# **Resource Summary Report**

Generated by FDI Lab - SciCrunch.org on Apr 16, 2025

# POA

RRID:SCR 024172

Type: Tool

### **Proper Citation**

POA (RRID:SCR\_024172)

#### 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 toolkit, software resource

**Defining Citation:** DOI:10.1093/bioinformatics/bth126

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

alignment, handle indels in alignment,

**Funding:** 

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:** 20250416T063958+0000

### Ratings and Alerts

No rating or validation information has been found for POA.

No alerts have been found for POA.

### **Data and Source Information**

Source: SciCrunch Registry

## **Usage and Citation Metrics**

We have not found any literature mentions for this resource.