

# Resource Summary Report

Generated by [ASWG](#) on Aug 26, 2026

## Wessim

RRID:SCR\_002567

Type: Tool

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### Proper Citation

Wessim (RRID:SCR\_002567)

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### 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:** 20260821T193645+0000

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### 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](#)

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## Usage and Citation Metrics

We found 3 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [ASWG](#) .

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.

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

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.