Resource Summary Report

Generated by NIF on Apr 18, 2025

cnvCapSeq

RRID:SCR_012126
Type: Tool

Proper Citation

cnvCapSeq (RRID:SCR_012126)

Resource Information

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

Proper Citation: cnvCapSeq (RRID:SCR_012126)

Description: Software for accurate and sensitive CNV discovery and genotyping in long-range targeted resequencing.

Resource Type: software resource

Defining Citation: PMID:25228465

Keywords: standalone software, java

Funding:

Availability: GNU Lesser General Public License

Resource Name: cnvCapSeq

Resource ID: SCR_012126

Alternate IDs: OMICS_05722

Record Creation Time: 20220129T080308+0000

Record Last Update: 20250410T070230+0000

Ratings and Alerts

No rating or validation information has been found for cnvCapSeq.

No alerts have been found for cnvCapSeq.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 2 mentions in open access literature.

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

Kumar V, et al. (2022) Variation in CFHR3 determines susceptibility to meningococcal disease by controlling factor H concentrations. American journal of human genetics, 109(9), 1680.

Zare F, et al. (2017) An evaluation of copy number variation detection tools for cancer using whole exome sequencing data. BMC bioinformatics, 18(1), 286.