

# Resource Summary Report

Generated by [RRID](#) on Aug 2, 2026

## SWIPE

RRID:SCR\_012771

Type: Tool

### Proper Citation

SWIPE (RRID:SCR\_012771)

### Resource Information

**URL:** <https://github.com/torognes/swipe>

**Proper Citation:** SWIPE (RRID:SCR\_012771)

**Description:** A software tool for performing rapid local alignment searches in amino acid or nucleotide sequence databases.

**Abbreviations:** SWIPE

**Synonyms:** Smith-Waterman database searches with inter-sequence SIMD parallelisation

**Resource Type:** software resource

**Defining Citation:** [PMID:21631914](#)

**Resource Name:** SWIPE

**Resource ID:** SCR\_012771

**Alternate IDs:** OMICS\_00998

**Record Creation Time:** 20220129T080312+0000

**Record Last Update:** 20260801T190451+0000

### Ratings and Alerts

No rating or validation information has been found for SWIPE.

No alerts have been found for SWIPE.

### Data and Source Information

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

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## Usage and Citation Metrics

We found 2 mentions in open access literature.

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

Zong P, et al. (2024) TSTA: thread and SIMD-based trapezoidal pairwise/multiple sequence-alignment method. GigaByte (Hong Kong, China), 2024, gigabyte141.

Chen LY, et al. (2022) Phylogenomic Analyses of Alismatales Shed Light into Adaptations to Aquatic Environments. Molecular biology and evolution, 39(5).