

Resource Summary Report

Generated by [nidm-terms](#) on Sep 21, 2026

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

Defining Citation: [PMID:23335014](#)

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

Availability: Free, Available for download, Freely available

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: 20260919T195504+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 [nidm-terms](#) .

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