StatAlign
RRID:SCR_001892
Type: Tool

Proper Citation

StatAlign (RRID:SCR_001892)

Resource Information

URL: http://statalign.github.io/

Proper Citation: StatAlign (RRID:SCR_001892)

Description: Software package for Bayesian analysis of protein, DNA and RNA sequences. It utilizes multiple alignments, phylogenetic trees and evolutionary parameters to quantify uncertainty in these analyses. It is written in Java.

Synonyms: StatAlign 2.0

Resource Type: software resource, data processing software, sequence analysis software, data analysis software, software application

Defining Citation: PMID:23335014

Keywords: software package, bayesian, protein, dna, rna, sequencing, java, bio.tools

Availability: Open source

Resource Name: StatAlign

Resource ID: SCR_001892

Alternate IDs: OMICS_03743, biotools:StatAlign

Alternate URLs: https://bio.tools/StatAlign

Ratings and Alerts
No rating or validation information has been found for StatAlign.

No alerts have been found for StatAlign.

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**Data and Source Information**

**Source:** SciCrunch Registry

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**Usage and Citation Metrics**

We found 1 mentions in open access literature.

**Listed below are recent publications.** The full list is available at RRID.