

Resource Summary Report

Generated by [dkNET](#) on Sep 2, 2026

Adaptive Immune Receptor Repertoire Rearrangement Schema

RRID:SCR_022592

Type: Tool

Proper Citation

Adaptive Immune Receptor Repertoire Rearrangement Schema (RRID:SCR_022592)

Resource Information

URL: <https://docs.airr-community.org/en/stable/datarep/rearrangements.html>

Proper Citation: Adaptive Immune Receptor Repertoire Rearrangement Schema (RRID:SCR_022592)

Description: Part of AIRR Data Model, defines annotations needed for rearrangements, which are sequences describing rearranged adaptive immune receptor chain (e.g., antibody heavy chain or TCR beta chain). Data for Rearrangement objects are stored as rows in tab delimited file and should be compatible with any TSV reader. Dataset is defined in this context as: TSV file, TSV with companion YAML file containing metadata, or directory containing multiple TSV files and YAML files.

Resource Type: data or information resource, narrative resource, portal, standard specification, topical portal

Defining Citation: [PMID:29144493](#)

Keywords: AIRR Data Model, annotations needed for rearrangements, rearranged adaptive immune receptor chain sequences,

Availability: Free, Freely available

Resource Name: Adaptive Immune Receptor Repertoire Rearrangement Schema

Resource ID: SCR_022592

Alternate URLs: <https://fairsharing.org/FAIRsharing.zwjNAh>

Record Creation Time: 20220728T050150+0000

Record Last Update: 20260829T182804+0000

Ratings and Alerts

No rating or validation information has been found for Adaptive Immune Receptor Repertoire Rearrangement Schema.

No alerts have been found for Adaptive Immune Receptor Repertoire Rearrangement Schema.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1 mentions in open access literature.

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

Dudzic P, et al. (2024) RIOT-Rapid Immunoglobulin Overview Tool-annotation of nucleotide and amino acid immunoglobulin sequences using an open germline database. Briefings in bioinformatics, 26(1).