# Resource Summary Report

Generated by FDI Lab - SciCrunch.org on Apr 18, 2025

## 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/

**Proper Citation:** Center for Inherited Disease Research (RRID:SCR_007339)

**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, resource, biomaterial analysis service, service resource, material analysis service, training service resource, production service resource, analysis 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:** 20250418T055147+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 40 mentions in open access literature.

**Listed below are recent publications.** The full list is available at FDI Lab - SciCrunch.org.


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.

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

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.

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

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.

Cole JB, et al. (2016) Genomewide Association Study of African Children Identifies Association of SCHIP1 and PDE8A with Facial Size and Shape. PLoS genetics, 12(8), e1006174.

Ha NH, et al. (2016) The Circadian Rhythm Gene Arntl2 Is a Metastasis Susceptibility Gene for Estrogen Receptor-Negative Breast Cancer. PLoS genetics, 12(9), e1006267.

Druley TE, et al. (2016) Candidate gene resequencing to identify rare, pedigree-specific variants influencing healthy aging phenotypes in the long life family study. BMC geriatrics, 16, 80.

Younkin SG, et al. (2014) A genome-wide study of de novo deletions identifies a candidate locus for non-syndromic isolated cleft lip/palate risk. BMC genetics, 15, 24.

Hasstedt SJ, et al. (2013) Five linkage regions each harbor multiple type 2 diabetes genes in the African American subset of the GENNID Study. Journal of human genetics, 58(6), 378.

Wiener H, et al. (2013) Principal components of heritability from neurocognitive domains differ between families with schizophrenia and control subjects. Schizophrenia bulletin, 39(2), 464.

Cole JW, et al. (2012) Rare variants in ischemic stroke: an exome pilot study. PloS one, 7(4), e35591.

Lien YJ, et al. (2011) A genome-wide linkage scan for distinct subsets of schizophrenia characterized by age at onset and neurocognitive deficits. PloS one, 6(8), e24103.

Greenwood CM, et al. (2011) A genome-wide linkage study of mammographic density, a risk factor for breast cancer. Breast cancer research : BCR, 13(6), R132.

Hasstedt SJ, et al. (2011) Pleiotropy of type 2 diabetes with obesity. Journal of human genetics, 56(7), 491.

Wijsman EM, et al. (2011) Genome-wide association of familial late-onset Alzheimer's disease replicates BIN1 and CLU and nominates CUGBP2 in interaction with APOE. PLoS genetics, 7(2), e1001308.

Freedman BI, et al. (2011) Differential effects of MYH9 and APOL1 risk variants on FRMD3 Association with Diabetic ESRD in African Americans. PLoS genetics, 7(6), e1002150.