# **Resource Summary Report**

Generated by NIF on Apr 22, 2025

# <u>Aline</u>

RRID:SCR\_016886 Type: Tool

**Proper Citation** 

Aline (RRID:SCR\_016886)

#### **Resource Information**

URL: http://www.bondxray.org/software/aline.html

Proper Citation: Aline (RRID:SCR\_016886)

**Description:** Software interactive perl/tk application which can read common sequence alignment formats which the user can then alter, embellish, markup etc to produce the kind of sequence figure commonly found in biochemical articles. Extensible WYSIWYG protein sequence alignment editor for publication quality figures.

Resource Type: software resource, software application

Defining Citation: PMID:19390156

**Keywords:** protein, sequence, alignment, editor, publication, quality, alter, embellish, markup, biochemistry, bioinformatics

**Funding:** 

Availability: Free, Available for download, Freely available

Resource Name: Aline

Resource ID: SCR\_016886

Record Creation Time: 20220129T080332+0000

Record Last Update: 20250421T054139+0000

**Ratings and Alerts** 

No rating or validation information has been found for Aline.

No alerts have been found for Aline.

## Data and Source Information

Source: <u>SciCrunch Registry</u>

### **Usage and Citation Metrics**

We found 2 mentions in open access literature.

Listed below are recent publications. The full list is available at <u>NIF</u>.

Gabrielsen M, et al. (2019) Identification and Characterization of Mutations in Ubiquitin Required for Non-covalent Dimer Formation. Structure (London, England : 1993), 27(9), 1452.

Rack JGM, et al. (2018) (ADP-ribosyl)hydrolases: Structural Basis for Differential Substrate Recognition and Inhibition. Cell chemical biology, 25(12), 1533.