# Mastering the Invariant Maps in SARvision|Biologics

Once you have created a Sequence Table and want to perform advance sequence analysis, the Invariants table view is a good way to study individual mutations. This table shows which residues have been tried at each position in the sequence alignment and how many times. 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 *Invariant map*. A new tab will be added to workspace. The invariant map 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 times a specific residue has been tried at a given position. Empty cells are residue-position combinations that have not been tried ("holes"). The user can mouse over any cell to see the data for that cell in a popup.
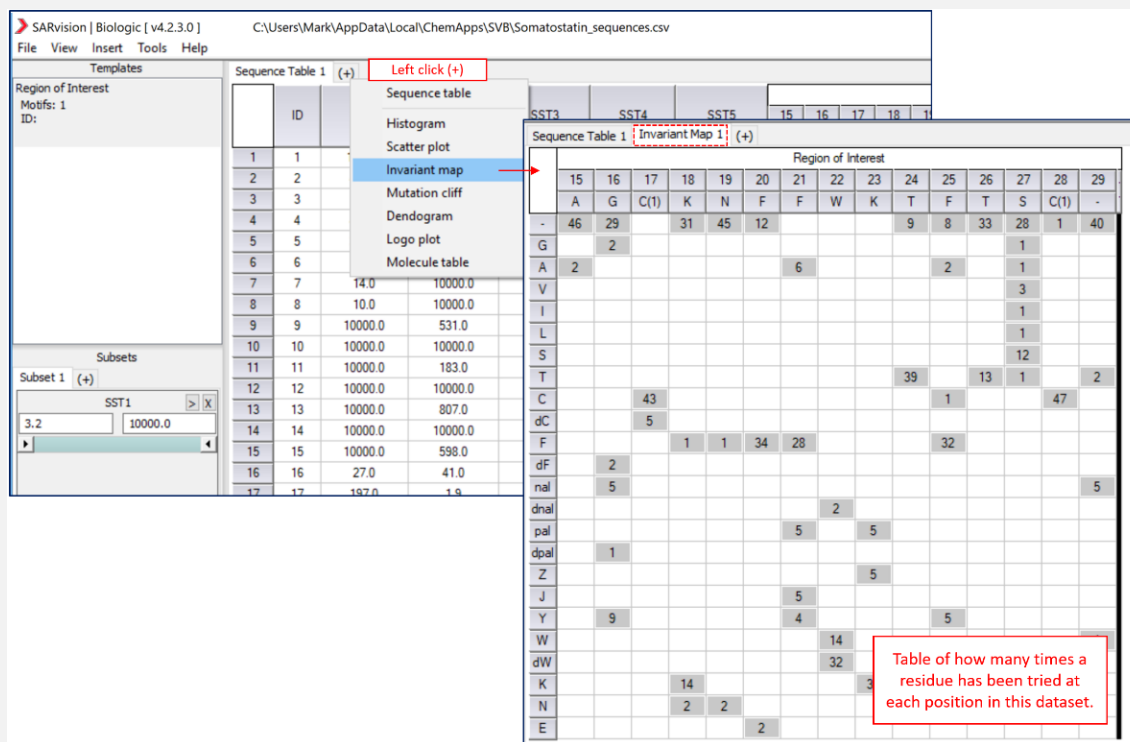
2. Use the bottom control bar to heatmap the table based on data for rows belonging to each cell. Data in each cell can be aggregated using (average, minimum or maximum) and heatmapped to specified color and data range. Below, the SST1 column is averaged and then heat mapped from blue(3.55nM) to red(10000nM).
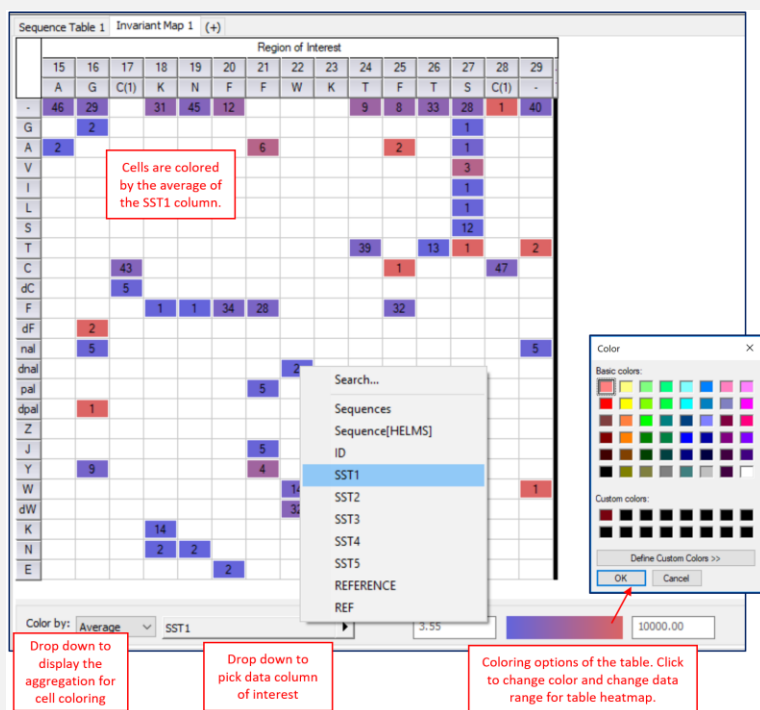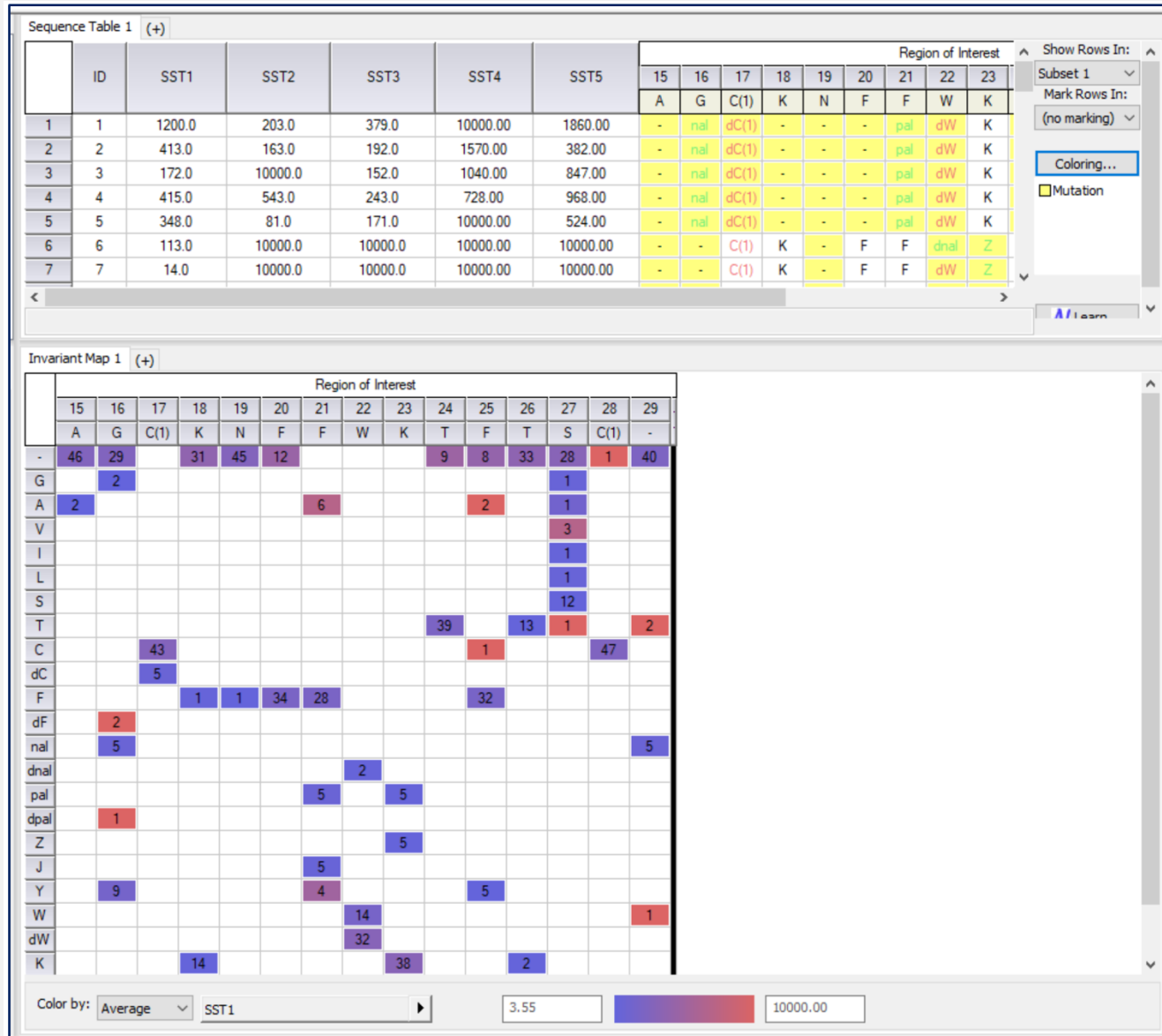

3. To visualize two views simultaneously, select under *main menu->view->Both panels* to create stacked views in the SARvision workspace.
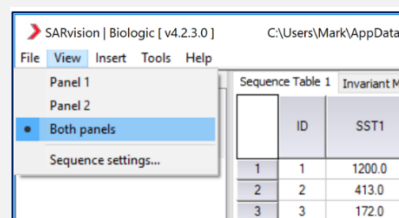

4. Then *right click on the Invariant map tab* and *Move to other panel* will move the invariant map to the bottom panel.

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

Sequence Table 1 (+)

	ID	SST1	SST2	SST3	SST4	SST5	15	16	17	18	19	20	21	22	23
							A	G	C(1)	K	N	F	F	W	K
1	1	1200.0	203.0	379.0	10000.00	1860.00	-	nal	dC(1)	-	-	-	pal	dW	K
2	2	413.0	163.0	192.0	1570.00	382.00	-	nal	dC(1)	-	-	-	pal	dW	K
3	3	172.0	10000.0	152.0	1040.00	847.00	-	nal	dC(1)	-	-	-	pal	dW	K
4	4	415.0	543.0	243.0	728.00	968.00	-	nal	dC(1)	-	-	-	pal	dW	K
5	5	348.0	81.0	171.0	10000.00	524.00	-	nal	dC(1)	-	-	-	pal	dW	K
6	6	113.0	10000.0	10000.0	10000.00	10000.00	-	-	C(1)	K	-	F	F	dnal	Z
7	7	14.0	10000.0	10000.0	10000.00	10000.00	-	-	C(1)	K	-	F	F	dW	Z

Region of Interest

Show Rows In: Subset 1

Mark Rows In: (no marking)

Coloring...

☐ Mutation

Invariant Map 1 (+)

Region of Interest

	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29
	A	G	C(1)	K	N	F	F	W	K	T	F	T	S	C(1)	-
-	46	29		31	45	12				9	8	33	28	1	40
G		2											1		
A	2						6				2		1		
V													3		
I													1		
L													1		
S													12		
T										39		13	1		2
C			43								1			47	
dC			5												
F				1	1	34	28				32				
dF		2													
nal		5													5
dnal								2							
pal								5	5						
dpal		1													
Z									5						
J								5							
Y		9						4			5				
W								14						1	
dW								32							
K				14					38			2			

Color by: Average SST1 ▶ 3.55 10000.00

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 Invariant map* at the bottom of the subset. Now any selection inside of the Invariant map becomes subset2. 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 Invariant map in real time. Note that using ctrl-right click to select cells in the Invariant map will allow the user to filter by sequence motifs. For example (C--WN).
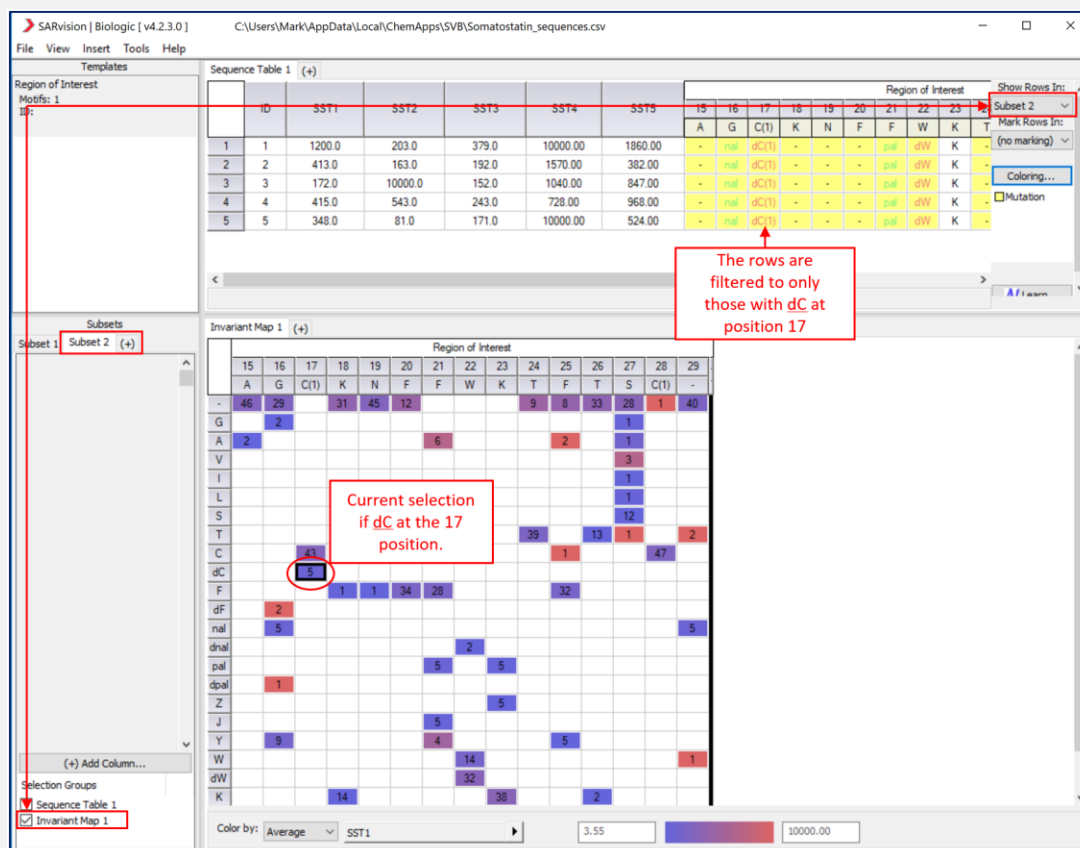
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