

Welcome to TCRselect

This instruction describes TCRselect V1.0 and will be updated if necessary.

TCRselect provides an easy visualization of T cell receptor (TCR) sharing between repertoires and can be used to select candidate clonotypes after epitope-specific expansion cultures with subsequent TCR identification (ESPEC-SUIT) (see also protocols.io).

Input

The expected input is a single file containing information on clonotype frequencies across multiple samples of a single patient.

- **File type:** accepted input file types are .txt, .csv, .xlsx
- Such files can be generated e.g. with the 'JoinSamples' routine of [vdjtools](https://vdjtools.org) or exported after performing the 'repLoad' routine of [Immunarch](https://immunarch.org).
- The minimally required content of the input file is a column with CDR3 information and columns specifying the frequency of each CDR3 sequence/clonotype in at least two samples, such as an antigen-stimulated and a control-stimulated culture.
- Additional information, e.g. on TCR reactivity, can be included in the input file for further visualization options. Categorical information associated with specific CDR3 sequences can also be provided in a separate file (to be uploaded later).
- Click [here](#) to download an example dataset generated using vdjtools. Note that this file has been modified for complete de-identification, including removal of some columns and replacement of CDR3 amino acid information with randomly generated numeric identifiers.

Using TCRSelect

After uploading your input data, select a column with CDR3 amino acid or nucleotide information. This is required to enable the mouse-over function.

In the 'View Data' tab, **select which samples to display on the x- and y-axis (Step 1)**. For post-ESPEC candidate selection, plot an antigen-stimulated culture against a control culture not exposed to any antigen.

Data points can be sized based on a third sample (**Step 2**). Plot information can be edited to fit your data (**Step 3**).

For data filtering, multiple numeric cut-offs can be defined. Data points meeting these criteria will be highlighted in the plot and can be exported using the "export filtered data" button. Use the mouse-over function for data exploration.

For visualization of categorical information, switch to 'Option 2: Categorical Filtering'. Select a column for filtering from your dataset, or upload an additional file linking CDR3 information to a categorical variable, e.g. 'reactivity'.

If you use TCRSelect in your research, publication, or any derived work, please cite:

TCRSelect, DKFZ, 2025, DOI: [10.1136/jitc-2025-012216](https://doi.org/10.1136/jitc-2025-012216)