

NCBI Epigenomics

Roadmap Epigenomics project data is also being hosted at NCBI's new dedicated Epigenomics database at <http://www.ncbi.nlm.nih.gov/epigenomics/>. This resource enables users to explore Roadmap Epigenomics data alongside hundreds of other richly-annotated epigenomic datasets. The NCBI Epigenomics home page provides a portal to the Roadmap Epigenomics project. Links are provided to take you to the Roadmap Project page at NIH, the Mapping Consortium page, the Human Epigenome Atlas, which is hosted at Baylor College of Medicine (the Epigenomic Data Analysis and Coordination Center). Links also are provided for the GEO Roadmap data listings page and data access policies.

The screenshot shows the NCBI Epigenomics homepage. At the top, there is a search bar with the text 'Epigenomics' and a 'Search' button. Below the search bar, there is a navigation menu with 'Resources' and 'How To' options. The main content area is divided into several sections: 'How to...' with links for 'Use the Sample Browser', 'Manage Collections of Samples', 'View Genome Tracks', and 'Download Genome Tracks'; 'Epigenomics Tools' with links for 'Sample Browser' and 'Advanced Search'; 'Scientific Background' with links for 'About Epigenomics', 'About DNA Methylation', 'About Histone Modification', and 'About Chromatin Structure'; 'Latest Studies' with a list of recent research articles; 'NIH Roadmap Epigenomics' (highlighted with a red box) with links for 'About the Project', 'Epigenomics Mapping Consortium', 'Human Epigenome Atlas', 'Roadmap Data in GEO', and 'Data Access Policies'; and 'Recent Review Articles' with a list of recent review papers.

Visualizing epigenomics data on NCBI's Sequence Viewer

A popular approach to analyzing epigenomic data is to display the results as 'tracks' on a genome browser. Tracks represent continuous-value data aligned against the genome; enriched regions are depicted as peaks in the track. After selecting one or more tracks from the Roadmap Epigenomics data listings table (previous page), click the "View Track" button in the column header to redirect to the NCBI Sequence Viewer.

The Sequence Viewer has many navigation and display features, including the ability to go to a specific location either by entering a gene symbol or genomic coordinates into the search box (A). The queried gene, and the surrounding locus, is displayed in the lower 'Gene models' track (B). Corresponding epigenomic results for that locus are displayed in the middle (blue) tracks.

The track labels of the example to the right indicate that histone H3 trimethylated at lysine 4 (H3K4me3) ChIP-Seq results in H1 cells (upper track) and IMR90 cells (lower track) are being displayed. Peaks in the tracks indicate areas of the genome that are enriched for this histone modification (C). Additionally, the slider/zoom tool can be used to expand or narrow the viewing region (D). A viewing window can also be defined by resizing and/or repositioning the slider tab in the overview panel (E).

