

# Resource Summary Report

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## Shimmer

RRID:SCR\_001164

Type: Tool

### Proper Citation

Shimmer (RRID:SCR\_001164)

### Resource Information

**URL:** <https://github.com/nhansen/Shimmer>

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**Description:** Software package that detects somatic single-nucleotide variants using statistical hypothesis testing with multiple testing correction. It uses Fisher's exact test along with multiple testing correction (Benjamini-Hochberg) to find significant differences between allele composition with a specified false discovery rate.

**Resource Type:** software resource

**Defining Citation:** [PMID:23620360](#)

**Keywords:** standalone software, bam

**Availability:** Free, Available for download, Freely available

**Resource Name:** Shimmer

**Resource ID:** SCR\_001164

**Alternate IDs:** OMICS\_03612

**Record Creation Time:** 20220129T080205+0000

**Record Last Update:** 20260815T182153+0000

### Ratings and Alerts

No rating or validation information has been found for Shimmer.

No alerts have been found for Shimmer.

### Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We have not found any literature mentions for this resource.