

# Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 2026

## POA

RRID:SCR\_024172

Type: Tool

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### Proper Citation

POA (RRID:SCR\_024172)

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### Resource Information

**URL:** <https://sourceforge.net/projects/poamsa/>

**Proper Citation:** POA (RRID:SCR\_024172)

**Description:** Software application for multiple sequence alignment in bioinformatics. Has superior ability to handle branching / indels in the alignment.

**Synonyms:** poa, Partial Order Alignment

**Resource Type:** software library, software resource, software toolkit

**Defining Citation:** [DOI:10.1093/bioinformatics/bth126](https://doi.org/10.1093/bioinformatics/bth126)

**Keywords:** sequence alignment, multiple sequence alignment, handle branching in alignment, handle indels in alignment,

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

**Resource Name:** POA

**Resource ID:** SCR\_024172

**Alternate IDs:** OMICS\_14254

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

**License:** GNU General Public License version 2.0 (GPLv2)

**Record Creation Time:** 20230824T050212+0000

**Record Last Update:** 20260905T133105+0000

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### Ratings and Alerts

No rating or validation information has been found for POA.

No alerts have been found for POA.

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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.