Resource Summary Report

Generated by NIF on May 25, 2025

vcfR

RRID:SCR_023453
Type: Tool

Proper Citation

vcfR (RRID:SCR_023453)

Resource Information

URL: https://CRAN.R-project.org/package=vcfR

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Description: Software R package to read, write, manipulate and analyze variant call format data. Facilitates easy manipulation of variant call format (VCF) data.

Synonyms: variant call format in R

Resource Type: software resource, software toolkit

Keywords: Manipulate and visualize VCF data, variant call format data, VCF data, extract data matrices, genomic data visualization, VCF file, variant call format files,

Funding:

Availability: Free, Available for download, Freely available

Resource Name: vcfR

Resource ID: SCR_023453

Alternate URLs: https://knausb.github.io/vcfR_documentation/, https://github.com/knausb/vcfR, https://cran.r-project.org/web/packages/vcfR/vignettes/intro_to_vcfR.html,

License: GPL v3

Record Creation Time: 20230411T050206+0000

Record Last Update: 20250525T032617+0000

Ratings and Alerts

No rating or validation information has been found for vcfR.

No alerts have been found for vcfR.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 5 mentions in open access literature.

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

Chen C, et al. (2024) GWAS reveals a rapidly evolving candidate avirulence effector in the Cercospora leaf spot pathogen. Molecular plant pathology, 25(1), e13407.

Aribi HB, et al. (2024) NeuroVar: an open-source tool for the visualization of gene expression and variation data for biomarkers of neurological diseases. GigaByte (Hong Kong, China), 2024, gigabyte143.

Brown N, et al. (2024) Replication stress increases de novo CNVs across the malaria parasite genome. bioRxiv : the preprint server for biology.

Barbosa CFC, et al. (2023) Genome-Wide SNP and Indel Discovery in Abaca (Musa textilis Née) and among Other Musa spp. for Abaca Genetic Resources Management. Current issues in molecular biology, 45(7), 5776.

Howard-McCombe J, et al. (2023) Genetic swamping of the critically endangered Scottish wildcat was recent and accelerated by disease. Current biology : CB, 33(21), 4761.