# Spectrus JS



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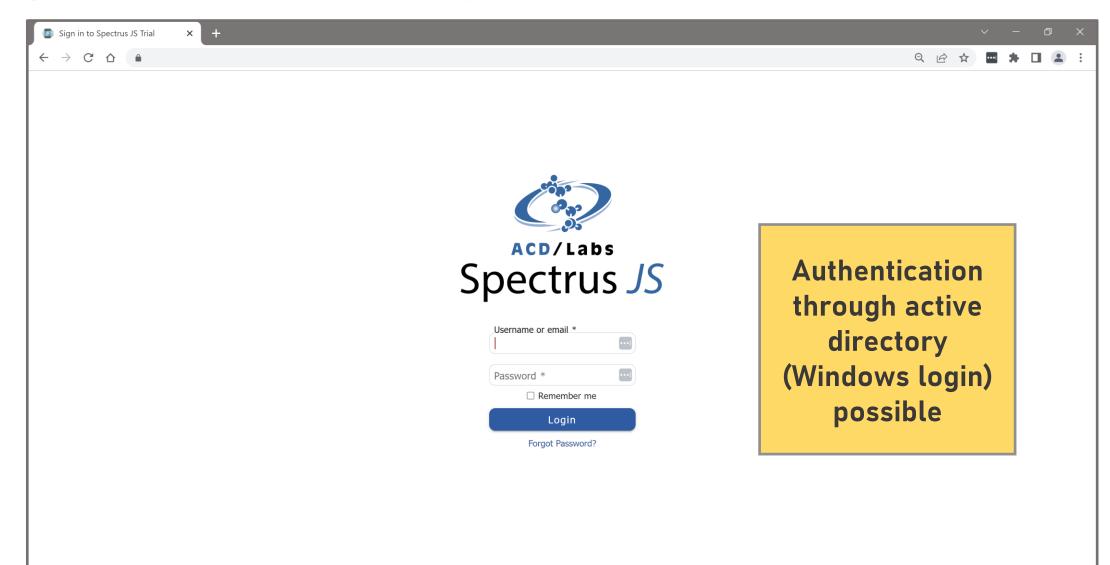
#### Spectrus JS – Overview

- Browser-based NMR processing software developed by ACD/Labs
- The NMR analyst only requires a web browser and access to the internet
- Hosted on your organizational intranet or (private) cloud
- For individual users, there is no need to perform installation and/or software updates
- Data pick-up from shared NMR server possible





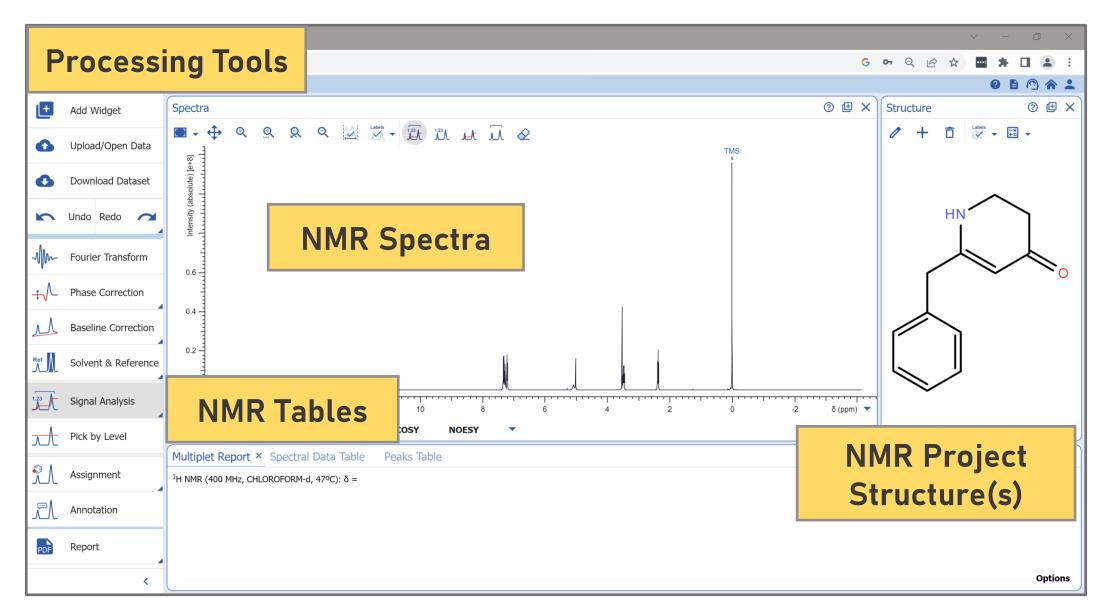
#### Spectrus JS – Home Page



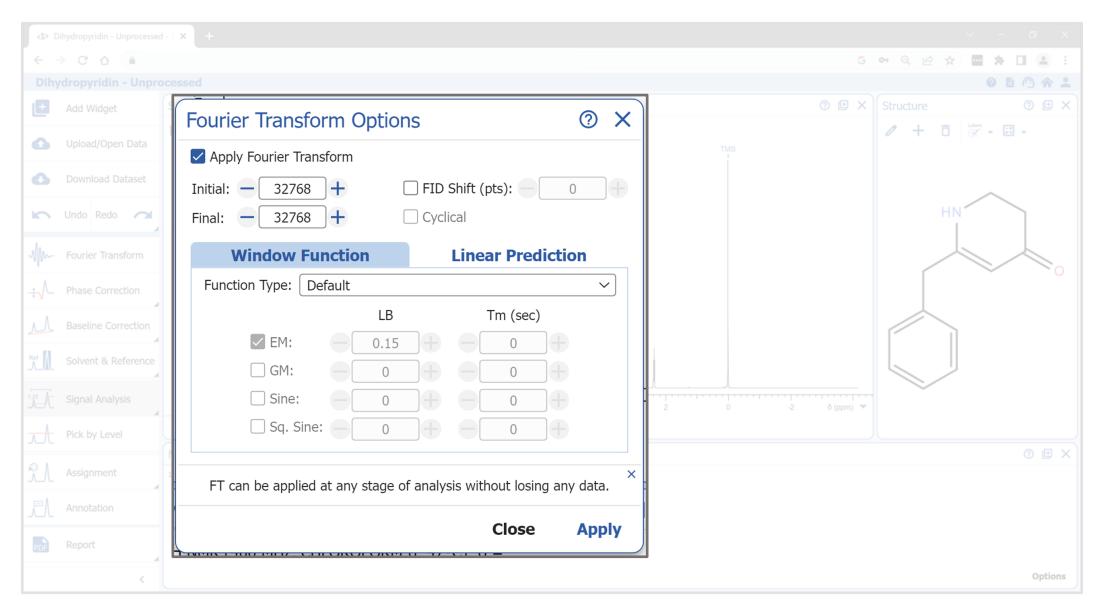
### Spectrus JS – Home Page

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Home Page				0 8 6 3
	Name	Last Modified	filter by name	
	Dihydropyridin - Unprocessed	Mar 17, 2023		
	Felodipine - NMR Data	Feb 10, 2023		
	Felodipine - LC-MS Data	Jan 26, 2023		
	Dihydropyridin - Fully Processed	Dec 20, 2022		
	GC-MS_Eugenol	Dec 1, 2022	•••	
	LC-MS_Verapamil_Rat_0min	Nov 28, 2022	•••	
	NMR Projects			
		+ Create New Dataset		

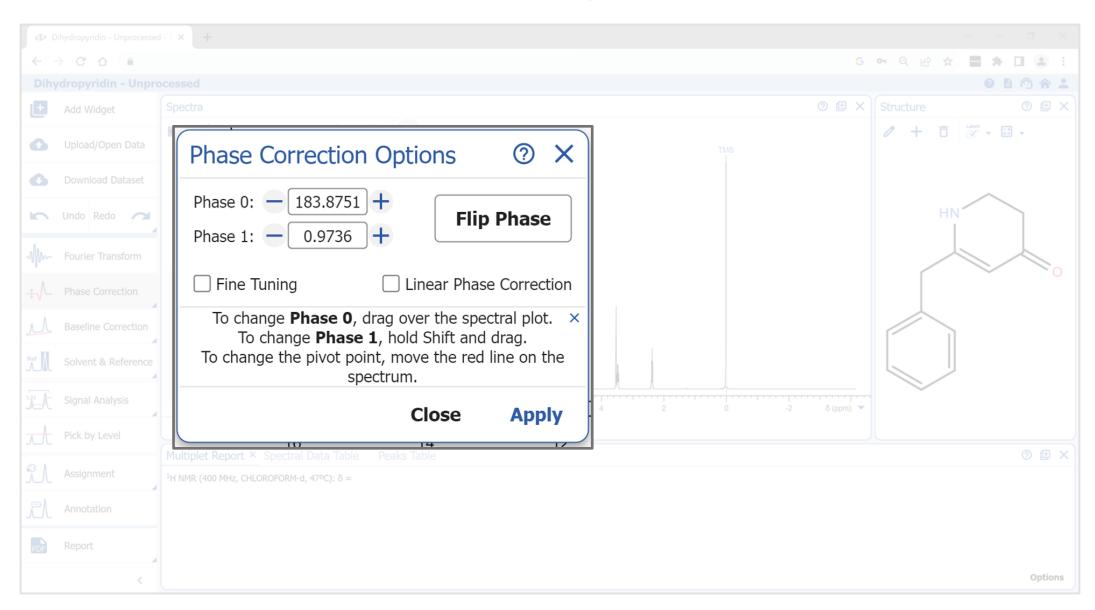
#### Spectrus JS – Dashboard



### Spectrus JS – Fourier Transformation Options



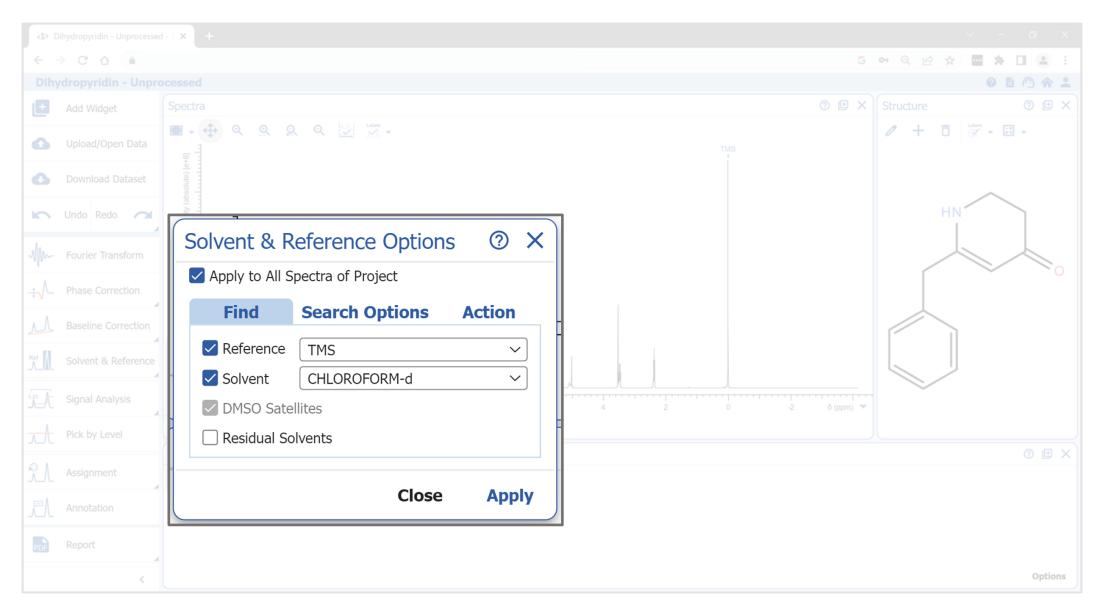
#### Spectrus JS – Phase Correction Options



### Spectrus JS – Baseline Correction Options

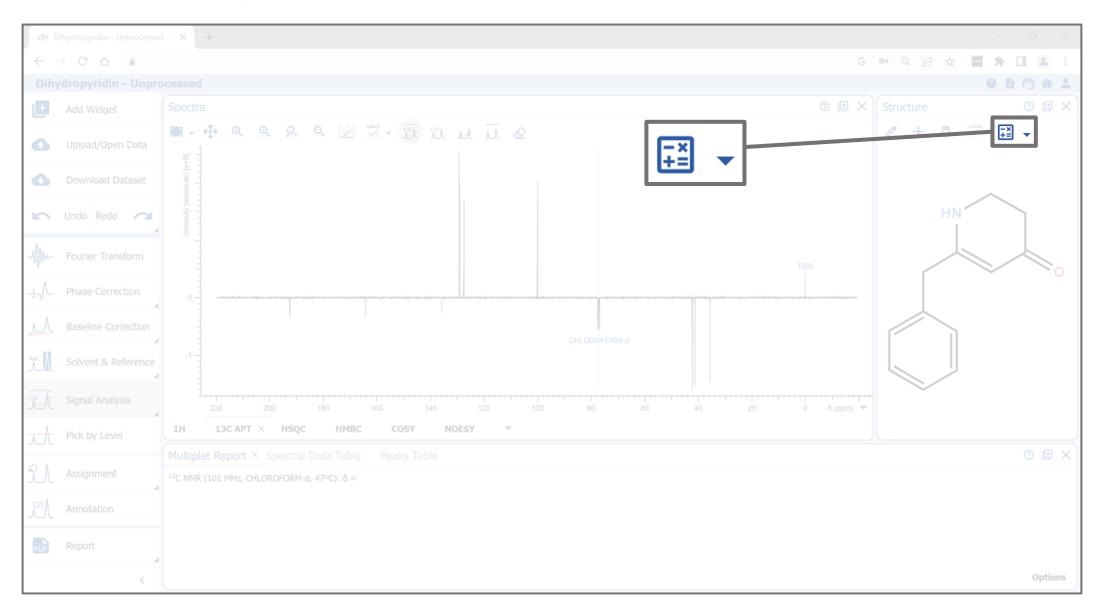
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1 <u>7</u> 7	Signal Analysis	Spectrum Averaging	2 0 -2 δ (ppm) ▼
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₹.L	Assignment	To add a point to the baseline, click the spectral plot. × To delete a point on the baseline, select it.	
17	Annotation	To correct the baseline, move the baseline point.	
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#### Spectrus JS – Solvent and Referencing Options

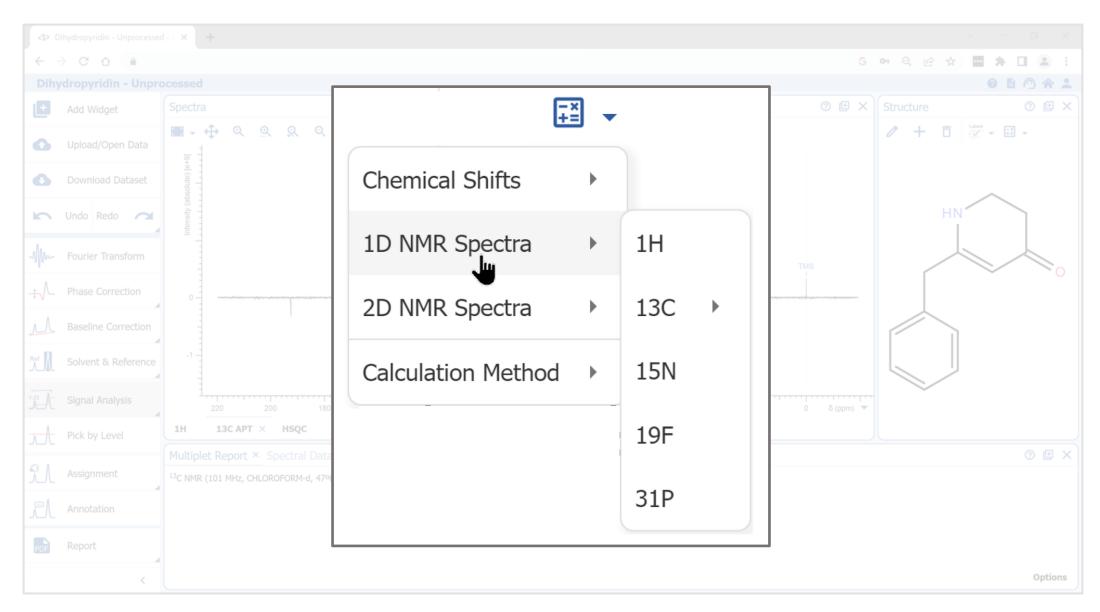


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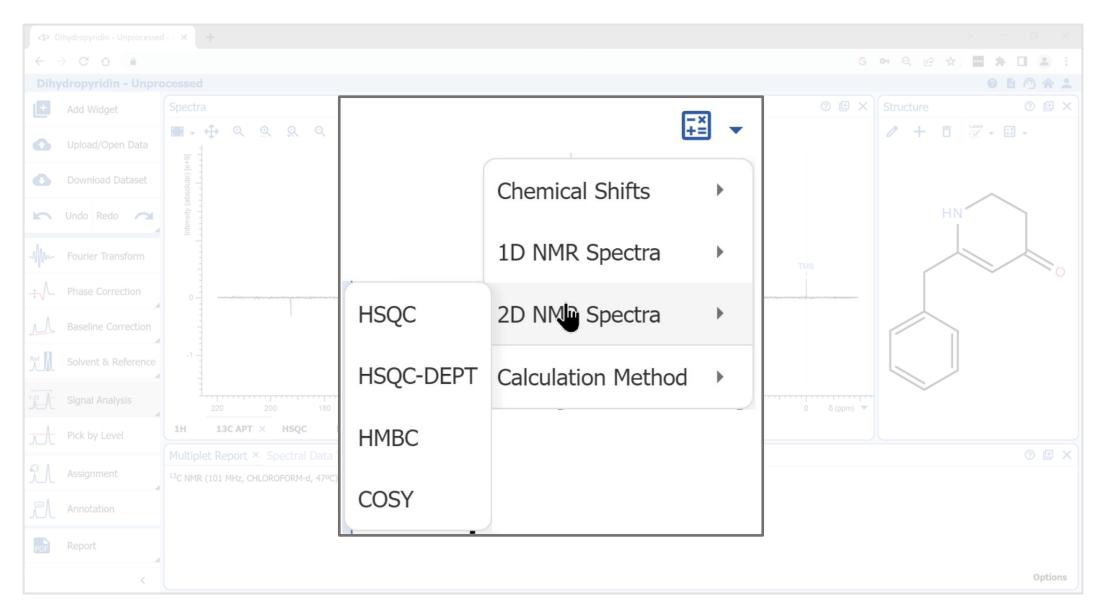
#### **Spectrus JS – Spectrum Prediction**



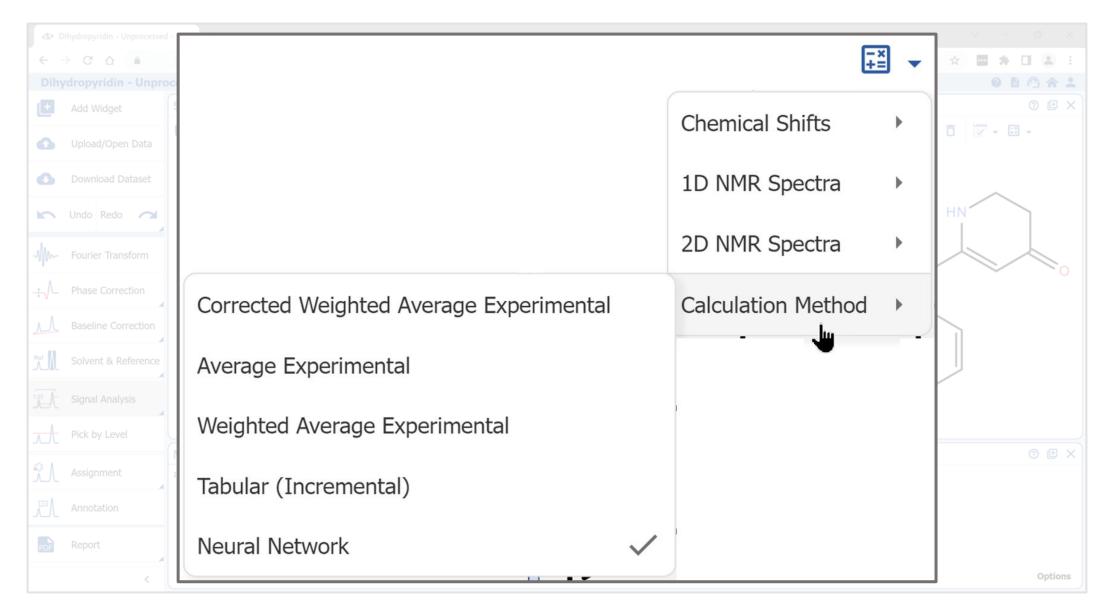
### Spectrus JS – 1D NMR Predictions



### Spectrus JS – 2D NMR Predictions

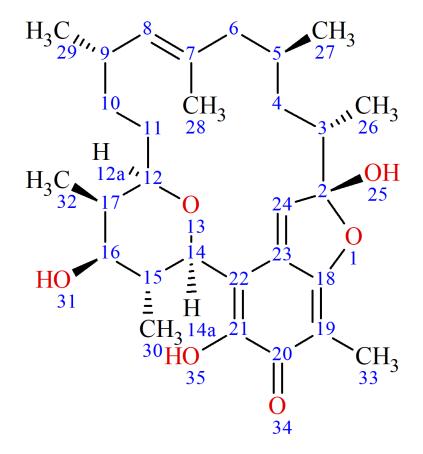


#### Spectrus JS – Prediction Algorithms



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#### Spectrus JS – Predicted <sup>13</sup>C APT



Internal databse with <sup>1</sup>H and <sup>13</sup>C data of ~300k structures

	÷	Ref	1H Shift 🔸	Atom No. 🔸
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		1	1.23 <'>	4
		1	1.39 <">	4
		1	1.79	5
		1	1.53 <'>	6
		1	2.02 <">	6
		1	4.47	8
		1	2.24	9
		1	1.08 <'>	10
		1	1.25 <">	10
		1	1.12 <'>	11
		1	1.36 <">	11
		1	3.39	12a
		1	4.19	14a
		1	1.6	15
		1	3.39	16
		1	1.75	17
		1	7.01	24
		1	0.53	26
V		1	0.83	27

#### Formula: C<sub>29</sub>H<sub>42</sub>O<sub>6</sub>

FW: 486.6402

Name: (1*R*,9*S*,10*S*,12*S*,14*E*,16*S*,19*R*,20*R*,21*S*,22*R*)-3,9,21-trihydrox<sup>-</sup> Trivial Name: kendomycin

Ref: J. Nat. Prod.,2020,v.83,p.965(HNMR: HSQC; 600 MHz; 300 K)

Monoisotopic Mass: 486.298139

[M+H]+: 487.305415



### Spectrus JS – Predicted <sup>13</sup>C APT

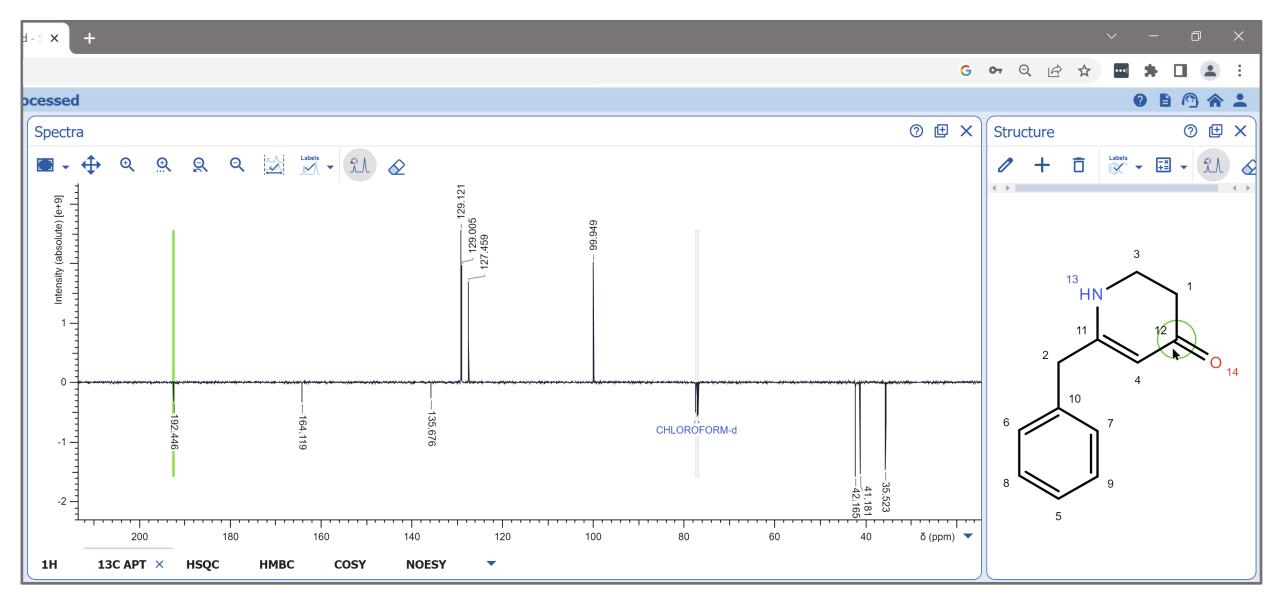
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		3	2	CH2	M02	H 8	3.52	3.38	s	41.18	40.16	S				
PDF	Report	4	3<'>	CH2	M03	H 7	3.47	3.67	td (7.62x(2), 2.39)	42.17	40.25	S				
	<	5	4	CH	M04	H 9	5.01	4.88	S	99.95	98.27	S				
	×	6	5, 8, 9	СН	M05	H 11	7.26	7.27, 7.20	m	127.46	128.52, 127.33	S				* *

### Spectrus JS – Predicted HSQC-DEPT

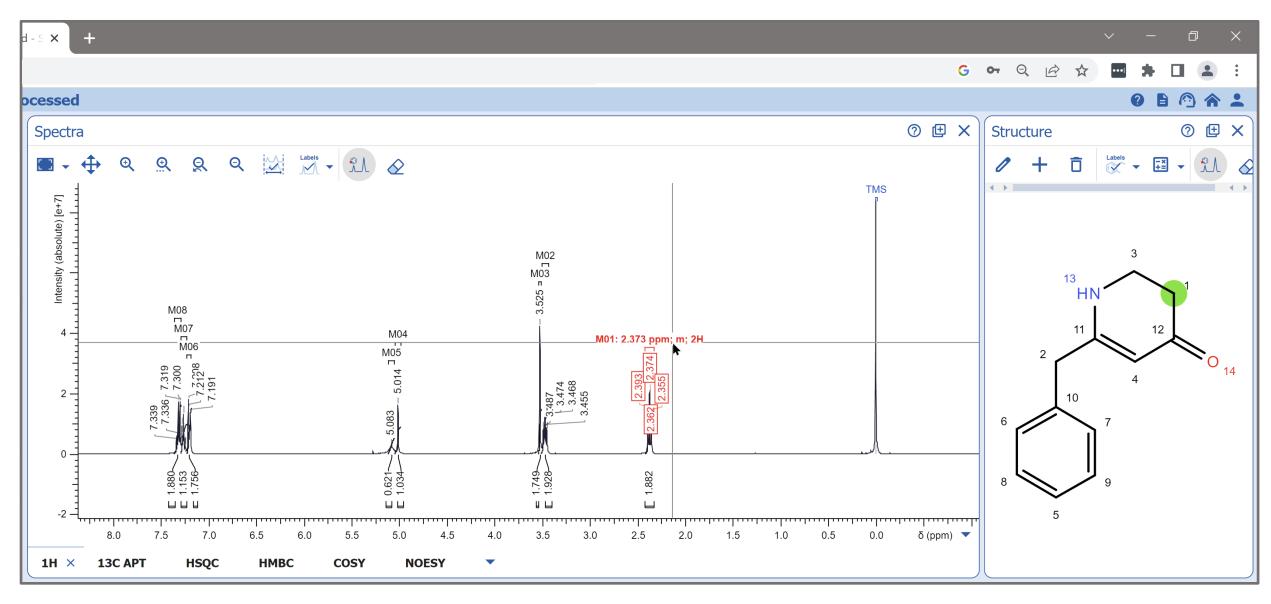
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	Depart	1	13	NH		M05	5.08	5.79	br s							
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		3	3<">	CH2	C 11	H 15	3.67	3.67	u	40.21	40.25	u				
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	× .	6		СН	C 14					129.00		u				* *

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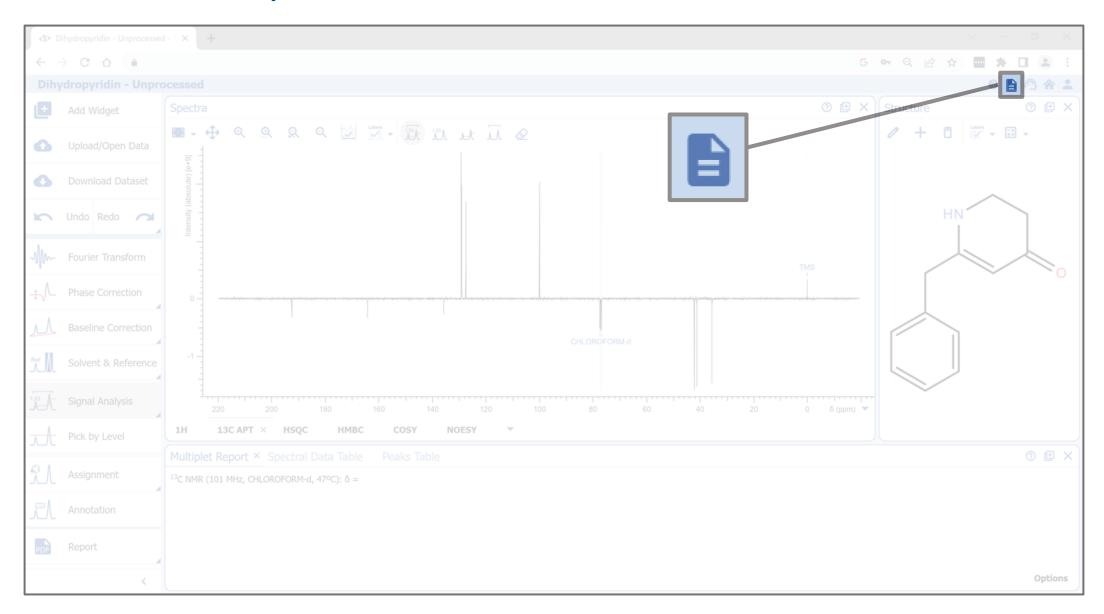
#### Spectrus JS – Manual Assignment <sup>13</sup>C



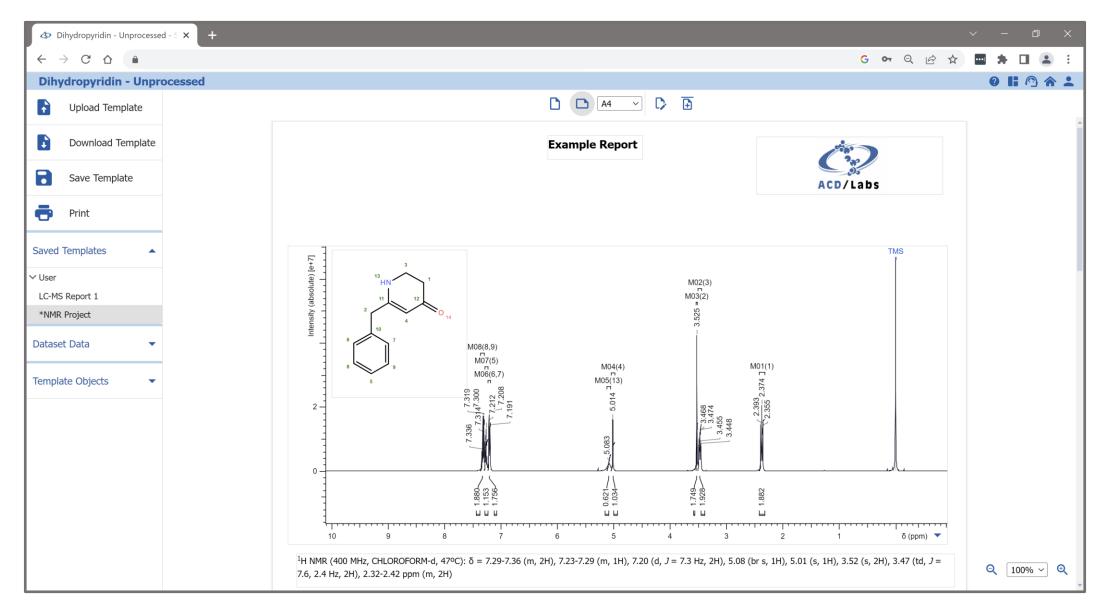
#### Spectrus JS – Manual Assignment <sup>1</sup>H



#### Spectrus JS – Report Editor



#### Spectrus JS – Report Editor



#### 🚱 ACD/Labs

### Spectrus JS – Summary

- Compatible with every operating system and browser
- Intuitive interface
- Easy to operate for both 1D and 2D NMR processing
- Prediction of 1D and 2D NMR experiments
- Effortless report generation



#### **Click here for a free trial version.**

# Questions?

## ⊠ Vincent.Zwicker@acdlabs.com



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