

BANCOS DE DADOS FANTASTICOS E ONDE HABITAM

CRISTAL VILLALBA

SCRIPT

O QUE TEMOS PRA HOJE?

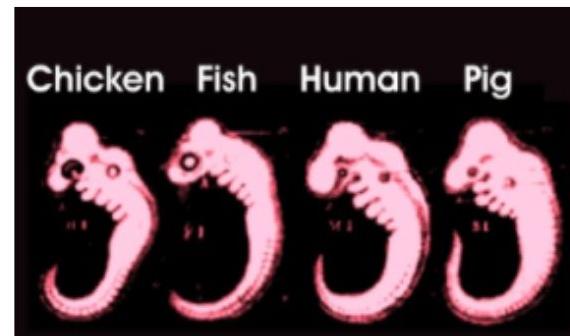
Bioinformática: Você sabia que ela tem mãe?

O que são bancos de dados?

O que são bancos de dados biológicos?

Tipos de bancos de dados

Exemplos



MENSAGEM (10) MOTIVACIONAL

SOMOS TODOS IGUAIS!

INTRO - A MÃE DA BIOINFO

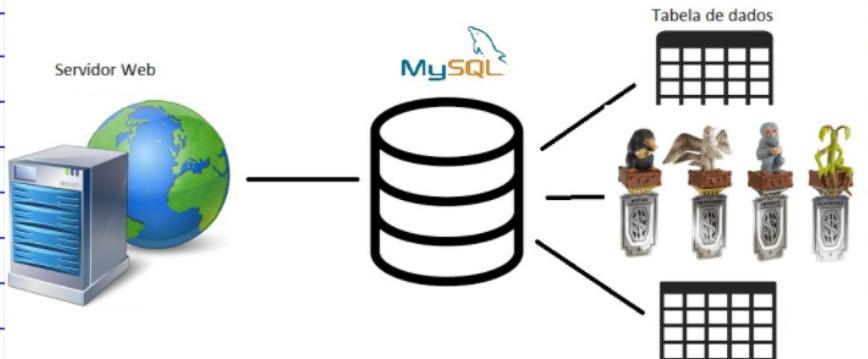
Margaret Oakley Dayhoff - Físico-química, professora e pesquisadora do National Biomedical Research Foundation, pioneira na aplicação de métodos matemáticos e computacionais ao campo da Bioquímica;

Criadora do Atlas de Sequências de Proteínas, nosso primeiro banco de dados biológico;

Também criou uma das primeiras matrizes de substituição, "Point accepted mutations" (PAM), para reduzir o tamanho dos arquivos utilizados para escrever sequências de aminoácidos na era da computação por cartões perfurados.

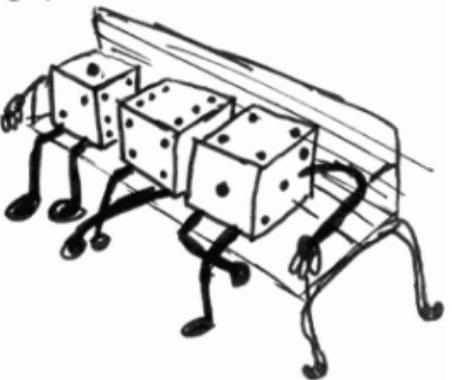
MARGARET OAKLEY DAYHOFF





O QUE SÃO BANCOS DE DADOS?

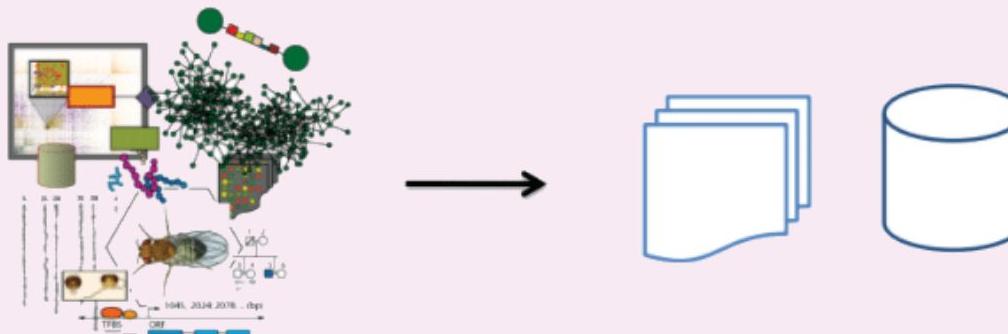
O BANCO DE DADOS



BANCOS DE DADOS BIOLÓGICOS

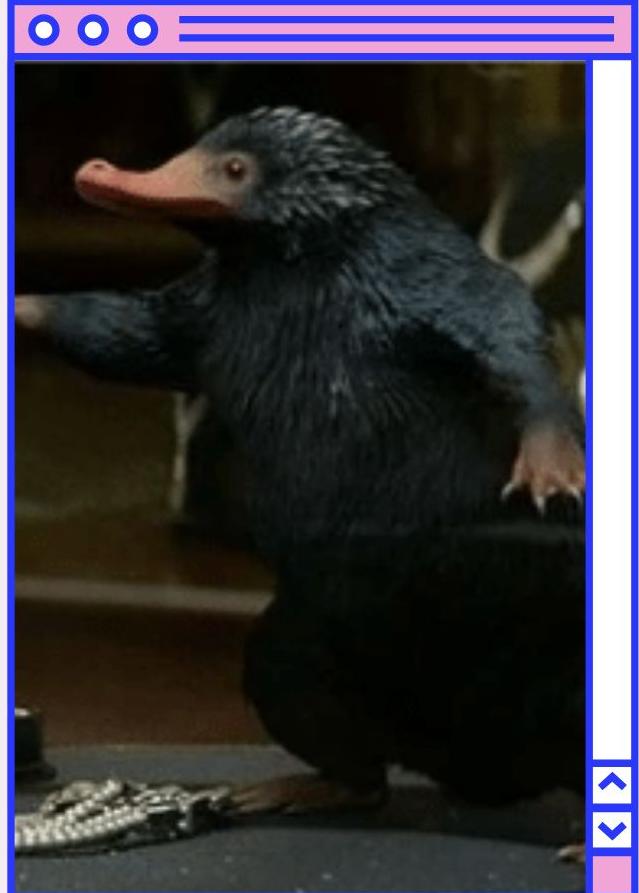
DADOS BIOLÓGICOS SÃO DADOS OU MEDIDAS COLETADAS A PARTIR DE FONTES BIOLÓGICAS

SÃO ARMAZENADOS EM BANCO DE DADOS BIOLÓGICOS (BDBS) ATRAVÉS DE ARQUIVOS



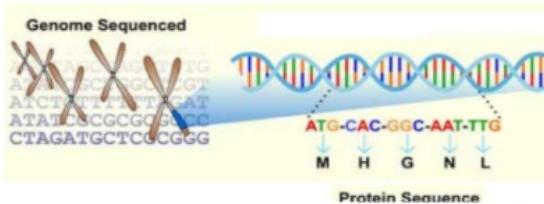
BANCOS DE DATOS DE SEQUENCIAS BIOLOGICAS
BANCOS DE DATOS DE ESTRUTURAS BIOLOGICAS
BANCOS DE DATOS DE ENRIQUECIMENTO FUNCIONAL

BANCOS PRIMARIOS
BANCOS SECUNDARIOS
BANCOS ESPECIALIZADOS



Bancos primários

- armazenam informações biológicas originais
 - sequências de nucleotídeos ou de proteínas



- Utilizam-se basicamente arquivos de tipo texto simples (e.g., tipo fasta) para armazenar essas informações.
- Dentre os principais BDBs primários destacam-se o **GenBank**, o **EMBL** e o **DDBJ** (Xiong, 2006).



Bancos secundários

- armazenam resultados de análises feitas a partir de dados primários
 - a partir de sequências de nucleotídeos ou de proteínas armazenas em BDBs primários
- O **SWISS-Prot** e o **PIR** (*Protein Information Resources*) são exemplos de BDBs secundários que armazenam informações referentes às proteínas, incluindo:
 - anotações de funcionalidades
 - estruturas tridimensionais e
 - literatura associada

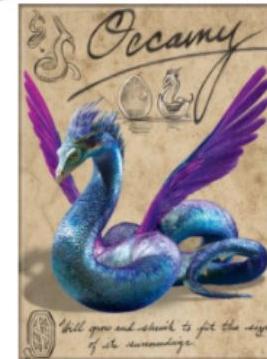


Bancos especializados

- são aqueles que atendem a um interesse particular de pesquisa.
- Dados são armazenados utilizando SGBDs ou arquivos
- Por exemplo, ***Flybase***, **HIV sequence database**, e **RDP** (*Ribossomal Database Project*) são BDBs especializados para um particular organismo ou tipo de dado



HIV DATABASES



EXEMPLOS



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NCBI National Center for Biotechnology Information

NCBI Home Resource List (A-Z) All Resources Chemicals & Bioassays Data & Software DNA & RNA Domains & Structures Genes & Expression Genetics & Medicine Genomes & Maps Homology Literature Proteins Sequence Analysis Taxonomy Training & Tutorials Variation

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NCBI News & Blog

Visit the new ClinVar for easier variant interpretation! 11 Oct 2019

The new ClinVar The new design for ClinVar names is now our default visual

New publication on AMRFinder, a tool that identifies resistance genes in pathogen genomes! 09 Oct 2019

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The NCBI Handbook [Internet]. 2nd edition.

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Small Molecules and Biological Assays

■ [Tools](#)

■ [The BLAST Sequence Analysis Tool](#)

■ [The Entrez Search and Retrieval System](#)

■ [C++ Toolkit](#)

■ [LinkOut: Linking to External Resources from NCBI Databases](#)

■ [Metadata](#)

Glossary

<https://www.ncbi.nlm.nih.gov/books/NBK169443/>

NCBI - Tutoriais

U.S. National Library of Medicine > NCBI National Center for Biotechnology Information

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Demonstrate How to Analyze NextGen Sequence
Data and Access Genetic Variation Population
Data

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Tutorials

Tutorials, Training materials in HTML, PDF and video formats



Documentation

Online manuals, handbooks, fact sheets and FAQs



Data & Software

All Databases Downloads Submissions Tools How To

Databases

[NCBI C++ Toolkit Manual](#)

A comprehensive manual on the NCBI C++ toolkit, including its design and development framework, a C++ library reference, software examples and demos, FAQs and release notes. The manual is searchable online and can be downloaded as a series of PDF documents.

Downloads

[BLAST \(Stand-alone\)](#)

BLAST executables for local use are provided for Solaris, LINUX, Windows, and Mac OSX systems. See the README file in the ftp directory for more information. Pre-formatted databases for BLAST nucleotide, protein, and translated searches also are available for downloading under the db subdirectory.

[FTP: BLAST Databases](#)

Sequence databases for use with the stand-alone BLAST programs. The files in this directory are pre-formatted databases that are ready to use with BLAST.

[FTP: CDD](#)

This site provides full data records for CDD, along with individual Position Specific Scoring Matrices (PSSMs), FASTA sequences and annotation data for each conserved domain. See the README file for full details.

[FTP: ClinVar Data](#)

This site provides full data extractions in XML and summary data in VCF format. It contains files with information about standard terms used in ClinVar, MedGen, and GTR.

[FTP: Fasta BLAST Databases](#)

Sequence databases in FASTA format for use with the stand-alone BLAST programs. These databases must be formatted using formattab before they can be used with BLAST.

[FTP: GenBank](#)

This site contains files for all sequence records in GenBank in the default flat file format. The GenBank division, and the full contents are described in the README.genbank file.

[FTP: GenPept](#)

The protein sequences corresponding to the translations of coding sequences (CDS) in GenBank. These files are in the GenPept format. Please see the README file in this directory for more information.



Quick Links

[BLAST \(Stand-alone\)](#)

[GenBank: BaitDB](#)

[GenBank: Sequin](#)

[GenBank: tbt2asn](#)

[SNP Submission Tool](#)

[Basic Local Alignment Search Tool \(BLAST\)](#)

[CDD](#)

[Conserved Domain Search Service \(CD Search\)](#)

[E-Utilities](#)

[Genome Workbench](#)

[Protein-BLAST](#)

[ProSplign](#)

[PubChem Structure Search](#)

[Splign](#)

[Vector Alignment Search Tool \(VAST\)](#)

UCSC Genome Browser

Our tools

- **Genome Browser**
interactively visualize genomic data
- **BLAT**
rapidly align sequences to the genome
- **Table Browser**
download data from the Genome Browser database
- **Variant Annotation Integrator**
get functional effect predictions for variant calls
- **Data Integrator**
combine data sources from the Genome Browser database
- **Gene Sorter**
find genes that are similar by expression and other metrics
- **Genome Browser in a Box (GBIB)**
run the Genome Browser on your laptop or server
- **In-Silico PCR**
rapidly align PCR primer pairs to the genome
- **LiftOver**
convert genome coordinates between assemblies
- **Track Hubs**
import and view external data tracks
- More tools...

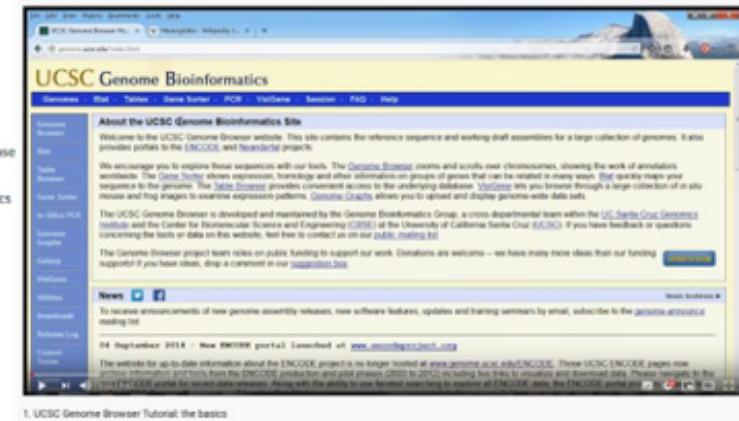
Our story

On June 22, 2000, UCSC and the other members of the

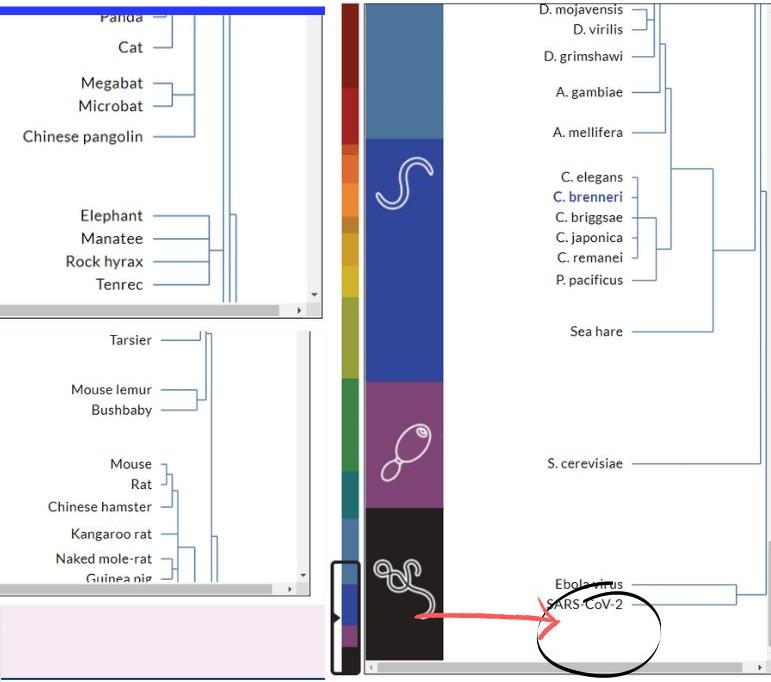
What's new

... news items

UCSC Genome Browser tutorial - the basics
<https://www.youtube.com/watch?v=DNXI-M9oQI8>



1. UCSC Genome Browser Tutorial: the basics



Browse>Select Species

POPULAR SPECIES



Enter species, common name or assembly ID

[HTTPS://GENOME.UCSC.EDU/CGI-BIN/HGGATEWAY](https://genome.ucsc.edu/cgi-bin/hgGateway)
Can't find a genome assembly?

GeneNetwork

University of Tennessee: www.genenetwork.org

Use GeneNetwork 2



Welcome!

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GeneWiki Entries

GeneWiki enables you to enrich the annotation of genes and transcripts. Please submit or edit a GeneWiki note (500 characters max) related to a gene, its transcripts, or proteins. When possible include PubMed identifiers or web resource links (URL addresses). Please ensure that the additions will have widespread use. For additional information, check the GeneWiki [help document](#).

Please enter a gene symbol in the box below and then click submit.

Select and search

Species: [Make Default](#)

Group:

Type:

Dataset: [Info](#)

Get Any:

Enter terms, genes, ID numbers in the **Search** field.

Use * or ? wildcards (Cyp*a?, synap*).

Use quotes for terms such as "tyrosine kinase".

Combined:

[Search](#)

Advanced commands

You can also use advanced commands. Copy these simple examples into the Get Any field for single term searches and Combined for searches with multiple terms:

- **POSITION=(chr1 25 30)** finds genes, markers, or transcripts on chromosome 1 between 25 and 30 Mb.
- **MEAN=(15 16)** in the Combined field finds highly expressed genes (15 to 16 log₂ units).
- **RANGE=(1.5 2.5)** in the Any field finds traits with values with a specified fold-range (minimum = 1). Useful for finding "housekeeping genes" (1.0-1.2) or highly variable molecular assays (10-100).

Affiliates

- Genome Browser at UTHSC
- Systems Genetics at EPFL
- Bayesian Network Web Server at UTHSC
- GeneNetwork 1 at UTHSC
- GeneWeaver
- WebGestalt at Baylor

News

- New SPARQLProg modules for @DisGeNET @un @WikiPathways @wikidata are being developed c #biohack19 !!! Nice work and thanks for the demo !!! Check them at <https://github.com/crmungall/sparqlprog>

Posted on Sep 4, 2019

- NOA for "Systems Genetic Analysis of Cognitive F Multi-Parent Crosses" came bright and early this award is very special - a collaboration between @KaczkowskiLab, Herskowitz lab, @timothyjohn, @MacCossLab. Multi-scale, Mouse-human, Rose

Posted on Aug 31, 2019

- Join JAX's @ElissaJChesler at @SIRweets's Neu discuss benefits and approaches for bringing gen

Github

- GN2 Source Code
- GN1 Source Code
- System Maintenance Code

Links

Human (hg19)
Mouse (mm10)
Rat (rn6)
Drosophila
Arabidopsis thaliana
Barley
Poplar
Soybean
Tomato



You are here: OMIA / Home

WELCOME TO OMIA

Online Mendelian Inheritance in Animals (OMIA) is a catalogue/compendium of inherited disorders, other (single-locus) traits, and genes in 261 animal species (other than [human](#) and [mouse](#) and [rats](#), which have their own resources) co-authored by [Professor Frank Nicholas](#) and [Associate Professor Imke Tammen](#) of the [University of Sydney](#), Australia, with help from [many people](#) over the years. OMIA information is stored in a database that contains textual information and references, as well as links to relevant [PubMed](#) and [Gene](#) records at the NCBI, and to [OMIM](#) and [Ensembl](#).

OMIA is manually curated by a [team](#) of specialists. If you see an error or wish to submit an entry, please [contact us](#).

To join the OMIA Support Group, register at [OMIA Support Group](#).

From 1st September 2011, the OMIA ID is binomial, with the format OMIA xxxxxx-yyyy.., where xxxxxx is the 6-digit number for a trait/disorder, and yyyy.. is the NCBI species taxonomy id (usually four digits, but sometimes longer).

Summary

dog cattle cat pig sheep horse chicken rabbit goat Other TOTAL

RECENT NEWS

HAPPY MENDEL DAY 2021!

Today (8th March) marks the 156th anniversary of Mendel completing the reading of his paper to the Natural History Society of Brünn (Brno in the Czech Republic) in 1865.

Mendel Day sits symbolically between Darwin Day in February and DNA Day in April, neatly replicating the chronology of three of the most important discoveries in

DOG
CATTLE
CAT
PIG
SHEEP
HORSE
CHICKEN
RABBIT
GOAT

TURKEY
WATER BUFFALO
GUINEA PIG
AMERICAN MINK
ROCK PIGEON
RHESUS MONKEY

LLAMA
ASS
NORTH AMERICAN DEER MOUSE
CRAB-EATING MACAQUE
ALPACA
DUCKS
JAPANESE MEDAKA
FERRET
OVIS SP.
DEER
MEADOW VOLES
AOUDAD
RED FOX
ARABIAN CAMEL
MONGOLIAN GERBIL

GRAY WOLF
YAK
CHIMPANZEE
RACCOON DOG
WESTERN ROE DEER
BIGHORN SHEEP
WHITE-TUFTED-EAR MARMOSET
CHEETAH
SUMATRAN TIGER
MALLARD
SPRINGBOK
ZEBU
RED DEER
SHORT-TAILED CHINCHILLA
DEGU
LION
BUDGERIGAR
ARCTIC FOX
OTHER

[HTTPS://OMIA.ORG/BROWSE/](https://omia.org/browse/)

	dog	cattle	cat	pig	sheep	horse	chicken	rabbit	goat	Other	TOTAL
TOTAL TRAITS/DISORDERS	787	556	363	286	258	242	223	103	90	691	3689
Mendelian trait/disorder	364	261	117	92	112	59	132	62	20	272	1556
Mendelian trait/disorder; likely causal variant(s) known	299	167	84	41	59	46	51	11	15	144	933
Likely causal variants	436	227	132	51	76	98	66	14	26	127	1271
Potential models for human disease	474	230	229	134	117	134	53	57	41	357	1859

Mendelian trait / disorder	Mendelian trait / disorder; likely causal variant(s) known	Likely causal variants	Potential models for human disease	Inborn error of metabolism	Dwarfism	Congenital heart disease	Inherited bleeding disorder	Lysosomal storage disease	Colour	Progressive retinal atrophy (PRA)
Stationary retinal disorder	Retinal disorder	Disorder of Sexual Development (DSD)	Embryonic lethal	Blood group system	Intrinsic platelet disorder	Extrinsic platelet disorder	Cancer	Leukodystrophy	Claw disorders	Hyperostotic disorder

TOTAL TRAITS / DISORDERS

3689

HTTPS://OMIA.ORG/BROWSE/



THE UNIVERSITY OF
SYDNEY

OMIA - ONLINE MENDELIAN INHERITANCE IN ANIMALS

OMIA

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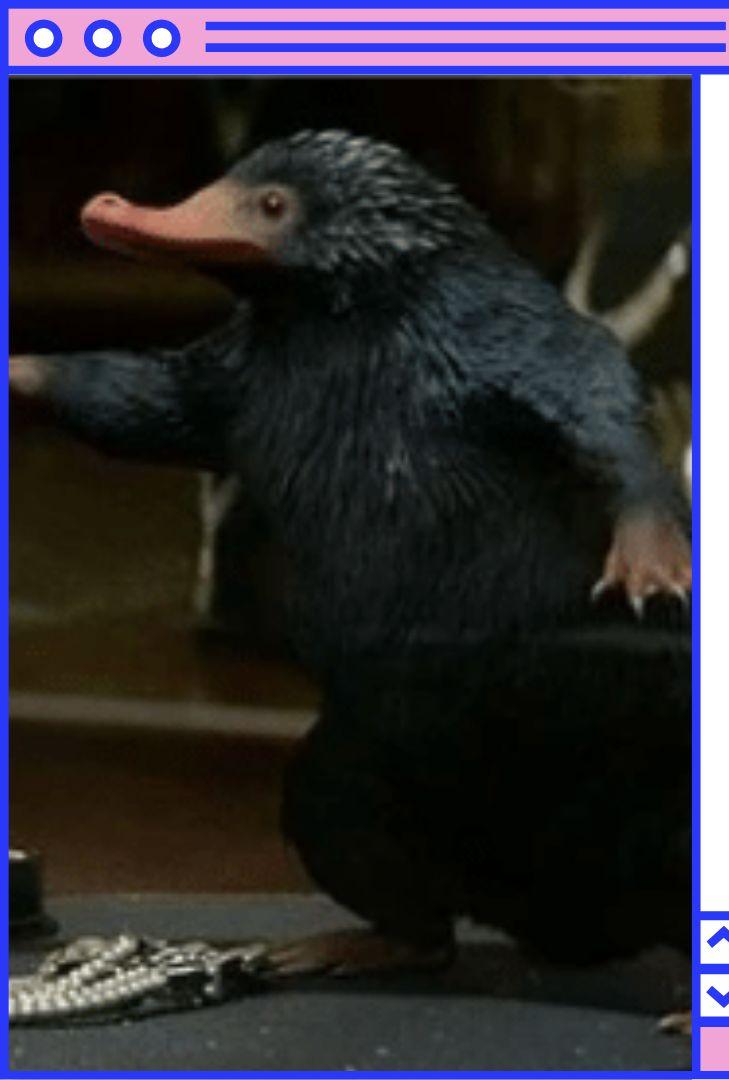
Links

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LINKS

- [Online Mendelian Inheritance in Man \(OMIM\)](#)
- [Inherited Disorders in Dogs](#)
- [Canine Inherited Disorders Database](#)
- [International Partnership for Dogs: Harmonization of Genetic Testing for Dogs](#)
- [WSAVA/PennGen Canine and Feline Hereditary Disease \(DNA\) Testing Laboratories](#)



**ONDE ENCONTRAR
FERRAMENTAS
PARA MINHAS
ANÁLISES?**

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Organism, repository, gene, tissue, accession

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9/2023

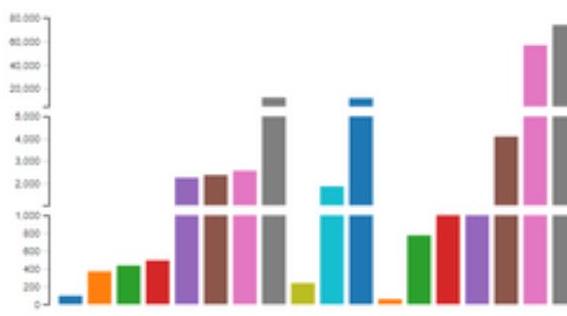
Examples: Cancer, Homo sapiens, Orbitrap, QSHALUS, Phospho, Hela, PXD001456

further mechanisms through effects
generated patients disease derived
extracted related
novel more regulation overall molecular
factor tumor samples analysis
including sequencing target
transcriptome sample pathways

Description  Sample  Data 



Tissues Organisms Diseases



Resources • Omics

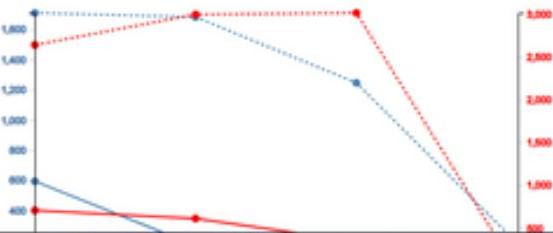
Latest Datasets

- [Jun 26 FLNC d18-21 BiolD experiment](#)
 - [Jun 6 FILIP1 CT pull-down](#)
 - [Apr 17 Liver cancer is one of the most prevalent and lethal human cancers.](#)
 - [Mar 9 Oliveira2020 - E. coli Extended Central Carbon Metabolism from Glycerol](#)
 - [Mar 9 Rare genetic variants affect urine metabolite concentrations: linking populatio...](#)
 - [Mar 8 Schölie2020 - Modular Modelica Implementation of the Hodgkin-Huxley mod...](#)
 - [Mar 8 Schölie2021 - Modular model of the human cardiac conduction system base...](#)
 - [Mar 5 Mutant FUS triggers age-dependent synaptic impairment in presymptomatic ...](#)

Most Accessed Datasets

- 2604 M *musculus* - Heart, Protein peptide count (Kislinger cell 2006)
 - 2789 Inodovirus and Microsporidian Linked to Honey Bee Colony Decline
 - 2176 SNP profiling of pancreatic adenocarcinoma (PDAC) xenografts
 - 4408 Khodolenko1999 - EGFR signaling
 - 2244 Funin deficiency effect on T cells
 - 2303 RNA-seq time course analysis of human and mouse T helper type 2 and typ
 - 2555 Cytokine interactome alterations promote oropharyngeal Epstein-barr virus (
 - 3229 Identification of proteins interacting with lncRNA (braveheart in mouse using

New Datasets Per Year



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Essential scientific and technical information about software tools, databases and services for bioinformatics and the life sciences.

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bio.tools COVID-19 related tools

See the bio.tools <https://covid-19.bio.tools> subdomain for a list COVID-19 related tools.

If you believe any tools are missing, please feel free to update the list as specified in the instructions at <https://covid-19.bio.tools>.



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About *Bioconductor*

Bioconductor provides tools for the analysis and comprehension of high-throughput genomic data.

Bioconductor uses the R statistical programming language, and is open source and open development. It has two releases each year, and an active user community. *Bioconductor* is also available as an [AMI](#) (Amazon Machine Image) and [Docker](#) images.

News

- [Bioconductor 3.12](#) is available.
- See our [google calendar](#) for events, conferences, meetings, forums, etc. Add your event with email to events at [bioconductor.org](#).

BioC 2021

Visit the [BioC 2021](#) website for complete conference information! The virtual conference will be held August 4-6, 2021!

News highlights:

- Abstract Submission Deadline for talk, demo, long workshop, digital poster, or Birds-of-a-feather is next Tuesday March 16! Submit [here](#)
- Registration opening soon.
- See the list of confirmed speakers on the [website home page](#)

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answers

34
views

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deseq2 apeglm rna-seq

written 22 hours ago by Chris-OHRI • 10

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0
answers

11
views

rna-seq

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votes
1
answer

42
views

gene R rna-seq

gencode gtf file derived genelD can't be annotated to gene symbol following Deseq2 manual

written 2 hours ago by Kai_Qi • 100

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0
answers

37
views

gene R rna-seq edger

Bioinformatics researcher looking for an answer on edgeR and DESeq2

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0
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bioinformatics internship co-op job

Job: Bioinformatics internships and co-ops (2021) at Stoke Therapeutics. Remote locations in the US.

written 3 hours ago by Eric Lim • 1.7k

1
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2
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1.2k
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variant calling vcf snp

How to split Double or Multiple Nucleotide Polymorphisms (DNP) into Single Nucleotide Polymorphisms (SNP)?

written 3.9 years ago by rafa.rios.50 • 60 • updated 3 hours ago by Biostar • 20

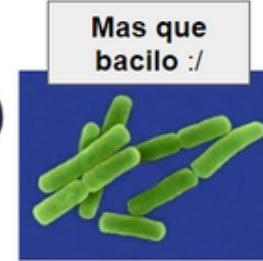
Recent Votes

- A: Deeptools Sorting for score values
- ATAC-seq sample normalization
- A: ATAC-seq sample normalization (quantil normalization)
- A: ATAC-seq sample normalization (quantil normalization)
- C: gencode gtf file derived genelD can't be annotated to gene symbol following Dese
- C: gencode gtf file derived genelD can't be annotated to gene symbol following Dese
- A: samtools addreplacerg gives error

Recent Locations • All »

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- Norway, 1 minute ago
- London, UK, 4 minutes ago
- United States, 4 minutes ago
- INBIOSIS, 7 minutes ago
- France/Nantes/Institut du Thorax - INSERM UMR1087, 8 minutes ago

MICRORGANISMOS PLANTAS ANIMAIS HUMANOS



Microrganismos

SpeciesFinder - <https://cge.cbs.dtu.dk/services/SpeciesFinder/>

MG Rast e RAST - <http://rast.theseed.org/FIG/rast.cgi>

Burkholderia DB - <https://burkholderia.com/>

Interação entre patógeno e hospedeiro - <https://hpidb.igbb.msstate.edu/>

DOOR: a database for prokaryotic operons - <http://csbl1.bmb.uga.edu/OperonDB>

PRODORIC: prokaryotic database of gene regulation - <http://prodoric.tu-bs.de/>

DoriC 10.0: database of replication origins including chromosomes and plasmids - <http://tubic.tju.edu.cn/doric/public/index.php/index>

DEG 5.0: database of essential genes in both prokaryotes and eukaryotes - <http://www.essentialgene.org/>

Plantas

FLAGDB <http://urgv.evry.inra.fr/projects/FLAGdb++/HTML/screenshots.shtml>

Genoma de Arabidopsis <http://www.gabipd.org/materials/>

PlantGDB <http://www.plantgdb.org/cgi-bin/GeneSeger/index.cgi> (em desenvolvimento)

Frutas tuberculos e afins <http://pgdbj.jp/plantdb/plantdb.html?ln=en>

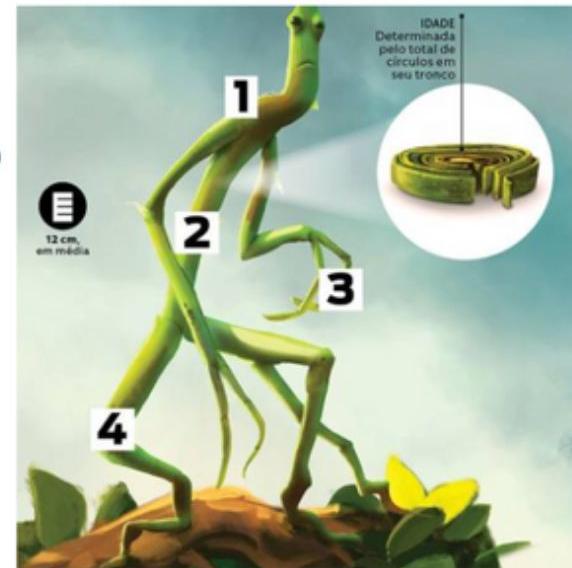
Asteraceae - http://www.etnobiotic.cat/gsad_v2/

The Plant Genome resource <https://phytozome.jgi.doe.gov/pz/portal.html>

Citogenética Molecular de Plantas <http://www.plantrndnadbatabase.com>

Fatores de Transcriçao em plantas <http://planttfdb.cbi.pku.edu.cn/help.php>

Brassica genômica e genética <http://www.brassica.info>



PlantGDB



...resources for comparative
plant genomics

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PlantGDB

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Sequence

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[EST Assemblies](#)
[FTP Server](#)
[More...](#)

Genomes

[Genome Browsers](#)
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Welcome to plantgdb.org! Tools and resources for plant genomics

► Quick tips for using PlantGDB...



Public Plant Sequence Release 187 is current.
Species-parsed [protein sequences](#) from GenBank and UniProt.

► More about Release 187...



PlantGDB-assembled unique transcripts (EST) and Genome Survey Sequence assemblies (GSS).

► More about Assemblies...



Online tools for pattern matching, sequence query, and spliced alignment.

► More about Tools...



BioExtract Server provides powerful database queries, analysis tools, and online workflows.

Genome Browsers



Genome browsers for emerging & completed plant genomes.

Video Tutorial (6 min) [View Quicktime](#) [View Flash](#)

► More about Genome Browsers...

Community Annotation



Tools and databases for gene structure annotation.

Video Tutorial (3 min) [View Quicktime](#) [View Flash](#)

► More about Community Annotation...

Special Datasets



Special datasets for transposon insertion sites, splicing-related genes, and more.

► More about Special Datasets...

Outreach



Plant Genome Research Outreach Portal (POROP) for locating activities, programs and resources; Outreach Program for Native Americans (OPNA).

New & Noteworthy

Click below or [view all news](#) | Twitter

- [What comes after PlantGDB?](#) (July 1, 2010)
- [New Location for PlantGDB](#) (July 23, 2010)
- [Br008 - Brassica rapa chromosome-based genome browser](#) (July 10, 2010)
- [Sm008 - Solanum tuberosum new genome browser](#) (July 16, 2010)
- [Br008 - Brassica rapa chromosome-based genome browser](#) (July 16, 2010)
- [Vc008 - Volvox carteri new genome browser](#) (July 16, 2010)
- [Medicago genome updated](#) (July 27, 2010)
- [Rice genome updated](#) (July 27, 2010)
- [Cassava genome updated](#) (July 27, 2010)
- [Populus annotation updated](#) (July 27, 2010)
- [Mimulus annotation updated](#) (July 27, 2010)
- [Chlamydomonas annotation updated](#) (July 27, 2010)
- [Brachypodium annotation updated](#) (July 27, 2010)
- [PlantGDB NSF Grant](#) (June 24, 2010)
- [PlantGDB at Maize Genetics Conf.](#) (June 24, 2010)
- [GenBank Release 187](#) (June 24, 2010)
- [New Add Track feature for Genome Browsers](#) (July 15, 2010)

What's Coming?

phytozome.jgi.doe.gov/pz/portal.html

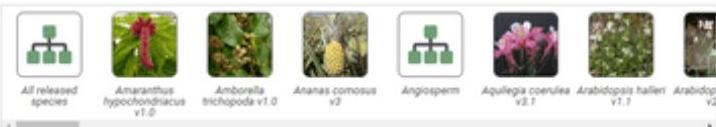


JGI HOME LOG IN

Species Tools Info Download Help Cast Subscribe

Phytozome quick search (advanced)

Flagships Clustered Genomes and Families Unclustered Genomes



Search in Click an image or type species/node name for Enter keywords or sequence

12.1.6

About Phytozome

Note: all genome releases since May 2019 are available only in Phytozome v13, our newest version of Phytozome. Access it at [Phytozome-Next](#).

Phytozome, the Plant Comparative Genomics portal of the Department of Energy's Joint Genome Institute, provides JGI users and the broader plant science community a hub for accessing, visualizing and analyzing JGI-sequenced plant genomes, as well as selected genomes and datasets that have been sequenced elsewhere. As of release v12.1.6, Phytozome hosts 93 assembled and annotated genomes, from 82 Viridiplantae species. More than half of these genomes have been sequenced, assembled and/or annotated with JGI Plant Science program resources. By integrating this large collection of plant genomes into a single resource and performing comprehensive and uniform annotation and analyses, Phytozome facilitates accurate and insightful comparative genomics studies.

All gene sets in Phytozome have been annotated with KOG, KEGG, ENZYME, Pathway and the InterPro family of protein analysis tools. Inparanoid pairwise orthology and paralogy groups have been calculated across all Phytozome proteomes. Families of related genes representing the modern descendants of putative ancestral genes are constructed at key phylogenetic nodes. These families provide additional insight into clade-specific orthology/paralogy relationships as well as clade-specific novelties and expansions. Search and visualization tools let users quickly find and analyze genes or genomic regions of interest. Query-based data access is provided by Phytozome's InterMine and BioMart instances, while bulk data sets can be accessed via the JGI's Genome Portal. JBrowse genome browsers are available for all genomes.

News (details...)

(2020-07-14)

BULK DATA ACCESS is back!

(2020-07-02)

Limited DATA ACCESS Jul 10-14!

(2020-04-15)

All new genomes are released in Phytozome v13.



Help with Phytozome

Documentation

- View a tree representation of the species in Phytozome v12.1!
- View a Quick Start Guide to using Phytozome
- Check out the FAQs

System Status (2021-03-12 13:50)

- ✓ Search
- ✓ BLAST
- ✓ Database
- ✓ PhytoMine
- ✓ PhytoMine-Web

Plantas

Listinha marota - <https://www.hsls.pitt.edu/obrc/index.php?page=general>

- ① AgBase -- a unified resource for functional analysis in agriculture
Search and analyze functional genomics datasets in agricultural species.
- ② AutoSNPdb -- an annotated single nucleotide polymorphism database for crop plants
Identify SNPs from assembled EST sequences for the crops rice, barley and Brassica.
- ③ BarleyBase -- an expression profiling database for plant genomics
Analyze and visualize plant microarray data.
- ④ CR-EST -- a resource for crop ESTs
Search for sequence, classification, clustering and annotation data of crop EST projects.
- ⑤ CSIROB -- a small RNA integrated database and browser resource for cereals
Search for sequence information on rice, maize and other cereal crops small RNAs.
- ⑥ ChroMDB -- the Chromatin Database
Locate chromatin-associated proteins, including RNA-associated proteins, for a broad range of organisms.
- ⑦ DRASTICx97INSIGHTS -- querying information in a plant gene expression database
Search for information of plant gene expression in response to pathogens and environmental changes.
- ⑧ FLAGdb++ -- A Database for the Functional Analysis of the Arabidopsis Genome
Search and visualize data for high-throughput functional analysis of *Arabidopsis*, rice, and other plant genomes.
- ⑨ GCP -- The Generation Challenge Programme
An online resource documenting stress-responsive genes comparatively across plant species.
- ⑩ GGT -- Graphical GenoTypes
Software for visualization and analysis of genetic data.
- ⑪ GabIPD -- a plant integrative 'omics' database
Search for comprehensive and extensive information on various plant genomes generated by a German collaborative network of plant genomics research.
- ⑫ GeneSequer@PlantGDB -- gene structure prediction in plant genomes
Predict gene structures of plant genomes.
- ⑬ GrainGenes -- The genome database for small-grain crops
Search for molecular and phenotypic information on wheat, barley, rye, triticale, and oats.
- ⑭ Gramene -- a resource for comparative grass genomics
Curated resource for genetic, genomic and comparative genomics data for the major crop species, including rice, maize, wheat and many other plant (mainly grass) species.
- ⑮ MIPS -- analysis and annotation of genome information
Search for protein sequence-related information based on whole-genome analysis.
- ⑯ MetaCrop -- a detailed database of crop plant metabolism
A database that summarizes diverse information about metabolic pathways in crop plants and allows automatic export of information for the creation of detailed metabolic models.
- ⑰ NASGBdb -- National Institute of Agrobiological Sciences Gene Bank DataBase
Find information about agricultural plant genetics and diseases.
- ⑱ P3DB -- Plant Protein Phosphorylation Database
Find information about protein phosphorylation in plants.
- ⑲ PHYTOPROT -- A Database of Clusters of Plant Proteins
Search for clustered plant protein sequences available from SwissProt/TrEMBL.
- ⑳ PIP -- a database of potential intron polymorphism markers
A database of potential intron polymorphism markers in plants.
- ㉑ PLACE -- Plant cis-acting regulatory DNA elements
Search for documented motifs found in plant cis-acting regulatory DNA elements.
- ㉒ PLANT-Pis -- A database for protease inhibitors and their genes in higher plants
Search for information on plant protease inhibitors (Pis) and related genes.
- ㉓ PLecDom -- Plant Lectin Domains server
Find information about plant lectin domains.
- ㉔ PMRD -- Plant MicroRNA Database
Find information about microRNA sequences and targets in plants.
- ㉕ PMRD -- Plant MicroRNA Database
Find information about microRNAs in plants.
- ㉖ PODB -- the Plant Organelles Database



Animais

Online Mendelian Inheritance in Animals - <https://omia.org/help/>

AggBase - Animais de interesse agrícola, plantas... <https://agbase.arizona.edu/index.html>

Mouse Genome Information <http://www.informatics.jax.org>

Insetinhos - <https://flybase.org/>

InSatDB <http://cdfd.org.in/INSATDB/home.php>

Beebase <http://hymenopteragenome.org/beebase/>



The screenshot shows the Ensembl homepage with several tools and databases:

- Tools**: BioMart > (Copy custom datasets from Ensembl with this data mining tool)
- BLAST/BLAST >**: Search our genomes for your DNA or protein sequence
- Variant Effect Predictor >**: Analyse your own variants and predict the functional consequences of known and unknown variants

A large search bar at the top right says "Search all species".

The main content area features a large blue banner with the text "Animais e +". Below it are sections for "All genomes", "Favourite genomes" (Human, Rattus, Mouse, Zebrafish), and various comparison and analysis tools like "Compare genes across species", "Find SNPs and other variants for my gene", "Gene expression in different tissues", "Retrieve gene sequence", and "Find & Data Download".

The right side of the page has a sidebar titled "Transcript-based displays" which includes a tree view of transcript components (Summary, Sequence, Exons, cDNA, Protein, Protein Information, Domains & features, Variants, 3D Protein model, Genetic Variation, External References, and ID History). It also shows a detailed "Transcript: 28TBT1A-2H1" view and a "Variant Effect Predictor" section.

At the bottom, there's a footer with links to "Ensembl", "BLAST/BLAST", "VEP", "Tools", "BioMart", "Downloads", "Help & Docs", and "Blog".

Find a Genome

This page lists all Ensembl species and their available genomes. - [View all species](#) (over 3000). To view other sites containing environmental, genomic, bioactive, etc.

Species tree

[View tree](#) [View genome tree](#)

Available genomes

Note: To find out which species were in previous releases, please see the [list of assemblies](#).

Common name	Atlantic herring	C. elegans	Common wombat	Elephant	Hedgehog ♂ (Prc)	Lesser Egyptian jerboa	Tongan sole						
Aardvark (Prc)													
Abingdon island giant tortoise													
Agassiz's desert tortoise													
Algerian mouse													
Alpaca													
Alpine marmot													
Amazon molly													
American beaver													
American black bear													
American mink													
Angola colobus													
Anole lizard													
Arctic ground squirrel													
Argentine black and white tegu													
Armadillo													
Asian hairytongue													

Links to Animal Genomics Research Web Sites and Database Resources

Cattle (*Bos taurus*)

- NRSP-8 Cattle Coordination
- Genome sequencing - Baylor
- NCBI Cattle Resources
- Ensembl cattle genome
- UCSC Cattle Genome Browser
- Arkdb: Cattle - Roslin, UK
- Bovine Genome Database (TXAM)
- Ruminant Genome Biology Consortium
- INRA Bovine map - France
- Cattle GDB - Australia
- Cattle SNP/Genome (CSIRO)
- Dairy Cattle QTL database
- Cattle QTL Viewer
- Iowa State U. CattleQTLdb
- Gene Indices (GIGI)
- Wageningen Cattle db
- microRNA genes
- Ortholog genes DB

Pigs (*Sus scrofa*)

- NRSP-8 Pig Coordination
- Genome sequencing - Sanger
- Genome Pre-Ensemble
- NCBI Pig Resources
- Arkdb: Pig - Roslin, UK
- ISU Pig QTLDb
- Pig Cytogenetic map - France
- PIGenome database - Korea
- RH Map: INRA, France
- RH Map: Reno, UNR
- RH Map: UIUC
- Sino-Danmark Sequencing Project
- Pig genome blast - NCBI
- Gene Indices (SeGI)
- PIGenome DB (Korea)
- Wageningen Pigs db

Chicken (*Gallus gallus*)

- NRSP-8: Chicken - Michigan
- Genome sequencing - WUSTL
- NCBI Chicken Resources
- NIH Chicken Resources
- Ensembl chicken genome
- UCSC Chicken Genome Browser
- ClickNet - Roslin, UK
- ISU Chicken QTLDb

Sheep (*Ovis aries*)

- NRSP-8 Sheep Coordination
- International Sheep Genome Consortium
- NCBI Sheep Resources
- UK Sheep Map - Roslin, UK
- Arkdb: Sheep - Roslin, UK
- Sheep - Melbourne, AU
- Sheep BACend seq (CSIRO)

Goat (*Capra hircus*)

- Goat Genome Consortium
- Goat - INRA, France

NCBI Goat Resource

Goat Genome Database

Horse (*Equus caballus*)

- NRSP-8 Horse Coordination
- NCBI Horse Genome
- NCBI Horse Resources
- Horse Transcriptome - Georgia
- Horse Genetics, UC-Davis
- Arkdb: Horse - Roslin, UK
- Horse - INRA, France

Buffalo

- Buffalo Genome ORG
- Water Buffalo Genome (India)
- Buffalo Genome Resource (NCBI)
- Buffalo genome db (France)

Turkey

- Arkdb: Turkey - Roslin, UK
- Turkey genome - Minnesota
- NCBI Turkey Resources

Camel

- Arabian Camel Genome

Rabbit

- Rabbit Genome - INRA, France

Cat

- Cat Genome: Roslin, UK
- NCBI Cat Resources

Dog

Aquaculture

- NRSP-8 AquaGenomics
- Catfish - Auburn, Alabama
- CatfishGenome ORG (Auburn)
- Catfish Gene Indices (CGI)
- FishBase - Japan
- Fugu Genomics Project - UK
- Fugu genome - Ensembl
- KillifishGene Indices (FlGI)
- Marine Genomics - MUSC
- Medaka Genome - Japan
- Oyster Genome Mapping - Rutgers
- Pufferfish Genome - France
- Rainbow Trout - INRA, France
- Shrimp Map - CSIRO, Australia
- Shrimp EST - Brazil
- Shrimp Genes 101
- Salmon Gene Indices (AsGI)
- Tetraodon Genome - Ensembl
- Tilapia Genome - Univ. Maryland
- Tilapia Genome Proj - Univ. of NH
- Trout Gene Indices (RTGI)
- ZebrafishGene Indices (ZGI)
- Zebrafish (ZFIN | Ensembl | NCBI)

Mouse

- Mouse - Jackson Lab
- Mouse - NCBI
- Mouse genome - NCBI
- Mouse - Ensembl
- Mouse Gene Indices (MGI)
- Mouse Gene Family - Japan

Rat

- Rat - NCBI
- Rat - Ensembl
- Rat - Medical College of Wisc.
- Rat Gene Indices (RGI)

Fly

- Fly Genetics: Harvard
- Fly Genetics: Indiana
- Drosophila - Berkley
- Drosophila Gene Indices
- Honey Bee genome

bioinformatics - resources, tools

- ISU Chicken QTLDb
- Chicken - Wageningen, NL
- GMOD Tracks - U Del
- ChickEST - Manchester, UK
- Birdbase - U. of Arizona
- Chicken RH Map - INRA
- GEISHA proj - U. of Arizona
- GallusReactome
- Gene Indices (GIGI)
- Wageningen Chicken db
- microRNA genes
- Ortholog genes DB

Dog

- Dog - NCBI
- DogMap Collaboration
- Dog - UC-Berkeley
- Dog - Univ. of Berne
- Dog - FHCRC
- Dog Gene Indices (DogGI)
- Dog - RH Project

Human

- Projects: NIH | DOE | UK
- Maps: RH map | 99 map | Launchpad
- Genes: Gene Indices (HsGI)
- Phenotypes: Associate db |
- Genome: Ensembl | Pharm | GDB

AgEncode

- ENCODEpedia Of DNA Elements
- EnCode explorer
- medEncode
- ENCODE data
- FAANG

Taxonomy

- NCBI Taxonomy DB
- Catalogue of Life
- GBIF Classification
- Taxonomy DB with Breeds

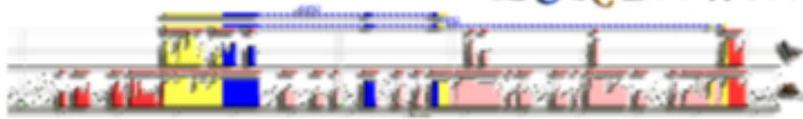
Related:

- Agricultural Genome Information Server (AGIS: a historical information archive)
- Genetic Resources by Organisms - A 1999 list
- Taxonomy Database with Breeds
- Community links | cattle | chicken | pigs |



Dcode.org ECR Browser ECRBase Mulan zPicture DIRE SynoR iVista 2.0 multiTF Array2BIO eShadow

ECR Browser



base genome	feature or position (chrN from-to)
Human	chr14:57264985-57279624
Human	<input type="text"/>
Mouse	<input type="text"/>
Chimpanzee	<input type="text"/>
Dog	<input type="text"/>
Opossum	<input type="text"/>
Rat	<input type="text"/>
Cow	<input type="text"/>
Chicken	<input type="text"/>
Frog	<input type="text"/>
Fugu	<input type="text"/>
Zebrafish	<input type="text"/>
Tetraodon	<input type="text"/>

Search in ECR Browser :: Align your sequence to a genome

[ECR Browser Guide](#)

SV

I coreECRs, **r** - reset parameters to default, **refresh** the page, **?** help



Humanos

Human Protein Atlas <https://www.proteinatlas.org>

Linhagens celulares <https://web.expasy.org/cellosaurus/>

HUGO <https://www.genenames.org>

Atlas das regiões UTR - <http://aura.science.unitn.it/>

Proteínas - <https://www.uniprot.org> / <http://www.wwpdb.org>

Biomoléculas - <https://www.ebi.ac.uk/chembl/>

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

MetaCyc / Biocyc <https://biocyc.org> / <https://biocyc.org/metacyc/index.shtml>

Enzimas <https://www.brenda-enzymes.org>

Reactome <https://reactome.org>

Domínios proteicos <https://pfam.xfam.org>

Ontologia gênica <http://geneontology.org/>



Humanos

GeneCardsSuite GeneCards MalaCards LifeMap Discovery PathCards TGEx VarElect GeneAnalytics GeneALaCarte

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

Keywords ▾ Search Term

Home User Guide Analysis Tools News And Views About ▾

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 ~150 web sources, including genomic, transcriptomic, proteomic, genetic, clinical and functional information.



Explore a Gene

CFTR

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
VARIANT ELECTRICITY

Affiliated Databases

MalaCards
HUMAN DISEASE DATABASE

LifeMap®
DISCOVERY

PathCards
PATHWAY CARDIOLOGY

GeneLoc
GENE LOCALIZATION

Analysis Tools

GeneAnalytics
GENE SET ANALYSIS

GeneALaCarte
GENOME ALARM CARTE

GenesLikeMe
GENE SIMILARITIES

GeneHancer
GENOME & TARGET SITES

ZBTB7A Gene (Protein Coding) *

Zinc Finger And BTB Domain Containing 7A

Jump to section

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



Proteins Antibodies Assays
Genes shRNA Primers CRISPR,
Lentiviral Particles



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



ORF Clones CRISPR
Cloning Vectors Lentiviral Vect

GeneID: GC19M004045 ⓘ
GIFS: 41 ⓘ



Genes Participants LDN
Unpublished Uncurated News



Aliases for ZBTB7A gene

Aliases for ZBTB7A Gene

- Zinc Finger And BTB Domain Containing 7A [2][3]
- Zinc Finger And BTB Domain Containing 7A: HIV-1 Inducer Of Short Transcripts Binding Protein [2]
- Factor That Binds To Inducer Of Short Transcripts Protein [1][2]
- POLY And Krueppel Erythroid Myeloid Oncogenic Factor [3]
- Zinc Finger And BTB Domain-Containing Protein 7A [3]
- POK Erythroid Myeloid Oncogenic Factor [3]
- Leukemia/Lymphoma-Related Factor [3]
- Factor Binding IST Protein [1][2]
- TTF-1-Interacting Peptide 21 [1]
- HIV-1 1st-Binding Protein [1][2]
- Zinc Finger Protein 857A [3]
- Lymphoma Related Factor [3]

Pokémon [1][2]

Pokémon [2]

ZHF57A [3]

ZBTB7 [2]

FBI-1 [3]

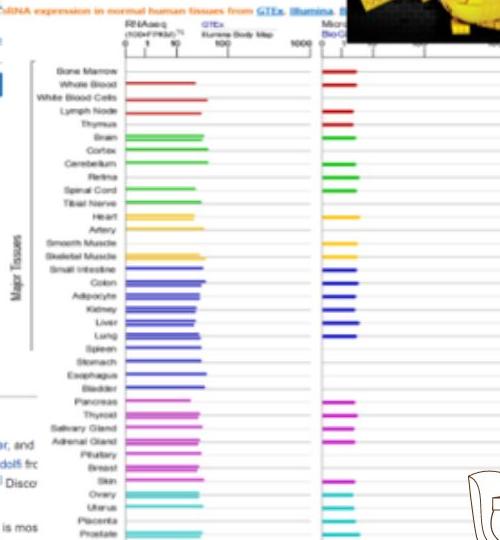
TIP21 [3]

FBI1 [2]

LSR [3]

HIV-1 Inducer Of Short Transcripts Binding Protein [3]

Zinc Finger And BTB Domain Containing 7 [2]



■ Immune ■ Nervous ■ Muscle ■ Intestinal

Zbtb7

From Wikipedia, the free encyclopedia

Zbtb7, originally named **Pokémon**, is a gene that may act as a master switch for cancer, and cells. The leader of the research team which discovered this, geneticist Pier Paolo Pandolfi fr City, said the gene is unique in that it is needed for other oncogenes to cause cancer.^[1] Disc Nature.^[2]

The original name, *Pokémon*, stands for "POK erythroid myeloid oncogenic factor" and is mos Company, not wanting the bad press inherent with its trademark sharing a name with a cancer 2005, at which point MSKCC decided to rename it as *Zbtb7*.^[3]

Zbtb7 are the member of the ZBTB protein family that contains zinc finger and BTB domain.^[4] (osteoclast-derived zinc finger),^[5] and FBI1 (1-3) (fourteen-three-three beta interactant).^[6]

External IDs for ZBTB7A Gene

HGNC: 18078 Entrez Gene: 51341 Ensembl: ENSG00000178951 OMIM:

Previous HGNC Symbols for ZBTB7A Gene

ZBTB7

Previous GeneCards Identifiers for ZBTB7A Gene

GC19M004000, GC19M004001, GC19M00389

Search aliases for ZBTB7A gene in PubMed and other databases





E AGORA?

[HTTPS://WWW.VETERINARIYPRACTICENEWS.COM/HOW-BIOINFORMATICS-RESEARCH-COULD-AFFECT-VETERINARY-PRACTICES-COMPANION-ANIMAL-HEALTH/](https://www.veterinarianpracticenews.com/how-bioinformatics-research-could-affect-veterinary-practices-companion-animal-health/)

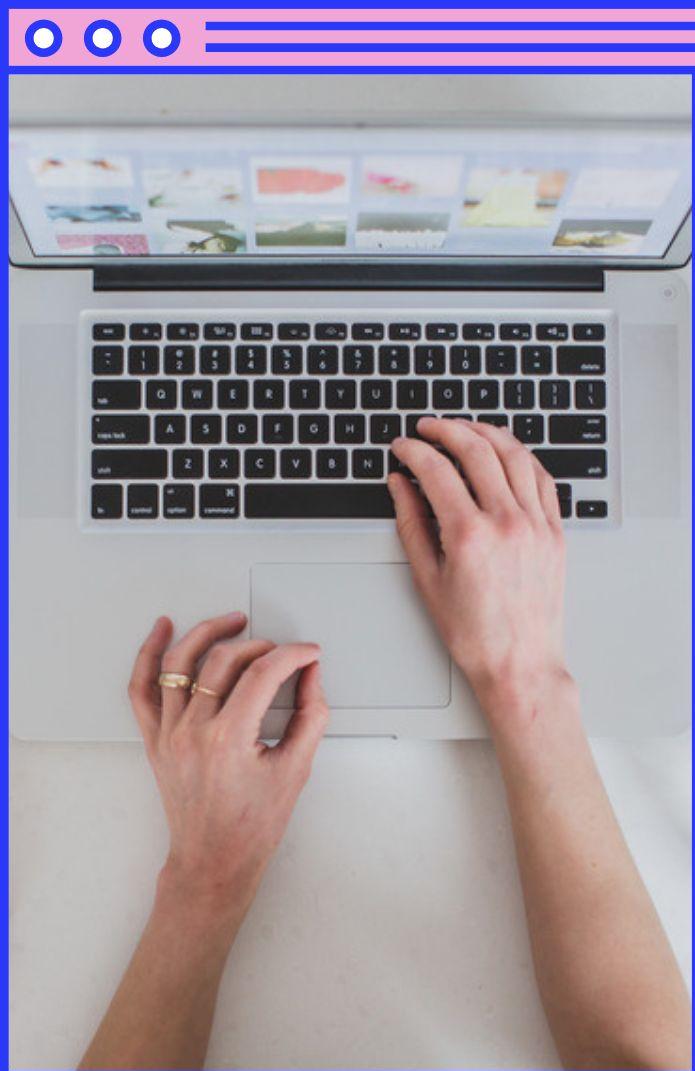
GOOD NEWS FOR HORSES: INTERRELATED INFORMATICS LEND INSIGHT INTO MULTIFACTORIAL DISEASE

THE FUTURE OF MEDICINE IN MICRO RNA



GOOD NEWS FOR DOGS: BIOINFORMATICS INFORM CANCER VACCINES

GOOD NEWS FOR CATS: THE BUILDING BLOCKS FOR DIAGNOSTICS, THERAPEUTICS



MOMENTO SELF PROPAGANDA

[HTTPS://GITHUB.COM/KURISUTARU/FANTASTIC_DATABASES_AND_WHERE_TO_FIND_THEM](https://github.com/kurisutaru/fantastic_databases_and_where_to_find_them)

fantastic_databases_and_where_to_find_them

Repository of databases for omic data

[View on GitHub](#)

Genetics and Molecular Biology



Case study: Exploratory ACE2 analysis using multi-omic web tools

Table of contents

- Step 1 Searching basic information on ACE2
- Step 2 Genomic and sequence databases
- Step 3 Searching of ACE2 Gene expression
- Step 4 Searching in Cancer databases
- Step 5 Comparative databases
- Step 6 Alternative splicing databases
- Step 7 Methylation databases
- Step 8 Regulatory Databases
- Step 9 miRNA, lncRNA and circRNA Databases
- Step 10 Metabolic databases
- Step 11 Disease-specific and variant-disease association
- Step 12 Proteome databases
- Step 13 Other databases
- Complete list of databases



Fantastic Databases and where to find them: Web applications for researchers in a rush

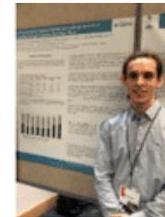
Journal:	<i>Genetics and Molecular Biology</i>
Manuscript ID:	GMB-2020-0203.R3
Manuscript Type:	Original Article
Date Submitted by the Author:	14-Feb-2021
Complete List of Authors:	Villalba Silva, Gerda Cristal; Universidade Federal do Rio Grande do Sul, Genetics and Molecular Biology; Hospital de Clínicas de Porto Alegre, Centro de Pesquisa Experimental Matte, Ursula; Universidade Federal do Rio Grande do Sul Instituto de Biociências, ; Hospital de Clínicas de Porto Alegre, ; Instituto Nacional de Ciencia e Tecnologia de Genetica Medica Populacional
Keyword:	Human databases, Bioinformatics tools, Web application, data mining, Big data

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[HTTPS://WWW.UFRGS.BR/MPSBASE/](https://www.ufrgs.br/mpsbase/)

Mais merchan :D

- MPSBase, TCC do Luis Soares - Núcleo de Bioinfo HCPA ➔



Currently, MPSBase consists of a total of 13 studies previously deposited in the GEO and ArrayExpress publicly, including 6 MPS types and 4 species. Crossing sample features on the same dataset, we could analyze more than 50 comparisons of normal/control tissues and MPS tissues. Here, we provide gene expression analysis and enrichment analysis to help researchers understand the pathophysiology of Mucopolysaccharidoses. The database was developed by researchers from the Gene Therapy Center and from the Bioinformatics Core of the Hospital de Clínicas de Porto Alegre, from the Universidade Federal do Rio Grande do Sul - Brazil.

Browse experiments by:

Species

MPS Type

Tissue type

Or insert a term below:

Select Species Select type of ID

Beta Version

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OBRIGADA



Slides aqui:

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