

Resource Summary Report

Generated by [Kravitz](#) on Sep 16, 2026

[migec](#)

RRID:SCR_016337

Type: Tool

Proper Citation

migec (RRID:SCR_016337)

Resource Information

URL: <https://github.com/mikessh/migec>

Proper Citation: migec (RRID:SCR_016337)

Description: Software package for analysis of immune repertoire sequencing data. Used for recovery of T Cell Receptor (TCR) data from bulk population data.Used for high-throughput sequencing data analysis. Allows for error correction while preserving the natural diversity of complex immune repertoires.

Abbreviations: MIGEC

Synonyms: Molecular Identifier Guided Error Correction

Resource Type: data analysis software, data processing software, software application, software resource, software toolkit

Defining Citation: [PMID:24793455](#)

Keywords: high sequencing, molecular, identifier, guided, error, correction, data, analysis, immune, recovery, T cell receptor,

Funding: European Regional Development Fund ;
Molecular and Cell Biology program RAS ;
Russian Foundation for Basic Research ;
Russian President

Availability: Free, Available for download, Freely available

Resource Name: migec

Resource ID: SCR_016337

Record Creation Time: 20220129T080330+0000

Record Last Update: 20260912T195838+0000

Ratings and Alerts

No rating or validation information has been found for migec.

No alerts have been found for migec.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 11 mentions in open access literature.

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

Shin YW, et al. (2026) Systemic T Cell Receptor Profiling Reveals Adaptive Immune Activation and Potential Immune Signatures of Diagnosis and Brain Atrophy in Epilepsy. *Annals of clinical and translational neurology*, 13(2), 296.

Principe N, et al. (2026) Comparative analysis of malignant pleural effusion and peripheral blood reveals unique T cell signatures associated with survival in mesothelioma patients. *Oxford open immunology*, 7(1), iqaf008.

Gao L, et al. (2025) Microbiota-Derived Inosine Suppresses Systemic Autoimmunity via Restriction of B Cell Differentiation and Migration. *Advanced science (Weinheim, Baden-Wurttemberg, Germany)*, 12(20), e2409837.

Racle J, et al. (2023) Machine learning predictions of MHC-II specificities reveal alternative binding mode of class II epitopes. *Immunity*, 56(6), 1359.

Mihai A, et al. (2023) E protein binding at the Tcra enhancer promotes Tcra repertoire diversity. *Frontiers in immunology*, 14, 1188738.

Russell ML, et al. (2022) Combining genotypes and T cell receptor distributions to infer genetic loci determining V(D)J recombination probabilities. *eLife*, 11.

Vetter J, et al. (2022) ImmunoDataAnalyzer: a bioinformatics pipeline for processing barcoded and UMI tagged immunological NGS data. *BMC bioinformatics*, 23(1), 21.

Mudd PA, et al. (2022) SARS-CoV-2 mRNA vaccination elicits a robust and persistent T follicular helper cell response in humans. *Cell*, 185(4), 603.

Komech EA, et al. (2022) TCR repertoire profiling revealed antigen-driven CD8+ T cell clonal groups shared in synovial fluid of patients with spondyloarthritis. *Frontiers in immunology*, 13, 973243.

Principe N, et al. (2020) Tumor Infiltrating Effector Memory Antigen-Specific CD8+ T Cells Predict Response to Immune Checkpoint Therapy. *Frontiers in immunology*, 11, 584423.

Pogorelyy MV, et al. (2017) Persisting fetal clonotypes influence the structure and overlap of adult human T cell receptor repertoires. PLoS computational biology, 13(7), e1005572.