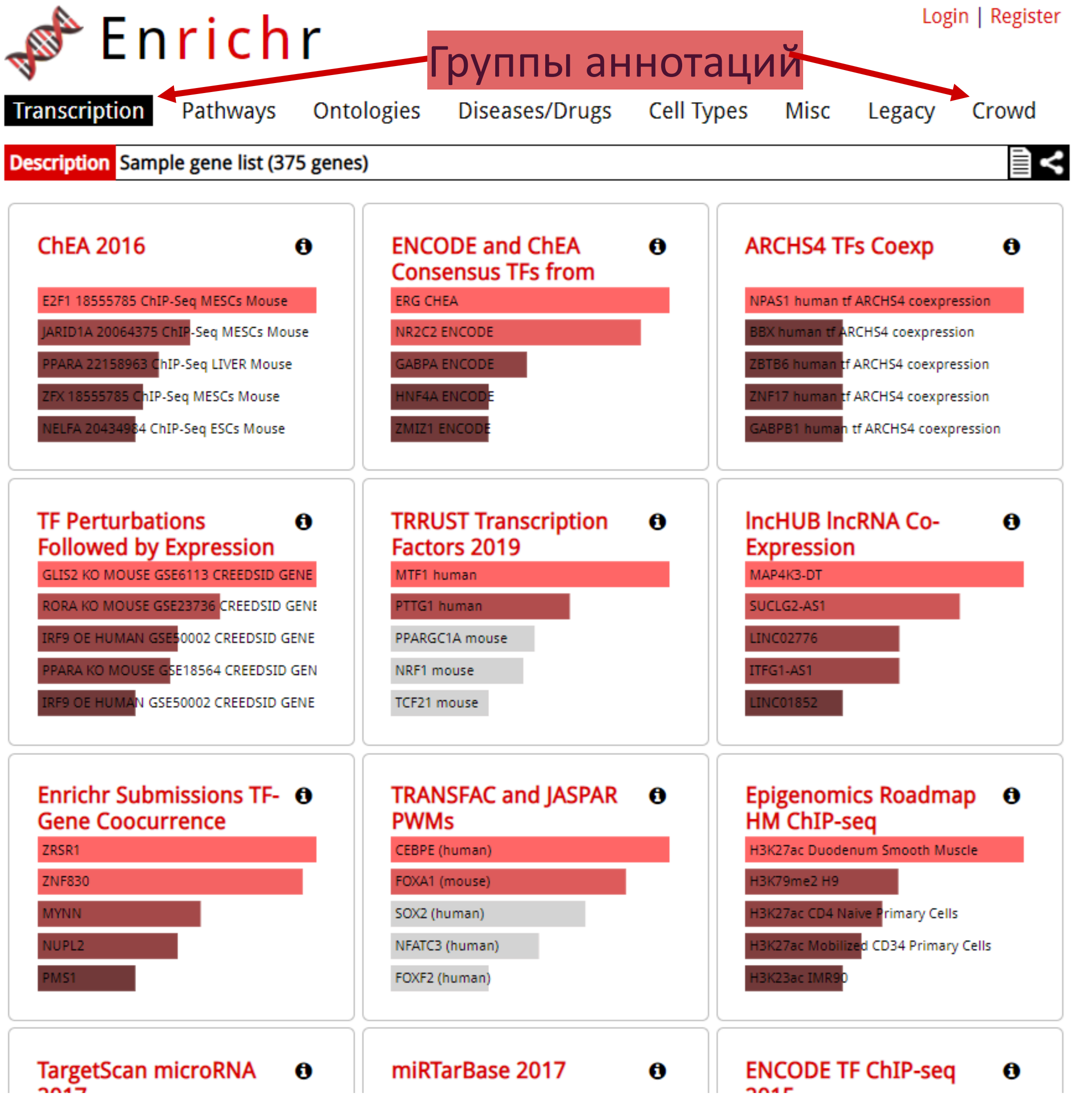
☐ Contribute your list so it can be searched by others

1. Задали список интересных генов:

2. Жмякнули кнопку

Получили результат - радуемся!

Еще больше результатов по разным аннотациям



Группы аннотаций

Sample gene list (375 genes)

ChEA 2016
- E2F1 18555785 ChIP-Seq MESCs Mouse
- JARID1A 20064375 ChIP-Seq MESCs Mouse
- PPARA 22158963 ChIP-Seq LIVER Mouse
- ZFX 18555785 ChIP-Seq MESCs Mouse
- NELFA 20434984 ChIP-Seq ESCs Mouse

ENCODE and ChEA Consensus TFs from
- ERG CHEA
- NR2C2 ENCODE
- GABPA ENCODE
- HNF4A ENCODE
- ZMIZ1 ENCODE

ARCHS4 TFs Coexp
- NPAS1 human tf ARCHS4 coexpression
- BBX human tf ARCHS4 coexpression
- ZBTB6 human tf ARCHS4 coexpression
- ZNF17 human tf ARCHS4 coexpression
- GABPB1 human tf ARCHS4 coexpression

TF Perturbations Followed by Expression
- GLIS2 KO MOUSE GSE6113 CREEDSID GENE
- RORA KO MOUSE GSE23736 CREEDSID GENE
- IRF9 OE HUMAN GSE50002 CREEDSID GENE
- PPARA KO MOUSE GSE18564 CREEDSID GEN
- IRF9 OE HUMAN GSE50002 CREEDSID GENE

TRRUST Transcription Factors 2019
- MTF1 human
- PTTG1 human
- PPARGC1A mouse
- NRF1 mouse
- TCF21 mouse

lncHUB lncRNA Co-Expression
- MAP4K3-DT
- SUCLG2-AS1
- LINC02776
- ITFG1-AS1
- LINC01852

Enrichr Submissions TF-Gene Coocurrence
- ZRSR1
- ZNF830
- MYNN
- NUPL2
- PMS1

TRANSFAC and JASPAR PWMs
- CEBPE (human)
- FOXA1 (mouse)
- SOX2 (human)
- NFATC3 (human)
- FOXF2 (human)

Epigenomics Roadmap HM ChIP-seq
- H3K27ac Duodenum Smooth Muscle
- H3K79me2 H9
- H3K27ac CD4 Naive Primary Cells
- H3K27ac Mobilized CD34 Primary Cells
- H3K23ac IMR90

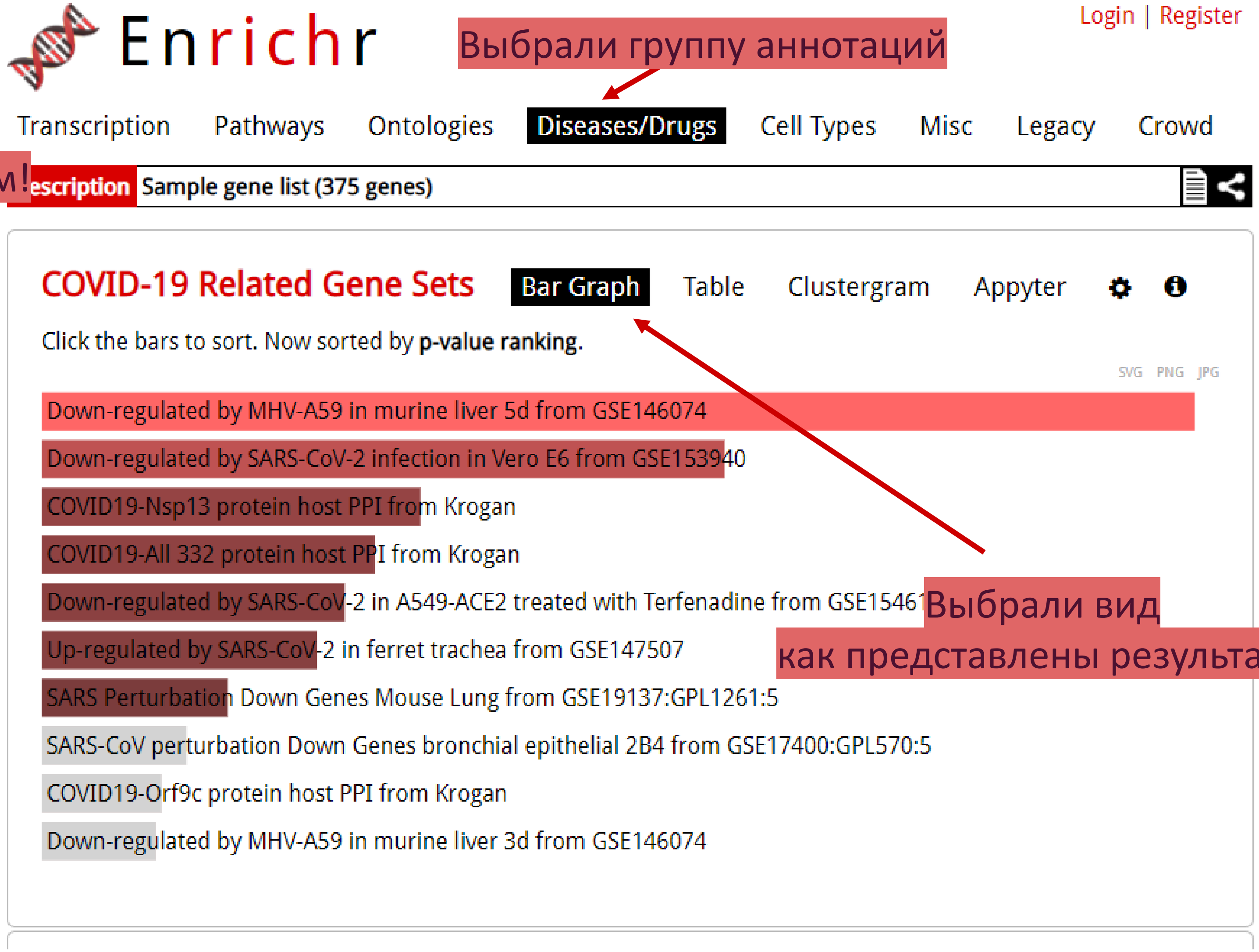
TargetScan microRNA

miRTarBase 2017

ENCODE TF ChIP-seq

Выбрали группу аннотаций

Изучили результаты
о нужным аннотациям!



escription Sample gene list (375 genes)

COVID-19 Related Gene Sets

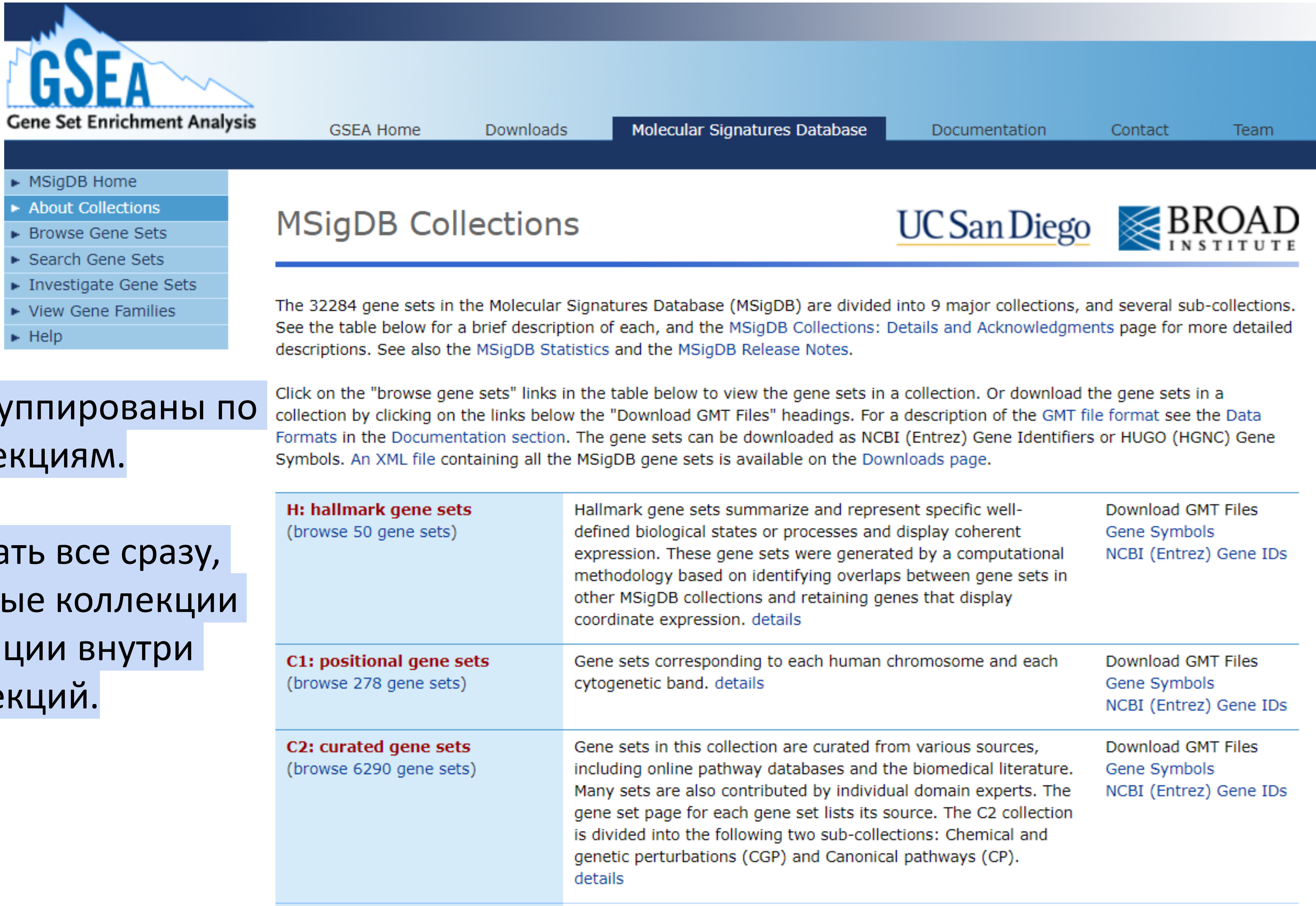
Click the bars to sort. Now sorted by **p-value ranking**.

- 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 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.

H: hallmark gene sets (browse 50 gene sets)	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	Download GMT Files Gene Symbols NCBI (Entrez) Gene IDs
C1: positional gene sets (browse 278 gene sets)	Gene sets corresponding to each human chromosome and each cytogenetic band. details	Download GMT Files Gene Symbols NCBI (Entrez) Gene IDs
C2: curated gene sets (browse 6290 gene sets)	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	Download GMT Files Gene Symbols NCBI (Entrez) Gene IDs

Аннотации сгруппированы по 9 коллекциям.

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

http://www.gsea-msigdb.org/gsea/msigdb/collections.jsp

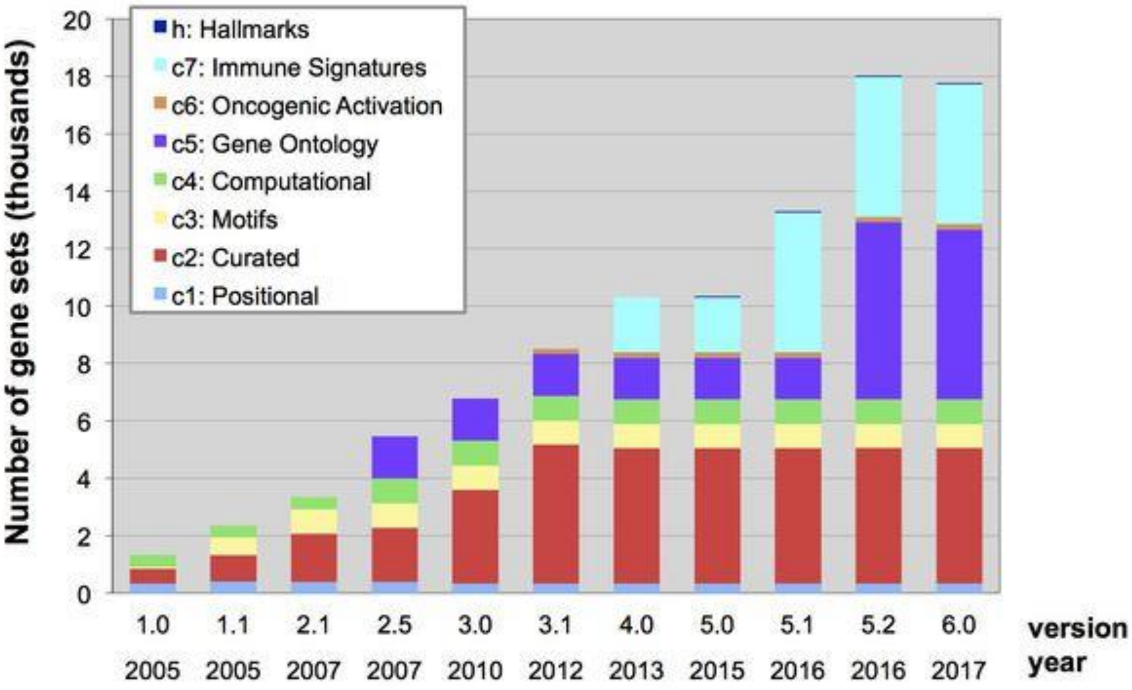
Коллекции включают в себя и широко известные GO, KEGG, Reactome…
так и более специализированные коллекции:

- связанные с иммунной

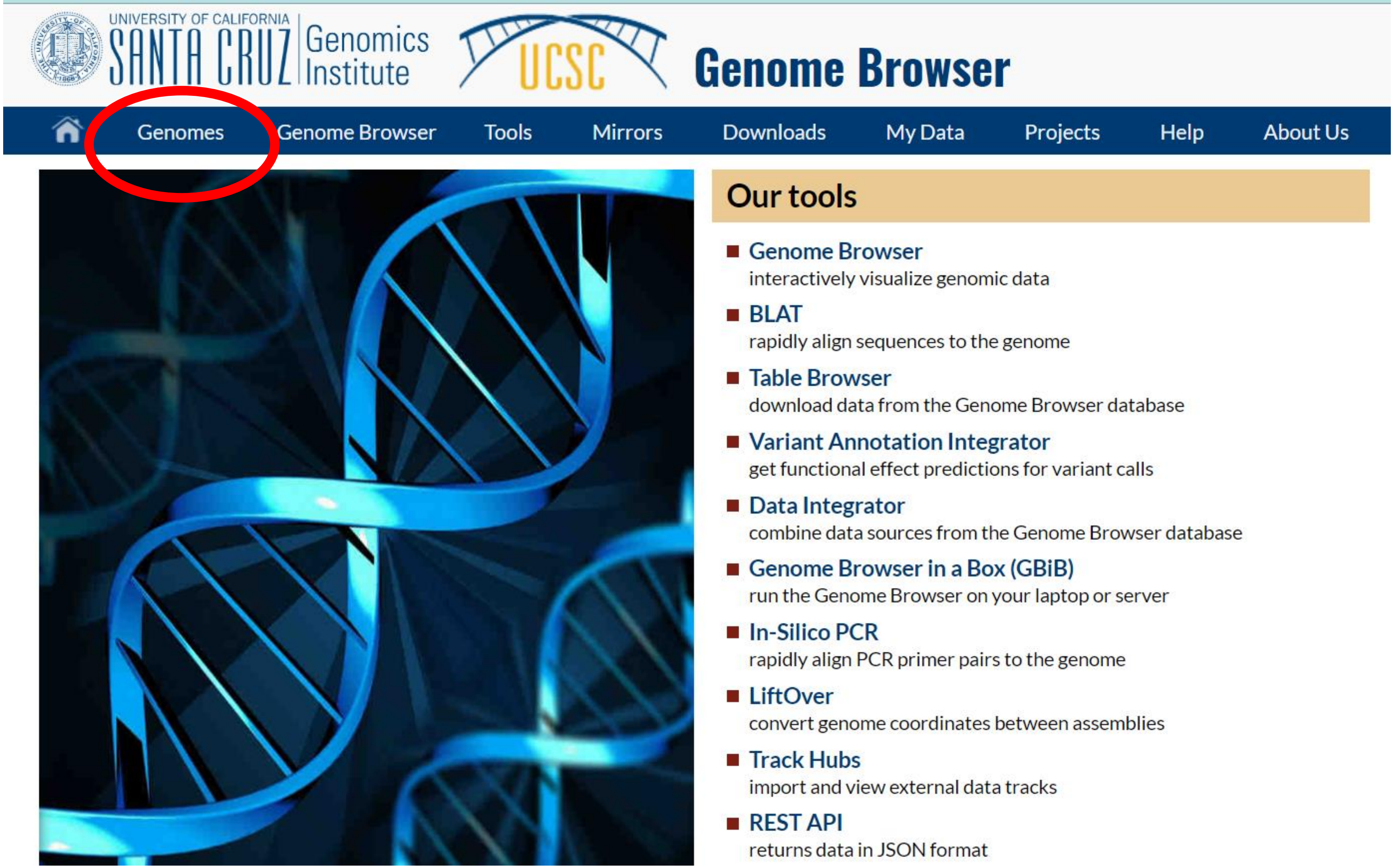
Есть и маркеры клеточных типов, собранные по нескольким scRNA-seq публикациям.

На этом же сайте можно скачать ПО для GSEA анализа.

Так же можно использовать веб-сервис https://www.genepattern.org/



https://genome.ucsc.edu/



Our tools

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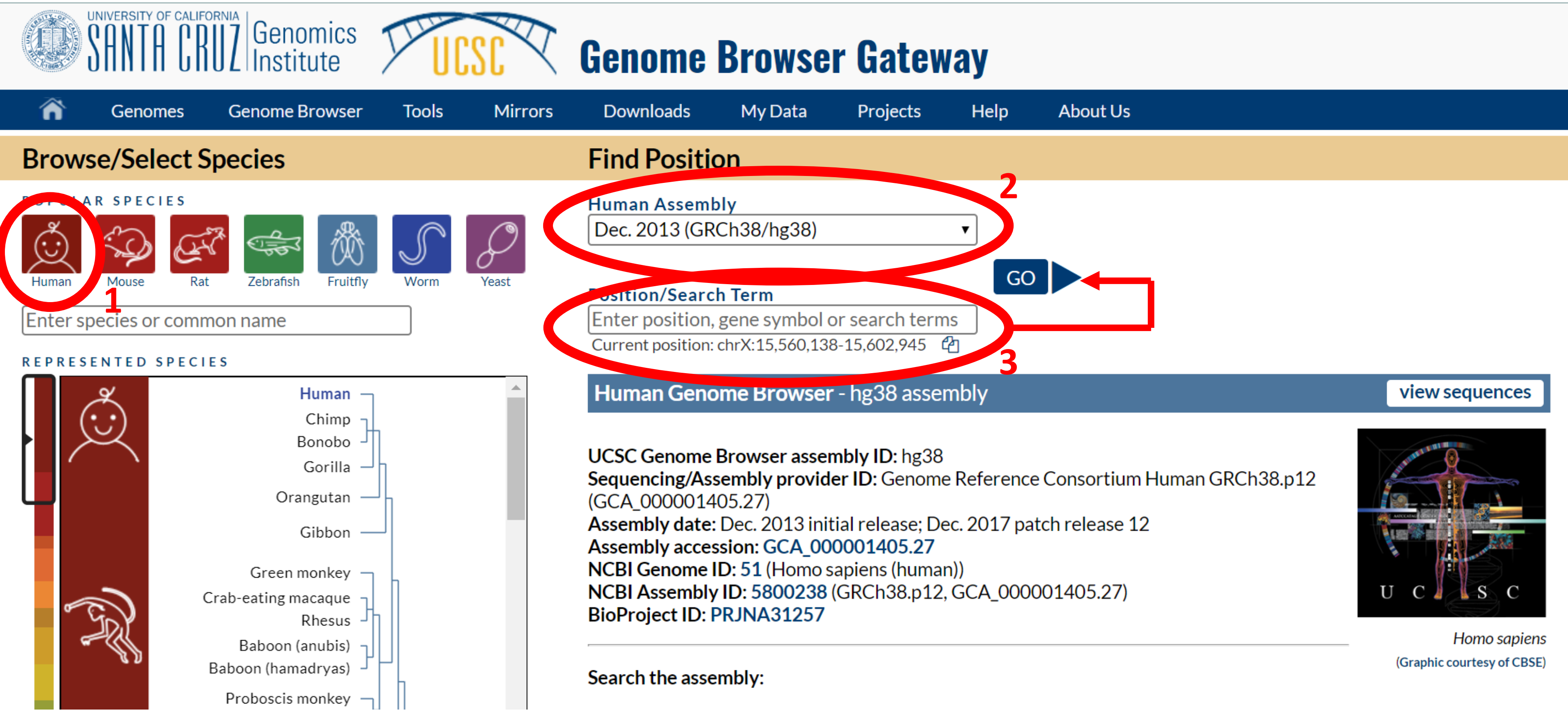


Browse/Select Species

Enter species or common name

Find Position

Human Assembly: Dec. 2013 (GRCh38/hg38)

Position/Search Term: Enter position, gene symbol or search terms

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

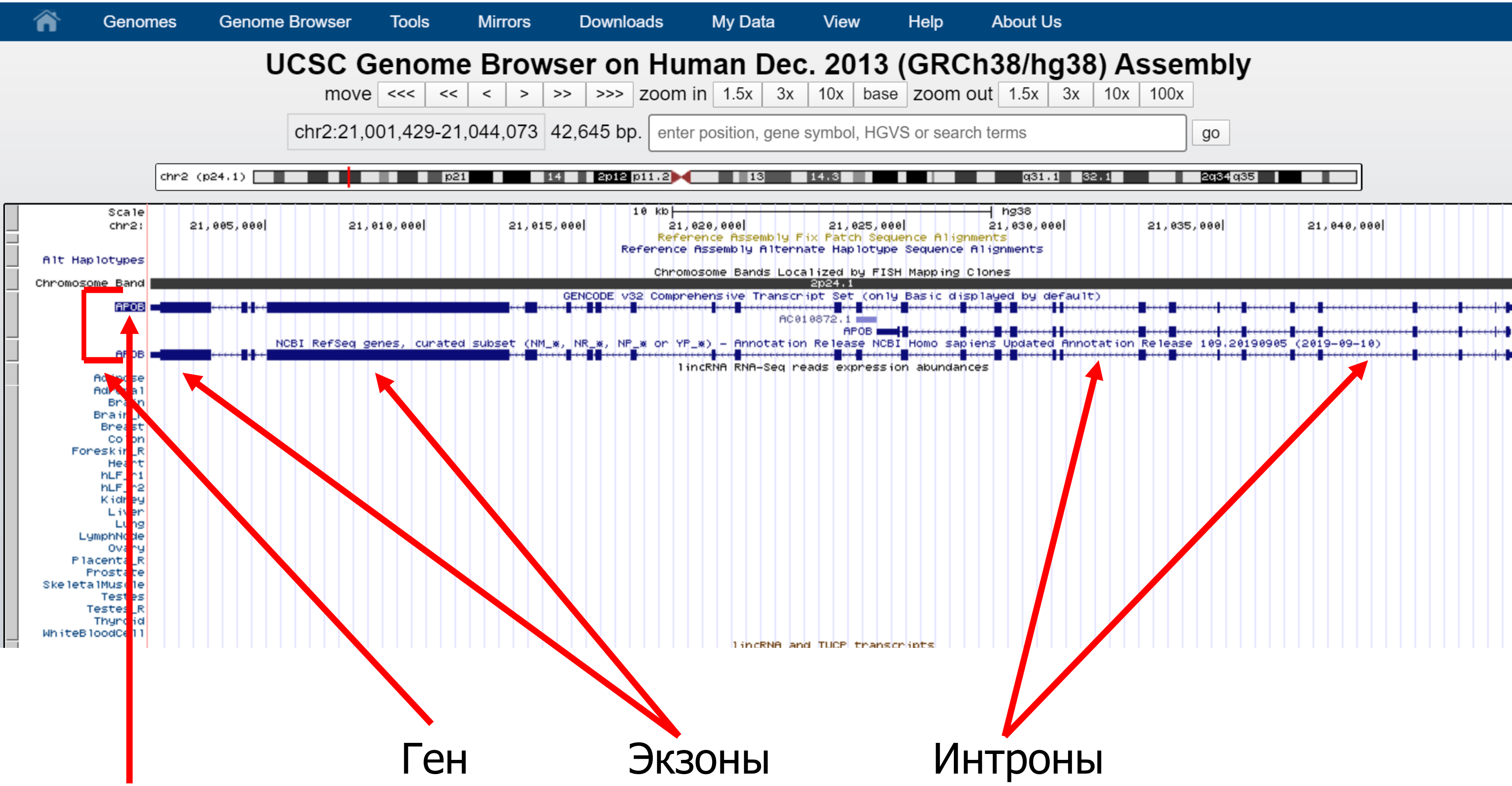
Human Genome Browser - hg38 assembly

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

chr2:21,001,429-21,044,073 42,645 bp.

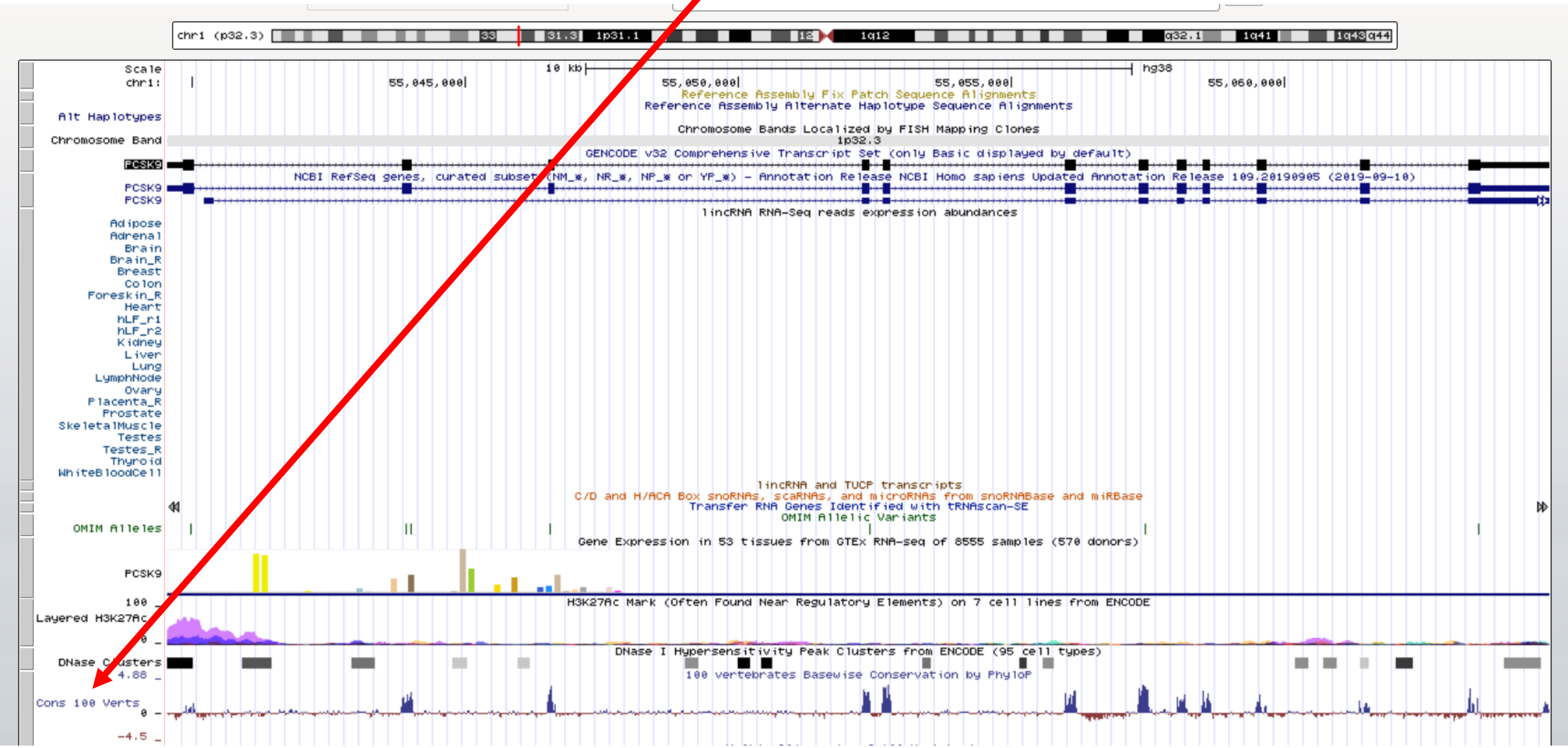
Ген

Экзоны

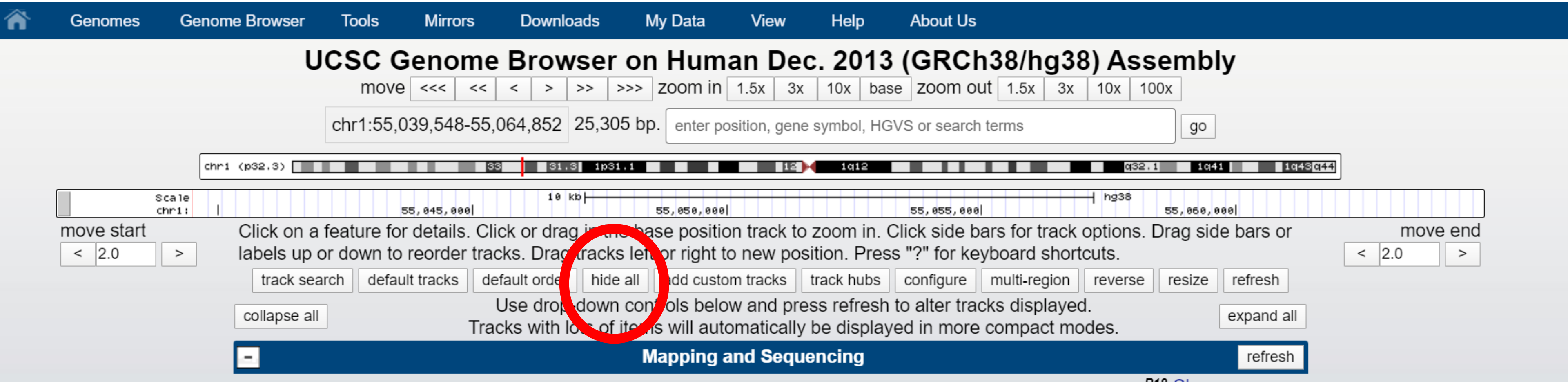
Интроны

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

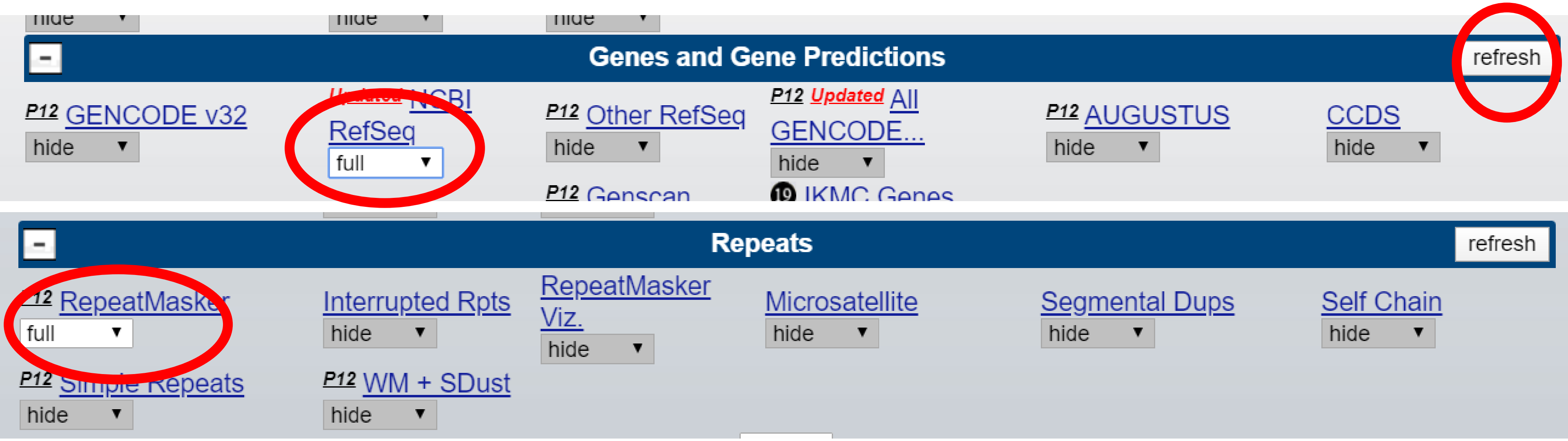
chr1:55,039,548-55,064,852 25,305 bp.

enter position, gene symbol, HGVS or search terms

Click on a feature for details. Click or drag in the base position track to zoom in. Click side bars for track options. Drag side bars or labels up or down to reorder tracks. Drag tracks left or right to new position. Press "?" for keyboard shortcuts.

Use drop down controls below and press refresh to alter tracks displayed. Tracks with lots of items will automatically be displayed in more compact modes.

Открыть только некоторые



P12 GENCODE v32: hide

Updated NCBI RefSeq: full

P12 Other RefSeq: hide

P12 Updated All GENCODE...: hide

P12 AUGUSTUS: hide

CCDS: hide

P12 Genscan

IKMC Genes

P12 RepeatMasker: full

Interrupted Rpts: hide

RepeatMasker Viz.: hide

Microsatellite: hide

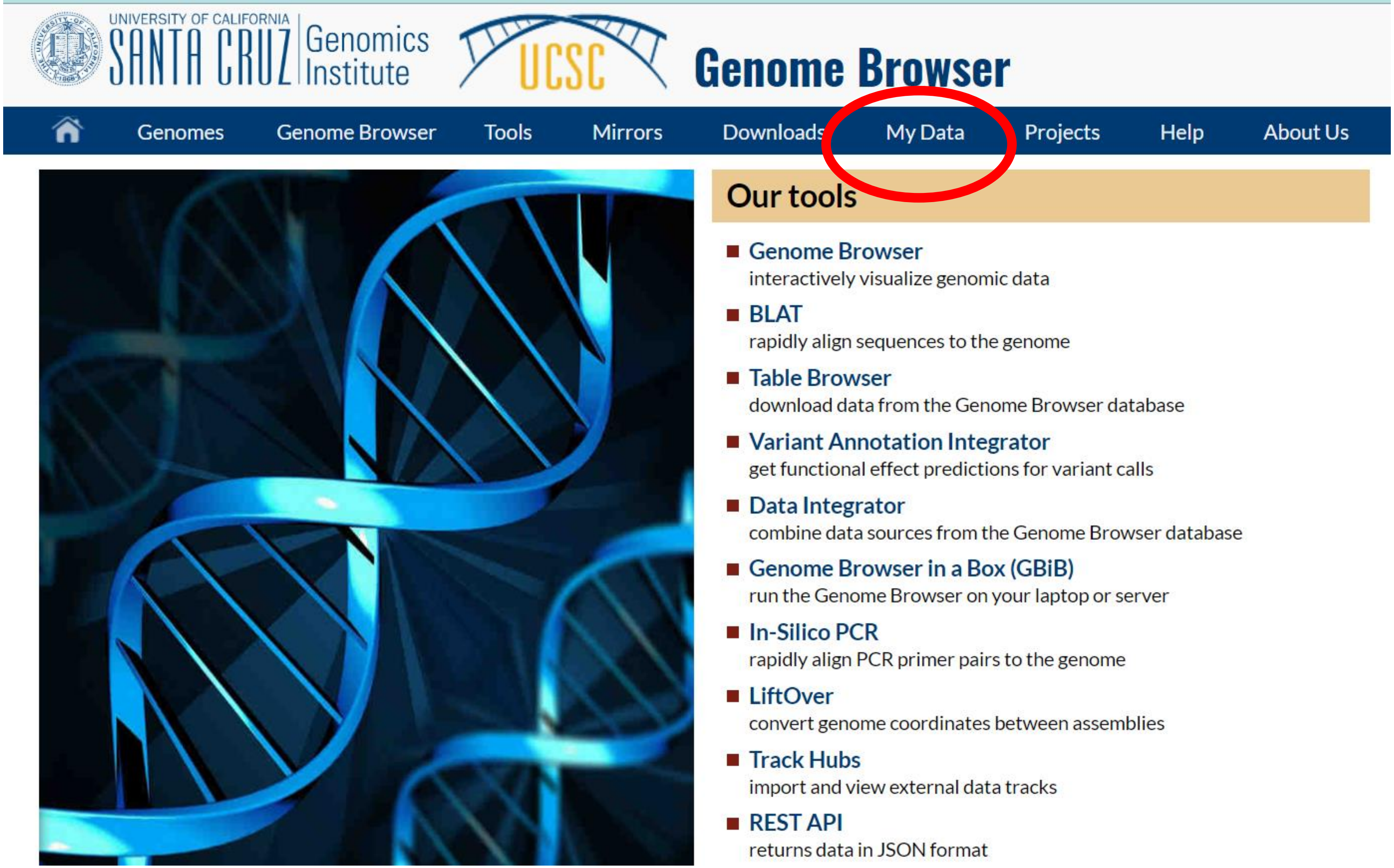
Segmental Dups: hide

Self Chain: hide

P12 Simple Repeats: hide

P12 WM + SDust: hide

https://genome.ucsc.edu/



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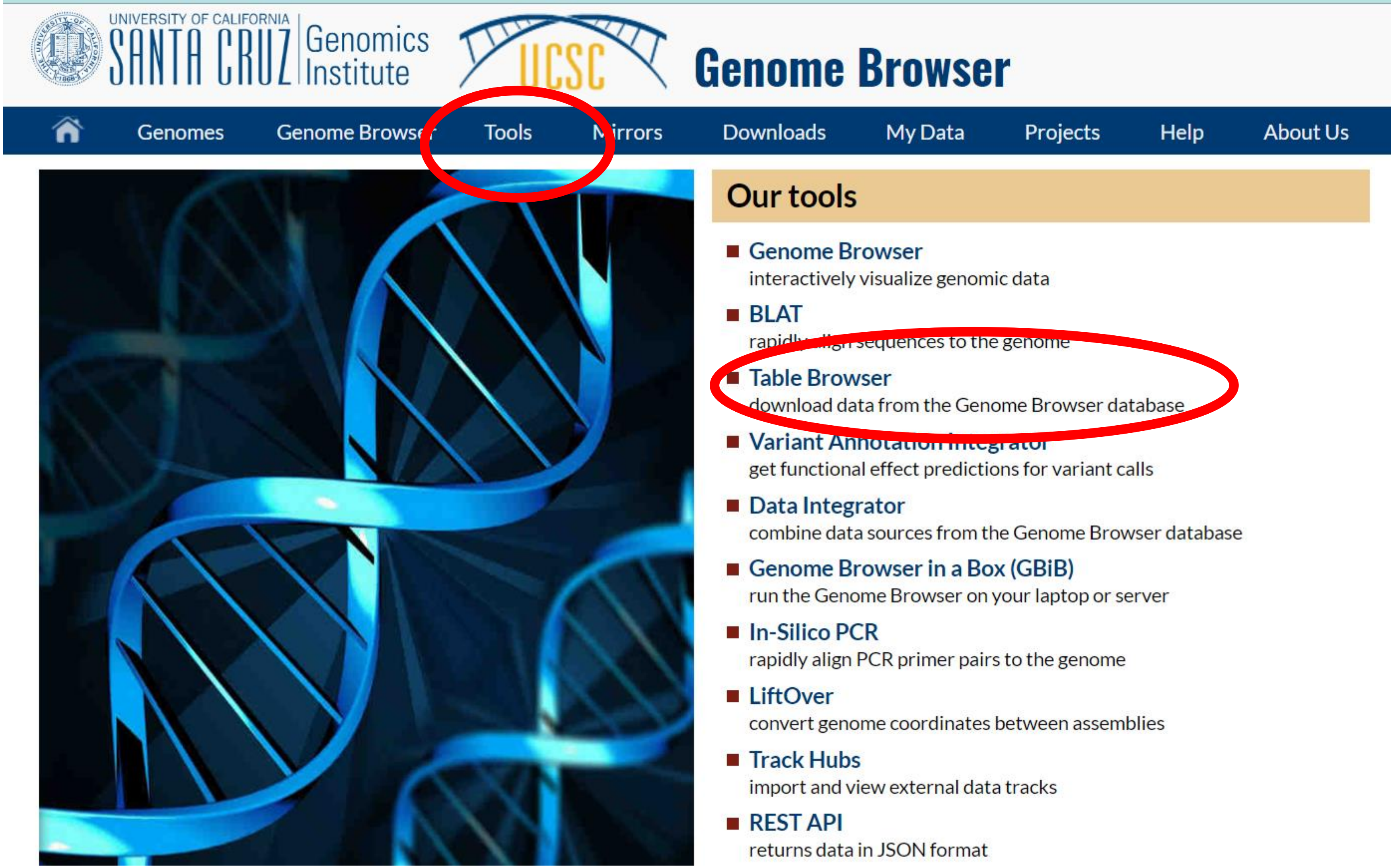
https://genome.ucsc.edu/



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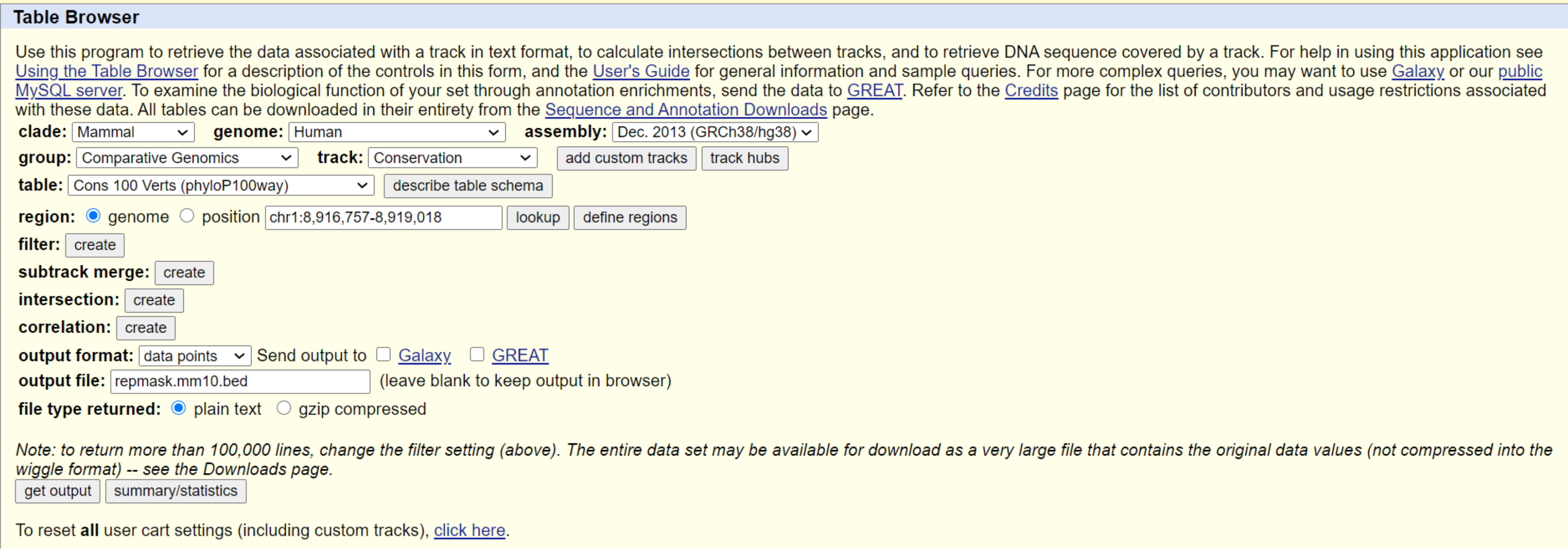


Table Browser

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: Mammal **genome:** Human **assembly:** Dec. 2013 (GRCh38/hg38)

group: Comparative Genomics **track:** Conservation

table: Cons 100 Verts (phyloP100way)

region: ● genome ○ position chr1:8,916,757-8,919,018

filter:

subtrack merge:

intersection:

correlation:

output format: data points Send output to ☐ Galaxy ☐ GREAT

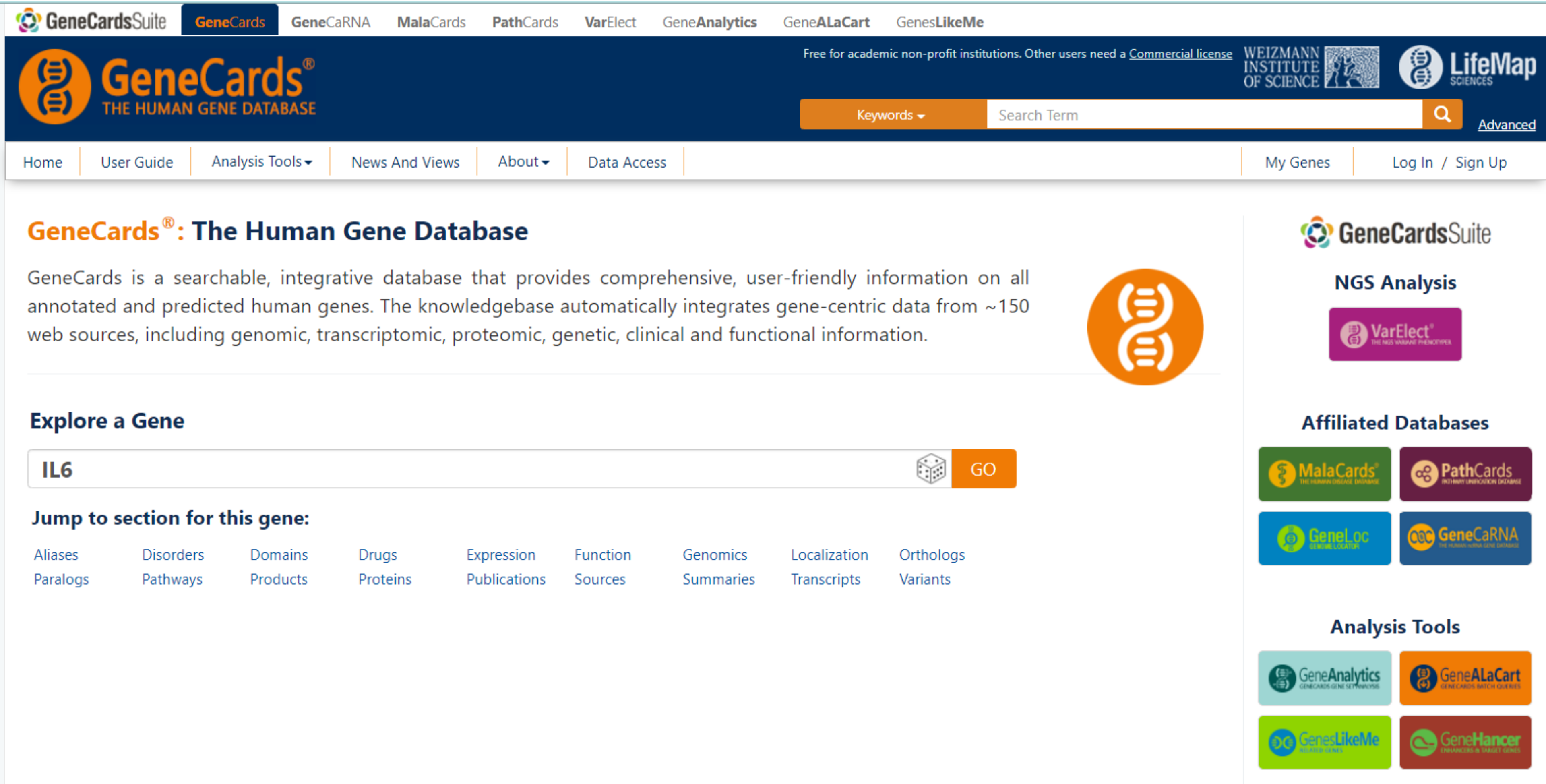
output file: repmask.mm10.bed (leave blank to keep output in browser)

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.

https://www.genecards.org/



Free for academic non-profit institutions. Other users need a Commercial license

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

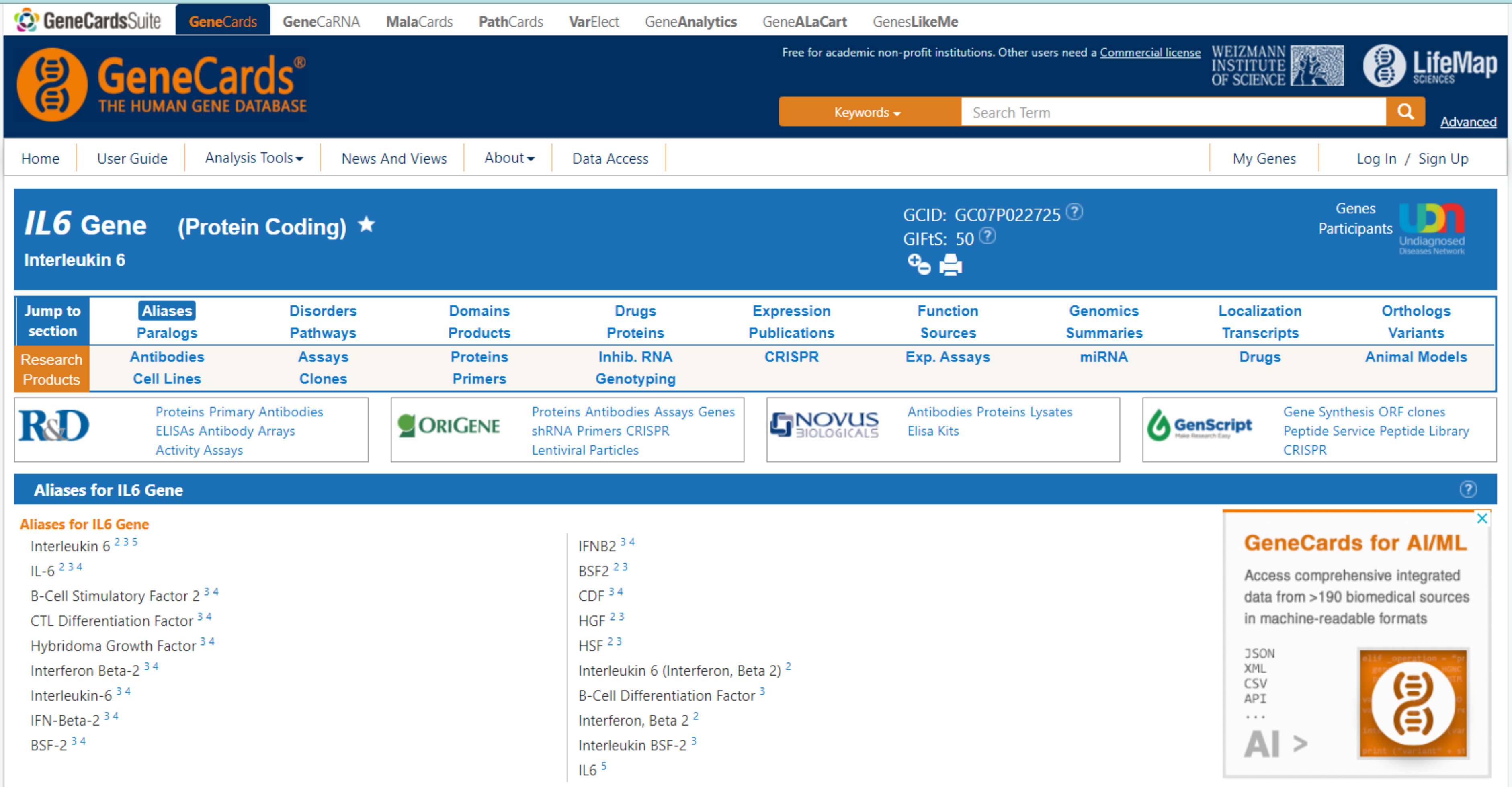
Jump to section for this gene:

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

NGS Analysis

Affiliated Databases

Analysis Tools



IL6 Gene (Protein Coding) ★

Interleukin 6

GCID: GC07P022725

GIFtS: 50

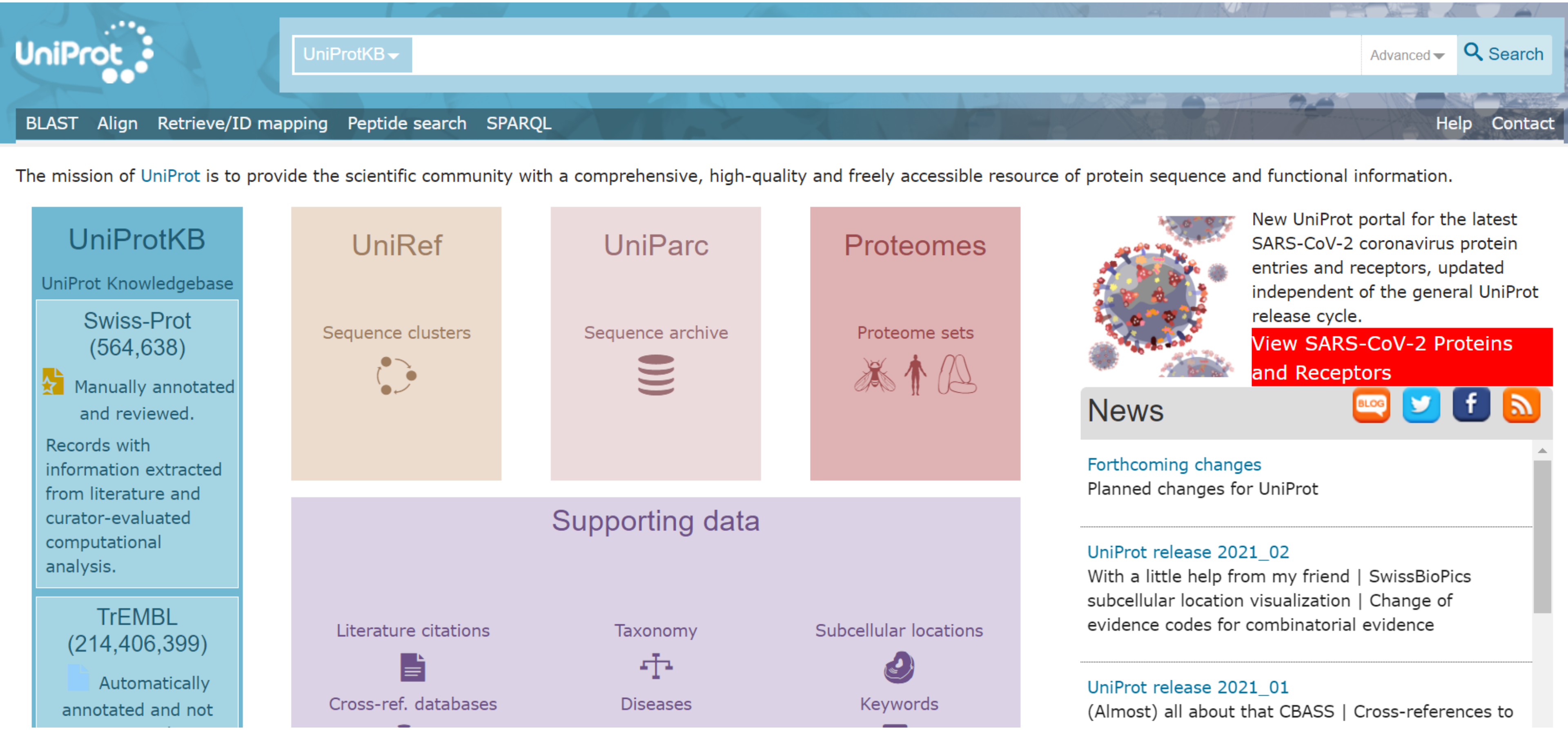
Aliases for IL6 Gene

Aliases for IL6 Gene

Interleukin 6 [2,3,5]
IL-6 [2,3,4]
B-Cell Stimulatory Factor 2 [3,4]
CTL Differentiation Factor [3,4]
Hybridoma Growth Factor [3,4]
Interferon Beta-2 [3,4]
Interleukin-6 [3,4]
IFN-Beta-2 [3,4]
BSF-2 [3,4]

IFNB2 [3,4]
BSF2 [2,3]
CDF [3,4]
HGF [2,3]
HSF [2,3]
Interleukin 6 (Interferon, Beta 2) [2]
B-Cell Differentiation Factor [3]
Interferon, Beta 2 [2]
Interleukin BSF-2 [3]
IL6 [5]

https://www.uniprot.org/



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

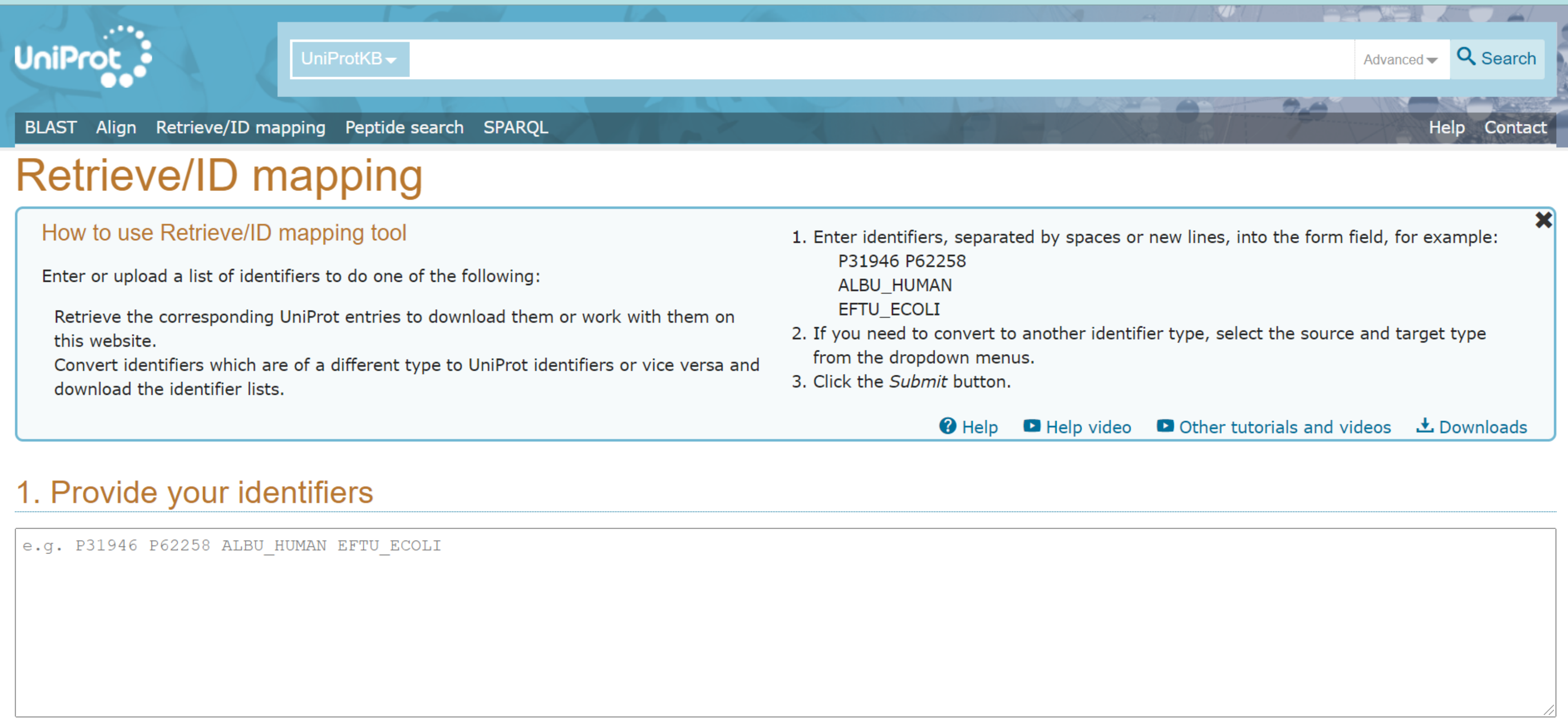
Planned changes for UniProt

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

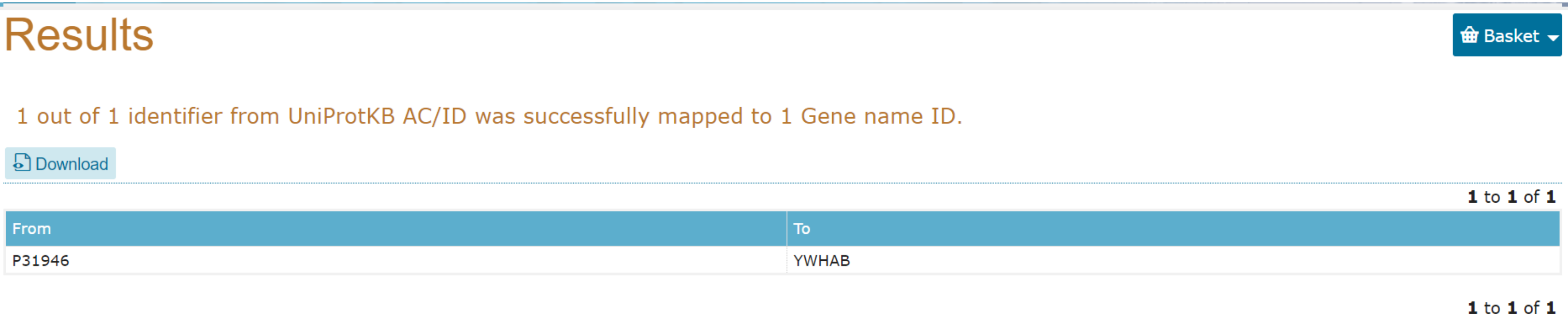
Enter or upload a list of identifiers to do one of the following:

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.

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.

1 to **1** of **1**

From	To
P31946	YWHAB

1 to **1** of **1**