

Resource Summary Report

Generated by [kravitz2](#) on Jul 31, 2026

tigger

RRID:SCR_024310

Type: Tool

Proper Citation

tigger (RRID:SCR_024310)

Resource Information

URL: <https://cran.r-project.org/package=tigger>

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Description: Software R package infers V genotype of individual from immunoglobulin repertoire sequencing data like AIRR-Seq, Rep-Seq. Includes detection of any novel alleles. This information is then used to correct existing V allele calls from among sample sequences.

Resource Type: software toolkit, software resource

Keywords: infer V genotype of individual, immunoglobulin repertoire sequencing data, AIRR-Seq, Rep-Seq, detection of novel alleles, correct existing V allele calls, sample sequences,

Availability: Free, Available for download, Freely available,

Resource Name: tigger

Resource ID: SCR_024310

Alternate IDs: OMICS_07533

Alternate URLs: <https://sources.debian.org/src/r-cran-tigger/>

License: AGPL-3

Record Creation Time: 20230830T050217+0000

Record Last Update: 20260729T044603+0000

Ratings and Alerts

No rating or validation information has been found for tigger.

No alerts have been found for tigger.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 8 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

McIntire KM, et al. (2024) Maturation of germinal center B cells after influenza virus vaccination in humans. The Journal of experimental medicine, 221(8).

Scharf L, et al. (2023) Longitudinal single-cell analysis of SARS-CoV-2-reactive B cells uncovers persistence of early-formed, antigen-specific clones. JCI insight, 8(1).

Mathew NR, et al. (2021) Single-cell BCR and transcriptome analysis after influenza infection reveals spatiotemporal dynamics of antigen-specific B cells. Cell reports, 35(12), 109286.

Hoehn KB, et al. (2021) Human B cell lineages associated with germinal centers following influenza vaccination are measurably evolving. eLife, 10.

Mikocziova I, et al. (2021) Germline polymorphisms and alternative splicing of human immunoglobulin light chain genes. iScience, 24(10), 103192.

Tang C, et al. (2020) AID Overlapping and Pol?? Hotspots Are Key Features of Evolutionary Variation Within the Human Antibody Heavy Chain (IGHV) Genes. Frontiers in immunology, 11, 788.

Omer A, et al. (2020) VDJbase: an adaptive immune receptor genotype and haplotype database. Nucleic acids research, 48(D1), D1051.

Mikocziova I, et al. (2020) Polymorphisms in human immunoglobulin heavy chain variable genes and their upstream regions. Nucleic acids research, 48(10), 5499.