

Use Table Browser to extract peak sequences

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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 controls in this form, and the [User's Guide](#) for general information and sample queries. For more complex queries, you may want to use [Galaxy](#) or 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 de

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

group: Custom Tracks **track:** P53 peaks **manage custom tracks** track hubs

table: ct_P53peaks_3940 describe table schema

region: ☒ genome ☐ ENCODE Pilot regions ☐ position chr6:36,641,517-36,657,836 **lookup** define regions

identifiers (names/accessions): paste list upload list

filter: create

intersection with cpGISlandExt: edit clear

1. select manage custom tracks

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Manage Custom Tracks

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

Name	Description	Type	Doc	Items	Pos	delete
P53 peaks	P53 ChIPseq peaks	bed		1700	chr12:	<input type="checkbox"/>

view in Genome Browser go

add custom tracks

2. Add custom track with Top 300 peaks

Managing Custom Tracks

Use Table Browser to extract peak sequences

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Add Custom Tracks

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

Display your own data as custom annotation tracks in the browser. Data must be formatted in [bigBed](#), [bigBarChart](#), [bigChain](#), [bigG-interact](#), [MAF](#), [narrowPeak](#), [Personal Genome SNP](#), [PSL](#), or [WIG](#) formats. To configure the display, set [track](#) and [browser](#) line attrib

Data in the bigBed, bigWig, bigGenePred, BAM and VCF formats can be provided via only a URL or embedded in a track line in the the Track Hub Help documentation.

Please note a much more efficient way to load data is to use [Track Hubs](#), which are loaded from the [Track Hubs Portal](#) found in the

Paste URLs or data: Or upload Choose File p53_macs_pe...00.bed.txt Submit Clear

3. upload the Top 300 peaks file

Rename to
Top300

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Manage Custom Tracks

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

Name	Description	Type	Doc	Items	Pos	delete
User Track	User Supplied Track	bed		300	chr6:	<input type="checkbox"/>
P53 peaks	P53 ChIPseq peaks	bed		1700	chr12:	<input type="checkbox"/>

view in Genome Browser go add custom tracks

4. rename

Managing Custom Tracks

This section provides a brief description of the columns in custom track management table. For more details about managing custom tracks, see

- Name** - a hyperlink to the update page where you can edit your track data.

Use Table Browser to extract peak sequences

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 more information, see the [User's Guide](#) for general information and sample queries. For more complex queries, you may want to use [Galaxy](#) or our [public MySC](#) to 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 the [Table Browser](#).

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

group: Custom Tracks track: Top300

table: ct_Top300_6377 describe table schema

region: ☒ genome ☐ ENCODE Pilot regions ☐ position chr6:36,641,517-36,657,836 lookup define regions

identifiers (names/accessions): paste list upload list

filter: create

intersection with cpGLSlandExt: edit clear

correlation: create

output format: sequence Send output to ☐ Galaxy ☐ GREAT

output file: top300.fasta (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](#).

Go to Table Browser

6. select the Top300 track

7. remove (clear) intersection if any still exists

8. select sequence as output format and specify output file

9. get output

Use Table Browser to extract peak sequences

The screenshot shows the 'Top300 Genomic Sequence' web interface. At the top is a blue navigation bar with links: Home, Genomes, Genome Browser, Tools, Mirrors, Downloads, My Data, Projects, Help, and About Us. Below this is a light blue header for the tool. The main content area is yellow and contains two sections: 'Sequence Retrieval Region Options:' and 'Sequence Formatting Options:'. In the first section, there are two input boxes for upstream and downstream bases, both containing the number '0'. This section is highlighted with a red rectangle, and a red arrow points to it from the annotation '10. make sure no extra bases are added'. Below this is a note about truncation. The second section contains radio buttons for 'All upper case.' (selected) and 'All lower case.', a checkbox for 'Mask repeats:' with sub-options 'to lower case' (selected) and 'to N', and a checkbox for 'Reverse complement (get '-' strand sequence)'. At the bottom of this section are 'get sequence' and 'cancel' buttons. A red arrow points to the 'get sequence' button from the annotation '11. get sequences'.

Top300 Genomic Sequence

Sequence Retrieval Region Options:

Add extra bases upstream (5') and extra downstream (3')

10. make sure no extra bases are added

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

Sequence Formatting Options:

☒ All upper case.
☐ All lower case.
☐ Mask repeats: ☒ to lower case ☐ to N
☐ Reverse complement (get '-' strand sequence)

11. get sequences

Use MEME-ChIP to predict TFBS motif from top 300 P53 ChIPseq peak sequences

MEME Suite 5.0.5

► Motif Discovery

► Motif Enrichment

► Motif Scanning

► Motif Comparison

► Gene Regulation

► Manual

► Guides & Tutorials

► Sample Outputs

► File Format Reference

► Databases


► Download & Install

► Help

► Alternate Servers

► Authors & Citing

► Recent Jobs



MEME-ChIP

Motif Analysis of Large Nucleotide Datasets

Version 5.0.5

MEME-ChIP performs **comprehensive motif analysis** (including motif discovery) on LARGE sets of (typically **nucleotide**) sequences such as those identified by ChIP-seq or CLIP-seq experiments (sample output from [sequences](#)).
Note: The input sequences should be centered on a 100 character region expected to contain motifs. See this [Manual](#) for more information.

Data Submission Form

Perform motif discovery, motif enrichment analysis and clustering on large nucleotide datasets.

Select the motif discovery and enrichment mode [?](#)

☒ Classic mode ☐ Discriminative mode ☐ Differential Enrichment mode [?](#)

Select the sequence alphabet

Use sequences with a standard alphabet or specify a custom alphabet. [?](#)

☒ DNA, RNA or Protein ☐ Custom No file chosen

Input the primary sequences

Enter the (equal-length) nucleotide sequences to be analyzed. [?](#)

Upload sequences [?](#) top300.fasta [?](#)

Input the motifs

Select, upload or enter a set of known motifs. [?](#)

JASPAR (NON-REDUNDANT) DNA [?](#)

JASPAR CORE (2018) [?](#)

Input job details

(Optional) Enter your email address. [?](#)

(Optional) Enter a job description. [?](#)

► Universal options

► MEME options

► DREME options

► CentriMo options

Note: if the combined form inputs exceed 80MB the job will be rejected.

Sequence alphabet is DNA

Upload the top300.fasta file

specify Jaspas motif database to compare the predicted motif

Start the search

Version 5.0.5

Please send comments and questions to: meme-suite@uic.edu

Powered by Opal

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