

Resource Summary Report

Generated by [PRECISE-TBI](#) on Sep 8, 2026

IVA

RRID:SCR_024044

Type: Tool

Proper Citation

IVA (RRID:SCR_024044)

Resource Information

URL: <https://github.com/sanger-pathogens/iva>

Proper Citation: IVA (RRID:SCR_024044)

Description: Software tool as de novo assembler designed to assemble virus genomes that have no repeat sequences, using Illumina read pairs sequenced from mixed populations at extremely high and variable depth.

Synonyms: Iterative Virus Assembler - de novo virus assembler of Illumina paired reads., iva

Resource Type: data analysis software, data processing software, software application, software resource

Defining Citation: [PMID:25725497](#)

Keywords: de novo assembler, assemble virus genomes, no repeat sequences, Illumina reads, pairs sequenced from mixed populations,

Availability: Free, Available for download, Freely available,

Resource Name: IVA

Resource ID: SCR_024044

Alternate IDs: OMICS_08188

Alternate URLs: <https://sources.debian.org/src/iva/>, <http://sanger-pathogens.github.io/iva/>

License: GNU GENERAL PUBLIC LICENSE

Record Creation Time: 20230824T050211+0000

Record Last Update: 20260905T133028+0000

Ratings and Alerts

No rating or validation information has been found for IVA.

No alerts have been found for IVA.

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](#) .

Koul M, et al. (2025) VITALdb: to select the best viroinformatics tools for a desired virus or application. Briefings in bioinformatics, 26(2).