



- Custom Tracks
- My Sessions
- Track Hubs
- GBiB Shared Data Folder
- Track Collection Builder
- Public Sessions

ser
alize genomic data
earch
-2 genome browser and explore coronavirus datasets

- 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

[More tools...](#)

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>, along with the initial prototype of a graphical viewing tool, the UCSC Genome Browser. In the ensuing years, the website has grown to include a broad collection of vertebrate and model organism assemblies and annotations, along with a large suite of tools for viewing, analyzing and downloading data. Learn more about our history on the [UCSC Genome Browser Project History](#) page and by [contacting this site](#).

What's new

- July. 20, 2021 - [Updated GENCODE gene tracks for hg38, hg19...](#)
- Jul. 14, 2021 - [gnomAD v3.1.1 track available for hg38](#)
- Jul. 08, 2021 - [Updated NCBI RefSeq tracks for hg38](#)

[More news...](#)

[Subscribe](#)

The UCSC Genome Browser is developed and maintained by the [Genome Bioinformatics Group](#), a cross-departmental team within the [UCSC Genomics Institute](#).

