# 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, service resource, database, storage service resource, data repository

**Defining Citation:** PMID:23193291, PMID:24174537

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

**Funding:**

**Availability:** Free, Freely available

**Resource Name:** Database of Genomic Variants Archive (DGVa)

**Resource ID:** SCR_004896

**Alternate IDs:** nlx_86626

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

**Record Creation Time:** 20220129T080227+0000

**Record Last Update:** 20250521T061022+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 128 mentions in open access literature.

**Listed below are recent publications.** The full list is available at FDI Lab - SciCrunch.org.

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.

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

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.

Lu Q, et al. (2024) Prenatal chromosomal microarray analysis in a large Chinese cohort of fetuses with congenital heart defects: a single center study. Orphanet journal of rare diseases, 19(1), 307.

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

Yuan N, et al. (2024) Comprehensive assessment of long-read sequencing platforms and

calling algorithms for detection of copy number variation. Briefings in bioinformatics, 25(5).

Riedhammer KM, et al. (2024) Implication of transcription factor FOXD2 dysfunction in syndromic congenital anomalies of the kidney and urinary tract (CAKUT). Kidney international, 105(4), 844.

Fang X, et al. (2024) Exome sequencing confirms the clinical diagnosis of both joubert syndrome and klinefelter syndrome with keratoconus in a han Chinese family. Frontiers in genetics, 15, 1417584.

Xu Z, et al. (2024) Application of Chromosomal Microarray Analysis in Genetic Reasons of Miscarriage Tissues. The application of clinical genetics, 17, 85.

Zhang L, et al. (2024) Prenatal diagnosis in fetal right aortic arch using chromosomal microarray analysis and whole exome sequencing: a Chinese single-center retrospective study. Molecular cytogenetics, 17(1), 22.

Zhao Y, et al. (2024) Prenatal diagnosis and postnatal follow-up of 15 fetuses with 16p13.11 microduplication syndrome. Frontiers in genetics, 15, 1486974.

Xiao B, et al. (2024) Combining optical genome mapping and RNA-seq for structural variants detection and interpretation in unsolved neurodevelopmental disorders. Genome medicine, 16(1), 113.

Khan H, et al. (2024) Biallelic variants identified in 36 Pakistani families and trios with autism spectrum disorder. Scientific reports, 14(1), 9230.

Li H, et al. (2024) Chromosomal abnormalities detected by chromosomal microarray analysis and pregnancy outcomes of 4211 fetuses with high-risk prenatal indications. Scientific reports, 14(1), 15920.

Seo Y, et al. (2024) Two novel non-coding single nucleotide variants in the DNase1 hypersensitivity site of PRDM13 causing North Carolina macular dystrophy in Korea. Molecular vision, 30, 58.

Azidane S, et al. (2024) Identification of novel driver risk genes in CNV loci associated with neurodevelopmental disorders. HGG advances, 5(3), 100316.

Huang J, et al. (2024) Associations between genomic aberrations, increased nuchal translucency, and pregnancy outcomes: a comprehensive analysis of 2,272 singleton pregnancies in women under 35. Frontiers in medicine, 11, 1376319.

Amin AK, et al. (2024) 11p13 microduplication: a differential diagnosis of Silver-Russell syndrome? Molecular cytogenetics, 17(1), 5.

Alkhidir S, et al. (2024) The genetic basis and the diagnostic yield of genetic testing related to nonsyndromic hearing loss in Qatar. Scientific reports, 14(1), 4202.

Li W, et al. (2024) Case report: Second report of neuromuscular syndrome caused by biallelic variants in ASCC3. Frontiers in genetics, 15, 1382275.