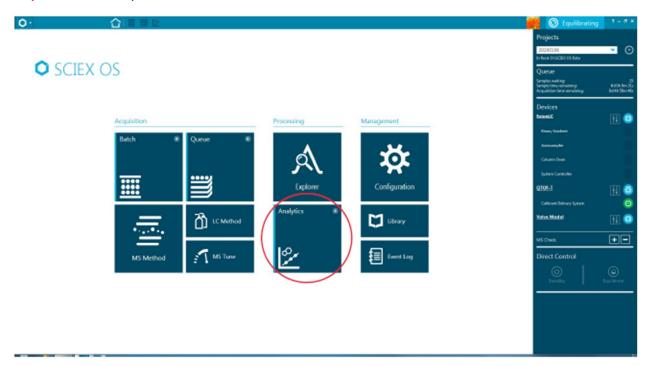
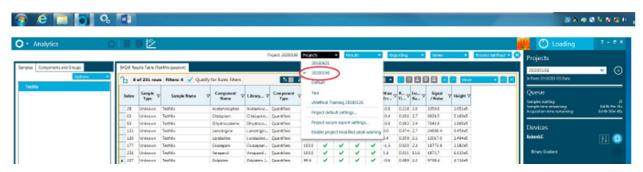
## **Processing Guide – QTOF**

Step 1: Select "Analytics" from the "Home" screen.



Step 2: Go to the "Project" drop-down and select the date analyzed.

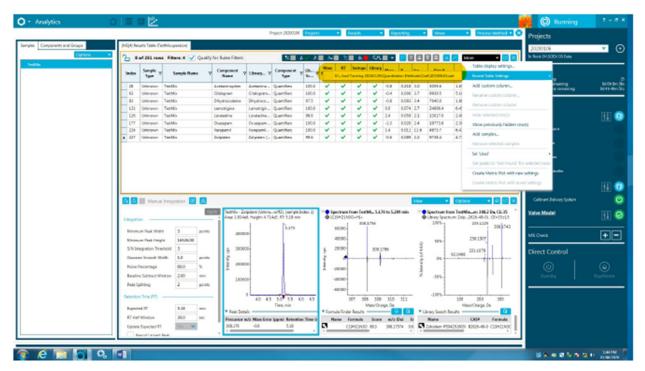


Step 3: Go to the "Results" drop-down and select "Open"

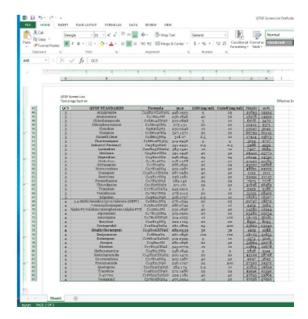


Step 4: Select the file to process – should be the data "2021XXXX"

**Step 5:** Go to the "More" drop-down located on the right-side of the data toolbar. Select "Recent Table Settings". Select the INITIAL option (this will re-format the data to include only the information relevant)



**Step 7:** Process the data. Fill out the "QC Supplement Form" for the Positive Controls and the QTOF Screen List spreadsheet (Shown below)



To see the Tables: Select the

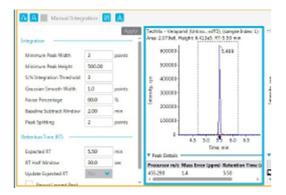
icon on the toolbar (located next to the grayed out boxes).



The Retention Times need to be updated for all the analytes included in the control— Starting with the Positive QCs can assist in the rest of the data.

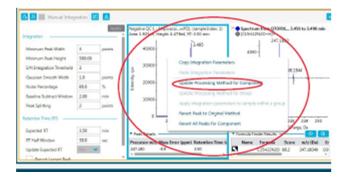
## To update retention times:

Click and Drag in the "Peak Table" (Highlighted in a blue outline below). The Retention time will automatically update.



## To save the retention times:

Right-click in the "Peak Table" and select "Update Processing Method for Component". The new retention time will now be applied to the other case samples.



Then go to the "Process Method" drop-down, select "Save Embedded method as" and overwrite the "QSCREEN20191231" method. (Recommend doing this after both Positive QCs have been processed)

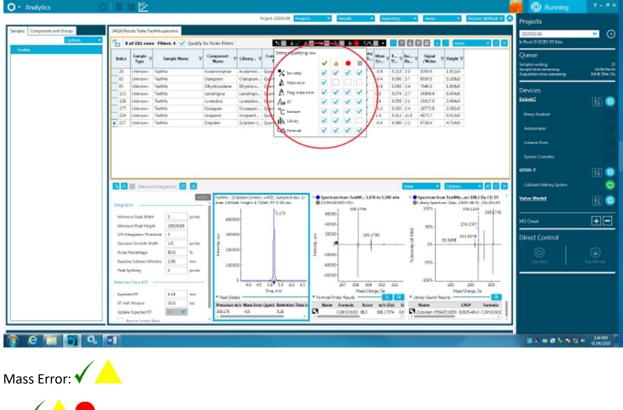


**Negative QCs:** should only have "Mepivacaine" but if anything with Four (✓) is seen, it needs to be included in the "Summary Report".

**Positive QCs:** Reference the QTOF Screen List for what should be included in the Sample. Make sure to include the analytes that should be there on the "Summary Report".

Step 8: After the Controls have been processed – process the case data.

Remove analytes without library matches first, then evaluate the below criteria – For summary page:



RT: √ △

Isotope: ✓ △

Library: 

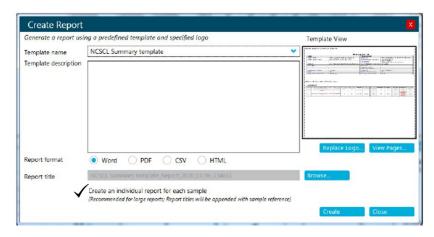
(as long as it matches to a library)

Step 9: To Print the "Summary Report" – select all the samples

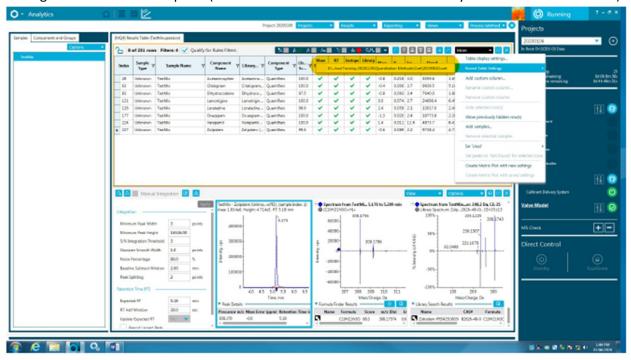
Go to the "Reporting" drop-down and select "Create report and save Results table"



Select the "NCSCL Summary Template3" option. *CHECK the "Create an individual report"*. Click "Create". The folder containing the reports will be under Data(D:)→ Reports (rename the folder: Date-Summary)



**Step 10:** Go to the "More" drop-down located on the right-side of the data toolbar. Select "Recent Table Settings". Select the FINAL option (this will re-format the data to include only the information relevant)

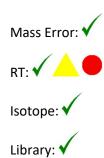


Re-process the data. This is the "Final Report" step.

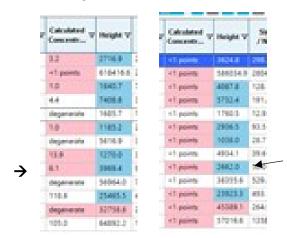
**Negative QCs:** should only include analytes with Four (✓)

**Positive QCs:** should only include analytes with Four (✓)

**Case Data:** the table will include the following criteria:



Note: This is where the height/concentration criteria comes into play.



**Calculated Concentration:** These are only used for analytes contained in a **QCS** – A red block with a numeric value indicates it is below 90% of the cut-off for that analyte and therefore <u>cannot</u> be reported.

**Height:** These are only for analytes <u>NOT</u> contained in a <u>QCS</u> – A <u>blue block</u> indicates it is below the LLOQ for that analyte and therefore <u>cannot</u> be reported.

<u>IF</u> an analyte in a QCS has a blue height block, but <u>NOT</u> a red concentration block, it will be left on the *FINAL* page.

\*\*Red height blocks need to be noted and submitted to the QTOF coordinator

Step 11: To print the "Final Report" – select all the samples

Go to the "Reporting" drop-down and select "Create report and save Results table"



Select the "NCSCL Final Template3" option. *CHECK the "Create an individual report"*. Click "Create". The folder containing the reports will be under Data(D:) → Reports (rename the folder: Date-Final)