# Resource Summary Report

Generated by RRID on Apr 17, 2025

# 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

**Funding:**

**Resource Name:** CNVnator

**Resource ID:** SCR_010821

**Alternate IDs:** OMICS_00343

**Record Creation Time:** 20220129T080300+0000

**Record Last Update:** 20250410T070023+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 458 mentions in open access literature.

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

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.

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.

Petrohilos C, et al. (2025) AMPed up immunity: 418 whole genomes reveal intraspecific diversity of koala antimicrobial peptides. Immunogenetics, 77(1), 11.

Hemara LM, et al. (2025) Identification and Characterization of Innate Immunity in Actinidia melanandra in Response to Pseudomonas syringae pv. actinidiae. Plant, cell & environment, 48(2), 1037.

Koponen L, et al. (2025) A deep intronic PHEX variant associated with X-linked hypophosphatemia in a Finnish family. JBMR plus, 9(2), ziae169.

Sapozhnikov DM, et al. (2024) Genetic confounds of transgenerational epigenetic inheritance in mice. Epigenetics, 19(1), 2318519.

Cuamatzi-Flores J, et al. (2024) Enhanced oxidative stress resistance in Ustilago maydis and its implications on the virulence. International microbiology : the official journal of the Spanish Society for Microbiology, 27(5), 1501.

Odrzywolski A, et al. (2024) Gollop-Wolfgang Complex Is Associated with a Monoallelic Variation in WNT11. Genes, 15(1).

Xiang X, et al. (2024) Populus cathayana genome and population resequencing provide insights into its evolution and adaptation. Horticulture research, 11(1), uhad255.

Muthusamy PV, et al. (2024) Hybrid de novo and haplotype-resolved genome assembly of Vechur cattle - elucidating genetic variation. Frontiers in genetics, 15, 1338224.

Tian S, et al. (2024) Evolutionary accumulation of FKS1 mutations from clinical echinocandin-resistant Candida auris. Emerging microbes & infections, 13(1), 2377584.

Ås J, et al. (2024) Whole genome case-control study of central nervous system toxicity due to antimicrobial drugs. PloS one, 19(2), e0299075.

Peers JA, et al. (2024) Tools for pathogen genetic surveillance: Lessons from the ash dieback invasion of Europe. PLoS pathogens, 20(5), e1012182.

Bloomfield M, et al. (2024) European Autism GEnomics Registry (EAGER): protocol for a multicentre cohort study and registry. BMJ open, 14(6), e080746.

Hirayasu K, et al. (2024) Identification of the hybrid gene LILRB5-3 by long-read sequencing and implication of its novel signaling function. Frontiers in immunology, 15, 1398935.

Karstensen JG, et al. (2024) Re-evaluating the genotypes of patients with adenomatous polyposis of unknown etiology: a nationwide study. European journal of human genetics : EJHG, 32(5), 588.

Wang X-Q, et al. (2024) Profiling the interplay and coevolution of Microcystis aeruginosa and cyanosiphophage Mic1. Microbiology spectrum, 12(6), e0029824.

Li-Bao L, et al. (2024) Regulation of Myc transcription by an enhancer cluster dedicated to pluripotency and early embryonic expression. Nature communications, 15(1), 3931.

Liu HK, et al. (2024) A Cysteinyl-tRNA Synthetase Mutation Causes Novel Autosomal-Dominant Inheritance of a Parkinsonism/Spinocerebellar-Ataxia Complex. Neuroscience bulletin, 40(10), 1489.

Chain FJJ, et al. (2024) Epigenetic diversity of genes with copy number variations among natural populations of the three-spined stickleback. Evolutionary applications, 17(7), e13753.