Resource Summary Report

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NIMH Repository and Genomics Resources (NRGR)

RRID:SCR_016318
Type: Tool

Proper Citation

NIMH Repository and Genomics Resources (NRGR) (RRID:SCR_016318)

Resource Information

URL: https://www.nimhgenetics.org/

Proper Citation: NIMH Repository and Genomics Resources (NRGR) (RRID:SCR_016318)

Description: Stores biosamples, genetic, pedigree and clinical data collected in designated NIMH-funded human subject studies. RGR database likewise links to other repositories holding data from same subjects, including dbGAP, GEO and NDAR. Allows to access these data and biospecimens (e.g., lymphoblastoid cell lines, induced pluripotent cell lines, fibroblasts) and further expand genetic and molecular characterization of patient populations with severe mental illness.

Abbreviations: NRGR, RGR

Synonyms: NRGR, Repository and Genomics Resources, NIMH, RGR

Resource Type: institution

Keywords: biosamples, genetic, pedigree, clinical, data

Funding: NIMH

Availability: Restricted

Resource Name: NIMH Repository and Genomics Resources (NRGR)

Resource ID: SCR_016318

Alternate IDs: grid.482687.7

Alternate URLs: https://ror.org/026dax180

Record Creation Time: 20220129T080330+0000

Record Last Update: 20260903T235334+0000

Ratings and Alerts

No rating or validation information has been found for NIMH Repository and Genomics Resources (NRGR).

No alerts have been found for NIMH Repository and Genomics Resources (NRGR).

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 29 mentions in open access literature.

Listed below are recent publications. The full list is available at kravitz2 .

Cirnigliaro M, et al. (2025) Common and rare variant genetic contributions in African Americans with autism. medRxiv : the preprint server for health sciences.

Kozlova A, et al. (2025) PICALM Alzheimer's risk allele causes aberrant lipid droplets in microglia. Nature, 646(8087), 1178.

Lu Z, et al. (2025) Substantia nigra related gene polymorphisms associated with antipsychotic-induced acute movement disorders: a genome-wide association study and multi-ancestry validation in schizophrenia. Military Medical Research, 12(1), 50.

Drago A, et al. (2024) Calcium Signaling and Molecular Adhesion Processes May Hold the Key to Genetic Risk for Autism: A Molecular Pathway Analysis on Two Independent Samples. Genes, 15(12).

Oliva V, et al. (2024) Polygenic scores of subcortical brain volumes as possible modulators of treatment response in depression. Neuroscience applied, 3, 103937.

Li K, et al. (2023) Racial differences in the major clinical symptom domains of bipolar disorder. International journal of bipolar disorders, 11(1), 17.

Garrison MA, et al. (2023) Genomic data resources of the Brain Somatic Mosaicism Network for neuropsychiatric diseases. Scientific data, 10(1), 813.

Crowley JJ, et al. (2023) Latin American Trans-ancestry INitiative for OCD genomics (LATINO): Study Protocol. medRxiv : the preprint server for health sciences.

Fanelli G, et al. (2022) A meta-analysis of polygenic risk scores for mood disorders, neuroticism, and schizophrenia in antidepressant response. European neuropsychopharmacology : the journal of the European College of Neuropsychopharmacology, 55, 86.

Khunsriraksakul C, et al. (2022) Integrating 3D genomic and epigenomic data to enhance target gene discovery and drug repurposing in transcriptome-wide association studies.

Nature communications, 13(1), 3258.

Gill PS, et al. (2021) Molecular Dysregulation in Autism Spectrum Disorder. Journal of personalized medicine, 11(9).

Elam JS, et al. (2021) The Human Connectome Project: A retrospective. NeuroImage, 244, 118543.

Chen X, et al. (2021) Artificial image objects for classification of schizophrenia with GWAS-selected SNVs and convolutional neural network. Patterns (New York, N.Y.), 2(8), 100303.

Chen J, et al. (2020) Polygenic Risk Scores for Subtyping of Schizophrenia. Schizophrenia research and treatment, 2020, 1638403.

Fabbri C, et al. (2020) A polygenic predictor of treatment-resistant depression using whole exome sequencing and genome-wide genotyping. Translational psychiatry, 10(1), 50.

Alexander-Bloch AF, et al. (2020) Imaging local genetic influences on cortical folding. Proceedings of the National Academy of Sciences of the United States of America, 117(13), 7430.

Rowe B, et al. (2019) Biological and practical implications of genome-wide association study of schizophrenia using Bayesian variable selection. NPJ schizophrenia, 5(1), 19.

Fang G, et al. (2019) Discovering genetic interactions bridging pathways in genome-wide association studies. Nature communications, 10(1), 4274.

Patowary A, et al. (2019) Family-based exome sequencing and case-control analysis implicate CEP41 as an ASD gene. Translational psychiatry, 9(1), 4.

Xavier RM, et al. (2018) Polygenic signal for symptom dimensions and cognitive performance in patients with chronic schizophrenia. Schizophrenia research. Cognition, 12, 11.