Resource Summary Report

Generated by NIF on Apr 18, 2025

International Human Epigenome Consortium

RRID:SCR_016937
Type: Tool

Proper Citation

International Human Epigenome Consortium (RRID:SCR_016937)

Resource Information

URL: http://ihec-epigenomes.org/

Proper Citation: International Human Epigenome Consortium (RRID:SCR_016937)

Description: Consortium to coordinate epigenome mapping and characterization worldwide to avoid redundant research effort, to implement high data quality standards, to coordinate data storage, management and analysis and to provide free access to the high resolution reference human epigenome maps for normal and disease cell types to the research community. Promotes data sharing. You may view, search and download the data already released by the different IHEC associated projects via the IHEC Data Portal.

Abbreviations: IHEC

Synonyms: International Human Epigenome Consortium, IHEC

Resource Type: portal, consortium, organization portal, data or information resource

Keywords: reference, human, epigenome, map, normal, disease, cell, data, quality, standard, sharing

Funding:

Availability: Free access to the research community, Open and controlled access to datasets according to policies and guidelines

Resource Name: International Human Epigenome Consortium

Resource ID: SCR_016937

Alternate URLs: https://epigenomesportal.ca/ihec/

Record Creation Time: 20220129T080332+0000

Record Last Update: 20250418T055501+0000

Ratings and Alerts

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

No alerts have been found for International Human Epigenome Consortium.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 21 mentions in open access literature.

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

Bruner WS, et al. (2024) Translation of genome-wide association study: from genomic signals to biological insights. Frontiers in genetics, 15, 1375481.

O'Neill K, et al. (2024) Long-read sequencing of an advanced cancer cohort resolves rearrangements, unravels haplotypes, and reveals methylation landscapes. Cell genomics, 4(11), 100674.

Bell CG, et al. (2024) Epigenomic insights into common human disease pathology. Cellular and molecular life sciences : CMLS, 81(1), 178.

Mohammadi-Shemirani P, et al. (2023) From 'Omics to Multi-omics Technologies: the Discovery of Novel Causal Mediators. Current atherosclerosis reports, 25(2), 55.

Moss J, et al. (2023) Megakaryocyte- and erythroblast-specific cell-free DNA patterns in plasma and platelets reflect thrombopoiesis and erythropoiesis levels. Nature communications, 14(1), 7542.

Arkhipova IR, et al. (2023) Meeting report: transposable elements at the crossroads of evolution, health and disease 2023. Mobile DNA, 14(1), 19.

Romualdo Cardoso S, et al. (2022) Functional annotation of breast cancer risk loci: current progress and future directions. British journal of cancer, 126(7), 981.

Kircher M, et al. (2022) Systematic assays and resources for the functional annotation of non-coding variants. Medizinische Genetik : Mitteilungsblatt des Berufsverbandes Medizinische Genetik e.V, 34(4), 275.

Ebert P, et al. (2021) Fast detection of differential chromatin domains with SCIDDO. Bioinformatics (Oxford, England), 37(9), 1198.

Islam R, et al. (2021) CRIS: complete reconstruction of immunoglobulin V-D-J sequences from RNA-seq data. Bioinformatics advances, 1(1), vbab021.

Ram-Mohan N, et al. (2021) Profiling chromatin accessibility responses in human neutrophils with sensitive pathogen detection. Life science alliance, 4(8).

Campagna MP, et al. (2021) Epigenome-wide association studies: current knowledge, strategies and recommendations. Clinical epigenetics, 13(1), 214.

Lutz PE, et al. (2021) Non-CG methylation and multiple histone profiles associate child abuse with immune and small GTPase dysregulation. Nature communications, 12(1), 1132.

Lee BH, et al. (2021) Molecular and computational approaches to map regulatory elements in 3D chromatin structure. Epigenetics & chromatin, 14(1), 14.

Cho YD, et al. (2021) Current advances of epigenetics in periodontology from ENCODE project: a review and future perspectives. Clinical epigenetics, 13(1), 92.

Luo Y, et al. (2020) New developments on the Encyclopedia of DNA Elements (ENCODE) data portal. Nucleic acids research, 48(D1), D882.

Ban M, et al. (2020) Transcript specific regulation of expression influences susceptibility to multiple sclerosis. European journal of human genetics : EJHG, 28(6), 826.

Toh TB, et al. (2019) Epigenetics of hepatocellular carcinoma. Clinical and translational medicine, 8(1), 13.

Adoue V, et al. (2019) The Histone Methyltransferase SETDB1 Controls T Helper Cell Lineage Integrity by Repressing Endogenous Retroviruses. Immunity, 50(3), 629.

Kumar V, et al. (2016) Comprehensive benchmarking reveals H2BK20 acetylation as a distinctive signature of cell-state-specific enhancers and promoters. Genome research, 26(5), 612.