

Resource Summary Report

Generated by [nidm-terms](#) on Aug 30, 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: 20260829T182511+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 [nidm-terms](#) .

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.

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.

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.

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.

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

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.