

Table Browser

Use this tool to retrieve and export data from the Genome Browser annotation track database. You can limit retrieval based on data attributes and intersect or merge with data from another track, or retrieve DNA sequence covered by a track. [More...](#)

Select dataset

clade: **genome:** **assembly:**
group: **track:**
table:

Define region of interest

region: genome position
identifiers (names/accessions):

Optional: Subset, combine, compare with another track

filter:
intersection:

Retrieve and display data

output format: Send output to [Galaxy](#) [GREAT](#)
output filename: (add .csv extension if opening in Excel, leave blank to keep output in browser)
output field separator: tsv (tab-separated) csv (for excel)
file type returned: plain text gzip compressed

Using the Table Browser

This section provides brief line-by-line descriptions of the Table Browser controls. For more information on using this program, see the [Table Browser User's Guide](#).

- **clade:** Specifies which clade the organism is in.
- **genome:** Specifies which organism data to use.
- **assembly:** Specifies which version of the organism's genome sequence to use.
- **group:** Selects the type of tracks to be displayed in the *track* list. The options correspond to the track groupings shown in the Genome Browser. Select 'All Tracks' for an alphabetical list of all available tracks in all groups. Select 'All Tables' to see all tables including those not associated with a track.
- **database:** (with "All Tables" group option) Determines which database should be used for options in table menu.
- **track:** Selects the annotation track data to work with. This list displays all tracks belonging to the group specified in the *group* list. Some tracks are not available when the region is set to *genome* due to the data provider's restrictions on sharing.
- **table:** Selects the SQL table data to use. This list shows all tables associated with the track specified in the *track* list. Some tables may be unavailable due to the data provider's restrictions on sharing.
- **describe table schema:** Displays schema information for the tables associated with the selected track.
- **region:** Restricts the query to a particular chromosome or region. Select *genome* to apply the query to the entire genome (not available for certain tracks with restrictions on data sharing). In some Human assemblies, you may select *ENCODE* to examine only the ENCODE Pilot regions. To limit the query to a specific position, type a chromosome name, e.g. *chrX*, or a chromosome coordinate range, such as *chrX:100000-200000*, or a gene name or other id in the text box. You can select multiple genomic regions by clicking the "define regions" button and entering up to 1,000 regions in a 3- or 4-field [BED](#) file format.
- **lookup:** Press this button after typing in a gene name or other id in the position text box to look up the chromosome position
- **identifiers** (selected tracks only): Restricts the output to table data that match a list of identifiers, for instance RefSeq accessions for the RefSeq track. If no identifiers are entered, all table data within the specified region will be displayed.
- **filter:** Restricts the query to only those items that match certain criteria, e.g. genes with a single exon. Click the *Create* button to add a filter, the *Edit* button to modify an existing filter, or the *Clear* button to remove an existing filter.
- **intersection** (selected tracks only): Combines the output of two queries into a single set of data based on specific join criteria. For example, this can be used to find all SNPs that intersect with RefSeq coding regions. The intersection can be configured to retain

the existing alignment structure of the table with a specified amount of overlap, or discard the structure in favor of a simple list of position ranges using a base-pair intersection or union of the two data sets. The button functionalities are similar to those of the *filter* option.

- **output:** Specifies the output format (not all options are available for some tracks). Formats include:
 - ***all fields from selected table*** - data from the selected table displayed in a tab-separated format suitable for import into spreadsheets and relational databases. The ASCII format may be read in any web browser or text editor.
 - ***selected fields from primary and related tables*** - user-selected set of tab-separated fields from the selected table and (optionally) other related tables as well.
 - ***sequence*** - DNA (or protein sequence, in some cases) associated with the table.
 - ***BED*** - positions of data items in a standard UCSC Browser format with the [name](#) column containing exon information separated by underscores.
 - ***GTF*** - positions of all data items in a [limited gene transfer format](#) (both BED and GTF formats can be used as the basis for custom tracks).
 - ***CDS FASTA alignment from multiple alignment*** - FASTA alignments of the CDS regions of a gene prediction track using any of the multiple alignment tracks for the current database. Output sequence can be in either nucleotide-space or translated to protein-space. Available only for genePred tracks.
 - ***custom track*** - customized Genome Browser annotation track based on the results of the query.
 - ***hyperlinks to Genome Browser*** - returns a page full of hyperlinks to the UCSC Genome Browser, one for each item in the table.
 - ***data points*** - the data points that make up a graph (aka wiggle) track.
 - ***MAF*** - multiple alignments in MAF format

Note that all start-end coordinate ranges are returned in UCSC's internal zero-based/half-open format, see our [FAQ](#), with the exception of the formats GTF, data points (aka "wiggle") and hyperlinks, which are one-based/closed.

- **Send output to Galaxy:** displays results of query in [Galaxy](#), a framework for interactive genome analysis.
- **Send output to GREAT:** displays the functional enrichments of the query results in [GREAT](#), a tool for analysis of the biological function of cis-regulatory regions.
- **file type returned:** When a filename is entered in the "output file" text box, specifies the format of the output file:
 - ***plain text*** - data is in ASCII format
 - ***gzip compressed*** - data is compressed in gzip format
- **get output:** Submits a data query based on the specified parameters and returns the output.
- **summary/statistics:** Displays statistics about the data specified by the parameters.