

Resource Summary Report

Generated by PRECISE-TBI on Sep 8, 2026

JOINSOLVER

RRID:SCR_016619

Type: Tool

Proper Citation

JOINSOLVER (RRID:SCR_016619)

Resource Information

URL: <https://joinsolver.niaid.nih.gov>

Proper Citation: JOINSOLVER (RRID:SCR_016619)

Description: Software tool to analyze human immunoglobulin V(D)J recombination and performing Ig nucleotide and amino acid alignment, as well as extensive mutation and Complementarity Determining Region 3 (CDR3H) analysis.

Resource Type: alignment software, data analysis software, data processing software, image analysis software, service resource, software application, software resource

Defining Citation: [DOI:10.4049/jimmunol.172.11.6790](https://doi.org/10.4049/jimmunol.172.11.6790)

Keywords: human, immunoglobulin, analysis, recombination, nucleotide, amino acid, alignment, mutation, CDR3H

Availability: Free, Available for download, Freely available

Resource Name: JOINSOLVER

Resource ID: SCR_016619

Alternate URLs: <https://dcb.cit.nih.gov/HTJoinSolver/>

Record Creation Time: 20220129T080331+0000

Record Last Update: 20260905T132811+0000

Ratings and Alerts

No rating or validation information has been found for JOINSOLVER.

No alerts have been found for JOINSOLVER.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We have not found any literature mentions for this resource.