Resource Summary Report

Generated by dkNET on Aug 5, 2026

CNVnator

RRID:SCR_010821
Type: Tool

Proper Citation

CNVnator (RRID:SCR_010821)

Resource Information

URL: http://sv.gersteinlab.org/cnvnator/

Proper Citation: CNVnator (RRID:SCR_010821)

Description: An approach to discover, genotype, and characterize typical and atypical CNVs from family and population genome sequencing.

Abbreviations: CNVnator

Resource Type: software resource

Resource Name: CNVnator

Resource ID: SCR_010821

Alternate IDs: OMICS_00343

Record Creation Time: 20220129T080300+0000

Record Last Update: 20260801T190358+0000

Ratings and Alerts

No rating or validation information has been found for CNVnator.

No alerts have been found for CNVnator.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 510 mentions in open access literature.

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

Garcia GL, et al. (2025) Aged and BRCA-Mutated Stromal Cells Drive Epithelial Cell Transformation. Cancer discovery, 15(6), 1203.

Hemara LM, et al. (2025) Genomic Biosurveillance of the Kiwifruit Pathogen Pseudomonas syringae pv. actinidiae Biovar 3 Reveals Adaptation to Selective Pressures in New Zealand Orchards. Molecular plant pathology, 26(2), e70056.

Hu L, et al. (2025) Regulating cellular metabolism and morphology to achieve high-yield synthesis of hyaluronan with controllable molecular weights. Nature communications, 16(1), 2076.

Ma W, et al. (2025) Whole-genome and whole-exome sequencing of Mayer-Rokitansky-Küster-Hauser syndrome-discordant monozygotic twins. Journal of assisted reproduction and genetics, 42(5), 1577.

Zhao M, et al. (2025) RNA sequencing and genome-wide association analysis reveal key genes responsible for different feather colors in Youjiang goose. Poultry science, 104(8), 105305.

Lindelöf H, et al. (2025) Genome sequencing in a cohort of 32 fetuses with genetic skeletal disorders. European journal of human genetics : EJHG, 33(11), 1474.

Marín-Garzón NA, et al. (2025) Detection and functional assessment of structural variants using whole-genome re-sequencing data in Nellore cattle. Scientific reports, 15(1), 30364.

Zhang Y, et al. (2025) Liquid crystal-guided DNA information storage: Nondestructive recovery and long-term preservation. Science advances, 11(39), eadu3957.

Xu J, et al. (2025) Clinical use of whole-genome sequencing in children with developmental delay or intellectual disability. BMC medical genomics, 18(1), 188.

Ye H, et al. (2025) Integrated chloroplast genomics and whole-genome resequencing reveals demographic history and selection signatures of black walnuts. The plant genome, 18(4), e70172.

Vani S, et al. (2025) Genome-wide copy number variation regions in indigenous (Bos indicus) cattle breeds of Tamil Nadu, India. Animal bioscience, 38(3), 395.

Mouton A, et al. (2025) Genetic and Anatomical Determinants of Olfaction in Dogs and Wild Canids. Molecular biology and evolution, 42(3).

Yang Y, et al. (2025) A De Novo Frameshift Variant in SMC1A Causes Non-Classic Cornelia de Lange Syndrome With Epilepsy: A Case Report and Literature Review. Molecular genetics & genomic medicine, 13(1), e70058.

De La Vega FM, et al. (2025) Benchmarking of germline copy number variant callers from whole genome sequencing data for clinical applications. Bioinformatics advances, 5(1), vbaf071.

Sugawara R, et al. (2025) A Pleiotropic and Functionally Divergent RAC3 Variant Disrupts Neurodevelopment and Impacts Organogenesis. Cells, 14(19).

Samano A, et al. (2025) Genome Structural Variants Shape Adaptive Success of an Invasive Urban Malaria Vector Anopheles stephensi. Molecular biology and evolution, 42(6).

Khor SS, et al. (2025) LILR genotype imputation with attribute bagging (LIBAG): leukocyte immunoglobulin-like receptor copy number imputation system. Frontiers in immunology, 16, 1559301.

Ehn E, et al. (2025) A de novo, mosaic and complex chromosome 21 rearrangement causes APP triplication and familial autosomal dominant early onset Alzheimer disease. Scientific reports, 15(1), 2912.

Behera S, et al. (2025) Comprehensive genome analysis and variant detection at scale using DRAGEN. Nature biotechnology, 43(7), 1177.

Zhang DF, et al. (2025) Prediction of mild cognitive impairment using blood multi-omics data. Frontiers in genetics, 16, 1552063.