Resource Summary Report

Generated by RRID on Aug 5, 2026

dbVar

RRID:SCR_003219
Type: Tool

Proper Citation

dbVar (RRID:SCR_003219)

Resource Information

URL: http://www.ncbi.nlm.nih.gov/dbvar/

Proper Citation: dbVar (RRID:SCR_003219)

Description: Structural variation database designed to store data on variant DNA > / = 1 bp in size from all organisms. Associations of defined variants with phenotype information is also provided. Users can browse data containing number of variant cells from each study, and filter studies by organism, study type, method and genomic variant. Organisms include human, mouse, cattle and several additional animals.

Abbreviations: dbVar

Synonyms: dbVar, Database of Genomic Structural Variation, NCBI dbVar

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

Defining Citation: PMID:23193291

Keywords: structure, variation, structural variation, genetics, insertion, deletion, copy number variant, inversion, translocation, genomic imbalance, genotype, gene expression, dna, genomics, phenotype, genetic code

Availability: Free, Freely available

Resource Name: dbVar

Resource ID: SCR_003219

Alternate IDs: nlx_157217, r3d100010758

Alternate URLs: https://doi.org/10.17616/R3V610

Record Creation Time: 20220129T080217+0000

Record Last Update: 20260805T044051+0000

Ratings and Alerts

No rating or validation information has been found for dbVar.

No alerts have been found for dbVar.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 190 mentions in open access literature.

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

Quarello P, et al. (2026) DNA Methylation Episignature as a Novel Diagnostic Tool for Diamond-Blackfan Anemia Syndrome. American journal of hematology, 101(2), 228.

Gong T, et al. (2025) Rare pathogenic structural variants show potential to enhance prostate cancer germline testing for African men. Nature communications, 16(1), 2400.

Chen J, et al. (2025) Neonatal seizures associated with a rare familial 16p11.2 microduplication: A case report. The Journal of international medical research, 53(7), 3000605251358613.

Poriswanish N, et al. (2025) Multiple origins and phenotypic implications of an extended human pseudoautosomal region shown by analysis of the UK Biobank. American journal of human genetics, 112(4), 927.

Wang H, et al. (2025) Structural variation detection and association analysis of whole-genome-sequence data from 16,543 Alzheimer's disease sequencing project subjects. Alzheimer's & dementia : the journal of the Alzheimer's Association, 21(6), e70277.

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.

Ghorbani M, et al. (2025) Near-complete Middle Eastern genomes refine autozygosity and enhance disease-causing and population-specific variant discovery. Nature genetics, 57(5), 1119.

Sun T, et al. (2025) Impact of schizophrenia-associated risk genes on brain functional networks and executive deficits: a study of individuals with schizophrenia and genetic high risk. Psychological medicine, 55, e240.

Cheng S, et al. (2025) Constellation illuminates rare disease genetics. medRxiv : the preprint server for health sciences.

Tokac RH, et al. (2025) Cross-Sectional Analysis of Metabolic Tumor Burden Detected by F-18 FDG PET/CT and Circulating Tumor DNA in Advanced Breast Cancer. Cancer medicine, 14(16), e71049.

Rodrigues Alves Barbosa V, et al. (2024) Single variant, yet "double trouble": TSC and KBG syndrome because of a large de novo inversion. Life science alliance, 7(4).

Wang Z, et al. (2024) VarCards2: an integrated genetic and clinical database for ACMG-AMP variant-interpretation guidelines in the human whole genome. Nucleic acids research, 52(D1), D1478.

Hayes V, et al. (2024) Rare pathogenic structural variants show potential to enhance prostate cancer germline testing for African men. Research square.

Schrauwen I, et al. (2024) Optical genome mapping unveils hidden structural variants in neurodevelopmental disorders. Scientific reports, 14(1), 11239.

Ma Y, et al. (2024) Complete F9 Gene Deletion, Duplication, and Triplication Rearrangements: Implications for Factor IX Expression and Clinical Phenotypes. Thrombosis and haemostasis, 124(4), 374.

Järvelä I, et al. (2024) Heterogeneous genetic patterns in bilateral perisylvian polymicrogyria: insights from a Finnish family cohort. Brain communications, 6(3), fcae142.

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).

Guner Yilmaz B, et al. (2024) Rapid genome sequencing for critically ill infants: an inaugural pilot study from Turkey. Frontiers in pediatrics, 12, 1412880.

Wang Y, et al. (2024) Quantifying the regulatory potential of genetic variants via a hybrid sequence-oriented model with SVEN. Nature communications, 15(1), 10917.

Du H, et al. (2024) HMZDupFinder: a robust computational approach for detecting intragenic homozygous duplications from exome sequencing data. Nucleic acids research, 52(4), e18.