Resource Summary Report

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NIMH Repository and Genomics Resources

RRID:SCR_006698
Type: Tool

Proper Citation

NIMH Repository and Genomics Resources (RRID:SCR_006698)

Resource Information

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

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Description: Collaborative venture between the National Institute of Mental Health (NIMH) and several academic institutions. Repository facilitates psychiatric genetic research by providing patient and control samples and phenotypic data for wide-range of mental disorders and Stem Cells.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: NIMH: Center for Collaborative Genetic Studies, NIMH Human Genetics Initiative, NIMH Center for Genetic Studies, NIMH Genetics, Center for Collaborative Genomic Studies on Mental Disorders, NIMH Repository and Genomics Resources (NRGR)

Resource Type: institution

Keywords: biosamples, genetic, pedigree, clinical, data

Related Condition: Bipolar Disorder, Schizophrenia, Alzheimer's disease, Autism, Attention deficit-hyperactivity disorder, Depression, Control, Obsessive-Compulsive Disorder, Anorexia Nervosa, Relative, Mental disorder, Brain disorder, Relative

Funding: NIH Blueprint for Neuroscience Research ;
National Institute for Mental Health

Availability: Restricted

Resource Name: NIMH Repository and Genomics Resources

Resource ID: SCR_006698

Alternate IDs: grid.482687.7, nif-0000-00186, SCR_016318

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

Record Creation Time: 20220129T080237+0000

Record Last Update: 20250519T203445+0000

Ratings and Alerts

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

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

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 60 mentions in open access literature.

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

Zhou B, et al. (2024) Resolving the 22q11.2 deletion using CTLR-Seq reveals chromosomal rearrangement mechanisms and individual variance in breakpoints. Proceedings of the National Academy of Sciences of the United States of America, 121(31), e2322834121.

Chen X, et al. (2024) Classification of Schizophrenia, Bipolar Disorder and Major Depressive Disorder with Comorbid Traits and Deep Learning Algorithms. Research square.

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

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

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

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.

Fabbri C, et al. (2022) Imputed expression of schizophrenia-associated genes and cognitive measures in patients with schizophrenia. Molecular genetics & genomic medicine, 10(6), e1942.

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.

Shumake J, et al. (2021) Inclusion of genetic variants in an ensemble of gradient boosting decision trees does not improve the prediction of citalopram treatment response. Scientific reports, 11(1), 3780.

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

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

Konte B, et al. (2021) HLA-DQB1 6672G>C (rs113332494) is associated with clozapine-induced neutropenia and agranulocytosis in individuals of European ancestry. Translational psychiatry, 11(1), 214.

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.

Magri C, et al. (2021) Alterations observed in the interferon ? and ? signaling pathway in MDD patients are marginally influenced by cis-acting alleles. Scientific reports, 11(1), 727.

McPartland JC, et al. (2020) The Autism Biomarkers Consortium for Clinical Trials (ABC-CT): Scientific Context, Study Design, and Progress Toward Biomarker Qualification. Frontiers in integrative neuroscience, 14, 16.

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

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.

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.

Ali AT, et al. (2020) Analysis of mitochondrial m1A/G RNA modification reveals links to nuclear genetic variants and associated disease processes. Communications biology, 3(1), 147.

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.