Resource Summary Report

Generated by NIF on May 20, 2025

ViReMa

RRID:SCR_000566
Type: Tool

Proper Citation

ViReMa (RRID:SCR_000566)

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 application, software toolkit, data analysis software, data processing software, software resource

Defining Citation: PMID:24137010

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

Funding:

Availability: MIT License

Resource Name: ViReMa

Resource ID: SCR_000566

Alternate IDs: OMICS_00225

Record Creation Time: 20220129T080202+0000

Record Last Update: 20250519T203056+0000

Ratings and Alerts

No rating or validation information has been found for ViReMa.

No alerts have been found for ViReMa.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 2 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

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.