

Resource Summary Report

Generated by [SPARC SAWG](#) on Jul 28, 2026

iReceptor

RRID:SCR_022294

Type: Tool

Proper Citation

iReceptor (RRID:SCR_022294)

Resource Information

URL: <http://ireceptor.irmacs.sfu.ca/>

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Description: Data discovery platform that facilitates curation, analysis and sharing of antibody/B-cell and T-cell receptor repertoires from multiple labs and institutions. Used to increase value of data through sharing with community. Platform for querying and analyzing antibody/B-cell and T-cell receptor repertoire data across federated repositories.

Resource Type: data or information resource, topical portal, portal

Defining Citation: [PMID:29944754](#)

Keywords: Adaptive Immune Receptor Repertoire, AIRR-seq data, querying and analyzing, antibody, B-cell, T-cell, receptor, federated repositories, data discovery

Availability: Free, Freely available

Resource Name: iReceptor

Resource ID: SCR_022294

Record Creation Time: 20220602T050139+0000

Record Last Update: 20260729T044529+0000

Ratings and Alerts

No rating or validation information has been found for iReceptor.

No alerts have been found for iReceptor.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 5 mentions in open access literature.

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

Jeon J, et al. (2025) EpicPred: predicting phenotypes driven by epitope-binding TCRs using attention-based multiple instance learning. *Bioinformatics (Oxford, England)*, 41(3).

Kato H, et al. (2023) Immune repertoire profiling for disease pathobiology. *Pathology international*, 73(1), 1.

Wan K, et al. (2023) Establishment and identification of cardiomyocyte arhGEF18 gene conditional knockout mice. *Pediatric discovery*, 1(2), e20.

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

Chen SY, et al. (2021) TCRdb: a comprehensive database for T-cell receptor sequences with powerful search function. *Nucleic acids research*, 49(D1), D468.