

# Resource Summary Report

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## Genomic Datasharing

RRID:SCR\_005233

Type: Tool

### Proper Citation

Genomic Datasharing (RRID:SCR\_005233)

### Resource Information

**URL:** <http://gds.nih.gov/>

**Proper Citation:** Genomic Datasharing (RRID:SCR\_005233)

**Description:** NIH established expectations for sharing data obtained through NIH-funded genome-wide association studies (GWAS) with the implementation of the GWAS Policy. Information and resources related to the GWAS Policy can be found on this website.

**Abbreviations:** GDS

**Synonyms:** GWAS, Genome-Wide Association Studies

**Resource Type:** data or information resource, feed, narrative resource, standard specification, listserv

**Keywords:** genome-wide association study, genome, data sharing

**Funding:** NIH

**Resource Name:** Genomic Datasharing

**Resource ID:** SCR\_005233

**Alternate IDs:** OMICS\_00272

**Record Creation Time:** 20220129T080229+0000

**Record Last Update:** 20260810T040408+0000

### Ratings and Alerts

No rating or validation information has been found for Genomic Datasharing.

No alerts have been found for Genomic Datasharing.

## Data and Source Information

**Source:** [SciCrunch Registry](#)

## Usage and Citation Metrics

We found 5 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [NIF](#) .

Falk MJ, et al. (2015) Mitochondrial Disease Sequence Data Resource (MSeqDR): a global grass-roots consortium to facilitate deposition, curation, annotation, and integrated analysis of genomic data for the mitochondrial disease clinical and research communities. *Molecular genetics and metabolism*, 114(3), 388.

Lehner T, et al. (2015) Convergence of advances in genomics, team science, and repositories as drivers of progress in psychiatric genomics. *Biological psychiatry*, 77(1), 6.

Frank E, et al. (2015) All the world's a (clinical) stage: rethinking bipolar disorder from a longitudinal perspective. *Molecular psychiatry*, 20(1), 23.

Berger S, et al. (2015) Effectiveness of shrinkage and variable selection methods for the prediction of complex human traits using data from distantly related individuals. *Annals of human genetics*, 79(2), 122.

Paltoo DN, et al. (2014) Data use under the NIH GWAS data sharing policy and future directions. *Nature genetics*, 46(9), 934.