

Resource Summary Report

Generated by [kravitz2](#) on Sep 4, 2026

Bio-Tools-Run-Alignment-Clustalw

RRID:SCR_024067

Type: Tool

Proper Citation

Bio-Tools-Run-Alignment-Clustalw (RRID:SCR_024067)

Resource Information

URL: <https://metacpan.org/dist/Bio-Tools-Run-Alignment-Clustalw>

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Description: Software package for performing multiple sequence alignment from set of unaligned sequences and/or sub-alignments by means of the clustalw program.

Synonyms: libbio-tools-run-alignment-clustalw-perl, Bio-Tools-Run-Alignment-Clustalw - Object for the calculation of a multiple sequence alignment from a set of unaligned sequences or alignments using the Clustalw program

Resource Type: software resource, software toolkit

Keywords: performing multiple sequence alignment, set of unaligned sequences,

Availability: Free, Available for download, Freely available,

Resource Name: Bio-Tools-Run-Alignment-Clustalw

Resource ID: SCR_024067

Alternate URLs: <https://sources.debian.org/src/libbio-tools-run-alignment-clustalw-perl/>

License: perl_5

Record Creation Time: 20230824T050211+0000

Record Last Update: 20260904T000026+0000

Ratings and Alerts

No rating or validation information has been found for Bio-Tools-Run-Alignment-Clustalw.

No alerts have been found for Bio-Tools-Run-Alignment-Clustalw.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We have not found any literature mentions for this resource.