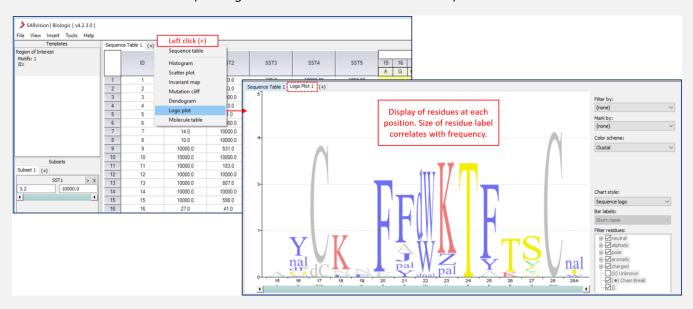
Mastering the Logo and Bar Plots in SARvision|Biologics

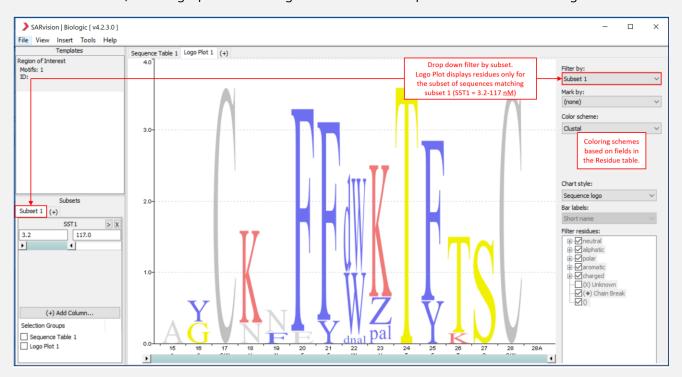
Once you have created a Sequence Table and want to perform advance sequence analysis, the Logo and Bar plot views are another way to visualize your data.

1. Left click on the (+) tab next to the Sequence Table to add a new view. Select the Logo plot. A new tab will be added to workspace containing the Logo plot view. The Logo plot will have the reference sequence and the numbering plotted along the bottom of the view and contains residue or monomer abbreviations stacked at each position. The size of the letters for each monomer reflect the frequency for which that residue appears. For example, below at position 17, Cappears in the dataset much more frequently than its enantiomeric counterpart dC.

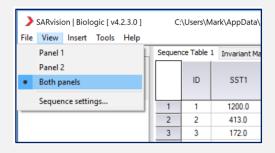


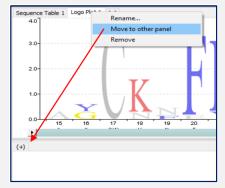
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2. Using the filter subsets, the Logo plot can be tuned to those residues that increase potency or to those that decrease potency. In Subset 1, the data is filtered to sequences with SST1 activity between 3.2 and 117 nM. Setting the *Filter by: Subset1* in the right hand control, the Logo plot now only reflects those sequence that fit this range.



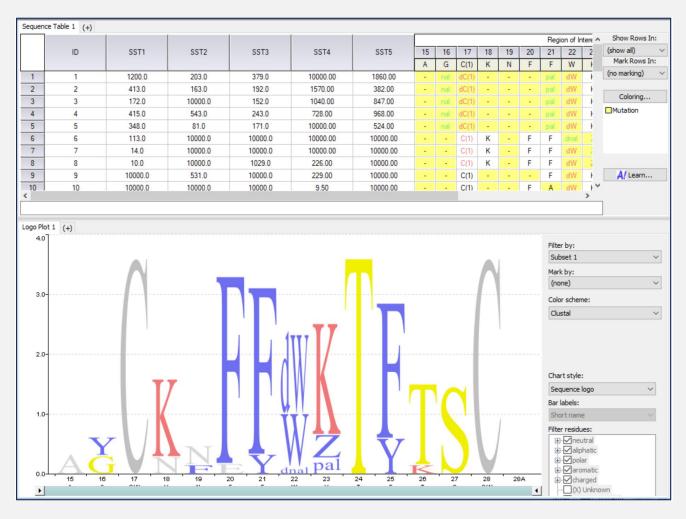
3. To visualize two views simultaneously, select under *main menu->view->Both panels* to create stacked views in the SARvision workspace.





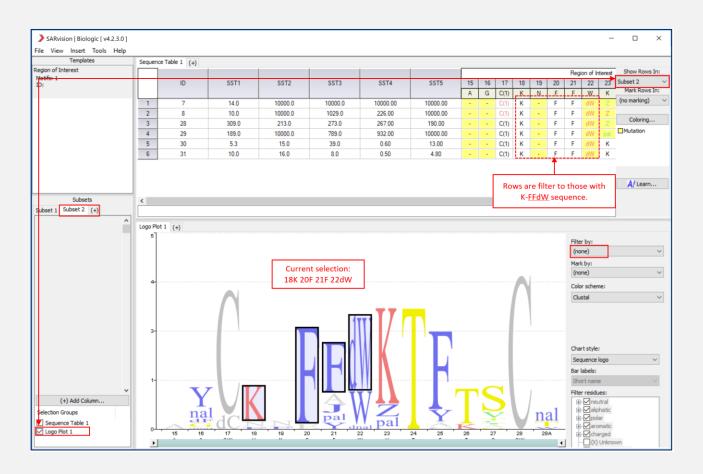
4. Then *right click on the Logo plot tab* and *Move to other panel* will move the Logo plot to the bottom panel.

5. You will now have stacked view that look similar to the one below.



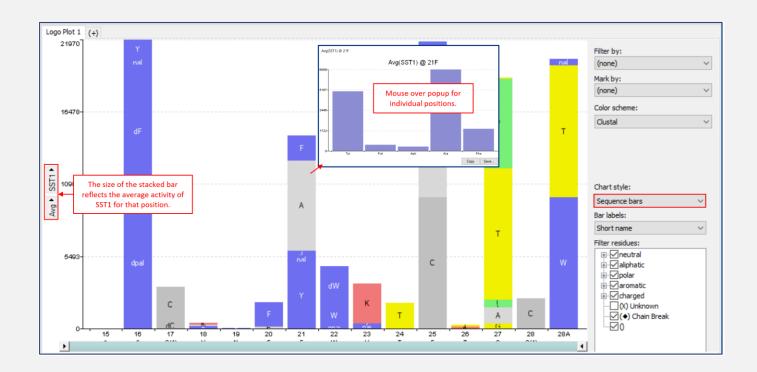
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6. These two views can be linked together using the subsets panel in the lower right. Create a new subset by *left clicking on the (+) in the subset tab*. Then *check the Logo Plot* at the bottom of Subset 2. Now any selection inside of the Logo Plot becomes subset 2. Setting the *Filter by: subset 2* in the right-hand control panel of sequence table will filter the sequence table by the selection in the Logo plot in real time. Note that using ctrl-right click to select residues in the Logo plot will allow the user to filter by sequence motifs. For example (K-FFdW). Note, be sure to set the *Filter by: method to '(none)'*.



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7. Last, the Logo Plot can be transformed into a bar plot. Instead of plotting letter of different sizes, it will now plot stacked bars such that the bar size reflects some property in the dataset. On the left had side of the plot, select a property and an aggregation method (eg. Average of SST1). Mouse over on any position in the bar plot will pop up a 1D representation of the residues at that position.



Next you may want to learn about Invariant Maps and Mutation Cliffs

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