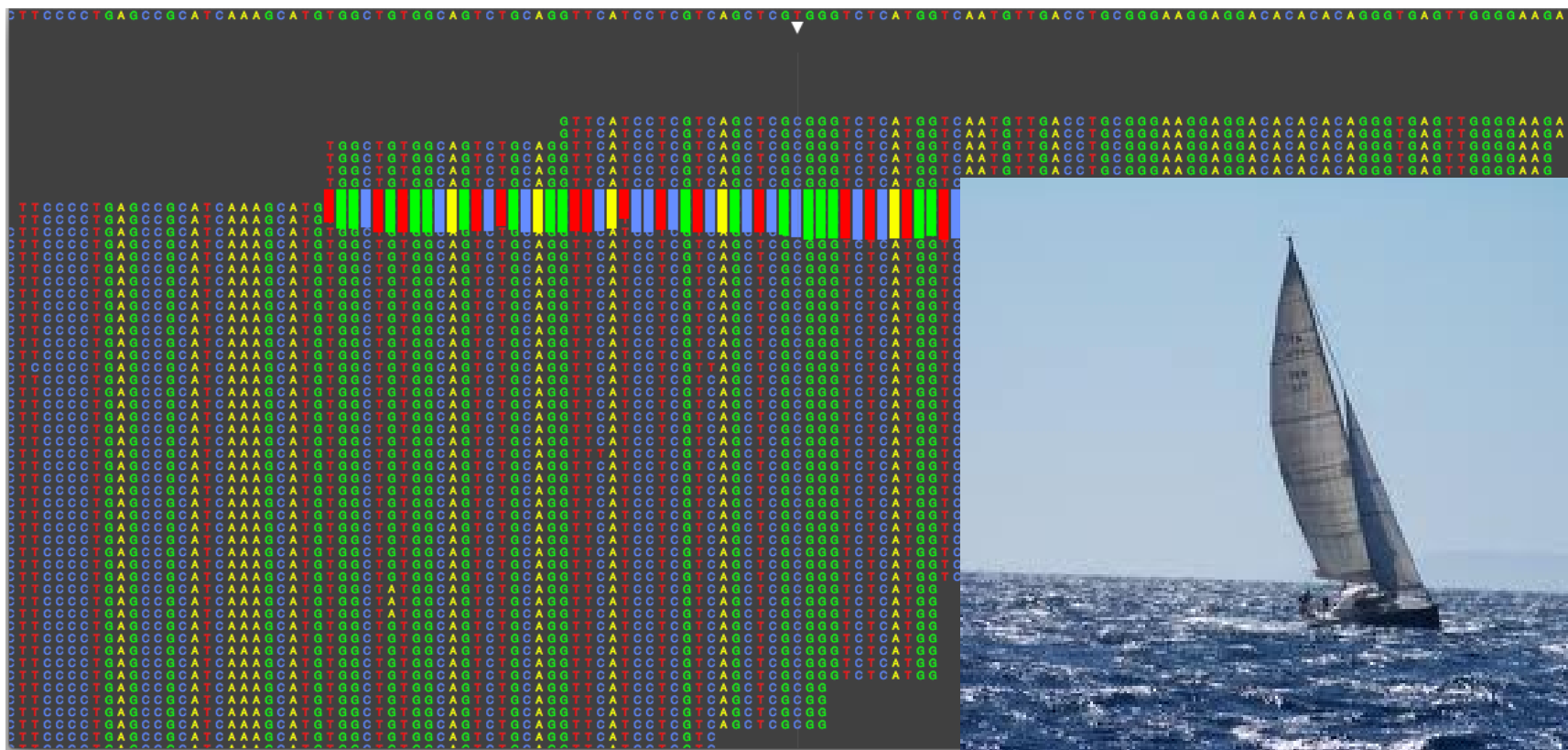


# HTS data visualization in genome browsers: the UCSC Genome Browser

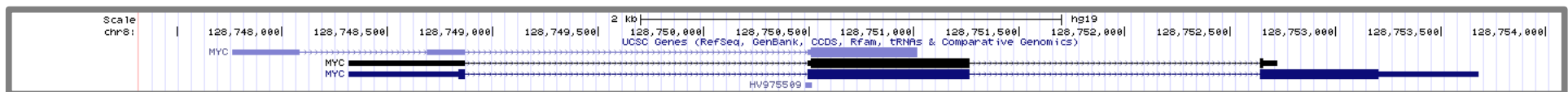


# What is a Genome Browser

- The Human Genome Project (2001) marks the beginning of a massive production of sequencing and genomic annotation data.



- For the first time there is a need to develop *ad hoc* tools to organize and manage this huge data amount → the first genome browsers appear:  
**MapViewer** (<http://www.ncbi.nlm.nih.gov/mapview/>), l'**Ensembl Genome Browser** (<http://www.ensembl.org/>) and the **UCSC Genome Browser** (<http://genome.ucsc.edu/>)



# University of California Santa Cruz (UCSC) Genome Browser



Site map and tools menu

## 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
  - **VisiGene**  
interactively view in situ images of mouse and frog
- More tools...

News

## Our story

On June 22, 2000, UCSC and the other members of the International Human Genome Project consortium completed the first working draft of the human genome assembly, forever ensuring free public access to the genome and the information it contains. A few weeks later, on July 7, 2000, the newly assembled genome was released on the web at <http://genome.ucsc.edu>,

## What's new

Feb. 20, 2018 - **New video: Visibility control in the Browser**  
Feb. 16, 2018 - **New search support for chromosome aliases**  
Feb. 08, 2018 - **New video: in-silico PCR (isPCR)**  
[More news...](#)

<http://genome.ucsc.edu/>



# The Genome Browser Gateway

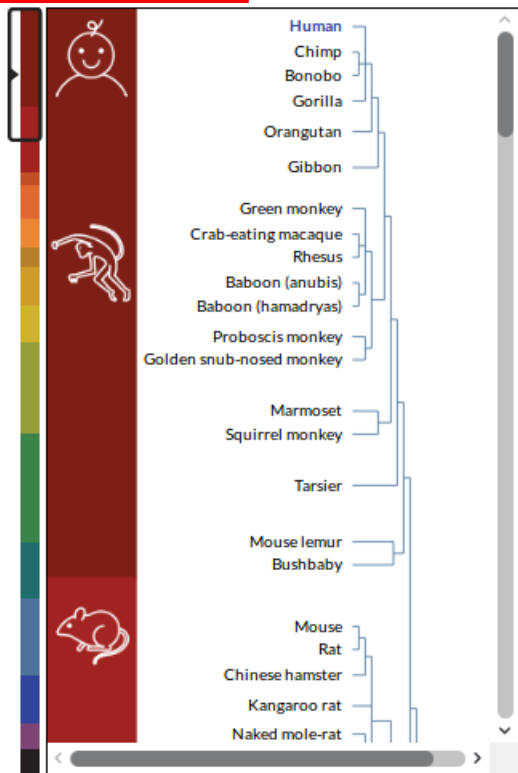
## Browse/Select Species

### POPULAR SPECIES



Enter species or common name

### REPRESENTED SPECIES



## Find Position

### Human Assembly

Dec. 2013 (GRCh38/hg38)

### Position/Search Term

Enter position, gene symbol or search terms

Current position: chr1:11,102,837-11,267,747

GO

## Human Genome Browser - hg38 assembly

view sequences

UCSC Genome Browser assembly ID: hg38

Sequencing/Assembly provider ID: Genome Reference Consortium Human GRCh38 (GCA\_000001405.15)

Assembly date: Dec. 2013

Accession ID: GCA\_000001405.15

NCBI Genome ID: 51 (Homo sapiens (human))

NCBI Assembly ID: 883148 (GRCh38, GCA\_000001405.15)

BioProject ID: 31257



Homo sapiens

(Graphic courtesy of CBSE)

### Search the assembly:

- **By position or search term:** Use the "position or search term" box to find areas of the genome associated with many different attributes, such as a specific chromosomal coordinate range; mRNA, EST, or STS marker names; or keywords from the GenBank description of an mRNA. [More information](#), including sample queries.
- **By gene name:** Type a gene name into the "search term" box, choose your gene from the drop-down list, then press "submit" to go directly to the assembly location associated with that gene. [More information](#).
- **By track type:** Click the "track search" button to find Genome Browser tracks that match specific selection criteria. [More information](#).

### Download sequence and annotation data:

- [Using rsync](#) (recommended)
- [Using FTP](#)
- [Using HTTP](#)
- [Data use conditions and restrictions](#)
- [Acknowledgments](#)

## Assembly Details

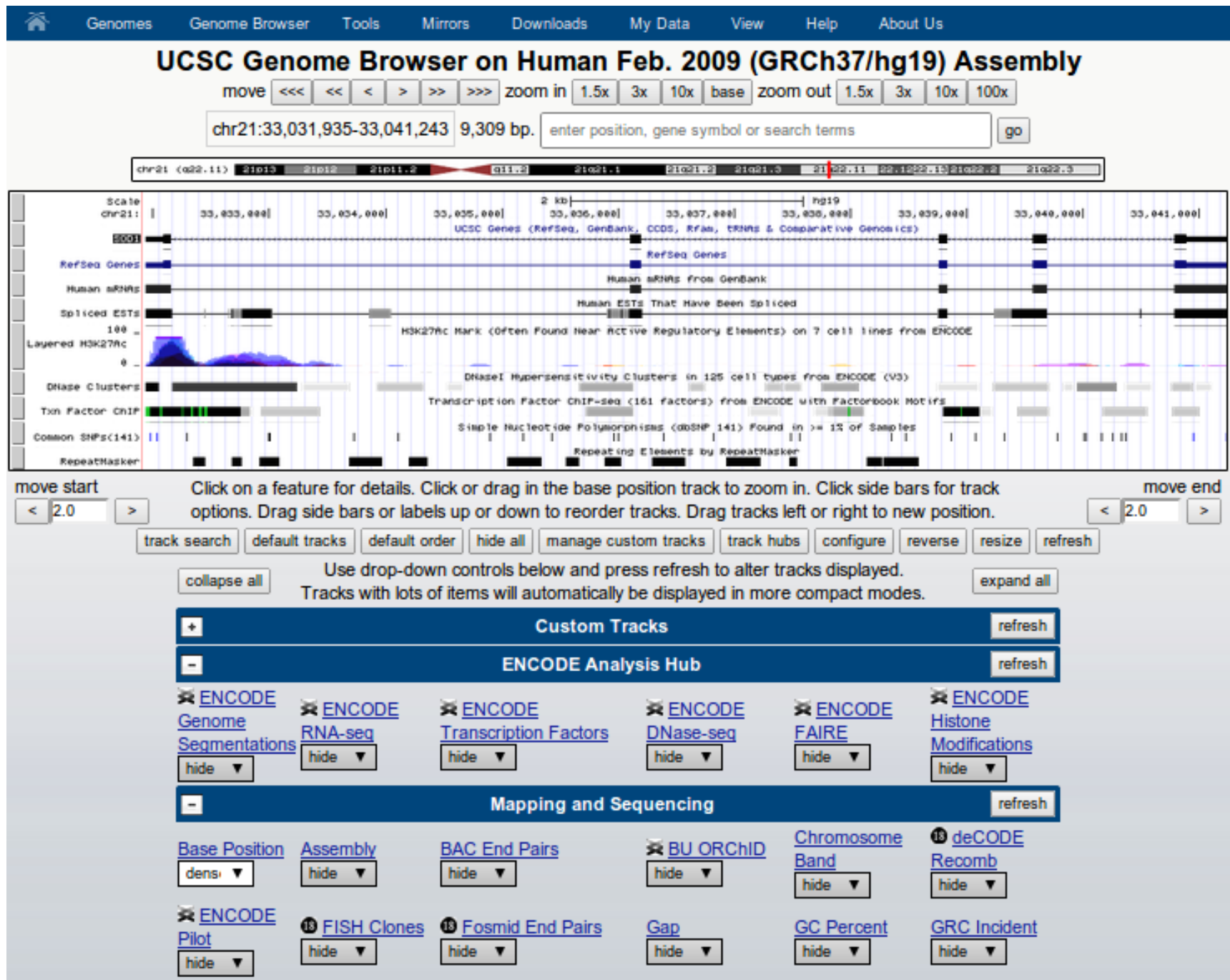
### Request:

chr7  
chrUn\_gl000212  
20p13  
chr3:1-1000000  
chr3:1000000+2000

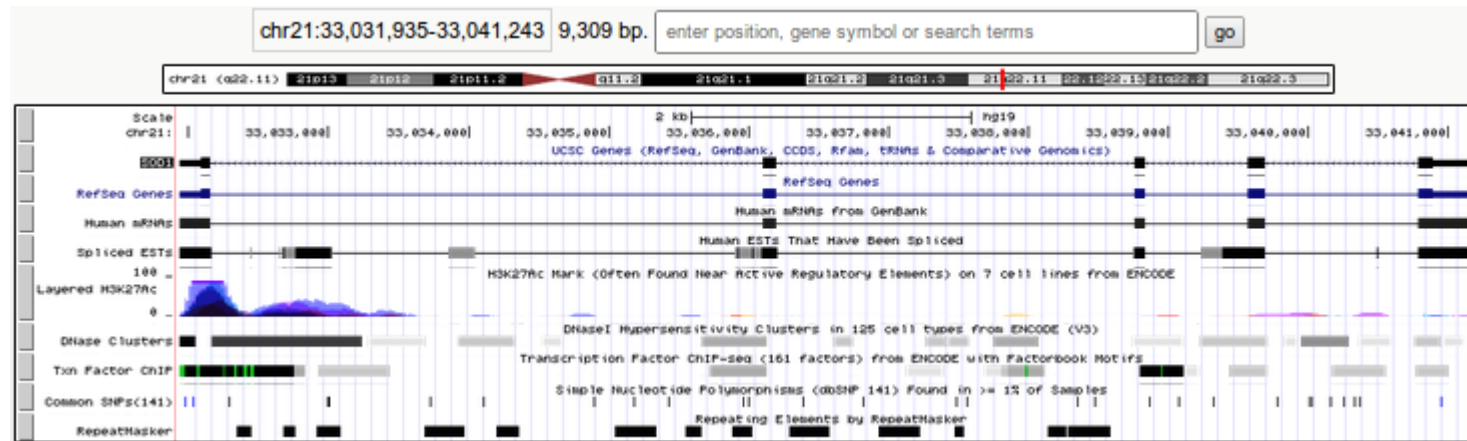
### Genome Browser Response:

Displays all of chromosome 7  
Displays all of the unplaced contig gl000212  
Displays region for band p13 on chr 20  
Displays first million bases of chr 3, counting from p-arm telomere  
Displays a region of chr3 that spans 2000 bases, starting with position 1000000

# Search result



# Search results: page structure



sequence

Annotation Tracks

**Reference Genome:** chromosome & coordinates

chromosome band

known genes

predicted genes

phenotype and disease

enhancer/promoter data

microarray/expression data

evolutionary conservation

SNPs and structural variation

repeated regions

more...

*Links to detail pages*

# Annotation Tracks



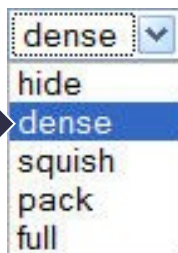


**Genome viewer**

**Groups of data (Tracks)**

- Mapping and Sequencing Tracks
- Genes and Gene Prediction Tracks  
(including sno/miRNA data)
- Phenotype, Disease, Literature Tracks
- mRNA and EST Tracks
- Expression (such as microarray)
- Regulation (including TFBS)
- Comparative Genomics
  - As a group
  - Individual species
- Neandertal, Denisova
- Variation, Repeats  
(including SNPs, copy number variation)

to add or remove,  
or change visibility





move to left or right

increase / decrease  
genomic interval

Red bar indicates the  
genomic interval in view

UCSC Genome Browser on Human Feb. 2009 (GRCh37/hg19) Assembly

move <<< << < > >> >>> zoom in 1.5x 3x 10x base zoom out 1.5x 3x 10x 100x

chr21:33,036,032-33,036,314 283 bp. enter position, gene symbol or search terms

go

chr21 (q22.11) 21p13 21p12 21p11.2 11.2 21q21.1 q21.2 21q21.3 21q22.11

Scale chr21: 33,033,000| 33,034,000| 33,035,000| 33,036,000| 33,037,000| 33,038,000| 33,039,000| 33,040,000| 33,041,000| hg19

UCSC Genes (RefSeq, GenBank, CCDS, Rfam, tRNAs & Comparative Genomics)

SOD1

Allelic Variant SNPs

147450.0014  
147450.0012  
147450.0020  
147450.0029  
147450.0025  
147450.0022

147450.0001  
147450.0002  
147450.0003  
147450.0004  
147450.0005  
147450.0006  
147450.0013

147450.0028  
147450.0031  
147450.0024  
147450.0006  
147450.0015  
147450.0033  
147450.0007  
147450.0008  
147450.0032  
147450.0009  
147450.0016  
147450.0010  
147450.0011

147450.0026  
147450.0023  
147450.0017  
147450.0018  
147450.0021

**Drag-and-select** ✕

chr21:33,036,032-33,036,314

☐ Don't show this dialog again and always zoom.  
(Re-enable highlight via the 'configure' menu at any time.)

Zoom In Highlight Cancel

Click or drag in the base position track to  
track options. Drag side bars or labels up or  
tracks left or right to new position.

manage custom tracks track hubs configure reverse

refresh

expand all

Custom Tracks refresh

ENCODE Analysis Hub refresh

ENCODE ENCODE ENCODE ENCODE ENCODE ENCODE

Extract a genomic sequence of interest ('View' → 'DNA')

UCSC Genome Browser on Human Feb. 2009 (GRCh37/hg19)

move <<< << < > >> >>> zoom in 1.5x 3x 10x base zoom out 1.5x

chr21:33,036,080-33,036,226 147 bp.

enter position, gene symbol or search terms

chr21 (q22.11) 21p13 21p12 21p11.2 11.2 21q21.1 q21.2 21q21.3 q22.11 q22.2 21q22

Scale chr21: 33,036,100 | 50 bases | 33,036,150 | 33,036,200 | hg19

UCSC Genes (RefSeq, GenBank, CCDS, Rfam, tRNAs & Comparative Genomics)

SOD1

OMIM Allelic Variant SNPs

147450.0001 147450.0005

147450.0002 147450.0030

147450.0003

147450.0004

147450.0013

Click on a feature for details. Click or drag in the base position track to zoom in. Click side bars for track options. Drag side bars or labels up or down to reorder tracks. Drag tracks left or right to new position.

move start < 2.0 > move end < 2.0 >

track search default tracks default order hide all manage custom tracks track hubs configure

reverse resize refresh

collapse all Use drop-down controls below and press refresh to alter tracks displayed. Tracks with lots of items will automatically be displayed in more compact modes. expand all

Custom Tracks refresh

ENCODE Analysis Hub refresh

ENCODE ENCODE ENCODE ENCODE ENCODE

PDF/PS  
DNA  
In Other Genomes  
Ensembl  
NCBI  
Configure Browser  
Default Tracks  
Default Track Order  
Reset All User Settings

Extract a genomic sequence of interest ('View' → 'DNA')

UCSC Genome Browser on Human Feb. 2009 (GRCh37/hg19)

move <<< << < > >> >>> zoom in 1.5x 3x 10x base zoom out 1.5x

chr21:33,036,080-33,036,226 147 bp.

enter position, gene symbol or search terms

chr21 (q22.11) 21p13 21p12 21p11.2 11.2 21q21.1 q21.2 21q21.3 q22.11 q22.2 21q22

Scale chr21: 33,036,100| 50 bases | 33,036,150| 33,036,200| hg19

UCSC Genes (RefSeq, GenBank, CCDS, Rfam, tRNAs & Comparative Genomics)

SOD1

OMIM Allelic Variant SNPs

147450.0001 147450.0005

147450.0002 147450.0030

147450.0003

147450.0004

PDF/PS

DNA

In Other Genomes

Ensembl

NCBI

Configure Browser

Default Tracks

Default Track On/Off

Reset All User Settings

Get DNA in Window (hg19/Human)

Get DNA for

Position chr21:33,036,080-33,036,226

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)

move end

< 2.0 >

track hubs configure

d. codes. expand all

refresh

refresh

ENCODE



Extract a genomic sequence of interest ('View' → 'DNA')

UCSC Genome Browser on Human Feb. 2009 (GRCh37/hg19)

move <<< << < > >> >>> zoom in 1.5x 3x 10x base zoom out 1.5x

chr21:33,036,080-33,036,226 147 bp.

enter position, gene symbol or search terms

chr21 (q22.11) 21p13 21p12 21p11.2 11.2 21q21.1 q21.2 21q21.3 q22.11 q22.2 21q22

Scale chr21: 33,036,100| 50 bases | 33,036,150| 33,036,200| hg19

UCSC Genes (RefSeq, GenBank, CCDS, Rfam, tRNAs & Comparative Genomics)

SOD1

Get DNA in Window (hg19/Human)

Get DNA for

Position chr21:33,036,080-33,036,226

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)

get DNA extended case/color options

Tracks with lots of items will automatically be displayed in more compact modes.

Custom Tracks

refresh

PDF/PS  
DNA  
In Other Genomes  
Ensembl  
NCBI  
Configure Browser  
Default Tracks  
Default Track On  
Reset All User Settings

base  
k options.  
acks.  
om tracks  
track hubs  
configure  
tracks displayed.  
expand all

move end  
< 2.0 >

collapse

+

-

ENCODE ENCODE

```
>hg19_dna range=chr21:33036080-33036226 5'pad=0 3'pad=0 strand=+ repeatMasking=none
CCAACTTTGCACTTTTCTTAAAGGAAAGTAATGGACCACTGAAGGTGTGG
GGAAGCATTAAAGGACTGACTGAAGGCCTGCATGGATTCCATGTTTCATGA
GTTTGGAGATAATACAGCAGGTGGGTGTTGTGCTGTGCTGGTGACCC
```

## Mapping of a sequence (Tool → 'Blat')

The screenshot shows the UCSC Genome Browser interface. The top navigation bar includes links for Genomes, Genome Browser, Tools, Mirrors, Downloads, My Data, View, Help, and About Us. The 'Tools' menu is open, highlighting 'Blat'. Other tools listed include Table Browser, Variant Annotation Integrator, Gene Sorter, Genome Graphs, In-Silico PCR, LiftOver, VisiGene, and Other Utilities. The main content area displays genomic tracks for chromosome 8, including gene annotations (MYC), alignments, and various genomic features. The 'move start' and 'move end' controls are visible at the bottom, along with track search, default tracks, default order, hide all, manage custom tracks, track hubs, configure, reverse, resize, refresh, collapse all, and expand all buttons.

**BLAT = BLAST-like Alignment Tool**

# Mapping of a sequence (Tool → 'Blat')

[Home](#) [Genomes](#) [Genome Browser](#) [Tools](#) [Mirrors](#) [Downloads](#) [My Data](#) [Help](#) [About Us](#)

## Human BLAT Search

### BLAT Search Genome

Genome:

Assembly:

Query type:

Sort output:

Output type:

Human ▼

Feb. 2009 (GRCh37/hg19) ▼

BLAT's guess ▼

query,score ▼

hyperlink ▼

```
>mm10_dna range=chr15:61989359-61989931 5'pad=0 3'pad=0 strand=- repeatMasking=none
GCTCCTCCTCGAGTTAGGTCAGTTTATGCAACCAGAGTTTCGAAGCTGTTT
GAGTTTGTGTTTCAACTGTTCTCGTCTGTTTCTCAATAAGTCTTTTCAG
AGGTGAGCTTGTGCTGCTGCTTGAATGGACAGGATGTAGGCGGTGGCT
TTTTTGAGGATCACTACCTTGGGGGCTTTTGTGTTTTOCAATTCAGG
GATCTGGTCAOCCAGGGCAAAAAGCTGCGCTTCAGCTGTTCTCTCTCT
GACGTTCAAGACGTTGTGTGTCGCTCTTGTGTTTCTCTCTCTCTCT
GAGGAOCTGGGGCTGGAGCACTTGGCGTTGTTGCTGATCTGCTTCAGGAC
CCTGOCCTGTCTCAACTTGGCCCTCTTGGCAGCTGGATAGTCTCTCTTG
TGGAGGGGGGTGCGCGTAGTTGTGCTGGTGAAGTGGAGACGTGGCAOCTC
TTGAGGACCAAGTGGGCTGTGCGGAGGTTTGTCTGTGGCTCGGGATGGAGA
TGAGCCCGACTCCGACCTCTTGGCAGGGGTTTGGCTCTTCTCCACAGACA
CCACATCAATTTCTCTCTCATCT
```

submit

I'm feeling lucky

clear

Paste in a query sequence to find its location in the 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 chosen 

submit file

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.



## Mapping of a sequence (Tool → 'Blat')

## Human BLAT Results

## BLAT Search Results

ACTIONS	QUERY	SCORE	START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
<a href="#">browser details</a>	mm10_dna	405	43	573	573	88.2%	8	-	128752655	128753185	531
<a href="#">browser details</a>	mm10_dna	37	64	178	573	70.5%	2	+	176335018	176335109	92
<a href="#">browser details</a>	mm10_dna	22	537	564	573	89.3%	4	-	55760470	55760497	28
<a href="#">browser details</a>	mm10_dna	20	537	556	573	100.0%	1	-	162268090	162268109	20

### Side by Side Alignment

[illegible]

The screenshot shows the UCSC Genome Browser interface for the human genome assembly (GRCh37/hg19). The main track displays the B1at Sequence for chromosome 8, with a red arrow pointing to the region chr8:128,752,522-128,753,318. Below the main track, several other tracks are visible, including UCSC Genes (RefSeq, GenBank, CCDS, Rfam, tRNAs & Comparative Genomics), conservation tracks for human, mouse, and dog, and tracks for non-placental vertebrate genomes. The interface also includes navigation tools at the top, such as 'move', 'zoom in', and 'zoom out', and a search bar for entering positions, gene symbols, or search terms.

# Viewing our data in the genome browser: The BED format

The **BED** (**B**rowser **E**xtensible **D**ata) format is a tab-delimited text format where each line specifies a genomic interval.

The first three BED fields (mandatory) are:

**chrom** - The name of the chromosome (e.g. chr3, chrY, chr2\_random).

**chromStart** - The starting position of the feature in the chromosome (0-based).

**chromEnd** - The ending position of the feature in the chromosome. The chromEnd base is not included in the display of the feature. For example, the first 100 bases of a chromosome are defined as chromStart=0, chromEnd=100, and span the bases numbered 0-99.

The above can be followed by up to 9 additional (optional) BED fields, of which the most commonly used are:

**name** - Defines the name of the BED line.

**score** - A score between 0 and 1000.

**strand** - Defines the strand - either '+' or '-'.

Finally, a BED file can also include an header line describing its visual settings in the UCSC Genome Browser

Example of BED format (including header line):

```
track name='my track' description='my track description' color=255,0,0 visibility=2
```

```
chr8 128867449 128867455 geneA 99 +  
chr8 128902915 128902921 geneB 1000 +  
chr8 129001512 129001518 geneC 0 +
```

# Viewing our data in the Genome Browser ('add custom track')

The screenshot displays the UCSC Genome Browser interface for Human Feb. 2009 (GRCh37/hg19) Assembly. The top navigation bar includes links for Genomes, Genome Browser, Tools, Mirrors, Downloads, My Data, View, Help, and About Us. The main title is "UCSC Genome Browser on Human Feb. 2009 (GRCh37/hg19) Assembly". Below the title, there are navigation controls for moving and zooming, a search bar with the text "chr8:128,747,765-128,751,018 3,254 bp.", and a track visualization showing various genomic features. A red arrow points to the "manage custom tracks" button, which is highlighted with a black box and the text "Manage your custom tracks".

Genomes Genome Browser Tools Mirrors Downloads My Data View Help About Us

## UCSC Genome Browser on Human Feb. 2009 (GRCh37/hg19) Assembly

move <<< << < > >> >>> zoom in 1.5x 3x 10x base zoom out 1.5x 3x 10x 100x

chr8:128,747,765-128,751,018 3,254 bp. enter position, gene symbol or search terms go

chr8 (624.21) 22.1 22.2 22.3 22.4 22.5 22.6 22.7 22.8 22.9 23.0 23.1 23.2 23.3 23.4 23.5 23.6 23.7 23.8 23.9 24.0

scale chr8: 1 kb hg19 128,748,500 128,749,000 128,749,500 128,750,000 128,750,500 128,751,000

move start < 2.0 > move end < 2.0 >

Click on a feature for details. Click or drag in the base position track to zoom in. Click side bars for track options. Drag side bars or labels up or down to reorder tracks. Drag tracks left or right to new position.

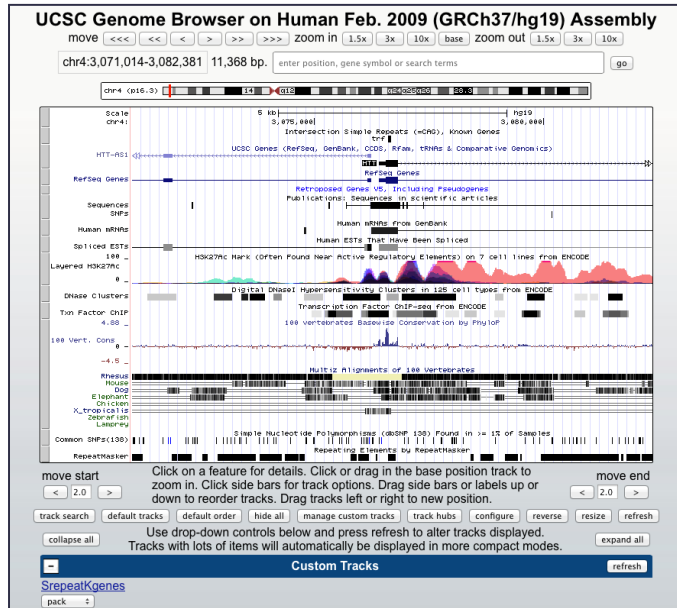
track search default tracks default order hide all manage custom tracks track hubs configure reverse resize refresh

collapse all Use drop-down controls below a Tracks with lots of items will automatically be expand all

**Manage your custom tracks**



# Querying the UCSC Genome Browser

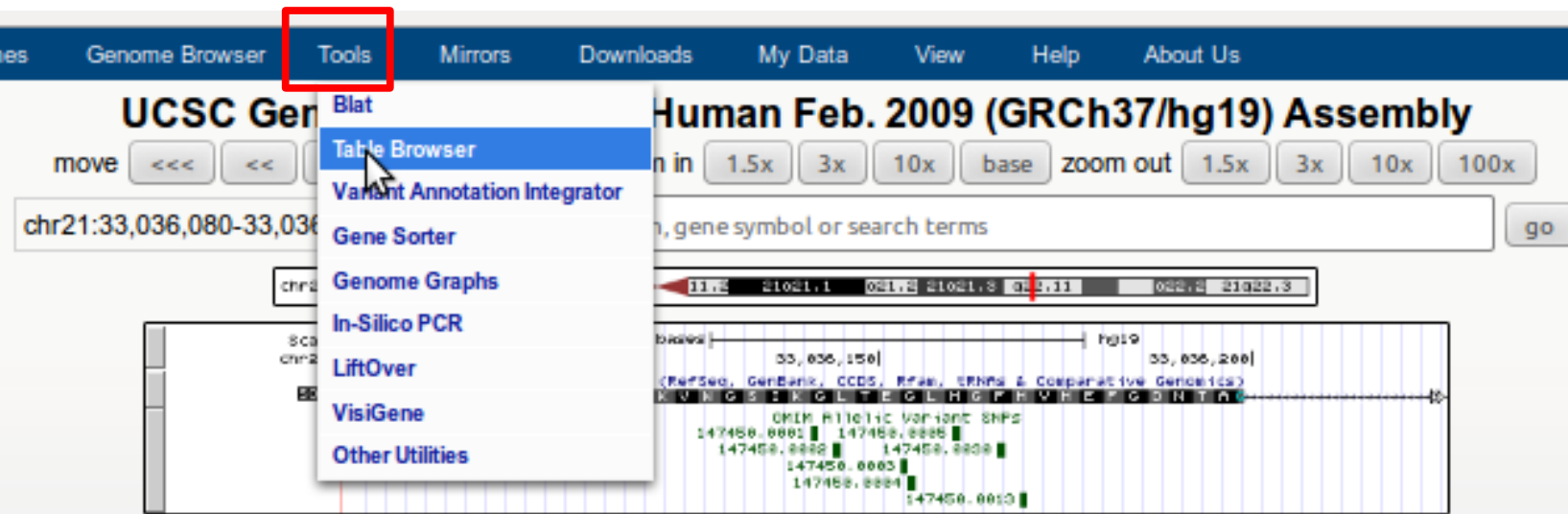


(MySQL)

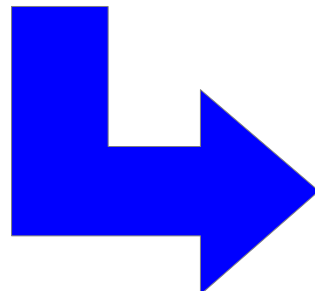
#chrom	chromStart	chromEnd	name	class	func
chr17	38451241	38451242	rs28897699	single	coding-nonsynon,untranslated,cc
chr17	38451354	38451355	rs8176316	single	untranslated,intron
chr17	38452072	38452073	rs8176315	single	untranslated,intron
chr17	38452146	38452147	rs8176314	single	untranslated,intron
chr17	38452200	38452201	rs9896925	single	untranslated,intron
chr17	38452527	38452528	rs8176313	single	untranslated,intron
chr17	38452648	38452649	rs8176312	single	untranslated,intron
chr17	38452664	38452665	rs8176311	single	untranslated,intron
chr17	38452703	38452704	rs8068463	single	untranslated,intron
chr17	38453219	38453220	rs4438367	single	coding-synon,untranslated,cds-3
chr17	38453227	38453228	rs28897698	single	coding-nonsynon,untranslated,cc
chr17	38453438	38453439	rs8176310	single	untranslated,intron
chr17	38453634	38453635	rs4793190	single	untranslated,intron
chr17	38453634	38453635	rs7406700	single	untranslated,intron
chr17	38453818	38453819	rs4792971	single	untranslated,intron
chr17	38453895	38453896	rs8176308	single	untranslated,intron
chr17	38454062	38454063	rs4792972	single	untranslated,intron
chr17	38454062	38454063	rs7405512	single	untranslated,intron
chr17	38454595	38454596	rs8176307	single	untranslated,intron
chr17	38454870	38454871	rs8176306	single	untranslated,intron
chr17	38454889	38454890	rs8176305	single	untranslated,intron
chr17	38454957	38454958	rs8176304	single	untranslated,intron
chr17	38454990	38454991	rs8176303	single	untranslated,intron
chr17	38455227	38455228	rs3092988	single	untranslated,intron
chr17	38455362	38455363	rs8176302	single	untranslated,intron
chr17	38455548	38455549	rs8176301	single	untranslated,intron
chr17	38455820	38455821	rs8176300	single	untranslated,intron
chr17	38455966	38455967	rs8176299	single	untranslated,intron
chr17	38456104	38456105	rs12949768	single	untranslated,intron
chr17	38456115	38456116	rs11079053	single	untranslated,intron

chrX 132991	160020	NM_018390	+	140854	156002	0	9	70,203,148,157,158,159,160,161,162,163,164,165,166,167,168,169,170,171,172,173,174,175,176,177,178,179,180,181,182,183,184,185,186,187,188,189,190,191,192,193,194,195,196,197,198,199,200,201,202,203,204,205,206,207,208,209,210,211,212,213,214,215,216,217,218,219,220,221,222,223,224,225,226,227,228,229,230,231,232,233,234,235,236,237,238,239,240,241,242,243,244,245,246,247,248,249,250,251,252,253,254,255,256,257,258,259,260,261,262,263,264,265,266,267,268,269,270,271,272,273,274,275,276,277,278,279,280,281,282,283,284,285,286,287,288,289,290,291,292,293,294,295,296,297,298,299,300,301,302,303,304,305,306,307,308,309,310,311,312,313,314,315,316,317,318,319,320,321,322,323,324,325,326,327,328,329,330,331,332,333,334,335,336,337,338,339,340,341,342,343,344,345,346,347,348,349,350,351,352,353,354,355,356,357,358,359,360,361,362,363,364,365,366,367,368,369,370,371,372,373,374,375,376,377,378,379,380,381,382,383,384,385,386,387,388,389,390,391,392,393,394,395,396,397,398,399,400,401,402,403,404,405,406,407,408,409,410,411,412,413,414,415,416,417,418,419,420,421,422,423,424,425,426,427,428,429,430,431,432,433,434,435,436,437,438,439,440,441,442,443,444,445,446,447,448,449,450,451,452,453,454,455,456,457,458,459,460,461,462,463,464,465,466,467,468,469,470,471,472,473,474,475,476,477,478,479,480,481,482,483,484,485,486,487,488,489,490,491,492,493,494,495,496,497,498,499,500,501,502,503,504,505,506,507,508,509,510,511,512,513,514,515,516,517,518,519,520,521,522,523,524,525,526,527,528,529,530,531,532,533,534,535,536,537,538,539,540,541,542,543,544,545,546,547,548,549,550,551,552,553,554,555,556,557,558,559,560,561,562,563,564,565,566,567,568,569,570,571,572,573,574,575,576,577,578,579,580,581,582,583,584,585,586,587,588,589,590,591,592,593,594,595,596,597,598,599,600,601,602,603,604,605,606,607,608,609,610,611,612,613,614,615,616,617,618,619,620,621,622,623,624,625,626,627,628,629,630,631,632,633,634,635,636,637,638,639,640,641,642,643,644,645,646,647,648,649,650,651,652,653,654,655,656,657,658,659,660,661,662,663,664,665,666,667,668,669,670,671,672,673,674,675,676,677,678,679,680,681,682,683,684,685,686,687,688,689,690,691,692,693,694,695,696,697,698,699,700,701,702,703,704,705,706,707,708,709,710,711,712,713,714,715,716,717,718,719,720,721,722,723,724,725,726,727,728,729,730,731,732,733,734,735,736,737,738,739,740,741,742,743,744,745,746,747,748,749,750,751,752,753,754,755,756,757,758,759,760,761,762,763,764,765,766,767,768,769,770,771,772,773,774,775,776,777,778,779,780,781,782,783,784,785,786,787,788,789,790,791,792,793,794,795,796,797,798,799,800,801,802,803,804,805,806,807,808,809,810,811,812,813,814,815,816,817,818,819,820,821,822,823,824,825,826,827,828,829,830,831,832,833,834,835,836,837,838,839,840,841,842,843,844,845,846,847,848,849,850,851,852,853,854,855,856,857,858,859,860,861,862,863,864,865,866,867,868,869,870,871,872,873,874,875,876,877,878,879,880,881,882,883,884,885,886,887,888,889,890,891,892,893,894,895,896,897,898,899,900,901,902,903,904,905,906,907,908,909,910,911,912,913,914,915,916,917,918,919,920,921,922,923,924,925,926,927,928,929,930,931,932,933,934,935,936,937,938,939,940,941,942,943,944,945,946,947,948,949,950,951,952,953,954,955,956,957,958,959,960,961,962,963,964,965,966,967,968,969,970,971,972,973,974,975,976,977,978,979,980,981,982,983,984,985,986,987,988,989,990,991,992,993,994,995,996,997,998,999,1000,1001,1002,1003,1004,1005,1006,1007,1008,1009,1010,1011,1012,1013,1014,1015,1016,1017,1018,1019,1020,1021,1022,1023,1024,1025,1026,1027,1028,1029,1030,1031,1032,1033,1034,1035,1036,1037,1038,1039,1040,1041,1042,1043,1044,1045,1046,1047,1048,1049,1050,1051,1052,1053,1054,1055,1056,1057,1058,1059,1060,1061,1062,1063,1064,1065,1066,1067,1068,1069,1070,1071,1072,1073,1074,1075,1076,1077,1078,1079,1080,1081,1082,1083,1084,1085,1086,1087,1088,1089,1090,1091,1092,1093,1094,1095,1096,1097,1098,1099,1100,1101,1102,1103,1104,1105,1106,1107,1108,1109,1110,1111,1112,1113,1114,1115,1116,1117,1118,1119,1120,1121,1122,1123,1124,1125,1126,1127,1128,1129,1130,1131,1132,1133,1134,1135,1136,1137,1138,1139,1140,1141,1142,1143,1144,1145,1146,1147,1148,1149,1150,1151,1152,1153,1154,1155,1156,1157,1158,1159,1160,1161,1162,1163,1164,1165,1166,1167,1168,1169,1170,1171,1172,1173,1174,1175,1176,1177,1178,1179,1180,1181,1182,1183,1184,1185,1186,1187,1188,1189,1190,1191,1192,1193,1194,1195,1196,1197,1198,1199,1200,1201,1202,1203,1204,1205,1206,1207,1208,1209,1210,1211,1212,1213,1214,1215,1216,1217,1218,1219,1220,1221,1222,1223,1224,1225,1226,1227,1228,1229,1230,1231,1232,1233,1234,1235,1236,1237,1238,1239,1240,1241,1242,1243,1244,1245,1246,1247,1248,1249,1250,1251,1252,1253,1254,1255,1256,1257,1258,1259,1260,1261,1262,1263,1264,1265,1266,1267,1268,1269,1270,1271,1272,1273,1274,1275,1276,1277,1278,1279,1280,1281,1282,1283,1284,1285,1286,1287,1288,1289,1290,1291,1292,1293,1294,1295,1296,1297,1298,1299,1300,1301,1302,1303,1304,1305,1306,1307,1308,1309,1310,1311,1312,1313,1314,1315,1316,1317,1318,1319,1320,1321,1322,1323,1324,1325,1326,1327,1328,1329,1330,1331,1332,1333,1334,1335,1336,1337,1338,1339,1340,1341,1342,1343,1344,1345,1346,1347,1348,1349,1350,1351,1352,1353,1354,1355,1356,1357,1358,1359,1360,1361,1362,1363,1364,1365,1366,1367,1368,1369,1370,1371,1372,1373,1374,1375,1376,1377,1378,1379,1380,1381,1382,1383,1384,1385,1386,1387,1388,1389,1390,1391,1392,1393,1394,1395,1396,1397,1398,1399,1400,1401,1402,1403,1404,1405,1406,1407,1408,1409,1410,1411,1412,1413,1414,1415,1416,1417,1418,1419,1420,1421,1422,1423,1424,1425,1426,1427,1428,1429,1430,1431,1432,1433,1434,1435,1436,1437,1438,1439,1440,1441,1442,1443,1444,1445,1446,1447,1448,1449,1450,1451,1452,1453,1454,1455,1456,1457,1458,1459,1460,1461,1462,1463,1464,1465,1466,1467,1468,1469,1470,1471,1472,1473,1474,1475,1476,1477,1478,1479,1480,1481,1482,1483,1484,1485,1486,1487,1488,1489,1490,1491,1492,1493,1494,1495,1496,1497,1498,1499,1500,1501,1502,1503,1504,1505,1506,1507,1508,1509,1510,1511,1512,1513,1514,1515,1516,1517,1518,1519,1520,1521,1522,1523,1524,1525,1526,1527,1528,1529,1530,1531,1532,1533,1534,1535,1536,1537,1538,1539,1540,1541,1542,1543,1544,1545,1546,1547,1548,1549,1550,1551,1552,1553,1554,1555,1556,1557,1558,1559,1560,1561,1562,1563,1564,1565,1566,1567,1568,1569,1570,1571,1572,1573,1574,1575,1576,1577,1578,1579,1580,1581,1582,1583,1584,1585,1586,1587,1588,1589,1590,1591,1592,1593,1594,1595,1596,1597,1598,1599,1600,1601,1602,1603,1604,1605,1606,1607,1608,1609,1610,1611,1612,1613,1614,1615,1616,1617,1618,1619,1620,1621,1622,1623,1624,1625,1626,1627,1628,1629,1630,1631,1632,1633,1634,1635,1636,1637,1638,1639,1640,1641,1642,1643,1644,1645,1646,1647,1648,1649,1650,1651,1652,1653,1654,1655,1656,1657,1658,1659,1660,1661,1662,1663,1664,1665,1666,1667,1668,1669,1670,1671,1672,1673,1674,1675,1676,1677,1678,1679,1680,1681,1682,1683,1684,1685,1686,1687,1688,1689,1690,1691,1692,1693,1694,1695,1696,1697,1698,1699,1700,1701,1702,1703,1704,1705,1706,1707,1708,1709,1710,1711,1712,1713,1714,1715,1716,1717,1718,1719,1720,1721,1722,1723,1724,1725,1726,1727,1728,1729,1730,1731,1732,1733,1734,1735,1736,1737,1738,1739,1740,1741,1742,1743,1744,1745,1746,1747,1748,1749,1750,1751,1752,1753,1754,1755,1756,1757,1758,1759,1760,1761,1762,1763,1764,1765,1766,1767,1768,1769,1770,1771,1772,1773,1774,1775,1776,1777,1778,1779,1780,1781,1782,1783,1784,1785,1786,1787,1788,1789,1790,1791,1792,1793,1794,1795,1796,1797,1798,1799,1800,1801,1802,1803,1804,1805,1806,1807,1808,1809,1810,1811,1812,1813,1814,1815,1816,1817,1818,1819,1820,1821,1822,1823,1824,1825,1826,1827,1828,1829,1830,1831,1832,1833,1834,1835,1836,1837,1838,1839,1840,1841,1842,1843,1844,1845,1846,1847,1848,1849,1850,1851,1852,1853,1854,1855,1856,1857,1858,1859,1860,1861,1862,1863,1864,1865,1866,1867,1868,1869,1870,1871,1872,1873,1874,1875,1876,1877,1878,1879,1880,1881,1882,1883,1884,1885,1886,1887,1888,1889,1890,1891,1892,1893,1894,1895,1896,1897,1898,1899,1900,1901,1902,1903,1904,1905,1906,1907,1908,1909,1910,1911,1912,1913,1914,1915,1916,1917,1918,1919,1920,1921,1922,1923,1924,1925,1926,1927,1928,1929,1930,1931,1932,1933,1934,1935,1936,1937,1938,1939,1940,1941,1942,1943,1944,1945,1946,1947,1948,1949,1950,1951,1952,1953,1954,1955,1956,1957,1958,1959,1960,1961,1962,1963,1964,1965,1966,1967,1968,1969,1970,1971,1972,1973,1974,1975,1976,1977,1978,1979,1980,1981,1982,1983,1984,1985,1986,1987,1988,1989,1990,1991,1992,1993,1994,1995,1996,1997,1998,1999,2000,2001,2002,2003,2004,2005,2006,2007,2008,2009,2010,2011,2012,2013,2014,2015,2016,2017,2018,2019,2020,2021,2022,2023,2024,2025,2026,2027,2028,2029,2030,2031,2032,2033,2034,2035,2036,2037,2038,2039,2040,2041,2042,2043,2044,2045,2046,2047,2048,2049,2050,2051,2052,2053,2054,2055,2056,2057,2058,2059,2060,2061,2062,2063,2064,2065,2066,2067,2068,2069,2070,2071,2072,2073,2074,2075,2076,2077,2078,2079,2080,2081,2082,2083,2084,2085,2086,2087,2088,2089,2090,2091,2092,2093,2094,2095,2096,2097,2098,2099,2100,2101,2102,2103,2104,2105,2106,2107,2108,2109,2110,2111,2112,2113,2114,2115,2116,2117,2118,2119,2120,2121,2122,2123,2124,2125,2126,2127,2128,2129,2130,2131,2132,2133,2134,2135,2136,2137,2138,2139,2140,2141,2142,2143,2144,2145,2146,2147,2148,2149,2150,2151,2152,2153,2154,2155,2156,2157,2158,2159,2160,2161,2162,2163,2164,2165,2166,2167,2168,2169,2170,2171,2172,2173,2174,2175,2176,2177,2178,2179,2180,2181,2182,2183,2184,2185,2186,2187,2188,2189,2190,2191,2192,2193,2194,2195,2196,2197,2198,2199,2200,2201,2202,2203,2204,2205,2206,2207,2208,2209,2210,2211,2212,2213,2214,2215,2216,2217,2218,2219,2220,2221,2222,2223,2
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# Querying the UCSC Genome Browser (Tool → 'Table Browser')



The screenshot shows the UCSC Genome Browser homepage. The 'Tools' menu is open, and 'Table Browser' is highlighted. The background shows a genomic track for Human Feb. 2009 (GRCh37/hg19) Assembly, with a search bar and zoom controls.



### Table Browser

Use this program to retrieve the data associated with a track in text format, to calculate intersections between tracks, and to retrieve DNA sequence covered by a track. For help in using this application see [Using the Table Browser](#) for a description of the controls in this form, the [User's Guide](#) for general information and sample queries, and the OpenHelix Table Browser [tutorial](#) for a narrated presentation of the software features and usage. For more complex queries, you may want to use [Galaxy](#) or our [public MySQL server](#). To examine the biological function of your set through annotation enrichments, send the data to [GREAT](#). Send data to [GenomeSpace](#) for use with diverse computational tools. Refer to the [Credits](#) page for the list of contributors and usage restrictions associated with these data. All tables can be downloaded in their entirety from the [Sequence and Annotation Downloads](#) page.

clade:  genome:  assembly:

group:  track:  [manage custom tracks](#) [track hubs](#)

table:  [describe table schema](#)

region: ☒ genome ☐ ENCODE Pilot regions ☐ position  [lookup](#) [define regions](#)

identifiers (names/accessions): [paste list](#) [upload list](#)

filter: [create](#)

intersection with ensGene: [edit](#) [clear](#)

correlation: [create](#)

output format:  Send output to ☐ [Galaxy](#) ☐ [GREAT](#) ☐ [GenomeSpace](#)

output file:  (leave blank to keep output in browser)

file type returned: ☒ plain text ☐ gzip compressed

*Note: The all fields and selected fields output formats are not available when an intersection has been specified.*

[get output](#) [summary/statistics](#)

To reset all user cart settings (including custom tracks), [click here](#).

# Querying the UCSC Genome Browser (Tool → 'Table Browser')

## Table Browser

Use this program to retrieve the data associated with a track in text format, to calculate intersections between tracks, and to retrieve DNA sequence covered by a track. For help in using this application see [Using the Table Browser](#) for a description of the controls in this form, the [User's Guide](#) for general information and sample queries, and the OpenHelix Table Browser [tutorial](#) for a narrated presentation of the software features and usage. For more complex queries, you may want to use [Galaxy](#) or our [public MySQL server](#). To examine the biological function of your set through annotation enrichments, send the data to [GREAT](#). Send data to [GenomeSpace](#) for use with diverse computational tools. Refer to the [Credits](#) page for the list of contributors and usage restrictions associated with these data. All tables can be downloaded in their entirety from the [Sequence and Annotation Downloads](#) page.

**clade:** Mammal ▼ **genome:** Human ▼ **assembly:** Feb. 2009 (GRCh37/hg19) ▼

**group:** Repeats ▼ **track:** Simple Repeats ▼ [manage custom tracks](#) [track hubs](#)

**table:** simpleRepeat ▼ [describe table schema](#)

**region:** ☒ genome ☐ ENCODE Pilot regions ☐ position  [lookup](#) [define regions](#)

**identifiers (names/accessions):** [paste list](#) [upload list](#)

**filter:** [create](#)

**intersection with ensGene:** [edit](#) [clear](#)

**correlation:** [create](#)

**output format:** BED - browser extensible data ▼ Send output to ☐ [Galaxy](#) ☐ [GREAT](#) ☐ [GenomeSpace](#)

**output file:**  (leave blank to keep output in browser)

**file type returned:** ☒ plain text ☐ gzip compressed

*Note: The all fields and selected fields output formats are not available when an intersection has been specified.*

[get output](#) [summary/statistics](#)

To reset all user cart settings (including custom tracks), [click here](#).



# Querying the UCSC Genome Browser (Tool → 'Table Browser')

**Table Browser**

Use this program to retrieve the data associated with a track in text format, to calculate intersections between tracks, and to retrieve DNA sequence covered by a track. For help in using this application see [Using the Table Browser](#) for a description of the controls in this form, the [User's Guide](#) for general information and sample queries, and the OpenHelix Table Browser [tutorial](#) for a narrated presentation of the software features and usage. For more complex queries, you may want to use [Galaxy](#) or our [public MySQL server](#). To examine the biological function of your set through annotation enrichments, send the data to [GREAT](#). Refer to the [Credits](#) page for the list of contributors and usage restrictions associated with these data. All table downloaded in their entirety from the [Sequence and Annotation Downloads](#) page.

clade: ☒ Mammal ☐ Vertebrate ☐ Deuterostome ☐ Insect ☐ Nematode ☐ Other

group: ☐ Tracks ☐ DE Pi

table: ☐ (ns):

region: ☐ chr21:33031557-33041576

identifi

filter:

intersection:

correlation:

output format:

output file:

file type returned: ☒ plain text ☐

To reset all user cart settings (includ

ome: ☒ Human ☐ Chimpanzee ☐ Gorilla ☐ Orangutan ☐ Gibbon ☐ Rhesus ☐ Baboon ☐ Squirrel monkey ☐ Marmoset ☐ Tarsier ☐ Mouse lemur ☐ Bushbaby ☐ Tree shrew ☐ Mouse ☐ Rat ☐ Kangaroo rat ☐ Naked mole-rat ☐ Guinea pig ☐ Rabbit ☐ Squirrel ☐ Pika ☐ Pig ☐ Alpaca ☐ Dolphin ☐ Sheep ☐ Cow ☐ Horse ☐ White rhinoceros ☐ Cat ☐ Ferret ☐ Dog ☐ Panda ☐ Microbat ☐ Megabat ☐ Hedgehog

assembly: ☒ Feb. 2009 (GRCh37/hg19) ☐ Mar. 2006 (NCBI36/hg18) ☐ May 2004 (NCBI35/hg17) ☐ July 2003 (NCBI34/hg16)

Send output to ☐ [Galaxy](#) ☐ [GREAT](#)

to keep output in browser)

[click here.](#)

Define genome of interest

# Querying the UCSC Genome Browser (Tool → 'Table Browser')

**Table Browser**

Use this program to retrieve the data associated with a track in text format, to calculate intersections between tracks, and to retrieve DNA sequence covered by a track. For help in using this application see [Using the Table Browser](#) for a description of the controls in this form, the [User's Guide](#) for general information and sample queries, and the OpenHelix Table Browser [tutorial](#) for a narrated presentation of the software features and usage. For more complex queries, you may want to use [Galaxy](#) or our [public MySQL server](#). To examine the biological function of your set through annotation enrichments, send the data to [GREAT](#). Refer to the [Credits](#) page for the list of contributors and usage restrictions associated with these data. All tables can be downloaded in their entirety from the [Sequence and Annotation Downloads](#) page.

clade: Mammal genome: Human assembly: Feb. 2009 (GRCh37/hg19)

group: Genes and Gene Predictions track: UCSC Genes add custom tracks track hubs

table: Custom Tracks describe table UCSC Genes  
ENCODE Analysis Hub RefSeq Genes

region: Mapping and Sequencing regions 7-33041570 lookup define regions

identify: Genes and Gene Predictions

filter: Phenotype and Literature  
mRNA and EST  
Expression  
Regulation

intersect: Comparative Genomics

correlate: Neanderthal Assembly and Analysis  
Denisova Assembly and Analysis

output: Variation  
Repeats

output: All Tracks

file type: All Tables

(leave in browser)

get output summary/statistics

To reset all user cart settings (including custom tracks), [click here](#).

Define table of interest

# Querying the UCSC Genome Browser (Tool → 'Table Browser')

## Table Browser

Use this program to retrieve the data associated with a track in text format, to calculate intersections between tracks, and to retrieve DNA sequence covered by a track. For help in using this application see [Using the Table Browser](#) for a description of the controls in this form, the [User's Guide](#) for general information and sample queries, and the OpenHelix Table Browser [tutorial](#) for a narrated presentation of the software features and usage. For more complex queries, you may want to use [Galaxy](#) or our [public MySQL server](#). To examine the biological function of your set through annotation enrichments, send the data to [GREAT](#). Refer to the [Credits](#) page for the list of contributors and usage restrictions associated with these data. All tables can be downloaded in their entirety from the [Sequence and Annotation Downloads](#) page.

clade:  genome:  assembly:

group:  track:

table:

region: ☒ genome ☐ ENCODE Pilot regions ☐ position

identifiers (names/accessions):

filter:

intersection:

correlation:

output format:  Send output to ☐ [Galaxy](#) ☐ [GREAT](#)

output file:  (leave blank to keep output in browser)

file type returned: ☒ plain text ☐ gzip compressed

Define the region

To reset all user cart settings (including custom tracks), [click here](#).

# Querying the UCSC Genome Browser (Tool → 'Table Browser')

## Table Browser

Use this program to retrieve the data associated with a track in text format, to calculate intersections between tracks, and to retrieve DNA sequence covered by a track. For help in using this application see [Using the Table Browser](#) for a description of the controls in this form, the [User's Guide](#) for general information and sample queries, and the OpenHelix Table Browser [tutorial](#) for a narrated presentation of the software features and usage. For more complex queries, you may want to use [Galaxy](#) or our [public MySQL server](#). To examine the biological function of your set through annotation enrichments, send the data to [GREAT](#). Refer to the [Credits](#) page for the list of contributors and usage restrictions associated with these data. All tables can be downloaded in their entirety from the [Sequence and Annotation Downloads](#) page.

**clade:** Mammal ▾ **genome:** Human ▾ **assembly:** Feb. 2009 (GRCh37/hg19) ▾

**group:** Genes and Gene Prediction Tracks ▾ **track:** UCSC Genes ▾ [add custom tracks](#) [track hubs](#)

**table:** knownGene ▾ [describe table schema](#)

**region:** ☒ genome ☐ ENCODE Pilot regions ☐ position chr21:33031597-33041570 [lookup](#) [define regions](#)

**identifiers (names/accessions):** [paste list](#) [upload list](#)

**filter:** [create](#)

**intersection:** [create](#)

**correlation:** [create](#)

**output format:** all fields from selected table ▾ Send output to ☐ [Galaxy](#) ☐ [GREAT](#)

**output file:**  (leave blank to keep output in browser)

**file type returned:** ☒ plain text ☐ gzip compressed

[get output](#) [summary/statistics](#)

Limit search  
to a subset of  
genes

To reset all user cart settings (including custom tracks), [click here](#).



# Querying the UCSC Genome Browser (Tool → 'Table Browser')

**Table Browser**

Use this program to retrieve the data associated with a track in text format, to calculate intersections between tracks, and to retrieve DNA sequence covered by a track. For help in using this application see [Using the Table Browser](#) for a description of the controls in this form, the [User's Guide](#) for general information and sample queries, and the OpenHelix Table Browser [tutorial](#) for a narrated presentation of the software features and usage. For more complex queries, you may want to use [Galaxy](#) or our [public MySQL server](#). To examine the biological function of your set through annotation enrichments, send the data to [GREAT](#). Refer to the [Credits](#) page for the list of contributors and usage restrictions associated with these data. All tables can be downloaded in their entirety from the [Sequence and Annotation Downloads](#) page.

**clade:** Mammal ▾ **genome:** Human ▾ **assembly:** Feb. 2009 (GRCh37/hg19) ▾

**group:** Genes and Gene Prediction Tracks ▾ **track:** UCSC Genes ▾ [add custom tracks](#) [track hubs](#)

**table:** knownGene ▾ [describe table schema](#)

**region:** ☒ genome ☐ ENCODE Pilot regions ☐ position chr21:33031597-33041570 [lookup](#) [define regions](#)

**identifiers (names/accessions):** [paste list](#) [upload list](#)

**filter:** [create](#)

**intersections:** [create](#)

**correlations:** [create](#)

**output:**  **Send output to** ☐ [Galaxy](#) ☐ [GREAT](#)

**output file type:**  [get output](#) [summary/stats](#)

To reset all user cart settings (including filters) [click here](#)

**Filter on Fields from hg19.knownGene**

name	does ▾	match	*	
chrom	does ▾	match	*	AND
strand	does ▾	match	*	AND
txStart	is ignorec ▾		0	AND
txEnd	is ignorec ▾		0	AND
cdsStart	is ignorec ▾		0	AND
cdsEnd	is ignorec ▾		0	AND
exonCount	is ignorec ▾		0	AND
exonStarts	does ▾	match	*	
exonEnds	does ▾	match	*	
proteinID	does ▾	match	*	AND
alignID	does ▾	match	*	AND
<b>AND ▾ Free-form query:</b> <input type="text"/>				
<a href="#">submit</a> <a href="#">cancel</a>				

Define filters

# Querying the UCSC Genome Browser (Tool → 'Table Browser')

## Table Browser

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**group:** Genes and Gene Prediction Tracks ▾ **track:** UCSC Genes ▾ [add custom tracks](#) [track hubs](#)

**table:** knownGene ▾ [describe table schema](#)

**region:** ☒ genome ☐ ENCODE Pilot regions ☐ position chr21:33031597-33041570 [lookup](#) [define regions](#)

**identifiers (names/accessions):** [paste list](#) [upload list](#)

**filter:** [create](#)

**intersection:** [create](#)

**correlation:** [create](#)

**output format:** all fields from selected table ▾ Send output to ☐ [Galaxy](#) ☐ [GREAT](#)

**output file:**  (leave blank to keep output in browser)

**file type returned:** ☒ plain text ☐ gzip compressed

[get output](#) [summary/statistics](#)

**Combined search**  
(eg: SNPs overlapping with RefSeq genes)

To reset all user cart settings (including custom tracks), [click here](#).

# Querying the UCSC Genome Browser (Tool → 'Table Browser')

**Table Browser**

Use this program to retrieve the data associated with a track in text format, to calculate intersections between tracks, and to retrieve DNA sequence covered by a track. For help in using this application see [Using the Table Browser](#) for a description of the controls in this form, the [User's Guide](#) for general information and sample queries, and the OpenHelix Table Browser [tutorial](#) for a narrated presentation of the software features and usage. For more complex queries, you may want to use [Galaxy](#) or our [public MySQL server](#). To examine the biological function of your set through annotation enrichments, send the data to [GREAT](#). Refer to the [Credits](#) page for the list of contributors and usage restrictions associated with these data. All tables can be downloaded in their entirety from the [Sequence and Annotation Downloads](#) page.

**clade:** Mammal ▾ **genome:** Human ▾ **assembly:** Feb. 2009 (GRCh37/hg19) ▾

**group:** Genes and Gene Prediction Tracks ▾ **track:** UCSC Genes ▾ [add custom tracks](#) [track hubs](#)

**table:** knownGene ▾ [describe table schema](#)

**region:** ☒ genome ☐ ENCODE Pilot regions ☐ position chr21:33031597-33041570 [lookup](#) [define regions](#)

**identifiers (names/accessions):** [paste list](#) [upload list](#)

**filter:** [create](#)

**intersection:** [create](#)

**correlation:** [create](#)

**output format:** all fields from selected table ▾ **Send output to:** ☐ [Galaxy](#) ☐ [GREAT](#)

**output file:** ☐ all fields from selected table  
☐ selected fields from primary and related tables  
☐ sequence  
☐ GTF - gene transfer format  
☐ CDS FASTA alignment from multiple alignment  
☐ BED - browser extensible data  
☐ custom track  
☐ hyperlinks to Genome Browser

**file type return:** [get output](#) [submit](#)

To reset all user cart settings (including custom tracks), [click here](#).

Define output  
format

## Same item, different names in different databases

Ensembl Gene ID	Associated Gene Name	HGNC symbol
<a href="#">ENSG00000108958</a>	<a href="#">AC016292.3</a>	
<a href="#">ENSG00000123009</a>	<a href="#">NME2P1</a>	<a href="#">NME2P1</a>
<a href="#">ENSG00000124399</a>	<a href="#">NDUFB4P12</a>	<a href="#">NDUFB4P12</a>
<a href="#">ENSG00000126005</a>	<a href="#">MMP24-AS1</a>	<a href="#">MMP24-AS1</a>
<a href="#">ENSG00000128692</a>	<a href="#">EIF2S2P4</a>	<a href="#">EIF2S2P4</a>
<a href="#">ENSG00000144158</a>	<a href="#">RP11-395L14.17</a>	
<a href="#">ENSG00000146677</a>	<a href="#">AC004453.8</a>	
<a href="#">ENSG00000153363</a>	<a href="#">LINC00467</a>	<a href="#">LINC00467</a>
<a href="#">ENSG00000173727</a>	<a href="#">CMB9-22P13.1</a>	
<a href="#">ENSG00000174977</a>	<a href="#">AC026271.5</a>	
<a href="#">ENSG00000175701</a>	<a href="#">LINC00116</a>	<a href="#">LINC00116</a>
<a href="#">ENSG00000178660</a>	<a href="#">ARMC10P1</a>	<a href="#">ARMC10P1</a>
<a href="#">ENSG00000179082</a>	<a href="#">C9orf106</a>	<a href="#">C9orf106</a>
<a href="#">ENSG00000179799</a>	<a href="#">OR7E22P</a>	<a href="#">OR7E22P</a>
<a href="#">ENSG00000179967</a>	<a href="#">PPP1R14BP3</a>	<a href="#">PPP1R14BP3</a>
<a href="#">ENSG00000180574</a>	<a href="#">EIF2S3L</a>	
<a href="#">ENSG00000181126</a>	<a href="#">HLA-V</a>	<a href="#">HLA-V</a>
<a href="#">ENSG00000181524</a>	<a href="#">RPL24P4</a>	<a href="#">RPL24P4</a>
<a href="#">ENSG00000185275</a>	<a href="#">CD24P4</a>	<a href="#">CD24P4</a>

	A	B	C	D
1	Acc	TGM 1h Notx	TGM 1h Kdo2	Log2 Fold
2	NM_010510	5.675	13.865	8.19
3	NM_008361	7.865	16.015	8.15
4	NM_008176	8.47	15.975	7.505
5	NM_009140	6.785	14.055	7.27
6	NM_013693	9.775	16.77	6.995
7	AK152177	9.09	16.06	6.97
8	L38281	9.1	15.94	6.84
9	NM_009404	6.085	12.765	6.68
10	NM_030612	7.95	14.485	6.535
11	NM_010554	7.715	13.98	6.265
12	NM_013652	11.255	17.215	5.96
13	NM_011337	10.305	15.65	5.345
14	NM_138648	7.26	12.26	5
15	NM_021274	8.99	13.93	4.94
16	NM_008331	7.775	12.415	4.64
17	NM_010907	12.6	17.17	4.57
18	NM_010276	6.29	10.725	4.435
19	NM_007707	11.895	16.23	4.335

### Step 2: Select Identifier

AFFYMETRIX\_3PRIME\_IVT\_ID ▾

DICTYBASE\_ID

ENSEMBL\_GENE\_ID

ENSEMBL\_TRANSCRIPT\_ID

ENTREZ\_GENE\_ID

FLYBASE\_GENE\_ID

GENBANK\_ACCESSION

GENOMIC\_GI\_ACCESSION

GENPEPT\_ACCESSION

LOCUS\_TAG

MGI\_ID

MIRBASE\_ID

MRNA\_GI\_ACCESSION

Typically, a bioinformatics process at this search of the agreement

### Integrated

Functional Annotation

Numerous Databases

Co-occurrence

Use Homologs

Dynamic Pathways

Disease Association