

Resource Summary Report

Generated by [PRECISE-TBI](#) on Aug 2, 2026

MedGen

RRID:SCR_000111

Type: Tool

Proper Citation

MedGen (RRID:SCR_000111)

Resource Information

URL: <http://www.ncbi.nlm.nih.gov/medgen/>

Proper Citation: MedGen (RRID:SCR_000111)

Description: A database of organized information related to human medical genetics, such as attributes of conditions with a genetic contribution.

Abbreviations: MedGen

Resource Type: data or information resource, database

Defining Citation: [PMID:32329672](#)

Keywords: medical genetics, medical, genetics, disease, clinical

Funding: NLM 1ZIHLM200888-05

Resource Name: MedGen

Resource ID: SCR_000111

Alternate IDs: nlx_156941, OMICS_01549

Record Creation Time: 20220129T080159+0000

Record Last Update: 20260801T190853+0000

Ratings and Alerts

No rating or validation information has been found for MedGen.

No alerts have been found for MedGen.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 6 mentions in open access literature.

Listed below are recent publications. The full list is available at [PRECISE-TBI](#) .

Hayman GT, et al. (2016) The Disease Portals, disease-gene annotation and the RGD disease ontology at the Rat Genome Database. Database : the journal of biological databases and curation, 2016.

Pratte-Santos R, et al. (2016) Analysis of chromosomal abnormalities by CGH-array in patients with dysmorphic and intellectual disability with normal karyotype. Einstein (Sao Paulo, Brazil), 14(1), 30.

Bornstein AT, et al. (2016) Tracking medical genetic literature through machine learning. Molecular genetics and metabolism, 118(4), 255.

Sayitoğlu M, et al. (2016) Clinical Interpretation of Genomic Variations. Turkish journal of haematology : official journal of Turkish Society of Haematology, 33(3), 172.

, et al. (2015) Database resources of the National Center for Biotechnology Information. Nucleic acids research, 43(Database issue), D6.

Landrum MJ, et al. (2014) ClinVar: public archive of relationships among sequence variation and human phenotype. Nucleic acids research, 42(Database issue), D980.