Resource Summary Report

Generated by dkNET on Apr 30, 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: 20250420T014510+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 dkNET.

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.

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

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.

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

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

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

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.

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

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.

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.

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

Al-Yazeedi T, et al. (2024) The contribution of an X chromosome QTL to non-Mendelian inheritance and unequal chromosomal segregation in Auanema freiburgense. Genetics, 227(1).

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.

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.