Genome browsers
Suppose we want to explore a gene...
http://genome.ucsc.edu

UCSC Genome Bioinformatics

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 portals to the ENCODE and Neandertal projects.

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.

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 (CBSIE) 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

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

8 September 2011 - New Navigation and Display Features

We've added several new features to the Genome Browser that make it easier to quickly configure and navigate around in the browser's annotation tracks window.

Automatic image resizing: The first time the annotation track window is displayed, or after the Genome Browser has been reset, the size of the track window is now set by default to the width that best fits your Internet browser window. If you subsequently resize your browser window, you can automatically adjust the annotation track image size to the new width by clicking the resize button under the track image. The default width can still be manually overridden on the Track Configuration page.

Scrolling left or right in the track window: You can now scroll (pan) horizontally through the tracks image by clicking on the image, dragging the cursor to the left or right, then releasing the mouse button. The view may be scrolled by up to one image width.
Mouse (Mus musculus) Genome Browser Gateway

The UCSC Genome Browser was created by the Genome Bioinformatics Group of UC Santa Cruz.
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Click here to reset the browser user interface settings to their defaults.

About the Mouse July 2007 (NCBI37/mm9) assembly (sequences)

The July 2007 mouse (Mus musculus) genome data were obtained from the Build 37 assembly by NCBI and the Mouse Genome Sequencing Consortium.

Sample position queries

A genome position can be specified by the accession number of a sequenced genomic region, an mRNA or EST, a chromosomal coordinate range, or keywords from the GenBank description of an mRNA. The following list shows examples of valid position queries for the Mouse genome. See the User's Guide for more information.

Request: Genome Browser Response:

chr16 Displays all of chromosome 16
chr16:1-5000000 Displays first 5 million bases of chr 16
chr16:1000000+2000 Displays a region of chr 16 that spans 2000 bases, starting with position 1000000
AC072048.4 Displays region of contig AC072048.4
D16Mit120 Displays region around STS marker DMit16120 from the MGI consensus genetic map, including 100,000 bases on each side as well
D16Mit120-D16Mit140 Displays region between STS markers D16Mit120 and D16Mit140
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<thead>
<tr>
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</tr>
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<tbody>
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<td>Displays region between STS markers D16Mit120 and D16Mit140</td>
</tr>
</tbody>
</table>
DNA downloading, BLAT searching
Get DNA for

Position: chr1:134,219,195-134,226,39

Note: This page retrieves genomic DNA for a single region. If you would prefer to get DNA for many items in a particular track, or get DNA with formatting options based on gene structure (introns, exons, UTRs, etc.), try using the Table Browser with the "sequence" output format.

Sequence Retrieval Region Options:

Add 0 extra bases upstream (5') and 0 extra downstream (3')

Note: if a feature is close to the beginning or end of a chromosome and upstream/downstream bases are added, they may be truncated in order to avoid extending past the edge of the chromosome.

Sequence Formatting Options:

- All upper case.
- All lower case.
- Mask repeats: to lower case to N
- Reverse complement (get '- strand sequence)

Note: The "Mask repeats" option applies only to "get DNA", not to "extended case/color options".
BLAT Search Genome

Paste in a query sequence to find its location in the genome. Multiple sequences may be searched if separated by lines starting with `>` followed by the sequence name.

File Upload: Rather than pasting a sequence, you can choose to upload a text file containing the sequence.

Upload sequence: [Choose File] no file selected

Only DNA sequences of 25,000 or fewer bases and protein or translated sequence of 10000 or fewer letters will be processed. Up to 25 sequences can be submitted at the same time. The total limit for multiple sequence submissions is 50,000 bases or 25,000 letters.

For locating PCR primers, use [In-Silico PCR] for best results instead of BLAT.
BLAT Search Genome

Genome:    Assembly:     Query type:     Sort output:     Output type:
Mouse       July 2007 (NCBI37/mm9)   BLAT's guess  query,score  hyperlink

Paste in a query sequence to find its location in the genome. Multiple sequences may be searched if separated by lines starting with '>' followed by the sequence name.

File Upload: Rather than pasting a sequence, you can choose to upload a text file containing the sequence.
Upload sequence: Choose File  no file selected  submit file

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## BLAT Search Results

<table>
<thead>
<tr>
<th>ACTIONS</th>
<th>QUERY</th>
<th>SCORE</th>
<th>START</th>
<th>END</th>
<th>QSIZE</th>
<th>IDENTITY</th>
<th>CHRO</th>
<th>STRAND</th>
<th>START</th>
<th>END</th>
<th>SPAN</th>
</tr>
</thead>
<tbody>
<tr>
<td>browser details</td>
<td>YourSeq</td>
<td>50</td>
<td>1</td>
<td>50</td>
<td>50</td>
<td>100.0%</td>
<td>1</td>
<td>+</td>
<td>134219195</td>
<td>134219244</td>
<td>50</td>
</tr>
</tbody>
</table>
Databases of human genome mutations
ANNOUNCEMENT

8/15/2011: dbSNP Build 134 Release

Please see the build announcement for more details

Search by IDs on All Assemblies

Note: rs# and ss# must be prefixed with "rs" or "ss", respectively (i.e. rs25, ss25)

ID:

Search  Reset

Submission Information

- By Submitter
- New Submitted Batches
- Method
- Population
- Publication

Batch

- Enter List
  - NCBI Assay ID(ss)
Database connection error. Please try again later.