

Resource Summary Report

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Genomic HyperBrowser

RRID:SCR_010909

Type: Tool

Proper Citation

Genomic HyperBrowser (RRID:SCR_010909)

Resource Information

URL: <http://hyperbrowser.uio.no/hb/>

Proper Citation: Genomic HyperBrowser (RRID:SCR_010909)

Description: A generic web-based system, providing statistical methodology and computing power to handle a variety of biological inquiries on genomic datasets.

Abbreviations: Genomic HyperBrowser

Synonyms: The Genomic HyperBrowser

Resource Type: analysis service resource, data analysis service, production service resource, service resource

Defining Citation: [PMID:23632163](#), [PMID:21182759](#)

Keywords: genomic, genomic track, gene regulation, disease association, epigenetic modification, genome

Resource Name: Genomic HyperBrowser

Resource ID: SCR_010909

Alternate IDs: OMICS_00638

Record Creation Time: 20220129T080301+0000

Record Last Update: 20260905T133200+0000

Ratings and Alerts

No rating or validation information has been found for Genomic HyperBrowser.

No alerts have been found for Genomic HyperBrowser.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 20 mentions in open access literature.

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

Fan Q, et al. (2020) LXR α Regulates ChREBP α Transactivity in a Target Gene-Specific Manner through an Agonist-Modulated LBD-LID Interaction. *Cells*, 9(5).

Bonnefont J, et al. (2019) Cortical Neurogenesis Requires Bcl6-Mediated Transcriptional Repression of Multiple Self-Renewal-Promoting Extrinsic Pathways. *Neuron*, 103(6), 1096.

Sun Z, et al. (2018) Transcription-associated histone pruning demarcates macroH2A chromatin domains. *Nature structural & molecular biology*, 25(10), 958.

Kanduri C, et al. (2017) Genome build information is an essential part of genomic track files. *Genome biology*, 18(1), 175.

Simovski B, et al. (2017) GSuite HyperBrowser: integrative analysis of dataset collections across the genome and epigenome. *GigaScience*, 6(7), 1.

Romasko EJ, et al. (2016) Male-Specific Transcription Factor Occupancy Alone Does Not Account for Differential Methylation at Imprinted Genes in the mouse Germ Cell Lineage. *G3 (Bethesda, Md.)*, 6(12), 3975.

Handel AE, et al. (2016) Bioinformatics Analysis of Estrogen-Responsive Genes. *Methods in molecular biology (Clifton, N.J.)*, 1366, 29.

Saleh S, et al. (2016) HIV integration and the establishment of latency in CCL19-treated resting CD4(+) T cells require activation of NF- κ B. *Retrovirology*, 13(1), 49.

Lercher L, et al. (2015) Generation of a synthetic GlcNAcylated nucleosome reveals regulation of stability by H2A-Thr101 GlcNAcylation. *Nature communications*, 6, 7978.

Kocer A, et al. (2015) Oxidative DNA damage in mouse sperm chromosomes: Size matters. *Free radical biology & medicine*, 89, 993.

Mosquera Orgueira A, et al. (2015) Hidden among the crowd: differential DNA methylation-expression correlations in cancer occur at important oncogenic pathways. *Frontiers in genetics*, 6, 163.

Ricigliano VA, et al. (2015) EBNA2 binds to genomic intervals associated with multiple sclerosis and overlaps with vitamin D receptor occupancy. *PloS one*, 10(4), e0119605.

Bengtzen M, et al. (2015) c-Myb Binding Sites in Haematopoietic Chromatin Landscapes. *PloS one*, 10(7), e0133280.

- Watson CT, et al. (2015) Sequencing of the human IG light chain loci from a hydatidiform mole BAC library reveals locus-specific signatures of genetic diversity. *Genes and immunity*, 16(1), 24.
- Rydbeck H, et al. (2015) ClusTrack: feature extraction and similarity measures for clustering of genome-wide data sets. *PloS one*, 10(4), e0123261.
- Ragoczy T, et al. (2014) Functional redundancy in the nuclear compartmentalization of the late-replicating genome. *Nucleus (Austin, Tex.)*, 5(6), 626.
- Watson CT, et al. (2012) Age-associated hyper-methylated regions in the human brain overlap with bivalent chromatin domains. *PloS one*, 7(9), e43840.
- Kresse SH, et al. (2012) Integrative analysis reveals relationships of genetic and epigenetic alterations in osteosarcoma. *PloS one*, 7(11), e48262.
- Disanto G, et al. (2012) Genomic regions associated with multiple sclerosis are active in B cells. *PloS one*, 7(3), e32281.
- Disanto G, et al. (2012) Vitamin D receptor binding, chromatin states and association with multiple sclerosis. *Human molecular genetics*, 21(16), 3575.