Resource Summary Report

Generated by Kravitz on Sep 10, 2026

Wessim

RRID:SCR_002567
Type: Tool

Proper Citation

Wessim (RRID:SCR_002567)

Resource Information

URL: http://sak042.github.io/Wessim/

Proper Citation: Wessim (RRID:SCR_002567)

Description: Software simulator for a targeted resequencing generally known as exome sequencing. Wessim generates a set of artificial DNA fragments for next generation sequencing (NGS) read simulation.

Resource Type: data analysis software, data processing software, sequence analysis software, simulation software, software application, software resource

Defining Citation: PMID:23413434

Keywords: resequencing simulator, artificial dna fragments, exome sequencing, next generation sequencing, ngs, python

Availability: Free, Available for download, Freely available

Resource Name: Wessim

Resource ID: SCR_002567

Alternate IDs: OMICS_00259

Record Creation Time: 20220129T080214+0000

Record Last Update: 20260905T132955+0000

Ratings and Alerts

No rating or validation information has been found for Wessim.

No alerts have been found for Wessim.

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 Kravitz .

Kong J, et al. (2017) ExCNVSS: A Noise-Robust Method for Copy Number Variation Detection in Whole Exome Sequencing Data. BioMed research international, 2017, 9631282.

Hofmann AL, et al. (2017) Detailed simulation of cancer exome sequencing data reveals differences and common limitations of variant callers. BMC bioinformatics, 18(1), 8.

Bohnert R, et al. (2017) Comprehensive benchmarking of SNV callers for highly admixed tumor data. PloS one, 12(10), e0186175.