Resource Summary Report

Generated by dkNET on May 19, 2025

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 application, data analysis software, data processing software, sequence analysis software, software resource

Defining Citation: PMID:23335014

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

Funding:

Availability: Open source

Resource Name: StatAlign

Resource ID: SCR_001892

Alternate IDs: biotools:StatAlign, OMICS_03743

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

Record Creation Time: 20220129T080210+0000

Record Last Update: 20250517T055512+0000

Ratings and Alerts

No rating or validation information has been found for StatAlign.

No alerts have been found for StatAlign.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 1 mentions in open access literature.

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

Christensen AB, et al. (2015) Phylogeny of Echinoderm Hemoglobins. PloS one, 10(8), e0129668.