Resource Summary Report

Generated by T1D on Aug 9, 2026

Blueprint Epigenome

RRID:SCR_003844
Type: Tool

Proper Citation

Blueprint Epigenome (RRID:SCR_003844)

Resource Information

URL: http://www.blueprint-epigenome.eu/

Proper Citation: Blueprint Epigenome (RRID:SCR_003844)

Description: Consortium to further the understanding of how genes are activated or repressed in both healthy and diseased human cells with a focus on distinct types of haematopoietic cells from healthy individuals and on their malignant leukemic counterparts. They will generate at least 100 reference epigenomes and study them to advance and exploit knowledge of the underlying biological processes and mechanisms in health and disease. Reference epigenomes will be generated by state-of-the-art technologies from highly purified cells for a comprehensive set of epigenetic marks in accordance with quality standards set by International Human Epigenome Consortium (IHEC). Access to the data is provided as well as the protocols used to collect the different blood cell types, to perform the different types of epigenomic analyses, etc.). This resource-generating activity will be complemented by hypothesis-driven research into blood-based diseases, including common leukemias and autoimmune disease (Type 1 Diabetes), by discovery and validation of epigenetic markers for diagnostic use and by epigenetic target identification. Since epigenetic changes are reversible, they can be targets for the development of novel and more individualized medical treatments. The involvement of companies will energize epigenomic research in the private sector by the development of smart technologies for better diagnostic tests and by identifying new targets for compounds. Thus the results of the project may lead to targeted diagnostics, new treatments and preventive measures for specific diseases in individual patients, an approach known as "personalized medicine". The Blueprint Data Access Committee will consider applications for access to data sets stored in the European Genome-phenome Archive (EGA) when authorized to do so by the Blueprint consortium and the holders of the original consent documents. Access is conditional upon availability of samples and/or data and signed agreement by the researcher(s) and the responsible employing Institution to abide by policies related to publication, data disposal, ethical approval and confidentiality. At EBI, the ftp site with the data can be found. You can either opt to link to the track hubs yourself or you can add the track hub to a genome browser - UCSC or ENSEMBL. Also Meta Data files and README are available. The data can also be

accessed via the BIOMART system.

Abbreviations: BLUEPRINT

Synonyms: BLUEPRINT - A BLUEPRINT of Haematopoietic Epigenomes

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

Keywords: epigenome, hematopoiesis, gene, data set, biomaterial supply resource, antibody, blood cell, blood, cord blood precursor cell, cell, cord blood, bone marrow, rna-seq, dname-seq, dnasei-seq, chip-seq, monocyte, granulocyte neutrophil, eosinophil, macrophage, m0, m1, m2, naive cd4+, naive cd8+, pathway

Related Condition: Leukemia, Blood disease, Autoimmune disease, Type 1 diabetes, Diabetes

Funding: European Union FP7 282510

Availability: Authorization required, Application required, Data Access Agreement, Acknowledgement required

Resource Name: Blueprint Epigenome

Resource ID: SCR_003844

Alternate IDs: nlx_158155

Record Creation Time: 20220129T080221+0000

Record Last Update: 20260808T185805+0000

Ratings and Alerts

No rating or validation information has been found for Blueprint Epigenome.

No alerts have been found for Blueprint Epigenome.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 123 mentions in open access literature.

Listed below are recent publications. The full list is available at T1D .

Kroehling L, et al. (2026) A highly resolved integrated single-cell atlas of HPV-negative head and neck cancer. Communications medicine, 6(1).

Hu X, et al. (2026) The functional landscape of alternative splicing in hematopoietic lineage commitment. Nature communications, 17(1).

Ngwa JS, et al. (2026) A genome-wide meta-analysis identifies a sex-specific genetic effect for platelet aggregation in response to agonists. medRxiv : the preprint server for health sciences.

Kroehling L, et al. (2025) A highly resolved integrated single-cell atlas of HPV-negative head and neck cancer. bioRxiv : the preprint server for biology.

Chavan A, et al. (2025) Epigenetic regulation of MED12: a key contributor to the leukemic chromatin landscape and transcriptional dysregulation. Epigenetics & chromatin, 18(1), 44.

Benjamin JS, et al. (2025) 23ME-01473, an Fc Effector-Enhanced Anti-ULBP6/2/5 Antibody, Restores NK Cell-Mediated Antitumor Immunity through NKG2D and Fc??RIIIa Activation. Cancer research communications, 5(3), 476.

McNamara ME, et al. (2025) Circulating cell-free DNA methylation patterns indicate cellular sources of allograft injury after liver transplant. Nature communications, 16(1), 5310.

Tamburri S, et al. (2025) SP140 represses specific loci by recruiting polycomb repressive complex 2 and NuRD complex. Nucleic acids research, 53(4).

Li ZP, et al. (2025) Interpretable deep learning of single-cell and epigenetic data reveals novel molecular insights in aging. Scientific reports, 15(1), 5048.

Gabbutt C, et al. (2025) Fluctuating DNA methylation tracks cancer evolution at clinical scale. Nature, 645(8081), 764.

K??hnke T, et al. (2024) Human ASXL1-Mutant Hematopoiesis Is Driven by a Truncated Protein Associated with Aberrant Deubiquitination of H2AK119. Blood cancer discovery, 5(3), 202.

Murphy AE, et al. (2024) Predicting cell type-specific epigenomic profiles accounting for distal genetic effects. Nature communications, 15(1), 9951.

Chen L, et al. (2024) Agonistic anti-DCIR antibody inhibits ITAM-mediated inflammatory signaling and promotes immune resolution. JCI insight, 9(12).

Alda-Catalinas C, et al. (2024) Mapping the functional impact of non-coding regulatory elements in primary T cells through single-cell CRISPR screens. Genome biology, 25(1), 42.

Nylund P, et al. (2024) PVT1 interacts with polycomb repressive complex 2 to suppress genomic regions with pro-apoptotic and tumour suppressor functions in multiple myeloma. Haematologica, 109(2), 567.

Gustafsson J, et al. (2023) Generation and analysis of context-specific genome-scale metabolic models derived from single-cell RNA-Seq data. Proceedings of the National Academy of Sciences of the United States of America, 120(6), e2217868120.

Milner JJ, et al. (2023) Nursing Informatics and Epigenetics: Methodological Considerations for Big Data Analysis. Computers, informatics, nursing : CIN, 41(6), 369.

Trinidad EM, et al. (2023) Liquidhope: methylome and genomic profiling from very limited quantities of plasma-derived DNA. Briefings in bioinformatics, 24(1).

Hing ZA, et al. (2023) Dysregulation of PRMT5 in chronic lymphocytic leukemia promotes progression with high risk of Richter's transformation. Nature communications, 14(1), 97.

Zhang W, et al. (2023) Glucose-responsive, antioxidative HA-PBA-FA/EN106 hydrogel enhanced diabetic wound healing through modulation of FEM1b-FNIP1 axis and promoting angiogenesis. Bioactive materials, 30, 29.