Resource Summary Report

Generated by NIF on Aug 13, 2026

Database of Genomic Variants

RRID:SCR_007000
Type: Tool

Proper Citation

Database of Genomic Variants (RRID:SCR_007000)

Resource Information

URL: http://dgv.tcag.ca/

Proper Citation: Database of Genomic Variants (RRID:SCR_007000)

Description: Collection of curated structural variation in the human genome. Catalogue of human genomic structural variation identified in healthy control samples for studies aiming to correlate genomic variation with phenotypic data. It is continuously updated with new data from peer reviewed research studies. The Database is no longer accepting direct submission of data as they are currently part of a collaboration with two new archival CNV databases at EBI and NCBI, called DGVa and dbVAR, respectively. One of the changes to DGV as part of this collaborative effort is that they will no longer be accepting direct submissions, but rather obtain the datasets from DGVa (short for DGV archive). This will ensure that the three databases are synchronized, and will allow for an official accessioning of variants.

Abbreviations: DGV

Synonyms: DGV, Database of Genomic Variants

Resource Type: data or information resource, database

Defining Citation: PMID:24174537

Keywords: genome, chromosome, control, deletion, structure, insertion, inversion, segmental duplication, structural variation, genomic variation, phenotype, copy number variation, indel, genetics, gene expression, chromosome abnormality, human genome, variation, dna, statistics, chromosome, FASEB list

Related Condition: Healthy, Control

Funding: Genome Canada ;
Ontario Genomics Institute ;
McLaughlin Centre ;

Canadian Institutes of Health Research

Availability: Acknowledgement requested

Resource Name: Database of Genomic Variants

Resource ID: SCR_007000

Alternate IDs: nif-0000-02721, OMICS_00266, r3d100010346

Alternate URLs: http://projects.tcag.ca/variation/, https://doi.org/10.17616/R3NC8H

Record Creation Time: 20220129T080239+0000

Record Last Update: 20260811T043300+0000

Ratings and Alerts

No rating or validation information has been found for Database of Genomic Variants.

No alerts have been found for Database of Genomic Variants.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 419 mentions in open access literature.

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

Mishra S, et al. (2026) Decoding Genetic Risk Factors in Recurrent Pregnancy Loss: An Integrative Chromosomal and??Bioinformatics Approach. Biochemical genetics.

Yu K, et al. (2026) Roles of insulin-like growth factor 1 receptor in growth regulation in 15q26 deletion and duplication syndrome. Biomedical reports, 24(6), 78.

Wang J, et al. (2026) Complex de novo tetrasomy and trisomy of 2p22.2 involving EIF2AK2 in a child with global developmental delay: a case report and literature review. Frontiers in pediatrics, 14, 1755339.

Zhao J, et al. (2025) Clinical features and genetic analysis of a family with t(5;9) (p15;p24) balanced translocation leading to Cri-du-chat syndrome in offspring. Frontiers in genetics, 16, 1550937.

Iacoviello M, et al. (2025) Junctional Epidermolysis Bullosa Caused by a Hemiallelic Nonsense Mutation in LAMA3 Revealed by 18q11.2 Microdeletion. International journal of molecular sciences, 26(15).

Moskvitin GD, et al. (2025) A familial case of interstitial deletion of the short arm of chromosome 6p22.3-p24.3 in twins with severe delay in psychomotor and speech development. Vavilovskii zhurnal genetiki i selektsii, 29(5), 644.

Jiang M, et al. (2025) Sequential prenatal diagnosis of fetal skeletal dysplasia: A cohort study. Acta obstetricia et gynecologica Scandinavica, 104(5), 860.

Mao B, et al. (2025) Congenital muscular dystrophies and myopathies: the leading cause of genetic muscular disorders in eleven Chinese families. BMC musculoskeletal disorders, 26(1), 51.

Long X, et al. (2025) CLPP Gene Variants Causing Perrault Syndrome Type 3 in Han Chinese Families: A Genotype-Phenotype Study. Human genomics, 19(1), 60.

Zhou M, et al. (2025) A copy number variation detection method based on OCSVM algorithm using multi strategies integration. Scientific reports, 15(1), 3526.

Molaei N, et al. (2025) Genetic spectrum among 2009 Iranian individuals with neuromuscular disorders using next generation sequencing and multiple ligation dependent probe amplification methods. Scientific reports, 15(1), 42736.

Xiao H, et al. (2025) A retrospective study for the diagnostic value of chromosomal microarray analysis in fetuses with high-risk prenatal indications. Frontiers in genetics, 16, 1649253.

Bencheikh BOA, et al. (2025) Novel germline and somatic variants in familial and sporadic meningioma genes. NPJ genomic medicine, 10(1), 41.

Kashevarova AA, et al. (2025) Delineation of the Genetic Architecture and Clinical Polymorphism of 3q29 Duplication Syndrome: A Review of the Literature and a Report of Two Novel Patients With Single-Gene BDH1 Duplications. Molecular genetics & genomic medicine, 13(1), e70047.

Wang Y, et al. (2025) Influence of copy number variation of unknown significance on the pregnancy outcomes. Scientific reports, 16(1), 4079.

Vimercati A, et al. (2025) Distinguishing Genetic Alterations Versus (Epi)Mutations in Silver-Russell Syndrome and Focus on the IGF1R Gene. The Journal of clinical endocrinology and metabolism, 110(4), e932.

Qin Y, et al. (2025) Prenatal diagnosis of fetuses with renal abnormalities: a retrospective analysis of 329 Chinese cases. Orphanet journal of rare diseases, 20(1), 486.

Bertini V, et al. (2025) 22q11.21 Deletions: A Review on the Interval Mediated by Low-Copy Repeats C and D. Genes, 16(1).

Shekfeh M, et al. (2025) Prevalence and impact of molecular variation in the three-prime repair exonuclease 1 TREX1 and its implications for oncology. Human genomics, 19(1), 73.

Zhang T, et al. (2025) CYTO-SV-ML: A Machine Learning Tool for Cytogenetic Structural Variant Analysis in Somatic Cell Type Using Genome Sequences. Life (Basel, Switzerland), 15(6).