Resource Summary Report

Generated by NIF on Sep 9, 2026

NIGMS Human Genetic Cell Repository

RRID:SCR_004517
Type: Tool

Proper Citation

NIGMS Human Genetic Cell Repository (RRID:SCR_004517)

Resource Information

URL: http://ccr.coriell.org/Sections/Collections/NIGMS/?SsId=8

Proper Citation: NIGMS Human Genetic Cell Repository (RRID:SCR_004517)

Description: Highly characterized cell lines and high quality DNA for cell and genetic research representing a variety of disease states, chromosomal abnormalities, apparently healthy individuals and many distinct human populations. The NIGMS Repository contains more than 10,600 cell lines, primarily fibroblasts and transformed lymphoblasts, and over 5,500 DNA samples. The NIGMS Repository has a major emphasis on heritable diseases and chromosomally aberrant cell lines. In addition, it contains a large collection dedicated to understanding human variation that includes samples from populations around the world, the CEPH collection, the Polymorphism Discovery Resource, and many apparently healthy controls. Human induced pluripotent stem cell lines, many of which were derived from NIGMS Repository fibroblasts, have recently become available through the NIGMS Repository. Sample donation facilitates all areas of research by making available well-characterized materials to any qualified researcher who might have otherwise been unable to invest the time and resources to collect needed samples independently. Donations to the Repository have created a resource of unparalleled scope. Samples from the collection have been used in more than 5,500 publications and are distributed to scientists in more than 50 countries. This resource is continuously expanding to support new directions in human genetics.

Abbreviations: NIGMS Repository

Synonyms: Human Genetic Cell Repository

Resource Type: biomaterial supply resource, cell repository, material resource

Keywords: cell, gene, cell line, dna, fibroblast, transformed lymphoblast, lymphoblast, induced pluripotent stem cell line, chromosomal abnormality, healthy, single-gene disorder, complex polygenic disorder, multifactorial birth defect, unaffected first-degree relatives of individuals with genetic disease, heritable disease, genetic disease, human variation, control, clinical data, blood

Related Condition: Chromosomal abnormality, Healthy, Single-gene disorder, Complex polygenic disorder, Multifactorial birth defect, Unaffected first-degree relatives of individuals with genetic disease, Heritable disease, Genetic disease, Control

Funding: NIGMS ;
NIH Blueprint for Neuroscience Research

Availability: Public / non-commercial: Cell cultures and DNA samples are distributed only to qualified professional persons who are associated with recognized research, Medical, Educational, Or industrial organizations engaged in biomedical research with Statement of Research Intent and a MTA. Samples obtained from the Repository, And material derived from the samples, May not be used for commercial purposes, Although knowledge gained from their use may be used.

Resource Name: NIGMS Human Genetic Cell Repository

Resource ID: SCR_004517

Alternate IDs: nlx_143798

Record Creation Time: 20220129T080225+0000

Record Last Update: 20260905T133040+0000

Ratings and Alerts

No rating or validation information has been found for NIGMS Human Genetic Cell Repository.

No alerts have been found for NIGMS Human Genetic Cell Repository.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 4 mentions in open access literature.

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

Oeste CL, et al. (2014) An isoprenylation and palmitoylation motif promotes intraluminal vesicle delivery of proteins in cells from distant species. PloS one, 9(9), e107190.

Bleazard T, et al. (2013) Fine-scale mapping of meiotic recombination in Asians. BMC genetics, 14, 19.

Watanabe E, et al. (2012) Tumor necrosis factor -308 polymorphism (rs1800629) is associated with mortality and ventilator duration in 1057 Caucasian patients. Cytokine, 60(1), 249.

Pronold M, et al. (2012) Copy number variation signature to predict human ancestry. BMC bioinformatics, 13, 336.