Resource Summary Report

Generated by NIF on Sep 15, 2026

VFS

RRID:SCR_005138
Type: Tool

Proper Citation

VFS (RRID:SCR_005138)

Resource Information

URL: http://sourceforge.net/projects/viralfusionseq/

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Description: A versatile high-throughput sequencing (HTS) tool for discovering viral integration events and reconstruct fusion transcripts at single-base resolution. It combines soft-clipping information, read-pair analysis, and targeted de novo assembly to discover and annotate viral-human fusion events. A simple yet effective empirical statistical model is used to evaluate the quality of fusion breakpoints. Minimal user defined parameters are required.

Abbreviations: VFS

Synonyms: ViralFusionSeq, ViralFusionSeq (VFS)

Resource Type: software resource

Defining Citation: PMID:23314323

Keywords: ubuntu, debian, high-throughput sequencing, virus, reconstruct, fusion transcript, transcript, integration, fusion, bio.tools

Availability: GNU General Public License, v3

Resource Name: VFS

Resource ID: SCR_005138

Alternate IDs: OMICS_00224, biotools:viralfusionseq

Alternate URLs: https://bio.tools/viralfusionseq

Record Creation Time: 20220129T080228+0000

Record Last Update: 20260912T195621+0000

Ratings and Alerts

No rating or validation information has been found for VFS.

No alerts have been found for VFS.

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 NIF .

Aurrecoechea C, et al. (2013) EuPathDB: the eukaryotic pathogen database. Nucleic acids research, 41(Database issue), D684.