Resource Summary Report

Generated by RRID on Aug 5, 2026

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: storage service resource, data repository, service resource, database, data or information 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: 20260805T044114+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 145 mentions in open access literature.

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

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.

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

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.

Liu Y, et al. (2025) Parent-of-origin testing of prenatal copy number variations: a retrospective study of 167 family cases. Scientific reports, 15(1), 5979.

Zeng Y, et al. (2025) Prenatal genetic detection in foetus with gallbladder size anomalies: cohort study and systematic review of the literature. Annals of medicine, 57(1), 2440638.

Shi X, et al. (2025) Utility of whole exome sequencing in the evaluation of isolated fetal growth restriction in normal chromosomal microarray analysis. Annals of medicine, 57(1), 2476038.

Peng H, et al. (2025) Prenatal diagnosis of imprinted associated chromosome abnormalities identified by noninvasive prenatal testing (NIPT). Scientific reports, 15(1), 12830.

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.

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

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

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.

Pelgrims E, et al. (2025) The importance of intrafamilial cognitive phenotyping by the case of 22q11.2 deletion, 15q11.2 deletion, and families with inherited copy number variants of unknown significance. Journal of neurodevelopmental disorders, 17(1), 73.

Zhang M, et al. (2025) Incidental finding of a DMD exons 48-55 deletion during prenatal diagnosis. Frontiers in pediatrics, 13, 1541468.

Xie W, et al. (2025) Ultrasound and genetic findings in a case series of fetuses presenting vertebral defects. BMC pregnancy and childbirth, 25(1), 858.

Maeda K, et al. (2025) Copy Number Variations in a Case with Intractable Epilepsy, Intellectual Disability, and Hereditary Neuropathy with Liability to Pressure Palsies Having a 17p12 Deletion. Internal medicine (Tokyo, Japan), 64(19), 2897.

Haake J, et al. (2025) Chromosomal quality control in hPSCs: A practical guide to SNP array analysis with GenomeStudio. Frontiers in cell and developmental biology, 13, 1599923.

Li J, et al. (2025) Prenatal diagnostic value of medium-coverage WGS and clinical Exome sequencing in fetal congenital heart disease. Future science OA, 11(1), 2570035.

van Bever Y, et al. (2024) Genome-wide methylation analysis in patients with proximal hypospadias - a pilot study and review of the literature. Epigenetics, 19(1), 2392048.

??enk U, et al. (2024) Genetic background of high myopia in children. PloS one, 19(11), e0313121.

Yue F, et al. (2024) Prenatal diagnosis and pregnancy outcomes in fetuses with ventriculomegaly. Frontiers in medicine, 11, 1349171.