Package: alakazam (via r-universe)

May 31, 2026

Type Package

Version 1.4.3.999

Date 2026-05-01

Title Immunoglobulin Clonal Lineage and Diversity Analysis

Description Provides methods for high-throughput adaptive immune receptor repertoire sequencing (AIRR-Seq; Rep-Seq) analysis. In particular, immunoglobulin (Ig) sequence lineage reconstruction, lineage topology analysis, diversity profiling, amino acid property analysis and gene usage. Citations: Gupta and Vander Heiden, et al (2017) <doi:10.1093/bioinformatics/btv359>, Stern, Yaari and Vander Heiden, et al (2014) <doi:10.1126/scitranslmed.3008879>.

License AGPL-3

URL `https://alakazam.readthedocs.io/`

BugReports `https://github.com/immcantation/alakazam/issues`

LazyData true

BuildVignettes true

VignetteBuilder knitr, rmarkdown

Encoding UTF-8

LinkingTo Rcpp

biocViews Software, AnnotationData

Depends R (>= 4.0), ggplot2 (>= 3.4.0)

Imports airr (>= 1.4.1), ape, dplyr (>= 1.0), graphics, grid, igraph (>= 1.5.0), Matrix (>= 1.3-0), methods, progress, Rcpp (>= 0.12.12), readr, rlang, scales, seqinr, stats, stringi, tibble, tidyr (>= 1.0), utils, Biostrings (>= 2.56.0), GenomicAlignments (>= 1.24.0), IRanges (>= 2.22.2)

Suggests cigarillo, knitr, rmarkdown, testthat

RoxygenNote 7.3.3

Collate 'Alakazam.R' 'AminoAcids.R' 'Classes.R' 'Core.R' 'Data.R' 'Diversity.R' 'Deprecated.R' 'Fastq.R' 'Gene.R' 'Lineage.R' 'RcppExports.R' 'Sequence.R' 'Topology.R'

Config/pak/sysreqs libglpk-dev libbz2-dev libicu-dev liblzma-dev libxml2-dev libx11-dev xz-utils zlib1g-dev

Repository https://immcantation.r-universe.dev

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RemoteUrl https://github.com/immcantation/alakazam

RemoteRef HEAD

RemoteSha e85cde1e7f4d2b7b7750a70fe7c558d202887ff5