Resource Summary Report

Generated by PRECISE-TBI on Sep 8, 2026

dbVar

RRID:SCR_003219
Type: Tool

Proper Citation

dbVar (RRID:SCR_003219)

Resource Information

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

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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: data or information resource, data repository, database, service resource, storage service 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: 20260905T132459+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 198 mentions in open access literature.

Listed below are recent publications. The full list is available at PRECISE-TBI .

Ormond C, et al. (2026) BICEP: an extension to indels and copy number variants for rare variant prioritisation in pedigree analysis. bioRxiv : the preprint server for biology.

Savara J, et al. (2026) Multiplatform comparisons and annotation of structural variants highlight the utility of the T2T reference genome in human diagnostics. GigaScience, 15.

Kerkeni N, et al. (2026) First Detection of 1p36 Deletion by Whole-Exome Sequencing in a Tunisian Patient. Birth defects research, 118(1), e70017.

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).

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.

Zou XZ, et al. (2026) Phenome-wide analysis of copy number variants in 470,727 UK Biobank genomes. Nature, 652(8110), 675.

Di H, et al. (2026) Sequential sequencing reveals the architecture and complexity of genomic variants in patients with Alport syndrome. Nature communications, 17(1).

Perrone S, et al. (2025) How to Read a Next-Generation Sequencing Report for AML and MDS? What Hematologists Need to Know. Journal of clinical medicine, 14(24).

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.

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.

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.

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.

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.

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.

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.

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.

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.

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).

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.