

Resource Summary Report

Generated by [RRID](#) on Aug 2, 2026

ProDA

RRID:SCR_024171

Type: Tool

Proper Citation

ProDA (RRID:SCR_024171)

Resource Information

URL: <http://proda.stanford.edu/>

Proper Citation: ProDA (RRID:SCR_024171)

Description: Software for multiple alignment of protein sequences with repeated and shuffled elements.Used for automated detection and alignment of homologous regions in collections of proteins with arbitrary domain architectures.

Synonyms: proda

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

Defining Citation: [DOI:10.1093/nar/gkl511](https://doi.org/10.1093/nar/gkl511)

Keywords: sequence alignment, protein sequences, protein sequences multiple alignment, repeated sequences, shuffled elements,

Availability: Free, Available for download, Freely available,

Resource Name: ProDA

Resource ID: SCR_024171

Alternate IDs: OMICS_21692

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

Record Creation Time: 20230824T050212+0000

Record Last Update: 20260801T190800+0000

Ratings and Alerts

No rating or validation information has been found for ProDA.

No alerts have been found for ProDA.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We have not found any literature mentions for this resource.