Resource Summary Report

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Center for Inherited Disease Research

RRID:SCR_007339
Type: Tool

Proper Citation

Center for Inherited Disease Research (RRID:SCR_007339)

Resource Information

URL: http://www.cidr.jhmi.edu/

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Description: Next generation sequencing and genotyping services provided to investigators working to discover genes that contribute to disease. On-site statistical geneticists provide insight into analysis issues as they relate to study design, data production and quality control. In addition, CIDR has a consulting agreement with the University of Washington Genetics Coordinating Center (GCC) to provide statistical and analytical support, most predominantly in the areas of GWAS data cleaning and methods development. Completed studies encompass over 175 phenotypes across 530 projects and 620,000 samples. The impact is evidenced by over 380 peer-reviewed papers published in 100 journals. Three pathways exist to access the CIDR genotyping facility: * NIH CIDR Program: The CIDR contract is funded by 14 NIH Institutes and provides genotyping and statistical genetic services to investigators approved for access through competitive peer review. An application is required for projects supported by the NIH CIDR Program. * The HTS Facility: The High Throughput Sequencing Facility, part of the Johns Hopkins Genetic Resources Core Facility, provides next generation sequencing services to internal JHU investigators and external scientists on a fee-for-service basis. * The JHU SNP Center: The SNP Center, part of the Johns Hopkins Genetic Resources Core Facility, provides genotyping to internal JHU investigators and external scientists on a fee-for-service basis. Data computation service is included to cover the statistical genetics services provided for investigators seeking to identify genes that contribute to human disease. Human Genotyping Services include SNP Genome Wide Association Studies, SNP Linkage Scans, Custom SNP Studies, Cancer Panel, MHC Panels, and Methylation Profiling. Mouse Genotyping Services include SNP Scans and Custom SNP Studies.

Abbreviations: CIDR

Synonyms: CIDR - Center for Inherited Disease Research

Resource Type: data computation service, production service resource, resource, material analysis service, analysis service resource, training service resource, biomaterial analysis service, service resource

Keywords: gene, genome, array, custom, dna, genome wide association study, genotyping, genotyping service, linkage scan, methylation profiling, hereditary disease, single gene disorder, snp, statistical genetics, whole genome, whole exome, exome sequencing, high throughput sequencing, single nucleotide polymorphism, sequencing, disease

Related Condition: Aging

Funding: NHGRI ;
NCI ;
NEI ;
NIA ;
NIAAA ;
NIAMS ;
NICHD ;
NIDA ;
NIDCD ;
NIDCR ;
NIDDK ;
NIEHS ;
NIMH ;
NINDS ;
NHGRI N01-HG-65403;
US Department of Health and Human Services HHSN268200782096C;
S Department of Health and Human Services HHSN268201100011I;
S Department of Health and Human Services HHSN268201200008I;
NHGRI U01HG004438;
NHGRI U54HG006542

Resource Name: Center for Inherited Disease Research

Resource ID: SCR_007339

Alternate IDs: nif-0000-00223

Record Creation Time: 20220129T080241+0000

Record Last Update: 20260804T043320+0000

Ratings and Alerts

No rating or validation information has been found for Center for Inherited Disease Research .

No alerts have been found for Center for Inherited Disease Research .

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 206 mentions in open access literature.

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

Conry M, et al. (2026) Multiple myeloma risk linked to DNA damage response genes. Journal of hematology & oncology, 19(1), 10.

Liu D, et al. (2021) PRICKLE1 ?? FOCAD Interaction Revealed by Genome-Wide vQTL Analysis of Human Facial Traits. Frontiers in genetics, 12, 674642.

Liu D, et al. (2021) Impact of low-frequency coding variants on human facial shape. Scientific reports, 11(1), 748.

White JD, et al. (2021) Insights into the genetic architecture of the human face. Nature genetics, 53(1), 45.

Liu C, et al. (2021) Genome scans of facial features in East Africans and cross-population comparisons reveal novel associations. PLoS genetics, 17(8), e1009695.

Indencleef K, et al. (2021) The Intersection of the Genetic Architectures of Orofacial Clefts and Normal Facial Variation. Frontiers in genetics, 12, 626403.

Naqvi S, et al. (2021) Shared heritability of human face and brain shape. Nature genetics, 53(6), 830.

Pollard K, et al. (2020) A clinically and genomically annotated nerve sheath tumor biospecimen repository. Scientific data, 7(1), 184.

Orlova E, et al. (2019) Pilot GWAS of caries in African-Americans shows genetic heterogeneity. BMC oral health, 19(1), 215.

O'Reilly J, et al. (2018) The impact of common genetic variants in the mitochondrial glycine cleavage system on relevant metabolites. Molecular genetics and metabolism reports, 16, 20.

Klein AP, et al. (2018) Genome-wide meta-analysis identifies five new susceptibility loci for pancreatic cancer. Nature communications, 9(1), 556.

Zou LS, et al. (2018) BoostMe accurately predicts DNA methylation values in whole-genome bisulfite sequencing of multiple human tissues. BMC genomics, 19(1), 390.

Levy BR, et al. (2018) Positive age beliefs protect against dementia even among elders with high-risk gene. PloS one, 13(2), e0191004.

Huan T, et al. (2018) Age-associated microRNA expression in human peripheral blood is associated with all-cause mortality and age-related traits. Aging cell, 17(1).

Wang Z, et al. (2018) Multi-Omics Analysis Reveals a HIF Network and Hub Gene EPAS1 Associated with Lung Adenocarcinoma. EBioMedicine, 32, 93.

Roosenboom J, et al. (2018) Mapping genetic variants for cranial vault shape in humans. PloS one, 13(4), e0196148.

Mukhopadhyay N, et al. (2018) Identifying genetic risk loci for diabetic complications and showing evidence for heterogeneity of type 1 diabetes based on complications risk. PloS one, 13(2), e0192696.

Crist RC, et al. (2018) A polymorphism in the OPRM1 3'-untranslated region is associated with methadone efficacy in treating opioid dependence. The pharmacogenomics journal, 18(1), 173.

Teitelbaum AM, et al. (2018) Nicotine dependence is associated with functional variation in FMO3, an enzyme that metabolizes nicotine in the brain. The pharmacogenomics journal, 18(1), 136.

Duverger O, et al. (2018) Genetic variants in pachyonychia congenita-associated keratins increase susceptibility to tooth decay. PLoS genetics, 14(1), e1007168.