

# KnowItAll Quantitative Software for EI GC-MS

Version 2024

J. Little, MS Interpretation Services

12/16/2024

- Full videos including this one found on demand at the following link
- <https://sciencesolutions.wiley.com/webinars/>
- My excerpt **only** shows Introduction and EI GC-MS software demonstration part of the webinar

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## Webinar: Introducing KnowItAll Quantitation

Dec 13, 2023 - 10:00 am EST

**Register Now**

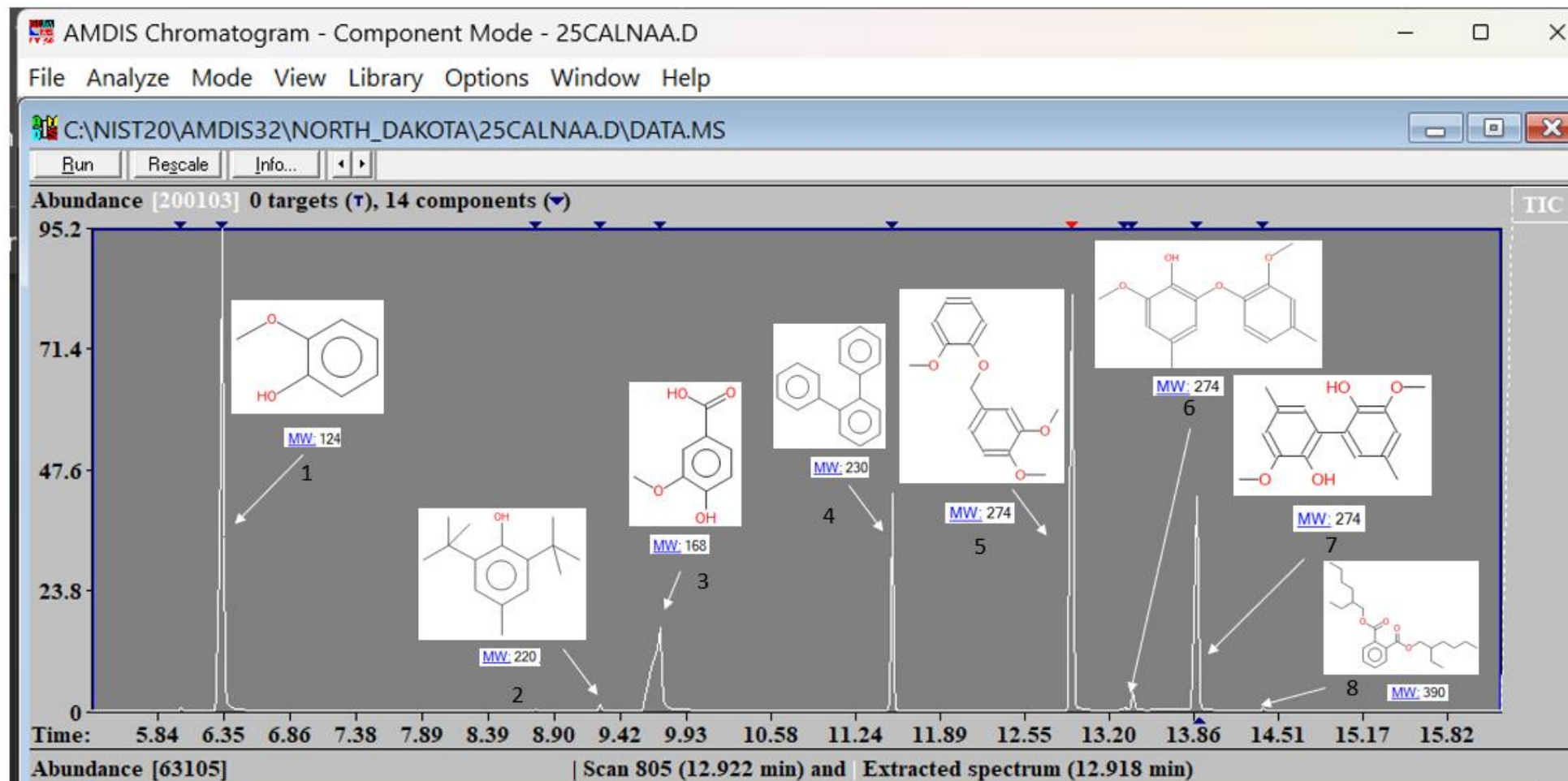


### Speaker: Dr. Leanna Ergin

Dr. Leanna Ergin is an Assistant Editor for Wiley Science Solutions, for which she helps create tools for spectroscopy, structural, and scientific standard reference data and helps create innovative software applications. Leanna completed her PhD in Clinical-Bioanalytical Chemistry from Cleveland State University, where she developed a protocol for processing hyperspectral image data that distinguishes the spectra, removes degeneracies caused by symmetry, and is generalized to work with any number of wavelength dimensions and spectra. The results are mapped to the full RGB colorspace of modern computer displays. Leanna joined Wiley in 2022.

## Files Used for Demonstration

- Files used for demo are found on my website in a zip file
- Obtained from University of North Dakota website and file names modified to match Wiley Webinar examples
- [https://arts-sciences.und.edu/academics/chemistry/kubatova-research-group/chrom\\_ms02.html](https://arts-sciences.und.edu/academics/chemistry/kubatova-research-group/chrom_ms02.html)
- North Dakota website does not totally show the identity of the species in file, my interpretation shown below



## More Information on Files from North Dakota Website

- Wiley used the files shown in the first screen capture shown below with concentrations in ug/mL added to end of file name
- Selected  $m/z$  124 for Compound 1 and  $m/z$  230 for internal standard, Compound 4
- Lower screen capture shows information for other files and species on their website
- Some of their species are NOT found in either the Wiley or NIST libraries

11CALNAB\_unknown.D

22CALNAD\_1\_60.D

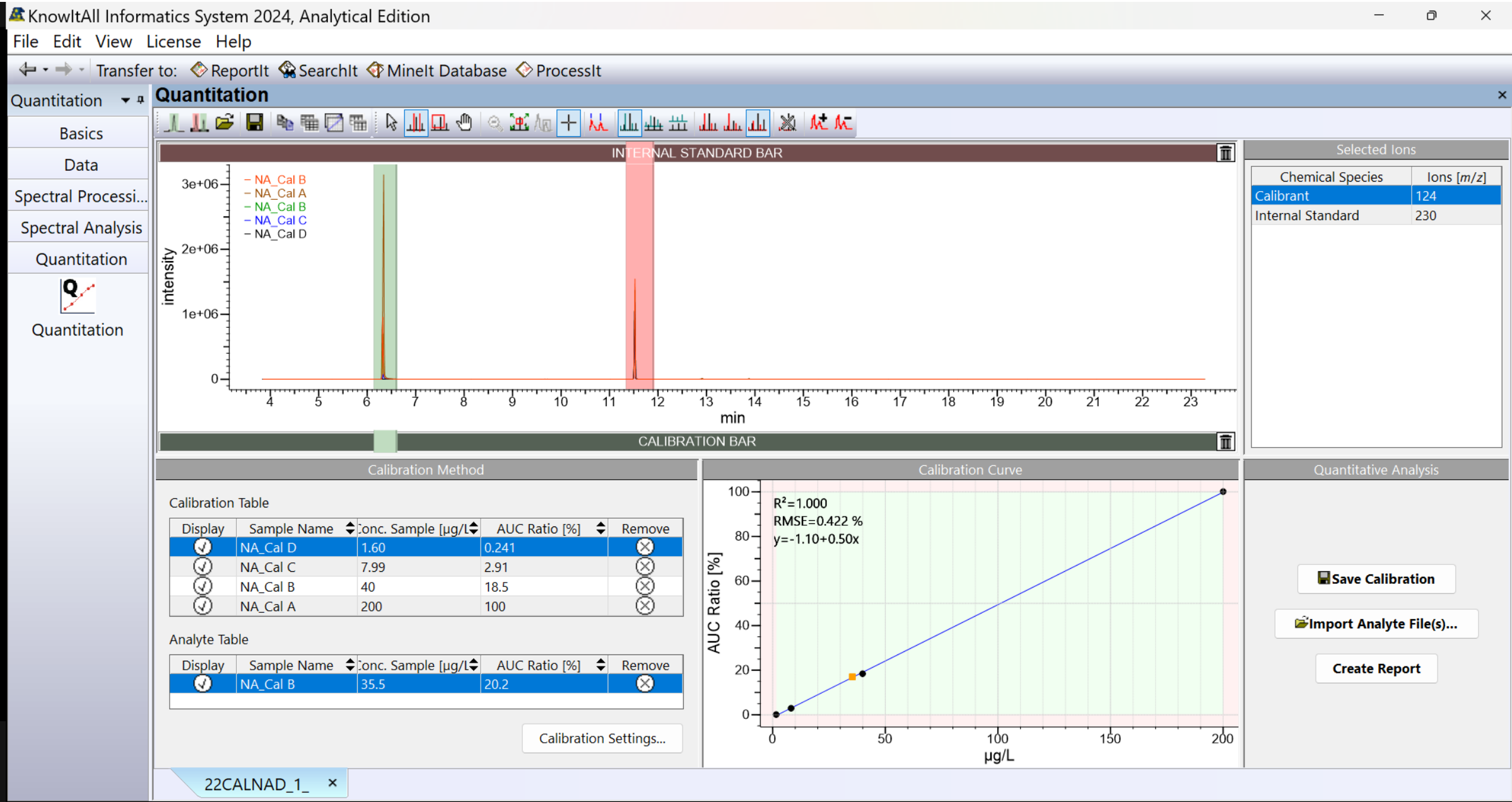
23CALNAC\_7\_99.D

24CALNAB\_40.D

25CALNAA\_200.D

Species		Formula	Mix F	Mix E	Mix D	Mix C	Mix B	Mix A
			NA2-74-F	NA2-74-E	NA2-74-D	NA2-74-C	NA2-74-B	NA2-74-A
1	Guaiacol	C <sub>7</sub> H <sub>8</sub> O <sub>2</sub>	0.064	0.320	1.60	7.99	40.0	200
3	Vanillic acid	C <sub>8</sub> H <sub>8</sub> O <sub>4</sub>	0.064	0.319	1.60	7.99	39.9	200
5	1,2-Dimethoxy-4-[(2-methoxyphenoxy)methyl]benzene	C <sub>16</sub> H <sub>18</sub> O <sub>4</sub>	0.064	0.320	1.60	8.00	40.0	200
7	Bicreosol	C <sub>16</sub> H <sub>18</sub> O <sub>4</sub>	0.064	0.320	1.60	8.00	40.0	200
4	o-Terphenyl (IS)	C <sub>18</sub> H <sub>14</sub>	62.0	62.0	62.0	62.0	62.0	62.0

Final Result Page from Demonstration



## Excerpt (13 Pages) of EI GC-MS Quantitation from Wiley Self-Guided Training Course

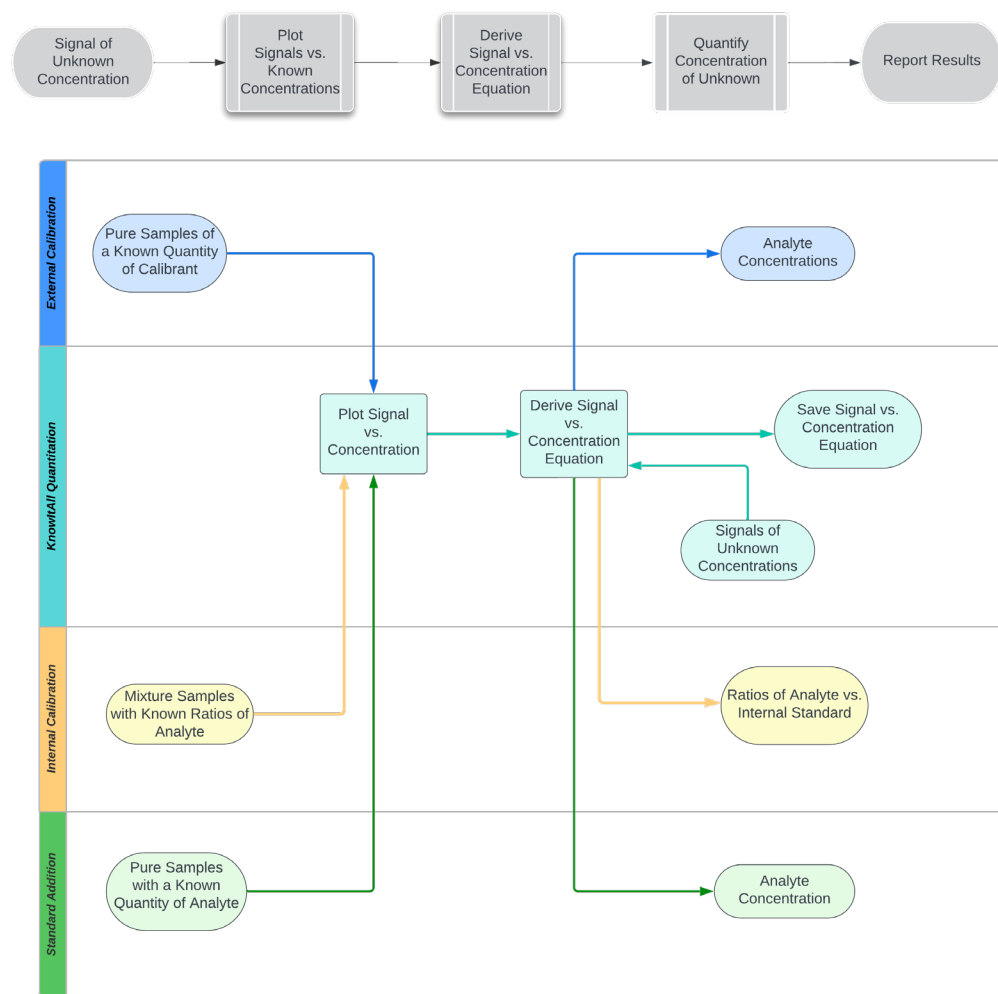
### Original Document Links:

<https://sciencesolutions.wiley.com/knowitall-software-training-course/>

[16\\_Training-Quantitation.pdf \(wiley.com\)](#)

EI GC-MS Quantitation Excerpts Found on Following 13 Pages:

## Quantitation Workflow

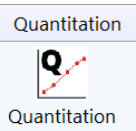


## GC-MS

*This exercise requires user to download sample datasets from [https://arts-sciences.und.edu/academics/chemistry/kubatova-research-group/chrom\\_ms02.html](https://arts-sciences.und.edu/academics/chemistry/kubatova-research-group/chrom_ms02.html). It is helpful to rename files so that analyte (Guaiacol) concentrations are reflected in the names.*

*Internal standard: o-Terphenyl (IS) RT 11.5192 62.0 ug/ml*

*Analyte: Guaiacol RT 6.3368 min*

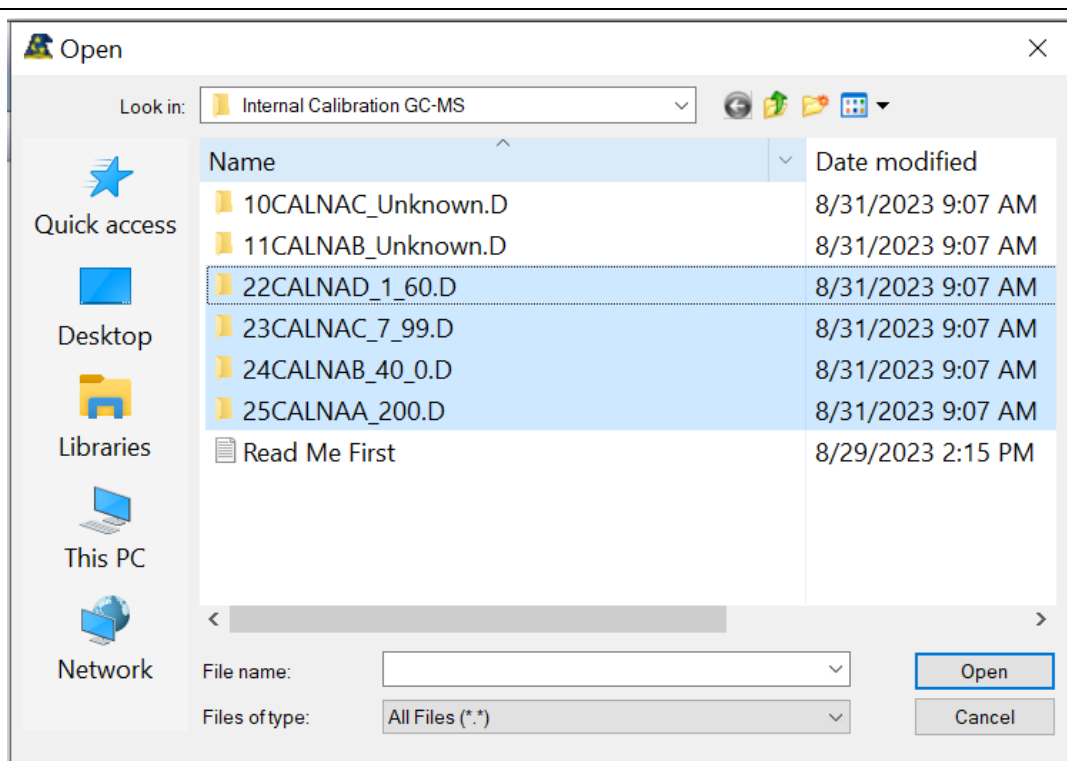
	Action	Result
1	Open the <b>Quantitation</b> application by clicking its icon, typically found in the <b>Quantitation</b> group.	 The icon for the Quantitation application, featuring a blue square with a white 'Q' and a red line graph, with the word 'Quantitation' written above and below the icon.
2	Click <b>New Internal Calibration</b> button.	KnowItAll prompts user to open calibrant files.



3 Navigate to the downloaded GC-MS file folder.

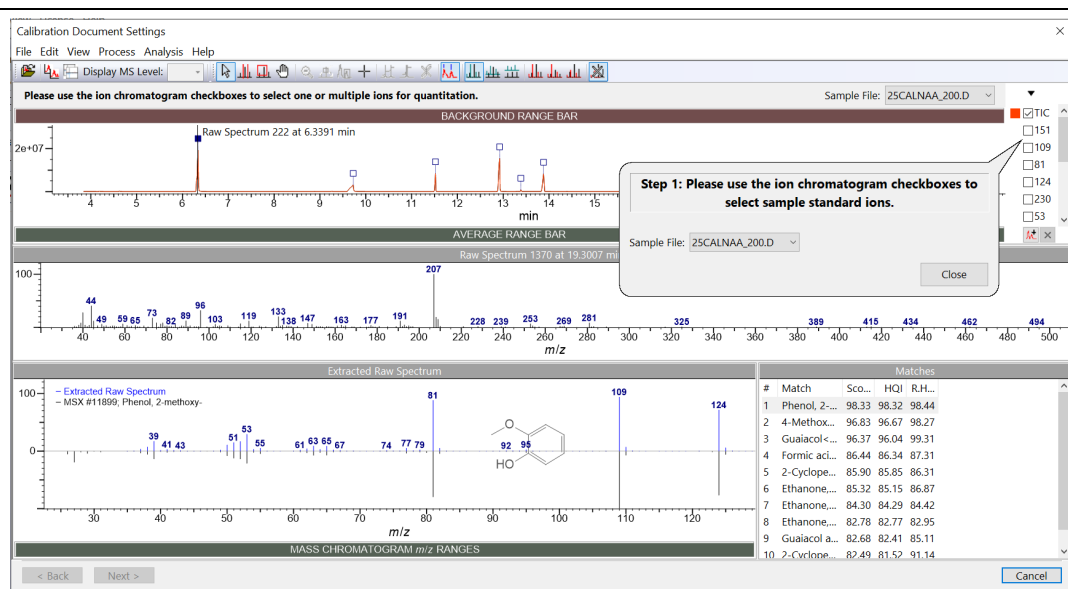
Select folders as shown in the right screenshot.

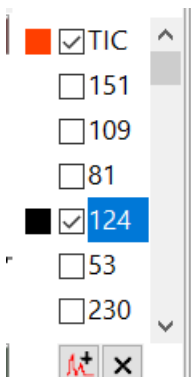
Click **Open**.





4 In the drop-down list, select the calibrant file where analyte concentration is the largest, in this example, it is the **25CALNAA\_200.D**

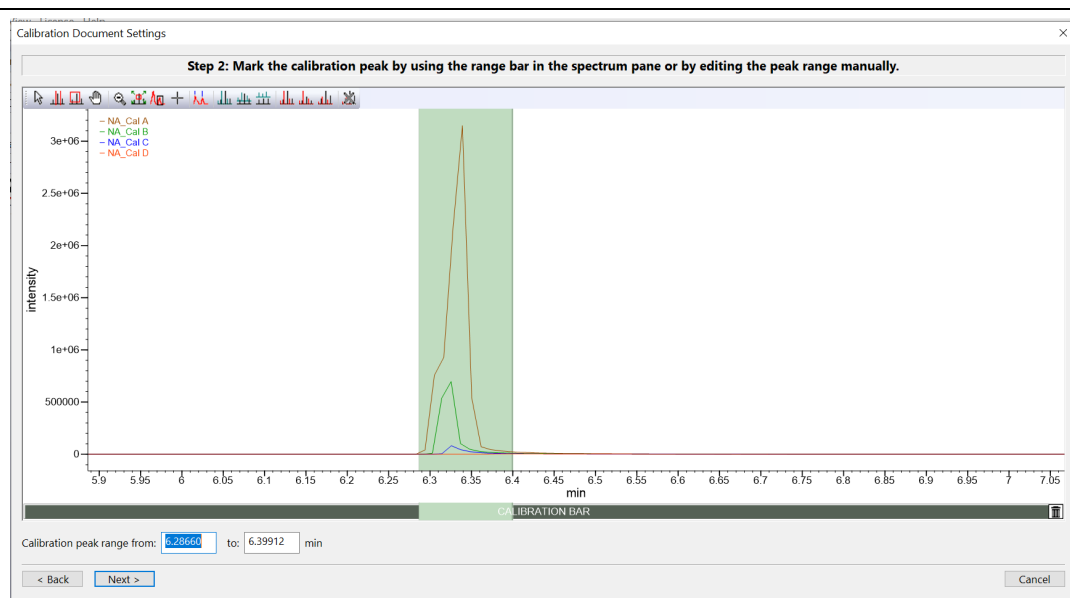


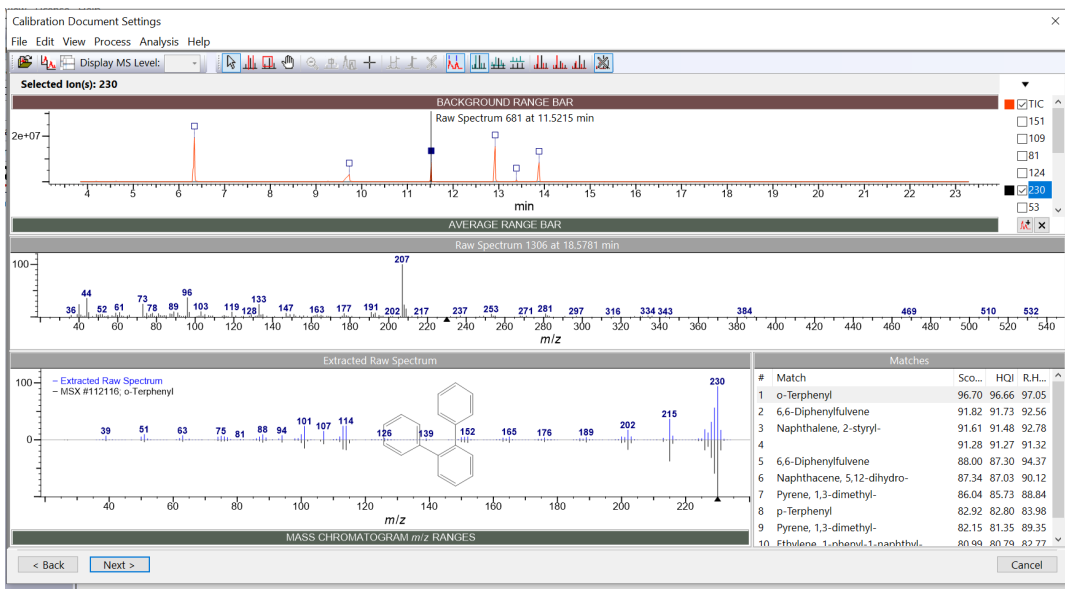
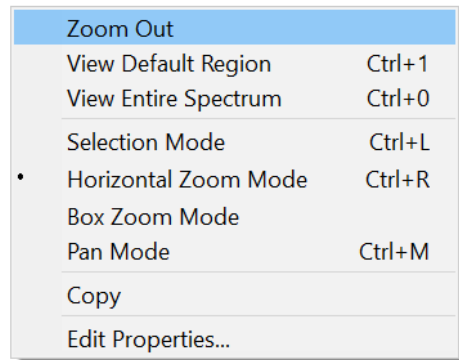
5	<p>Select a component from the <b>Raw Spectrum</b> pane, in our example, the interested component has a TIC peak at <b>6.45</b> min.</p> <p>Select an ion, in this case, we select its <b>molecular m/z 124</b>.</p> <p>Click <b>Next &gt;</b> (bottom left corner)</p>	
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6 Click the **Spectrum** pane, drag and drop mouse to zoom into region 6 – 6.5 min.

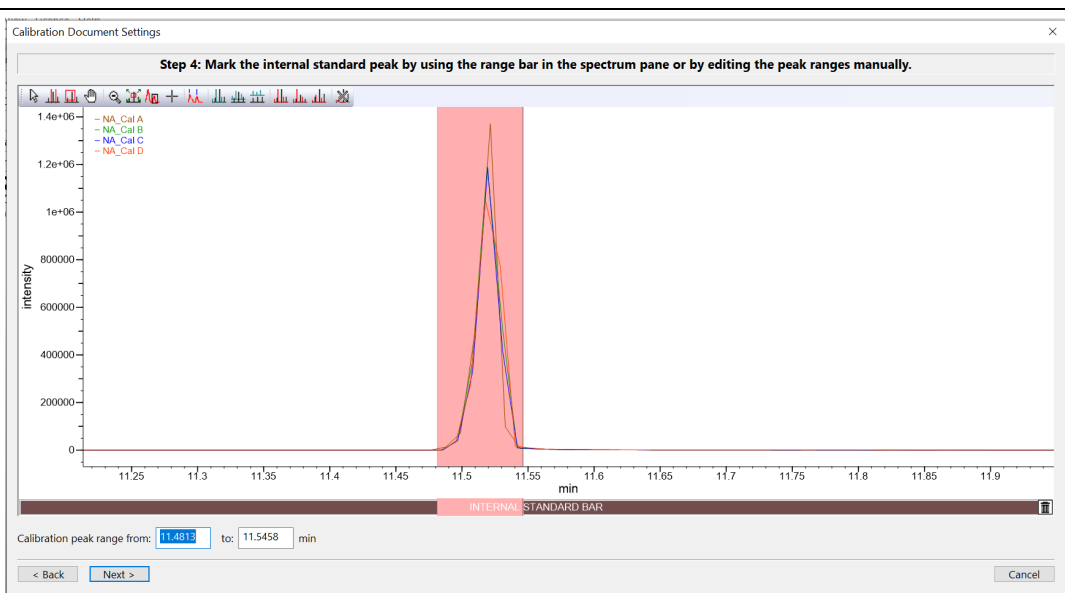
Select peak region by clicking down the CALIBRATION BAR (drag and drop).

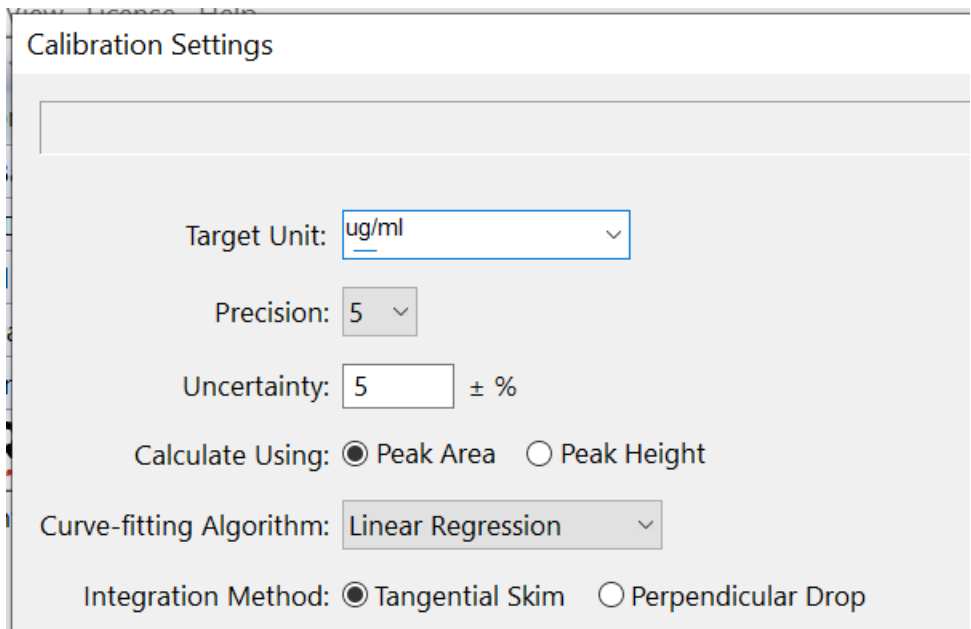
Click button **Next >**.



7	<p>Select a component from the <b>Raw Spectrum</b> pane, in our example, the interested component has a TIC peak at <b>11.5 min</b>.</p> <p>Select an ion, in this case, we select its <b>molecular m/z 230</b>.</p> <p>Click <b>Next &gt;</b> (bottom left corner)</p>	 <p>The screenshot shows the 'Calibration Document Settings' window. The 'Selected Ion(s): 230' is displayed. The 'Raw Spectrum 681 at 11.5215 min' is shown with a peak at 11.5215 min. The 'AVERAGE RANGE BAR' shows the mass range from 40 to 540 m/z. The 'Extracted Raw Spectrum' shows the mass spectrum with a peak at m/z 230. The 'MASS CHROMATOGRAM m/z RANGES' is also visible.</p>
8	<p>Right mouse click the spectrum pane.</p> <p>Select <b>Zoom out</b>.</p>	 <p>The screenshot shows the right-click context menu for the spectrum pane. The 'Zoom Out' option is highlighted. Other options include 'View Default Region', 'View Entire Spectrum', 'Selection Mode', 'Horizontal Zoom Mode', 'Box Zoom Mode', 'Pan Mode', 'Copy', and 'Edit Properties...'. The 'Zoom Out' option is associated with the Ctrl+1 keyboard shortcut.</p>

- 10 Click the **Spectrum** pane, drag and drop mouse to zoom into region 10.5 – 12 min region.
- Select peak region by clicking down the INTERNAL STANDARD BAR (drag and drop).
- Click button **Next >**.



9	<p>In the following window, define calibration settings.</p> <p>Target Unit: <b>ug/ml</b> (you have to type in)</p> <p>Calculate Using: <b>Peak Area</b></p> <p>Click button <b>Next &gt;</b>.</p>	 <p>Calibration Settings</p> <p>Target Unit: <input type="text" value="ug/ml"/></p> <p>Precision: <input type="text" value="5"/></p> <p>Uncertainty: <input type="text" value="5"/> ± %</p> <p>Calculate Using: <input checked="" type="radio"/> Peak Area <input type="radio"/> Peak Height</p> <p>Curve-fitting Algorithm: <input type="text" value="Linear Regression"/></p> <p>Integration Method: <input checked="" type="radio"/> Tangential Skim <input type="radio"/> Perpendicular Drop</p>
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- 10 Enter concentration and ratio values in the pop-up window.

Concentration (internal standard) 62 ug/ml

Calibrant File    Concentration [ug/ml]

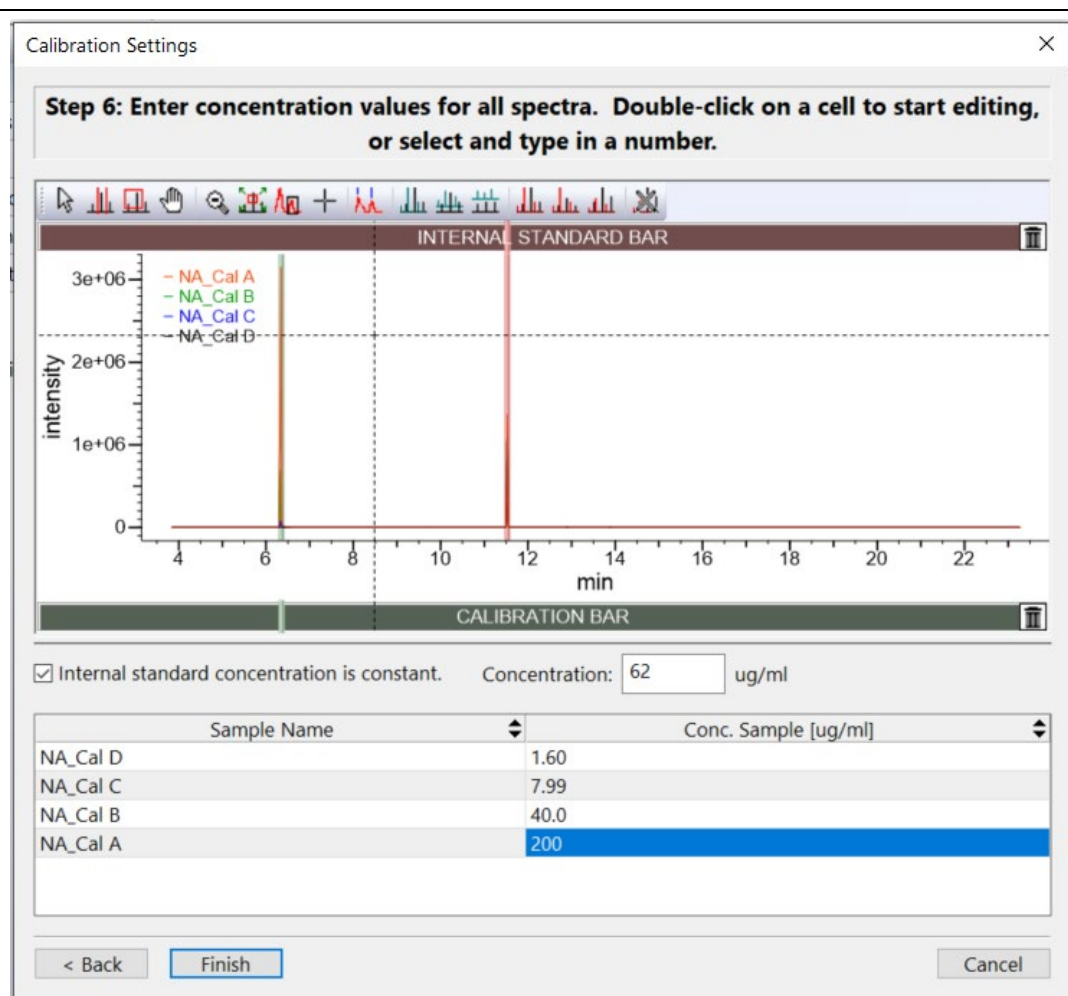
NA\_Cal D        1.60

NA\_Cal C        7.99

NA\_Cal B        40.0

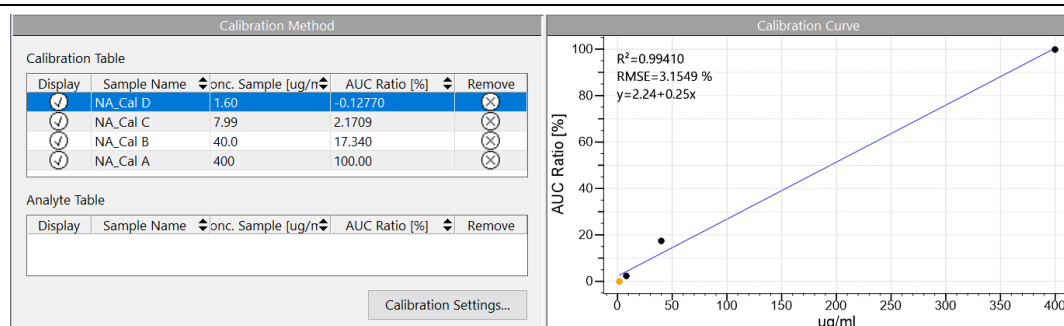
NA\_Cal A        200

Click **Finish** button.



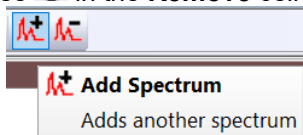


11



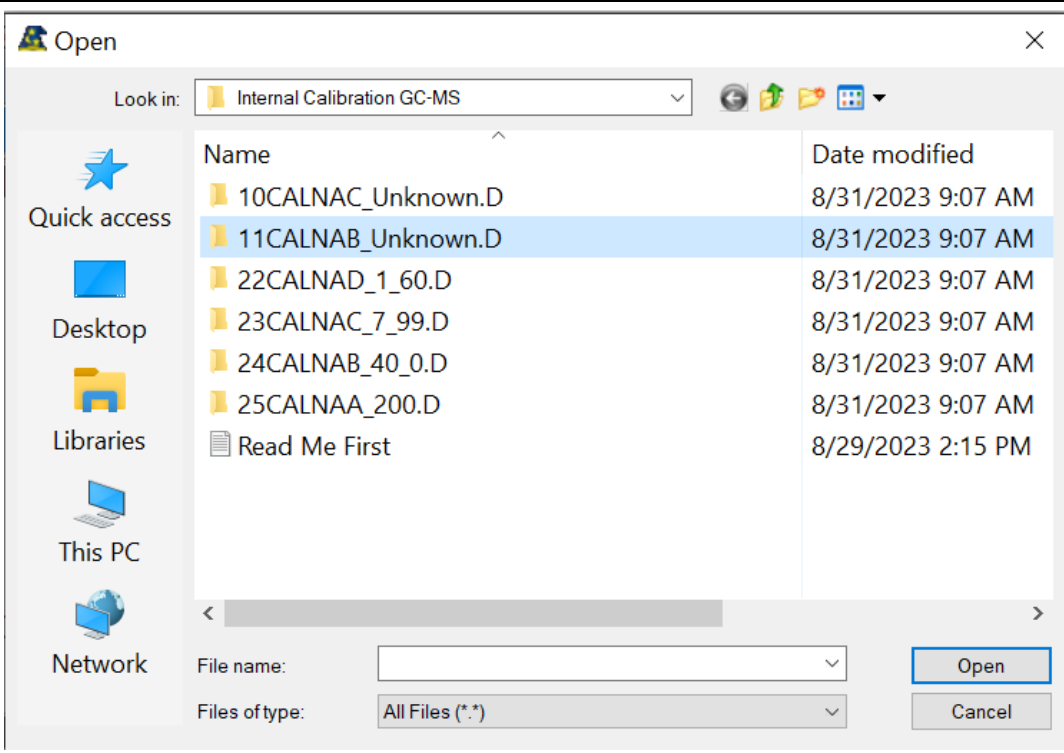
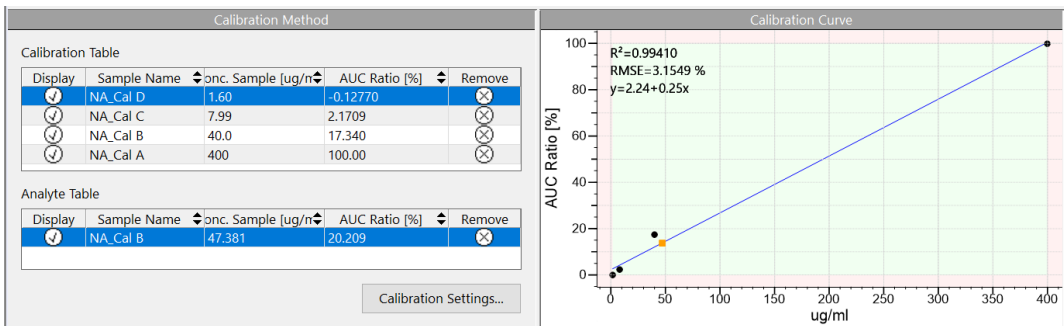
Statistics are reported in the calibration curve. The lower the **RMSE (root mean squared error)**, the better the curve is fitting. The closer the **R<sup>2</sup> (coefficient of determination)** is to 1, the better the curve is fitting.

One can use ☐ in the **Remove** cell to remove samples from calibration; and use **Add**



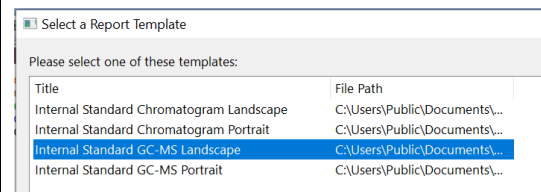
**Spectrum** to add new calibrants,

One can reset parameters using the **Calibration Settings** button. One can save this calibration for future use or sharing by clicking the **Save Calibration** button.

12	<p>Click the <b>Import Analyte File(s)</b> button.</p> <p>Select unknown file folder <b>11_CLANAB_Unknown.D</b> to calculate the concentrations.</p> <p>Click <b>Open</b>.</p>	
13		 <p>The concentration ratio of analyte to internal standard is shown in the <b>Analyte Table</b> and as a square spot in the <b>Calibration Curve</b>.</p>

14 Click **Transfer to: Report**

Select the **Internal Standard GC-MS Landscape** template



Click **OK**

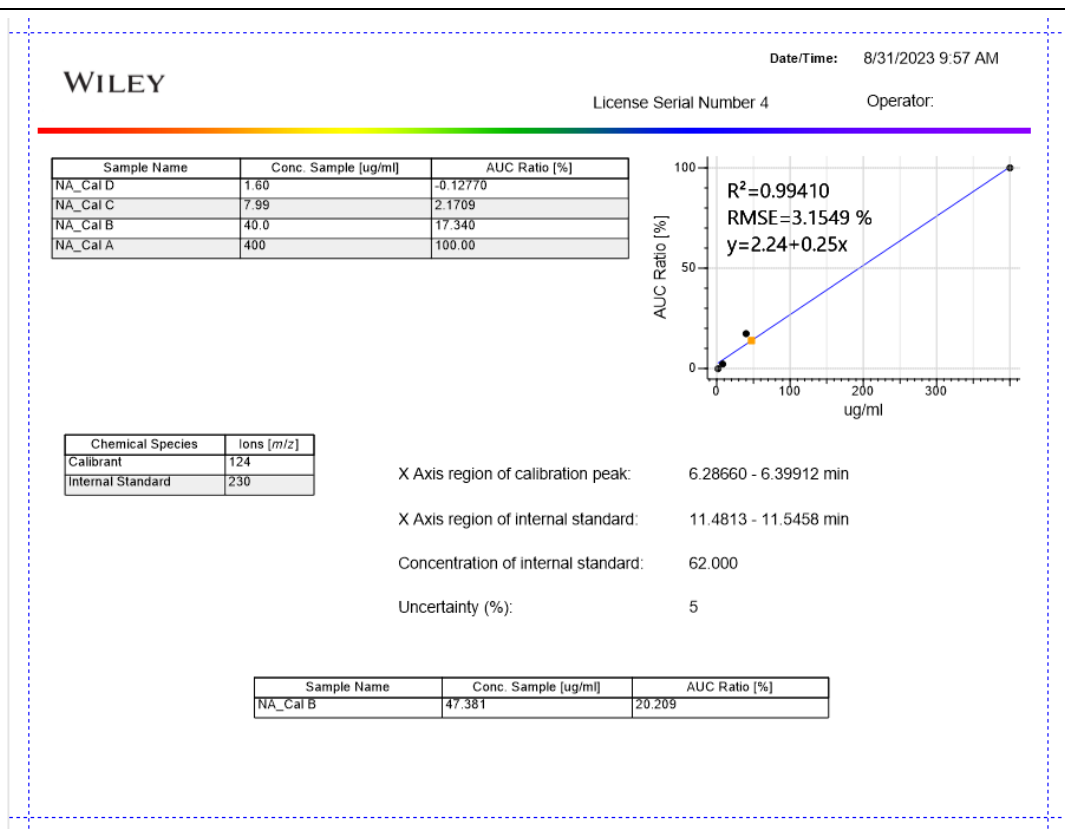
Note: if a template is used for the first time, user has to do the following before transfer data to ReportIt application:

**File > Edit Report Templates**

**Click Add button**

**Navigate to the template file**

**Open**



This is a basic report, one can select these objects and copy/paste to other applications.

## Wiley KnowItAll Training Resources (1 of 2)

<https://sciencesolutions.wiley.com/knowitall-software-training-course/>



**This self-guided training course will familiarize you with the KnowItAll software through a series of lessons.**

- This series is designed for you to follow along with in the KnowItAll software.
- The lessons are organized by category, each containing a series of short, easy to follow tutorials.

## Wiley KnowItAll Training Resources (2 of 2)

### Quantitation Training Link:

[16 Training-Quantitation.pdf](#)

#	Lesson	Lesson PDF
1	General Features: Introduction to the Basic Applications in the KnowItAll Informatics System	<a href="#">Download</a>
2	Simple Spectral Search/Identification with KnowItAll ID Expert	<a href="#">Download</a>
3	Searching: IR & Raman	<a href="#">Download</a>
4	Mixture Analysis: IR & Raman	<a href="#">Download</a>
5	Functional Group Analysis: IR, Raman, & Polymer	<a href="#">Download</a>
6	Mass Spectrometry Search	<a href="#">Download</a>
7	GC-MS Analysis Using KnowItAll MS Expert, ProcessIt and SearchIt	<a href="#">Download</a>
8	Create Databases	<a href="#">Download</a>
9	Drawing Structures & Reactions	<a href="#">Download</a> <a href="#">Hotkeys/Shortcuts</a>

10	Creating Reports	<a href="#">Download</a>
11	Data Mining & Analysis	<a href="#">Download</a>
12	Quality Control Analysis with QC Expert	<a href="#">Download</a>
13	NMR Processing Tools	<a href="#">Download</a>
14	NMR Analysis Tools	<a href="#">Download</a>
15	NMR Prediction	<a href="#">Download</a>
16	Quantitation	<a href="#">Download</a>
17	LC-MS Databases using Processing and Minelt	<a href="#">Download</a>
18	Using Predicted IR Spectra in KnowItAll	<a href="#">Download</a>