Resource Summary Report

Generated by NIF on Aug 19, 2026

CopySeq

RRID:SCR_010758
Type: Tool

Proper Citation

CopySeq (RRID:SCR_010758)

Resource Information

URL: http://www.embl.de/~korbel/CopySeq/

Proper Citation: CopySeq (RRID:SCR_010758)

Description: A computational tool that analyzes the depth-of-coverage of high-throughput DNA sequencing reads, and can integrate paired-end and breakpoint junction analysis based CNV-analysis approaches, to infer locus copy-number genotypes.

Abbreviations: CopySeq

Resource Type: software resource

Defining Citation: PMID:21085617

Keywords: java, bio.tools

Resource Name: CopySeq

Resource ID: SCR_010758

Alternate IDs: biotools:copyseq, OMICS_00055

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

Record Creation Time: 20220129T080300+0000

Record Last Update: 20260815T182407+0000

Ratings and Alerts

No rating or validation information has been found for CopySeq.

No alerts have been found for CopySeq.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 1 mentions in open access literature.

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

Zichner T, et al. (2013) Impact of genomic structural variation in Drosophila melanogaster based on population-scale sequencing. Genome research, 23(3), 568.