Resource Summary Report

Generated by dkNET on May 18, 2025

RDXplorer

RRID:SCR_013290
Type: Tool

Proper Citation

RDXplorer (RRID:SCR_013290)

Resource Information

URL: http://rdxplorer.sourceforge.net/

Proper Citation: RDXplorer (RRID:SCR_013290)

Description: A computational tool for copy number variants (CNV) detection in whole human genome sequence data using read depth (RD) coverage.

Abbreviations: RDXplorer

Resource Type: software resource

Keywords: bio.tools

Funding:

Resource Name: RDXplorer

Resource ID: SCR_013290

Alternate IDs: biotools:RDXplorer, OMICS_00349

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

Record Creation Time: 20220129T080315+0000

Record Last Update: 20250420T014639+0000

Ratings and Alerts

No rating or validation information has been found for RDXplorer.

No alerts have been found for RDXplorer.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 7 mentions in open access literature.

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

Luo F, et al. (2019) A systematic evaluation of copy number alterations detection methods on real SNP array and deep sequencing data. BMC bioinformatics, 20(Suppl 25), 692.

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

Magi A, et al. (2017) XCAVATOR: accurate detection and genotyping of copy number variants from second and third generation whole-genome sequencing experiments. BMC genomics, 18(1), 747.

Xia LC, et al. (2016) A genome-wide approach for detecting novel insertion-deletion variants of mid-range size. Nucleic acids research, 44(15), e126.

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

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.