

# Resource Summary Report

Generated by [kravitz2](#) on Aug 2, 2026

## ViReMa

RRID:SCR\_000566

Type: Tool

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### Proper Citation

ViReMa (RRID:SCR\_000566)

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### Resource Information

**URL:** <http://sourceforge.net/projects/virema/>

**Proper Citation:** ViReMa (RRID:SCR\_000566)

**Description:** Software Python package for detection, alignment and reporting of recombination events in Next-Generation Sequencing data. Detects and reports recombination or fusion events in virus genomes using deep sequencing datasets.

**Abbreviations:** ViReMa

**Synonyms:** Viral Recombination Mapper

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

**Defining Citation:** [PMID:24137010](#)

**Keywords:** virus genomes deep sequencing datasets, detection, alignment and reporting of recombination events, Next-Generation Sequencing data,

**Availability:** Free, Available for download, Freely available,

**Resource Name:** ViReMa

**Resource ID:** SCR\_000566

**Alternate IDs:** OMICS\_00225

**License:** MIT License

**Record Creation Time:** 20220129T080202+0000

**Record Last Update:** 20260801T190115+0000

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### Ratings and Alerts

No rating or validation information has been found for ViReMa.

No alerts have been found for ViReMa.

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## Data and Source Information

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

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## Usage and Citation Metrics

We found 2 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [kravitz2](#) .

Sotcheff S, et al. (2023) ViReMa: a virus recombination mapper of next-generation sequencing data characterizes diverse recombinant viral nucleic acids. GigaScience, 12.

Jaworski E, et al. (2021) Tiled-ClickSeq for targeted sequencing of complete coronavirus genomes with simultaneous capture of RNA recombination and minority variants. eLife, 10.