Database of Genomic Variants Archive (DGVa)

RRID:SCR_004896
Type: Tool

Proper Citation

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Resource Information

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

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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, Database of Genomic Variants Archive, DGVa,

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

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)
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 79 mentions in open access literature.

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


Rraku E, et al. (2023) The phenotypic spectrum of terminal and subterminal 6p deletions based on a social media-derived cohort and literature review. Orphanet journal of rare diseases, 18(1), 68.

Niceta M, et al. (2023) Delineation of the clinical profile of CNOT2 haploinsufficiency and overview of the IDNADFS phenotype. Clinical genetics, 103(2), 156.

Wigle TJ, et al. (2023) DPYD Exon 4 Deletion Associated with Fluoropyrimidine Toxicity and Importance of Copy Number Variation. Current oncology (Toronto, Ont.), 30(1), 663.


Zhao J, et al. (2022) Expanding the mutational spectrum of Rahman syndrome: A rare disorder with severe intellectual disability and particular facial features in two Chinese patients. Molecular genetics & genomic medicine, 10(3), e1825.


Wen Q, et al. (2022) Distribution and transmission of copy number variations of uncertain significance in 105 trios. Molecular genetics & genomic medicine, 10(9), e2030.

Breuer K, et al. (2022) Exome sequencing in individuals with cardiovascular laterality defects
identifies potential candidate genes. European journal of human genetics : EJHG, 30(8), 946.