

# FASTA-OMSSA Protein Peptide Visualiser - User Guide

## Introduction

This program allows the user to input a FASTA file containing one protein, and an OMSSA file containing peptides matching that protein. Then the protein sequence is displayed with peptides highlighted. The peptides and their properties are shown in a table and there is also a visual representation of the protein and its peptides.

## How to use the program

Opening the program displays a window with 4 sections.

1. Open the FASTA file by clicking 'File' > 'Open FASTA File' in the menu bar.
2. A dialogue window pops up from which you should navigate to the file, select it and click 'Open'.
3. Now the protein sequence from the FASTA file will appear in the 'Sequence Viewer' text box.
4. Next open the OMSSA CSV file by clicking 'File' > 'Open OMSSA File'. Select the file and open it.
5. The program now displays information in three sections: 'Protein Viewer' shows a visual representation of the protein (white) with the peptides (grey) at their relative positions in the protein, 'Sequence Viewer' shows the protein sequence with peptides highlighted (grey) with their start (green) and stop (red) positions indicated, and 'Peptide Viewer' contains a table containing the peptides' UniProt ID, Peptide (sequence), Start (position), Stop (position), and p-value.

Note: if the peptides in the Protein Viewer appear black, reopen the program and do not resize the window before running.