Resource Summary Report

Generated by NIF on Apr 26, 2025

PARASAIL

RRID:SCR_021805
Type: Tool

Proper Citation

PARASAIL (RRID:SCR_021805)

Resource Information

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

Proper Citation: PARASAIL (RRID:SCR_021805)

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

Synonyms: Pairwise Sequence Alignment Library

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

Defining Citation: DOI:10.1186/s12859-016-0930-z

Keywords: multiple sequence alignement, 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: 20250426T060828+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 2 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

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.