

Resource Summary Report

Generated by SPARC SAWG on Aug 1, 2026

VADR

RRID:SCR_024377

Type: Tool

Proper Citation

VADR (RRID:SCR_024377)

Resource Information

URL: <https://github.com/nawrockie/vadr>

Proper Citation: VADR (RRID:SCR_024377)

Description: Software suite of tools for classifying and analyzing sequences homologous to set of reference models of viral genomes or gene families.

Synonyms: ushahidi

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

Defining Citation: [PMID:35441162](https://pubmed.ncbi.nlm.nih.gov/35441162/)

Keywords: classifying and analyzing sequences, sequences homologous to set of reference models, viral genomes reference models, gene families reference models,

Availability: Free, Available for download, Freely available,

Resource Name: VADR

Resource ID: SCR_024377

Old URLs: <https://sources.debian.org/src/vadr/>

Record Creation Time: 20230830T050217+0000

Record Last Update: 20260801T190826+0000

Ratings and Alerts

No rating or validation information has been found for VADR.

No alerts have been found for VADR.

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 [SPARC SAWG](#) .

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