

Resource Summary Report

Generated by [Kravitz](#) on Sep 15, 2026

Aline

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 application, software resource

Defining Citation: [PMID:19390156](#)

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

Availability: Free, Available for download, Freely available

Resource Name: Aline

Resource ID: SCR_016886

Record Creation Time: 20220129T080332+0000

Record Last Update: 20260912T200254+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: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 2 mentions in open access literature.

Listed below are recent publications. The full list is available at [Kravitz](#) .

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.