Resource Summary Report

Generated by nidm-terms on Jul 28, 2026

cnvHiTSeq

RRID:SCR_013160
Type: Tool

Proper Citation

cnvHiTSeq (RRID:SCR_013160)

Resource Information

URL: http://sourceforge.net/projects/cnvhitseq/

Proper Citation: cnvHiTSeq (RRID:SCR_013160)

Description: A set of Java-based command-line tools for detecting Copy Number Variants (CNVs) using next-generation sequencing data.

Abbreviations: cnvHiTSeq

Synonyms: cnvHiTSeq - A set of tools for detecting CNVs using sequencing data

Resource Type: commercial organization, software resource

Defining Citation: PMID:23259578

Keywords: matlab

Availability: Commercial license

Resource Name: cnvHiTSeq

Resource ID: SCR_013160

Alternate IDs: OMICS_00342

Record Creation Time: 20220129T080314+0000

Record Last Update: 20260728T043421+0000

Ratings and Alerts

No rating or validation information has been found for cnvHiTSeq.

No alerts have been found for cnvHiTSeq.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 4 mentions in open access literature.

Listed below are recent publications. The full list is available at nidm-terms .

De T, et al. (2021) Signatures of TSPAN8 variants associated with human metabolic regulation and diseases. iScience, 24(8), 102893.

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

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

Bellos E, et al. (2012) cnvHiTSeq: integrative models for high-resolution copy number variation detection and genotyping using population sequencing data. Genome biology, 13(12), R120.