Resource Summary Report

Generated by PRECISE-TBI on Sep 18, 2026

CNAseg

RRID:SCR_010817
Type: Tool

Proper Citation

CNAseg (RRID:SCR_010817)

Resource Information

URL: http://www.compbio.group.cam.ac.uk/software/cnaseg/

Proper Citation: CNAseg (RRID:SCR_010817)

Description: A novel framework for the identification of CNA events that uses flowcell-to-flowcell variability to estimate the false positive rate and the depth of coverage to finalize copy number calls.

Abbreviations: CNAseg

Resource Type: software resource

Resource Name: CNAseg

Resource ID: SCR_010817

Alternate IDs: OMICS_00337

Record Creation Time: 20220129T080300+0000

Record Last Update: 20260912T195724+0000

Ratings and Alerts

No rating or validation information has been found for CNAseg.

No alerts have been found for CNAseg.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 3 mentions in open access literature.

Listed below are recent publications. The full list is available at PRECISE-TBI .

Nigam A, et al. (2019) Impact of next generation sequencing on our understanding of CAKUT. Seminars in cell & developmental biology, 91, 104.

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

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.