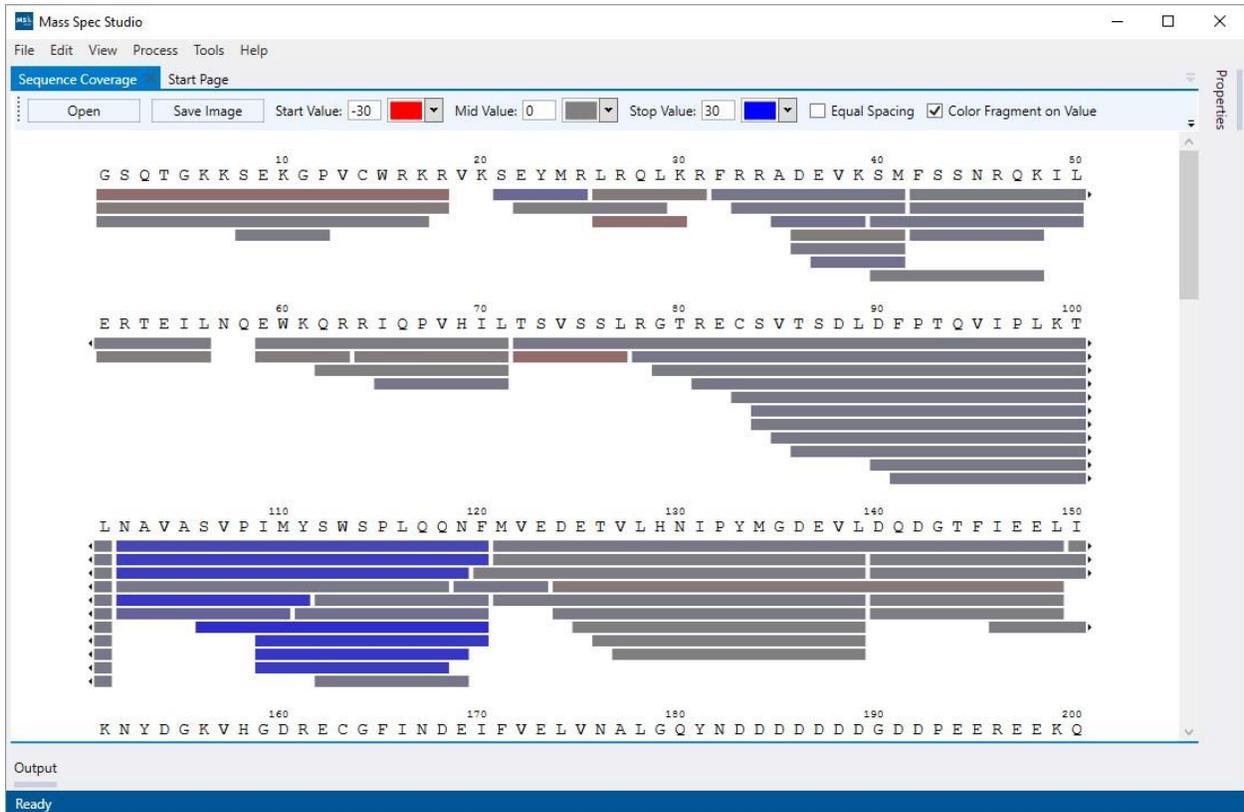


Sequence Coverage Visualizer 2.0



Installation and Usage Guide

vsarpe@gmail.com

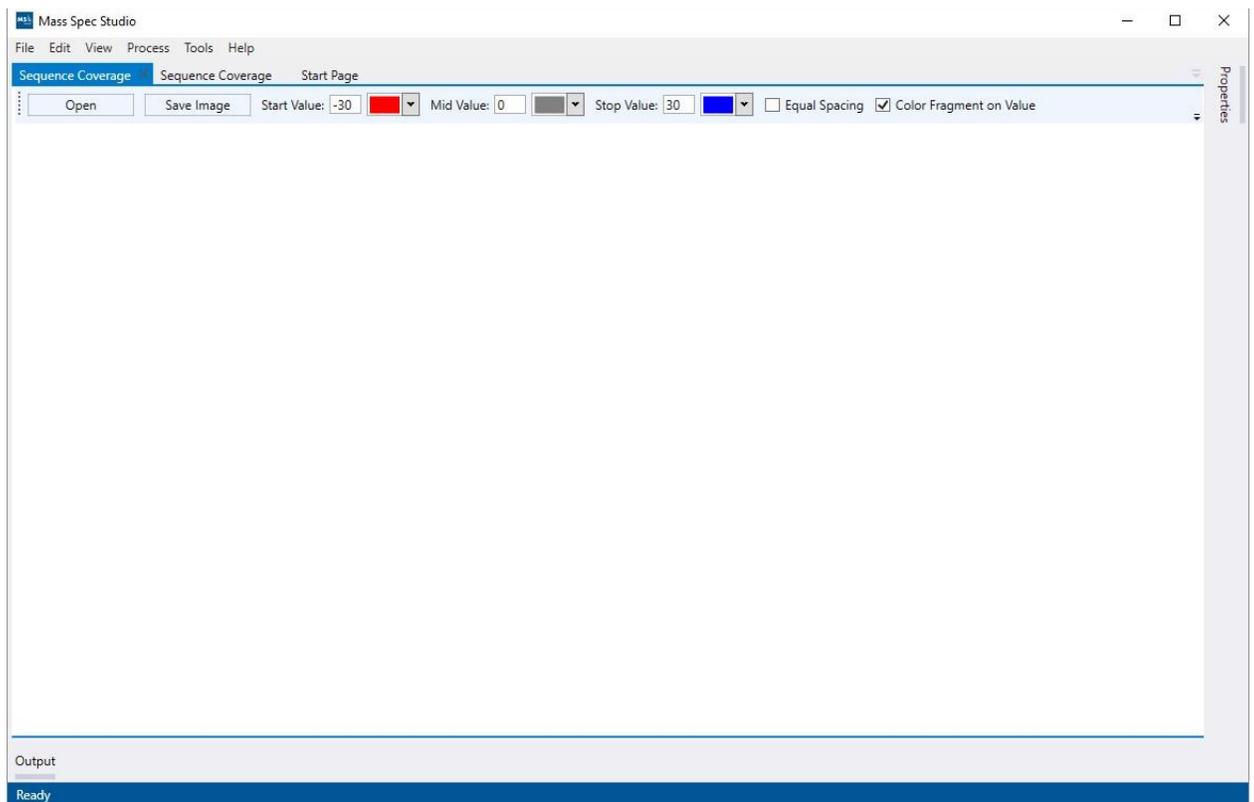
Installation:

1. Download and install the latest version of Mass Spec Studio 2.0 from <https://www.msstudio.ca/downloads/general/>.
2. Download the SequenceCoverageVisualizer plug-in from <https://mssdownloads.s3-us-west-2.amazonaws.com/releases/SequenceCoverageVisualizer.zip>.
3. Start MSStudio and open the “Tools -> Component Manager”
4. Click the Install button in the bottom left, select “Current User”, and select the SequenceCoverageViewer.zip file you downloaded in step 2. There should be a popup saying the installation was successful.
5. Hit “Apply” in the bottom right of the Component Manager window. MSStudio will restart and load the newly install plug-in.

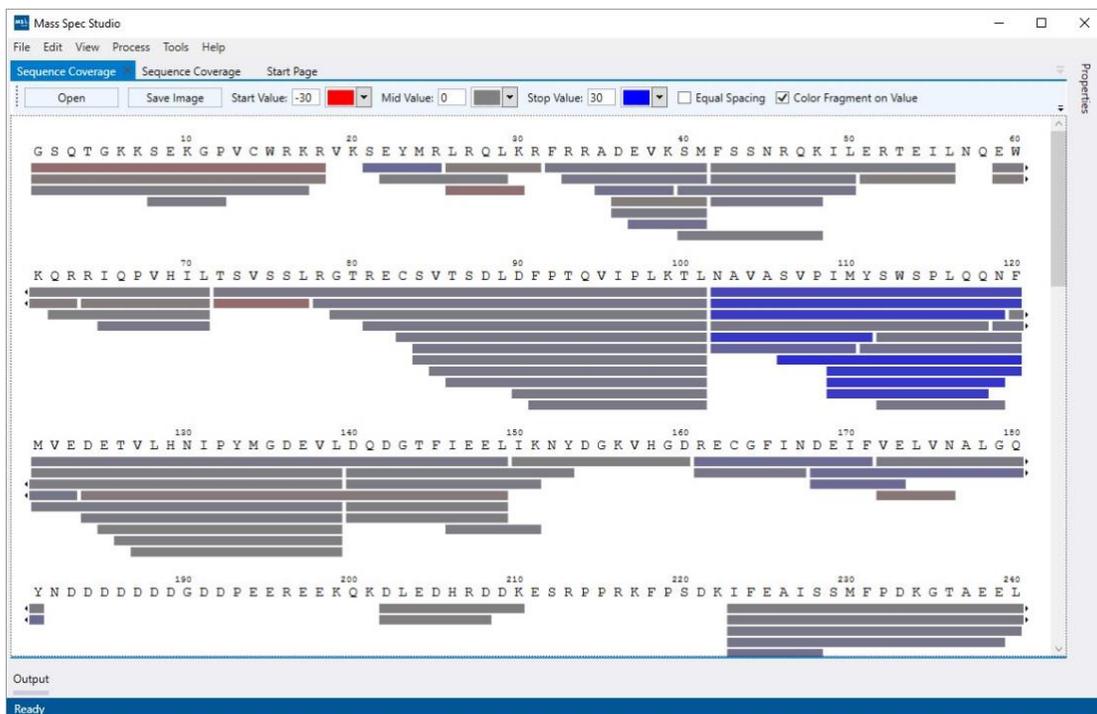
Usage:

This plugin will run whether you have a project open already or not.

1. Open the “Sequence Coverage Visualizer” from the “Tools -> External Tools -> Sequence Coverage Visualizer”.



2. Click Open and load in your CSV file and FASTA file. The FASTA file should contain only 1 sequence (otherwise the first will be selected by default). The CSV files should contain the following fields: **Start, Stop, Value** in any order. To plot a descending gradient for each peptide, you can add additional **Value** columns (Example: **Start, Stop, Value 1, Value 2, Value 3**). They will be rendered in a descending gradient on the peptide sequence.



3. You can change the settings to completely customize the view from the toolbar at the top.
 - a. Change the start value and color (Min).
 - b. Change the mid value and color.
 - c. Change the stop value and color (Max).
 - d. Change whether you want equal spacing between sequences.

- e. Change whether you want to color the fragments based on value of just the default fragment color.
 - f. Change the default color (will only show if the previous option is OFF).
 - g. Change whether you want to display a title on the viewer.
 - h. Change the title itself.
4. You can click “Save Image” to save a 300dpi TIFF image of the viewer. Note that the number of amino acids per row will match that of your view, so resize it to your liking before saving the image.
5. You can have multiple tabs of the sequence visualizer open at the same time, each with its own sequence and properties.