

# User Manual

## What does Peptide Viewer do?

Peptide viewer reads two file inputs, a fasta file and a .csv file that contains OMSSA output. Then it parses both files in order to find matching peptides between both files. After finding the matches, the program highlights identified peptides visually in three different areas by three different methods. First, it shows a graphic which contains a rectangle which represents identified peptide sequences as colored, while the unidentified sequences remain white. Second, it shows the whole input fasta sequence as a text with identified peptides as colored text. Finally, it shows a table of identified peptides with their various properties, such as the starting point, ending point, e-value, mass, p-value etc.

## How to use Peptide Viewer?

- Execute the PeptideViewer.jar file to open the program.

- Click on UPLOAD FASTA button at the top to upload a .fasta file that you want to analyse (If successful, you should see the file name on top, also the button will turn green)

- Click on UPLOAD OMSSA button at the top to upload a .csv file containing OMSSA output that you want to use to search for identified peptides in the .fasta file (If successful, you should see the file name on top, also the button will turn green)

- Click SHOW PEPTIDES button at the top, this will show:

- A visual rectangle graphic that highlights portions of the fasta sequence depending on identified peptides in the sequence

- Highlighted text of the fasta sequence where identified peptides are in green color

- A table at the bottom showing the various properties of identified peptides

- The recents panel at the right will show which fasta files you successfully analysed recently