Resource Summary Report

Generated by NIF on Sep 1, 2026

HipSci

RRID:SCR_003909
Type: Tool

Proper Citation

HipSci (RRID:SCR_003909)

Resource Information

URL: http://www.hipsci.org/

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Description: A UK national induced pluripotent stem (iPS) cell resource that will create and characterize more than 1000 human iPSCs from healthy and diseased tissue for use in cellular genetic studies. Between 2013 and 2016 they aim to generate iPS cells from over 500 healthy individuals and 500 individuals with genetic disease. They will then use these cells to discover how genomic variation impacts on cellular phenotype and identify new disease mechanisms. Strong links with NHS investigators will ensure that studies on the disease-associated cell lines will be linked to extensive clinical information. Further key features of the project are an open access model of data sharing; engagement of the wider clinical genetics community in selecting patient samples; and provision of dedicated laboratory space for collaborative cell phenotyping and differentiation.

Abbreviations: HipSci

Synonyms: Human Induced Pluripotent Stem Cells Initiative

Resource Type: biomaterial supply resource, material resource

Keywords: stem cell, genomic variation, cellular phenotype, disease mechanism, phenotype, disease, clinical data, clinical, genetics, male, female, cell line, induced pluripotent stem cell

Related Condition: Healthy, Genetic disease

Funding: Wellcome Trust ;
MRC

Availability: Acknowledgement required, Free, Public

Resource Name: HipSci

Resource ID: SCR_003909

Alternate IDs: nlx_158252

Record Creation Time: 20220129T080221+0000

Record Last Update: 20260829T183055+0000

Ratings and Alerts

No rating or validation information has been found for HipSci.

No alerts have been found for HipSci.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 131 mentions in open access literature.

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

Forbes CA, et al. (2026) A precision medicine approach to interpret a GATA4 genetic variant in a paediatric patient with congenital heart disease. Human genomics, 20(1), 29.

Lampersperger H, et al. (2026) Mechanical impact on neural stem cell lineage decisions in human brain organoids. EMBO reports, 27(6), 1393.

Lee BN, et al. (2026) Genetics of growth rate in induced pluripotent stem cells. Stem cell reports, 21(6), 102928.

Bertin M, et al. (2026) Dynamic allele usage of X-linked genes ameliorates neurodevelopmental disease phenotypes in brain organoids. Nature communications, 17(1), 599.

Feng C, et al. (2026) A genome-scale single-cell CRISPRi map of trans gene regulation across human pluripotent stem cell lines. Cell genomics, 6(2), 101076.

Ajasin D, et al. (2026) HIV heart inflammation is mediated by HIV infected myeloid cells, HIV-tat secretion, and aberrant function of Connexin43-containing channels. Scientific reports, 16(1).

Sumanaweera D, et al. (2025) Gene-level alignment of single-cell trajectories. Nature methods, 22(1), 68.

Quaid K, et al. (2025) iPSCs and iPSC-derived cells as a model of human genetic and epigenetic variation. Nature communications, 16(1), 1750.

Cuvertino S, et al. (2025) Epigenome and transcriptome changes in KMT2D-related Kabuki syndrome Type 1 iPSCs, neuronal progenitors and cortical neurons. PLoS genetics, 21(9), e1011608.

Johnson OD, et al. (2025) DNA-damage-associated protein co-expression network in cardiomyocytes informs on tolerance to genetic variation and disease. iScience, 28(5), 112474.

El Garwany O, et al. (2025) Splicing QTL mapping in stimulated macrophages associates low-usage splice junctions with immune-mediated disease risk. Nature communications, 16(1), 7205.

Todd CD, et al. (2025) Epigenetic priming of mammalian embryonic enhancer elements coordinates developmental gene networks. Genome biology, 26(1), 214.

Blair JD, et al. (2025) Phospho-seq: integrated, multi-modal profiling of intracellular protein dynamics in single cells. Nature communications, 16(1), 1346.

Ko??odziejczak-Guglas I, et al. (2025) Proteomic-based stemness score measures oncogenic dedifferentiation and enables the identification of druggable targets. Cell genomics, 5(6), 100851.

Meijer HA, et al. (2025) NOTCH1 S2513 is critical for the regulation of NICD levels impacting the segmentation clock in hiPSC-derived PSM cells and somitoids. Genes & development, 39(17-18), 1025.

Yuste-Checa P, et al. (2025) Structural analyses define the molecular basis of clusterin chaperone function. Nature structural & molecular biology.

Panousis NI, et al. (2025) Gene expression QTL mapping in stimulated iPSC-derived macrophages provides insights into common complex diseases. Nature communications, 16(1), 7204.

Shaw NC, et al. (2025) Functional characterization of the MED12 p.Arg1138Trp variant in females: implications for neural development and disease mechanism. Molecular medicine (Cambridge, Mass.), 31(1), 300.

Zhang Z, et al. (2025) Developing a general AI model for integrating diverse genomic modalities and comprehensive genomic knowledge. Nucleic acids research, 53(21).

Larrea Murillo L, et al. (2025) Blood vessels bioengineered from induced pluripotent stem cell derived mesenchymal stem cells and porous silk fibroin coated functional scaffolds. Journal of tissue engineering, 16, 20417314251355723.