

Resource Summary Report

Generated by [kravitz2](#) on Sep 5, 2026

PARASAIL

RRID:SCR_021805

Type: Tool

Proper Citation

PARASAIL (RRID:SCR_021805)

Resource Information

URL: <https://github.com/jeffdaily/parasail>

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Description: Software tool as multiple sequence alignment for global, local and semi global alignments.

Synonyms: Pairwise Sequence Alignment Library

Resource Type: alignment software, data processing software, image analysis software, software application, software resource

Defining Citation: [DOI:10.1186/s12859-016-0930-z](https://doi.org/10.1186/s12859-016-0930-z)

Keywords: multiple sequence alignment, global alignments, local alignments, semi global alignments,

Funding: Pacific Northwest National Laboratory

Availability: Free, Available for download, Freely available

Resource Name: PARASAIL

Resource ID: SCR_021805

Alternate URLs: <https://sources.debian.org/src/libparasail-dev/>

License: Battelle BSD-style

License URLs: <https://github.com/jeffdaily/parasail/blob/master/LICENSE.md>

Record Creation Time: 20220129T080357+0000

Record Last Update: 20260903T235726+0000

Ratings and Alerts

No rating or validation information has been found for PARASAIL.

No alerts have been found for PARASAIL.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 4 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

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

Luo H, et al. (2025) Large-Scale T-cell Receptor Repertoire Profiling Unveils Tumor-Specific Signals for Diagnosing Indeterminate Pulmonary Nodules. Cancer research, 85(24), 5141.

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

Vanni C, et al. (2022) Unifying the known and unknown microbial coding sequence space. eLife, 11.