

Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 2026

MiXCR

RRID:SCR_018725

Type: Tool

Proper Citation

MiXCR (RRID:SCR_018725)

Resource Information

URL: <https://milaboratory.com/software/mixcr/>

Proper Citation: MiXCR (RRID:SCR_018725)

Description: Software tool to processes big immunome data from raw sequences to quantitated clonotypes by MiLaboratory LLC. Universal software for analysis of T- and B-cell receptor repertoire high throughput sequencing data. Software for comprehensive adaptive immunity profiling.

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

Defining Citation: [PMID:25924071](#)

Keywords: Process immunome data, raw sequence, quantitated clonotype, B cell receptor, sequencing data analysis, T cell receptor, high throughput sequencing data, adaptive immunity profiling, MiLaboratory, bio.tools

Funding: Russian Science Foundation

Availability: Restricted

Resource Name: MiXCR

Resource ID: SCR_018725

Alternate IDs: biotools:MiXCR, BioTools:MiXCR

Alternate URLs: <https://github.com/milaboratory/mixcr>, <https://bio.tools/MiXCR>, <https://bio.tools/MiXCR>, <https://bio.tools/MiXCR>

License URLs: <https://github.com/milaboratory/mixcr/blob/develop/LICENSE>

Record Creation Time: 20220129T080341+0000

Ratings and Alerts

No rating or validation information has been found for MiXCR.

No alerts have been found for MiXCR.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 73 mentions in open access literature.

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

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.

Fritz L, et al. (2026) Differentiation-induced reduction in functional diversity restricts the ability of cytomegalovirus-specific CD8 T cells to eliminate virus-infected cells. EBioMedicine, 123, 106107.

Sanz-Garcia E, et al. (2026) Investigating Early Kinetics in Plasma ctDNA and Peripheral T-cell Receptor Repertoire to Predict Treatment Outcomes to PD-1 Inhibitors in Head and Neck Squamous Cell Carcinoma. Clinical cancer research : an official journal of the American Association for Cancer Research, 32(4), 735.

Machida E, et al. (2026) Microbiomic and immunogenic biomarkers of adjuvant chemotherapy efficacy in stage III colorectal cancer. JNCI cancer spectrum, 10(3).

Liu P, et al. (2026) Chain-specific remodeling of the ?? T-cell TCR repertoire in preterm infants with cCMV: a gestational-age-stratified case-control study. Frontiers in immunology, 17, 1713669.

Alhussien MN, et al. (2026) Deciphering interferon functions in avian influenza using receptor knockout models in the natural host. eLife, 14.

Campbell KM, et al. (2026) Cellular neighborhoods govern antitumor T-cell infiltration following anti-CTLA-4 in melanoma with primary resistance to anti-PD-1. Cancer discovery.

Hattori-Muroi K, et al. (2026) Dietary soy shapes the microbiome to induce commensal-specific T follicular helper cells and IgA production. Immunity, 59(6), 1616.

Aran A, et al. (2025) Minimally expanded breast cancer tumor-infiltrating-lymphocytes provide guidance for therapeutic selection. Frontiers in immunology, 16, 1699262.

Islam SMR, et al. (2025) Identification of HLA class II-restricted T cell receptors against shared PIK3CA mutations in patients with epithelial cancers. *Cancer immunology, immunotherapy* : CII, 75(1), 5.

Liu C, et al. (2025) Multiomics Reveals the Immunologic Features and the Immune Checkpoint Blockade Potential of Colorectal Medullary Carcinoma. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 31(4), 773.

Balko J, et al. (2025) Peripheral blood gene expression signatures of systemic immunity predict tumor microenvironment biology and therapeutic response in breast cancer. *Research square*.

Sun X, et al. (2025) Dynamic single-cell systemic immune responses in immunotherapy-treated early-stage HR+ breast cancer patients. *NPJ breast cancer*, 11(1), 65.

Lhomme G, et al. (2025) Deep exploration of the TCR CDR3? repertoire specific for viral CD4 T-cell epitopes inside the circulating T-cell repertoire. *Frontiers in immunology*, 16, 1713225.

Ren W, et al. (2025) Whole-genome sequencing reveals three follicular lymphoma subtypes with distinct cell of origin and patient outcomes. *Cell reports. Medicine*, 6(8), 102278.

Jiang J, et al. (2025) Malnutrition exacerbating neuropsychiatric symptoms on the Alzheimer's continuum is relevant to the cAMP signaling pathway: Human and mouse studies. *Alzheimer's & dementia : the journal of the Alzheimer's Association*, 21(2), e14506.

Fiore D, et al. (2025) A patient-derived T cell lymphoma biorepository uncovers pathogenetic mechanisms and host-related therapeutic vulnerabilities. *Cell reports. Medicine*, 6(4), 102029.

Wang W, et al. (2025) Liver transplant-facilitated CD161+V γ 7.2+ MAIT cell recovery demonstrates clinical benefits in hepatic failure patients. *Nature communications*, 16(1), 4022.

Yang J, et al. (2025) Transcriptomic Profiling and Tumor Microenvironment Classification Reveal Unique and Dynamic Immune Biology in HIV-Associated Kaposi Sarcoma. *Cells*, 14(2).

Lupyr KR, et al. (2025) Neighborhood enrichment for the identification of antigen-specific T-cell receptors. *Briefings in bioinformatics*, 26(5).