AlphaMap Tutorial

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This step-by-step guide helps you to get started with our software AlphaMap.

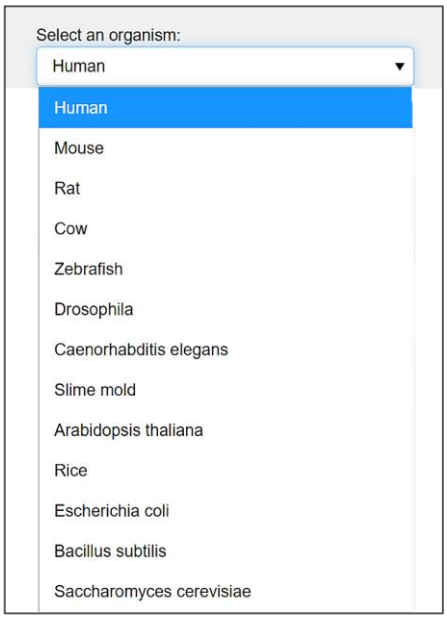
Program Description

This website enables the exploration of proteomic datasets on the peptide level. It is possible to evaluate the sequence coverage of any identified protein and its post-translational modifications (PTMs). AlphaMap further integrates all available UniProt sequence annotations as well as information about proteolytic cleavage sites.

Installation

How to use AlphaMap

1. Select the organism of your proteomic study. Currently, the 13 most popular organisms based on UniProt are available for selection, including: Human [Taxon identifier=9606], Mouse [10090], Rat [10116], Cow [9913], Zebrafish [7955], Drosophila [7227], Caenorhabditis elegans [6239], Slime mold [44689], Arabidopsis thaliana [3702], Rice [39947], Escherichia coli (strain K12) [83333], Bacillus subtilis (strain 168) [224308], Saccharomyces cerevisiae (strain ATCC 204508 / S288c) [559292].



2. Upload your proteomic datasets analyzed by AlphaPept, MaxQuant or Spectronaut:

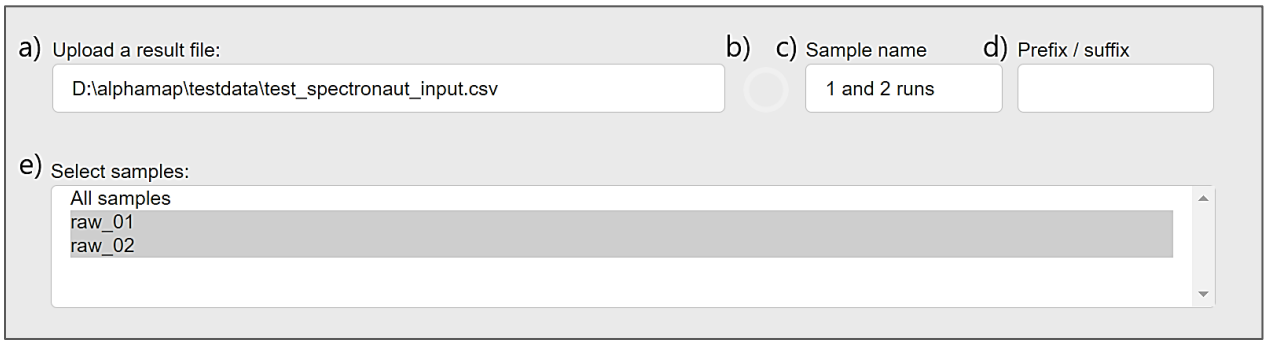
    a) Provide the filepath to the result file in the “Upload a result file:” field, e.g. “D:\spectronaut_output.csv”.

    b) Wait for samples to be displayed in the ”Select samples” field. The loading process is indicated by a spinner symbol.

    c) (optional) Select either all samples (default) or any specific sample(s) to visualize together as one trace.

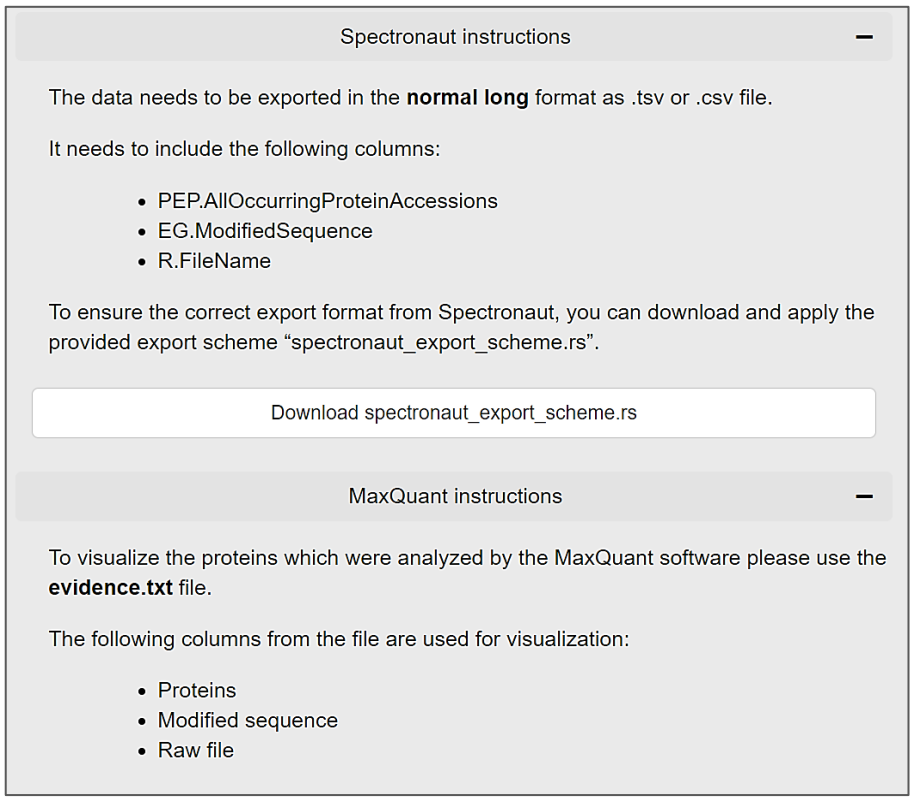
    d) (optional) Choose a name by which the selected sample(s) will be displayed in the figure. If no name is provided, the original names of all selected samples will be concatenated by semicolon. If ‘all samples’ were selected, the filename will be the default name.

    e) (optional) Provide a prefix or suffix to be removed from the original names of the selected samples. This option only applies if no user defined name is provided (see d).



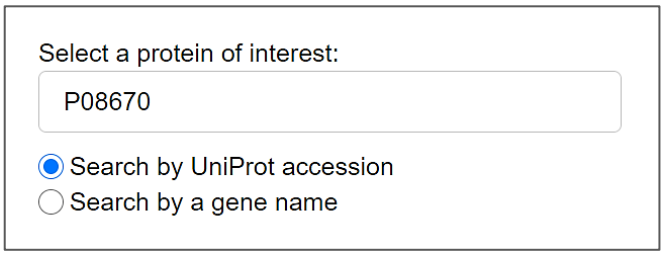
* Up to three datasets or sets of selected samples can be visualized together. For this, use the “Upload additional result files” option. If you would like to choose different samples from the same result file, you need to provide the same filepath and select the different samples.

* If you cannot upload the selected file, please take a look at the detailed instructions for Spectronaut and Maxquant input formats.

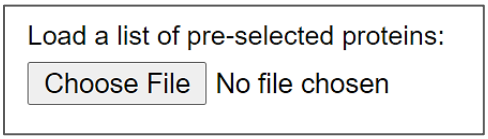


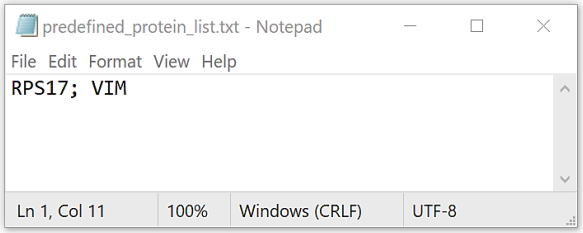
3. Press the "Upload Data" button. The loading process is indicated by a spinner symbol.

4. Select a protein of interest. Per default, you can choose from all UniProt accessions. Click the “Search by a gene name” option to select proteins by their gene name.



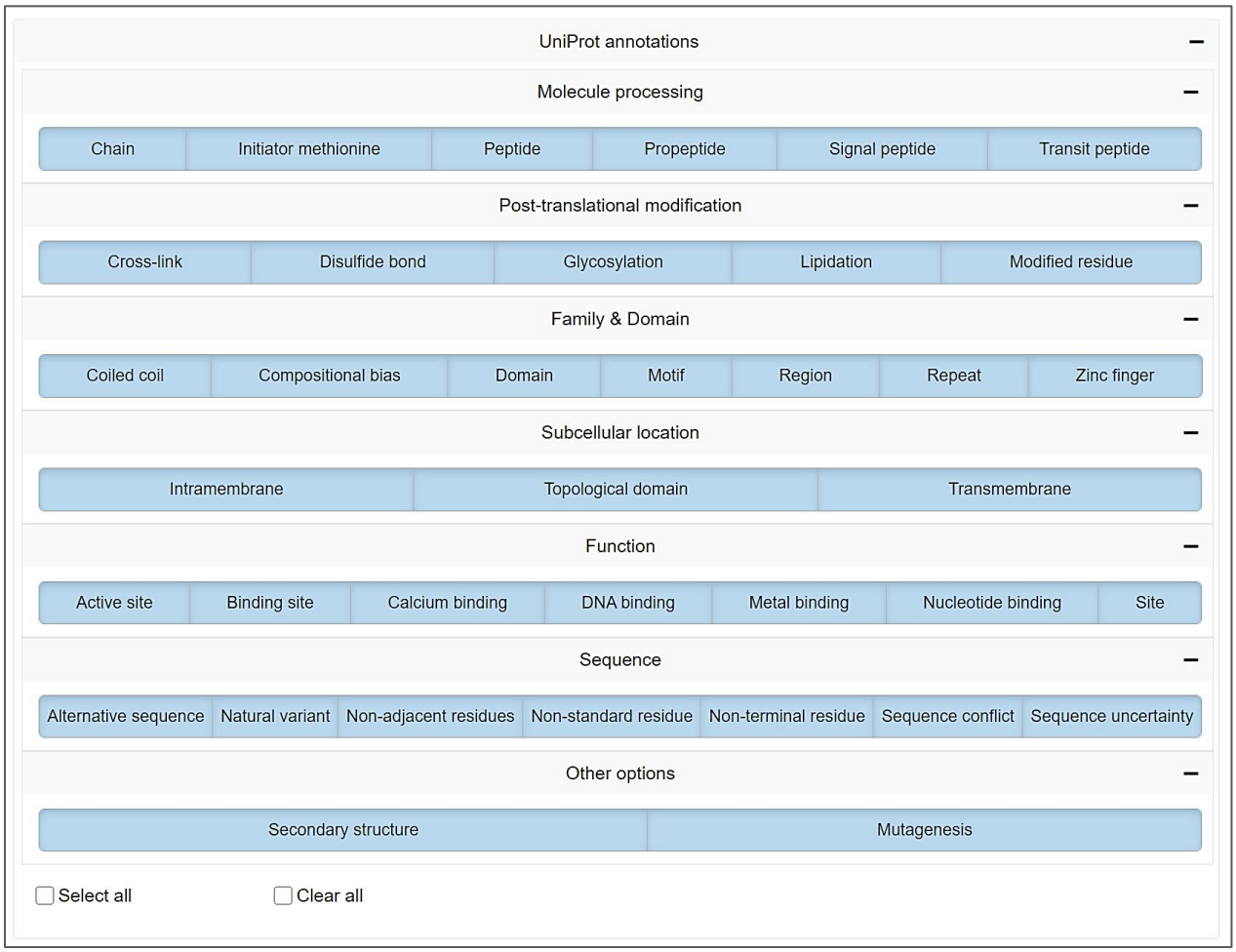
5. (optional) Load a list of pre-selected proteins. This can be a .txt file containing either UniProt accessions or gene names separated by semicolons. This will reduce the options available in the selection of proteins of interest (step 4).



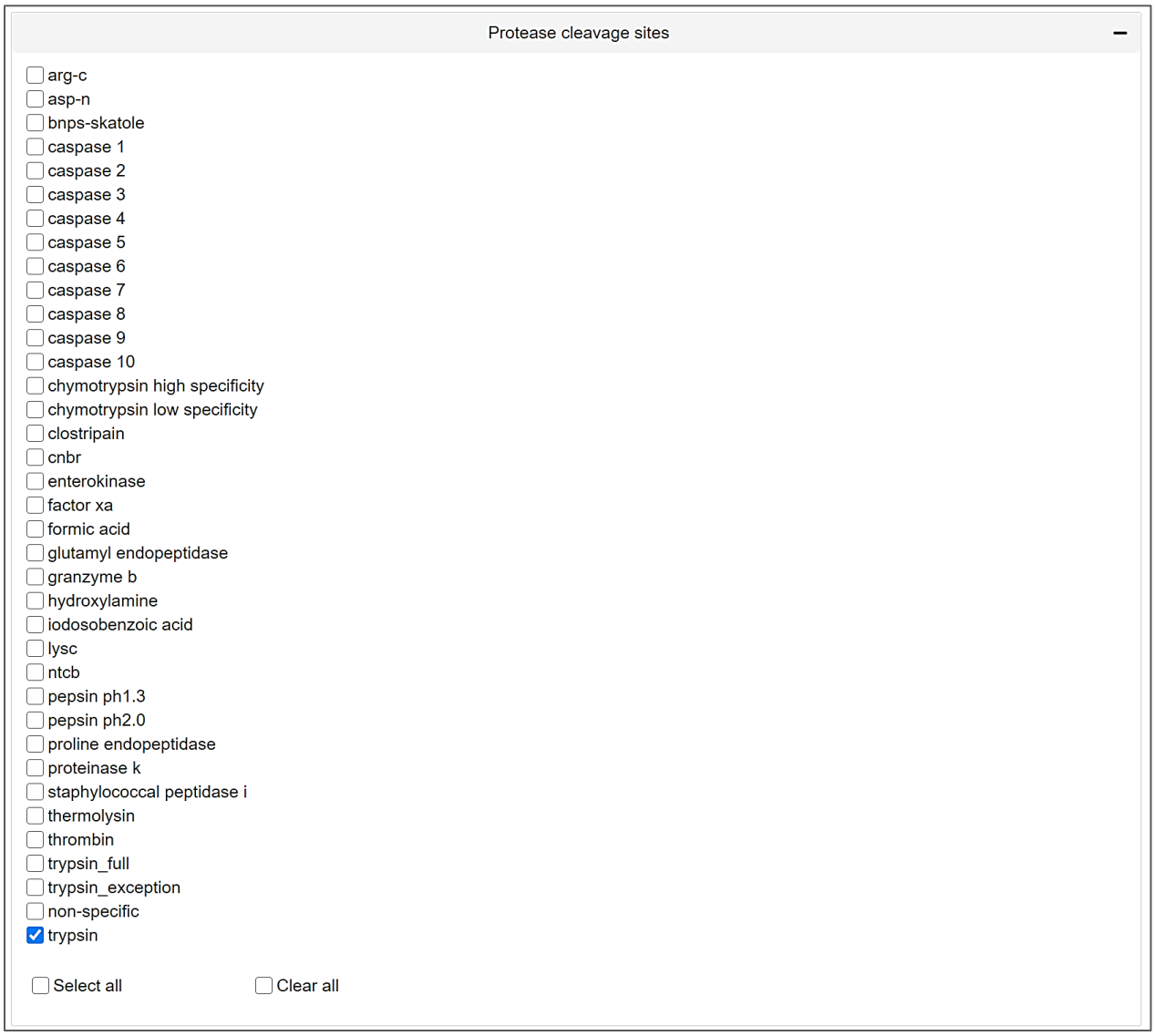


6. Select annotation options for the sequence visualization.

    - All sequence annotations from UniProt are available and displayed per default. You can choose a customized set of displayed annotations in the “UniProt annotation” selection.



- All theoretical cleavage sites for the most common proteases can be shown. Trypsin is selected by default. Alternative or additional proteases can be selected in the “Protease cleavage sites” selection.



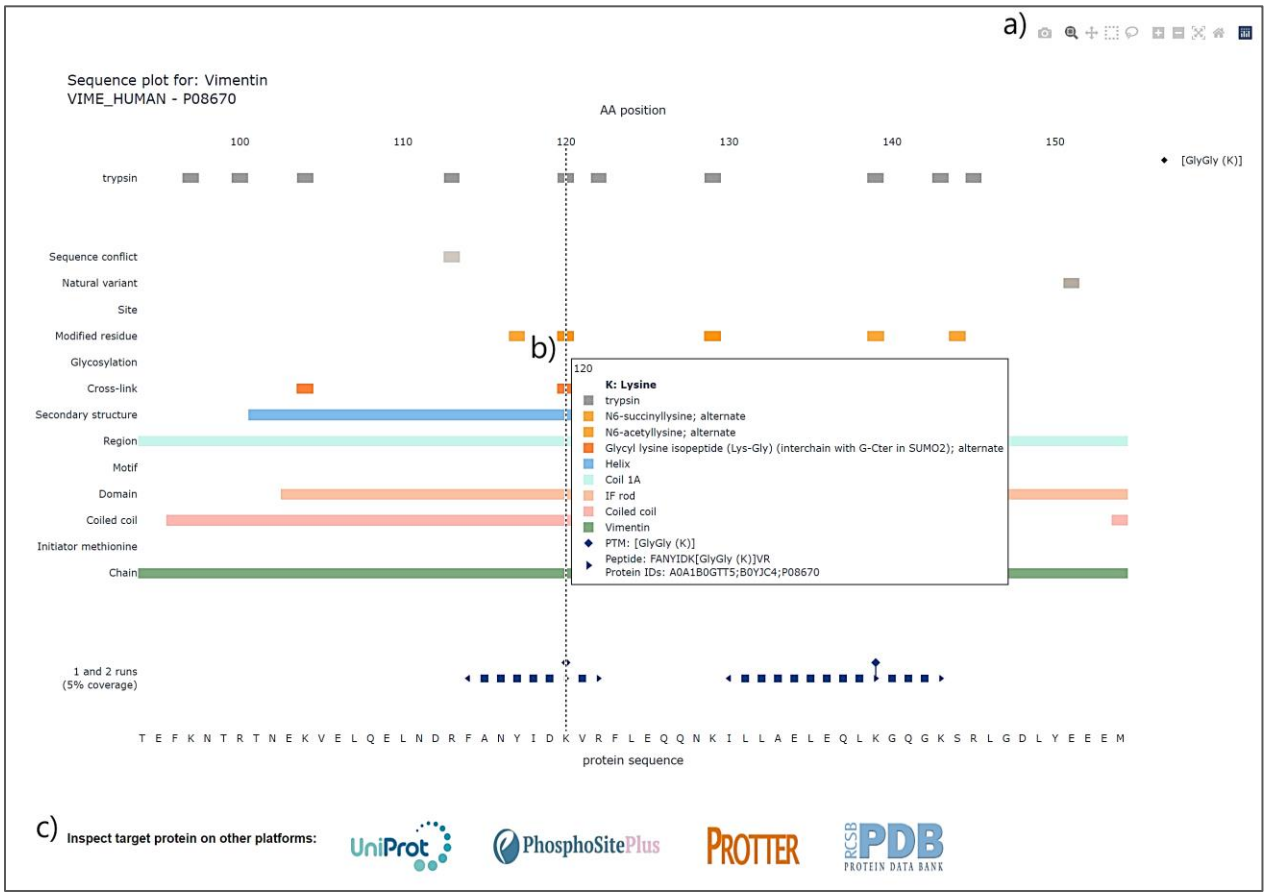
* You can use “Select all” or “Clear all” checkboxes to speed up the selection process.

7. Press the "Visualize Protein" button. The loading process is indicated by a spinner symbol.

   a) You can use the interactive toolbar to for example zoom in and out or to highlight specific sequence regions. Press the little camera icon to download a high-resolution .svg image of the currently displayed protein and sequence region.

   b) If you hover over the sequence, all annotation information for the current sequence position of the cursor will be displayed.

   c) You can directly visit other websites for further exploration of details on the selected protein of interest. UniProt, PhosphoSitePlus, Protter and PDB are available for direct access.



8. Enjoy exploring your data!