ENCODE: Encyclopedia of DNA Elements
www.encodeproject.org

Human and Mouse (below) data are available

Experiment Matrix visually summarizes types of data

Submitted ENCODE Datasets that are available to explore

Search offers various ways to locate data of interest

ENCODE data is integrated in the Genome Browser interface

Earliest access to new data via the Preview Browser

See sample visualizations of data

Learn about the resources ENCODE researchers are using

All ENCODE data is available to download and use with other tools or for other analyses

Mouse cell line and tissue details

Defined and controlled experimental aspects are described

Target proteins assessed in experiments are explained

Learn about ENCODE with tutorials, papers, presentations and more

Guidance on experimental strategies and platform characterizations

Details of file structures used

Collected information on software resources associated with ENCODE data and analysis

The ENCODE Experiment Matrix provides an up-to-date view of the breadth of ENCODE experiments, with an interface for selecting experiments for viewing in the browser or downloading underlying data for analysis

A downloadable spreadsheet of the data types, cell lines, factors, treatments, project teams, accession numbers, and data restriction dates

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The ENCODE Project (ENCODE) is an international consortium of researchers who are moving beyond the basic information of the reference genome sequence. Researchers are using many cutting-edge technologies to learn as much as possible about variations, genes, non-coding transcripts, regulatory elements, and genome structure and more, in extensive detail across the entire genome. The UCSC Genome Bioinformatics Group hosts the ENCODE DCC, or Data Coordination Center, aspects of the project.

The ENCODE data are now available for the entire human genome. All ENCODE data are free and available for immediate use via:

- Simple and Advanced search forms to locate data and tools that meet your specific needs
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ENCODE data is integrated in the Genome Browser interface

Encyclopedia of DNA Elements

The Encyclopedia of DNA Elements (ENCyclopedia of DNA Elements) Consortium is an international collaboration of research groups funded by the National Human Genome Research Institute (NHGRI). The goal of ENCODE is to build a comprehensive catalog of functional elements in the human genome, including elements that affect the protein and RNA levels, and regulatory elements that control cells and circumstances in which a gene is active.

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To search for ENCODE data related to your area of interest and set up a browser view, use the UCSC Experiment Search tool (Advanced features). The Experiment List (Human) and Experiment List (Mouse) links provide complete ENCODE data that is released or in preparation. Early access to pre-release ENCODE data is provided at http://encode.uchicago.edu. If you would like to receive notifications of ENCODE data releases and related news by email, encode-announce@lists.ens.de. For more information about how to access this data, see the quick online guide. All ENCODE data is freely available for download and analysis. However, before publishing research that uses ENCODE data, please read the ENCODE Data Sharing Policy, which places some restrictions on publication use of data for main data release. Read more about ENCODE data at UCSC.

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Signals detected in experiments can be shown in various modes. **Dense** mode compresses data into the most compact display style. Choosing other visibility types may provide further details. **Full display** offers the most expanded view of the underlying data, with additional graphical details that can provide signal histogram and designations of the “peak” locations.

ENCODE tracks can be found in many track groups. Hyperlinks provide access to track details, sometimes as a super-track page for a set, or to individual subtracks for specific technique and experimental details and filter options.

ENCODE data are identified in the browser annotation track menu by the NHGRI helix icon symbol.

ENCODE data can be visualized and queried like any other data in the UCSC Genome Browser, across the entire genome. For help with an overview of the UCSC foundations, see the OpenHelix tutorials that provide more background.

This "wiggle" track display shows the signal level in various cell lines (identified by color) which can be turned on and off (see below).

Tracks have different conventions and color codes, but many will offer both signal displays of the full results across a region, and also show a peak value in that region as well. Some tracks will offer filters to set threshold values.

Super-tracks combine related topic data using different techniques (such as open chromatin state here) that can be evaluated together.

Users can choose various aspects of the experiments to display. Peaks, signals, individual cell lines, replicates, and various treatment conditions may be available to select and explore.

Super-track and track Description sections will have crucial meta-data to understand the projects, and will explain the display conventions, color codes, and more. Citations for data or technologies may be provided when available. Credits and contacts for the project teams will also be provided.