

Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 2026

VizHub

RRID:SCR_006209

Type: Tool

Proper Citation

VizHub (RRID:SCR_006209)

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: analysis service resource, data analysis service, data or information resource, portal, production service resource, 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: 20260905T132549+0000

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 [Kravitz](#) .

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.