

# Package: alakazam (via r-universe)

August 31, 2024

**Type** Package

**Version** 1.3.1.999

**Date** 2024-08-01

**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](https://doi.org/10.1093/bioinformatics/btv359)>, Stern, Yaari and Vander Heiden, et al (2014) <[doi:10.1126/scitranslmed.3008879](https://doi.org/10.1126/scitranslmed.3008879)>.

**License** AGPL-3

**URL** <https://alakazam.readthedocs.io/>

**BugReports** <https://bitbucket.org/kleinstein/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** knitr, rmarkdown, testthat

**RoxygenNote** 7.3.2

2

**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'

**Repository** <https://ssnn-airr.r-universe.dev>

**RemoteUrl** <https://bitbucket.org/kleinstei/alakazam>

**RemoteRef** HEAD

**RemoteSha** e493319e4322c40abf422f057c26a2e2ff8a83b4