

# Resource Summary Report

Generated by [RRID](#) on Aug 2, 2026

## IVA

RRID:SCR\_024044

Type: Tool

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### Proper Citation

IVA (RRID:SCR\_024044)

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### 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 processing software, data analysis 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:** 20260801T190825+0000

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## Ratings and Alerts

No rating or validation information has been found for IVA.

No alerts have been found for IVA.

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## Data and Source Information

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

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## Usage and Citation Metrics

We found 1 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [RRID](#) .

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