

Genome Database

Genome Databases

- The study of genes and proteins has become an extremely important area in the modern day biology and they are better known as genomics and proteomics
- Genome databases store this information and differently from gene databases the genome databases contain both coding and non-coding inter-genic sequences.

Types of databases


- Many types of databases available for researchers in the field of biology
 - a) Primary sequence databases - for storage of raw experimental data
 - b) Secondary databases - contain information on sequence patterns and motifs
 - c) Organism specific databases and other databases like Saccharomyces genome database, Mouse genome database, Human genome database, European mutant mouse pathology database


Organism-specific genomic databases

Organism	Database/resource	URL
<i>Escherichia coli</i>	EcoGene EcoCyc (Encyclopedia of <i>E. coli</i> genes and metabolism) Colibri	http://bmb.med.miami.edu/EcoGene/EcoWeb http://ecocyc.pangeasystems.com/ecocyc/ecocyc.html http://genolist.pasteur.fr/Colibri
<i>Bacillus subtilis</i>	SubtiList	http://genolist.pasteur.fr/SubtiList
<i>Saccharomyces cerevisiae</i>	Saccharomyces Genome Database (SGD)	http://genome-www.stanford.edu/Saccharmyces
<i>Plasmodium falciparum</i>	PlasmoDB	http://PlasmoDB.org
<i>Arabidopsis thaliana</i>	MIPS <i>Arabidopsis thaliana</i> Database (MAtdB) The Arabidopsis information resource (TAIR)	http://mips.gsf.de/proj/thal/db http://www.arabidopsis.org
<i>Drosophila melanogaster</i>	FlyBase	http://flybase.bio.indiana.edu
<i>Caenorhabditis elegans</i>	A <i>C. elegans</i> DataBase (ACeDB)	http://www.acedb.org
Mouse	Mouse Genome Database (MGD)	http://www.informatics.jax.org
Human	OnLine Mendelian Inheritance in Man (OMIM)	http://www.ncbi.nlm.nih.gov/omim

NCBI Genome Page

<http://www.ncbi.nlm.nih.gov/sites/entrez?db=geno>





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Entrez Genome Help

Submitting Genome Project Genome sequence

Microbial Genome Projects

Genomic BLAST Microbial Eukaryotic

Archaea Chromosome Plasmid DraftAssembly

Bacteria Chromosome Plasmid DraftAssembly

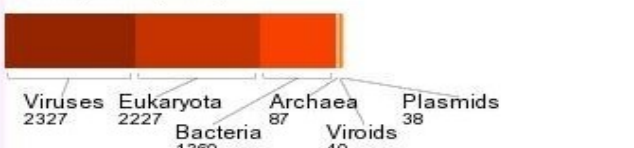
Eukaryota Chromosome Plasmid Organelles

Viruses Phages

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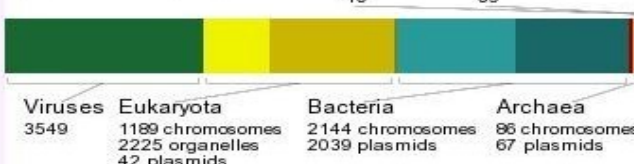
The Genome database provides views for a variety of genomes, complete chromosomes, sequence maps with contigs, and integrated genetic and physical maps. The database is organized in six major organism groups: [Archaea](#), [Bacteria](#), [Eukaryotae](#), [Viruses](#), [Viroids](#), and [Plasmids](#) and includes complete chromosomes, organelles and plasmids as well as draft genome assemblies.

Total species (6079)



Viruses	Eukaryota	Bacteria	Archaea	Viroids	Plasmids
2327	2227	1360	87	40	38

Total records (11420)



Viruses	Eukaryota	Bacteria	Archaea
3549	1189 chromosomes 2225 organelles 42 plasmids	2144 chromosomes 2039 plasmids	86 chromosomes 67 plasmids

Genome Sequencing Milestone Reached! There are now 1000 complete Prokaryotic Genomes available in Entrez Genome. See the full list of [complete bacterial and archaeal genomes](#). [Microbial Resources](#) are available for search, retrieval, and analysis of all genomes.

▶ **Related resources**

[Entrez Genome Project](#) complete and incomplete large-scale sequencing projects

[Entrez Protein Clusters](#) a collection of related protein sequences

[Eukaryotic genome projects and sequences](#)

[Genomes of Bacillus anthracis](#) reference genome and related sequences

[Influenza Virus Resource](#) sequence database and analyses

[Microbial Genomes](#) reference sequences and resources

[Organelle](#) reference sequences and tools

[Plant Genomes Central](#) major plant genome

Human Genome Resources


<http://www.ncbi.nlm.nih.gov/projects/genome/guide/human/>

NCBI • Genomic Biology • Homo sapiens

Search for


Browse your Genome
Click on the Chromosome to show


Genes



1 2 3 4 5 6 7 8
9 10 11 12 13 14 15 16
17 18 19 20 21 22 X Y

Find A Gene
Search for
from

The NCBI Handbook
 An online guide to the use of NCBI resources. Titles of selected chapters that refer to human genome resources are shown below.



Human Genome Resources

A challenge facing researchers today is that of piecing together and analyzing the plethora of data currently being generated through the Human Genome Project and scores of smaller projects. NCBI's Web site serves as an integrated, one-stop, genomic information infrastructure for biomedical researchers from around the world so that they may use these data in their research efforts. [More...](#)

Genes and Human Health

- ▶ **Gene Database**
A new database of genes and associated information is now available for searching in Entrez.
- ▶ **OMIM**
A guide to human genes and inherited disorders maintained by Johns Hopkins University and collaborators.
- ▶ **RefSeq**
Reference sequences of chromosomes, genomic contigs, mRNAs, and proteins for human and major model organisms.
- ▶ **dbSNP**
A database of single nucleotide polymorphisms (SNPs) and other nucleotide variations.

Reagents

UCSC Genome Bioinformatics

Genomes - Blat - Tables - Gene Sorter - PCR - VisiGene - Proteome - Session - FAQ - Help

Genome
Browser

ENCODE

Blat

Table
Browser

Gene Sorter

In Silico
PCR

Genome
Graphs

Galaxy

VisiGene

Proteome
Browser

Utilities

Downloads

Release Log

Custom
Tracks

About the UCSC Genome Bioinformatics Site

Welcome to the UCSC Genome Browser website. This site contains the reference sequence and working draft assemblies for a large collection of genomes. It also provides a portal to the ENCODE project.

We encourage you to explore these sequences with our tools. The [Genome Browser](#) zooms and scrolls over chromosomes, showing the work of annotators worldwide. The [Gene Sorter](#) shows expression, homology and other information on groups of genes that can be related in many ways. [Blat](#) quickly maps your sequence to the genome. The [Table Browser](#) provides convenient access to the underlying database. [VisiGene](#) lets you browse through a large collection of *in situ* mouse and frog images to examine expression patterns. [Genome Graphs](#) allows you to upload and display genome-wide data sets.

<http://genome.ucsc.edu>

The UCSC Genome Browser is developed and maintained by the Genome Bioinformatics Group, a cross-departmental team within the Center for Biomolecular Science and Engineering ([CBSE](#)) at the University of California Santa Cruz ([UCSC](#)). If you have feedback or questions concerning the tools or data on this website, feel free to contact us on our [public mailing list](#).

News

[News Archives](#) ►

To receive announcements of new genome assembly releases, new software features, updates and training seminars by email, subscribe to the [genome-announce](#) mailing list.

14 Dec. 2009 - New job posting: Biological Data Technician

The UCSC Genome Browser project is looking for a bioinformatician, biologist, or software engineer with a strong biology background to collect and import data into the UCSC Genome Browser database and website. This person will work closely with external research laboratories to capture their experimental results and methods and with internal software developers and database testing staff to make the data accessible to the worldwide scientific community.

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The UCSC Genome Browser Introduction

Tutorial and training materials by OpenHelix



Online Tutorial Suite

Learn to use the UCSC Genome Browser with this **free tutorial, sponsored by UCSC Genome Bioinformatics Group**. The UCSC Genome Browser provides a way to examine the data from many genomes, with extensive annotation tracks for various data types including known genes, predicted genes, SNPs, comparative multi-species analysis and much more. This introductory tutorial focuses on the foundation and framework for the organization and display of the data, and basic text and sequence searches. This tutorial, which is the first in a series of three tutorials on the UCSC Genome Browser, will get you on your way to expertly navigating this vital tool for genomic research.

You'll learn:

- to perform basic text searches on the UCSC Genome Browser
- to understand and customize the displays in genomic regions of interest
- to start with a sequence and find genomic regions of interest using BLAT

More about the resource:

The UCSC Genome Browser, sometimes referred to as the "Golden Path" browser, offers a well-organized and user-friendly view of the human genome, along with dozens of other genomes as well. The official genomic sequence is supplemented with many other data types which are useful to researchers: expression, variation, comparative genomics, and many more. The data can be accessed with simple text or sequence searches using BLAT, or probed in depth with customized queries. Be sure to see the other UCSC tutorials for advanced topics and additional tools as well.

Launch	Download	Download	Download	Link
Online Tutorial	PowerPoint Slides <small>(Optimized for Windows*)</small>	Slide Handouts <small>(PDF file)</small>	Hands-on Exercises <small>(PDF file)</small>	Visit the Resource

Related tutorials

This tutorial is a part of the tutorial group **UCSC Tutorials**. You might find the other tutorials in the group interesting:

UCSC Genome Browser: Custom Tracks and Table Browser: UCSC Genome Browser advanced topics
UCSC Genome Browser: The Additional Tools: Additional tools at the UCSC Genome Browser

Categories

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Algorithms and Analysis

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THANK YOU