

Package: EpitoScope (via r-universe)

September 25, 2026

Title Interactive QC, Visualization, and Immunogenicity Assessment of Immunopeptidomics Data

Version 1.0.0

Description An interactive R/Shiny application that unifies quality control, visualization, comparative statistics, and MHC class I/II binding prediction for mass-spectrometry-based immunopeptidomics data. It ingests search-engine outputs from PEAKS, FragPipe, DIA-NN, and Spectronaut through a configurable column-mapping layer, and provides publication-ready figure export and relational storage of processed results and binding predictions.

License GPL-3

URL <https://github.com/yannic-chen/EpitoScope>

BugReports <https://github.com/yannic-chen/EpitoScope/issues>

Encoding UTF-8

LazyData true

Depends R (>= 4.3)

Imports shiny, bs4Dash, DT, rhandsontable, shinyjs, DBI, RSQLite, dplyr, tidyr, purrr, stringr, data.table, arrow, memoise, curl, httr, jsonlite, ggplot2, ggrepel, ggseqlogo, ggVennDiagram, ggnewscale, eulerr, heatmaply, viridis, patchwork, plotly, igraph, ggraph, visNetwork, ComplexUpset, ComplexHeatmap, clusterProfiler, org.Hs.eg.db, rmarkdown, grid, grDevices, stats, utils, tools, limma, digest, viridisLite, scales, gtable, rlang, bslib, RColorBrewer

Suggests knitr, htmltools, fastcluster, testthat (>= 3.0.0)

Roxygen list(markdown = TRUE)

RoxygenNote 8.0.0

Config/testthat/edition 3

Config/pak/sysreqs

libcairo2-dev cmake libfontconfig1-dev libfreetype6-dev libglpk-dev make libmagick++-dev gsfonts libicu-dev libpng-dev libuv1-dev libxml2-dev libssl-dev perl zlib1g-dev libclang-dev

Repository <https://yannic-chen.r-universe.dev>
Date/Publication 2026-09-25 18:48:20 UTC
RemoteUrl <https://github.com/yannic-chen/EpitoScope>
RemoteRef HEAD
RemoteSha dd6d4b200a37d8f89d4a47b38ec154a53a6ea252

Contents

Colum_mapping_table	2
run_app	3
Index	4

Colum_mapping_table	<i>This function is to generate the table for column mapping. i.e. which columns are used for what info</i>
---------------------	---

Description

This function is to generate the table for column mapping. i.e. which columns are used for what info

Usage

```
Colum_mapping_table(df, max_chars = 20)
```

Arguments

- df data.frame to display
- max_chars integer, maximum number of characters to show before truncating. Avoid wide columns

Value

data.frame with HTML for truncated display

`run_app`*Launch the EpitoScope Shiny application*

Description

Launch the EpitoScope Shiny application

Usage

```
run_app(  
  input_variable = NULL,  
  generate_pseudo_sequence = FALSE,  
  custom_schema = NULL,  
  custom_signature = NULL,  
  replace_schema = FALSE,  
  db_path = NULL,  
  ...  
)
```

Arguments

`input_variable` Optional pre-loaded annotation table. Default NULL.

`generate_pseudo_sequence` Logical, passed to the server. Default FALSE.

`custom_schema, custom_signature` Optional named lists to extend/replace the schema.

`replace_schema` Logical; replace vs. extend the built-in schema.

`db_path` SQLite results DB path. Defaults under `tools::R_user_dir()`.

`...` Passed to `shiny::shinyApp()`.

Value

A Shiny app object

Index

`Colum_mapping_table`, [2](#)

`run_app`, [3](#)

`shiny::shinyApp()`, [3](#)

`tools::R_user_dir()`, [3](#)