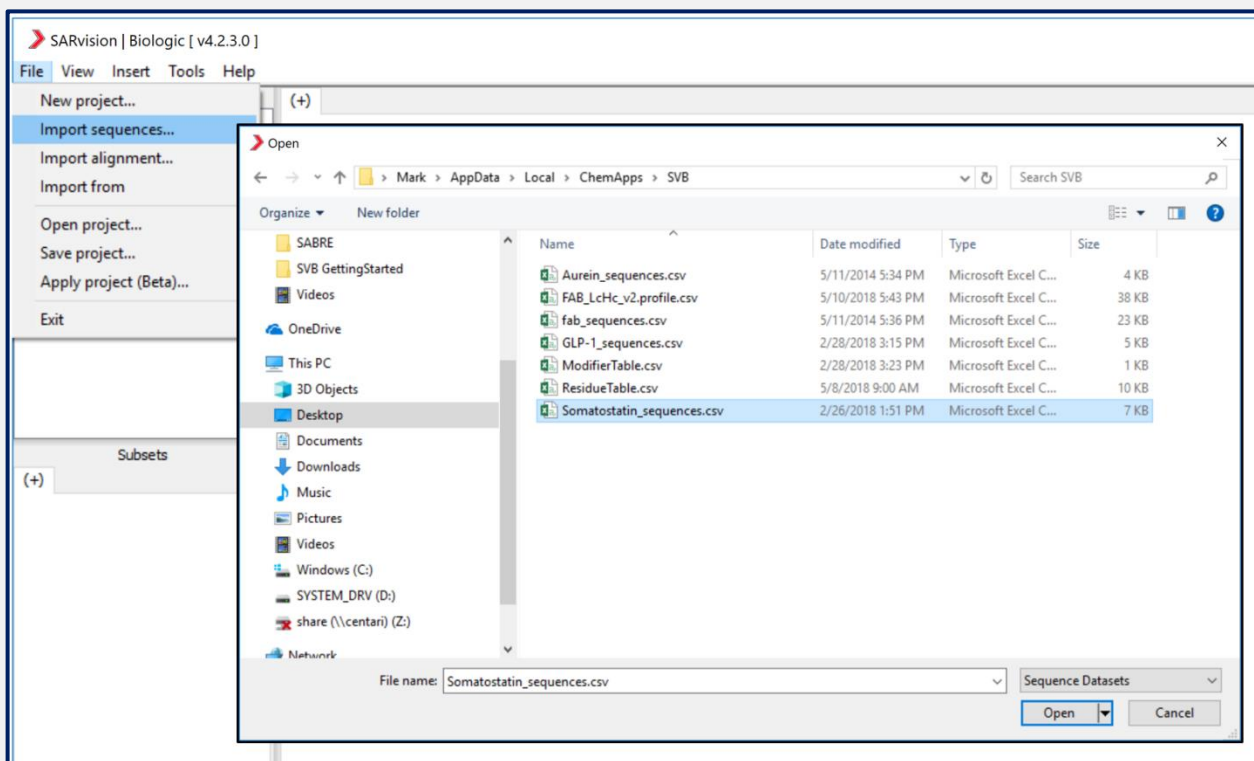
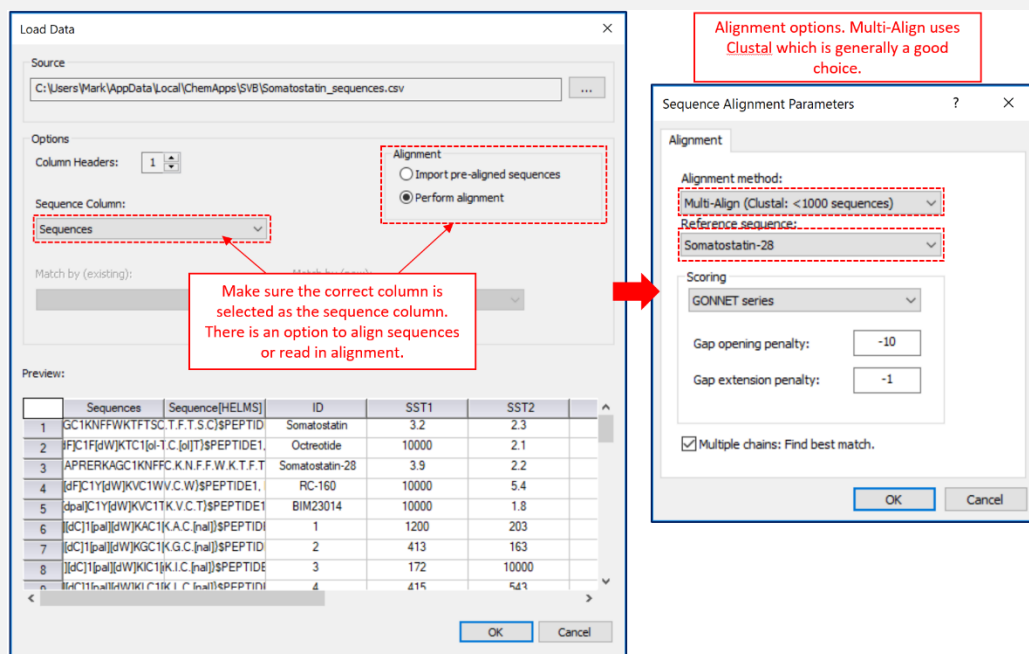


## Mastering the Sequence Table in SARvision|Biologics

1. Import some sequences to analyze. Under **Tools->open resource folder** are located some example files that you can experiment. In this example we will use the somatostatin example dataset (**Somatostatin\_sequences.csv**). Under main menu->Import sequences... open a sequence file.



- After loading, SARvision|biologics will display an import UI so that the proper parsing can be performed and the sequence identified. The sequence column defaults to a column that contains "Sequence" in the name. The decision to align sequences or import sequence alignment (sequences that contain '-' in them) is made here. The UI is the alignment UI for the user to choose the reference sequence, the alignment method and parameters to use in alignment.



3. Under right click on the Sequence Table Table tab ->Columns... and unclutter the Sequence table view by hiding unnecessary columns and locking the ID column on the left.

Right click tab

Too many columns clutter the display. Hide uninteresting columns and lock the ID column on the left.

Column Display

Hidden:

Displayed:

Lock/Unlock

Format...

4. Right click on data column to add some *heatmaps* and to *sort* columns.

Sequence Table 1 (+)

ID SST1 SST2 SST3 SST4 SST5

1 BIM23014 10000.0 1.8 0.62

2 17 197.0 1.9 43.00

3 Octreotide 10000.0 2.1 5.60

4 Somatostatin-28 3.9 2.2

5 Somatostatin 3.2 2.3

6 34 112.0 5.0

7 RC-160 10000.0 5.4

8 30 5.3 15.0

9 19 10.3 8.2 0.51

10 31 10.0 8.0 0.50

11 25 117.0 36.0 1.80

12 18 79.0 222.0 3.30

13 16 27.0 13.0 1.80

14 21 6.5 10.0 1.30

15 26 27.0 22.0 1.30

16 40 517.0 263.0 1.20

17 36 330.0 347.0 1.10

18 22 450.0 271.0 0.88

19 5 348.0 171.0 10000.0

20 33 59.0 189.0 1.20

21 20 5.3 13.0 0.70

22 2 413.0 163.0 1570.00 382.00

Sort increasing

Sort decreasing

Heatmap...

Remove heatmap

Format...

Rename...

Delete

Heatmap [SST2]

0 100

100 300

Set up some heatmap ranges to color individual columns.

Use values in: SST2

OK Cancel

Sequence Table 1 (+)

Data columns.

Reference sequence on top: Somatostatin-28 selected on import.

Macrocycle linkers are numbered.

Mutations highlighted with yellow background

Unnatural amino acid have user defined color coded font.

Data

Sequence alignment

ID	SST2	SST3	SST4	SST5	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	
1	BIM23014	1.8	43.0	66.00	0.62	S	A	N	S	N	P	A	M	A	P	R	E	R	K	A	G	C(1)	K	N	F	F	W	K	T	F	T	S	C(1)
2	17	1.9	52.0	1.00	43.00	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
3	Odreotide	2.1	4.4	10000.00	5.60	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
4	Somatostatin-28	2.2	7.1	3.80	3.90	S	A	N	S	N	P	A	M	A	P	R	E	R	K	A	G	C(1)	K	N	F	F	W	K	T	F	T	S	C(1)
5	Somatostatin	2.3	3.5	2.50	2.40	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
6	34	5.0	11.0	1.40	9.50	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
7	RC-160	5.4	3.1	10000.00	0.70	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
8	30	15.0	39.0	0.60	13.00	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
9	19	15.5	8.2	0.51	4.80	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
10	31	16.0	8.0	0.50	4.80	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
11	25	26.0	36.0	1.80	20.30	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
12	18	28.0	222.0	3.30	8.60	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
13	16	41.0	13.0	1.80	46.00	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
14	21	43.0	10.0	1.30	24.00	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
15	26	54.0	22.0	1.30	63.00	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
16	40	56.0	263.0	1.20	34.00	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
17	36	57.0	347.0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
18	22	71.0	271.0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
19	5	81.0	171.0	10000.00	524.00	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
20	33	95.0	189.0	1.20	31.00	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
21	20	130.0	13.0	0.70	14.00	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
22	2	163.0	192.0	1570.00	382.00	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
23	24	170.0	247.0	1.10	240.00	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
24	38	179.0	57.0	1.60	19.00	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
25	11	183.0	897.0	0.98	199.00	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
26	1	203.0	379.0	10000.00	1860.00	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
27	28	213.0	273.0	267.00	190.00	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
28	39	260.0	135.0	1.90	663.00	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
29	23	347.0	10000.0	1.20	10000.00	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
30	9	531.0	10000.0	229.00	10000.00	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
31	4	543.0	243.0	728.00	968.00	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
32	15	598.0	10000.0	10000.00	10000.00	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
33	37	622.0	624.0	2.00	692.00	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
34	13	807.0	750.0	0.84	633.00	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
35	3	10000.0	152.0	1040.00	847.00	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
36	6	10000.0	10000.0	10000.00	10000.00	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
37	7	10000.0	10000.0	10000.00	10000.00	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	

5. The sequence table should look something like what is shown below.

6. Since there is only one sequence that has an N-terminal tail on the peptide, the first 15 or so residues are not very interesting. The view can be filtered down to only the region of the alignment (Region of Interest) that is interesting. Right click in the Templates box and Edit template.... Change the range to "15-\*" or position 15 to the end of the sequence. The

SARvision | Biologic [ v4.2.3.0 ] C:\Users\Mark\AppData\Local\ChemApps\SVB\Somatostatin\_sequences.csv

File View Insert Tools Help

Templates

Region of Interest: 1

Notifs: 1

ID:

Right click

Edit template...

Save template...

Clone template

Delete template

Set to mutations only

Label sequences...

Subsets

Subset 1 (+)

Sequence Table 1 (+)

ID	SST1	SST2	SST3	SST4	SST5	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29
1	8	30	0.62	A	G	C(1)	K	N	F	F	W	K	T	F	T	S	C(1)	-	-	-
2	9	19	43.00	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3	10	31	5.60	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
4	11	25	3.90	A	G	C(1)	K	N	F	F	W	K	T	F	T	S	C(1)	-	-	-
5	12	18	2.40	A	G	C(1)	K	N	F	F	W	K	T	F	T	S	C(1)	-	-	-
6	13	16	2.40	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
7	14	21	9.50	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
8	15	26	0.70	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
9	16	40	13.00	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
10	17	36	4.80	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
11	18	22	4.80	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
12	19	5	20.30	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
13	20	33	8.60	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
14	21	20	46.00	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
15	22	71.0	24.00	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
16	23	171.0	63.00	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
17	24	347.0	31.00	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
18	25	189.0	14.00	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
19	26	192.0	240.00	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
20	27	247.0	199.00	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
21	28	57.0	692.00	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
22	29	897.0	968.00	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
23	30	379.0	10000.00	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
24	31	273.0	10000.00	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
25	32	135.0	10000.00	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
26	33	152.0	10000.00	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
27	34	1040.00	10000.00	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
28	35	847.00	10000.00	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
29	36	10000.00	10000.00	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
30	37	10000.00	10000.00	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-

Template Editor

Name: Region of Interest

Reference sequence: SARSNPANAPRRKAGCKRFFVKTFTSC

Current sequence: SARSNPANAPRRKAGCKRFFVKTFTSC

Notifs: 1

Name: Region of Interest

Range: 15-\*

Color: (none)

Start sequence numbering at: 1

OK Cancel

reference sequence can be change in the drop down box. The text displayed at the top of the alignment can be changed here as well.

7. Create Residue/monomer filters for sequence alignment columns. **Right click on a column** and select **Filter by residue....** The user can choose to display/hide rows based on the residue in this position of the alignment. Note that one can apply filters to multiple columns and filter by sequence motifs.

The screenshot shows a sequence alignment table with columns 15 to 29. A right-click context menu is open over column 16, with 'Filter by residue...' selected. The dialog box 'Filter by Residue' is shown, with 'Show rows where residue at 16 is:' and a list of residues with their frequencies: '-' (29), 'Y' (9), 'nal' (5), 'G' (2), 'dF' (2), and 'dpal' (1). The 'dpal' checkbox is checked. The resulting table shows only rows where column 16 contains 'dpal', 'dF', or 'nal'.

The column is filter to show only rows that have monomers: Dpal, dF, nal

8. Add addition filters using the Subset filter panel. Click on the **(+) Add Column...** in the lower left corner and add a property column (SST2). In the top part of the Subset panel a range filter gets added and the user can manually set a range to filter the table by. Because the

The screenshot shows the 'Subset' filter panel on the left, with 'SST2' selected in the 'Add Column...' list. The 'Range' filter is set to '1.8' to '81.0'. The main table shows the results of this filter, with rows 1, 2, 3, and 4 highlighted in green. The table has columns ID, SST1, SST2, SST3, SST4, SST5, and a 'Region of Interest' section with columns 15 to 29. The 'Show Rows In:' dropdown is set to 'Subset 1'.

Only rows are shown that have a SST2 value between 1.8 and 81.0.

The default is for the Sequence table view to 'listen' to Subset 1.

**Show Rows In:** is set to Subset1 in the right hand control of the Sequence table view, the rows will be filtered by the settings in Subset 1. Note that there are now two filtering schemes being applied the Sequence Table. First the table is filtered by column 16 residues selected by the user and second by the Subset 1 filter settings.

For more information please contact us at [info@altoris.com](mailto:info@altoris.com)