

# Resource Summary Report

Generated by [PRECISE-TBI](#) on Aug 2, 2026

## JAligner

RRID:SCR\_024050

Type: Tool

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### Proper Citation

JAligner (RRID:SCR\_024050)

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### Resource Information

**URL:** <https://github.com/ahmedmoustafa/JAligner>

**Proper Citation:** JAligner (RRID:SCR\_024050)

**Description:** Open source software Java implementation of the Needleman?Wunsch and Smith-Waterman algorithms for biological pairwise sequence alignment with the affine gap penalty model.

**Synonyms:** jaligner

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

**Keywords:** Java, pairwise sequence alignment, affine gap penalty model,

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

**Resource Name:** JAligner

**Resource ID:** SCR\_024050

**Alternate IDs:** OMICS\_20021

**Alternate URLs:** <https://sources.debian.org/src/jaligner/>

**License:** GPL-2.0 license

**Record Creation Time:** 20230824T050211+0000

**Record Last Update:** 20260803T040842+0000

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### Ratings and Alerts

No rating or validation information has been found for JAligner.

No alerts have been found for JAligner.

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## 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.