AlphaMap Tutorial

Developed by: Eugenia Voytik, Isabell Bludau.

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

Table of Contents

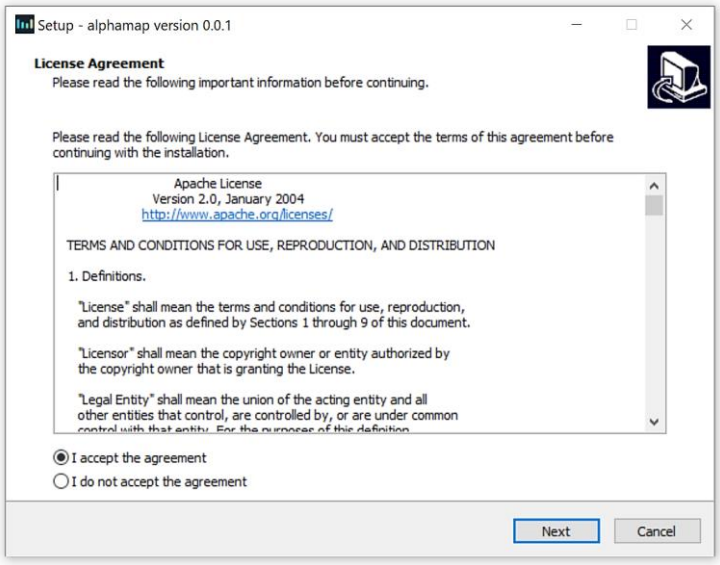
Program Description

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.

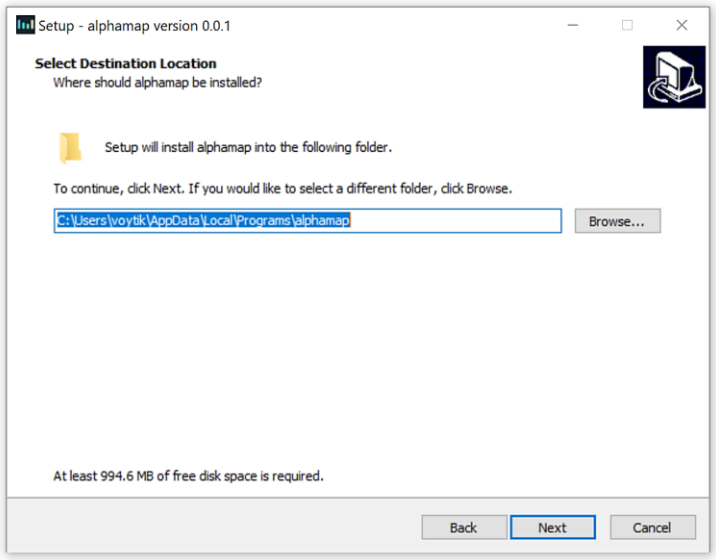
Installation

Windows:

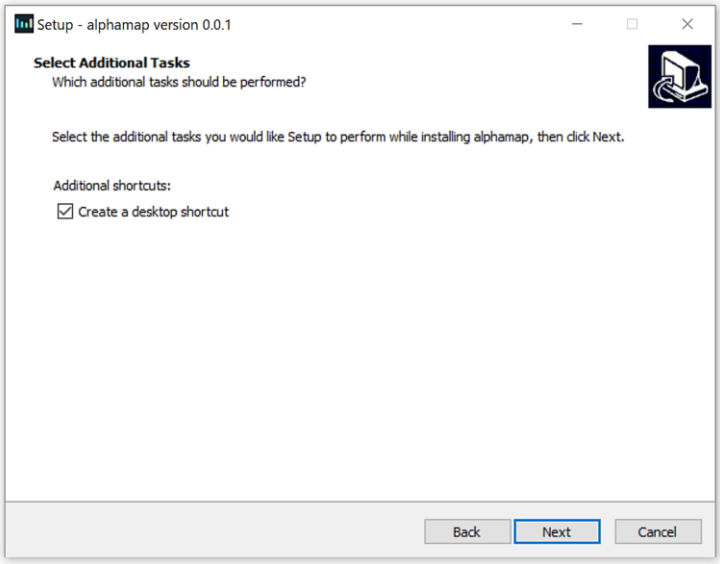
1. Download the latest release for Windows (alphamap_installer_windows.exe) from the GitHub repository and open the .exe file.
2. In the “User Account Control” dialog asking about permission for the app to make changes to your device press the “Yes” button.
3. In the appearing “Setup – alphamap version X.X.X” dialog window accept the License Agreement and press the “Next” button.



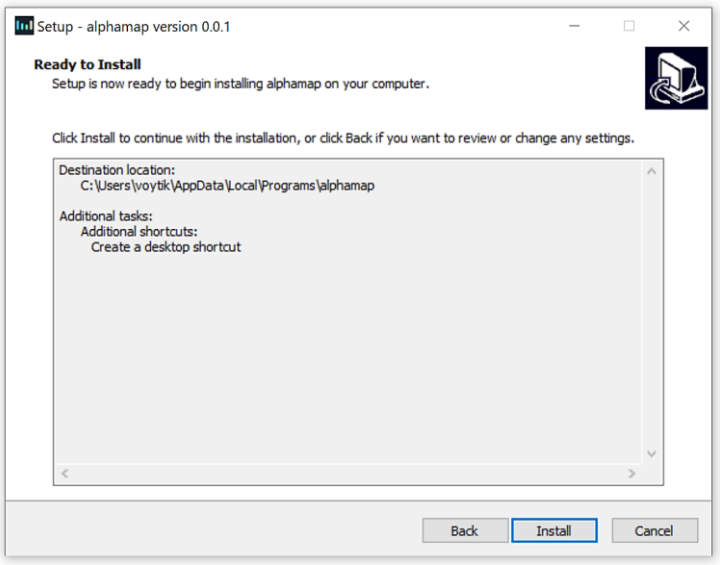
4. Select the destination location for the installation of AlphaMap software (the size of the whole package is 994.6 MB) and press the “Next” button.



5. In the next dialog window mark the “Create a desktop shortcut” check box and press the “Next” button.



6. Check the setting and if everything is correct, press “Install” button. You may go back to change some settings using the “Back” button or “Cancel” the installation.



7. Wait till the installation process is finished and with the marked “Launch alphamap” check box press the “Finish” button.
8. In the appearing “Windows Security Alert” dialog window press the “Allow access” button that will prevent the Windows Defender Firewall from blocking the AlphaMap tool on your PC.
9. Check your default browser (Google Chrome or Mozilla Firefox are suggested for the fast running of the AlphaMap) and start working with the tool.

* If you install AlphaMap for all users, you might need admin privileges to run it (right-click on the AlphaMap logo on your desktop and select "Run as administrator").

MacOS:

1. Download the latest release for macOS (alphamap.app.zip) from the GitHub repository, unzip the file and move it to your applications folder. By doing it, you accept the terms of the AlphaMap license agreement and all third-party licenses.
2. Launch the file and take into account that the first opening of the tool on macOS takes a long time to load. The loading time will be significantly reduced upon the second launch.
3. Check your default browser (Google Chrome or Mozilla Firefox are suggested for the fast running of the AlphaMap) and start working with the tool.

* If nothing happens when you launch AlphaMap, you might need to grant it permissions by going to the macOS menu "System Preferences | Security & Privacy | General". If the problem still persists, it is possible that macOS already quarantined the AlphaMap app. It can be

removed from quarantine by running <*xattr -dr com.apple.quarantine alphamap.app*> (copy everything between <>) in your terminal in the application folder where alphamap.app is located.

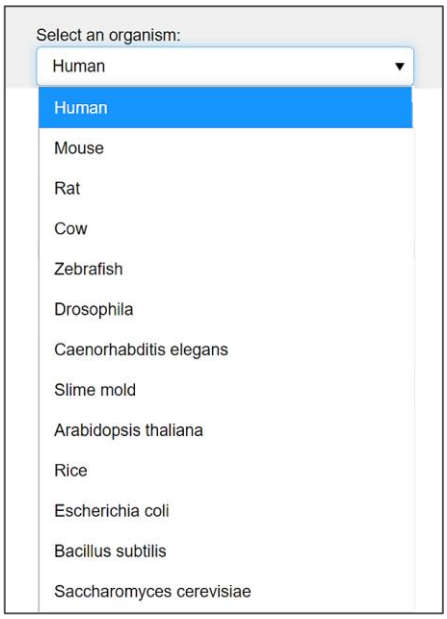
Linux:

1. Download the latest release for Linux (alphamap) from the GitHub repository to the desired location. By doing it, you accept the terms of the AlphaMap license agreement and all third-party licenses.
2. To run it, drag and drop the folder in the terminal and the GUI will open as a tab in your default browser. Google Chrome or Mozilla Firefox are suggested for the fast running of AlphaMap.

* If permissions are wrong, run <*chmod +x alphamap*> (copy everything between <>) in the terminal (at the right location).

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:

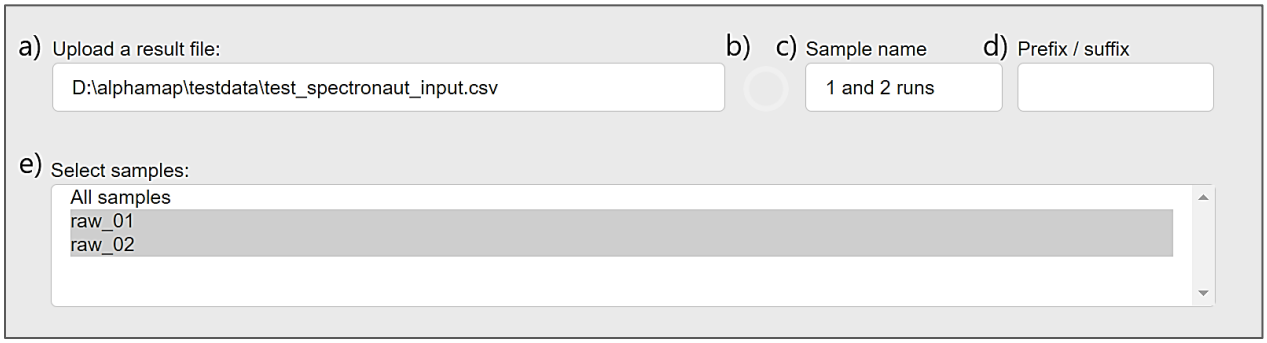
   a) Provide the filepath to the result file in the "Upload a result file:" field, e.g. "D:\spectronaut_output.csv".

   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.

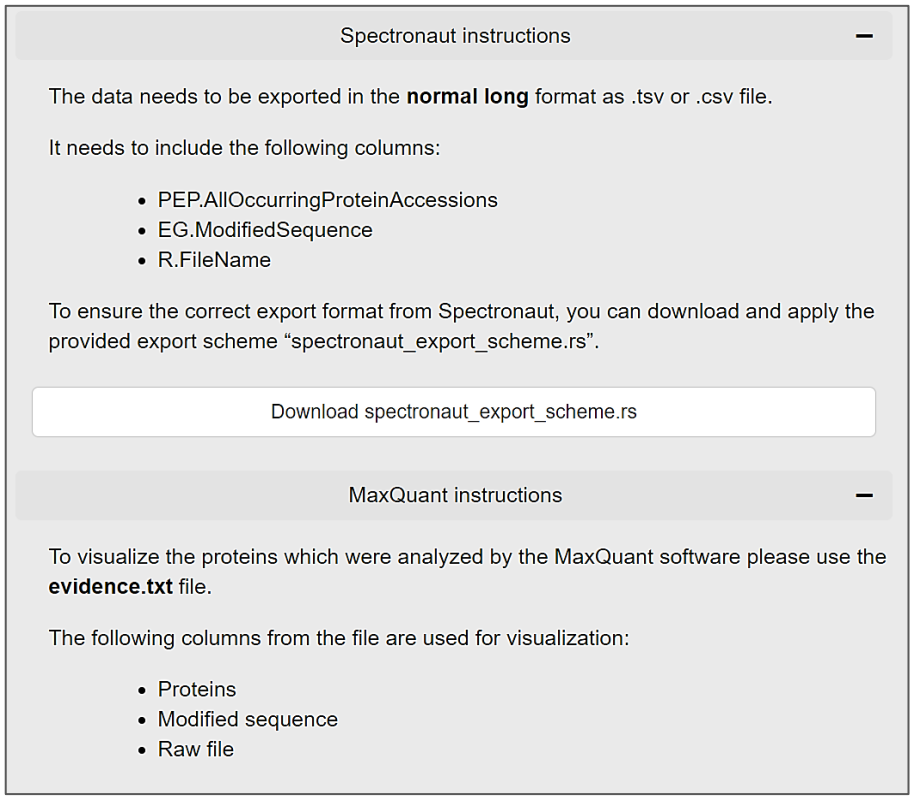
   d) (optional) Choose a name by which the selected sample(s) will be displayed in the figure. If no name is provided, the original names of all selected samples will be concatenated by semicolon. If 'all samples' were selected, the filename will be the default name.

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).



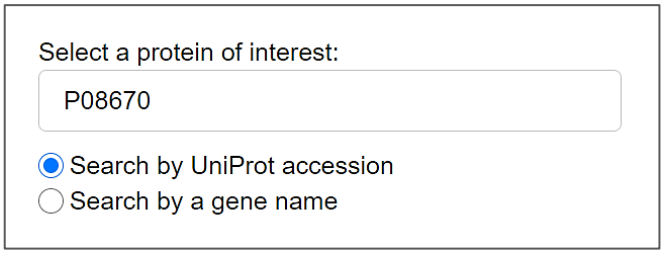
* Up to three datasets or sets of selected samples can be visualized together. For this, use the “Upload additional result files” option. If you would like to choose different samples from the same result file, you need to provide the same filepath and select the different samples.

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

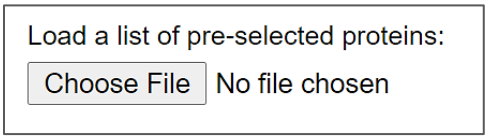


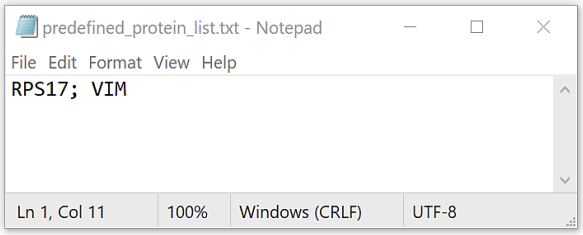
3. Press the "Upload Data" button. The loading process is indicated by a spinner symbol.

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.



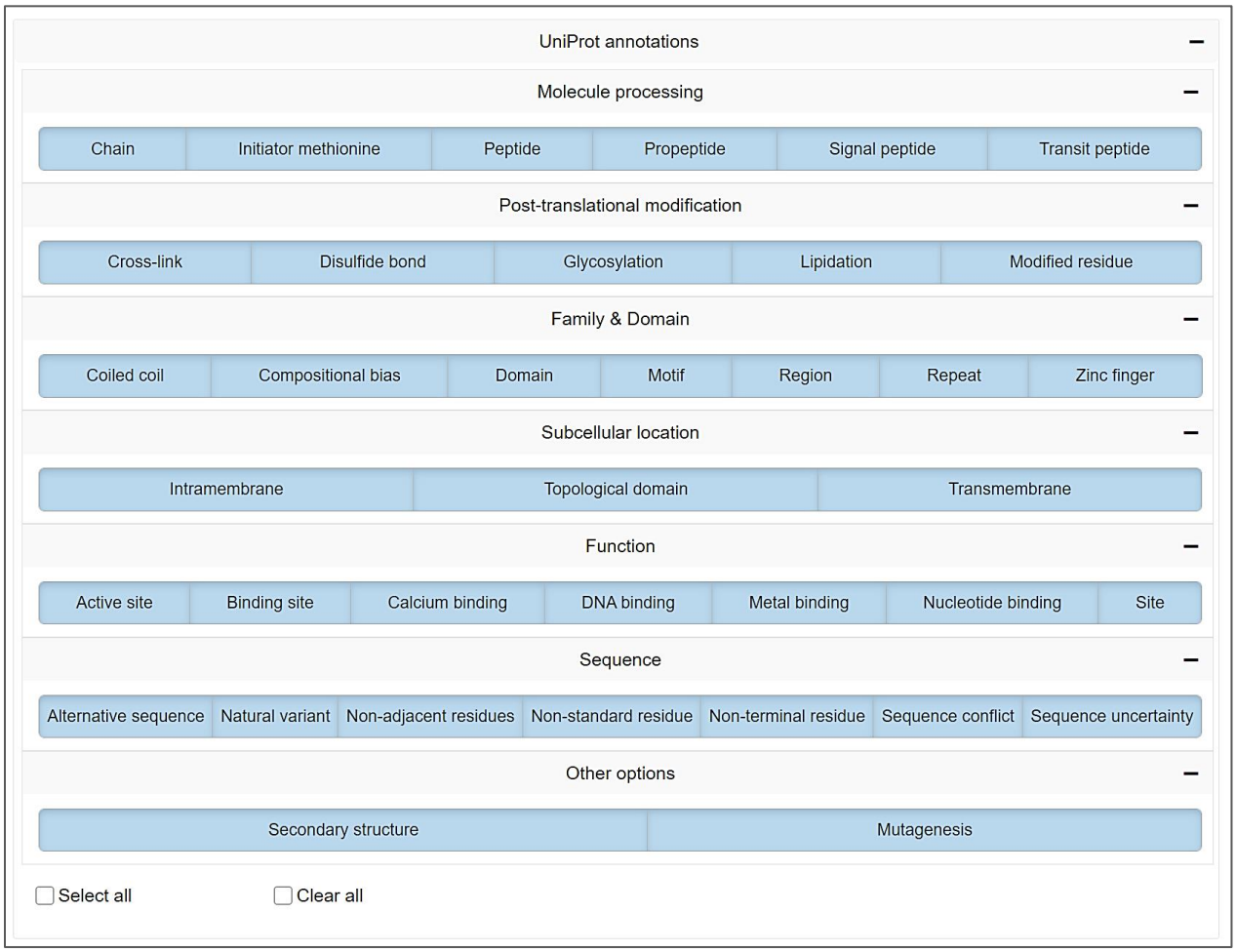
5. (optional) Load a list of pre-selected proteins. This can be a .txt file containing either UniProt accessions or gene names separated by semicolons. This will reduce the options available in the selection of proteins of interest (step 4).



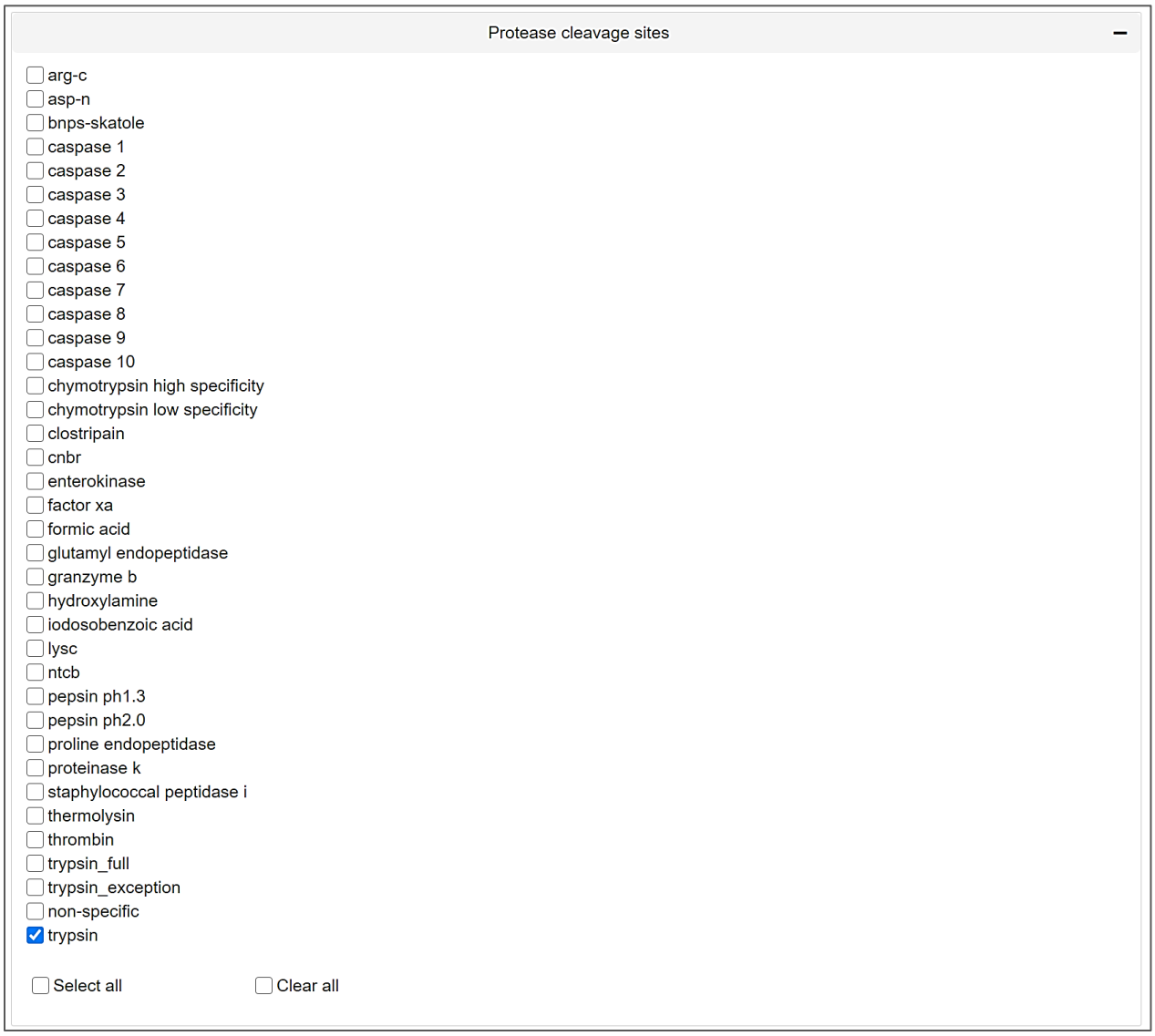


6. Select annotation options for the sequence visualization.

    - 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.



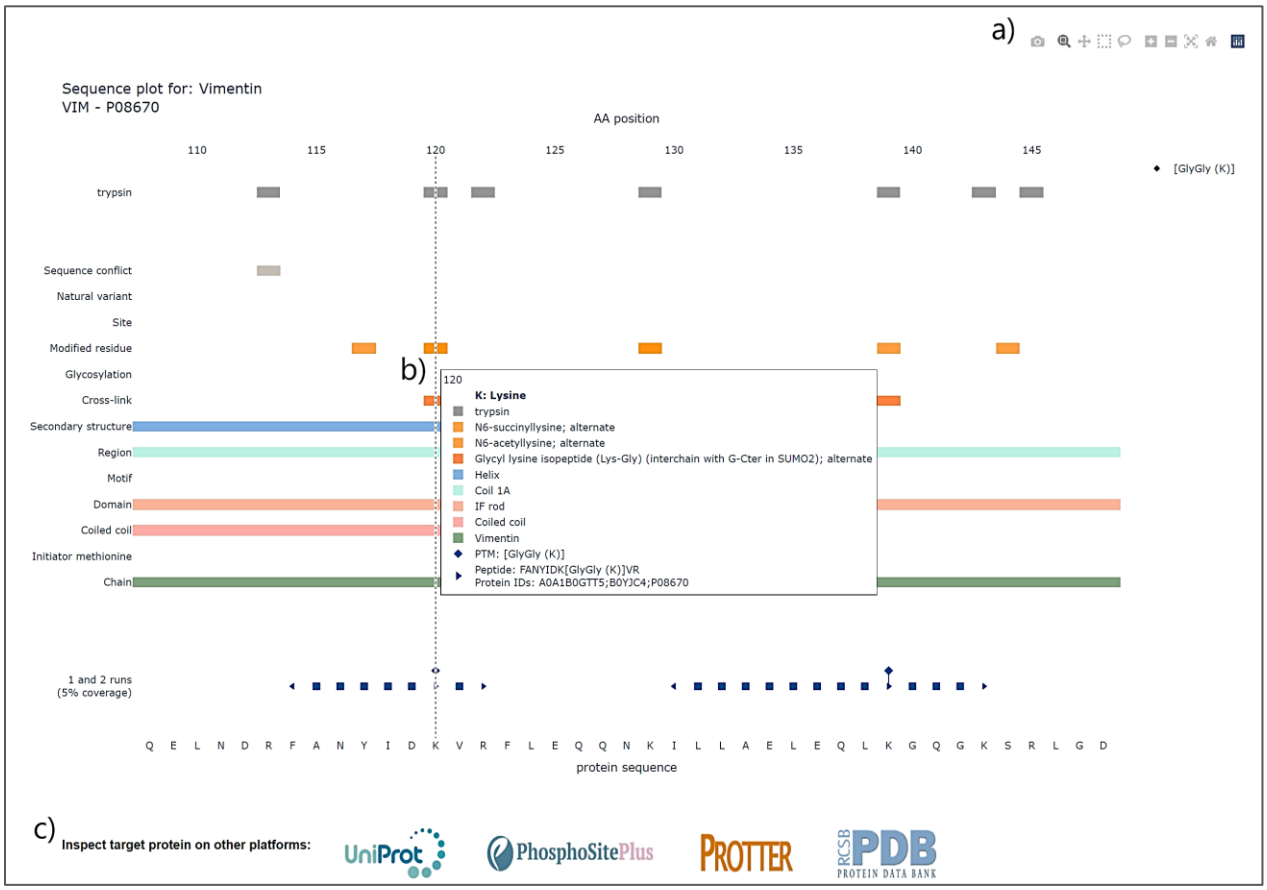
* You can use “Select all” or “Clear all” checkboxes to speed up the selection process.

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!

9. Please, press “Quit” button when your working session in AlphaMap is finished.

IMPORTANT WARNING! If you just close the browser tab and do not press the "Quit" button, AlphaMap will keep running in the background (potentially using a significant amount of RAM memory). This is especially important for **macOS**.