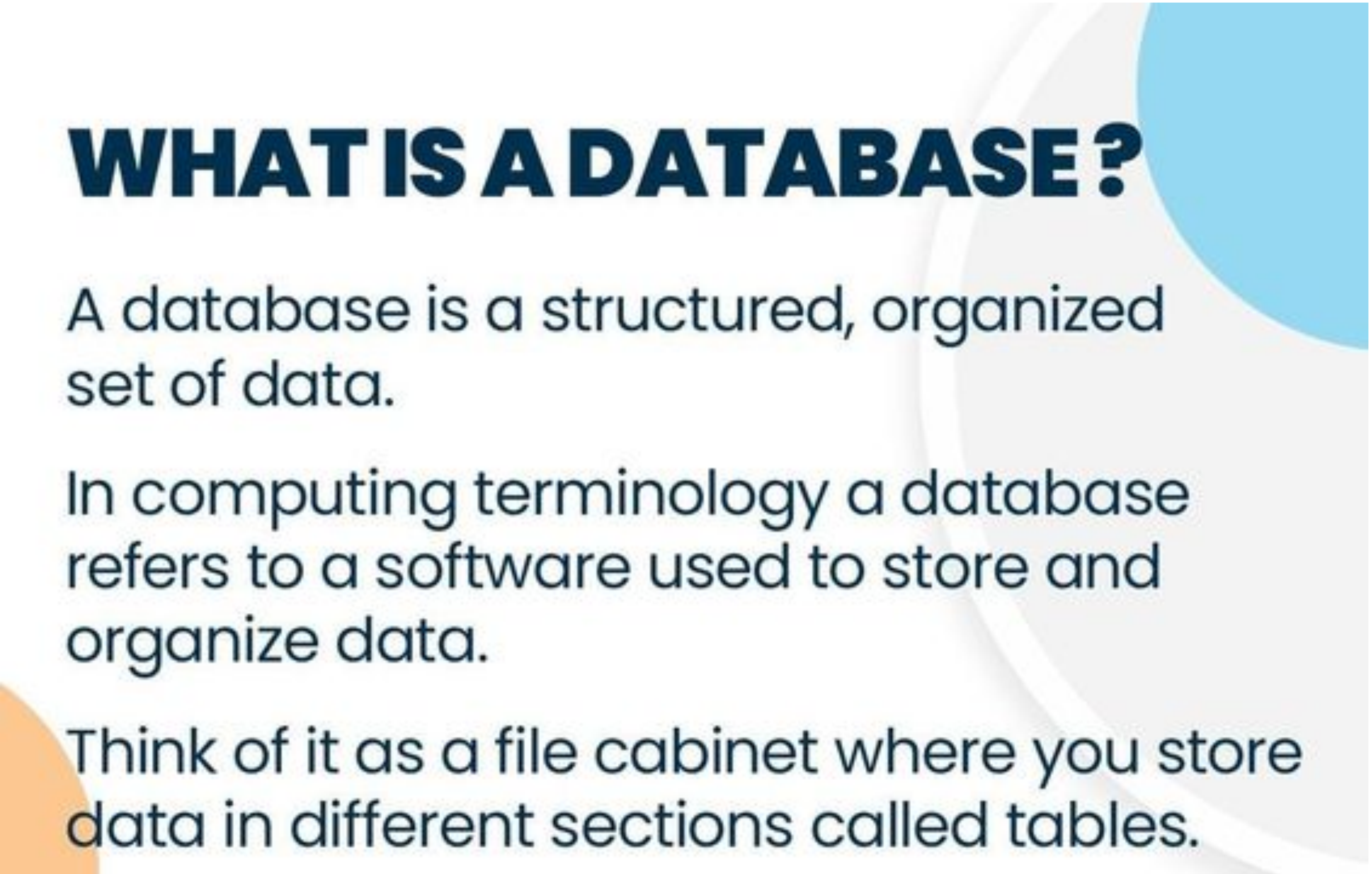
Databases

2025-03-24



WHAT IS A DATABASE?

A database is a structured, organized set of data.

In computing terminology a database refers to a software used to store and organize data.

Think of it as a file cabinet where you store data in different sections called tables.

Guess how many biological databases exist worldwide

We can find the answer in…

Database Commons

a catalog of worldwide biological databases

2024

Data Statistics

6389 DATABASES	13 CATEGORIES	1647 SPECIES
9872 PUBLICATIONS	2141 INSTITUTIONS	76 COUNTRIES / REGIONS

2025

Data Statistics

6952 DATABASES	13 CATEGORIES	1737 SPECIES
10434 PUBLICATIONS	2309 INSTITUTIONS	80 COUNTRIES / REGIONS

https://ngdc.cncb.ac.cn/databasecommons/

We can find the answer in…

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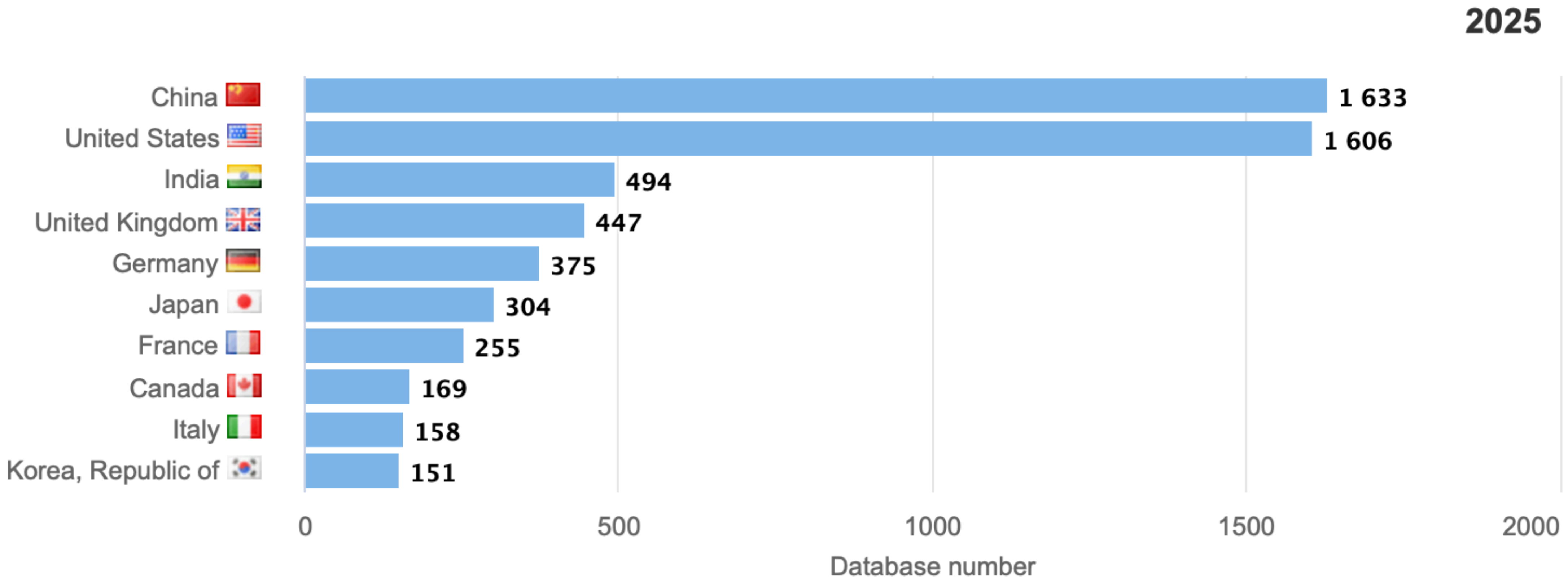
a catalog of worldwide biological databases



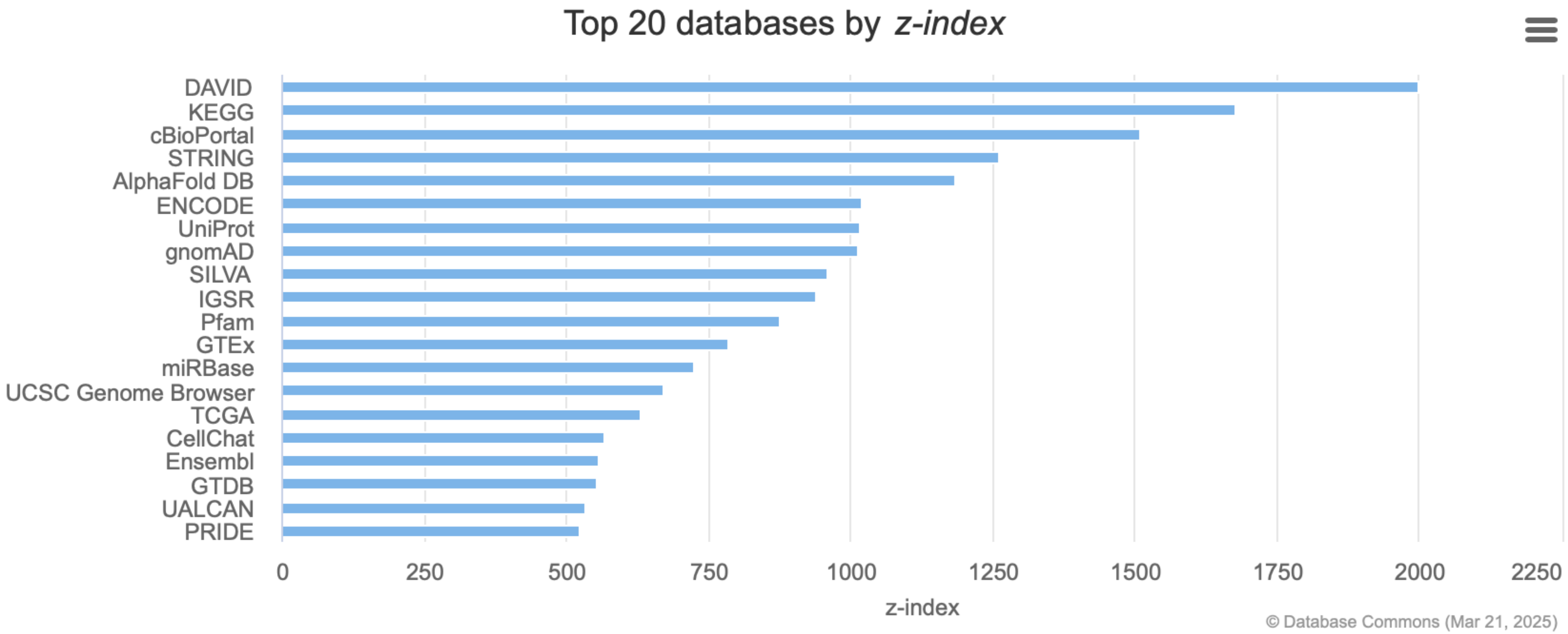
© Database Commons (Mar 21, 2025)
National Genomics Data Center

https://ngdc.cncb.ac.cn/databasecommons/

We can find the answer in…

Database Commons

a catalog of worldwide biological databases


Top 20 databases by *z-index*

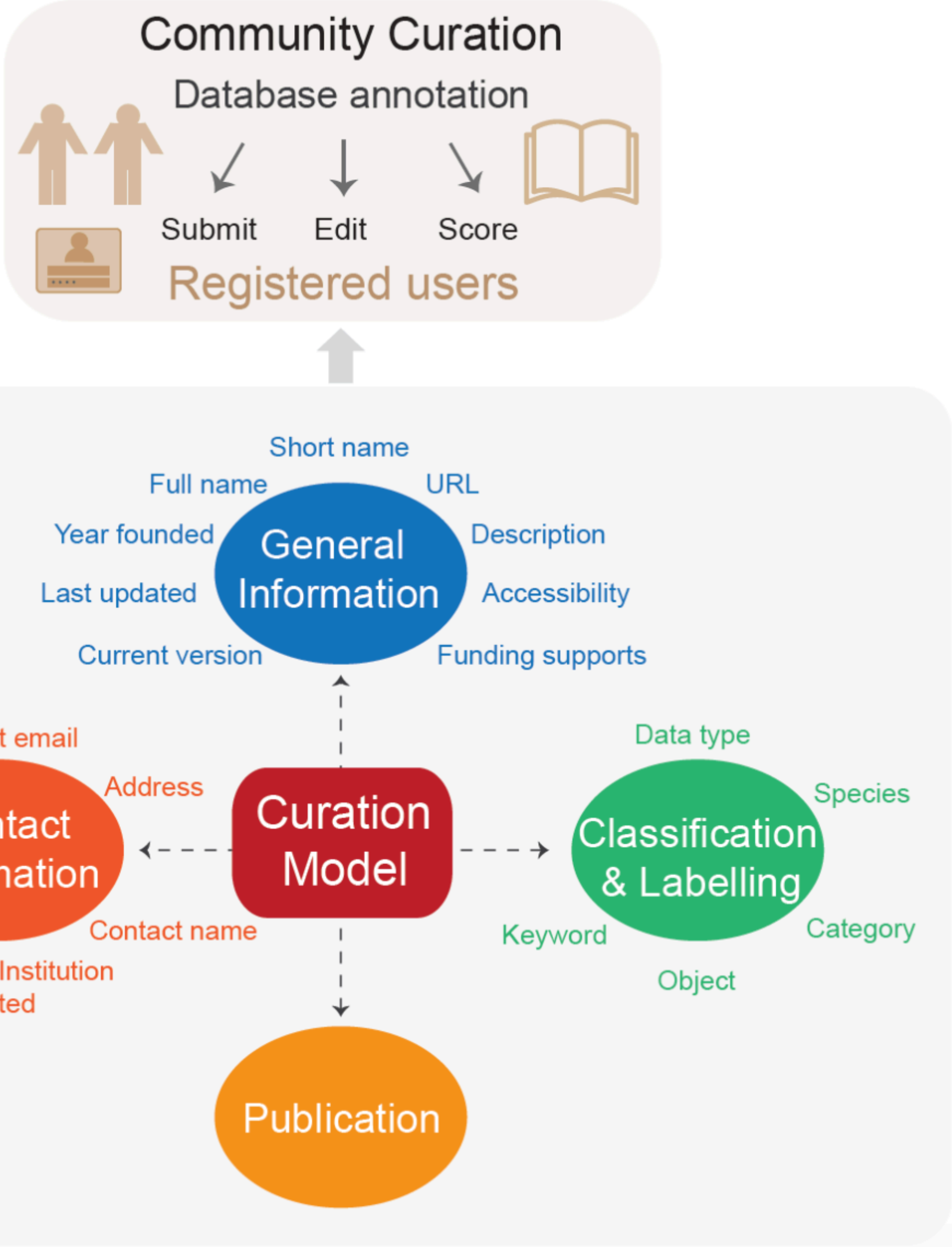
© Database Commons (Mar 21, 2025)
National Genomics Data Center

Z-index: Number of citations/Database age

https://ngdc.cncb.ac.cn/databasecommons/

Database Commons

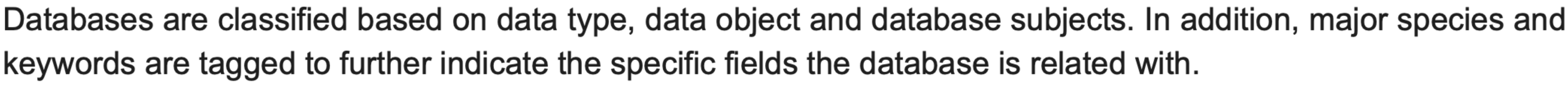
How it works



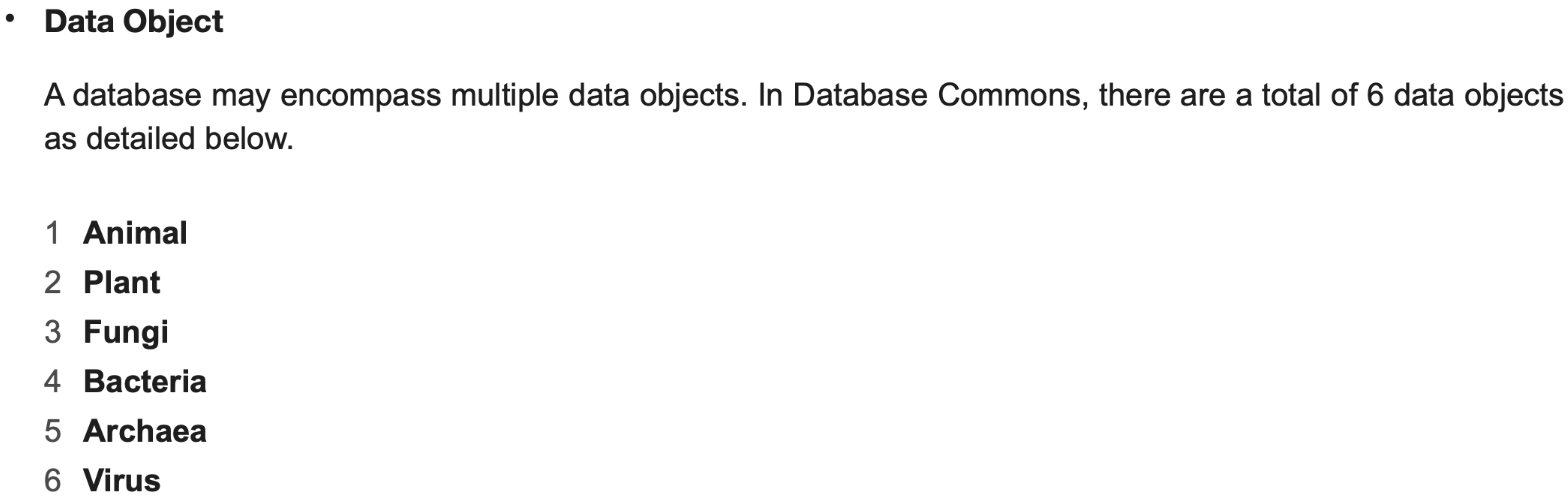
https://ngdc.cncb.ac.cn/databasecommons/

Database Commons

Classification and labelling



Databases are classified based on data type, data object and database subjects. In addition, major species and keywords are tagged to further indicate the specific fields the database is related with.



- **Data Object**

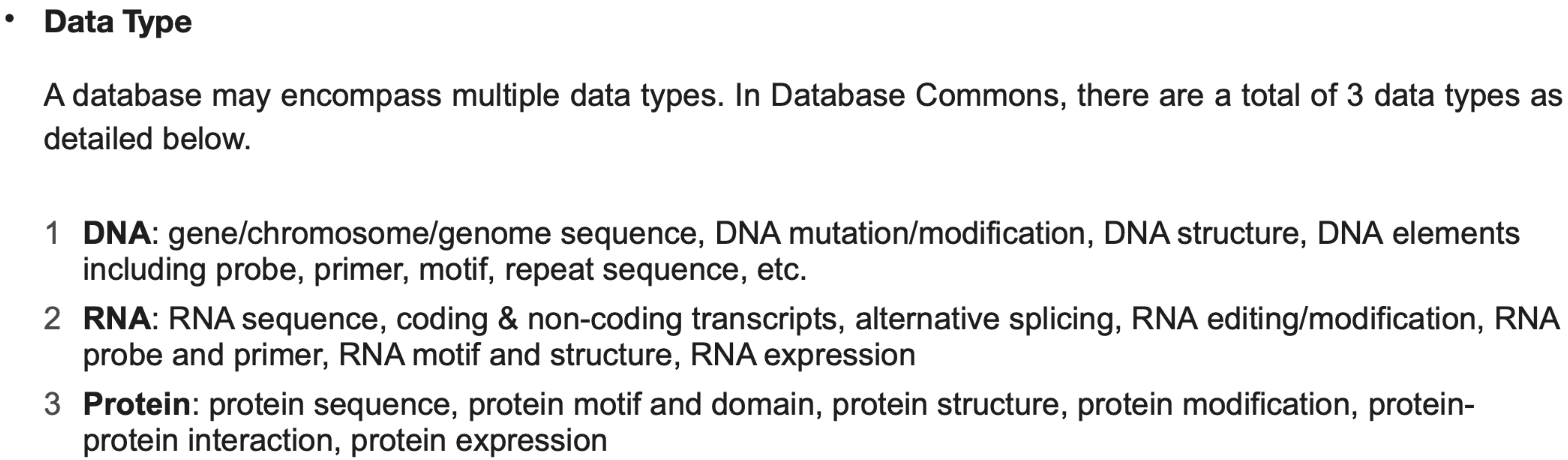
  A database may encompass multiple data objects. In Database Commons, there are a total of 6 data objects as detailed below.

  1. **Animal**
  2. **Plant**
  3. **Fungi**
  4. **Bacteria**
  5. **Archaea**
  6. **Virus**

https://ngdc.cncb.ac.cn/databasecommons/

Database Commons

Classification and labelling



- **Data Type**

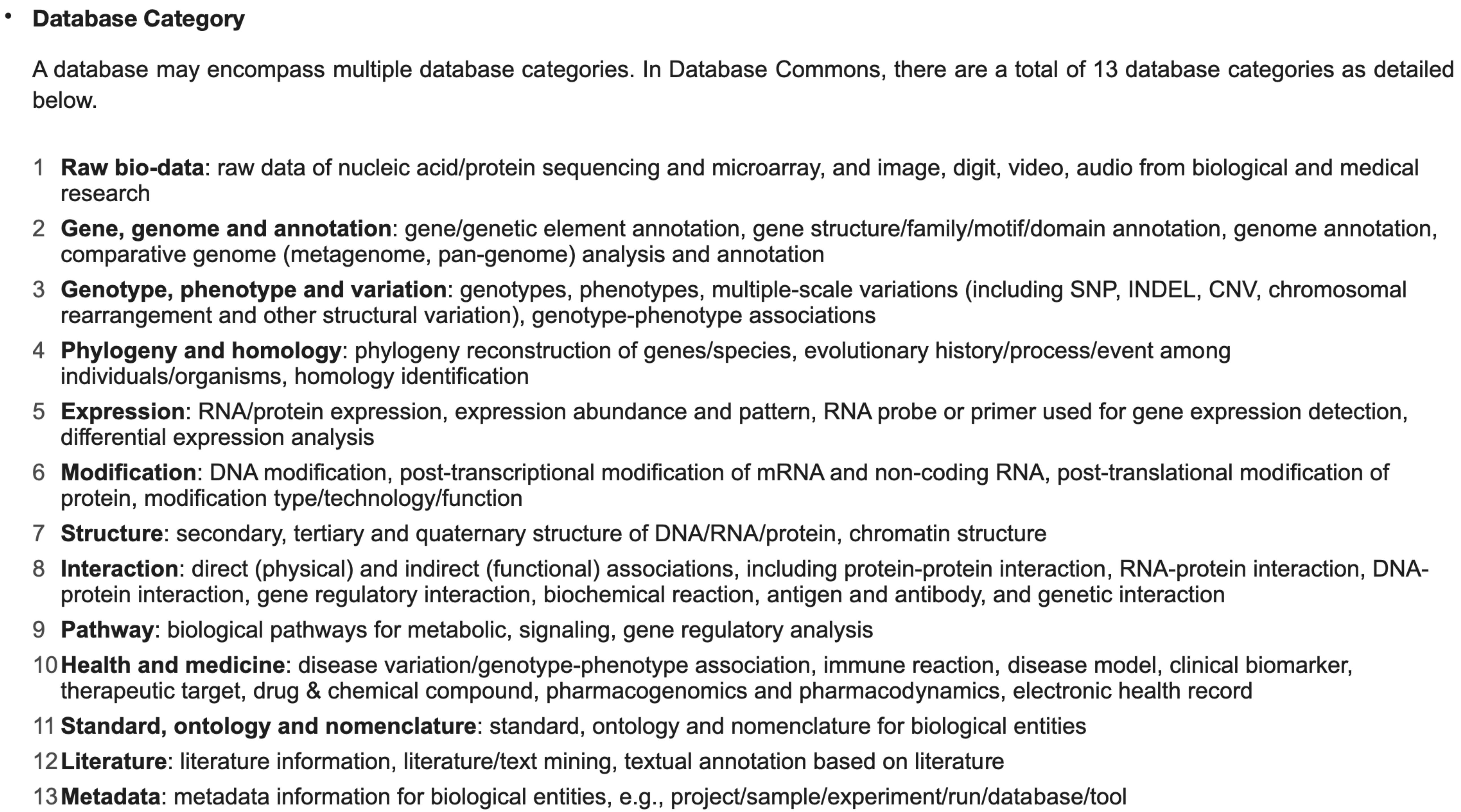
  A database may encompass multiple data types. In Database Commons, there are a total of 3 data types as detailed below.

  1. **DNA**: gene/chromosome/genome sequence, DNA mutation/modification, DNA structure, DNA elements including probe, primer, motif, repeat sequence, etc.
  2. **RNA**: RNA sequence, coding & non-coding transcripts, alternative splicing, RNA editing/modification, RNA probe and primer, RNA motif and structure, RNA expression
  3. **Protein**: protein sequence, protein motif and domain, protein structure, protein modification, protein-protein interaction, protein expression

https://ngdc.cncb.ac.cn/databasecommons/

Database Commons

Classification and labelling



- **Database Category**

A database may encompass multiple database categories. In Database Commons, there are a total of 13 database categories as detailed below.

1. **Raw bio-data**: raw data of nucleic acid/protein sequencing and microarray, and image, digit, video, audio from biological and medical research
2. **Gene, genome and annotation**: gene/genetic element annotation, gene structure/family/motif/domain annotation, genome annotation, comparative genome (metagenome, pan-genome) analysis and annotation
3. **Genotype, phenotype and variation**: genotypes, phenotypes, multiple-scale variations (including SNP, INDEL, CNV, chromosomal rearrangement and other structural variation), genotype-phenotype associations
4. **Phylogeny and homology**: phylogeny reconstruction of genes/species, evolutionary history/process/event among individuals/organisms, homology identification
5. **Expression**: RNA/protein expression, expression abundance and pattern, RNA probe or primer used for gene expression detection, differential expression analysis
6. **Modification**: DNA modification, post-transcriptional modification of mRNA and non-coding RNA, post-translational modification of protein, modification type/technology/function
7. **Structure**: secondary, tertiary and quaternary structure of DNA/RNA/protein, chromatin structure
8. **Interaction**: direct (physical) and indirect (functional) associations, including protein-protein interaction, RNA-protein interaction, DNA-protein interaction, gene regulatory interaction, biochemical reaction, antigen and antibody, and genetic interaction
9. **Pathway**: biological pathways for metabolic, signaling, gene regulatory analysis
10. **Health and medicine**: disease variation/genotype-phenotype association, immune reaction, disease model, clinical biomarker, therapeutic target, drug & chemical compound, pharmacogenomics and pharmacodynamics, electronic health record
11. **Standard, ontology and nomenclature**: standard, ontology and nomenclature for biological entities
12. **Literature**: literature information, literature/text mining, textual annotation based on literature
13. **Metadata**: metadata information for biological entities, e.g., project/sample/experiment/run/database/tool

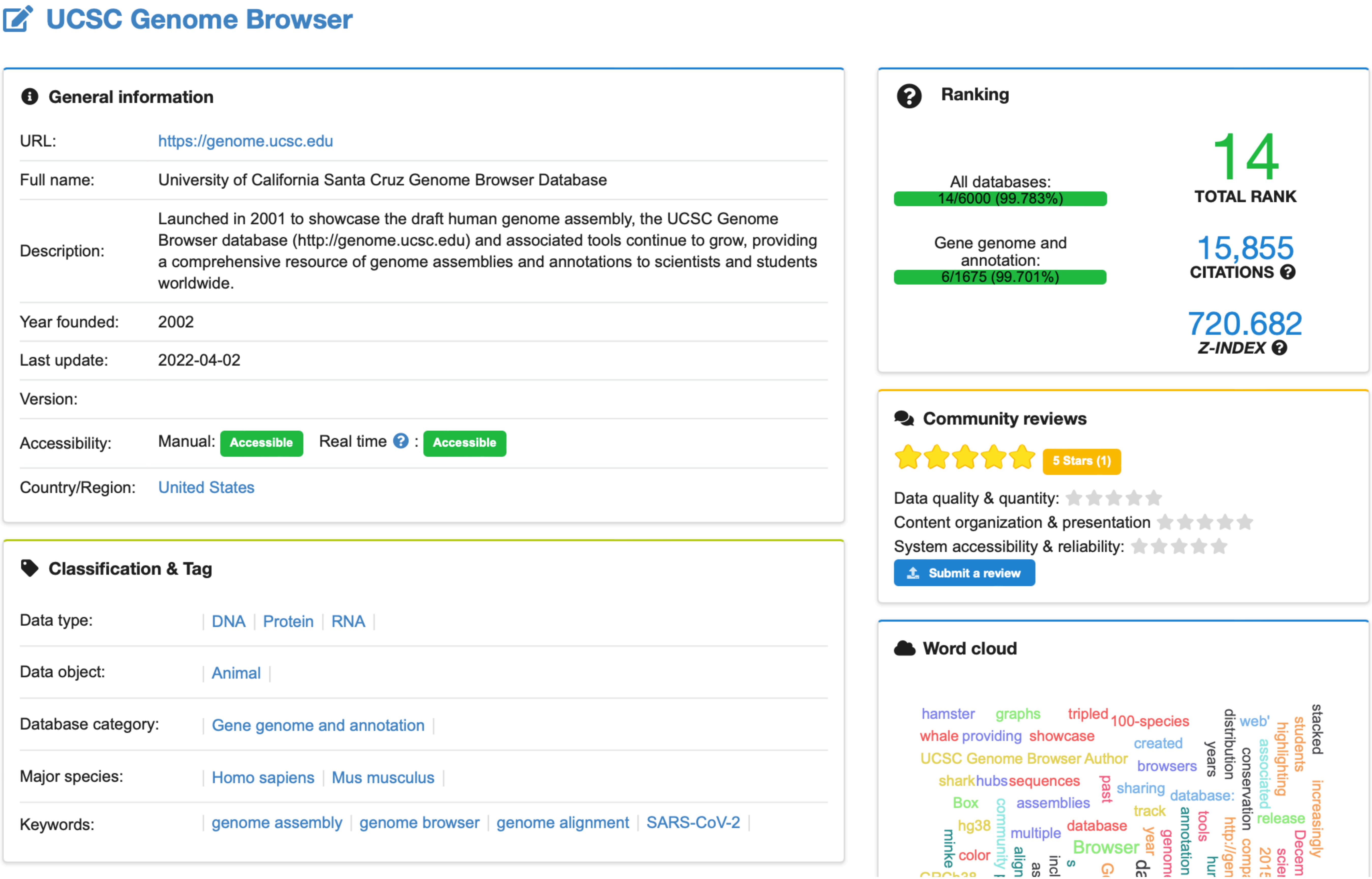
https://ngdc.cncb.ac.cn/databasecommons/

Databases we will see in more detail

We will explore:

- UCSC Genome Browser
- Kyoto Encyclopedia of Genes and Genomes (KEGG)
- The Cancer Genome Browser (TCGA)
- cBioPortal
- The Human Protein Atlas
- Known and Predicted Protein-Protein Interactions (STRING)
- Encyclopedia of DNA Elements (ENCODE)

UCSC Genome Browser



UCSC Genome Browser

General information

URL:	https://genome.ucsc.edu
Full name:	University of California Santa Cruz Genome Browser Database
Description:	Launched in 2001 to showcase the draft human genome assembly, the UCSC Genome Browser database (http://genome.ucsc.edu) and associated tools continue to grow, providing a comprehensive resource of genome assemblies and annotations to scientists and students worldwide.
Year founded:	2002
Last update:	2022-04-02
Version:	
Accessibility:	Manual: Accessible Real time ? : Accessible
Country/Region:	United States

Classification & Tag

Data type:	DNA | Protein | RNA
Data object:	Animal
Database category:	Gene genome and annotation
Major species:	Homo sapiens | Mus musculus
Keywords:	genome assembly | genome browser | genome alignment | SARS-CoV-2

Ranking

All databases: 14/6000 (99.783%)

Gene genome and annotation: 6/1675 (99.701%)

14 TOTAL RANK

15,855 CITATIONS ?

720.682 Z-INDEX ?

Community reviews

★★★★★ 5 Stars (1)

Data quality & quantity: ☆☆☆☆☆

Content organization & presentation ☆☆☆☆☆

System accessibility & reliability: ☆☆☆☆☆

Submit a review

Word cloud

https://ngdc.cncb.ac.cn/databasecommons/database/id/93

UCSC Genome Browser

Tools

- **Genome Browser** - Interactively visualize genomic data
- **BLAT** - Rapidly align sequences to the genome
- **In-Silico PCR** - Rapidly align PCR primer pairs to the genome
- **Table Browser** - Download and filter data from the Genome Browser
- **LiftOver** - Convert genome coordinates between assemblies
- **REST API** - Returns data requested in JSON format
- **Variant Annotation Integrator** - Annotate genomic variants
- **More tools...**

News

Mar. 14, 2025 - **denovo-db tracks for hg19 now available**

Mar. 06, 2025 - **New MITOMAP track for hg38 and hg19**

Mar. 05, 2025 - **New Splicing Impact super track and SpliceVarDB track for hg38**

Mar. 03, 2025 - **New highlight features for track hubs now available**

Feb. 24, 2025 - **enGenome VarChat track for human (hg38 and hg19)**

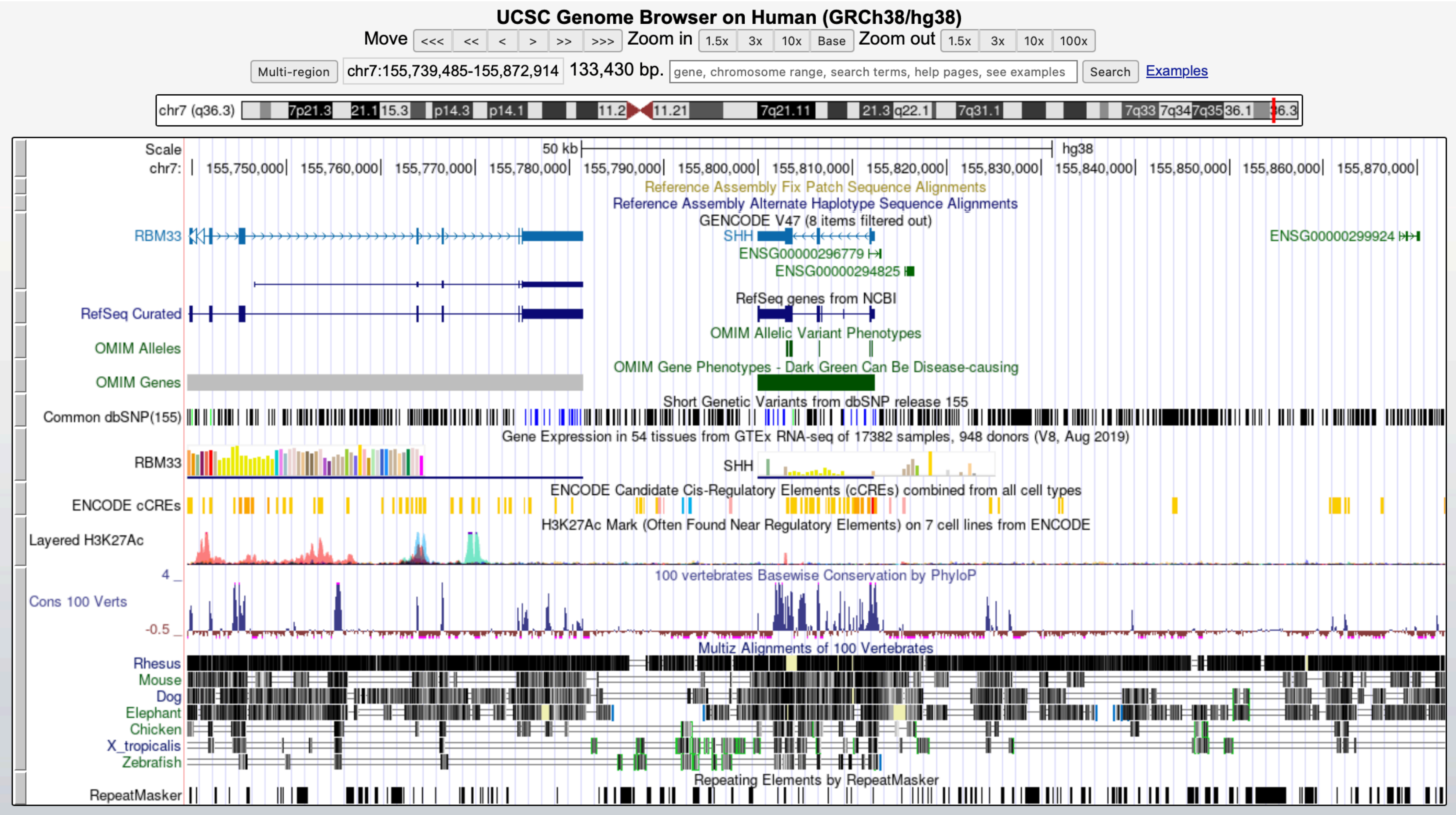
Feb. 21, 2025 - **New AlphaMissense tracks for Human (hg19/hg38)**

https://genome.ucsc.edu/

UCSC Genome Browser

Human Assembly: Dec. 2013 (GRCh38/hg38)

Current position: chr7:155,799,529-155,812,871

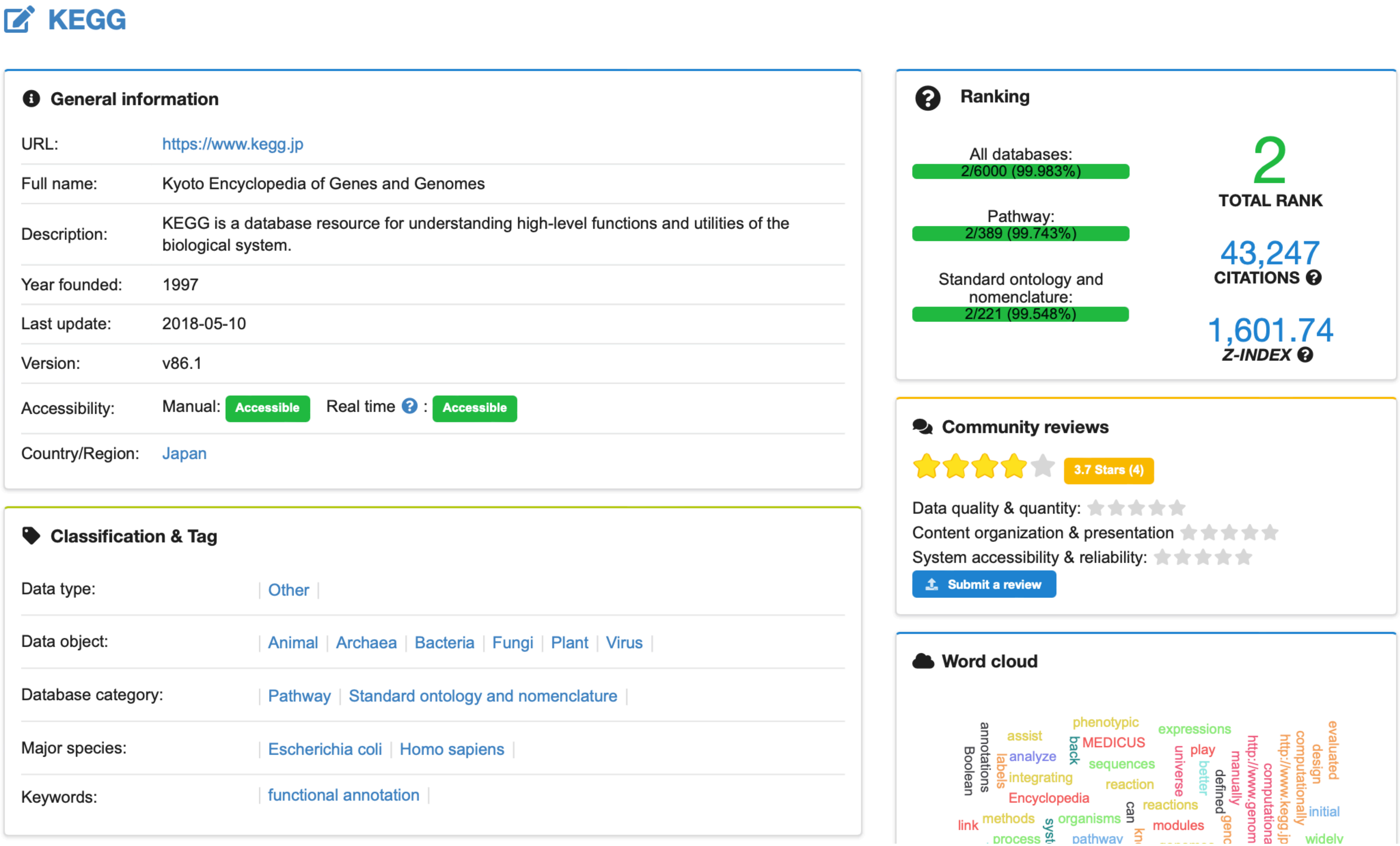


UCSC Genome Browser on Human (GRCh38/hg38)

chr7:155,739,485-155,872,914 133,430 bp.

https://genome.ucsc.edu/

Kyoto Encyclopedia of Genes and Genomes (KEGG)



KEGG

General information

URL:	https://www.kegg.jp
Full name:	Kyoto Encyclopedia of Genes and Genomes
Description:	KEGG is a database resource for understanding high-level functions and utilities of the biological system.
Year founded:	1997
Last update:	2018-05-10
Version:	v86.1
Accessibility:	Manual: **Accessible** Real time ? : **Accessible**
Country/Region:	Japan

Ranking

All databases:
2/6000 (99.983%)

Pathway:
2/389 (99.743%)

Standard ontology and nomenclature:
2/221 (99.548%)

2
TOTAL RANK

43,247
CITATIONS ?

1,601.74
Z-INDEX ?

Community reviews

★★★★☆ **3.7 Stars (4)**

Data quality & quantity: ☆☆☆☆☆
Content organization & presentation ☆☆☆☆☆
System accessibility & reliability: ☆☆☆☆☆

Submit a review

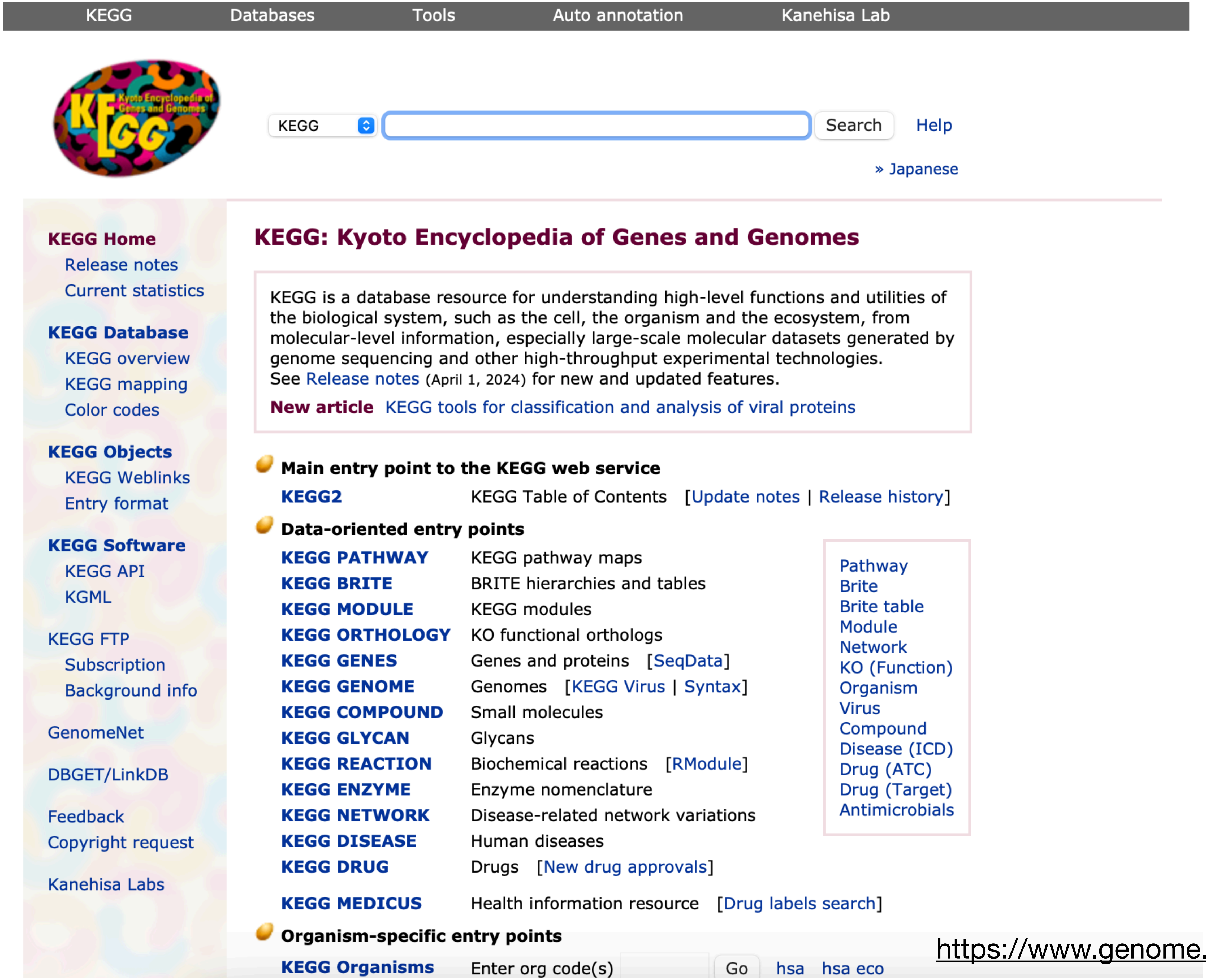
Classification & Tag

Data type:	Other
Data object:	Animal | Archaea | Bacteria | Fungi | Plant | Virus
Database category:	Pathway | Standard ontology and nomenclature
Major species:	Escherichia coli | Homo sapiens
Keywords:	functional annotation

Word cloud

https://ngdc.cncb.ac.cn/databasecommons/database/id/184

Kyoto Encyclopedia of Genes and Genomes (KEGG)



KEGG Home
- Release notes
- Current statistics

KEGG Database
- KEGG overview
- KEGG mapping
- Color codes

KEGG Objects
- KEGG Weblinks
- Entry format

KEGG Software
- KEGG API
- KGML

KEGG FTP
- Subscription
- Background info

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, 2024) for new and updated features.

New article KEGG tools for classification and analysis of viral proteins

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
KEGG GENES	Genes and proteins [SeqData]
KEGG GENOME	Genomes [KEGG Virus | Syntax]
KEGG COMPOUND	Small molecules
KEGG GLYCAN	Glycans
KEGG REACTION	Biochemical reactions [RModule]
KEGG ENZYME	Enzyme nomenclature
KEGG NETWORK	Disease-related network variations
KEGG DISEASE	Human diseases
KEGG DRUG	Drugs [New drug approvals]
KEGG MEDICUS	Health information resource [Drug labels search]

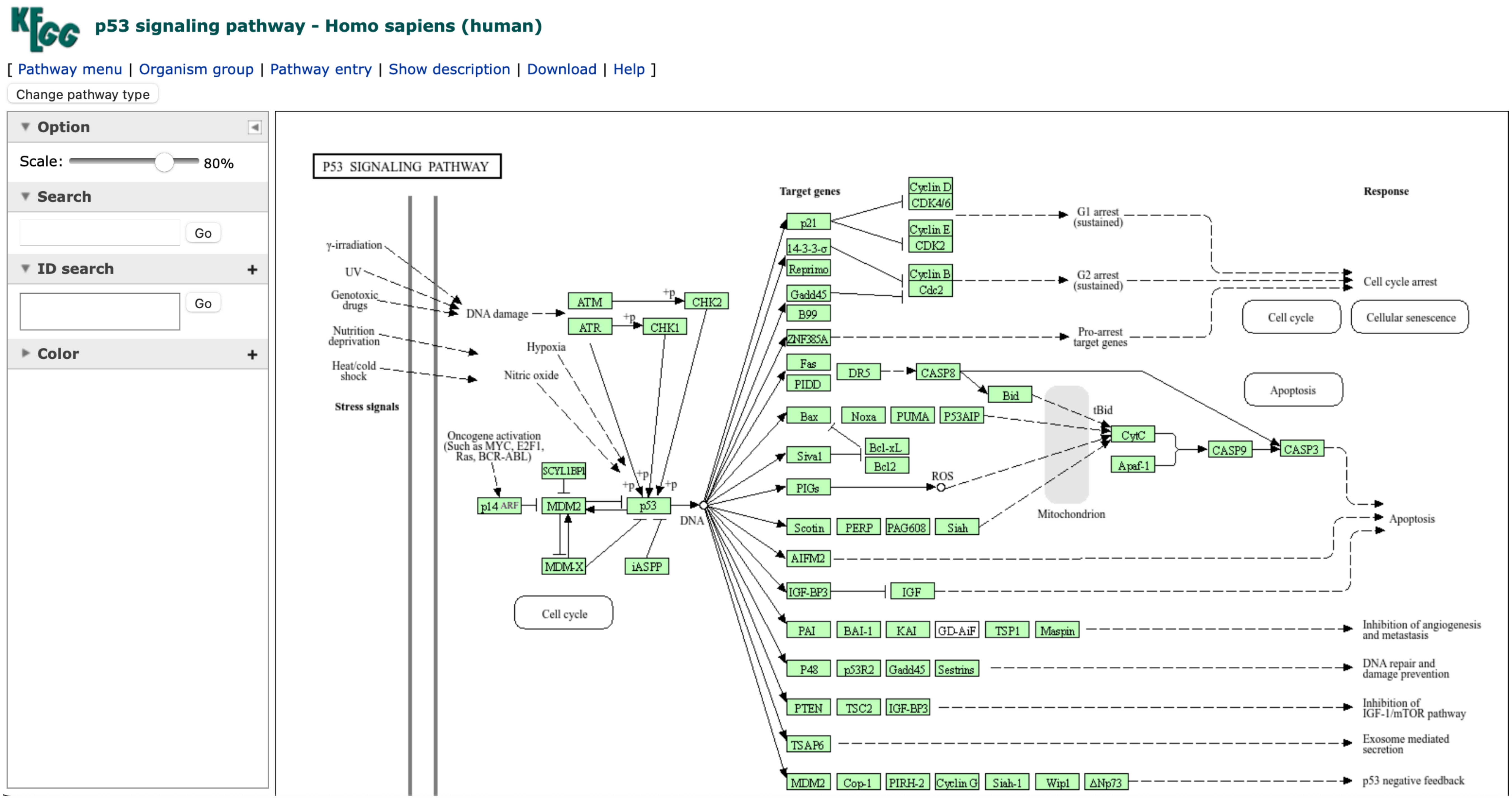
Pathway
Brite
Brite table
Module
Network
KO (Function)
Organism
Virus
Compound
Disease (ICD)
Drug (ATC)
Drug (Target)
Antimicrobials

Organism-specific entry points

KEGG Organisms Enter org code(s) Go hsa hsa eco

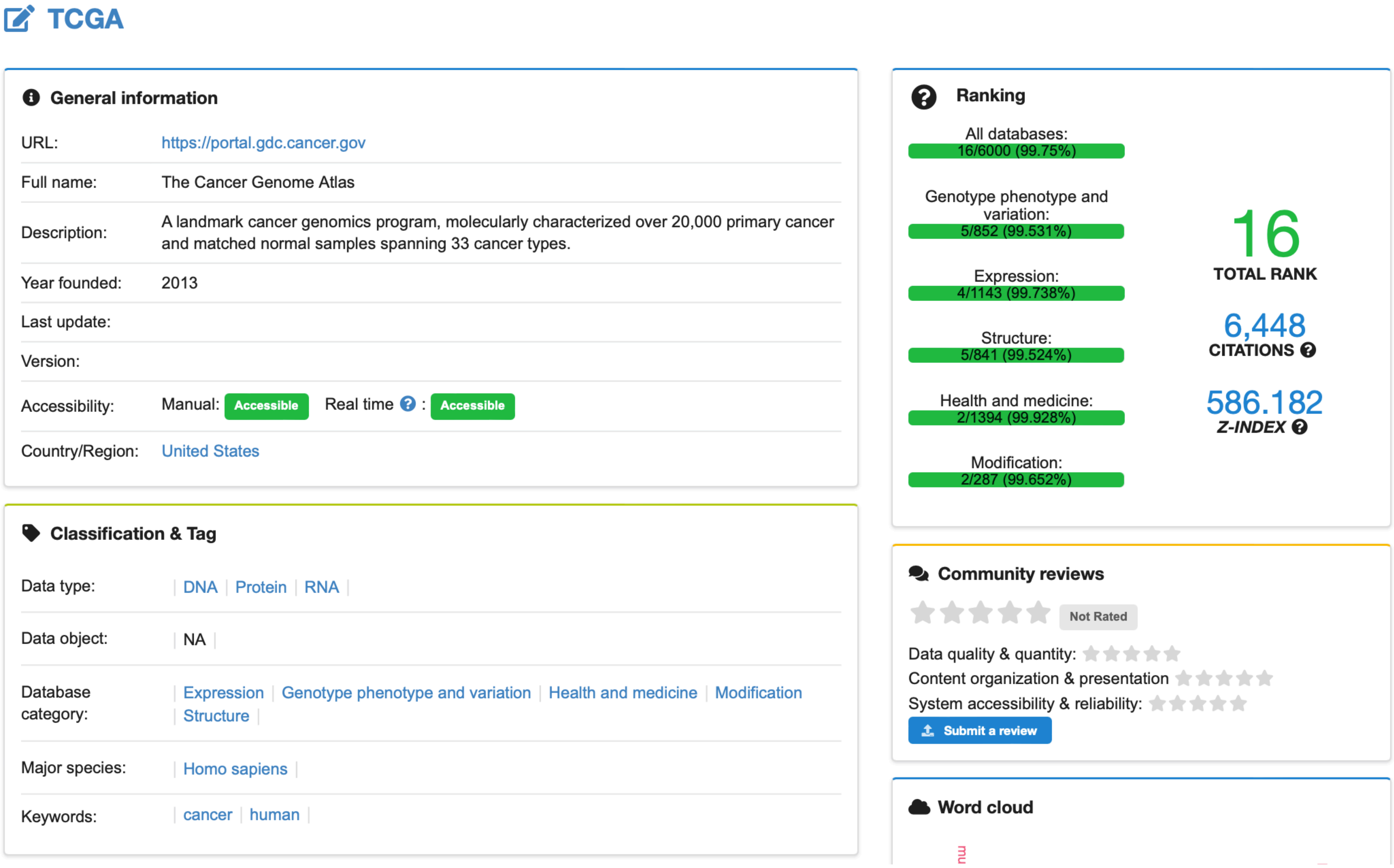
https://www.genome.jp/kegg/

Kyoto Encyclopedia of Genes and Genomes (KEGG)



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

The Cancer Genome Atlas (TCGA)



TCGA

General information

URL:	https://portal.gdc.cancer.gov
Full name:	The Cancer Genome Atlas
Description:	A landmark cancer genomics program, molecularly characterized over 20,000 primary cancer and matched normal samples spanning 33 cancer types.
Year founded:	2013
Last update:	
Version:	
Accessibility:	Manual: Accessible Real time ? : Accessible
Country/Region:	United States

Classification & Tag

Data type:	DNA | Protein | RNA
Data object:	NA
Database category:	Expression | Genotype phenotype and variation | Health and medicine | Modification | Structure
Major species:	Homo sapiens
Keywords:	cancer | human

Ranking

All databases: 16/6000 (99.75%)

Genotype phenotype and variation: 5/852 (99.531%)

Expression: 4/1143 (99.738%)

Structure: 5/841 (99.524%)

Health and medicine: 2/1394 (99.928%)

Modification: 2/287 (99.652%)

16
TOTAL RANK

6,448
CITATIONS ?

586.182
Z-INDEX ?

Community reviews

☆☆☆☆☆ Not Rated

Data quality & quantity: ☆☆☆☆☆

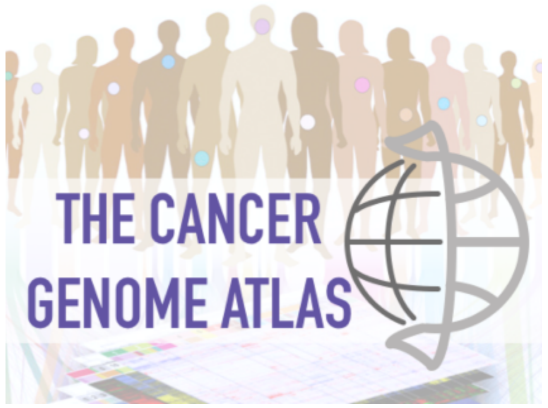
Content organization & presentation ☆☆☆☆☆

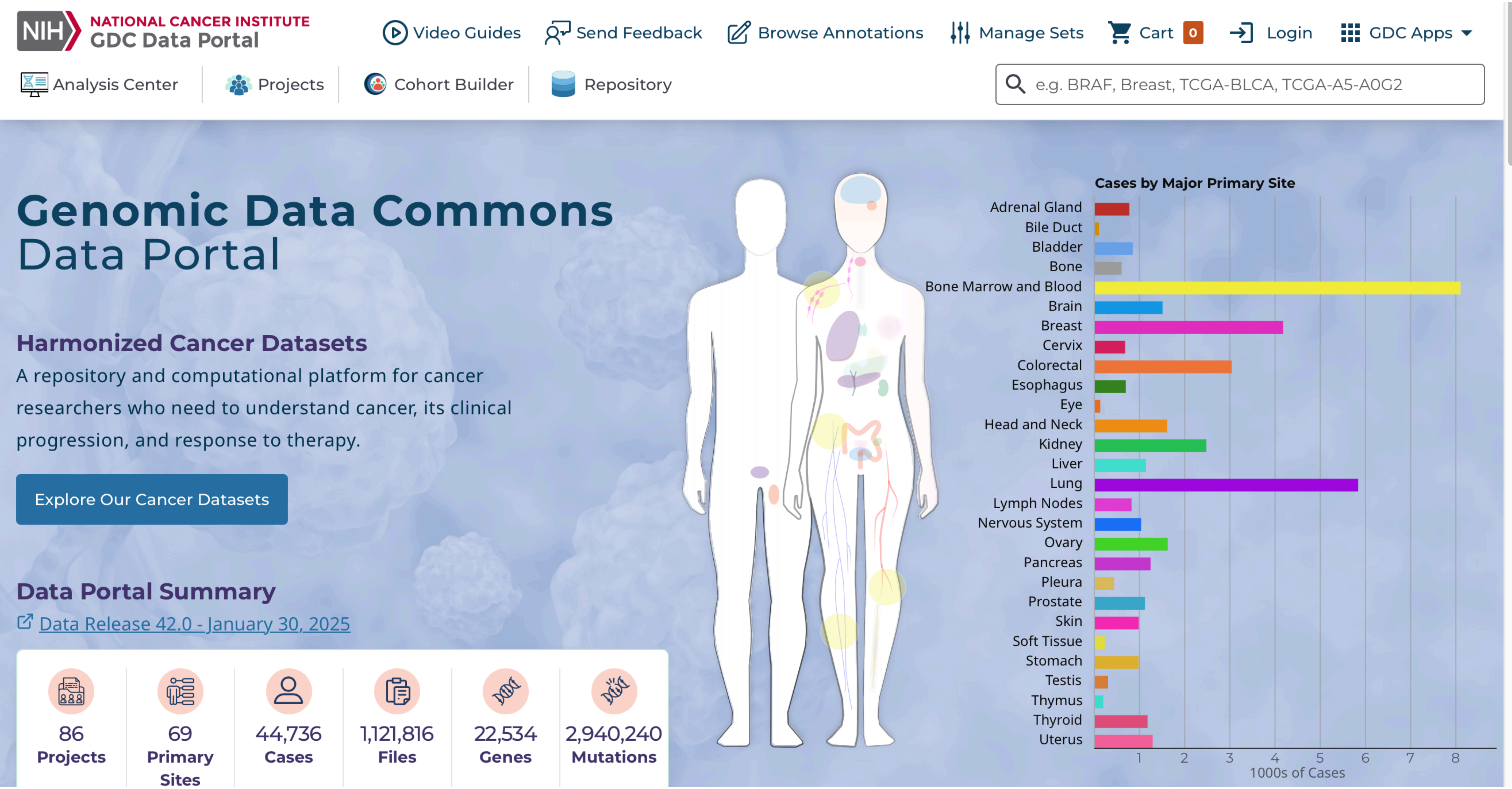
System accessibility & reliability: ☆☆☆☆☆

Word cloud

https://ngdc.cncb.ac.cn/databasecommons/database/id/6331

The Cancer Genome Atlas (TCGA)





Genomic Data Commons Data Portal

Harmonized Cancer Datasets

A repository and computational platform for cancer researchers who need to understand cancer, its clinical progression, and response to therapy.

Data Portal Summary

Data Release 42.0 - January 30, 2025

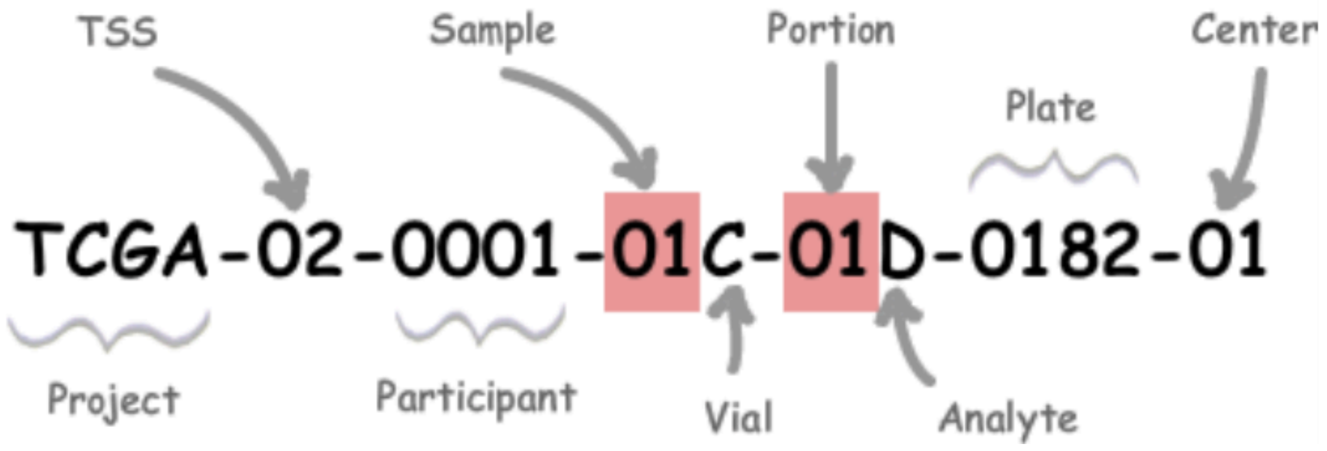
86	69	44,736	1,121,816	22,534	2,940,240
Projects	**Primary Sites**	**Cases**	**Files**	**Genes**	**Mutations**

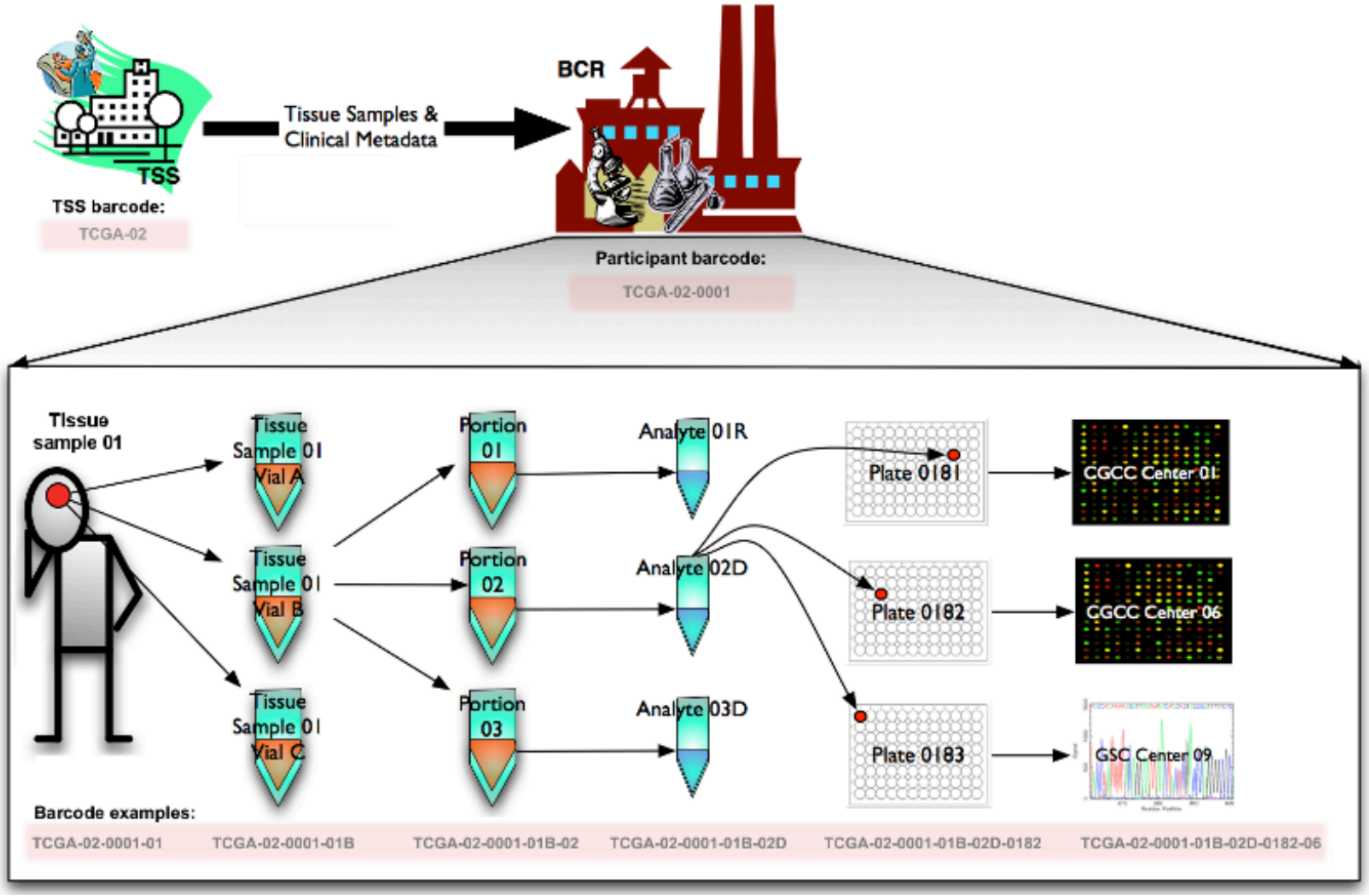
https://www.cancer.gov/ccg/research/genome-sequencing/tcga https://portal.gdc.cancer.gov/

The Cancer Genome Atlas (TCGA)

TCGA barcodes

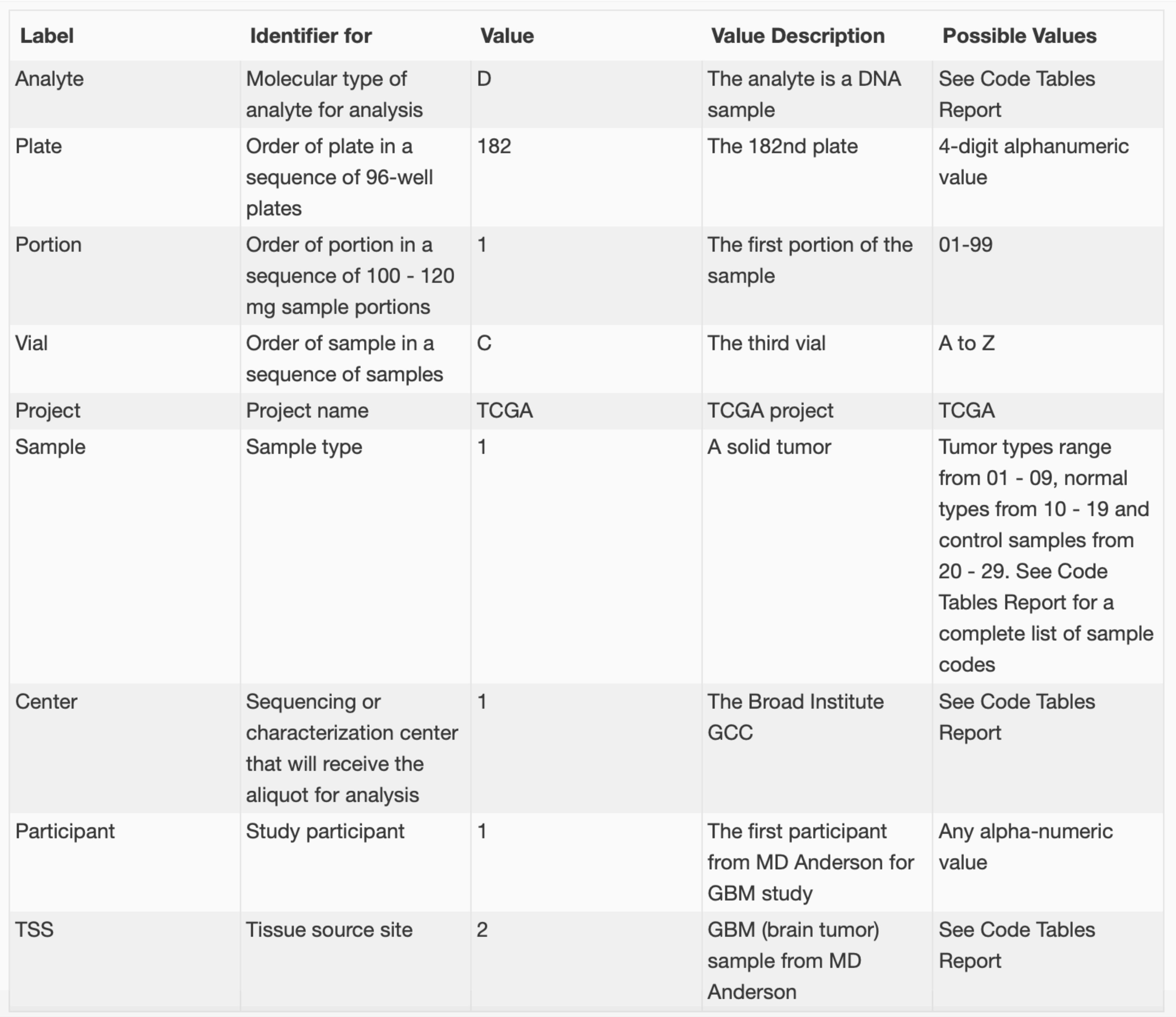
Each sample (i.e. sequencing experiment) presents a unique barcode that describe the patient, tissue, molecule etc.





The Cancer Genome Atlas (TCGA)

TCGA barcodes

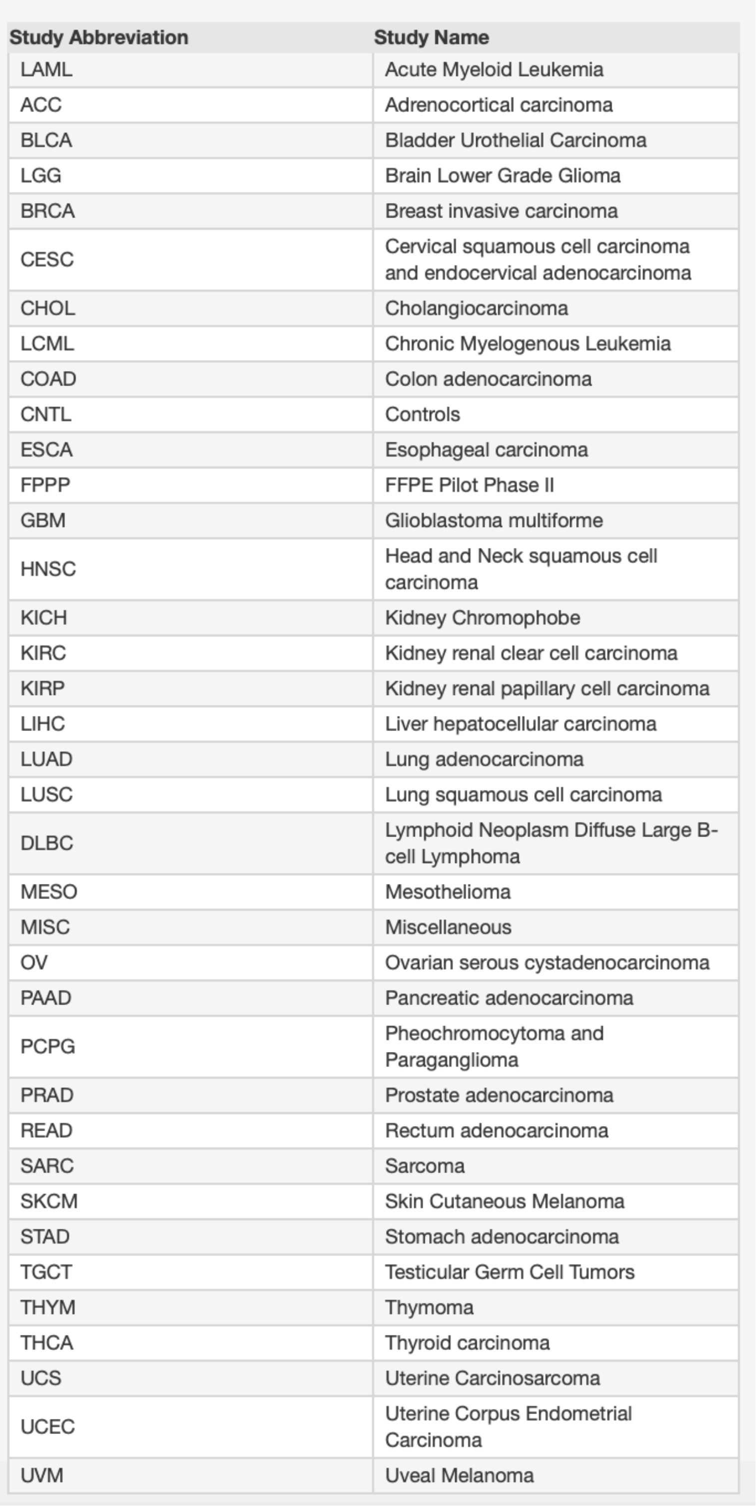


Label	Identifier for	Value	Value Description	Possible Values
Analyte	Molecular type of analyte for analysis	D	The analyte is a DNA sample	See Code Tables Report
Plate	Order of plate in a sequence of 96-well plates	182	The 182nd plate	4-digit alphanumeric value
Portion	Order of portion in a sequence of 100 - 120 mg sample portions	1	The first portion of the sample	01-99
Vial	Order of sample in a sequence of samples	C	The third vial	A to Z
Project	Project name	TCGA	TCGA project	TCGA
Sample	Sample type	1	A solid tumor	Tumor types range from 01 - 09, normal types from 10 - 19 and control samples from 20 - 29. See Code Tables Report for a complete list of sample codes
Center	Sequencing or characterization center that will receive the aliquot for analysis	1	The Broad Institute GCC	See Code Tables Report
Participant	Study participant	1	The first participant from MD Anderson for GBM study	Any alpha-numeric value
TSS	Tissue source site	2	GBM (brain tumor) sample from MD Anderson	See Code Tables Report

The Cancer Genome Atlas (TCGA)

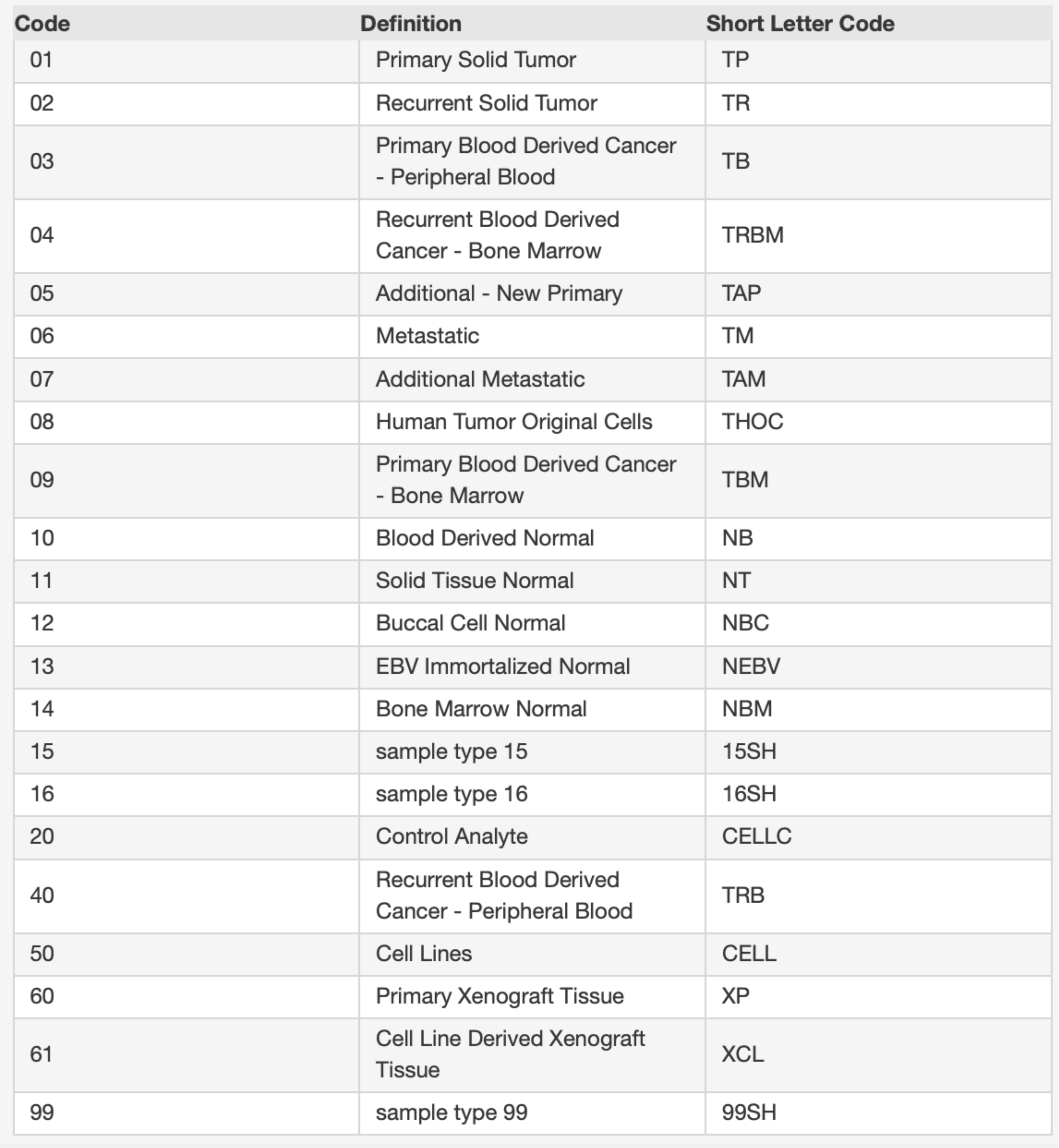
TCGA barcodes

https://gdc.cancer.gov/resources-tcga-users/tcga-code-tables/tcga-study-abbreviations



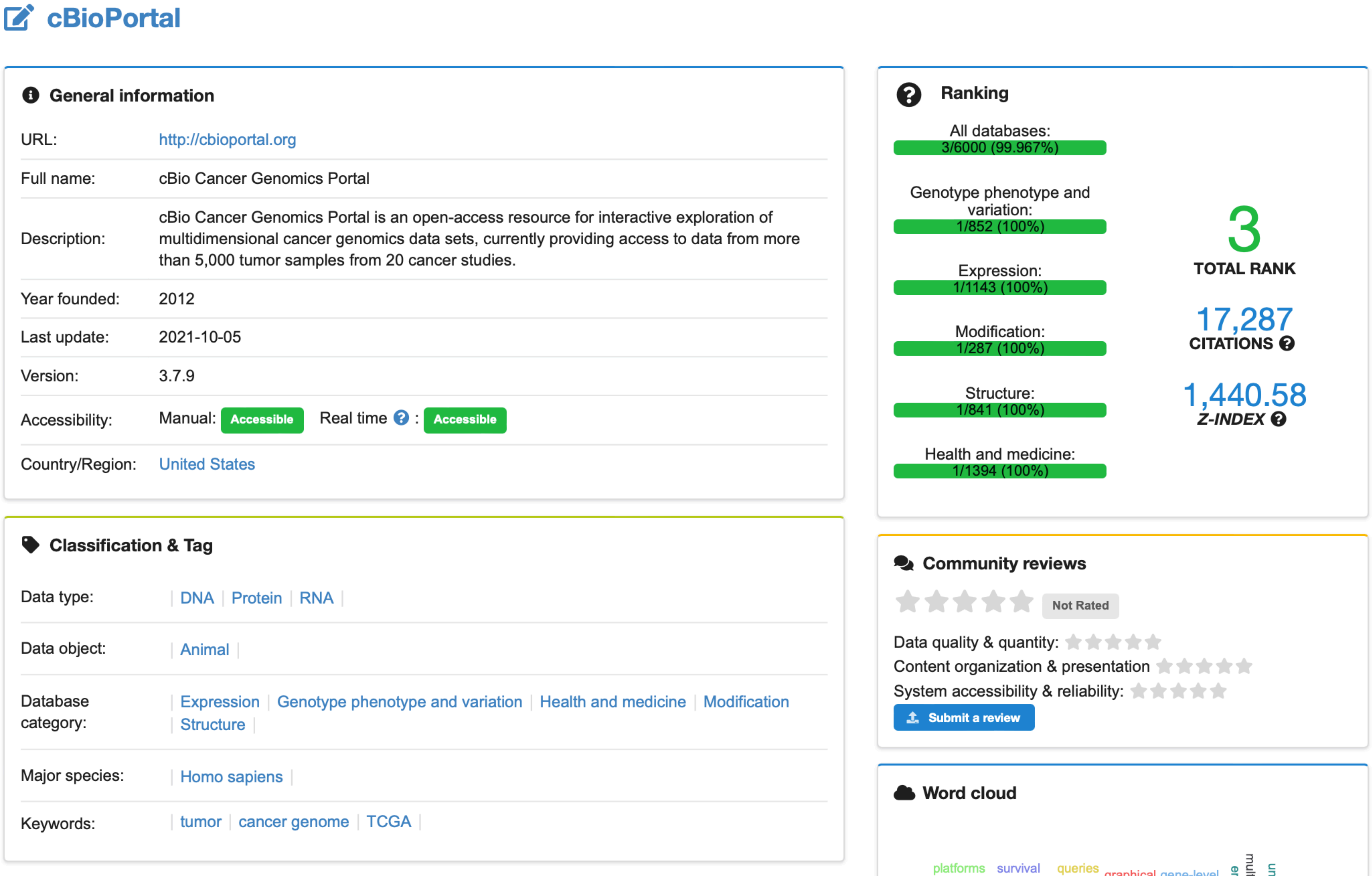
Study Abbreviation	Study Name
LAML	Acute Myeloid Leukemia
ACC	Adrenocortical carcinoma
BLCA	Bladder Urothelial Carcinoma
LGG	Brain Lower Grade Glioma
BRCA	Breast invasive carcinoma
CESC	Cervical squamous cell carcinoma and endocervical adenocarcinoma
CHOL	Cholangiocarcinoma
LCML	Chronic Myelogenous Leukemia
COAD	Colon adenocarcinoma
CNTL	Controls
ESCA	Esophageal carcinoma
FPPP	FFPE Pilot Phase II
GBM	Glioblastoma multiforme
HNSC	Head and Neck squamous cell carcinoma
KICH	Kidney Chromophobe
KIRC	Kidney renal clear cell carcinoma
KIRP	Kidney renal papillary cell carcinoma
LIHC	Liver hepatocellular carcinoma
LUAD	Lung adenocarcinoma
LUSC	Lung squamous cell carcinoma
DLBC	Lymphoid Neoplasm Diffuse Large B-cell Lymphoma
MESO	Mesothelioma
MISC	Miscellaneous
OV	Ovarian serous cystadenocarcinoma
PAAD	Pancreatic adenocarcinoma
PCPG	Pheochromocytoma and Paraganglioma
PRAD	Prostate adenocarcinoma
READ	Rectum adenocarcinoma
SARC	Sarcoma
SKCM	Skin Cutaneous Melanoma
STAD	Stomach adenocarcinoma
TGCT	Testicular Germ Cell Tumors
THYM	Thymoma
THCA	Thyroid carcinoma
UCS	Uterine Carcinosarcoma
UCEC	Uterine Corpus Endometrial Carcinoma
UVM	Uveal Melanoma

https://gdc.cancer.gov/resources-tcga-users/tcga-code-tables/sample-type-codes



Code	Definition	Short Letter Code
01	Primary Solid Tumor	TP
02	Recurrent Solid Tumor	TR
03	Primary Blood Derived Cancer - Peripheral Blood	TB
04	Recurrent Blood Derived Cancer - Bone Marrow	TRBM
05	Additional - New Primary	TAP
06	Metastatic	TM
07	Additional Metastatic	TAM
08	Human Tumor Original Cells	THOC
09	Primary Blood Derived Cancer - Bone Marrow	TBM
10	Blood Derived Normal	NB
11	Solid Tissue Normal	NT
12	Buccal Cell Normal	NBC
13	EBV Immortalized Normal	NEBV
14	Bone Marrow Normal	NBM
15	sample type 15	15SH
16	sample type 16	16SH
20	Control Analyte	CELLC
40	Recurrent Blood Derived Cancer - Peripheral Blood	TRB
50	Cell Lines	CELL
60	Primary Xenograft Tissue	XP
61	Cell Line Derived Xenograft Tissue	XCL
99	sample type 99	99SH

cBioPortal



cBioPortal

General information

URL:	http://cbioportal.org
Full name:	cBio Cancer Genomics Portal
Description:	cBio Cancer Genomics Portal is an open-access resource for interactive exploration of multidimensional cancer genomics data sets, currently providing access to data from more than 5,000 tumor samples from 20 cancer studies.
Year founded:	2012
Last update:	2021-10-05
Version:	3.7.9
Accessibility:	Manual: Accessible Real time ? : Accessible
Country/Region:	United States

Ranking

All databases:
3/6000 (99.967%)

Genotype phenotype and variation:
1/852 (100%)

Expression:
1/1143 (100%)

Modification:
1/287 (100%)

Structure:
1/841 (100%)

Health and medicine:
1/1394 (100%)

3
TOTAL RANK

17,287
CITATIONS ?

1,440.58
Z-INDEX ?

Classification & Tag

Data type:	DNA | Protein | RNA
Data object:	Animal
Database category:	Expression | Genotype phenotype and variation | Health and medicine | Modification | Structure
Major species:	Homo sapiens
Keywords:	tumor | cancer genome | TCGA

Community reviews

☆☆☆☆☆ Not Rated

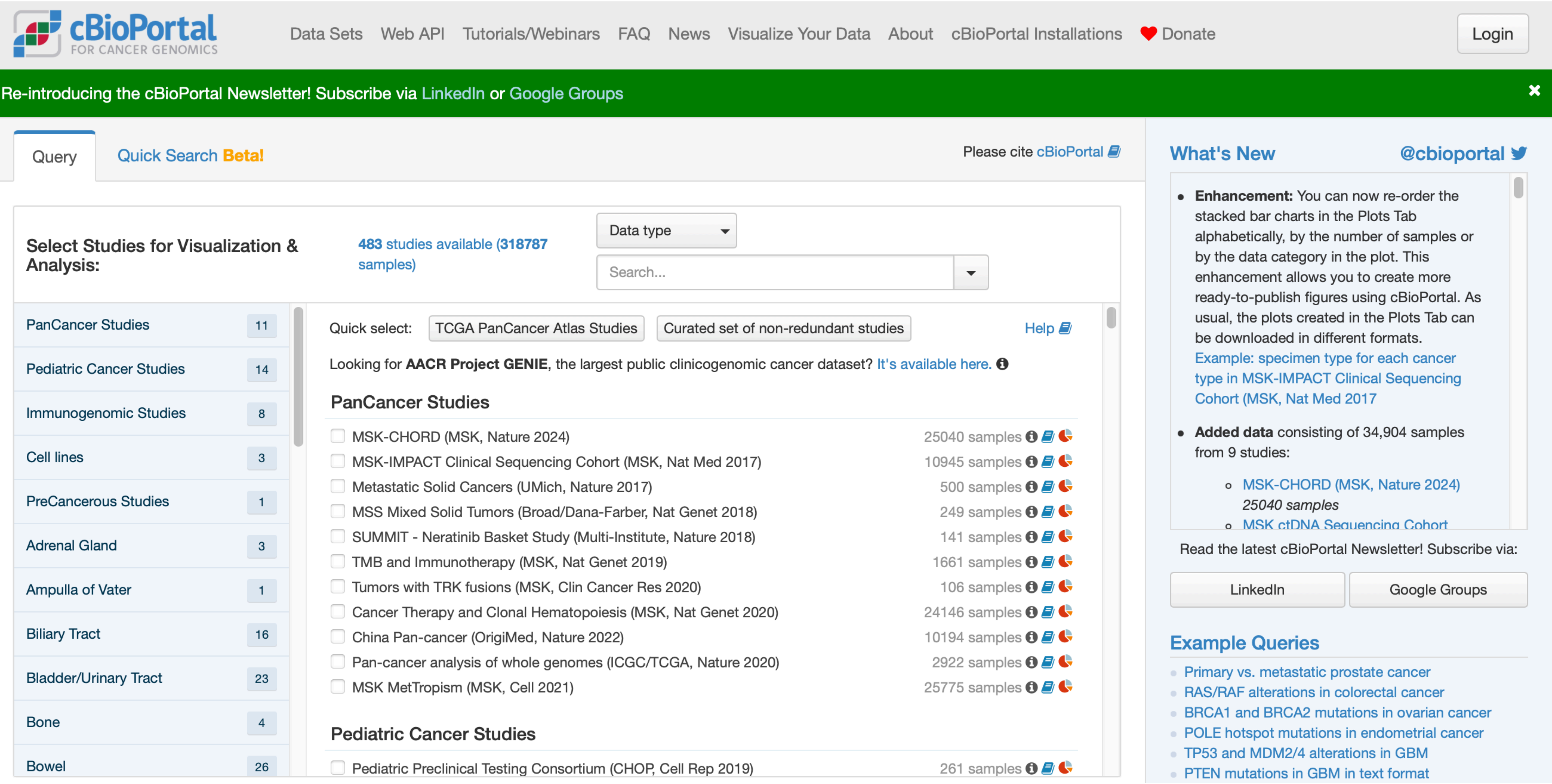
Data quality & quantity: ☆☆☆☆☆
Content organization & presentation ☆☆☆☆☆
System accessibility & reliability: ☆☆☆☆☆

Submit a review

Word cloud

https://ngdc.cncb.ac.cn/databasecommons/database/id/6569

cBioPortal



Re-introducing the cBioPortal Newsletter! Subscribe via LinkedIn or Google Groups

Please cite cBioPortal

Select Studies for Visualization & Analysis:

483 studies available (318787 samples)

PanCancer Studies	11
Pediatric Cancer Studies	14
Immunogenomic Studies	8
Cell lines	3
PreCancerous Studies	1
Adrenal Gland	3
Ampulla of Vater	1
Biliary Tract	16
Bladder/Urinary Tract	23
Bone	4
Bowel	26

Quick select: TCGA PanCancer Atlas Studies | Curated set of non-redundant studies | Help

Looking for **AACR Project GENIE**, the largest public clinicogenomic cancer dataset? It's available here.

PanCancer Studies

☐ MSK-CHORD (MSK, Nature 2024)	25040 samples
☐ MSK-IMPACT Clinical Sequencing Cohort (MSK, Nat Med 2017)	10945 samples
☐ Metastatic Solid Cancers (UMich, Nature 2017)	500 samples
☐ MSS Mixed Solid Tumors (Broad/Dana-Farber, Nat Genet 2018)	249 samples
☐ SUMMIT - Neratinib Basket Study (Multi-Institute, Nature 2018)	141 samples
☐ TMB and Immunotherapy (MSK, Nat Genet 2019)	1661 samples
☐ Tumors with TRK fusions (MSK, Clin Cancer Res 2020)	106 samples
☐ Cancer Therapy and Clonal Hematopoiesis (MSK, Nat Genet 2020)	24146 samples
☐ China Pan-cancer (OrigiMed, Nature 2022)	10194 samples
☐ Pan-cancer analysis of whole genomes (ICGC/TCGA, Nature 2020)	2922 samples
☐ MSK MetTropism (MSK, Cell 2021)	25775 samples

Pediatric Cancer Studies

☐ Pediatric Preclinical Testing Consortium (CHOP, Cell Rep 2019)	261 samples

What's New

@cbioportal

- **Enhancement:** You can now re-order the stacked bar charts in the Plots Tab alphabetically, by the number of samples or by the data category in the plot. This enhancement allows you to create more ready-to-publish figures using cBioPortal. As usual, the plots created in the Plots Tab can be downloaded in different formats. Example: specimen type for each cancer type in MSK-IMPACT Clinical Sequencing Cohort (MSK, Nat Med 2017
- **Added data** consisting of 34,904 samples from 9 studies:
    - MSK-CHORD (MSK, Nature 2024) *25040 samples*
    - MSK ctDNA Sequencing Cohort

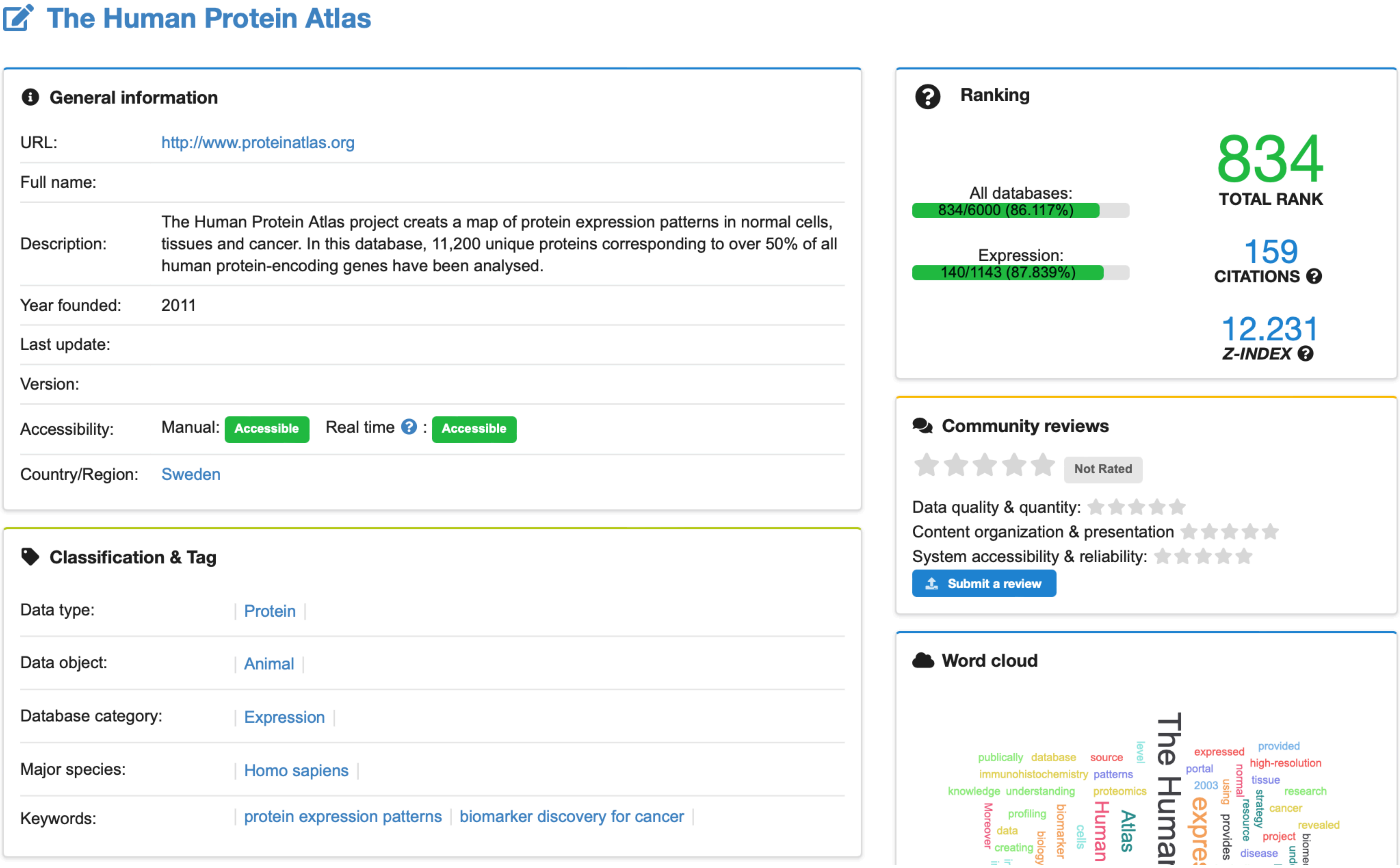
Read the latest cBioPortal Newsletter! Subscribe via:

Example Queries

- Primary vs. metastatic prostate cancer
- RAS/RAF alterations in colorectal cancer
- BRCA1 and BRCA2 mutations in ovarian cancer
- POLE hotspot mutations in endometrial cancer
- TP53 and MDM2/4 alterations in GBM
- PTEN mutations in GBM in text format

https://www.cbioportal.org/

The Human Protein Atlas



The Human Protein Atlas

General information

URL:	http://www.proteinatlas.org
Full name:	
Description:	The Human Protein Atlas project creats a map of protein expression patterns in normal cells, tissues and cancer. In this database, 11,200 unique proteins corresponding to over 50% of all human protein-encoding genes have been analysed.
Year founded:	2011
Last update:	
Version:	
Accessibility:	Manual: Accessible Real time ? : Accessible
Country/Region:	Sweden

Classification & Tag

Data type:	Protein
Data object:	Animal
Database category:	Expression
Major species:	Homo sapiens
Keywords:	protein expression patterns | biomarker discovery for cancer

Ranking

All databases: 834/6000 (86.117%)

Expression: 140/1143 (87.839%)

834 TOTAL RANK

159 CITATIONS ?

12.231 Z-INDEX ?

Community reviews

☆☆☆☆☆ Not Rated

Data quality & quantity: ☆☆☆☆☆

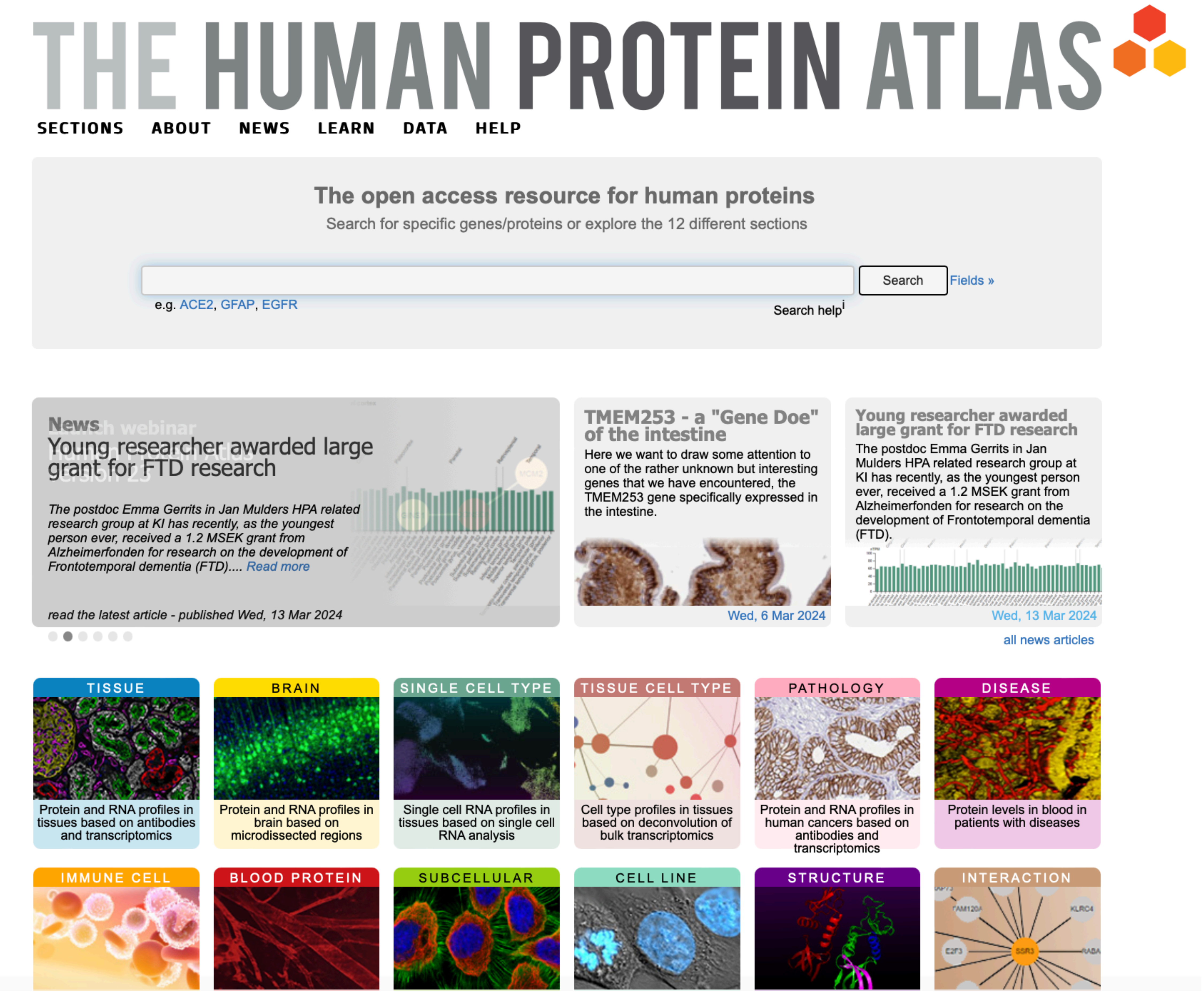
Content organization & presentation ☆☆☆☆☆

System accessibility & reliability: ☆☆☆☆☆

Submit a review

Word cloud

https://ngdc.cncb.ac.cn/databasecommons/database/id/4602



The open access resource for human proteins

Search for specific genes/proteins or explore the 12 different sections

e.g. ACE2, GFAP, EGFR

News

Young researcher awarded large grant for FTD research

The postdoc Emma Gerrits in Jan Mulders HPA related research group at KI has recently, as the youngest person ever, received a 1.2 MSEK grant from Alzheimerfonden for research on the development of Frontotemporal dementia (FTD).... Read more

read the latest article - published Wed, 13 Mar 2024

TMEM253 - a "Gene Doe" of the intestine

Here we want to draw some attention to one of the rather unknown but interesting genes that we have encountered, the TMEM253 gene specifically expressed in the intestine.

Wed, 6 Mar 2024

Young researcher awarded large grant for FTD research

The postdoc Emma Gerrits in Jan Mulders HPA related research group at KI has recently, as the youngest person ever, received a 1.2 MSEK grant from Alzheimerfonden for research on the development of Frontotemporal dementia (FTD).

Wed, 13 Mar 2024

all news articles

TISSUE: Protein and RNA profiles in tissues based on antibodies and transcriptomics

BRAIN: Protein and RNA profiles in brain based on microdissected regions

SINGLE CELL TYPE: Single cell RNA profiles in tissues based on single cell RNA analysis

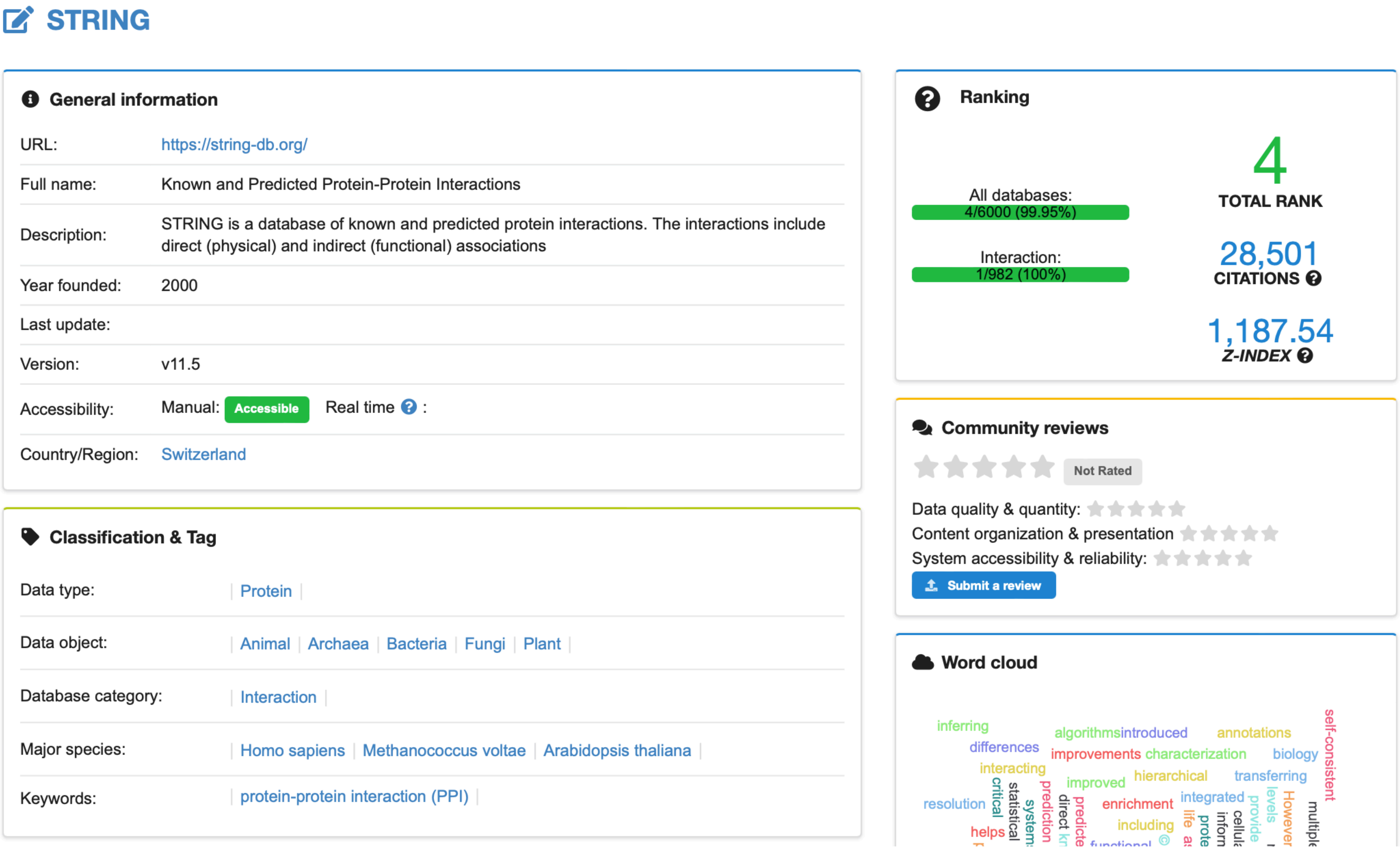
TISSUE CELL TYPE: Cell type profiles in tissues based on deconvolution of bulk transcriptomics

PATHOLOGY: Protein and RNA profiles in human cancers based on antibodies and transcriptomics

DISEASE: Protein levels in blood in patients with diseases

https://www.proteinatlas.org/

STRING



STRING

General information

URL:	https://string-db.org/
Full name:	Known and Predicted Protein-Protein Interactions
Description:	STRING is a database of known and predicted protein interactions. The interactions include direct (physical) and indirect (functional) associations
Year founded:	2000
Last update:	
Version:	v11.5
Accessibility:	Manual: Accessible Real time ? :
Country/Region:	Switzerland

Classification & Tag

Data type:	Protein
Data object:	Animal | Archaea | Bacteria | Fungi | Plant
Database category:	Interaction
Major species:	Homo sapiens | Methanococcus voltae | Arabidopsis thaliana
Keywords:	protein-protein interaction (PPI)

Ranking

All databases: 4/6000 (99.95%)

Interaction: 1/982 (100%)

4 TOTAL RANK

28,501 CITATIONS ?

1,187.54 *Z-INDEX* ?

Community reviews

☆☆☆☆☆ Not Rated

Data quality & quantity: ☆☆☆☆☆

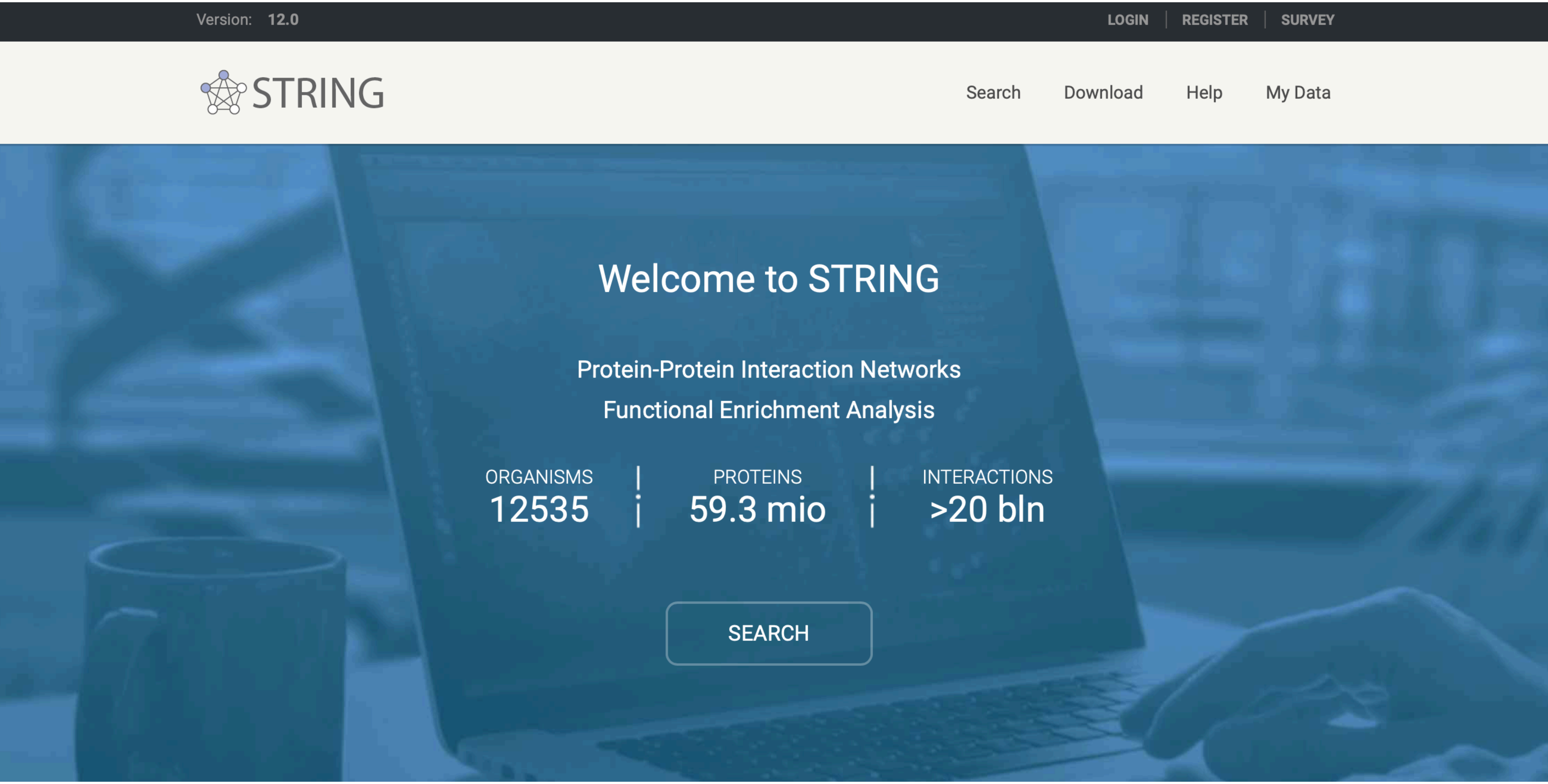
Content organization & presentation ☆☆☆☆☆

System accessibility & reliability: ☆☆☆☆☆

Word cloud

https://ngdc.cncb.ac.cn/databasecommons/database/id/62

STRING



Version: 12.0

LOGIN | REGISTER | SURVEY

STRING

Search Download Help My Data

Welcome to STRING

Protein-Protein Interaction Networks

Functional Enrichment Analysis

ORGANISMS 12535 | PROTEINS 59.3 mio | INTERACTIONS >20 bln

SEARCH

https://string-db.org/cgi/input?sessionId=buUIHtE4Ehj7&input_page_active_form=multiple_identifiers

STRING

1. Go to:

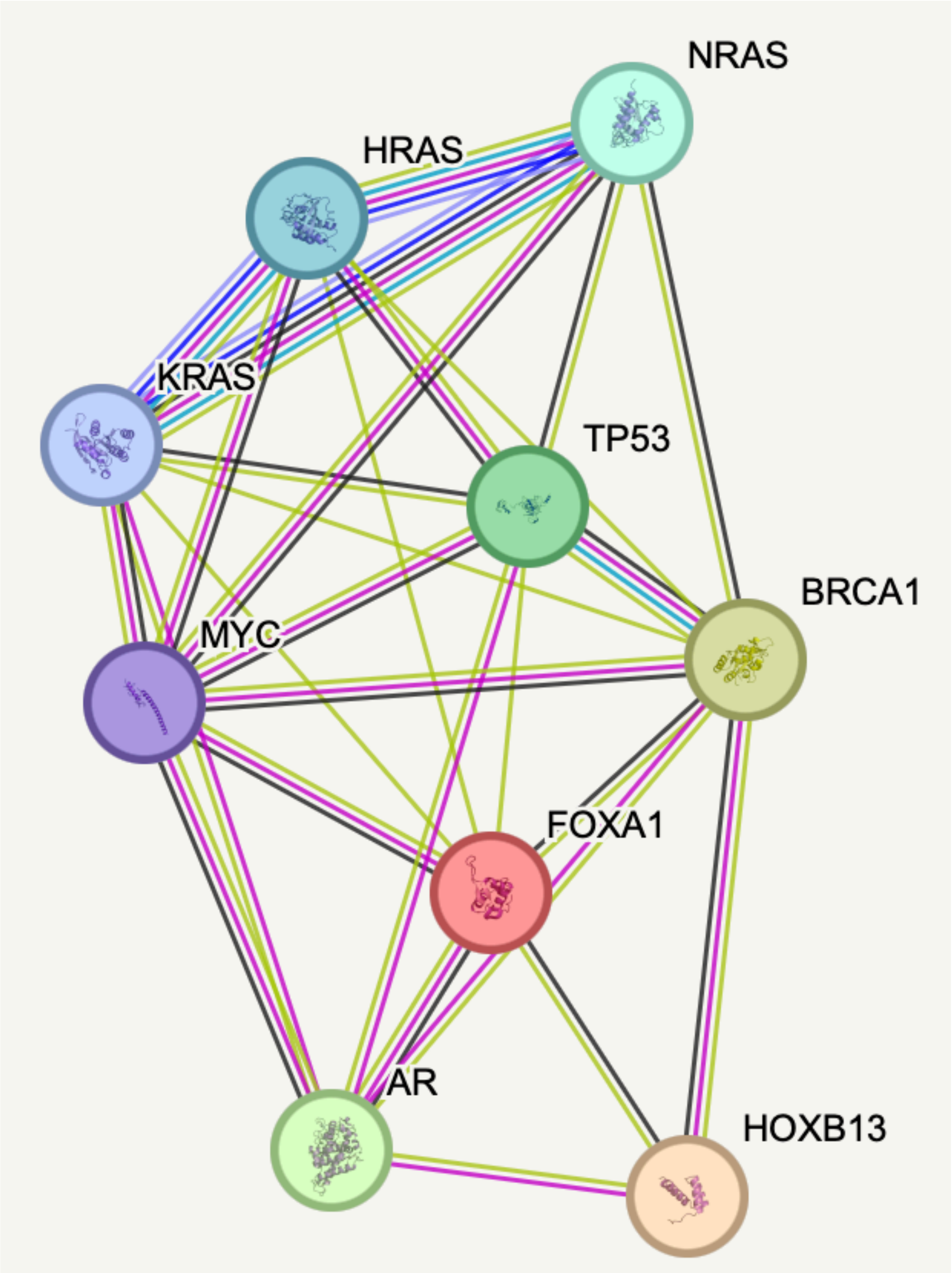
https://string-db.org/cgi/input?sessionId=buUIHtE4Ehj7&input_page_active_form=multiple_identifiers

2. Copy and paste the following gene names in the “List of names” panel:
FOXA1
AR
MYC
HOXB13
KRAS
TP53
NRAS
HRAS
NCOR
BRCA1

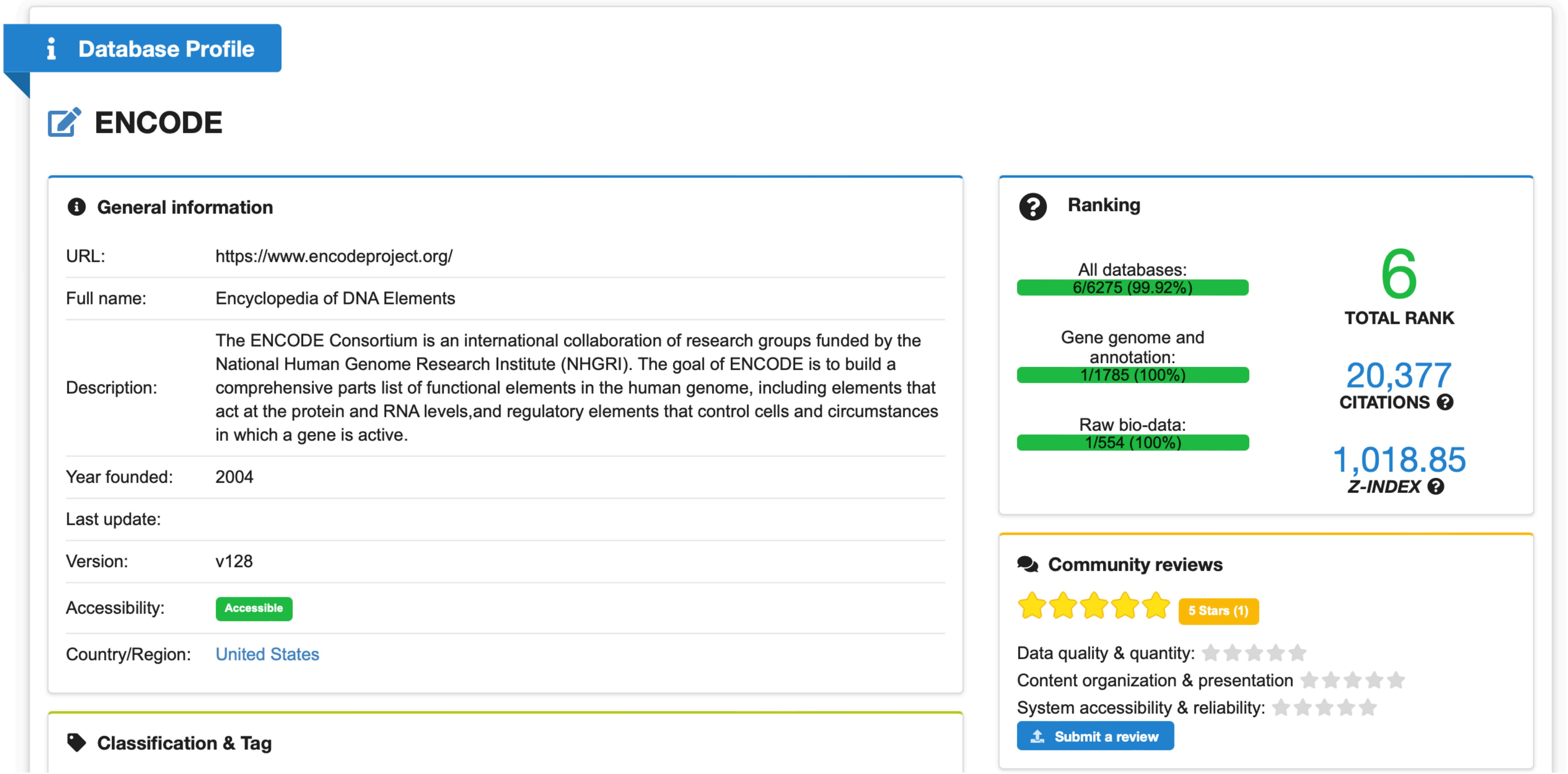
3. Choose the organism “Homo sapiens”

STRING

4. Explore the result



ENCODE



ENCODE

General information

URL:	https://www.encodeproject.org/
Full name:	Encyclopedia of DNA Elements
Description:	The ENCODE Consortium is an international collaboration of research groups funded by the National Human Genome Research Institute (NHGRI). The goal of ENCODE is to build a comprehensive parts list of functional elements in the human genome, including elements that act at the protein and RNA levels,and regulatory elements that control cells and circumstances in which a gene is active.
Year founded:	2004
Last update:	
Version:	v128
Accessibility:	Accessible
Country/Region:	United States

Ranking

All databases: 6/6275 (99.92%)

Gene genome and annotation: 1/1785 (100%)

Raw bio-data: 1/554 (100%)

6 TOTAL RANK

20,377 CITATIONS

1,018.85 *Z-INDEX*

Community reviews

★★★★★ 5 Stars (1)

Data quality & quantity: ☆☆☆☆☆

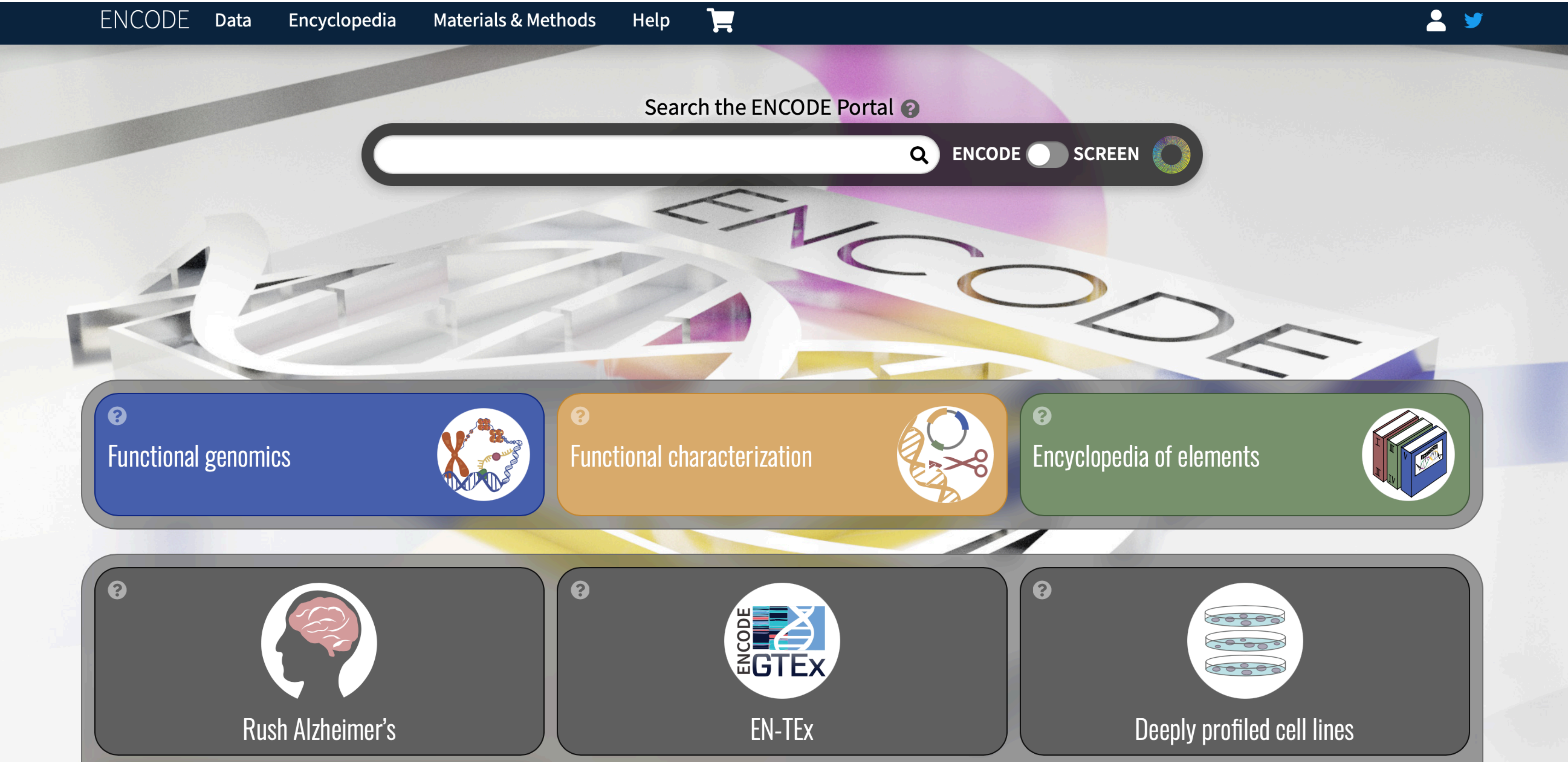
Content organization & presentation ☆☆☆☆☆

System accessibility & reliability: ☆☆☆☆☆

Classification & Tag

https://ngdc.cncb.ac.cn/databasecommons/database/id/317

ENCODE



https://www.encodeproject.org/

R packages associated to databases

https://bioconductor.org/packages/release/data/annotation/html/UCSCRepeatMasker.html

https://bioconductor.org/packages/release/data/experiment/html/msigdb.html

https://bioconductor.org/packages/release/bioc/html/cBioPortalData.html

https://bioconductor.org/packages/release/bioc/html/TCGAbiolinks.html

https://bioconductor.org/packages/release/bioc/html/hpar.html

https://www.bioconductor.org/packages/release/bioc/html/STRINGdb.html

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