

Resource Summary Report

Generated by [PRECISE-TBI](#) on Sep 19, 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: 20260912T195752+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](#)

Usage and Citation Metrics

We found 3 mentions in open access literature.

Listed below are recent publications. The full list is available at [PRECISE-TBI](#) .

Bonab RR, et al. (2025) SW-actors: accelerating the Smith-Waterman algorithm via actors. Bioinformatics advances, 5(1), vbaf173.

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).