Resource Summary Report

Generated by NIF on May 13, 2025

Coriell Cell Repositories

RRID:SCR_003244
Type: Tool

Proper Citation

Coriell Cell Repositories (RRID:SCR_003244)

Resource Information

URL: https://catalog.coriell.org/

Proper Citation: Coriell Cell Repositories (RRID:SCR_003244)

Description: A biorepository and biomaterial supply resource which establishes, verifies, maintains, and distributes cells, cultures and DNA derived from cell cultures to the scientific community around the world. Scientists can browse the sample catalog and request specific cell lines for their research studies. An inventory of the remaining stock of each cell line and DNA preparation is presented in real time. Coriell's significant cell biobank collections include: NIGMS Human Genetic Cell Repository, NINDS Human Genetics DNA and Cell Line Repository, NIA Aging Cell Repository, NHGRI Sample Repository for Human Genetic Research, NEI Age-Related Eye Disease Study (AREDS) Genetic Repository, HD Community BioRepository, American Diabetes Association, GENNID Study, and Autism Research Resource. The repositories are ISO 9000-2001 compliant.

Abbreviations: CCR

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

Keywords: cellular, molecular, genetics, cell line, culture, cell, dna, reagent, disease, family, gene, pharmacogenetics, population, single nucleotide polymorphism

Funding: NIH

Resource Name: Coriell Cell Repositories

Resource ID: SCR_003244

Alternate IDs: nif-0000-00182

Alternate URLs: http://ccr.coriell.org/ccr/, http://ccr.coriell.org/

Record Creation Time: 20220129T080217+0000

Record Last Update: 20250513T060514+0000

Ratings and Alerts

No rating or validation information has been found for Coriell Cell Repositories.

No alerts have been found for Coriell Cell Repositories.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 73 mentions in open access literature.

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

Oturkar CC, et al. (2024) ESR1 and p53 interactome alteration defines mechanisms of tamoxifen response in luminal breast cancer. iScience, 27(6), 109995.

Naama M, et al. (2023) Pluripotency-independent induction of human trophoblast stem cells from fibroblasts. Nature communications, 14(1), 3359.

Sharma SD, et al. (2023) Astrocytes mediate cell non-autonomous correction of aberrant firing in human FXS neurons. Cell reports, 42(4), 112344.

Zhang N, et al. (2023) Unique progerin C-terminal peptide ameliorates Hutchinson-Gilford progeria syndrome phenotype by rescuing BUBR1. Nature aging, 3(2), 185.

Fløyel T, et al. (2021) SKAP2, a Candidate Gene for Type 1 Diabetes, Regulates ?-Cell Apoptosis and Glycemic Control in Newly Diagnosed Patients. Diabetes, 70(2), 464.

Davis Armstrong NM, et al. (2021) Multi-omic analysis of stroke recurrence in African Americans from the Vitamin Intervention for Stroke Prevention (VISP) clinical trial. PloS one, 16(3), e0247257.

Iannuzzi F, et al. (2021) Might Fibroblasts from Patients with Alzheimer's Disease Reflect the Brain Pathology? A Focus on the Increased Phosphorylation of Amyloid Precursor Protein Tyr682 Residue. Brain sciences, 11(1).

Reis ALM, et al. (2020) A universal and independent synthetic DNA ladder for the

quantitative measurement of genomic features. Nature communications, 11(1), 3609.

Das Sharma S, et al. (2020) Cortical neurons derived from human pluripotent stem cells lacking FMRP display altered spontaneous firing patterns. Molecular autism, 11(1), 52.

Curtis ME, et al. (2020) Dysregulation of the Retromer Complex System in Down Syndrome. Annals of neurology, 88(1), 137.

Ahmed S, et al. (2019) MAPT p.V363I mutation: A rare cause of corticobasal degeneration. Neurology. Genetics, 5(4), e347.

Pan H, et al. (2019) The cell line ontology-based representation, integration and analysis of cell lines used in China. BMC bioinformatics, 20(Suppl 5), 179.

Hwang SM, et al. (2018) Comparison of Ion Personal Genome Machine Platforms for the Detection of Variants in BRCA1 and BRCA2. Cancer research and treatment, 50(1), 255.

Chen D, et al. (2018) Comparison of single cell sequencing data between two whole genome amplification methods on two sequencing platforms. Scientific reports, 8(1), 4963.

Kang JY, et al. (2018) Lysosomal Targeting Enhancement by Conjugation of Glycopeptides Containing Mannose-6-phosphate Glycans Derived from Glyco-engineered Yeast. Scientific reports, 8(1), 8730.

Zamponi E, et al. (2018) Nrf2 stabilization prevents critical oxidative damage in Down syndrome cells. Aging cell, 17(5), e12812.

Dolzhenko E, et al. (2017) Detection of long repeat expansions from PCR-free whole-genome sequence data. Genome research, 27(11), 1895.

Royba E, et al. (2017) Evaluation of ATM heterozygous mutations underlying individual differences in radiosensitivity using genome editing in human cultured cells. Scientific reports, 7(1), 5996.

Ong E, et al. (2017) Ontological representation, integration, and analysis of LINCS cell line cells and their cellular responses. BMC bioinformatics, 18(Suppl 17), 556.

Buchwalter A, et al. (2017) Nucleolar expansion and elevated protein translation in premature aging. Nature communications, 8(1), 328.