



开放的资源数据库

IMP 整合植物资源数据库



IMP
Integrated Medicinal Plantomics

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Integrated Medicinal Plantomics



IMP: Bridging the Gap for Medicinal Plant Genomics

Synthetic biology medicine is built on the molecular metabolic pathways of herbal plants. Finding functional genes and assembling the metabolic pathways requires a number of critical steps, one of which is the comparative genome and transcriptome analysis. We developed IMP as an integrated platform for organizing, analyzing, and sharing omics data of medicinal plantomics with 10 computation modules to deal with the volume of omics data and the complexity of analysis operations. Typing in either IDs, function descriptions, or pathway annotations would generate a list of matched genes. Users could choose several genes and send them to various programs, including (1) **Gene expression profile module** to compare their transcriptome profiles across various organs or treatment conditions to screen key functional genes, (2) **Gene fishing** to look for additional genes with similar expression profiles that may work together, (3) **Gene map viewer** to see if these genes could form gene clusters to be involved in one metabolite pathway, (4) **Multiple sequence alignments** to locate conserved catalytic sites for metabolite synthesis, (5) **Sequences fetch** to download related sequences, (6) **Primer design** to produce primers for experimental verification, and (7) **BLAST** to compare their hits across species. Users might also create an in-silico project to resolve the medicinal component synthetic pathways utilizing (8) **DE gene analysis model** to perform cross-organ comparison or along-inducing comparison. The identified differentially expressed genes could be used for function discovery in (9) **GO/KEGG**

Andrographis paniculata

cytochrome p450

Q Search



25,865,814

Genes



127,498,390,992

Genome bases



2,434

Samples



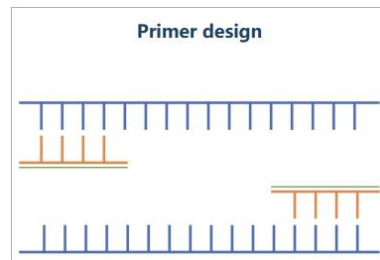
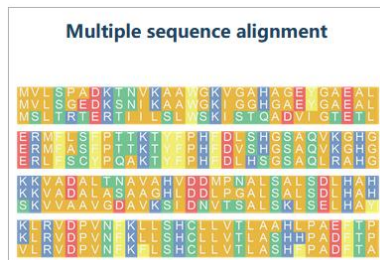
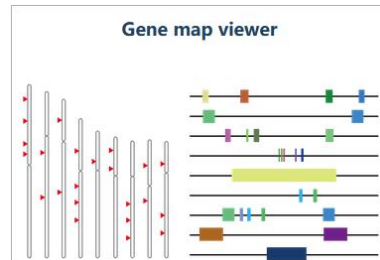
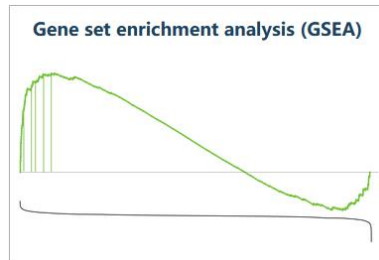
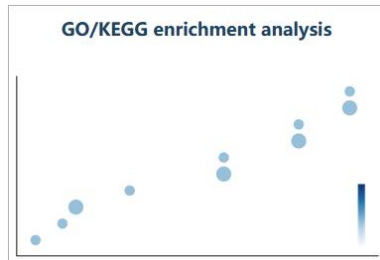
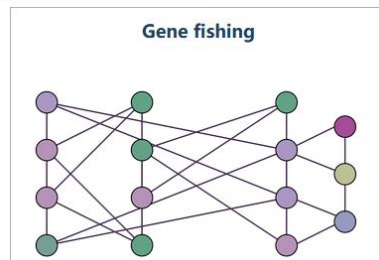
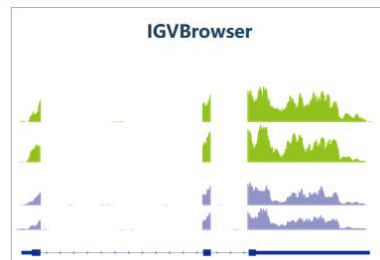
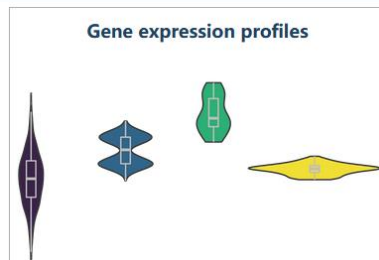
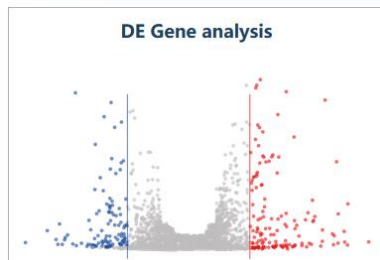
442

Species

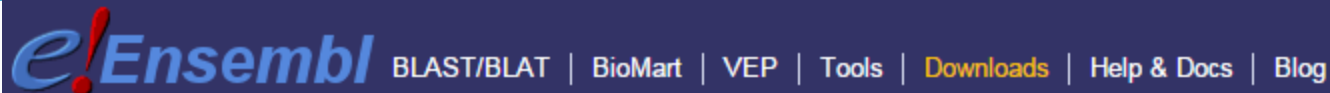
易生信, <https://www.bic.ac.cn/IMP/>



IMP 整合植物资源数据库 功能展示



Ensembl (<http://www.ensembl.org/index.html?redirect=no>)




Show	<div>10</div> entries	Show/hide columns											Filter			
★	Species	DNA (FASTA)	cDNA (FASTA)	CDS (FASTA)	ncRNA (FASTA)	Protein sequence (FASTA)	Annotated sequence (EMBL)	Annotated sequence (GenBank)	Gene sets	Whole databases	Variation (GVF)	Variation (VCF)	Variation (VEP)	Regulation (GFF)	Data files	BAM/BigWig
Y	Human <i>Homo sapiens</i>	FASTA	FASTA	FASTA	FASTA	FASTA	EMBL	GenBank	GTF GFF3	MySQL	GVF	VCF	VEP	Regulation (GFF)	Regulation data files	BAM/BigWig
Y	Mouse <i>Mus musculus</i>	FASTA	FASTA	FASTA	FASTA	FASTA	EMBL	GenBank	GTF GFF3	MySQL	GVF	VCF	VEP	Regulation (GFF)	Regulation data files	BAM/BigWig
Y	Zebrafish <i>Danio rerio</i>	FASTA	FASTA	FASTA	FASTA	FASTA	EMBL	GenBank	GTF GFF3	MySQL	GVF	VCF	VEP	-	-	BAM/BigWig
	Alpaca <i>Vicugna pacos</i>	FASTA	FASTA	FASTA	FASTA	FASTA	EMBL	GenBank	GTF GFF3	MySQL	-	-	VEP	-	-	-
	Amazon molly <i>Poecilia formosa</i>	FASTA	FASTA	FASTA	FASTA	FASTA	EMBL	GenBank	GTF GFF3	MySQL	-	-	VEP	-	-	BAM/BigWig
	Anole lizard <i>Anolis carolinensis</i>	FASTA	FASTA	FASTA	FASTA	FASTA	EMBL	GenBank	GTF GFF3	MySQL	-	-	VEP	-	-	BAM/BigWig
	Armadillo <i>Dasypus novemcinctus</i>	FASTA	FASTA	FASTA	FASTA	FASTA	EMBL	GenBank	GTF GFF3	MySQL	-	-	VEP	-	-	BAM/BigWig

<ftp://ftp.ensembl.org/pub/release->

ftp://ftp.ensembl.org/pub/release-104/assembly/dna/Mus_musculus.GRCm38.dna.primary_assembly.fa.gz

Ensembl - BioMart



 BLAST/BLAT | **BioMart** | BLAST | VEP | Tools | Downloads | Help & Docs | Blog

Login/Register

Search all species...

New | Count | Results

URL | XML | Perl | Help

Dataset

Human genes (GRCh38.p12)

Filters

[None selected]

Attributes

Gene stable ID

Transcript stable ID

Dataset

[None Selected]

Please select columns to be included in the output and hit 'Results' when ready

Missing non coding genes in your mart query output, please check the following [FAQ](#)

☒ Features

☐ Variant (Germline)

☐ Structures

☐ Variant (Somatic)

☐ Homologues

☐ Sequences

☐ GENE:

☐ EXTERNAL:

☐ PROTEIN DOMAINS AND FAMILIES:

Ensembl - BioMart (Features)



BLAST/BLAT | BioMart | BLAST | VEP | Tools | Downloads | Help & Docs | Blog

Login/Register

Search all species...

New Count Results

URL XML Perl Help

Dataset

Human genes (GRCh38.p12)

Filters

[None selected]

Attributes

Gene stable ID

Transcript stable ID

Gene name

Gene start (bp)

Gene end (bp)

Strand

NCBI gene ID

UniProtKB Gene Name ID

GO term definition

Dataset

[None Selected]

Export all results to ☐ Unique results only Go

Email notification to

View rows as ☐ Unique results only

Gene stable ID	Transcript stable ID	Gene name	Gene start (bp)	Gene end (bp)	Strand	NCBI gene ID	UniProtKB Gene Name ID	GO term definition
ENSG00000210049	ENST00000387314	MT-IF	577	647	1			
ENSG00000211459	ENST00000389680	MT-RNR1	648	1601	1	4549		
ENSG00000210077	ENST00000387342	MT-TV	1602	1670	1			
ENSG00000210082	ENST00000387347	MT-RNR2	1671	3229	1	4550		
ENSG00000209082	ENST00000386347	MT-TL1	3230	3304	1			
ENSG00000198888	ENST00000361390	MT-ND1	3307	4262	1	4535	P03886	"A lipid bilayer along with all the proteins and protein complexes embedded in it an attached to it." [GOC:dos, GOC:mah, ISBN:0815316194]
ENSG00000198888	ENST00000361390	MT-ND1	3307	4262	1	4535	P03886	"A metabolic process that results in the removal or addition of one or more electrons to or from a substance, with or without the concomitant removal or addition of a proton or protons." [GOC:dhl, GOC:ecd, GOC:ehp, GOC:ehp, GOC:ehp, GOC:ehp]

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Ensembl - BioMart (Structures)



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Search all species...

New | Count | Results

★ URL | XML | Perl | Help

Dataset

Human genes (GRCh38.p12)

Filters

[None selected]

Attributes

Gene stable ID

Gene start (bp)

Gene end (bp)

Strand

5' UTR start

5' UTR end

3' UTR start

3' UTR end

Gene type

Dataset

[None Selected]

Please select columns to be included in the output and hit 'Results' when ready

Missing non coding genes in your mart query output, please check the following [FAQ](#)

☐ Features

☐ Variant (Germline)

☒ Structures

☐ Variant (Somatic)

☐ Homologues

☐ Sequences

GENE:

Ensembl

☒ Gene stable ID

☐ Transcript stable ID

☐ Protein stable ID

☐ Chromosome/scaffold name

☒ Gene start (bp)

☒ Gene end (bp)

☐ Transcript start (bp)

☐ Transcript end (bp)

☐ Transcription start site (TSS)

☐ Transcript length (including UTRs and CDS)

☒ Strand

☐ Gene name

☐ Source of gene name

☒ 5' UTR start

☒ 5' UTR end

☒ 3' UTR start

☒ 3' UTR end

☐ CDS Length

☐ Transcript count

☐ Gene description

☒ Gene type

EXON:

Ensembl - BioMart (Sequences)



BLAST/BLAT | BioMart | BLAST | VEP | Tools | Downloads | Help & Docs | Blog

Login/Register

Search all species...

New Count Results

URL XML Perl Help

Dataset

Human genes (GRCh38.p12)

Filters

[None selected]

Attributes

Gene stable ID

Transcript stable ID

3' UTR

Dataset

[None Selected]

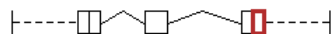
Please select columns to be included in the output and hit 'Results' when ready

Missing non coding genes in your mart query output, please check the following [FAQ](#)

- ☐ Features
- ☐ Variant (Germline)
- ☐ Structures
- ☐ Variant (Somatic)
- ☐ Homologues
- ☒ Sequences

SEQUENCES:

Sequences (max 1)



- ☐ Unspliced (Transcript)
- ☐ Unspliced (Gene)
- ☐ Flank (Transcript)
- ☐ Flank (Gene)
- ☐ Flank-coding region (Transcript)
- ☐ Flank-coding region (Gene)
- ☐ 5' UTR
- ☒ 3' UTR
- ☐ Exon sequences
- ☐ cDNA sequences
- ☐ Coding sequence
- ☐ Peptide

Upstream flank

☐ Upstream flank



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Ensembl - BioMart (Homologues)



Ensembl [BLAST/BLAT](#) | [BioMart](#) | [BLAST](#) | [VEP](#) | [Tools](#) | [Downloads](#) | [Help & Docs](#) | [Blog](#)

Search all species...

[New](#) [Count](#) [Results](#)

[★ URL](#) [XML](#) [Perl](#) [Help](#)

Dataset	Please select columns to be included in the output and hit 'Results' when ready
Human genes (GRCh38.p12)	Missing non coding genes in your mart query output, please check the following FAQ
Filters	
[None selected]	
Attributes	
Gene stable ID	<input type="radio"/> Features <input type="radio"/> Variant (Germline)
	<input type="radio"/> Structures <input type="radio"/> Variant (Somatic)
	<input checked="" type="radio"/> Homologues <input type="radio"/> Sequences
Dataset	
[None Selected]	<input type="checkbox"/> GENE:
	<input type="checkbox"/> ORTHOLOGUES (Max select 6 orthologues):
	<input type="checkbox"/> PARALOGUES:





GEO DataSets

GEO DataSets

Search

Create alert Advanced

Help

Entry type

DataSets (42)
Series (2,037)
Samples (28,863)
Platforms (24)

Organism

Customize ...

Study type

Expression profiling by array
Methylation profiling by array
Customize ...

Author

Customize ...

Attribute name

tissue (13,767)
strain (1,201)
Customize ...

Publication dates

30 days
1 year
Custom range...

Clear all

Show additional filters

Summary 20 per page Sort by Default order

Search results

Items: 1 to 20 of 30966

<< First < Prev Page 1 of 1549 Next > Last >>

Send to:

Filters: [Manage Filters](#)

Top Organisms [\[Tree\]](#)

More...

Find related data

Database:

Find items

Search details

"liver neoplasms" [MeSH Terms] OR liver cancer [All Fields]

Search

See more...

Recent activity

Turn Off Clear

liver cancer (30966)

GEO DataSets

RNA Sequencing [\[Icon\]](#) [\[Icon\]](#) [\[Icon\]](#) [\[Icon\]](#) [\[Icon\]](#) [\[Icon\]](#)

Normal liver developmental stages: embryonic and postnatal

1. Analysis of hepatoblasts, immature hepatocytes and hepatocytes from livers at different developmental timepoints (embryonic day 14, embryonic day 18, post-natal day 5, post-natal day 56). Results provide insight into molecular mechanisms underlying normal liver development.

Organism: Mus musculus
Type: Expression profiling by array, log2 ratio, 4 age, 3 cell type, 2 development stage sets
Platform: GPL7202 Series: GSE65063 11 Samples
Download data: TXT

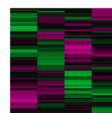
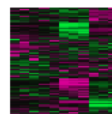
DataSet Accession: GDS5818 ID: 5818
[PubMed](#) [Full text in PMC](#) [Similar studies](#) [GEO Profiles](#) [Analyze DataSet](#)

Mutant isocitrate dehydrogenase 1 effect on hepatoblasts grown on uncoated plates

2. Analysis of mutant IDH1 (R132C)-expressing hepatoblasts that were grown on uncoated plates to induce hepatocyte differentiation. IDH genes are frequently mutated in intrahepatic cholangiocarcinoma (IHCC). Results provide insight into the role of IDH1 in hepatocyte differentiation.

Organism: Mus musculus
Type: Expression profiling by array, count, 2 genotype/variation sets
Platform: GPL8321 Series: GSE57002 4 Samples
Download data: CEL

DataSet Accession: GDS5677 ID: 5677
[PubMed](#) [Full text in PMC](#) [Similar studies](#) [GEO Profiles](#) [Analyze DataSet](#)



Entry type

DataSets (42)
Series (2,037)
Samples (28,863)
Platforms (24)

Organism

Customize ...

Study type

Expression profiling by array
Methylation profiling by array
Customize ...

Author

Customize ...

Attribute name

tissue (13,767)
strain (1,201)
Customize ...

Publication dates

30 days
1 year
Custom range...

[Clear all](#)

[Show additional filters](#)

Summary

Search results

Items: 1 to

☐ [Normal](#)

1. Analysis of day 56 development of Organism Type: Platform Download: DataSet PubMed

☐ [Mutant](#)

2. Analysis of plates t cholang differen Organism Type: Platform Download: DataSet PubMed

Entry type

DataSets (13)
Series (355)
Samples (1,80)
Platforms (5)

Organism

Customize ...

Study type

Expression pro

throughput s

Customize ...

Author

Customize ...

Attribute name

tissue (1,419)
strain (1,064)
Customize ...

Publication date

30 days

1 year

Custom range

[Clear all](#)

[Show additional](#)

Study type

- ☐ Expression profiling by MPSS
- ☐ Expression profiling by RT-PCR
- ☐ Expression profiling by SAGE
- ☐ Expression profiling by SNP array
- ☐ Expression profiling by array
- ☐ Expression profiling by genome tiling array
- ☒ Expression profiling by high throughput sequencing
- ☐ Genome binding/occupancy profiling by SNP array
- ☐ Genome binding/occupancy profiling by array
- ☐ Genome binding/occupancy profiling by genome tiling array
- ☐ Genome binding/occupancy profiling by high throughput sequencing
- ☐ Genome variation profiling by SNP array
- ☐ Genome variation profiling by array
- ☐ Genome variation profiling by genome tiling array
- ☐ Genome variation profiling by high throughput

Show

Summary 20 per page Sort by

wangzhimin07 My NCBI Sign Out

Search

Help

Filters: [Manage Filters](#)

Top Organisms [\[Tree\]](#)

More...

Find related data

Database: [Select](#)

Find items

Search details

liver neoplasms [MeSH Terms] OR liver cancer [All Fields]

Search

See more...

Recent activity

[Turn Off](#) [Clear](#)

liver cancer (30966)

GEO DataSets

RNA Sequencing: [\[Icon\]](#) [\[Icon\]](#) [\[Icon\]](#) [\[Icon\]](#) [\[Icon\]](#) [\[Icon\]](#)

ENCODE - Encyclopedia of DNA Elements



ENCODE

Data

Encyclopedia

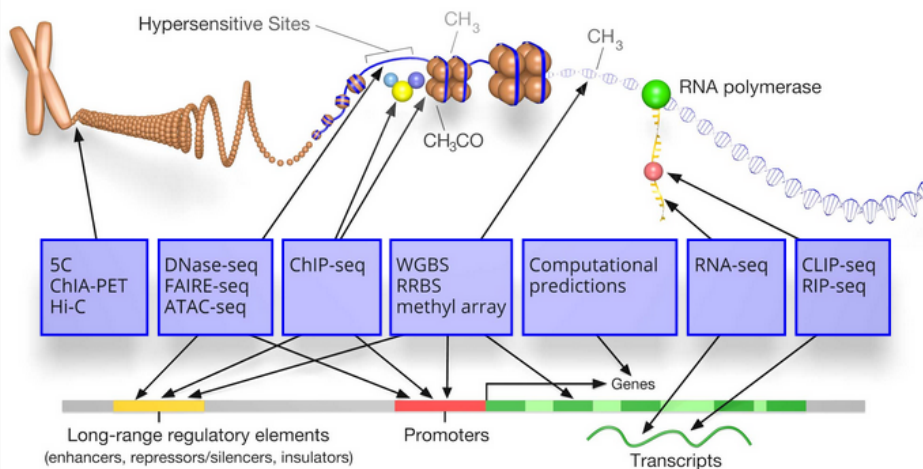
Materials & Methods

Help

Search...



ENCODE: Encyclopedia of DNA Elements



The ENCODE (Encyclopedia of DNA Elements)

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.

[Get Started](#)

Based on an image by Darryl Leja (NHGRI), Ian Dunham (EBI), Michael Pazin (NHGRI)



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ENCODE - Encyclopedia of DNA Elements



ENCODE

Data

Encyclopedia

Materials & Methods

Help

Search...



Experiment Matrix

Click or enter search terms to filter the experiments included in the matrix.

Enter search term(s)

Organism

<i>Homo sapiens</i>	9972
<i>Mus musculus</i>	1782
<i>Drosophila melanogaster</i>	1292
<i>Caenorhabditis elegans</i>	907
<i>Drosophila pseudoobscura</i>	4
<i>Drosophila mojavensis</i>	2

[- See fewer](#)

Biosample type

cell line	5508
tissue	4103
whole organisms	1861
primary cell	1398
in vitro differentiated cells	561

[+ See more...](#)

Organ

2410

Assay

ChIP-seq	8405
DNase-seq	839
polyA RNA-seq	756
shRNA RNA-seq	526
total RNA-seq	408

[+ See more...](#)

Assay category

DNA binding	8405
Transcription	3033
DNA accessibility	1098
RNA binding	590
DNA methylation	561

[+ See more...](#)

Target of assay

transcription factor	3724
histone	2945
histone modification	2945
control	2424
broad histone mark	1637

[+ See more...](#)

Date released

July, 2013	2161
March, 2014	829
July, 2016	609
May, 2016	527
October, 2016	462

[+ See more...](#)

Available data

fastq	13290
bam	12512
bigWig	11518
bed narrowPeak	7240
bigBed narrowPeak	7231

[+ See more...](#)

BIO SAMPLE

14119 results



Clear Filters

ASSAY

cell line

K562	669	8	19	271	11	185	3	7	1	1	10	1	2	9	1	50	6	1
HepG2	356	3	11	255	5	160	3	3	2		6		2	6	1		6	2
A549	374	14	27				2	9	1		5	2		2	3		2	1
GM12878	227	3	13	3		3	6	1	1		7	1	2	6	1		6	2
HEK293	244						2				1							2

[+ See 205 more...](#)

tissue

liver	161	9	20	3	1	1	9	7	7	2			7			1
heart	99	22	16	3			1	10	9	7	2		8			
stomach	94	21	15	5		3	4	10	4	6	5		4			1

...and
25
more

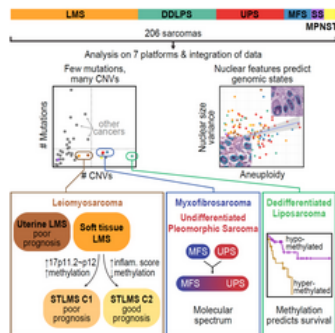
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TCGA - The Cancer Genome Atlas



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TCGA's Study of Soft Tissue Sarcoma

TCGA's analysis of six major types of adult soft tissue sarcomas reveals frequent copy number alterations, low mutational loads, and a diverse array of underlying molecular mechanisms. Certain sarcomas may benefit from immunotherapy.

[Learn More](#)

[Launch Data Portal](#)

The Genomic Data Commons (GDC) Data Portal is an interactive data system for researchers to search, download, upload, and analyze harmonized cancer genomic data sets, including TCGA.

Questions About Cancer

Visit www.cancer.gov

Call 1-800-4-CANCER

Use LiveHelp Online Chat

Multimedia Library

[Images](#)

[Videos and Animations](#)

[Podcasts](#)

[Interactive](#)

TCGA in Action



December 2016
CASE STUDY: A Researcher Mined
TCGA Data to Study Her Own Ovarian
Cancer

News and Announcements

November 02, 2017
TCGA Soft Tissue Sarcoma Study Charts Diverse
Landscape of Molecular Changes
TCGA's analysis of six major types of adult soft tissue

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TCGA data portal

TCGA数据库在线使用

原创 2017-08-26 陈同 生信宝典



NIH NATIONAL CANCER INSTITUTE
GDC Data Portal

Home

Projects

Exploration

Analysis

Repository

Q

Manage Sets

0

0

0

Harmonized Cancer Datasets

Genomic Data Commons Data Portal

Get Started by Exploring:



Projects



Exploration



Analysis



Repository

Q e.g. BRAF, Breast, TCGA-BLCA, TCGA-A5-A0G2

Data Portal Summary

[Data Release 10.1 - February 15, 2018](#)

PROJECTS



40

PRIMARY SITES



61

CASES



32,555

FILES



310,859

GENES



22,147

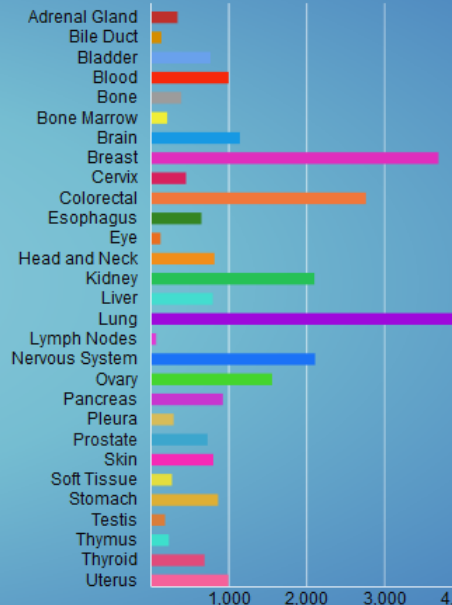
MUTATIONS



3,142,246



Cases by Major Primary Site



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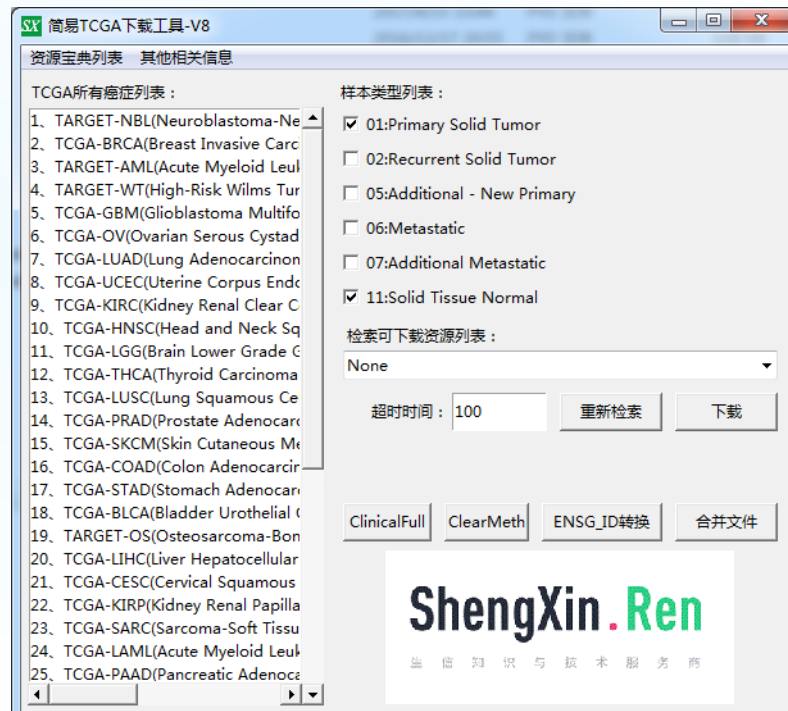
○ GDC Data Transfer Tool

<https://gdc.cancer.gov/access-data/gdc-data-transfer-tool>

<https://docs.gdc.cancer.gov/Data Transfer Tool/Users Guide/Data Download and Upload/>

[UCSC XENA \(集成分析TCGA, ICGC数据\)](#)

○ TCGA简易下载小工具 (生信人)



Human protein atlas (<http://www.proteinatlas.org/>)



THE HUMAN PROTEIN ATLAS

[MENU](#) [HELP](#) [NEWS](#)

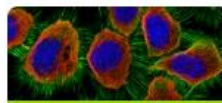
SEARCH¹

e.g. RBM3, insulin, CD36

[Search](#) [Fields »](#)



TISSUE ATLAS



CELL ATLAS



PATHOLOGY ATLAS

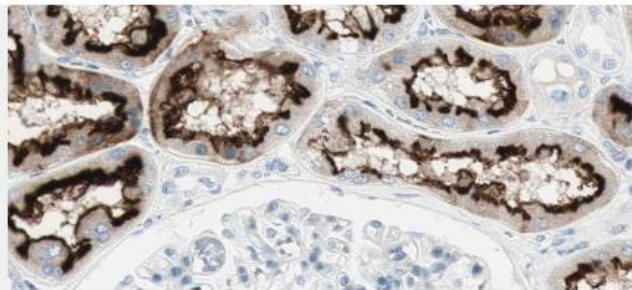


image of the day

Version: 18

Atlas updated: 2017-12-01

[release history](#)

Proteome analysis based on
26009 antibodies targeting
17000 unique proteins.

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Human protein atlas (<http://www.proteinatlas.org/>)



THE HUMAN PROTEIN ATLAS

≡ MENU HELP NEWS

SEARCHⁱ

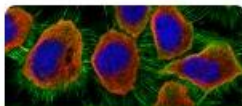
CD36

Search

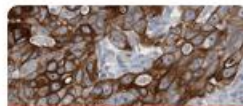
Fields »



TISSUE ATLAS



CELL ATLAS



PATHOLOGY ATLAS

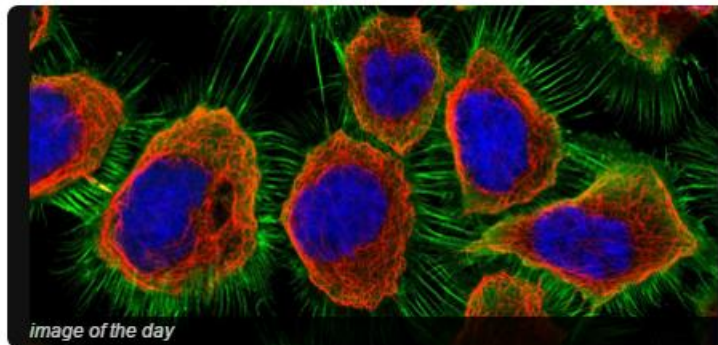


image of the day

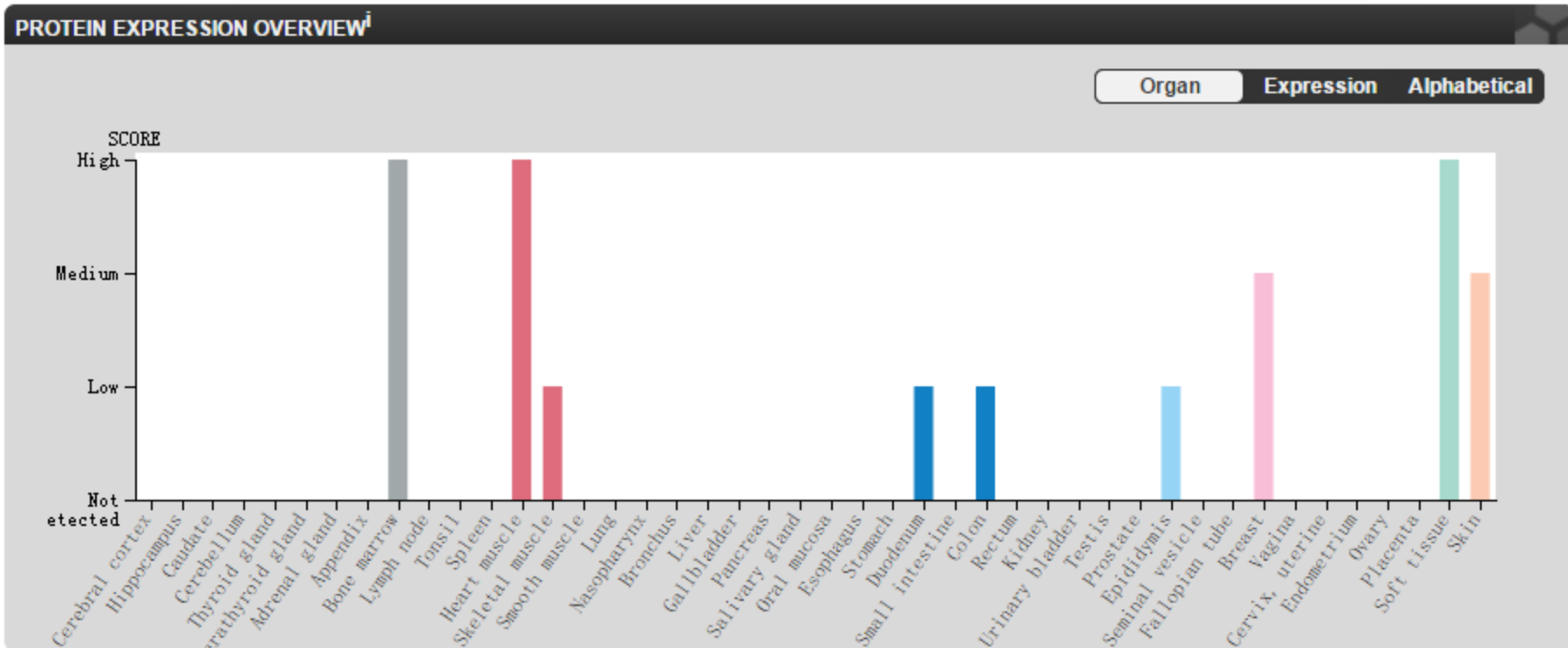
Version: 18
Atlas updated: 2017-12-01
[release history](#)

Proteome analysis based on
26009 antibodies targeting
17000 unique proteins.

在线查询目的基因的信息。



Human protein atlas - 蛋白表达水平



Human protein atlas - RNA表达水平



RNA EXPRESSION OVERVIEWⁱ

HPA datasetⁱ

TPM
GTEx datasetⁱ

FANTOM5 datasetⁱ

RNA tissue category: Expressed in all

Organ

Expression

Alphabetical

RNA tissue category: Group enriched (adipose tissue, breast, heart muscle, spleen)

Organ

Expression

Alphabetical

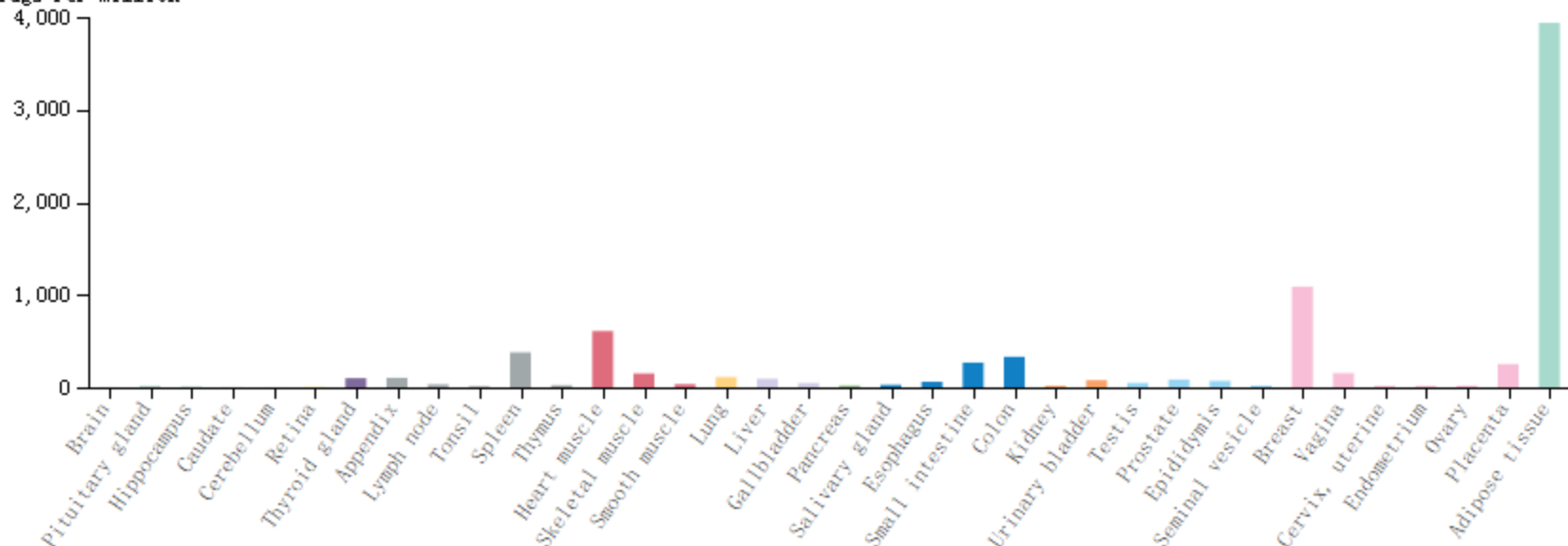
RNA tissue category: Tissue enhanced (adipose tissue)

Organ

Expression

Alphabetical

Tags Per Million



Human protein atlas (<http://www.proteinatlas.org/>)



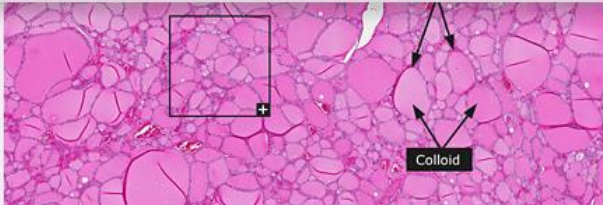
THE HUMAN PROTEIN ATLAS

MENU **HELP** **NEWS**

THE HUMAN PROTEOME	NEWS	THE PROJECT	TECHNICAL DATA
THE HUMAN TISSUES	NEWS ARTICLES	INTRODUCTION	ANTIBODY VALIDATION
THE HUMAN CELL	EVENTS	ORGANIZATION	ASSAYS & ANNOTATION
HUMAN PATHOLOGY	PRESS ROOM	PUBLICATIONS	DISCLAIMER
PROTEIN CLASSES		PUBLICATION DATA	DOWNLOADABLE DATA
PROTEIN EVIDENCE		ANTIBODY SUBMISSION	HELP & FAQ
		ANTIBODY AVAILABILITY	LICENCE & CITATION
		LINKS	PRIVACY STATEMENT
		CONTACT	RELEASE HISTORY

LEARN

- DICTIONARY
- METHODS
- CELL LINES



dictionary: histology of Thyroid gland

Version: 18
Atlas updated: 2017-12-01
[release history](#)

Proteome analysis based on
26009 antibodies targeting
17000 unique proteins.

下载数据进行本地分析。



Human protein atlas (<http://www.proteinatlas.org/>)



The data is based on The Human Protein Atlas version 18 and Ensembl version 88.38.

4 RNA gene data

RNA levels in 64 cell lines and 37 tissues based on RNA-seq. The tab-separated file includes Ensembl gene identifier ("Gene"), analysed sample ("Sample") and transcripts per million ("Value" and "Unit"). The data is based on The Human Protein Atlas version 18 and Ensembl version 88.38.

[RNA sequencing data for human tissue](#)

[RNA sequencing data for human cell lines](#)

[rna_tissue.tsv.zip](#)

TSV-file, 3.7 MB

[rna_cellline.tsv.zip](#)

TSV-file, 6.2 MB

5 RNA isoform data

RNA levels in 64 cell lines and 37 tissues based on RNA-seq. The tab-separated file includes Ensembl gene identifier ("Gene"), Ensembl transcript identifier ("Transcript"), analysed sample ("Sample") and transcript per million ("TPM"). The data is based on The Human Protein Atlas version 18 and Ensembl version 88.38.

[transcript_rna_tissue.tsv.zip](#)

TSV-file, 73.7 MB

[transcript_rna_cellline.tsv.zip](#)

TSV-file, 51.9 MB

6 Data from the Human Protein Atlas in tab-separated format

This file contains a subset of the data in the Human Protein Atlas version 18 corresponding to the data seen in the search result. This data can also be downloaded for a resulting gene set when using the search function (via the TSV link on the result page).

[proteinatlas.tsv.zip](#)

TSV-file (gzip compressed), 1.5 MB

7 Data from the Human Protein Atlas in XML format

The XML file contains most of the data in the Human Protein Atlas version 18.


[proteinatlas.xml.gz](#)

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GeneCards (<http://www.genecards.org/>)




 **GeneCardsSuite**


GeneCards MalaCards LifeMap Discovery PathCards TGex VarElect GeneAnalytics GeneALaCart GenesLikeMe

 **GeneCards®**
HUMAN GENE DATABASE

 **WEIZMANN INSTITUTE OF SCIENCE**

 **LifeMap**
SCIENCES


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Keywords ▾ Search Term  [Advanced](#)


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GeneCards®: The Human Gene Database

GeneCards is a searchable, integrative database that provides comprehensive, user-friendly information on all annotated and predicted human genes. It automatically integrates gene-centric data from ~125 web sources, including genomic, transcriptomic, proteomic, genetic, clinical and functional information.




Explore a Gene


ADAM10  **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 Tools


 **TGex™**
TRANSLATIONAL GENOMICS EXPERT


 **VarElect**
NGS PHENOTYPING

Affiliated Databases


 **MalaCards**
HUMAN DISEASE DATABASE


 **LifeMap®**
DISCOVERY

 **PathCards**
PATHWAY ANNOTATION DATABASE

 **GeneLoc**
GENOME BROWSER

Analysis Tools

 **GeneAnalytics**
GENE SET ANALYSIS

 **GeneALaCart**
GENE-RELATED GENE SOURCES

GeneCards (<http://www.genecards.org/>)



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OF SCIENCE



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Keywords ▾

Search Term



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[Log In / Sign Up](#)

ADAM10 Gene (Protein Coding)

ADAM Metallopeptidase Domain 10

GCID: GC15M058588 ?

GIFS: 63 ?

Genes
Participants



Undiagnosed
Diseases Network

[Jump to
section](#)

[Aliases](#) [Disorders](#) [Domains](#) [Drugs](#) [Expression](#) [Function](#) [Genomics](#) [Localization](#) [Orthologs](#)
[Paralogs](#) [Pathways](#) [Products](#) [Proteins](#) [Publications](#) [Sources](#) [Summaries](#) [Transcripts](#) [Variants](#)



Genes Peptides Proteins
CRISPR



Proteins Antibodies Assays
Genes shRNA Primers
CRISPR Lentiviral Particles



Genes (adenoviral)
Genes (lentiviral) miRNA
shRNA (AAV)



ORF Clones CRISPR
Cloning Vectors
Lentiviral Vectors

Aliases for ADAM10 Gene

Aliases for ADAM10 Gene

ADAM Metallopeptidase Domain 10^{2 3 5}
Mammalian Disintegrin-Metalloprotease^{3 4}
Kuzbanian Protein Homolog^{3 4}
EC 3.4.24.81^{4 5 6}
CDw156^{3 4}
MADM^{3 4}
Kuz^{3 4}
Disintegrin And Metalloproteinase Domain-Containing Protein 10³

CD156c Antigen⁴
EC 3.4.24^{5 6}
HsT18717³
ADAM 10⁴
CD156c³
AD10³
AD18³
RAK³



GeneAnalytics
GENE SET ANALYSIS

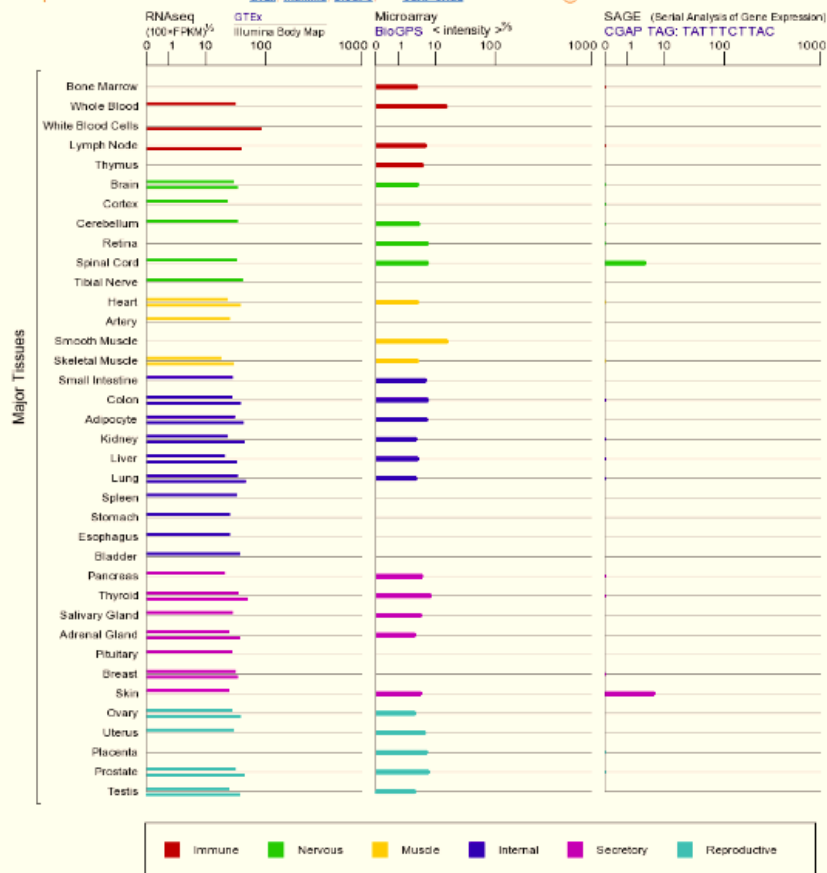
Cells, Diseases, Pathways,
Functions and Compounds
relevant to your gene set
Powered by GeneCards

[START 7 DAY FREE TRIAL >](#)

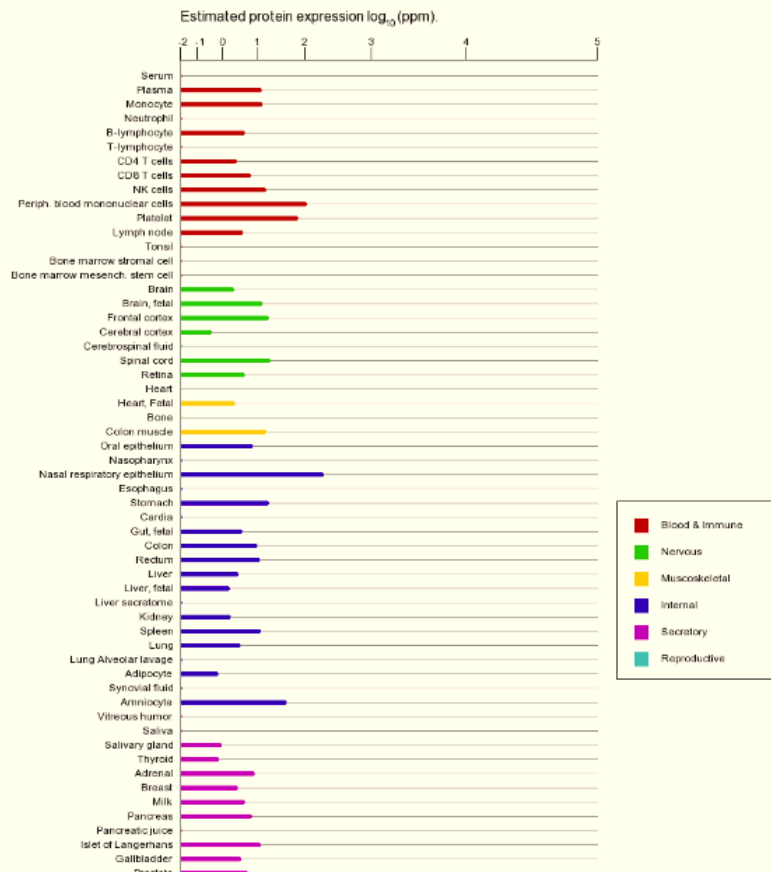
GeneCards - RNA和蛋白表达水平



mRNA expression in normal human tissues from [GTEx](#), [Illumina](#), [BioGPS](#), and [CGAP SAGE](#) for ADAM10 Gene



Integrated Proteomics: protein expression in normal tissues and cell lines from [ProteomicsDB](#), [MaxQB](#), and [MOPED](#) for ADAM10 Gene





Expression Atlas

Gene expression across species and biological conditions

[Home](#)[Download](#)[Release notes](#)[FAQ](#)[Help](#)[Licence](#)[About](#)[Feedback](#)

Search this project



Examples: [ASPM](#), [Apoptosis](#), [ENSMUSG00000021789](#), [zinc finger](#)



Exploring gene expression results across species under different biological conditions

Expression Atlas is an open science resource that gives users a powerful way to find information about gene and protein expression across species and biological conditions such as different tissues, cell types, developmental stages and diseases among others. Expression Atlas aims to help answering questions such as 'where is a certain gene expressed?' or 'how does its expression change in a disease?'.

[Read more about Expression Atlas](#)

Search

Gene set enrichment

Gene / Gene properties

Examples: [REG1B](#), [zinc finger](#), [O14777 \(UniProt\)](#), [GO:0010468 \(regulation of gene expression\)](#)

Organism

Homo sapiens

Biological conditions

Examples: [lung](#), [leaf](#), [valproic acid](#), [cancer](#)



EBI gxa支持多物种，动物，植物，真菌



By species

Animals

Plants

Fungi



Homo sapiens

1200 experiments

B 29 D 1171



Mus musculus

976 experiments

B 40 D 936



Arabidopsis thaliana

533 experiments

B 6 D 527



Rattus norvegicus

141 experiments

B 2 D 139



Drosophila melanogaster

128 experiments

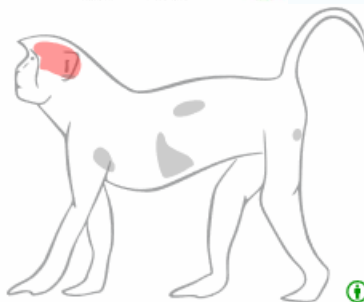
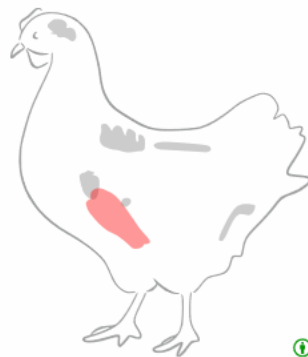
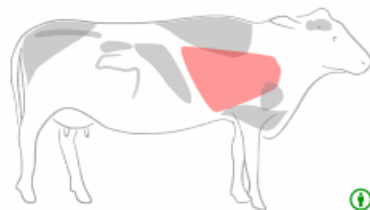
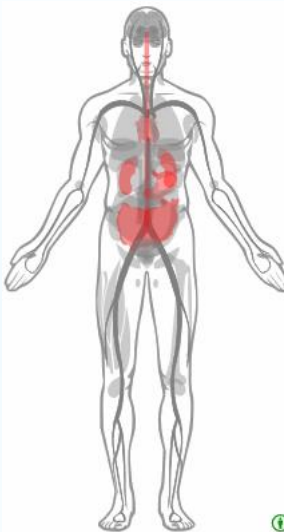
B 1 D 127



Saccharomyces cerevisiae

41 experiments

B 0 D 41



易生信，毕生缘；

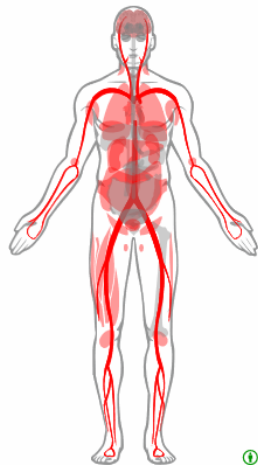


搜索基因Myc查看其表达



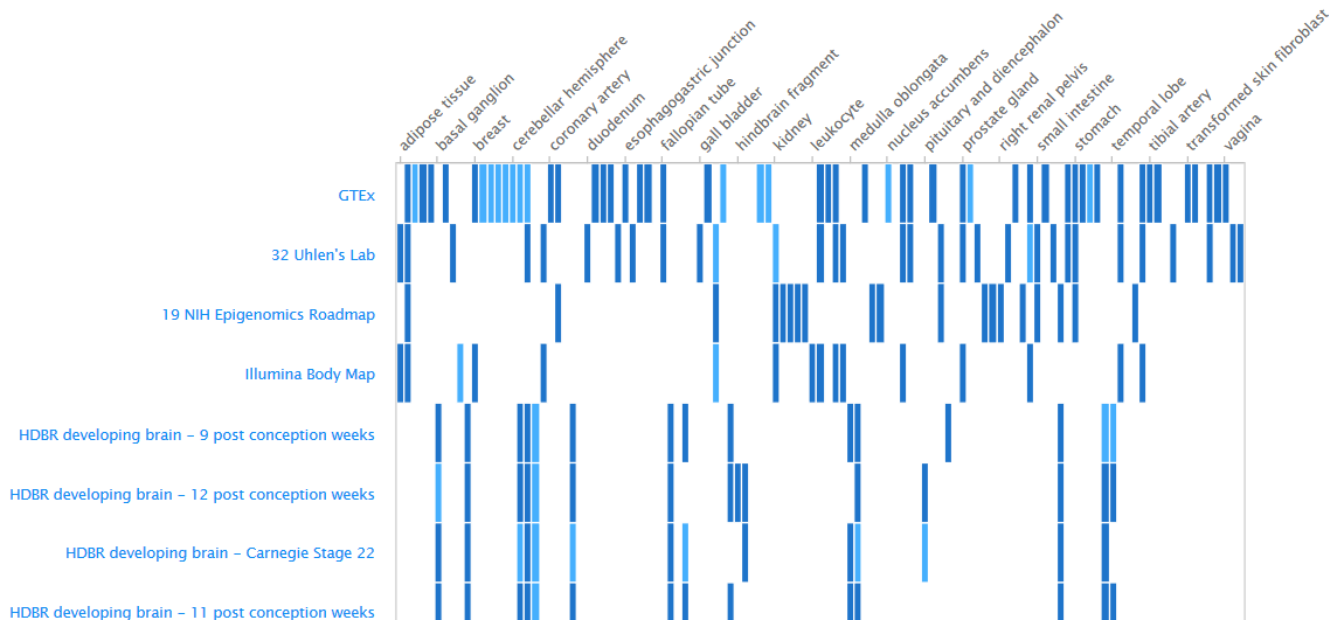
Homo sapiens — Organism part

Showing 30 experiments:



①

By experiment type Filters Download





Baseline expression

Differential expression

REG1B information



Show anatomograms

Organism part

Filter your results

Showing 9 experiments:

Sort By experiment type ▼

Filters

Download



Homo sapiens

☒ Organism part

☐ Cell line

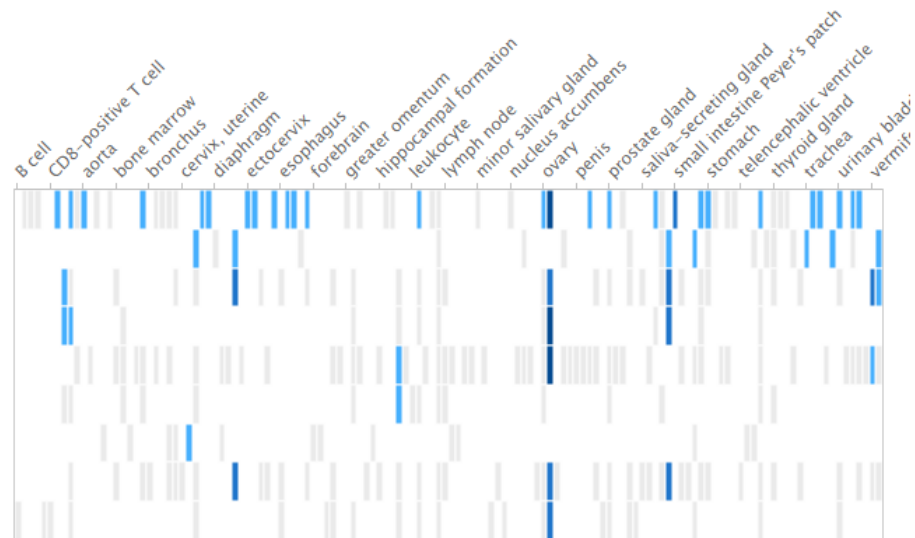


Developmental stage

☐ Disease

☐ Individual

68 FANTOM5 project - fetal
32 Uhlen's Lab
ENCODE (M. Snyder lab)
68 FANTOM5 project - adult
Illumina Body Map
HDBR developing brain - 10 post conception weeks
Human Protein Atlas
Human Proteome Map - adult



■ High ■ Medium ■ Low ■ Below cutoff ■ No data available



No data available



肿瘤和正常样本基因表达



GEPIA

GoPIA

Example

API

Help



GEPIA

Gene Expression Profiling Interactive Analysis

Single Gene Analysis

Cancer Type Analysis

Multiple Gene Analysis

Enter gene name:

9,736 tumors and 8,587 normal samples
from the TCGA and the GTEx projects

The indicators in search box are "symbol" or "alias (newest symbol)".

e.g. ERBB2/ENSG00000141736/2064

GoPIA!

Profile

Boxplots

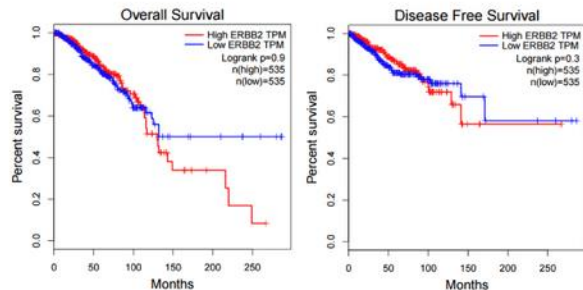
Stage Plots

Survival Analysis

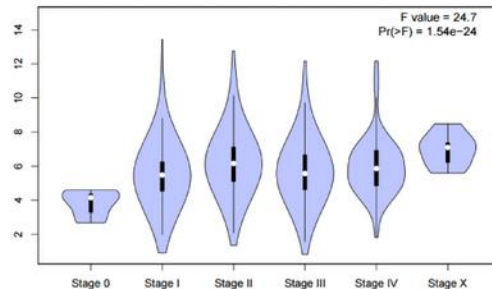
Similar



肿瘤和正常样本基因表达图谱绘制

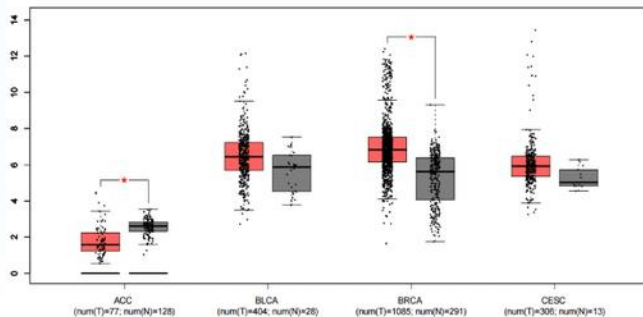


Survival analysis

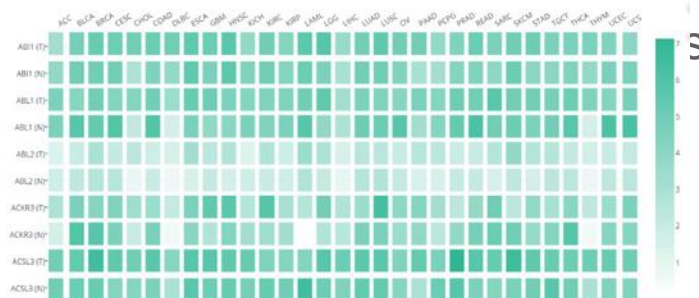


Analyze expression by stage

Normal/cancer comparison



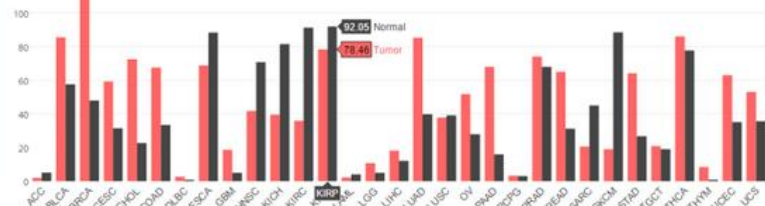
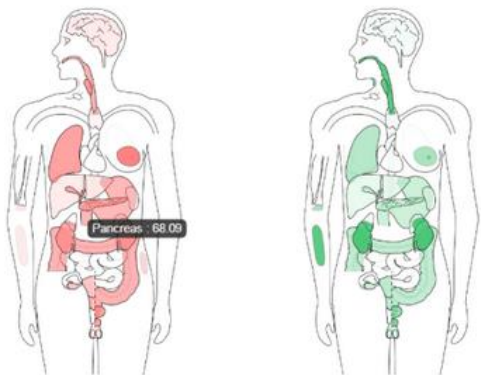
Gene comparison



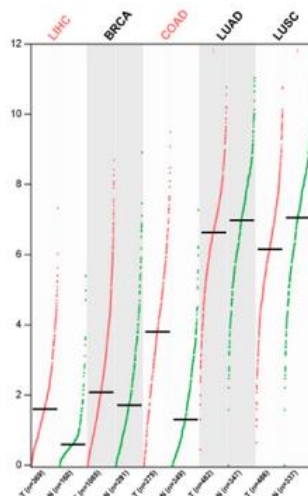
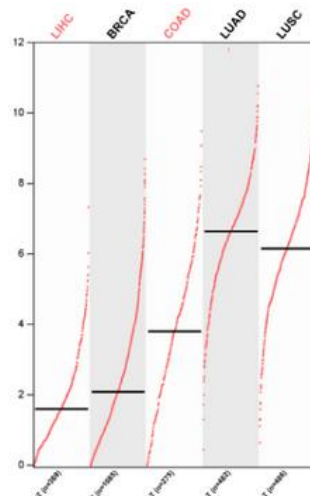
肿瘤和正常样本基因表达图谱绘制

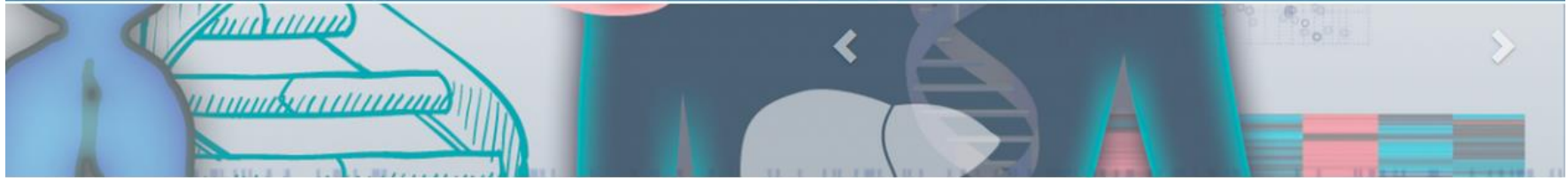


Interactive bodymap



Gene expression by cancer type / tissue type

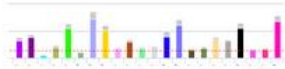




Current Release

Latest Version: V7

[Dataset Summary Statistics Report](#)



[How to cite](#)

[Browse eQTL](#)

Genetic Association

[Single-Tissue eQTLs](#)

Search eQTL by gene or SNP ID

[IGV eQTL Browser](#)



Transcriptome

Search expression by gene ID...

[Top 100 Expressed Genes in a Tissue \(e.g. Blood\)](#)

[Gene Expression in Tissues](#)



Portal for the Genotype-Tissue Expression (GTEx) project. Gene expression and quantitative trait loci from 53 human tissues. Visualization and download of all public data generated by the GTEx project.



BioGPS (<http://biogps.org/#goto=welcome>)



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BioGPS

A free *extensible* and *customizable* **gene annotation portal**, a complete resource for learning about **gene** and **protein function**.

[Plugins »](#) [Datasets »](#)



Simple to use

- 1  **Search**
for your gene of interest
- 2  **View**
the gene annotation report
- 3  **Browse**
the gene report layouts
- 4  **Build**
your own gene report

[Details »](#)

Search genes here:

CDK2
CDK3

Press Ctrl-Enter or click [Search](#)

Example Searches

(click to try these samples)

- Gene Symbol(s)
- Wildcard queries
- Gene Ontology
- Affymetrix IDs
- Interpro
- Genomic interval

User Love

 **User Love**

"BioGPS was so helpful in getting rich annotation for a sample of..."

News and Musings

Gene Wiki Data, BioThings, Mark2Cure, & more! A review of 2017 in the Su Lab
by ginger
Rather than summarize the 2017 progress on in each project in separate, project-specific posts, I'm putting it all in once [...] [\[view more\]](#)



BioGPS (<http://biogps.org/#goto=welcome>)



BioGPS

My Stuff Plugins Datasets Login here or Sign up Quick gene search

Current Gene List

View Undo Save

All (6)

☐ CDK2
☐ Cdk2
☐ Cdk2
☐ CDK3
☐ TEN1-CDK3
☐ Cdk3-ps

Saved Gene Lists

Load Export

All Gene Lists

Available after logging in.

Search Result Gene Report

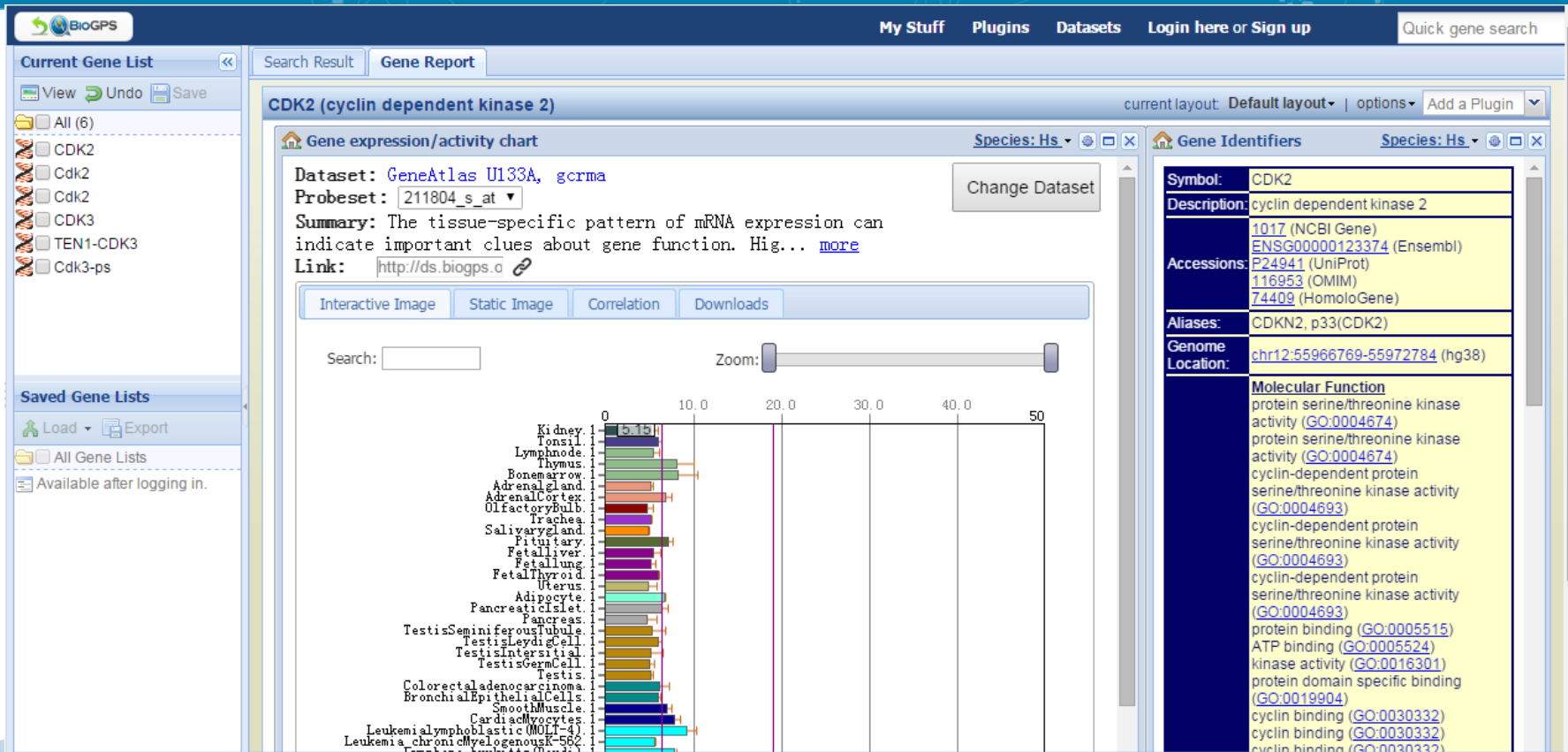
Your query returns 12 records, 6 records displayed:

NO.	QUERY	SYMBOL	ID	NAME	SPECIES
1	CDK2	CDK2	1017	cyclin dependent kinase 2	human
4	CDK3	CDK3	1018	cyclin dependent kinase 3	human
5	CDK3	TEN1-CDK3	100529145	TEN1-CDK3 readthrough (NMD candidate)	human
2	CDK2	Cdk2	12566	cyclin-dependent kinase 2	mouse
6	CDK3	Cdk3-ps	69681	cyclin-dependent kinase 3, pseudogene	mouse
3	CDK2	Cdk2	362817	cyclin dependent kinase 2	rat

Select species here:
☒ human (3)
☒ mouse (2)
☒ rat (1)
☐ fruitfly (1)
☐ nematode (0)
☐ zebrafish (1)
☐ thale-cress (1)
☐ frog (1)
☐ pig (2)
Select all



BioGPS (<http://biogps.org/#goto=welcome>)



Sequencing costs a lot and gains more



扫码关注生信宝典，学习更多生信知识



扫码关注宏基因组，获取专业学习资料

易生信，没有难学的生信知识



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