Resource Summary Report

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Database of Genomic Variants Archive (DGVa)

RRID:SCR_004896
Type: Tool

Proper Citation

Database of Genomic Variants Archive (DGVa) (RRID:SCR_004896)

Resource Information

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

Proper Citation: Database of Genomic Variants Archive (DGVa) (RRID:SCR_004896)

Description: Public repository that accepts direct submissions and provides archiving, accessioning and distribution of publicly available genomic structural variants, in all species. Variants are accessioned at the study and sample level, granting stable identifiers that can be used in publications. DGVa data is integrated with other EBI resources, including comprehensive EBI search and Ensembl genome browser. Exchanges data with companion database, dbVar, at National Center for Biotechnology Information.NOTE: since 2019 DGVa doesn't accept submissions. Please send the data for submission to European Variation Archive (EVA).

Abbreviations: DGVa

Synonyms: , DGVarchive, DGVa, Database of Genomic Variants Archive

Resource Type: data or information resource, data repository, database, service resource, storage service resource

Defining Citation: PMID:23193291, PMID:24174537

Keywords: genome, dna, gene, expression, genetics, mapping, structural, variant, gold standard

Availability: Free, Freely available

Resource Name: Database of Genomic Variants Archive (DGVa)

Resource ID: SCR_004896

Alternate IDs: nlx_86626, r3d100010814

Alternate URLs: https://doi.org/10.17616/R3HK7Z

Old URLs: http://www.ebi.ac.uk/dgva/page.php, http://www.ebi.ac.uk/dgva/

Record Creation Time: 20220129T080227+0000

Record Last Update: 20260905T132526+0000

Ratings and Alerts

No rating or validation information has been found for Database of Genomic Variants Archive (DGVa).

No alerts have been found for Database of Genomic Variants Archive (DGVa).

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 211 mentions in open access literature.

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

Lee SS, et al. (2026) HER2 Positivity as a Prognostic Biomarker and Therapeutic Target in Advanced Biliary Tract Cancer: A Multi-institutional Analysis. Clinical cancer research : an official journal of the American Association for Cancer Research, 32(9), 1745.

Xu T, et al. (2026) Prenatal phenotypes and pregnancy outcomes of fetuses with recurrent 16p13.11 microduplications. Medicine, 105(23), e49059.

Zhang Y, et al. (2026) Prenatal diagnosis of distal Xq28 duplication syndrome: case reports and literature review. Molecular cytogenetics, 19(1).

Zhang Y, et al. (2026) Prenatal diagnosis of 9p distal deletion associated with subependymal cysts: A case report and literature review. Medicine, 105(16), e48420.

Saia F, et al. (2026) Genetic architecture and clinical features of Tourette syndrome in a child and adolescent cohort: an explorative clinical exome-based study. Frontiers in psychiatry, 17, 1744145.

Wang Y, et al. (2026) Detection and evaluation of copy number variation using both linked-read and short-read sequencing in New Zealand dairy cattle. Frontiers in genetics, 17, 1856199.

Galv??o JMS, et al. (2026) Genomic landscape of pediatric germ cell tumors reveals oncogenic mutations and copy number alterations. Frontiers in oncology, 16, 1689022.

La Monica I, et al. (2026) Clinical Insights into the Neurodevelopmental Impact of 16p CNVs in an Italian Clinical Cohort. Genes, 17(2).

Lazarczyk E, et al. (2026) Novel compound heterozygous FAM20C variants cause Raine syndrome - retrospective prenatal diagnosis and literature review. Orphanet journal of rare diseases, 21(1).

Deng Y, et al. (2025) Effective detection of 148 cases chromosomal mosaicism by karyotyping, chromosomal microarray analysis and QF-PCR in 32,967 prenatal diagnoses. BMC medical genomics, 18(1), 70.

Peng Y, et al. (2025) A cross-sectional study comparing machine learning and logistic regression techniques for predicting osteoporosis in a group at high risk of cardiovascular disease among old adults. BMC geriatrics, 25(1), 209.

Chen Y, et al. (2025) Detection of chromosomal and gene abnormality with karyotyping, chromosomal microarray analysis and trio-based whole exome sequencing in pregnancies with fetal growth restriction: implications for precise prenatal diagnosis. BMC pregnancy and childbirth, 25(1), 1067.

Wen L, et al. (2025) Clinical application of single nucleotide polymorphism array in prenatal diagnosis: Experience with 8753 samples. PloS one, 20(9), e0332424.

Zhang Y, et al. (2025) Genetic and clinical features of microcephaly in a prenatal cohort. BMC pregnancy and childbirth, 26(1), 65.

Yin Y, et al. (2025) A Prospective Evaluation of the Diagnostic Utility for Low-Coverage Genome Sequencing in Prenatal Samples: A Comparison With Chromosomal Microarray Analysis. Prenatal diagnosis, 45(12), 1525.

Ding F, et al. (2025) A rare variation of ERCC8 gene cause Cockayne syndrome in a Chinese family. Frontiers in genetics, 16, 1531832.

Zeng Z, et al. (2025) Clinical utility of trio whole exome sequencing in fetuses with ultrasound anomalies. Human genomics, 19(1), 37.

Mirabella F, et al. (2025) Exploring Copy Number Variants in a Cohort of Children Affected by ADHD: Clinical Investigation and Translational Insights. Genes, 16(9).

Tao Y, et al. (2025) Uncovering genetic contributors to developmental delay and intellectual disability: a focus on CNVs in pediatric patients. Frontiers in genetics, 16, 1539902.

Mohamed AM, et al. (2025) Deciphering copy number variations and gene implications in an Egyptian cohort with autism spectrum disorders. BMC medical genomics, 18(1), 190.