Resource Summary Report

Generated by NIF on Aug 30, 2026

rSW-seq

RRID:SCR_010825
Type: Tool

Proper Citation

rSW-seq (RRID:SCR_010825)

Resource Information

URL: http://compbio.med.harvard.edu/Supplements/BMCBioinfo10-2.html

Proper Citation: rSW-seq (RRID:SCR_010825)

Description: Designed to identify CNVs between two genomes.

Abbreviations: rSW-seq

Resource Type: software resource

Defining Citation: PMID:20718989

Resource Name: rSW-seq

Resource ID: SCR_010825

Alternate IDs: OMICS_00351

Record Creation Time: 20220129T080300+0000

Record Last Update: 20260829T182338+0000

Ratings and Alerts

No rating or validation information has been found for rSW-seq.

No alerts have been found for rSW-seq.

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 NIF .

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.

Duan J, et al. (2013) Comparative studies of copy number variation detection methods for next-generation sequencing technologies. PloS one, 8(3), e59128.

Klambauer G, et al. (2012) cn.MOPS: mixture of Poissons for discovering copy number variations in next-generation sequencing data with a low false discovery rate. Nucleic acids research, 40(9), e69.

Malone JH, et al. (2012) Mediation of Drosophila autosomal dosage effects and compensation by network interactions. Genome biology, 13(4), r28.