Resource Summary Report

Generated by PRECISE-TBI on Aug 1, 2026

Magnolya

RRID:SCR_000164
Type: Tool

Proper Citation

Magnolya (RRID:SCR_000164)

Resource Information

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

Proper Citation: Magnolya (RRID:SCR_000164)

Description: A software which enables copy number variation (CNV) detections without using a reference genome. Magnolya directly compares the two next-generation sequences datasets.

Resource Type: software resource, software application, data analytics software

Defining Citation: PMID:23047563

Keywords: algorithm, copy number, next-generation, reference genome, dataset comparison

Availability: Free, Available for download, Freely available

Resource Name: Magnolya

Resource ID: SCR_000164

Alternate IDs: OMICS_00347

Record Creation Time: 20220129T080159+0000

Record Last Update: 20260801T042451+0000

Ratings and Alerts

No rating or validation information has been found for Magnolya.

No alerts have been found for Magnolya.

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 PRECISE-TBI .

Louw N, et al. (2023) Incorporating CNV analysis improves the yield of exome sequencing for rare monogenic disorders-an important consideration for resource-constrained settings. Frontiers in genetics, 14, 1277784.

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.