

# Resource Summary Report

Generated by PRECISE-TBI on Jul 31, 2026

## VizHub

RRID:SCR\_006209

Type: Tool

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### Proper Citation

VizHub (RRID:SCR\_006209)

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### Resource Information

**URL:** <http://vizhub.wustl.edu>

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**Description:** A visualization hub displaying sequencing data from the Roadmap Epigenomics project. It hosts high volume of tracks from ENCODE and Roadmap Epigenomics projects, supports multiple organisms, visualizes chromatin-interaction data (e.g. Hi-C), performs gene set view, gene plot, and many others. All delivered on the web at high performance.

**Abbreviations:** VizHub

**Synonyms:** Roadmap Epigenomics Visualization Hub, Visualization Hub

**Resource Type:** service resource, data analysis service, portal, data or information resource, production service resource, analysis service resource

**Keywords:** epigenomics, neandertal, genome, visualization, browser, sequencing

**Resource Name:** VizHub

**Resource ID:** SCR\_006209

**Alternate IDs:** nlx\_151756

**Record Creation Time:** 20220129T080234+0000

**Record Last Update:** 20260731T042720+0000

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### Ratings and Alerts

No rating or validation information has been found for VizHub.

No alerts have been found for VizHub.

## Data and Source Information

**Source:** [SciCrunch Registry](#)

## Usage and Citation Metrics

We found 6 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [PRECISE-TBI](#) .

Cazaly E, et al. (2019) Making Sense of the Epigenome Using Data Integration Approaches. *Frontiers in pharmacology*, 10, 126.

Lee MK, et al. (2017) Epigenome-wide association study of chronic obstructive pulmonary disease and lung function in Koreans. *Epigenomics*, 9(7), 971.

Li R, et al. (2016) 3Disease Browser: A Web server for integrating 3D genome and disease-associated chromosome rearrangement data. *Scientific reports*, 6, 34651.

Pennington KL, et al. (2015) Epigenetic Mechanisms of the Aging Human Retina. *Journal of experimental neuroscience*, 9(Suppl 2), 51.

Zhang B, et al. (2013) Functional DNA methylation differences between tissues, cell types, and across individuals discovered using the M&M algorithm. *Genome research*, 23(9), 1522.

Stevens M, et al. (2013) Estimating absolute methylation levels at single-CpG resolution from methylation enrichment and restriction enzyme sequencing methods. *Genome research*, 23(9), 1541.