Resource Summary Report

Generated by dkNET on Apr 29, 2025

CNVer

RRID:SCR_010820
Type: Tool

Proper Citation

CNVer (RRID:SCR_010820)

Resource Information

URL: http://compbio.cs.toronto.edu/CNVer/

Proper Citation: CNVer (RRID:SCR_010820)

Description: A method for CNV detection that supplements the depth-of-coverage with paired-end mapping information, where matepairs mapping discordantly to the reference serve to indicate the presence of variation.

Abbreviations: CNVer

Resource Type: software resource

Keywords: bio.tools

Funding:

Resource Name: CNVer

Resource ID: SCR_010820

Alternate IDs: biotools:cnver, OMICS_00341

Alternate URLs: https://bio.tools/cnver

Record Creation Time: 20220129T080300+0000

Record Last Update: 20250420T014510+0000

Ratings and Alerts

No rating or validation information has been found for CNVer.

No alerts have been found for CNVer.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 8 mentions in open access literature.

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

Louw N, et al. (2023) Incorporating CNV analysis improves the yield of exome sequencing for rare monogenic disorders-an important consideration for resource-constrained settings. Frontiers in genetics, 14, 1277784.

Berlow NE, et al. (2020) Deep Functional and Molecular Characterization of a High-Risk Undifferentiated Pleomorphic Sarcoma. Sarcoma, 2020, 6312480.

Dharanipragada P, et al. (2018) iCopyDAV: Integrated platform for copy number variations-Detection, annotation and visualization. PloS one, 13(4), e0195334.

Girard SL, et al. (2016) Paternal Age Explains a Major Portion of De Novo Germline Mutation Rate Variability in Healthy Individuals. PloS one, 11(10), e0164212.

Pirooznia M, et al. (2015) Whole-genome CNV analysis: advances in computational approaches. Frontiers in genetics, 6, 138.

Liu L, et al. (2015) Identification of hallmarks of lung adenocarcinoma prognosis using whole genome sequencing. Oncotarget, 6(35), 38016.

Keane TM, et al. (2014) Identification of structural variation in mouse genomes. Frontiers in genetics, 5, 192.

Zhao M, et al. (2013) Computational tools for copy number variation (CNV) detection using next-generation sequencing data: features and perspectives. BMC bioinformatics, 14 Suppl 11(Suppl 11), S1.