

Resource Summary Report

Generated by [PRECISE-TBI](#) on Sep 8, 2026

[seqinr](#)

RRID:SCR_022678

Type: Tool

Proper Citation

seqinr (RRID:SCR_022678)

Resource Information

URL: <https://cran.r-project.org/web/packages/seqinr/index.html>

Proper Citation: seqinr (RRID:SCR_022678)

Description: Software R package for exploratory data analysis and data visualization for biological sequence, DNA and protein, data.

Resource Type: software resource, software toolkit

Keywords: exploratory data analysis and data visualization, biological sequence data, DNA and protein data

Availability: Free, Available for download, Freely available

Resource Name: seqinr

Resource ID: SCR_022678

License: GPL v3

Record Creation Time: 20220817T050143+0000

Record Last Update: 20260905T133311+0000

Ratings and Alerts

No rating or validation information has been found for seqinr.

No alerts have been found for seqinr.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 12 mentions in open access literature.

Listed below are recent publications. The full list is available at [PRECISE-TBI](#) .

Hu SY, et al. (2025) Comprehensive sampling of mitochondrial genomes substantiates the Neoproterozoic origin of land plants. *Plant communications*, 6(11), 101497.

Amador CI, et al. (2025) Decoding the impact of interspecies interactions on biofilm matrix components. *Biofilm*, 9, 100271.

Gulyaeva A, et al. (2025) Identification and characterization of Faecalibacterium prophages rich in diversity-generating retroelements. *Microbiology spectrum*, 13(2), e0106624.

Voorter CEM, et al. (2024) Resolving unknown nucleotides in the IPD-IMGT/HLA database by extended and full-length sequencing of HLA class I and II alleles. *Immunogenetics*, 76(2), 109.

Xu ZM, et al. (2024) Joint host-pathogen genomic analysis identifies hepatitis B virus mutations associated with human NTCP and HLA class I variation. *American journal of human genetics*, 111(6), 1018.

Koncz M, et al. (2024) Genomic surveillance as a scalable framework for precision phage therapy against antibiotic-resistant pathogens. *Cell*, 187(21), 5901.

Li S, et al. (2023) Evolutionary conservation of sequence motifs at sites of protein modification. *The Journal of biological chemistry*, 299(5), 104617.

Dougherty K, et al. (2022) Computational curation and analysis of publicly available protein sequence data from a single protein family. *MethodsX*, 9, 101846.

Werner BT, et al. (2021) *Fusarium graminearum* DICER-like-dependent sRNAs are required for the suppression of host immune genes and full virulence. *PloS one*, 16(8), e0252365.

Iraola G, et al. (2017) Distinct *Campylobacter fetus* lineages adapted as livestock pathogens and human pathobionts in the intestinal microbiota. *Nature communications*, 8(1), 1367.

Duchoslav M, et al. (2015) Parallel subfunctionalisation of PsbO protein isoforms in angiosperms revealed by phylogenetic analysis and mapping of sequence variability onto protein structure. *BMC plant biology*, 15, 133.

Williams D, et al. (2012) Quantifying homologous replacement of loci between haloarchaeal species. *Genome biology and evolution*, 4(12), 1223.