

Resource Summary Report

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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 [NIF](#) .

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.