

# Resource Summary Report

Generated by [NIF](#) on Aug 28, 2026

## JOINSOLVER

RRID:SCR\_016619

Type: Tool

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### Proper Citation

JOINSOLVER (RRID:SCR\_016619)

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### 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:** 20260821T194054+0000

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### Ratings and Alerts

No rating or validation information has been found for JOINSOLVER.

No alerts have been found for JOINSOLVER.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We have not found any literature mentions for this resource.