

Resource Summary Report

Generated by [PRECISE-TBI](#) on Aug 31, 2026

[multiAlignFree](#)

RRID:SCR_013188

Type: Tool

Proper Citation

multiAlignFree (RRID:SCR_013188)

Resource Information

URL: <http://www-rcf.usc.edu/~fsun/Programs/multiAlignFree/multiAlignFreemain.html>

Proper Citation: multiAlignFree (RRID:SCR_013188)

Description: R package intended to implement a program for multiple alignment-free sequence comparison based on long genome sequence or NGS data.

Abbreviations: multiAlignFree

Synonyms: multiAlignFree: Multiple Alignment-free Sequence Comparison

Resource Type: software resource

Defining Citation: [PMID:23990418](#)

Availability: Free

Resource Name: multiAlignFree

Resource ID: SCR_013188

Alternate IDs: OMICS_00981

Record Creation Time: 20220129T080314+0000

Record Last Update: 20260829T182431+0000

Ratings and Alerts

No rating or validation information has been found for multiAlignFree.

No alerts have been found for multiAlignFree.

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 [PRECISE-TBI](#) .

Kumar H, et al. (2026) FusionTarget: Computational framework for drug repurposing against modeled fusion protein structures from genomic breakpoints. iScience, 29(6), 116076.