Resource Summary Report

Generated by RRID on Apr 8, 2025

Coriell Institute for Medical Research

RRID:SCR_003043
Type: Tool

Proper Citation

Coriell Institute for Medical Research (RRID:SCR_003043)

Resource Information

URL: http://www.coriell.org/

Proper Citation: Coriell Institute for Medical Research (RRID:SCR_003043)

Description: Non-profit research center dedicated to the study of the human genome. Expert staff and pioneering programs in the fields of personalized medicine, cell biology, cytogenetics, genotyping, and biobanking drive our mission. The emerging field of personalized medicine draws upon a person's genomic information to tailor treatments and prescription drug dosing to optimize health outcomes. The Coriell Personalized Medicine Collaborative (CPMC) research study is seeking to understand the usefulness of genetic risk and pharmacogenomics in clinical decision-making and healthcare management. Coriell has a distinguished history in cell biology. We are building upon this expertise by playing an important role in induced pluripotent stem (iPS) cell research. These powerful cells, which can be made from skin cells or blood, are revolutionizing the way human disease is studied and how drugs are developed. The decline of neurons afflicted with Alzheimer's disease or pancreatic cells fighting diabetes can be studied in a Petri dish. By proving efficacy within the diseased environment prior to clinical trial, drugs can move through the pipeline quicker to reach patients sooner. In addition to pioneering cutting-edge research initiatives, Coriell offers custom research services including cell culture, cytogenetic analyses, and molecular biology to the scientific community. Furthermore, Coriell's Genotyping and Microarray Center is one of the nation's largest centers, with high-throughput DNA analysis systems from Illumina and Affymetrix. The Center is CLIA-certified in 48 states.

Abbreviations: Coriell

Synonyms: Coriell Institute

Resource Type: production service resource, topical portal, service resource, portal, data or information resource

Keywords: genome, induced pluripotent stem cell

Funding:

Resource Name: Coriell Institute for Medical Research

Resource ID: SCR_003043

Alternate IDs: nif-0000-00169

Record Creation Time: 20220129T080216+0000

Record Last Update: 20250407T215338+0000

Ratings and Alerts

No rating or validation information has been found for Coriell Institute for Medical Research.

No alerts have been found for Coriell Institute for Medical Research.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 119 mentions in open access literature.

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

Son SM, et al. (2024) p300 nucleocytoplasmic shuttling underlies mTORC1 hyperactivation in Hutchinson-Gilford progeria syndrome. Nature cell biology, 26(2), 235.

Jerez PÁ, et al. (2024) African ancestry neurodegeneration risk variant disrupts an intronic branchpoint in GBA1. medRxiv : the preprint server for health sciences.

Gan P, et al. (2024) Development and validation of a pharmacogenomics reporting workflow based on the illumina global screening array chip. Frontiers in pharmacology, 15, 1349203.

Park J, et al. (2024) Inducing Pluripotency in Somatic Cells: Historical Perspective and Recent Advances. International journal of stem cells, 17(4), 363.

Álvarez Jerez P, et al. (2024) African ancestry neurodegeneration risk variant disrupts an

intronic branchpoint in GBA1. Nature structural & molecular biology, 31(12), 1955.

Alvarez Jerez P, et al. (2024) Characterizing a complex CT-rich haplotype in intron 4 of SNCA using large-scale targeted amplicon long-read sequencing. NPJ Parkinson's disease, 10(1), 136.

Genner R, et al. (2024) Assessing methylation detection for primary human tissue using Nanopore sequencing. bioRxiv : the preprint server for biology.

Lai SK, et al. (2024) A novel framework for human leukocyte antigen (HLA) genotyping using probe capture-based targeted next-generation sequencing and computational analysis. Computational and structural biotechnology journal, 23, 1562.

Obeidat L, et al. (2024) Genetic causes of primary immunodeficiency in the Jordanian population. Biomedical reports, 21(5), 160.

Akamatsu S, et al. (2024) Targeted nanopore sequencing using the Flongle device to identify mitochondrial DNA variants. Scientific reports, 14(1), 25161.

Engelbrecht E, et al. (2024) Resolving haplotype variation and complex genetic architecture in the human immunoglobulin kappa chain locus in individuals of diverse ancestry. Genes and immunity, 25(4), 297.

Kolmogorov M, et al. (2023) Scalable Nanopore sequencing of human genomes provides a comprehensive view of haplotype-resolved variation and methylation. bioRxiv : the preprint server for biology.

Ben-Mahmoud A, et al. (2023) A cryptic microdeletion del(12)(p11.21p11.23) within an unbalanced translocation t(7;12)(q21.13;q23.1) implicates new candidate loci for intellectual disability and Kallmann syndrome. Scientific reports, 13(1), 12984.

Smullen M, et al. (2023) Modeling of mitochondrial genetic polymorphisms reveals induction of heteroplasmy by pleiotropic disease locus 10398A>G. Scientific reports, 13(1), 10405.

Ben-Mahmoud A, et al. (2023) A microdeletion del(12)(p11.21p11.23) with a cryptic unbalanced translocation t(7;12)(q21.13;q23.1) implicates new candidate loci for intellectual disability and Kallmann syndrome. Research square.

Cherukuri PF, et al. (2022) Establishing analytical validity of BeadChip array genotype data by comparison to whole-genome sequence and standard benchmark datasets. BMC medical genomics, 15(1), 56.

Monternier PA, et al. (2022) Beneficial Effects of the Direct AMP-Kinase Activator PXL770 in In Vitro and In Vivo Models of X-Linked Adrenoleukodystrophy. The Journal of pharmacology and experimental therapeutics, 382(2), 208.

Xie H, et al. (2022) De novo assembly of human genome at single-cell levels. Nucleic acids research, 50(13), 7479.

Stojkovska I, et al. (2022) Rescue of ?-synuclein aggregation in Parkinson's patient neurons by synergistic enhancement of ER proteostasis and protein trafficking. Neuron, 110(3), 436.

Rusilowicz-Jones EV, et al. (2022) Benchmarking a highly selective USP30 inhibitor for enhancement of mitophagy and pexophagy. Life science alliance, 5(2).