

# Bases de Datos y Navegadores para plantas

# INSDC

International Nucleotide Sequence Database Collaboration

**NCBI**

National Center for Biotechnology Information

**EMBL-EBI**

European Bioinformatics Institute

**DDBJ**

DNA Data Bank of Japan

**Genbank**

Biosample

Bioproject

BLAST

Pubmed

SRA

RefSeq

Taxonomy

...



**ENA**

Biomodels

Expression Atlas

Enzyme Portal

EMBL Genomes

ArrayExpress

Uniprot

Wormbase

...



**DDBJ**

RefEx

CRISPR direct

WABI

TXSearch

DRA

GGGenome

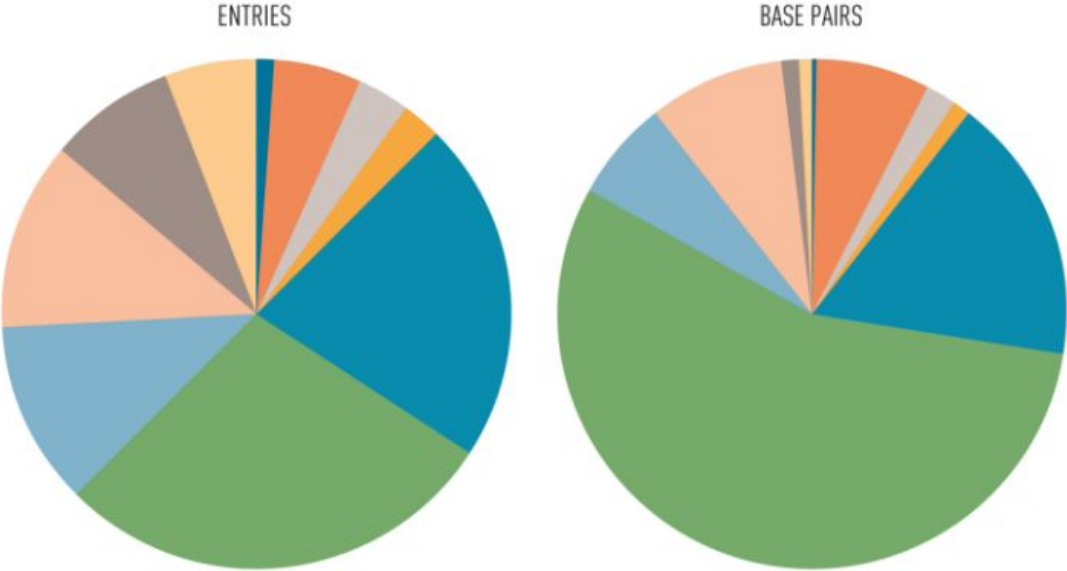
GEA

...

Connected and open network of archives, search tools, workspaces, external sources and analysis tools

# Nucleotide sequence Data

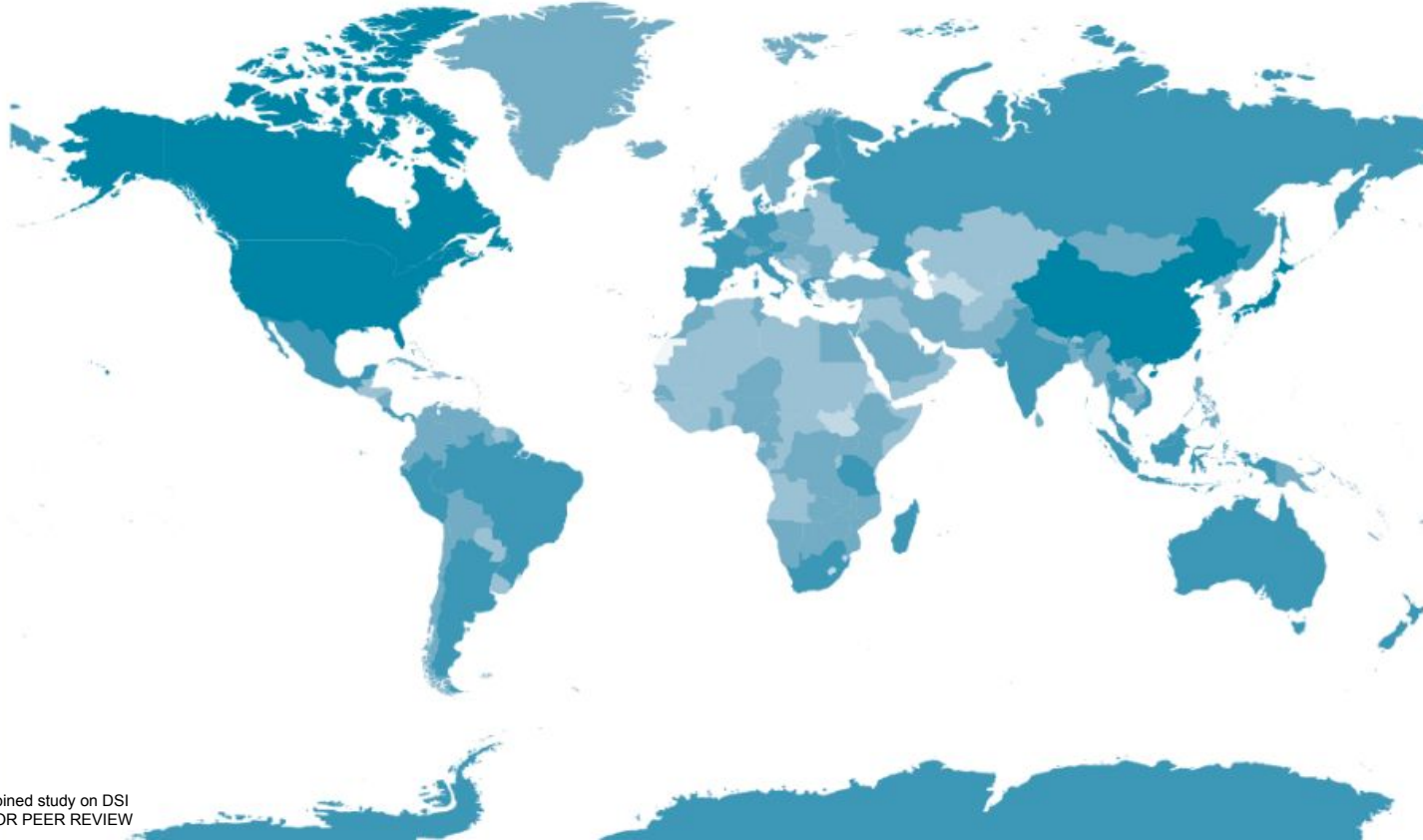
What is the biological scope of the NSD available in Genbank?



TAXONOMIC GROUP	ENTRIES	BASE PAIRS
Viruses	1.21%	0.32%
Bacteria/Archaea	5.60%	7.37%
Fungi	3.29%	1.95%
Single-celled Eukaryotes	2.56%	0.91%
Plants & Algae	21.61%	17.12%
Animals	28.45%	55.62%
Human	11.52%	6.25%
Model Organisms	11.93%	8.67%
Other/synthetic (microorganisms)	8.03%	1.16%
Unidentified (no tax. ID)	5.82%	0.61%

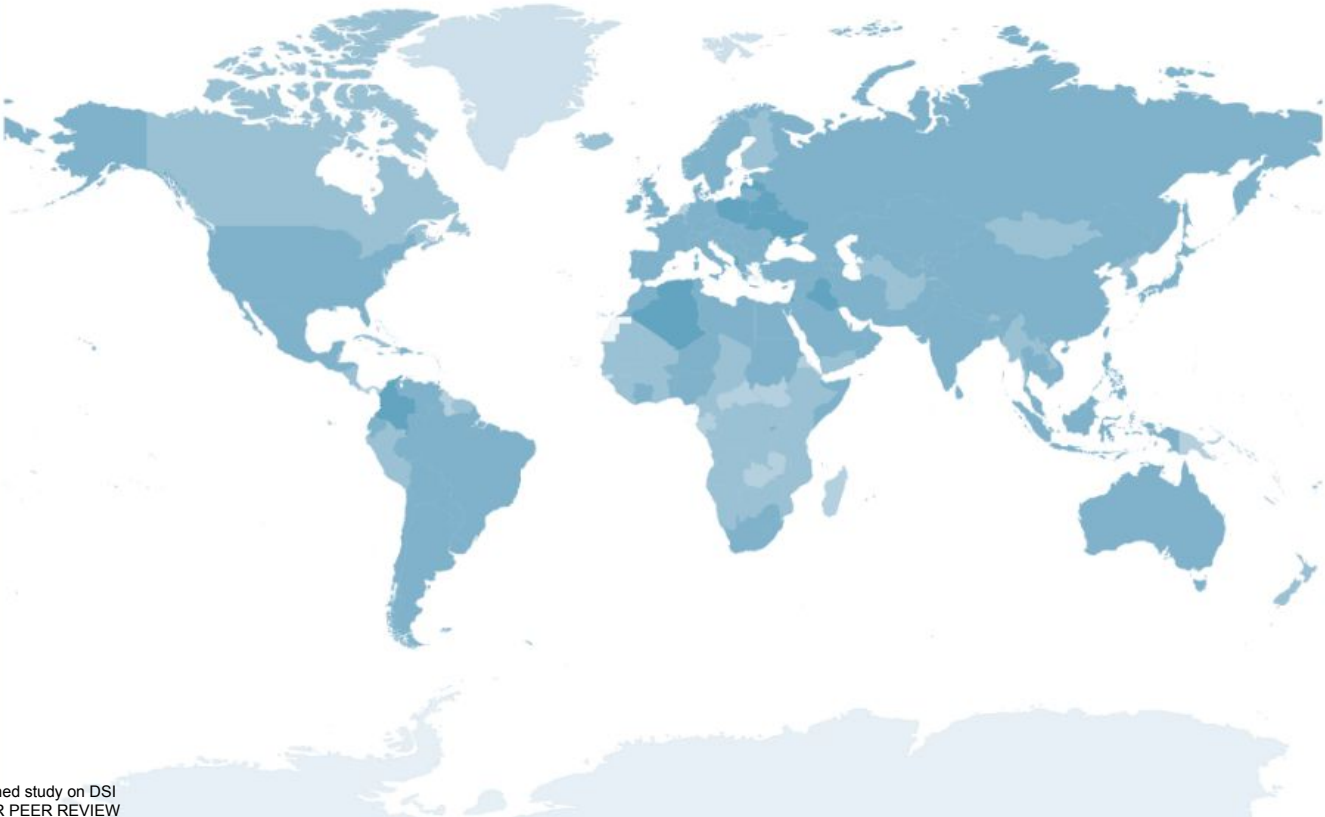
## What is the country of origin for non-human NSD?

1. China	18.23 %
2. United States	17.39 %
3. Canada	9.10 %
4. Japan	7.24 %
5. India	3.46 %
6. Australia	2.66 %
7. Mexico	2.54 %
8. Brazil	2.30 %
9. Germany	1.83 %
10. Spain	1.58 %



How does database usage  
compare to provided sequences?

1. Ukraine	4.91
2. Bahrain	2.97
3. Lebanon	1.55
4. Iraq	1.48
5. Albania	1.45
6. Colombia	1.31
7. Algeria	1.23
8. Singapore	1.20
9. Belarus	1.18
10. Poland	1.13





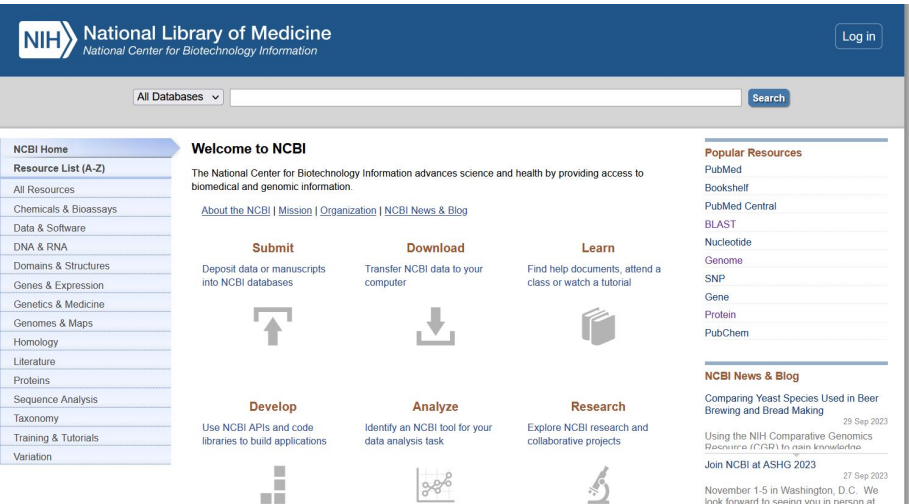
National  
Center for  
Biotechnology  
Information

# NCBI

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

Se estableció el 4 de Nov de 1988

Objetivo del NCBI Desarrollar bases de datos públicas, herramientas de software, difundir información biomédica



The screenshot shows the NCBI homepage with a blue header containing the NIH logo and 'National Library of Medicine' text. Below the header is a search bar with a dropdown menu set to 'All Databases' and a 'Search' button. The main content area is divided into three columns. The left column is a navigation menu with links like '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', and 'Variation'. The middle column is titled 'Welcome to NCBI' and includes a mission statement, links to 'About the NCBI', 'Mission', 'Organization', and 'NCBI News & Blog', and three main action buttons: 'Submit' (Deposit data or manuscripts into NCBI databases), 'Download' (Transfer NCBI data to your computer), and 'Learn' (Find help documents, attend a class or watch a tutorial). The right column is titled 'Popular Resources' and lists 'PubMed', 'Bookshelf', 'PubMed Central', 'BLAST', 'Nucleotide', 'Genome', 'SNP', 'Gene', 'Protein', and 'PubChem'. Below this is a 'NCBI News & Blog' section with articles like 'Comparing Yeast Species Used in Beer Brewing and Bread Making' and 'Using the NIH Comparative Genomics Resource (CCGP) in your browser', and a 'Join NCBI at ASHG 2023' announcement.

Funciones del NCBI

1.Mantenimiento de Bases de Datos Biológicas.

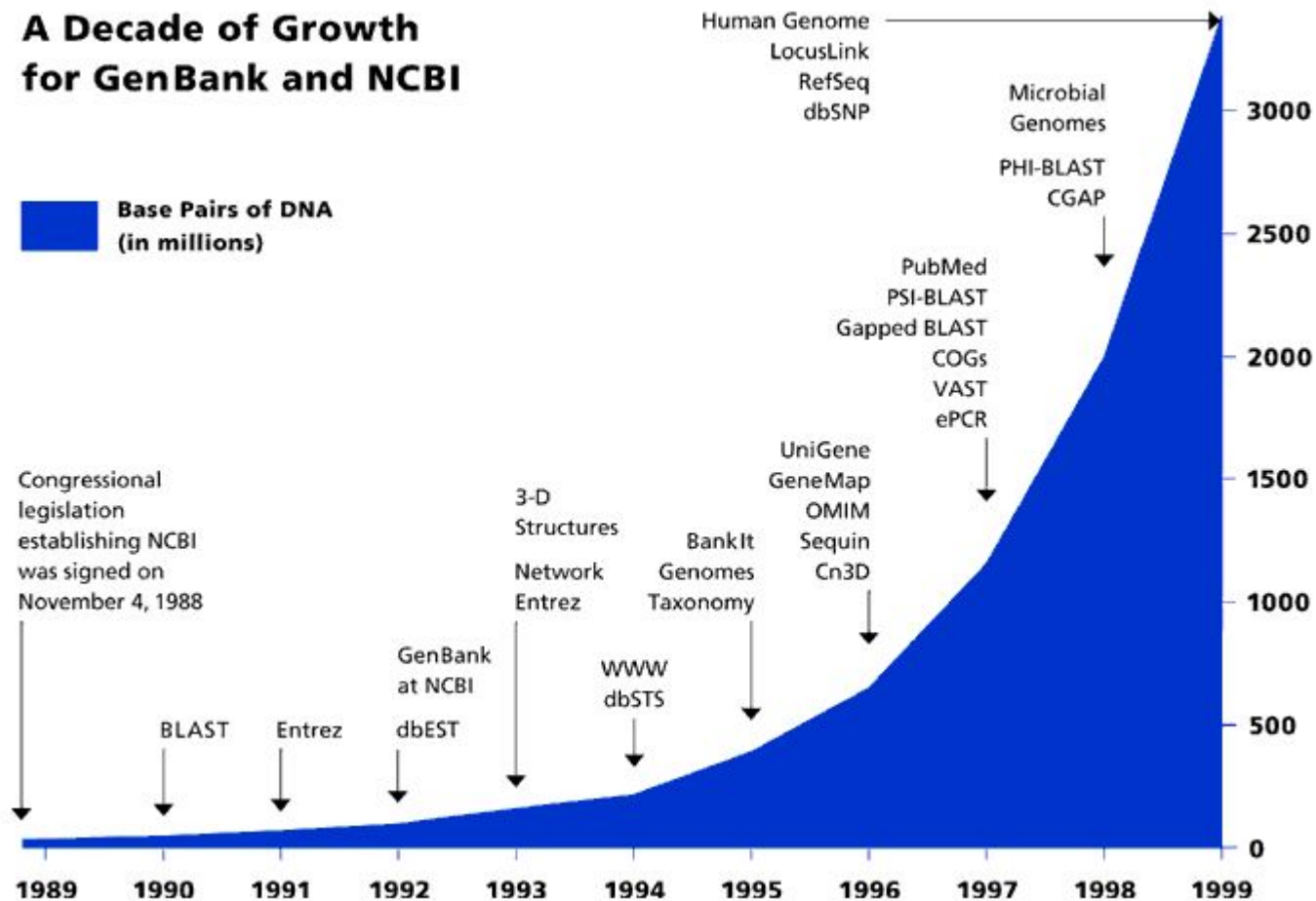
2. Proporcionar un sistema de recuperación de datos. p.ej. Entrez

3. Proporcionar recursos computacionales para el análisis de datos de GenBank.

“ NCBI ofrece además algunas herramientas bioinformáticas para el análisis de secuencias de ADN, ARN y proteínas, siendo BLAST una de las más usadas”

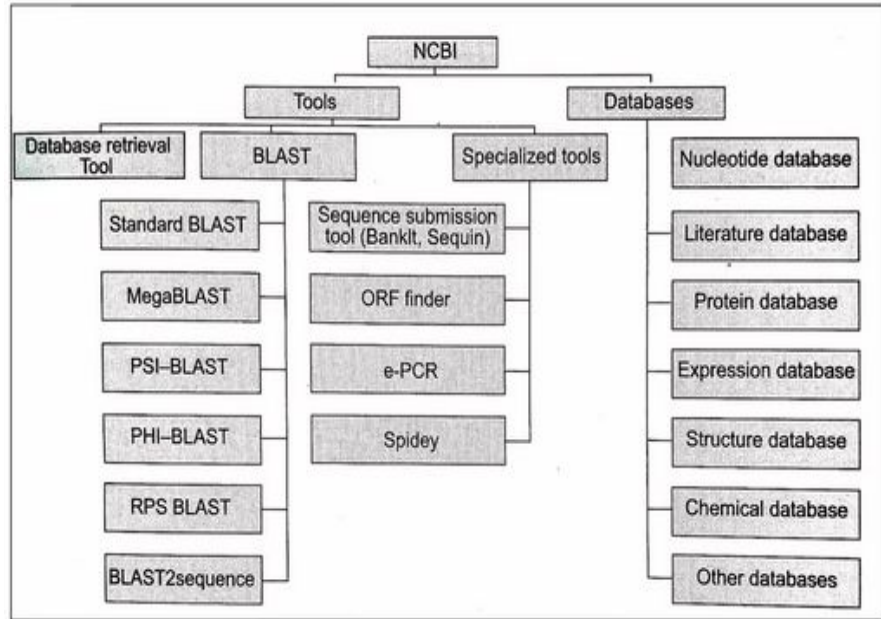
Cañedo, 2009)

# A Decade of Growth for GenBank and NCBI





# Herramientas de NCBI



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

[Batch Entrez](#)

[BLAST Microbial Genomes](#)

[BLAST RefSeqGene](#)

[BLAST Tutorials and Guides](#)

[CDTree](#)

[Cn3D](#)

[COBALT](#)

[Coffee Break](#)

[Comparative Genome Viewer \(CGV\)](#)

[Conserved Domain Architecture Retrieval Tool \(CDART\)](#)

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

[Ebot](#)

[E-Utilities](#)

[Gene Expression Omnibus \(GEO\) BLAST](#)

[Genetic Codes](#)

[Genome BLAST](#)

[Genome Data Viewer \(GDV\)](#)

[Genome Remapping Service](#)

[Genome Workbench](#)

[LinkOut](#)

[Map Viewer](#)

[Multiple Sequence Alignment Viewer](#)

[NCBI News](#)

[NCBI Toolbox](#)

[Open Reading Frame Finder \(ORF Finder\)](#)

[OSIRIS](#)

[Performs a BLAST search of the genomic sequences in the RefSeqGene/LRG set. The default display provides ready navigation to review alignments in the Graphics display.](#)

[Phenotype-Genotype Integrator \(PheGenI\)](#)

[Primer-BLAST](#)

[ProSplign](#)

[Provides a configurable graphical display of a nucleotide or protein sequence and features that have been annotated on that sequence. In addition to use on NCBI sequence database pages, this viewer is available as an embeddable webpage component. Detailed documentation including an API Reference guide is available for developers wishing to embed the viewer in their own pages.](#)

[PSSM Viewer](#)

[PubChem Power User Gateway \(PUG\)](#)

[PubChem Standardization Service](#)

[PubChem Structure Search](#)

[PubMed Clinical Queries](#)

[PubMed Tutorials](#)

[Related Structures](#)

[Sequence Viewer](#)

[SNP Database Specialized Search Tools](#)

[Splign](#)

[Taxonomy Browser](#)

[Taxonomy Common Tree](#)

[Taxonomy Statistics](#)

[Taxonomy Status Reports](#)

[Tree Viewer](#)

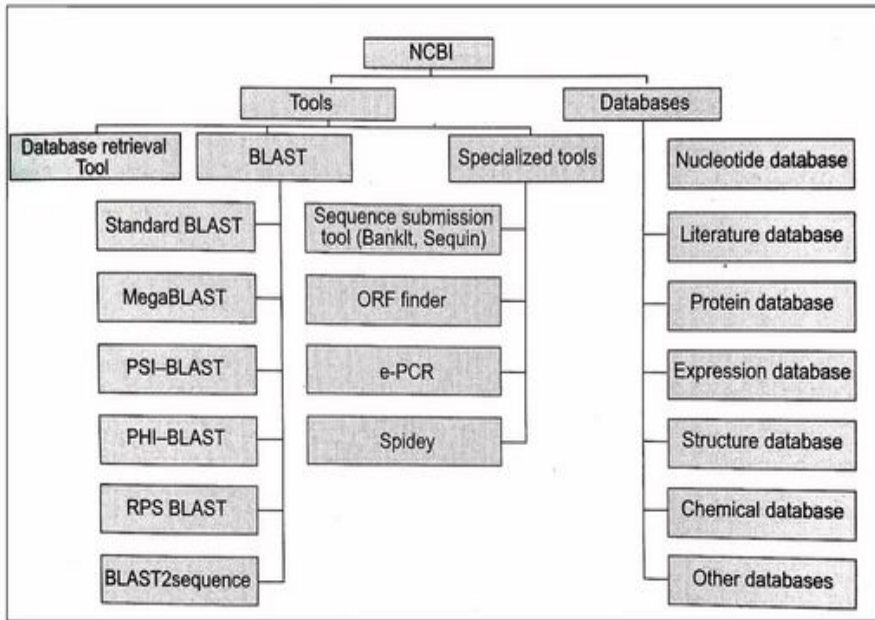
[Variation Viewer](#)

[VecScreen](#)

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

[Viral Genotyping Tool](#)

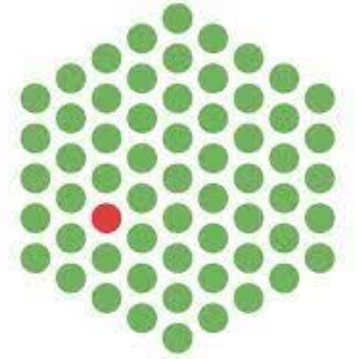
## Bases de DATOS



[Assembly](#)  
[BioCollections](#)  
[BioProject \(formerly Genome Project\)](#)  
[BioSample](#)  
[Bookshelf](#)  
[ClinicalTrials.gov](#)  
[ClinVar](#)  
[Computational Resources from NCBI's Structure Group](#)  
[Consensus CDS \(CCDS\)](#)  
[Conserved Domain Database \(CDD\)](#)  
[Database of Genomic Structural Variation \(dbVar\)](#)  
[Database of Genotypes and Phenotypes \(dbGaP\)](#)  
[Database of Short Genetic Variations \(dbSNP\)](#)  
[GenBank](#)  
[Gene](#)  
[Gene Expression Omnibus \(GEO\) Database](#)  
[Gene Expression Omnibus \(GEO\) Datasets](#)  
[Gene Expression Omnibus \(GEO\) Profiles](#)  
[GeneReviews](#)  
[Genes and Disease](#)  
[Genetic Testing Registry \(GTR\)](#)  
[Genome](#)  
[Genome Reference Consortium \(GRC\)](#)  
[Glycans](#)  
[HIV-1 Human Protein Interaction Database](#)  
[Identical Protein Groups](#)  
[Influenza Virus](#)  
[Journals in NCBI Databases](#)  
[MedGen](#)  
[MeSH Database](#)  
[National Library of Medicine \(NLM\) Catalog](#)  
[NCBI C++ Toolkit Manual](#)

[NCBI Education Page](#)  
[NCBI Glossary](#)  
[NCBI Handbook](#)  
[NCBI Help Manual](#)  
[NCBI Pathogen Detection Project](#)  
[Nucleotide Database](#)  
[Online Mendelian Inheritance in Man \(OMIM\)](#)  
[PopSet](#)  
[Protein Clusters](#)  
[Protein Database](#)  
[Protein Family Models](#)  
[PubChem BioAssay](#)  
[PubChem Compound](#)  
[PubChem Substance](#)  
[PubMed](#)  
[PubMed Central \(PMC\)](#)  
[Reference Sequence \(RefSeq\)](#)  
[RefSeqGene](#)  
[Retrovirus Resources](#)  
[SARS CoV](#)  
[Sequence Read Archive \(SRA\)](#)  
[Structure \(Molecular Modeling Database\)](#)  
[Taxonomy](#)  
[Third Party Annotation \(TPA\) Database](#)  
[Viral Genomes](#)  
[Virus Variation](#)

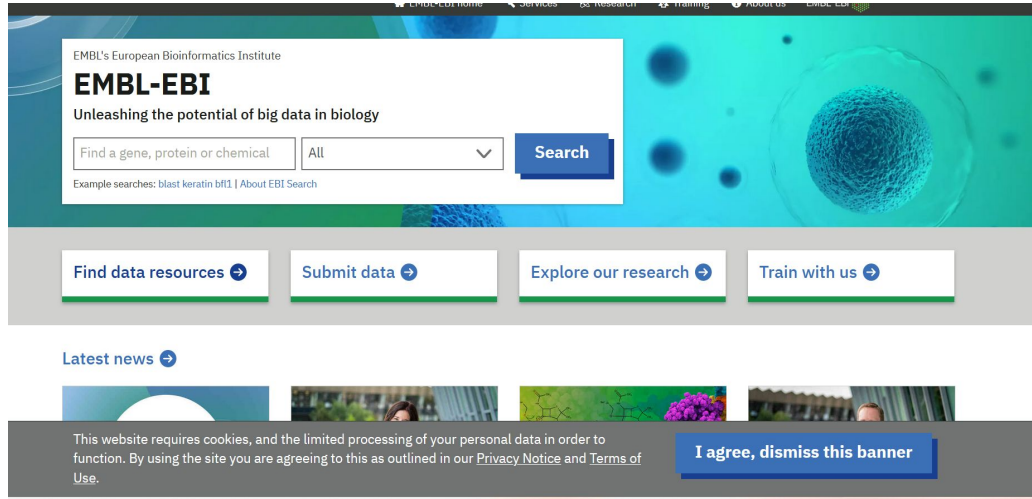
# EMBL-EBI



<https://www.ebi.ac.uk/>

# EMBL-EBI

[European Molecular Biology Laboratory \(EMBL\)](#)



EMBL's European Bioinformatics Institute

## EMBL-EBI

Unleashing the potential of big data in biology

Find a gene, protein or chemical  All

Example searches: [blast keratin bft1](#) | [About EBI Search](#)

[Find data resources](#) [Submit data](#) [Explore our research](#) [Train with us](#)

Latest news

This website requires cookies, and the limited processing of your personal data in order to function. By using the site you are agreeing to this as outlined in our [Privacy Notice](#) and [Terms of Use](#).

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En 1980, se creó en el EMBL Heidelberg la biblioteca de datos de secuencias de nucleótidos del EMBL (ahora parte del Archivo Europeo de Nucleótidos), con el objetivo de crear una base de datos central de secuencias de ADN.

# Herramientas de EMBL-EBI

## Featured data resources



### AlphaFold DB

Database for protein structure predictions for numerous species

CC-BY



### Complex Portal

A manually curated, encyclopaedic resource of macromolecular complexes from model organisms.

CCO



### ArrayExpress

A database of functional genomics experiments, including microarray and RNAseq expression data typically related to publications.

[Web API](#)

## Featured tools



### Clustal Omega

Multiple sequence alignment of DNA or protein sequences. Clustal Omega replaces the older ClustalW alignment tools.

[Web API](#)



### HMMER

Fast sensitive protein homology searches using profile hidden Markov models (HMMs) for querying against both sequence and HMM target databases.

[Web API](#)



### Annotation Platform

Consolidating text-mined and curated annotations

[Web API](#)



# DDBJ

<https://www.ddbj.nig.ac.jp/>

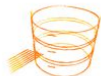


Bioinformation and DDBJ Center provides sharing and analysis services for data from life science researches and advances science.



## Search

Retrieve the data from the database



## Submission

Navigation for how to submit your data



## Services

Services available in DDBJ Center



## Super Computer

NIG Supercomputer



## Statistics

Statistics of DDBJ Center services



## Activities

Training sessions and achievements of DDBJ Center



## NEWS

### Updated tools related to Mass Submission System (MSS)

2023/09/27

[Announcement](#)

[DDBJ](#)

[DDBJ Center](#)

### [Resumed](September 27th) Suspension of DDBJ services due to NIG supercomputer maintenance

2023/09/22

[Maintenance](#)

[DDBJ](#)

[BioProject](#)

[BioSample](#)

[DRA](#)

[GEA](#)

[JGA](#)

[AGD](#)

[DDBJ Center](#)

### Planned policy revisions

2023/09/06

[Announcement](#)

[DDBJ](#)

[BioProject](#)

[BioSample](#)

[MetaboBank](#)

[DRA](#)

[GEA](#)

[JGA](#)

[AGD](#)

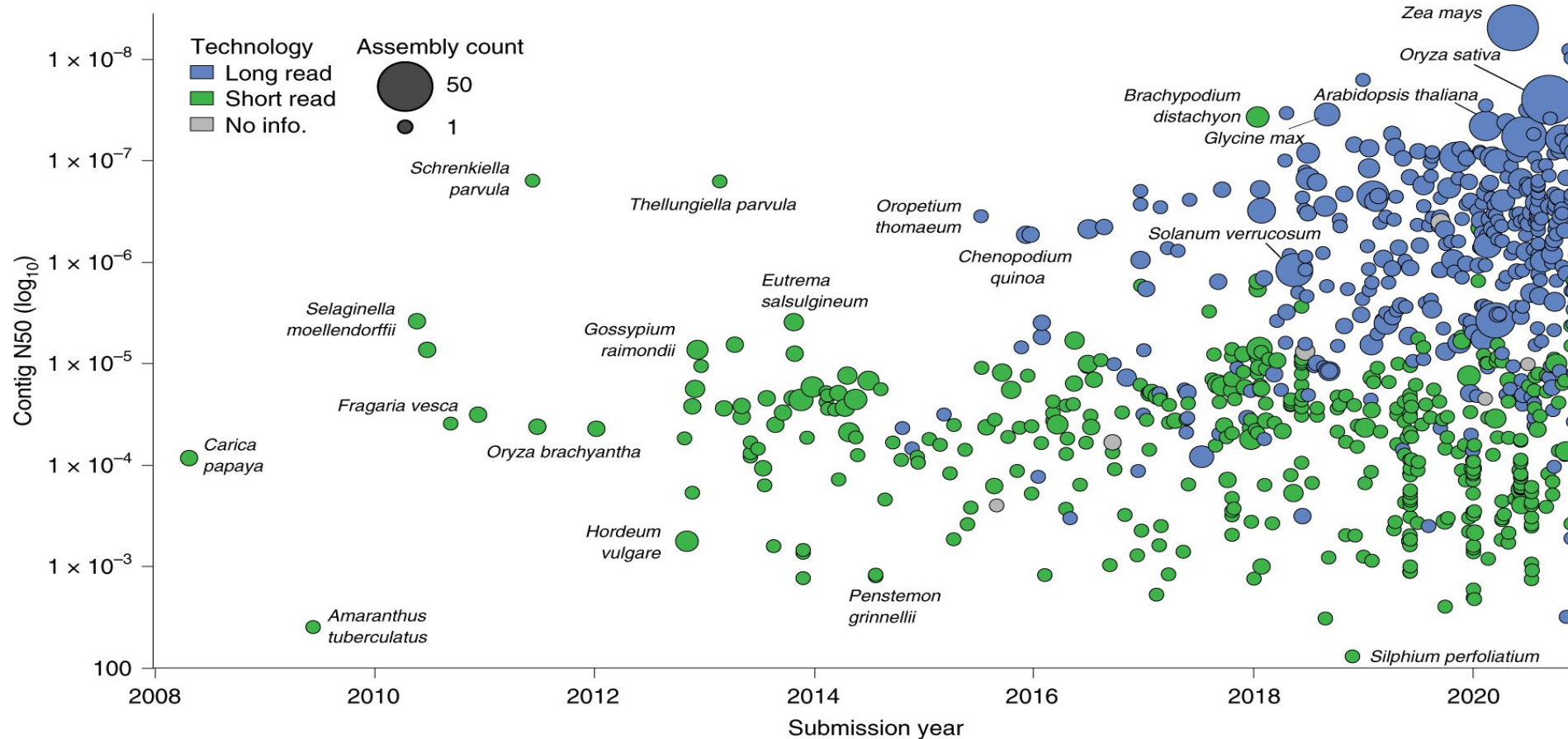
[DDBJ Center](#)

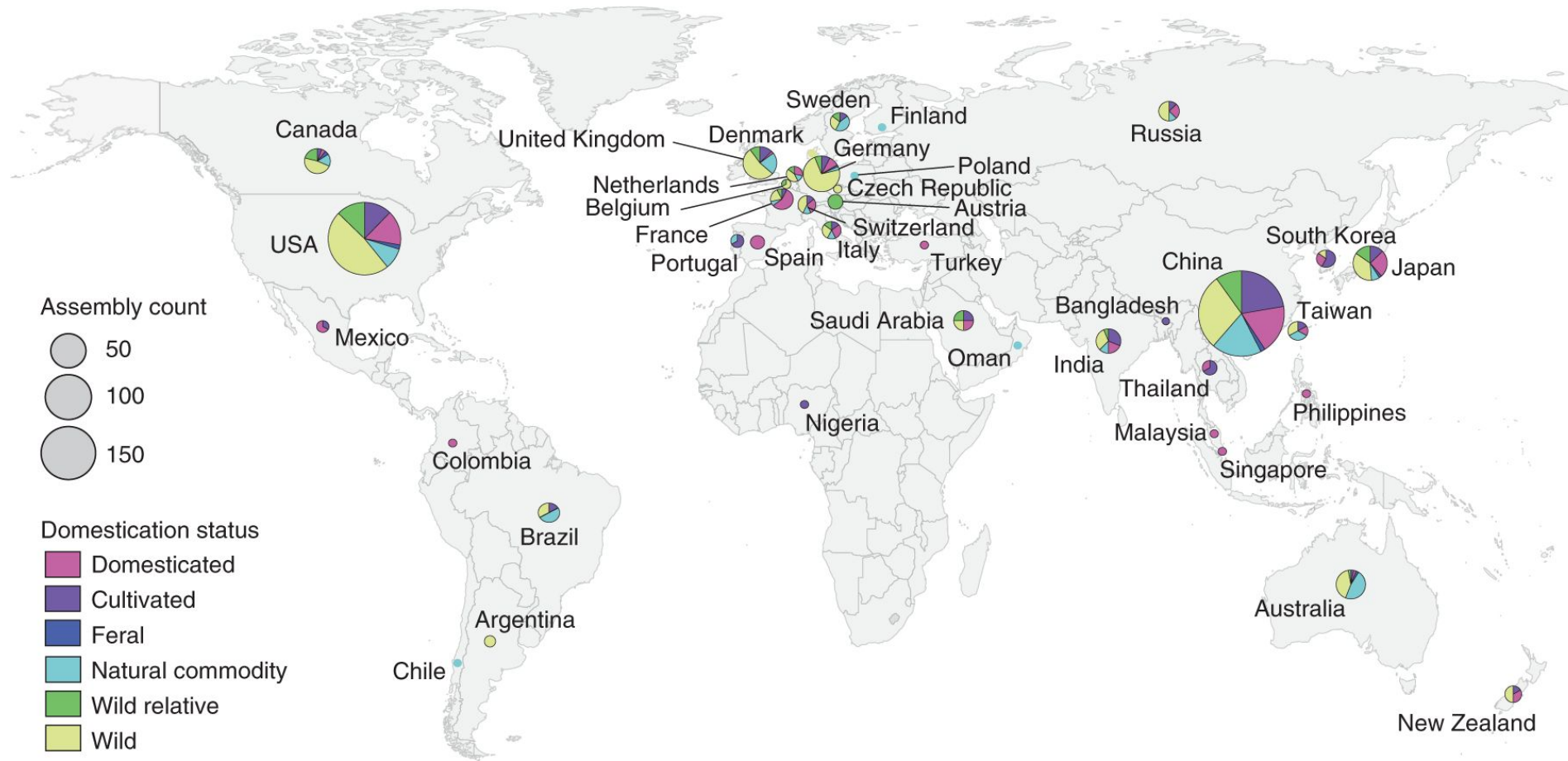
[more](#)

# Plantas



# Genomas secuenciados de Plantas





# Navegadores enfocados en Plantas



<http://eggnog5.embl.de/#/app/home>



<https://plants.ensembl.org/index.html>



<https://phytozome-next.jgi.doe.gov/>



<https://bioinformatics.psb.ugent.be/plaza/>



<https://www.genome.jp/kegg/genome/plant.html>

# Bases de Datos en Plantas

**Table 4.5** List of plant species of relevant agronomical interest, sorted by the year of publication of their genomes. The annotation version available for these species in different reference databases is also reported

Species	Year of publication	Annotation version						
		NCBI	Ensembl Plants	PlantGDB	Phytozome	Plaza	Egglog	KEGG
<i>Arabidopsis</i>	2000	TAIR 10	TAIR 10	TAIR 10	TAIR 10	TAIR 10	TAIR 10	TAIR 10
Rice	2002	RGAP 7	RGAP 7	RGAP 7	RGAP 7	RGAP 7	RGAP 7	RGAP 7
Grapevine	2007	GCF_000003745.3	V1 Cribi	V2 Genoscope	V2 Genoscope	V2 Genoscope	V1 Cribi	GCF_000003745.3
Maize	2009	B73_RefGen_v3	B73_RefGen_v4	B73_RefGen_v2	B73_RefGen_v3	B73_RefGen_v4	B73_RefGen_v4	B73_RefGen_v3
Potato	2011	GCF_000226075.1	GCF_000226075.1	PGSC v.3 2.1.10	PGSC v. 3.4	iTAG v. 1	GCF_000226075.1	GCF_000226075.1
Tomato	2012	GCF_000188115.3	iTAG v. 2.4	NA	iTAG v. 2.3	iTAG v. 2.3	iTAG v. 2.3	GCF_000188115.3
Sweet orange	2013	GCF_000317415.1	NA	NA	JGI v1	JGI v1	NA	GCF_000317415.1
Pepper	2014	GCF_000710875.1	NA	NA	NA	NA	NA	NA
Amborella	2013	GCF_000471905.1	GCF_000471905.1	NA	AmTr_v.0.10	AmTr_v.0.10	NA	GCF_000471905.1
Soybean	2006	GCF_000004515.4	GCF_000004515.1	Wm82.a2.v1	Wm82.a2.v1	Wm82.a2.v1	GCF_000004515.1	GCF_000004515.4
Apple	2010	GCF_000148765.1	NA	NA	M. Domestica v1.0	M. Domestica v1.0	NA	GCF_000148765.1
Sorghum	2009	GCF_000003195.2	GCF_000003195.2	Sbi1.4	Sbi3.1	NA	GCF_000003195.2	GCF_000003195.2
Barrel medic	2011	GCF_000219495.2	Mt4.0	Mt3.5	Mt4.0	Mt4.0	NA	GCF_000219495.2
Banana	2012	GCF_000313855.1	GCF_000313855.1	NA	M. acuminata v 1	NA	GCF_000313855.1	GCF_000313855.1
Cocoa	2011	GCF_000208745.1	GCF_000208745.1	NA	C. Matina v1.1	C. Matina v1.1	NA	GCF_000208745.1





# TAIR

*The Arabidopsis Information Resource (TAIR)*

-Bases de Datos y Browser

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

The Arabidopsis Information Resource

Home Help Contact About Us Subscribe Login Register Institution: Universidad Nacional Autonoma de Mexico (subscriber)

Search Browse Tools Portals Download Submit News Stocks

**Community Workshops**

ICAR 2024 July 15-20

SAN DIEGO 3rd INTERNATIONAL CONFERENCE ON ARABIDOPSIS RESEARCH

Proposals Due October 15, 2023

**Breaking News**

**ICAR2024 Call for proposals**  
[Aug 28, 2023]  
ICAR2024 Community Workshops Call for Proposals. Submissions due October 15, 2023.

**TAIR preparing to phase out SeqViewer and GBrowse**  
[Aug 16, 2023]  
TAIR is preparing to retire GBrowse and SeqViewer, focus on features and new tracks with JBrowse and JBrowse2

**AgBioData, TAIR and Phoenix at ASPB**  
[Jul 19, 2023]  
See you in Savannah. AgBioData is hosting two workshops at ASPB. Come to booth #406 to learn more about Phoenix Bioinformatics, TAIR and AgBioData.

**InterPro domain update**  
[Jul 19, 2023]  
TAIR protein domains have been updated to InterPro 95.0

**35th public release of TAIR@Phoenix data**  
[Jul 1, 2023]  
35th public release of data curated under TAIR's subscription-based funding model. Files contain new publications, annotations, gene models and other data through



<https://plants.ensembl.org/index.html>

**EnsemblPlants** · [HMMER](#) | [BLAST](#) | [BioMart](#) | [Tools](#) | [Downloads](#) | [Help & Docs](#) | [Blog](#)

[Login/Register](#)

Search Ensembl Plants

**Arabidopsis thaliana (TAIR10)** ▾

#### Search

Search Thale-cress...

Go

e.g. AT1G07820 or 1:2421089-2422066 or Carboxy\*

#### About *Arabidopsis thaliana*

*Arabidopsis thaliana* is a small flowering plant that is widely used as a model organism in plant biology. *Arabidopsis* is a member of the mustard (Brassicaceae) family, which includes cultivated species such as cabbage and radish. *Arabidopsis* is not of major agronomic significance, but its small genome size and ease of cultivation offer important advantages for basic research in genetics and molecular biology. *Arabidopsis thaliana* has a genome size of ~135 Mb, and a haploid chromosome number of five.

Taxonomy ID [3102](#)

Data source [The Arabidopsis Information Resource](#)

More information and statistics

#### Genome assembly: [TAIR10](#)

More information and statistics

Download DNA sequence (FASTA)

Convert your data to TAIR10 coordinates

Display your data in Ensembl Plants



View karyotype



Example region

#### Gene annotation

What can I find? Protein-coding and non-coding genes, splice variants, cDNA and protein sequences, non-coding RNAs.

More about this genebuild

Download genes, cDNAs, ncRNA, proteins - FASTA - GFF3

Update your old Ensembl IDs



Example gene



Example transcript

#### Comparative genomics

What can I find? Homologues, gene trees, and whole genome alignments across multiple species.

More about comparative analyses

Phylogenetic overview of gene families

Download alignments (EMF)



Example gene tree

Pan-taxonomic tree

#### Variation

What can I find? Short sequence variants.

More about variation in Ensembl Plants

Download all variants - GVCF - VCF - VEP

Variant Effect Predictor



Example variant

#### Regulation

What can I find? Microarray annotations.

More about the Ensembl Plants microarray annotation strategy



# Phytozome 12

THE PLANT GENOMICS RESOURCE



Phytozome 13  
THE PLANT GENOMICS RESOURCE



Welcome to

Phytozome ▼

Overview

Release Notes

News

## Recent Genome Releases

Pharus latifolius v1.1		Aug 5, 2021
Betula platyphylla v1.1	Asian white birch	Aug 5, 2021
Portulaca amilis v1.0	Paraguayan purslane	Aug 5, 2021
Zea mays B84 v1.2	Stiff stalk maize B84	Jun 8, 2021
Zea mays LH145 v1.2	Stiff stalk maize LH145	Jun 8, 2021
Zea mays NKH8431 v1.2	Stiff stalk maize NKH8431	Jun 8, 2021

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. 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.

# InterMINE - Phytozome

☐ Manage Columns

☐ Manage Filters

☐ Manage Relationships

Showing 1 to 9 of 9 rows

Gene Symbol	Gene Secondary Identifier	GO Annotation Ontology Term . Identifier	GO Annotation Ontology Term . Name	Code Code	Ontology Term Namespace
zen	CG1046	GO:0000978	RNA polymerase II cis-regulatory region sequence-specific DNA binding	IBA	molecular_function
zen	CG1046	GO:0000981	DNA-binding transcription factor activity, RNA polymerase II-specific	IBA	molecular_function
zen	CG1046	GO:0000981	DNA-binding transcription factor activity, RNA polymerase II-specific	IDA	molecular_function
zen	CG1046	GO:0005634	nucleus	IBA	cellular_component
zen	CG1046	GO:0006957	regulation of transcription by RNA polymerase II	IBA	biological_process



**LIS - Legume Information System**  
Information about legume traits for crop improvement



**LegumeMine v5.1.0.2** Genomic and expression data from LIS



**LIS - Legume Information System**  
Information about legume traits for crop improvement



**MedicagoMine v5.1.0.3** Medicago data from the Legume Information System

[LegumeMine](#) | [ArachisMine](#) | [CicerMine](#) | [GlycineMine](#) | [LensMine](#) | [LupinusMine](#) | [PhaseolusMine](#) | [VignaMine](#) | [MedicagoMine](#)



**MaizeMine v1.5**

An integrated data warehouse for [MaizeGDB](#). [Click here to go to MaizeMine v1.4 \(previous release\)](#)





# AgBioData

Toward enhanced genomics, genetics, and breeding research outcomes through standardization of practices and protocols across agricultural databases

AgBase

<https://agbase.arizona.edu/>

AgroPortal

<http://agroportal.lirmm.fr/>

Alfalfa Breeders Toolbox

<https://medicago.legumeinfo.org/>

Animal QTLdb

<http://www.animalgenome.org/cgi-bin/QTLdb/index>

Bovine Genome Database

<http://bovinegenome.org/>

CassavaBase

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

Citrus Genome Database

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

Citrus Greening

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

CottonGen

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

Crop Ontology

<https://cropontology.org/>

Cucurbit Genomics

<http://cucurbitgenomics.org/>

CyVerse

<http://www.cyverse.org>

EBS (Enterprise Breeding System)

<https://ebs.excellenceinbreeding.org/>

Ensembl

<https://useast.ensembl.org/index.html>

FAANG

<https://data.faang.org/home>

Genome Database for Rosaceae

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

Genome Database for Vaccinium

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

GOBii

<https://excellenceinbreeding.org/toolbox/tools/gobii-genomic-data-management-system-gobii-gdm>

GrainGenes

<https://wheat.pw.usda.gov/GG3/>

Gramene

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

GRIN

<https://www.ars-grin.gov>

Hardwood Genomics

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

Hymenoptera Genome Database

<http://hymenopteragenome.org/>

i5k Workspace@NAL

<https://i5k.nal.usda.gov/>

KitBase

<http://kitbase.ucdavis.edu/>

Legume Information System

<https://legumeinfo.org/>

MaizeGDB

<https://maizegdb.org/>

MusaBase

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

National Animal Disease Center

<https://www.ars.usda.gov/midwest-area/ames/nadc/>

PeanutBase

<https://peanutbase.org>

Planteome

<https://planteome.org/>

Plant Metabolic Pathway Databases

<https://plantcyc.org/>

Pulse Crop Database

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

Sol Genomics Network

<https://solgenomics.net/>

SorghumBase

<https://www.sorghumbase.org>

SoyBase

<https://www.soybase.org>

SweetPotatoBase

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

TAIR

<http://www.arabidopsis.org>

The Bio-Analytic Resource for Plant Biology (BAR)

<https://bar.utoronto.ca/>

The European Variation Archive

<https://www.ebi.ac.uk/eva/>

TreeGenes

<https://treegenesdb.org>

Triticeae toolbox, T3

<https://triticeaetoolbox.org/wheat/>

Wheat1S

<http://wheat1s.org/>

YamBase

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

<https://www.agbiodata.org/databases>