



Our tools

- **Genome Browser**
interactively visualize genomic data
- **BLAT**
rapidly align sequences to the genome
- **Table Browser**
download data from the Genome Browser
- **Variant Annotation Integrator**
get functional effect predictions for variants
- **Data Integrator**
combine data sources from the Genome Browser
- **Gene Sorter**
find genes that are similar by expression
- **Genome Browser in a Box (GBiB)**
run the Genome Browser on your laptop
- **In-Silico PCR**
rapidly align PCR primer pairs to the genome
- **LiftOver**
convert genome coordinates between assemblies
- **VisiGene**
interactively view in situ images of molecular

Table Browser

Use this program to retrieve the data associated with a track in text format, to calculate intersections between tracks, help in using this application see [Using the Table Browser](#) for a description of the controls in this form, the [User's Guide](#), the [OpenHelix Table Browser tutorial](#) for a narrated presentation of the software features and usage. For more complex queries, refer to the [MySQL server](#). To examine the biological function of your set through annotation enrichments, send the data to [Gene Set Enrichment Analysis](#) or [GSEA](#). For more complex computational tools. Refer to the [Credits](#) page for the list of contributors and usage restrictions associated with these tools. See 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:

output file: (leave blank)

file type returned: ☒ plain text ☐ gzip compressed

To reset all user cart settings (including custom tracks),

Using the Table Browser

Manage Custom Tracks

genome: Human **assembly:** Feb. 2009 (GRCh37/hg19) [hg19]

Name	Description	Type	Doc	Items	Pos	delete
User Track	User Supplied Track	bed		100	chr1:	<input type="checkbox"/>

view in