

# Resource Summary Report

Generated by [dkNET](#) on Aug 11, 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:** 20260808T190618+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 [dkNET](#) .

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.