

Resource Summary Report

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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: 20260801T190941+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 380 mentions in open access literature.

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

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.

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

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

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.

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.

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

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.

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

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.

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).

Vimercati A, et al. (2025) PEG10 loss of function causes Silver-Russell syndrome: a familial case with paternal deletion. *Scientific reports*, 15(1), 45070.

Bestetti I, et al. (2024) Long-read sequencing reveals chromothripsis in a molecularly unsolved case of Cornelia de Lange syndrome. *Frontiers in genetics*, 15, 1358334.

Peranzoni F, et al. (2024) 46 XX Ovotesticular Disorder of Sex Development with Gonadotropin-Releasing Hormone Receptor, Autosomal Recessive Heterozygous Missense Mutation and Autosomal Dominant Heterozygous Missense Mutation of the PROKR2 Gene: A Case Report. *Global medical genetics*, 11(3), 220.

Reshadmanesh A, et al. (2024) First Case of Macrocephaly, Dysmorphic Facies, and Psychomotor Retardation Harboring Co-inherited Variants in HERC1 and PMP22 Genes from Iran: Two Novel Variants. *Archives of Iranian medicine*, 27(12), 700.

Zhang F, et al. (2024) Prenatal diagnosis and family analysis of 17q12 microdeletion syndrome with fetal renal abnormalities. *Frontiers in genetics*, 15, 1401315.

De Bellis C, et al. (2024) Genomic, epigenomic and transcriptomic inter- and intra-tumor heterogeneity in desmoid tumors. *Clinical cancer research : an official journal of the American Association for Cancer Research*.

Yang L, et al. (2024) Efficiency of Non-Invasive Prenatal Testing in Detecting Fetal Copy Number Variation: A Retrospective Cohort Study. *International journal of women's health*, 16, 1661.

Cherubini A, et al. (2024) Exploring human pancreatic organoid modelling through single-cell RNA sequencing analysis. *Communications biology*, 7(1), 1527.

Chen Y, et al. (2024) Novel evidence of CNV deletion in KCTD13 related to the severity of isolated hypospadias in Chinese population. *Frontiers in pediatrics*, 12, 1409264.