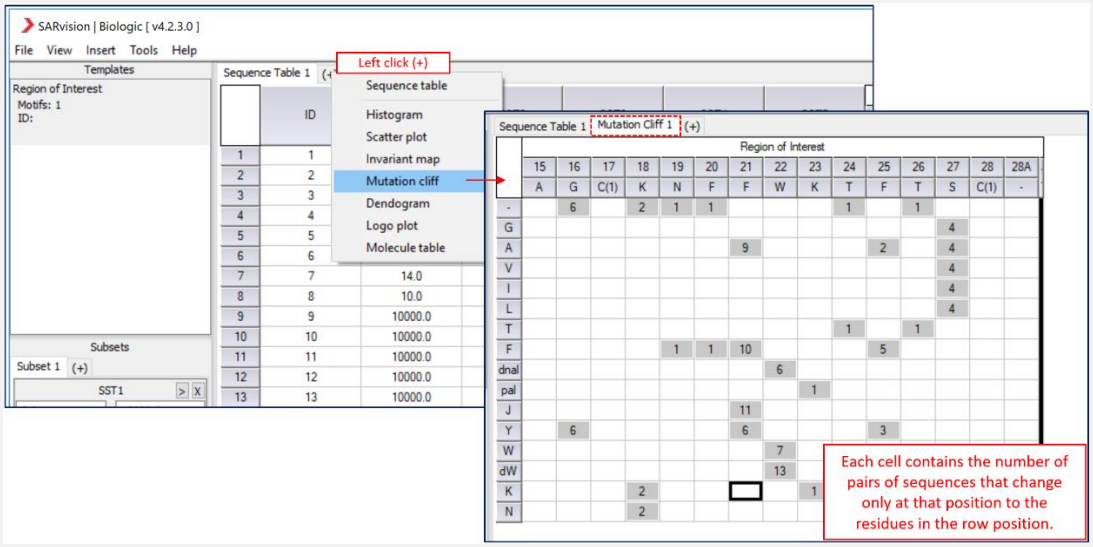
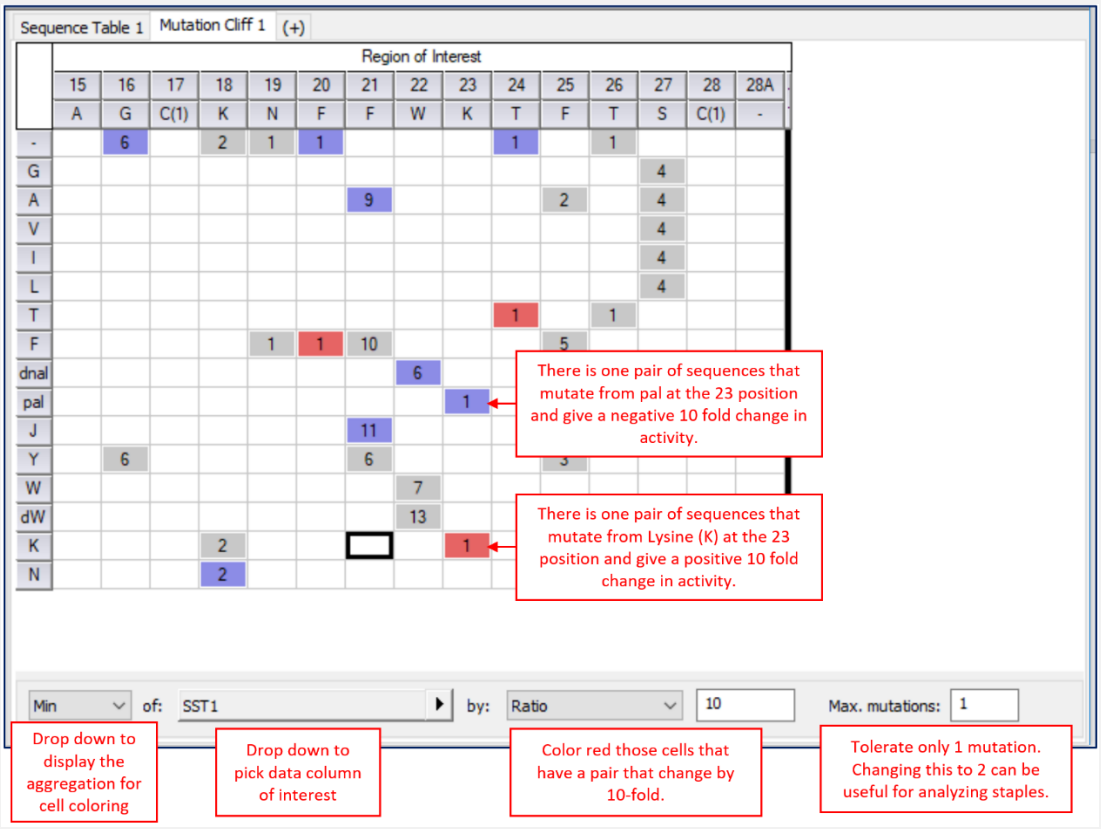
Mastering the Mutation Cliffs in SARvision|Biologics

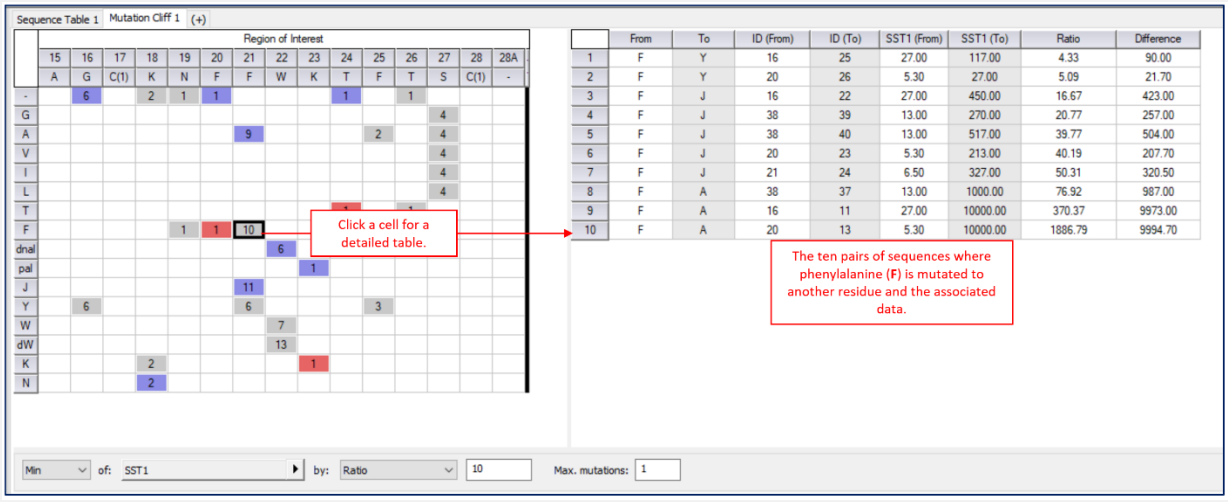
Once you have created a Sequence Table and want to perform advance sequence analysis, the Mutation Cliff table view is a good way to study individual mutations. It is set up to identify pairs of sequences that differ only at a single position and organize them by one of the mutations (rows) and sequence position (columns). For a more detailed description please read our article in J Chem Inf Model. 2013 53(10):2774-9. doi: 10.1021/ci400333x.

1. *Left click on the (+)* tab next to the Sequence Table to add a new view. Select the *Mutation cliff*. A new tab will be added to workspace. The Mutation cliff has the reference sequence and numbering along the top of the table and lists the residues (or monomers) along the left side as rows. Each cell displays the number of pairs of sequences that differ only at this position and have a mutation involving the residue on the row. For example, at position 16 there are 6 mutations involving Tyrosine (Y).



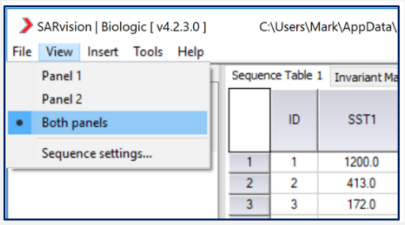


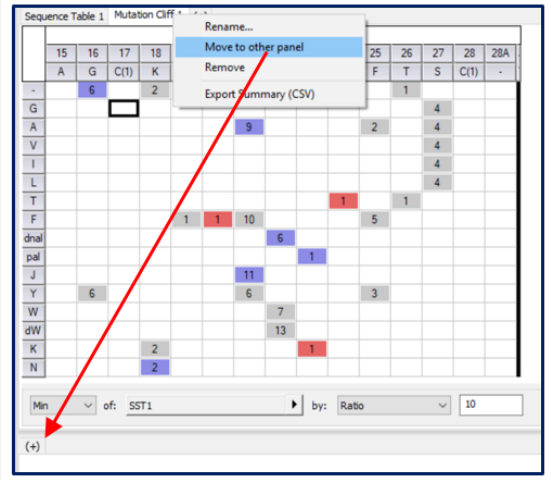
2. Use the bottom control bar to choose a column of data to study in the table. Data changes associated with cells can be aggregates as the minimum or maximum values. Cells are colored blue and red based on the magnitude of the change (ratio = 10 fold change).



3. To examine mutation pairs in greater detail, *left click on a cell* of interest. The components (pairs of sequences with data) will popup in a sub-table on the right. The sub-table can be sorted and answers the question how mutation of as specific residue affect activity. In the example below, the 10 mutation cliffs involving phenylalanine (F) at the 21 position are displayed with the corresponding mutation and data that exist in this dataset.

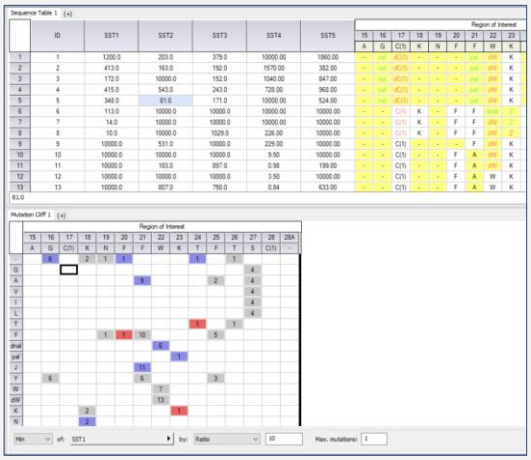
4. To visualize two views simultaneously, select under *main menu->view->Both panels* to create stacked views in the SARvision workspace.





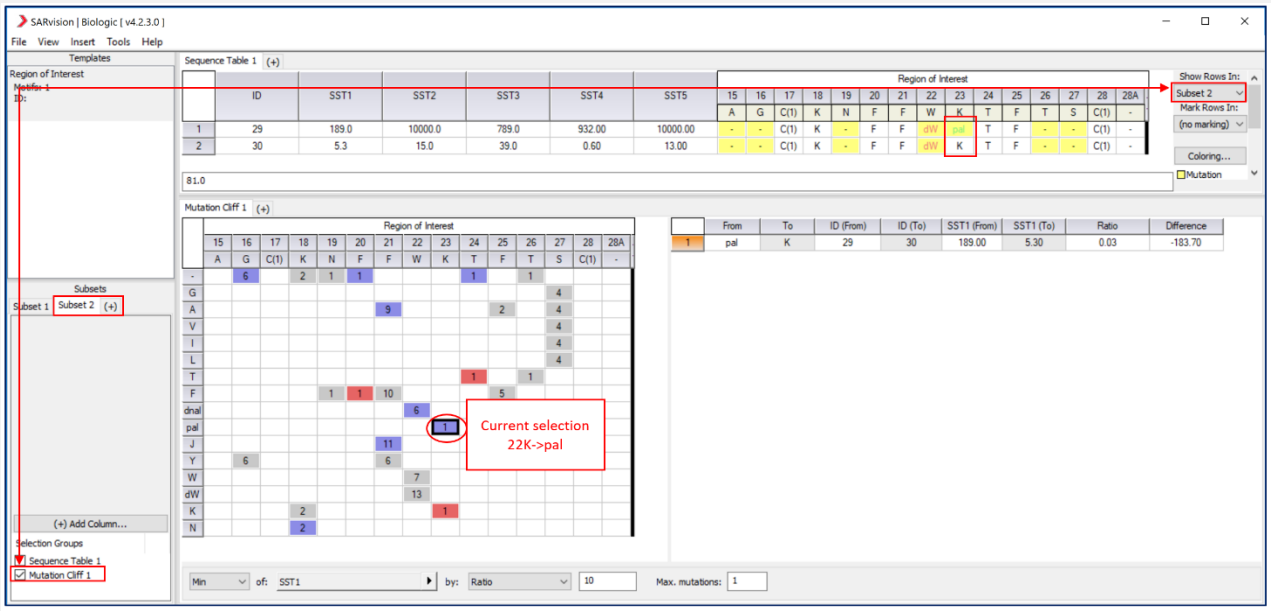
5. Then *right click on the Mutation cliff tab* and *Move to other panel* will move the Mutation cliff to the bottom panel.

6. You will now have stacked view that look similar to below.



7. These two views can be linked together using the subsets panel in the lower right.
    a. Create a new subset by *left clicking on the (+) in the subset tab*.
    b. Then *check the Mutation cliff* at the bottom of the subset. Now any selection inside of the Mutation cliff becomes subset 2. Setting the *Show Rows In: subset 2* in the right-hand control panel of sequence table will filter the sequence table by the selection in the Mutation cliff in real time. In this way the user can browse all the data (instead of just a single point as in the sub-table).

Note that selection can be done at the cell level in the mutation table to select a group of sequences, OR can be done at the sub-table level to select individual pairs of sequences.



For more information contact us at info@altoris.com