



GENOME BROWSER:- VEGA





1. The Vertebrate Genome Annotation (Vega) database (<http://vega.sanger.ac.uk>)

2. first made public in 2004 and has been designed to view manual annotation of human, mouse and zebrafish genomic sequences produced at the Wellcome Trust Sanger Institute.

3. Since its initial release, the number of human annotated loci has more than doubled to close to 33 000 and now contains comprehensive annotation on 20 of the 24 human chromosomes, four whole mouse chromosomes and around 40% of the zebrafish *Danio rerio* genome.



4. The Vega database is the central repository for the majority of genome sequencing centres to deposit their annotation of human chromosomes.

5. Unlike other browsers, Vega only displays a manually annotated gene set on the latest chromosome assemblies, which are often more up-to-date than the reference genome assembly generated by NCBI.

6. Currently, the human database contains twenty chromosomes annotated by eight different sequencing centres.

7. The Havana Group at the Wellcome Trust Sanger Institute (WTSI) is updating the annotation through its involvement in the consensus-coding sequence (CCDS) collaboration with UCSC, NCBI and Ensembl (<http://www.ncbi.nlm.nih.gov/CCDS/>) which aims to produce a reference set of protein-coding gene annotation across the entire human genome.



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vega browser first page.

This is an archived version of Vega. [Click here for more information.](#)






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Search: for






A repository for high-quality gene models produced by the manual annotation of vertebrate genomes.


Browse a genome

 Human [7-02-2017] [Ensembl]	 Mouse [7-02-2017] [Ensembl]
 Zebrafish [16-11-2016] [Ensembl]	 Rat [7-02-2017] [Ensembl]
	 Pig [25-08-2015] [Ensembl]

Browse a region


 Tasmanian devil [23-10-2013] [Ensembl]	 Chimpanzee [12-01-2012] [Ensembl]
 Gorilla [30-03-2009] [Ensembl]	 Wallaby [30-03-2009] [Ensembl]
 Dog [14-02-2005] [Ensembl]	

Major histocompatibility complex (MHC) annotation



Non-reference regions
Human: 6-COIL, 6-OBL, 6-SST2, 6-APD, 6-DPS, 6-MANN, 6-MCF
Mouse: NOD/MLTc, NOD/SHLJ
Pig: Large White
Further information on our MHC annotation.

Leucocyte receptor complex (LRC) annotation



Non-reference regions:
Human: COX_1, COX_2, PGF_1, PGF_2, DM1A, DM1B, MCTA, MCTB.
Further information on our LRC annotation.

Our Data

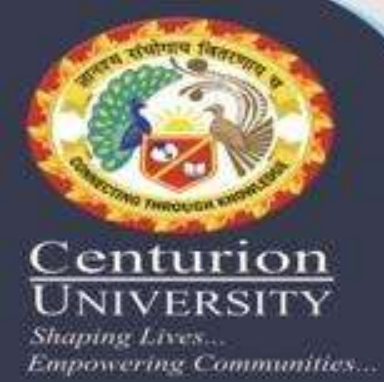
- High-quality manual annotation
- Human annotation incorporated into GENCODE-4
- Gene sets and regions of particular interest:
 - Genes with mouse knockout and human LOF transcripts
 - MHC and LRC regions
 - 327 candidate regions of NOO mice
- Inter- and intra-species comparative genomics
- Cross-referenced to other databases
- Complements Ensembl
- Downloadable datasets

What's New in release 58

- Final Vega update (all species)
- Mouse Annotation Updated (Mouse)
- Human Annotation Updated (Human)
- Rat Annotation Updated (Rat)
- No schema update (all species)

More news...

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UCSC -

- is an on-line, and downloadable, genome browser hosted by the University of California, Santa Cruz (UCSC).
- is an interactive website offering access to genome sequence data from a variety of vertebrate and invertebrate species and major model organisms, integrated with a large collection of aligned annotations.





- The Browser is a graphical viewer optimized to support fast interactive performance and is an open-source, web-based tool suite built on top of a MySQL database for rapid visualization, examination, and querying of the data at many levels. The Genome Browser Database, browsing tools, downloadable data files, and documentation can all be found on the UCSC Genome Bioinformatics website.



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interactively visualize genomic data
- COVID-19 Research**
use the SARS-CoV-2 genome browser and explore coronavirus datasets
- 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
- 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
- REST API**
returns data in JSON format

Type here to search

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