Resource Summary Report

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International Human Epigenome Consortium Data Portal

RRID:SCR_014625
Type: Tool

Proper Citation

International Human Epigenome Consortium Data Portal (RRID:SCR_014625)

Resource Information

URL: http://epigenomesportal.ca/ihec/

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Description: A data portal of the International Human Epigenome Consortium which provides access to comprehensive data sets of reference epigenomes relevant to health and disease. The IHEC Data Portal can be used to view, search and download data already released by different IHEC-associated projects. Data are organized by consortium, by tissue, and by assay category. Users can visualize data sets using the data grid provided or the UCSC Genome Browser.

Synonyms: International Human Epigenome Consortium (IHEC) Data Portal, IHEC Data Portal

Resource Type: data or information resource, portal

Keywords: portal, data portal, data set, epigenetic, consortium, human, epigenome, tissue, assay

Funding: Canadian Institutes of Health Research ;
Genome Quebec ;
Genome Canada

Availability: Public, Data sets available for download

Resource Name: International Human Epigenome Consortium Data Portal

Resource ID: SCR_014625

Record Creation Time: 20220129T080321+0000

Record Last Update: 20250419T055423+0000

Ratings and Alerts

No rating or validation information has been found for International Human Epigenome Consortium Data Portal.

No alerts have been found for International Human Epigenome Consortium Data Portal.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 11 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

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

Zhou J, et al. (2019) Elevated H3K27ac in aged skeletal muscle leads to increase in extracellular matrix and fibrogenic conversion of muscle satellite cells. Aging cell, 18(5), e12996.

Boži? T, et al. (2018) Variants of DNMT3A cause transcript-specific DNA methylation patterns and affect hematopoiesis. Life science alliance, 1(6), e201800153.

Zheng SC, et al. (2018) Identification of differentially methylated cell types in epigenome-wide association studies. Nature methods, 15(12), 1059.

Mandal M, et al. (2018) BRWD1 orchestrates epigenetic landscape of late B lymphopoiesis. Nature communications, 9(1), 3888.

Ohara K, et al. (2017) Genes involved in development and differentiation are commonly methylated in cancers derived from multiple organs: a single-institutional methylome analysis using 1007 tissue specimens. Carcinogenesis, 38(3), 241.

Jeon JP, et al. (2017) Differential DNA methylation of MSI2 and its correlation with diabetic traits. PloS one, 12(5), e0177406.

Stunnenberg HG, et al. (2016) The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. Cell, 167(5), 1145.

Farlik M, et al. (2016) DNA Methylation Dynamics of Human Hematopoietic Stem Cell Differentiation. Cell stem cell, 19(6), 808.

Lorzadeh A, et al. (2016) Nucleosome Density ChIP-Seq Identifies Distinct Chromatin Modification Signatures Associated with MNase Accessibility. Cell reports, 17(8), 2112.

Breeze CE, et al. (2016) eFORGE: A Tool for Identifying Cell Type-Specific Signal in Epigenomic Data. Cell reports, 17(8), 2137.