Psychiatric Genomics Consortium

RRID:SCR_004495
Type: Tool

Proper Citation

Psychiatric Genomics Consortium (RRID:SCR_004495)

Resource Information

URL: https://www.med.unc.edu/pgc/

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Description: Consortium conducting meta-analyses of genome-wide genetic data for psychiatric disease. Focused on autism, attention-deficit hyperactivity disorder, bipolar disorder, major depressive disorder, schizophrenia, anorexia nervosa (AN), Tourette syndrome (TS), and obsessive-compulsive disorder (OCD). Used to investigate common single nucleotide polymorphisms (SNPs) genotyped on commercial arrays, structural variation (copy number variation) and uncommon or rare genetic variation. To participate you are asked to upload data from your study to central computer used by this consortium. Genetic Cluster Computer serves as data warehouse and analytical platform for this study. When data from your study have been incorporated, account will be provided on central server and access to all GWAS genotypes, phenotypes, and meta-analytic results relevant to deposited data and participation aims. NHGRI GWAS Catalog contains updated information about all GWAS in biomedicine, and is usually excellent starting point to find comprehensive list of studies. Files can be obtained by any PGC member for any disease to which they contributed data. These files can also be obtained by application to NIMH Genetics Repository. Individual-level genotype and phenotype data requires application, material transfer agreement, and informed consent consideration. Some datasets are also in controlled-access dbGaP and Wellcome Trust Case-Control Consortium repositories. PGC members can also receive back cleaned and imputed data and results for samples they contributed to PGC analyses.

Abbreviations: PGC

Synonyms: Psychiatric GWAS Consortium, PGC, Psychiatric Genomics Consortium

Resource Type: storage service resource, computational hosting, analysis service resource,
consortium, community building portal, service resource, data or information resource, data repository, production service resource, portal, organization portal, data analysis service

**Defining Citation:** PMID:20955924, PMID:19895722, PMID:19648536, PMID:19339359, PMID:19002139

**Keywords:** structural variation, genetic variation, single nucleotide polymorphism, attention deficit-hyperactivity disorder, bipolar disorder, schizophrenia, mental disease, one mind ptsd, data sharing, visualization, genome-wide association study, genomic, genotype, phenotype, psychiatry, gwas, copy number variation, FASEB list

**Related Condition:** Mental disease, Attention deficit-hyperactivity disorder, Bipolar Disorder, Schizophrenia, Major Depressive Disorder, Autism, Cross-disorder

**Funding Agency:** Netherlands Genetic Cluster Computer, Hersenstichting Nederland, NIMH

**Availability:** Restricted

**Resource Name:** Psychiatric Genomics Consortium

**Resource ID:** SCR_004495

**Alternate IDs:** nlx_143769

**Old URLs:** https://pgc.unc.edu/

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**Ratings and Alerts**

No rating or validation information has been found for Psychiatric Genomics Consortium.

No alerts have been found for Psychiatric Genomics Consortium.

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**Data and Source Information**

**Source:** SciCrunch Registry

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**Usage and Citation Metrics**

We found 74 mentions in open access literature.

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


Widomska J, et al. (2023) Molecular Landscape of Tourette’s Disorder. International journal
Shoham N, et al. (2023) Investigating the association between schizophrenia and distance visual acuity: Mendelian randomisation study. BJPsych open, 9(2), e33.


Yang A, et al. (2022) Longer screen time utilization is associated with the polygenic risk for Attention-deficit/hyperactivity disorder with mediation by brain white matter microstructure. EBioMedicine, 80, 104039.


Cao C, et al. (2022) webTWAS: a resource for disease candidate susceptibility genes identified by transcriptome-wide association study. Nucleic acids research, 50(D1), D1123-D1130.

Reus LM, et al. (2021) Gene Expression Imputation Across Multiple Tissue Types Provides Insight Into the Genetic Architecture of Frontotemporal Dementia and Its Clinical Subtypes. Biological psychiatry, 89(8), 825-835.

