

(Favorite Approach Part 1 plus “Nearby Precursors” Enhancement)

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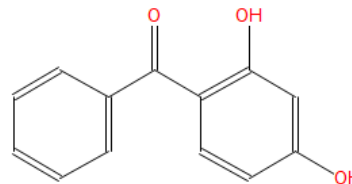
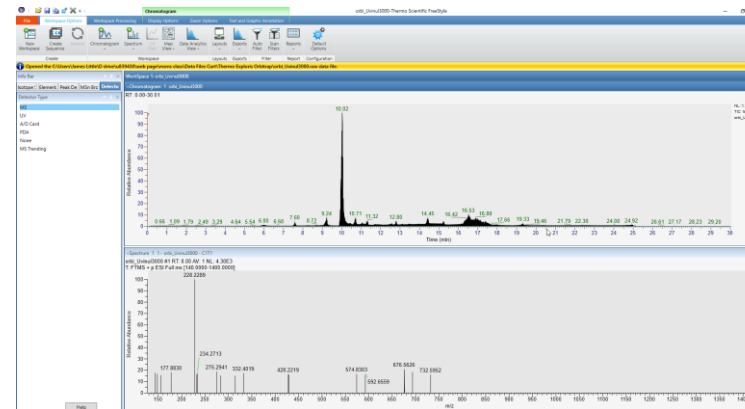
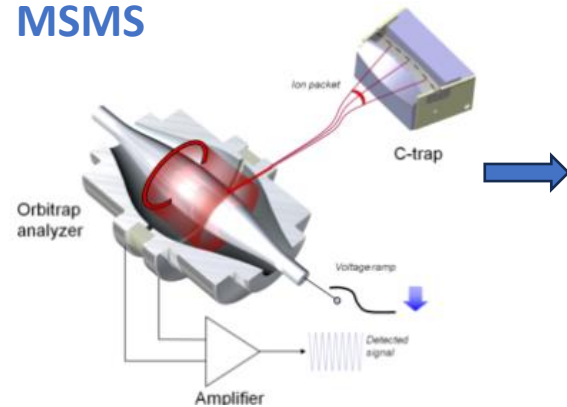
Ken Matuszak

 Thermo Fisher Scientific

● Sr. Product Specialist

Thermo Freestyle

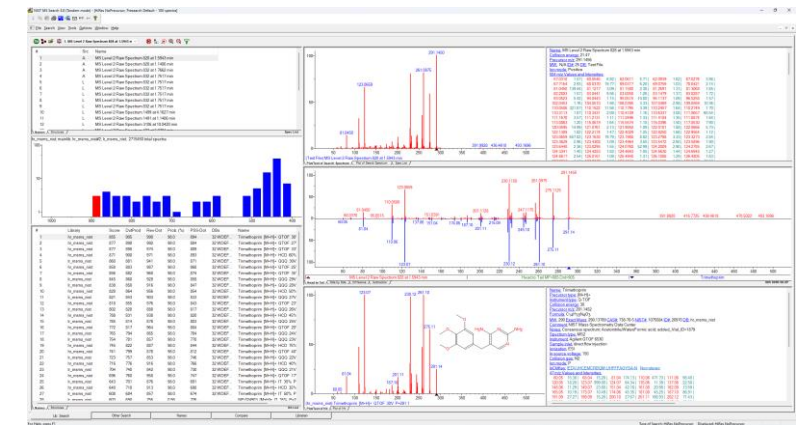
Thermo Orbitrap MSMS



Uvinul 3000
MW 214

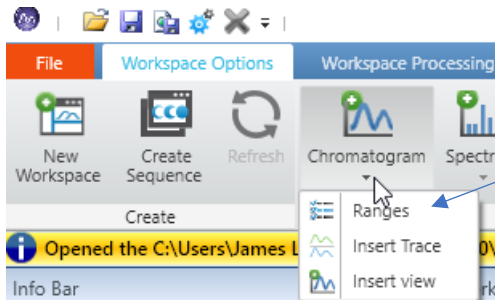
LC-MS and MSMS Analyses (Positive and Negative Mode) with Photo Array Detector Array (PDA) and UV-VIS Analyses

NIST MSMS Search



In My Opinion, Preferred Way of Processing Data (Do the Same Steps as in the Preferred Approach in Part 1)

- Open three windows in the bottom of Freestyle
- Top one is positive ion MS1
- Second one in negative MS2
- Bottom is either UV or PDA trace
- After setting up, be sure to save in Workspace Options/Layouts
- Then when new file opened, and layout is loaded, data is parsed into these three window automatically!



Chromatogram Ranges - Chromatogram 1											
Display	File Name	Detector Type	Filter	Trace Type	Mass Defect Range	Ranges	Smoothing	Chemical Formula	Mass Tolerance	Delay Time	
☒	C:\Users\James Li...	MS		TIC	MDF Ranges		None			0.00	
☐					MDF Ranges					0.00	

Bottom window will appear, keep adding windows to get three total

(Do the Same Steps as in the Preferred Approach in Part 1)

Three working boxes for processing

Spectrum window

Boxes for selecting functions

Select filter to change top one to positive ion and second one to negative ion, Select Detector type to get PDA or UV



Note, positive and negative options are last two items in the filter list when opened!

(Do the Same Steps as in the Preferred Approach in Part 1)

Positive MS1

Negative MS1

PDA

Spectrum

Note, Now be sure to save layout so when opening a new file, it will be automatically applied

Workspace Processing | Display Options | Zoom Options | Text and Graphic Annotation

Chromatogram | Spectrum | CV Plot | Map View | Data Analytics View | Layouts | Exports | Auto Filter

Workspace

Opened the C:\Users\James Little\Documents\workspace\msms class\Data Files Curt\Thermo Exploris Orbitrap\orbi_Uvinul3000.raw data file.

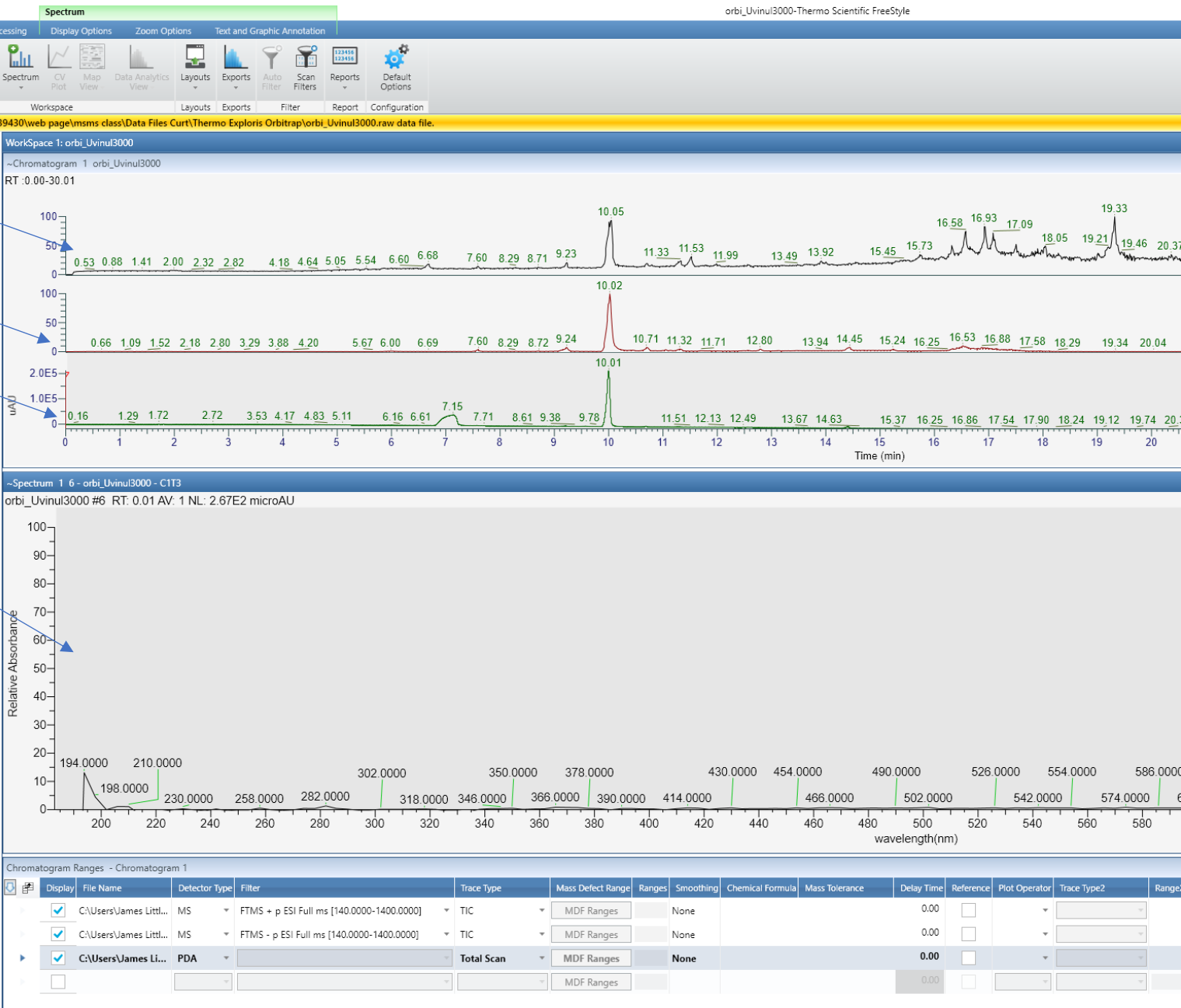
Workspace 1: orbi_Uvinul3000

~Chromatogram 1 orbi_Uvinul3000

RT: 0.00-30.01

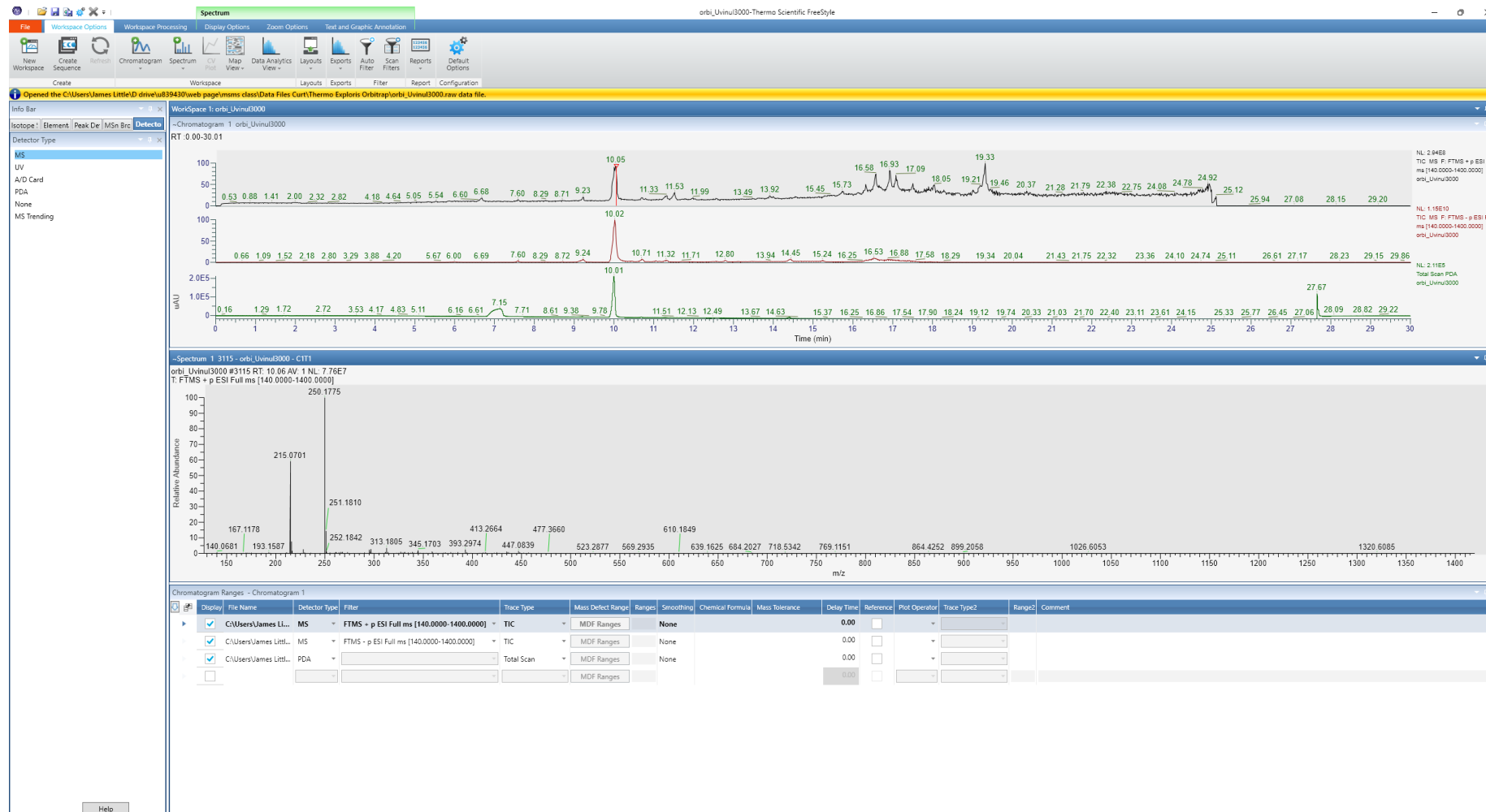
Detect | Scan F

Save As | Save As Default | Apply | Apply Default



Then Use Nearby Precursors Option

- Left click on any peak in either the positive or negative chromatogram
- Below, I clicked on the positive ion for chromatogram to get peak at 10.05 minutes
- That will give the spectrum for peak in second window from top
- Double left click on the purple circle, and the MS2 spectrum will appear as *shown in next slide*
- **NOTE: “Nearby Precursors” CANNOT be used with an averaged MS Spectrum!**

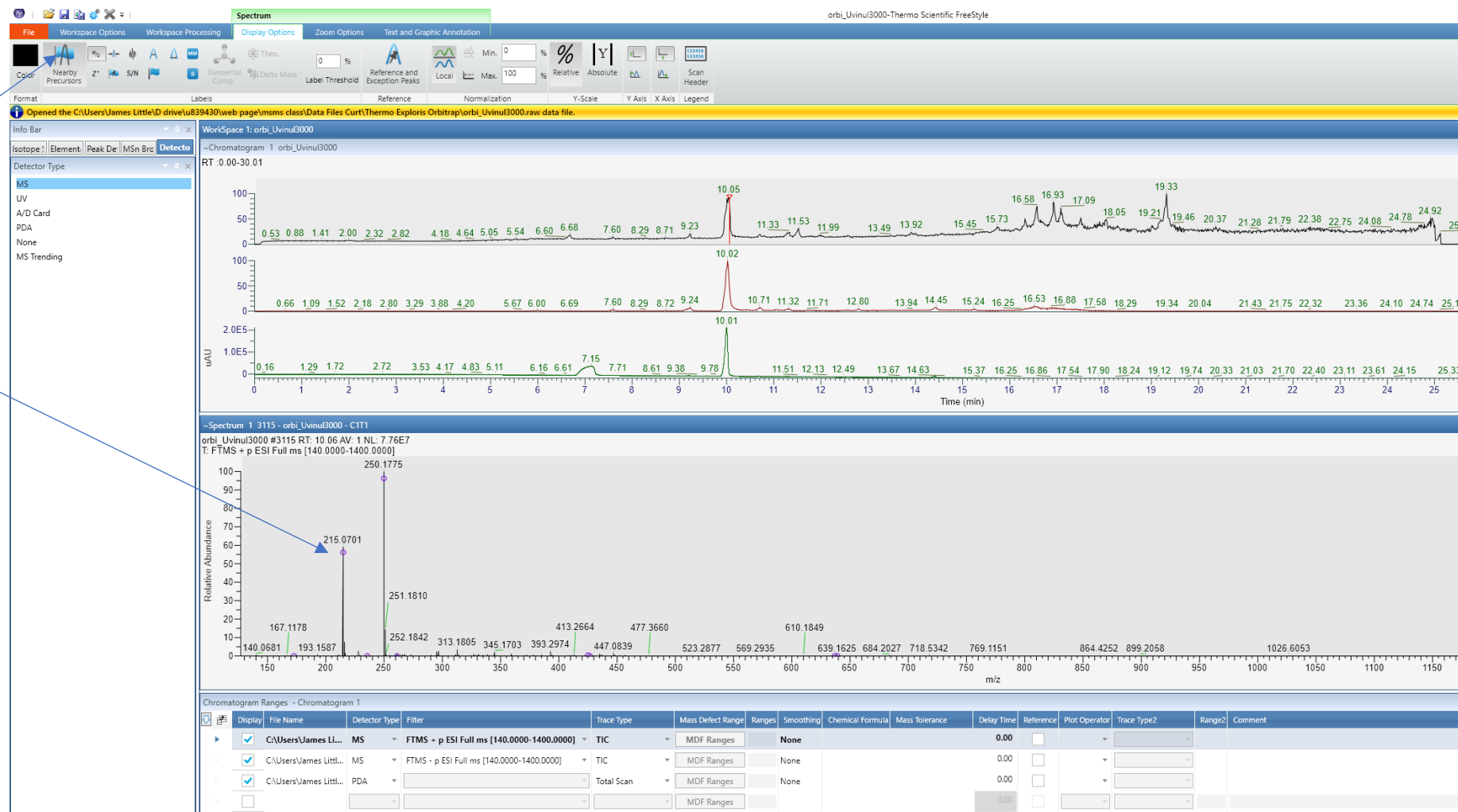


Then Use Nearby Precursors Option

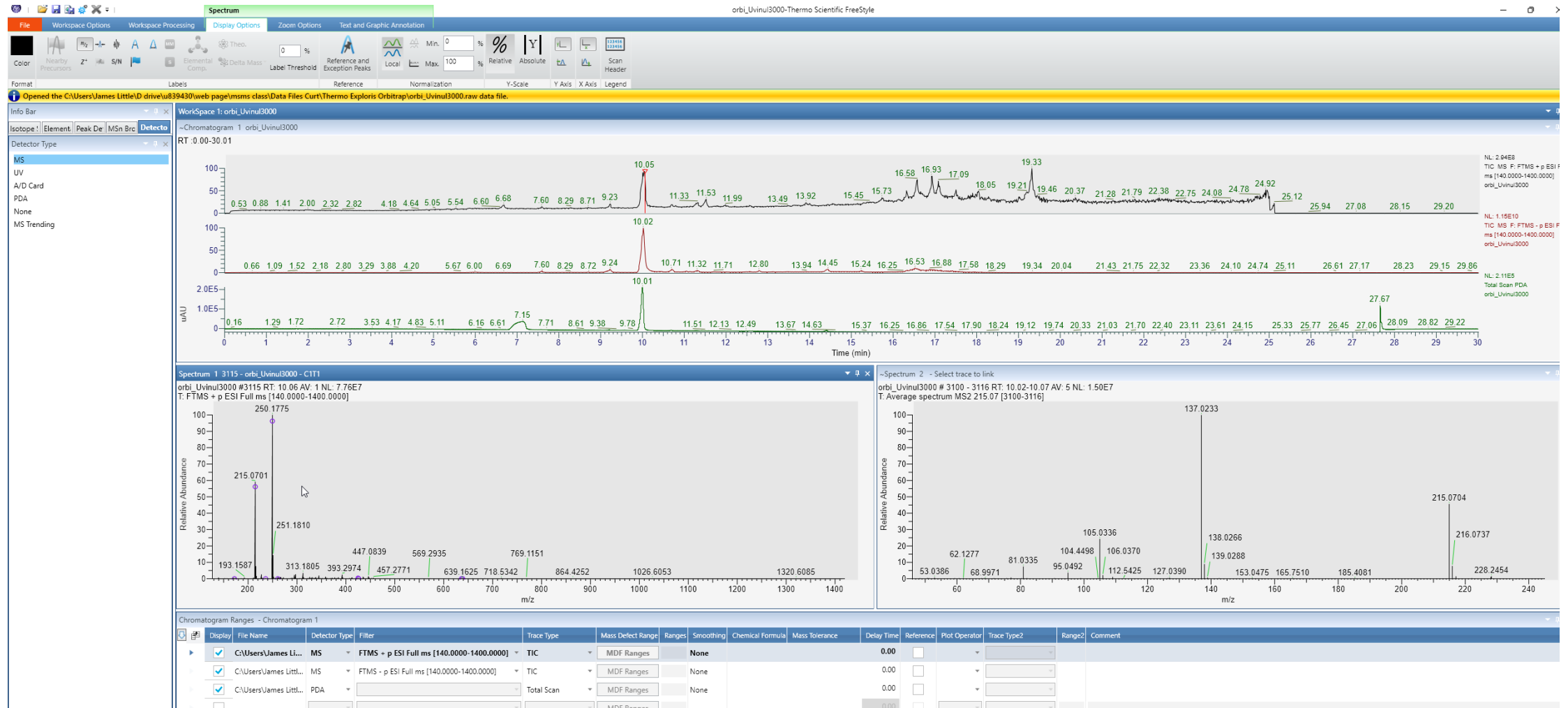
- All peaks with a purple circle have an associated MS2 spectrum
- Double left click on the purple circle, and the MS2 spectrum will appear as *shown in next slide*
- **NOTE: "Nearby Precursors" CANNOT be used with an averaged MS Spectrum!**

Nearby Precursors

Double Left Click on
Purple Circle to get
MSMS Spectrum
associated with ion



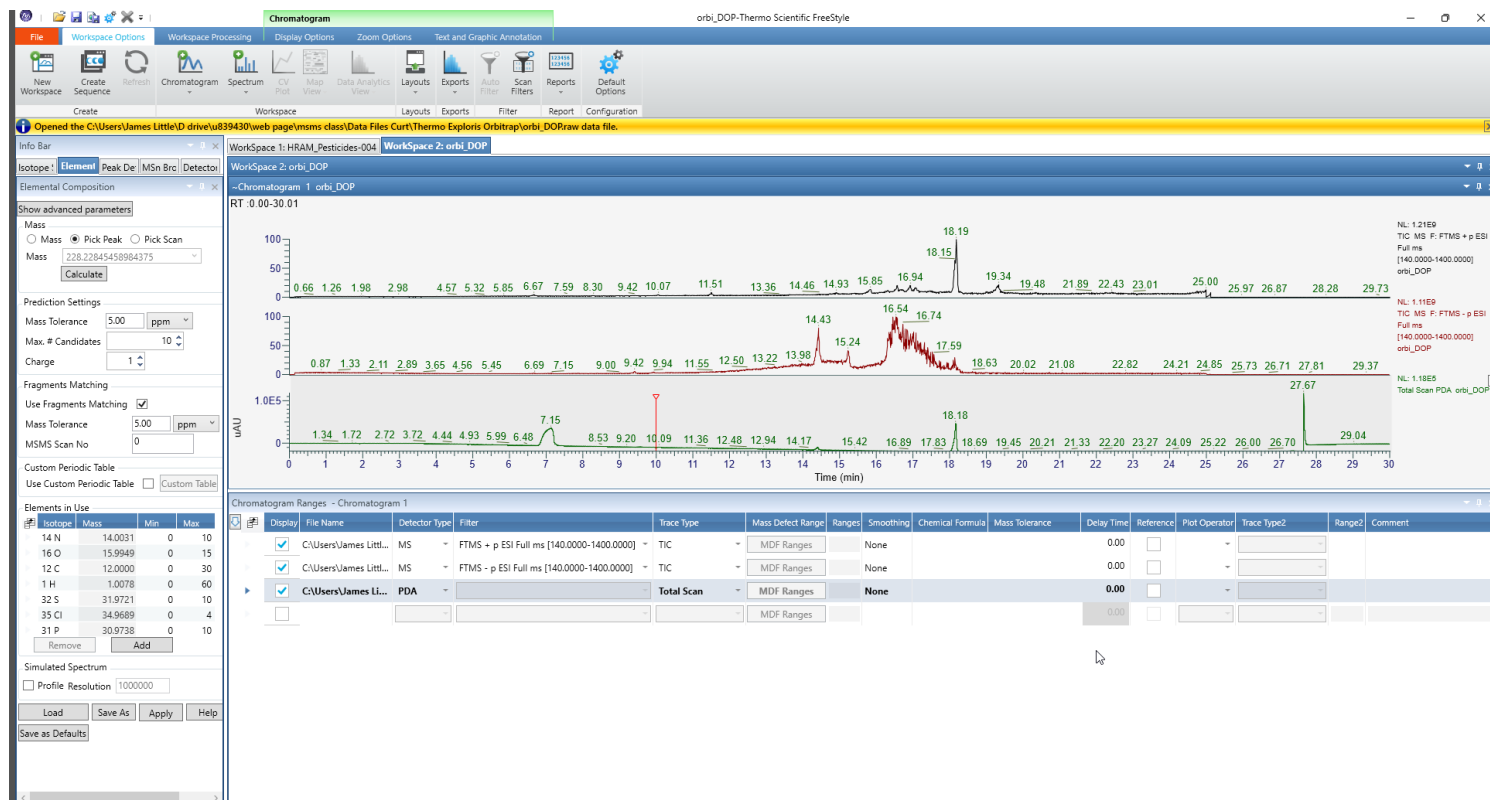
- After **double left clicking** on purple circle for ion at 215.0701, the MS2 spectrum for that peak is displayed
- Can then select bar above spectrum with left click and send to NIST search as before as detailed in Part 1 of this series
- Just click on the x in box to remove the MS2 spectrum and get ready to select another one
- If you inadvertently remove all the spectra, go to main toolbar Workspace Options/Spectrum/Insert View



If You Delete All the MS and MS2 Windows by Mistake

- If you remove all the spectra windows by mistake (1)
- Go to Workspace Options/Spectrum/Insert View (2)

(1)



(2)

