

Supporting Information

Computation-guided rational design of a peptide motif that reacts with
cyanobenzothiazoles via internal cysteine-lysine relay

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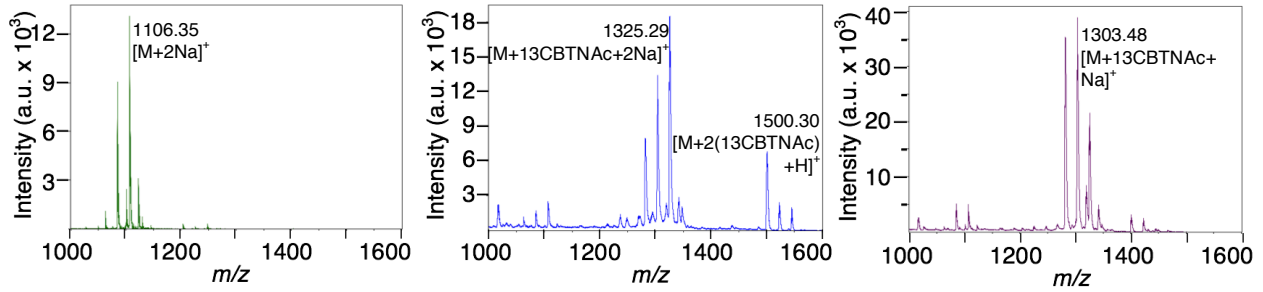
Table S1. List of sequences modeled using PEP-FOLD.²⁵⁻²⁶ Bolded peptides in blue-shaded cells were subsequently made by SPPS.

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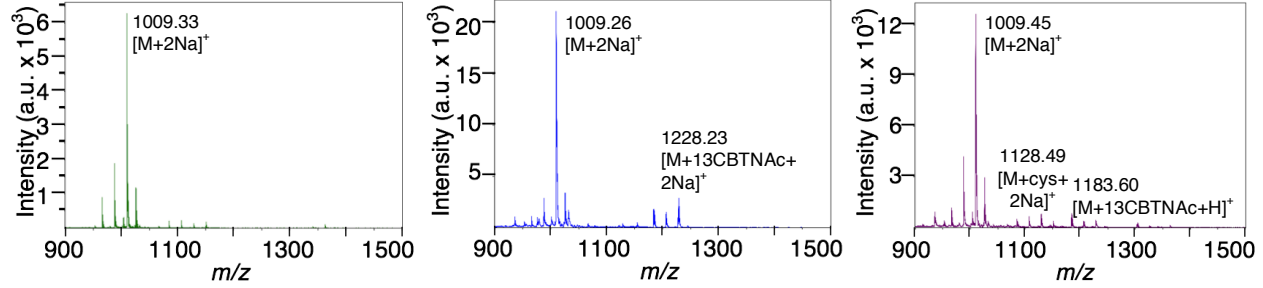
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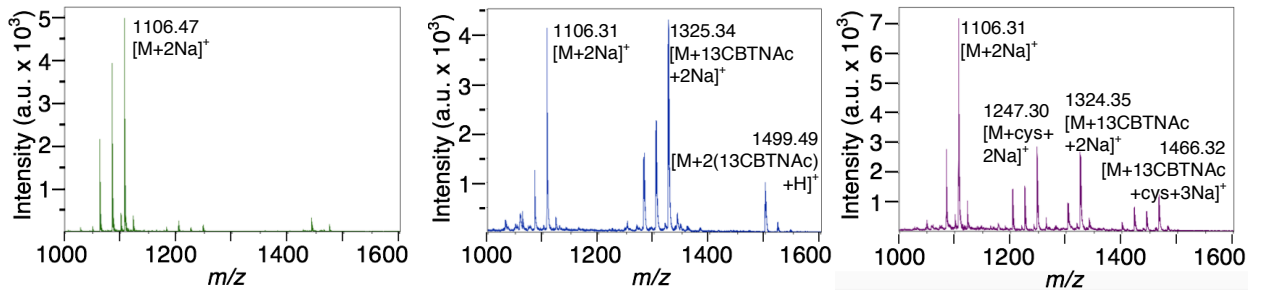
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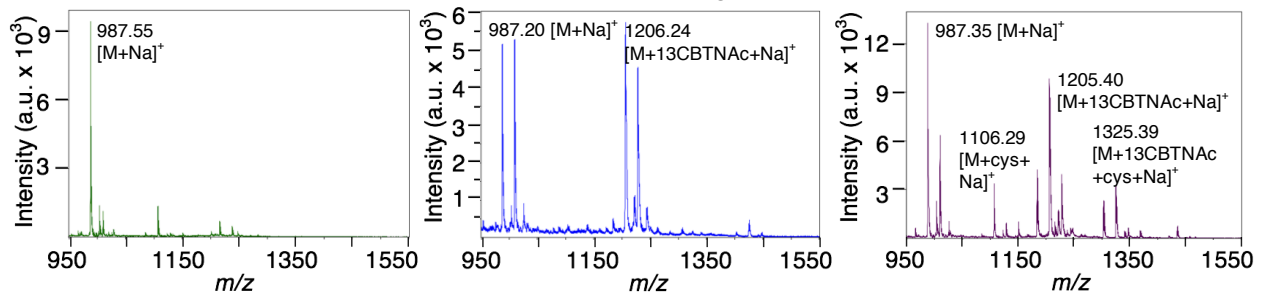
B. PEP-FOLD-4, Ac-GGDPHPCKGG-NH₂ (5): 964.42 g/mol



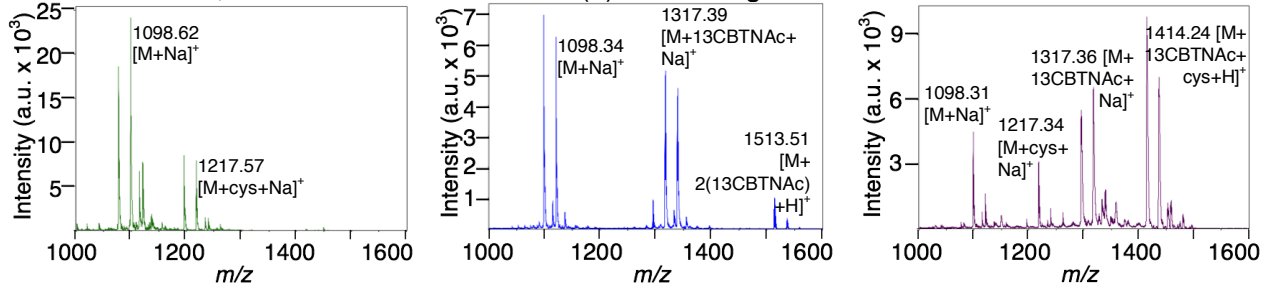
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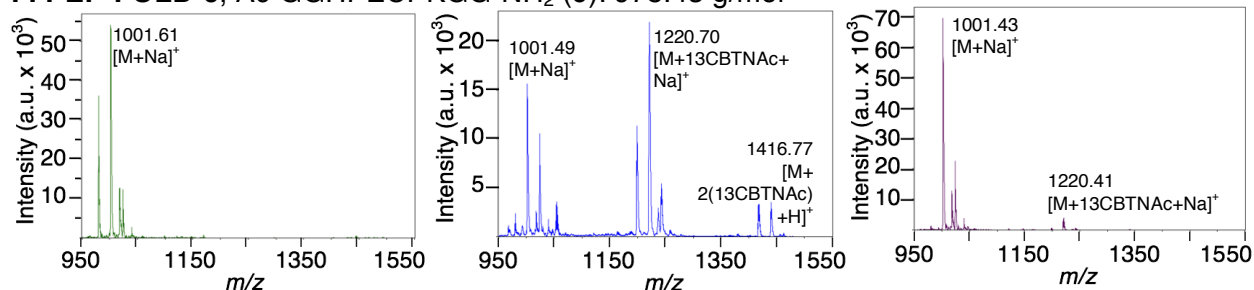
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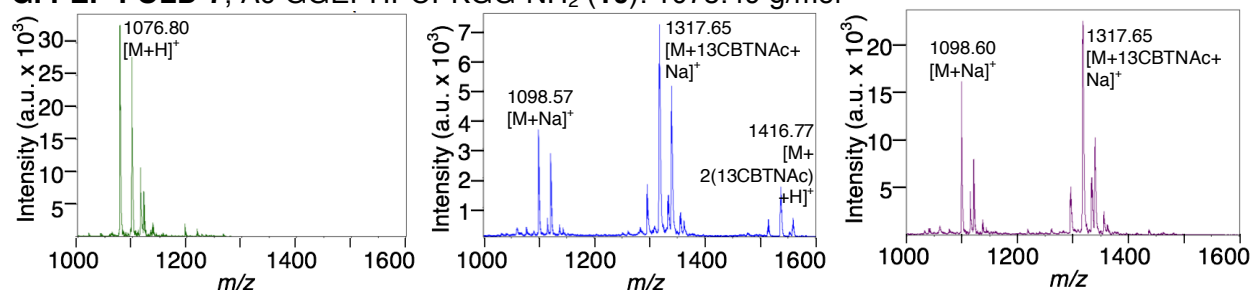
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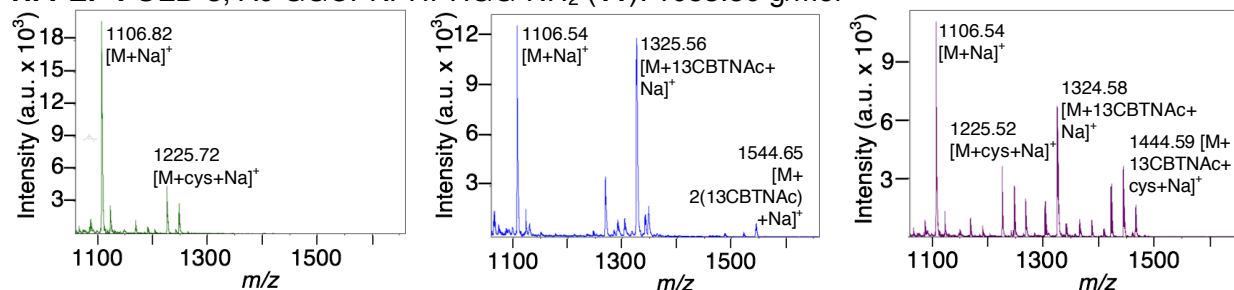
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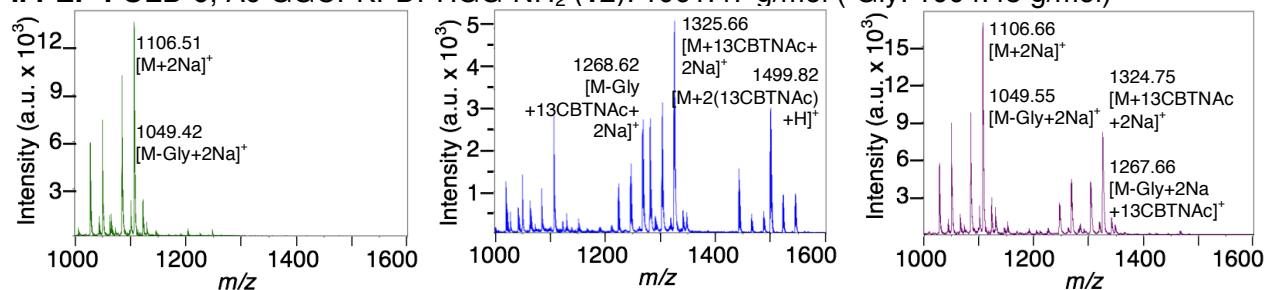
G. PEP-FOLD-7, Ac-GGEPHPCPKGG-NH₂ (10): 1075.49 g/mol



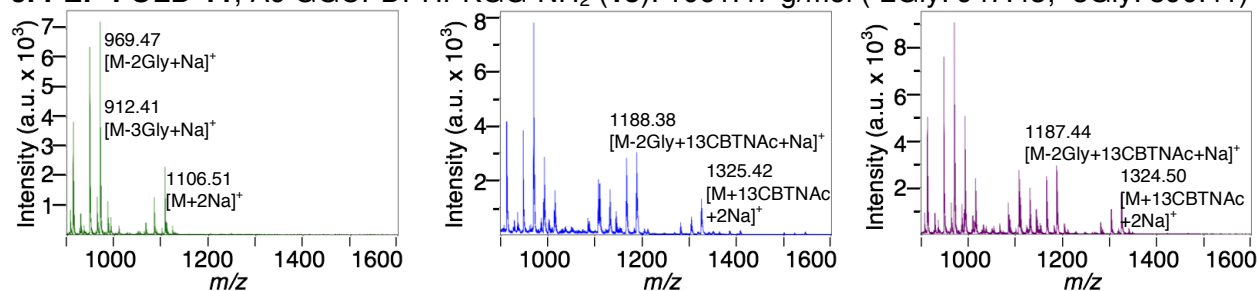
H. PEP-FOLD-8, Ac-GGCPKPHPHGG-NH₂ (11): 1083.50 g/mol



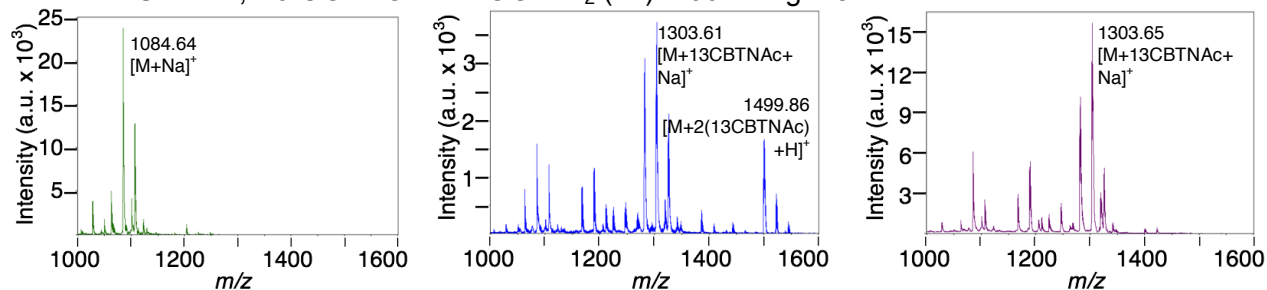
I. PEP-FOLD-9, Ac-GGCPKPDPHGG-NH₂ (12): 1061.47 g/mol (-Gly: 1004.45 g/mol)



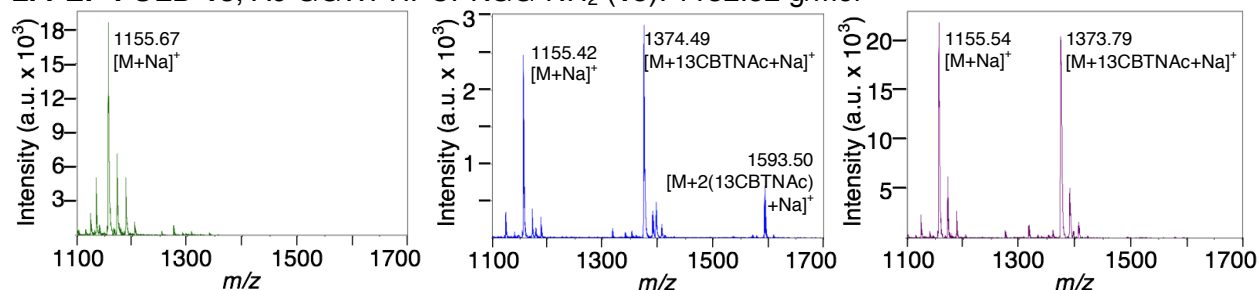
J. PEP-FOLD-11, Ac-GGCPDHPKGG-NH₂ (13): 1061.47 g/mol (-2Gly: 947.43; -3Gly: 890.41)



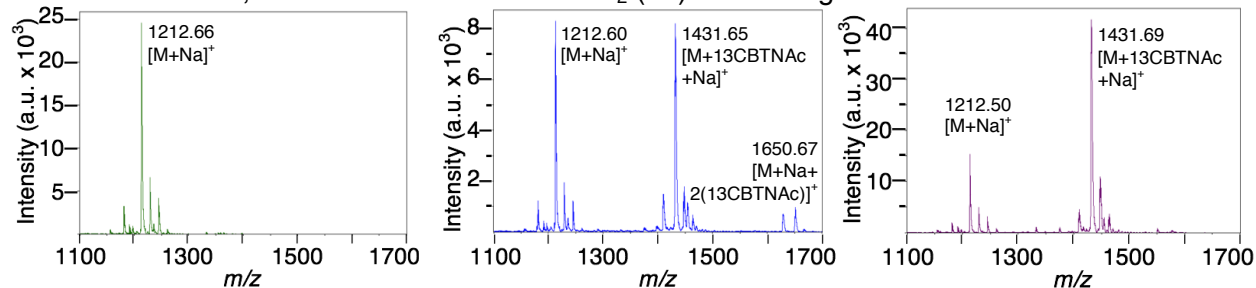
K. PEP-FOLD-12, Ac-GGKPCPHPDGG-NH₂ (14): 1061.47 g/mol



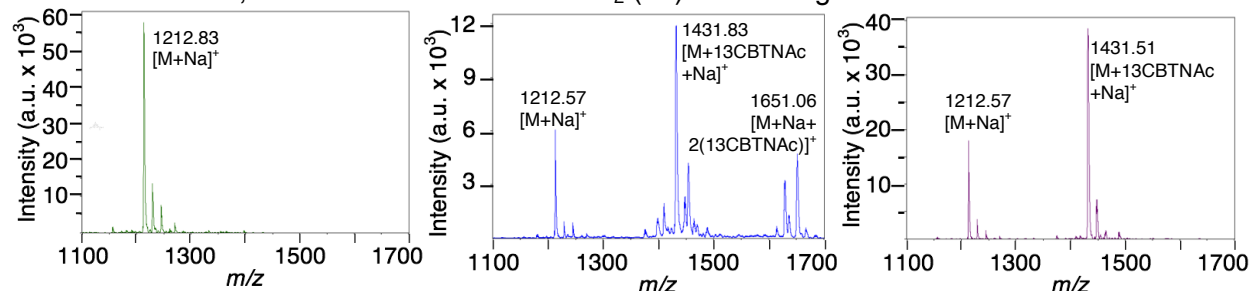
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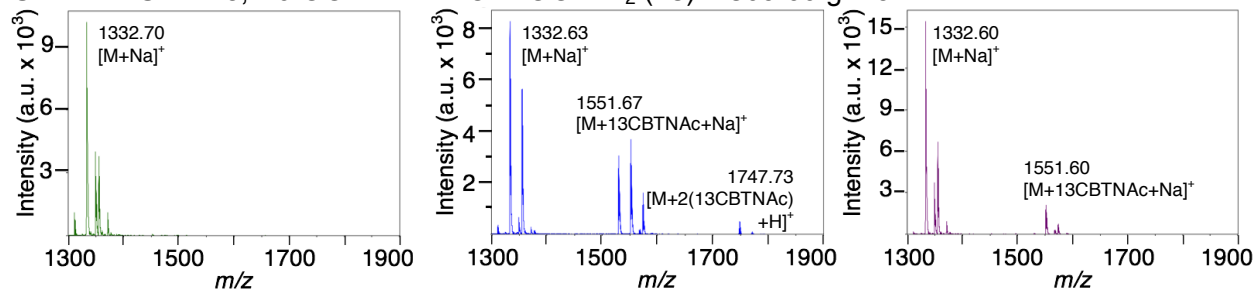
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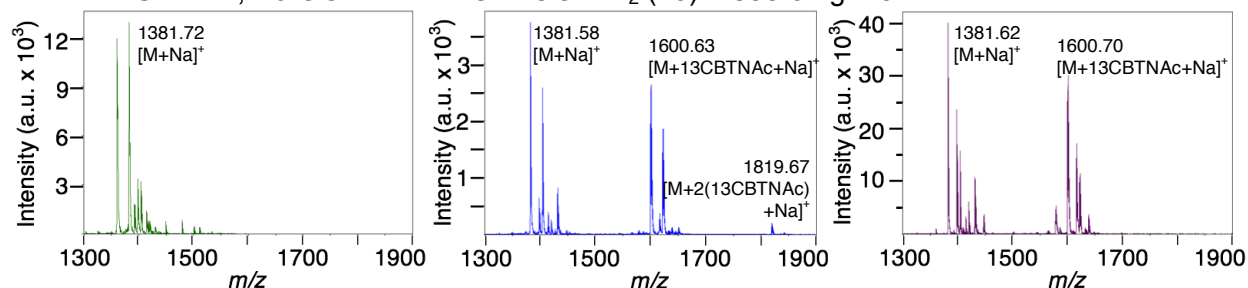
N. PEP-FOLD-15, Ac-GGKPCPGWPHGG-NH₂ (17): 1189.55 g/mol



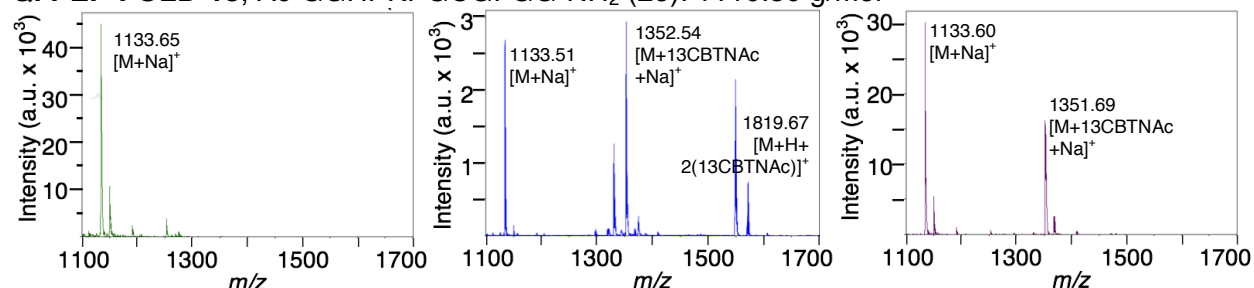
O. PEP-FOLD-16, Ac-GGHPHPKPCPEGG-NH₂ (18): 1309.60 g/mol



P. PEP-FOLD-17, Ac-GGHPWPKPCPEGG-NH₂ (19): 1358.62 g/mol



Q. PEP-FOLD-18, Ac-GGHPKPGCGFGG-NH₂ (20): 1110.50 g/mol



R. PEP-FOLD-19, Ac-GGHPKPGCGFGG-NH₂ (21): 1053.48 g/mol (-Gly: 996.46 g/mol)

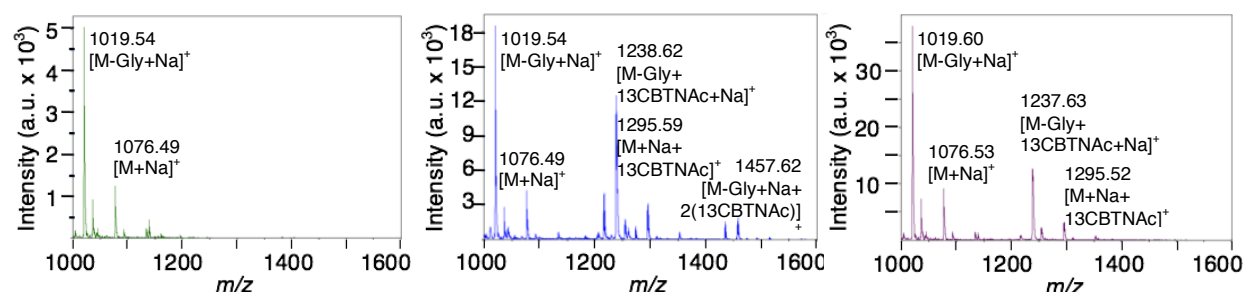


Figure S1. 13CBTNAc binding assay and cysteine competition MALDI-TOF-MS data for the eighteen peptides synthesized by SPPS. All peptides were re-purified by preparative RP-HPLC immediately prior to this experiment and all data in this figure were obtained in parallel in order to minimize sources of error. The binding assay and cysteine competition were as follows: 40 μ L of a 10% DMF in PBS solution of peptide (0.9 mM) with or without 13CBTNAc (1 mM) was incubated 48 h at r.t. Then, the negative control (without 13CBTNAc) and half (20 μ L) of the sample incubated with 13CBTNAc were each treated with an equal volume (20 μ L) of a solution of cysteine and DTT (10 and 15 mM, respectively) in PBS. The other half of the sample incubated with 13CBTNAc was treated with an equal volume of a solution of DTT (15 mM) in PBS. After 48 h at r.t., MALDI-TOF MS was used to analyze the negative control (left column, green spectra),

the sample incubated with ^{13}C BTNAc then DTT alone (middle column, blue spectra), and the sample incubated with ^{13}C BTNAc then cysteine and DTT (right column, purple spectra). Labels are in the format **Name of peptide**, Sequence (**Compound #**): Calculated exact mass (identity of major impurity and calculated exact mass, where applicable). **A**) CBTag 1.0 (**4**), analogous to Figure 3B. **B**) PEP-FOLD-4, analogous to Figure 3C (**5**). **C-R**) Other peptides tested. Peptides in **I**, **J**, and **R** have additional peaks corresponding to glycine deletions, but the residues that confer reactivity (e.g., Cys, Lys) were not affected.

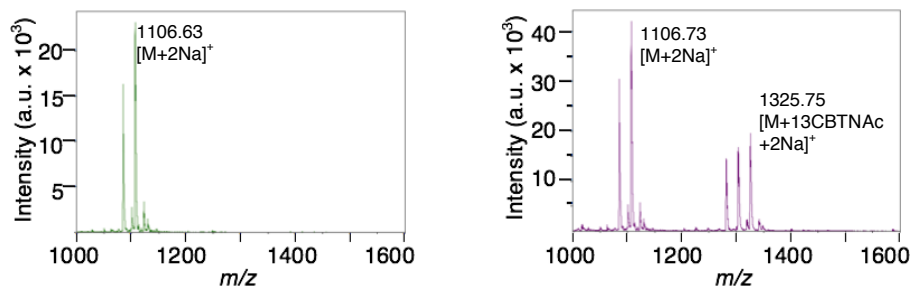


Figure S2. Results of the ¹³CBTNAC binding assay and cysteine treatment for CBTag 1.0 when conducted in the presence of 5 mM glutathione (reduced). Left (green spectrum), negative control after treatment with cysteine and DTT. Right (purple spectrum), CBTag 1.0 treated with 1.1 equiv. of ¹³CBTNAC then with 10 equiv. cysteine and 15 equiv. DTT relative to ¹³CBTNAC. CBTag 1.0-¹³CBTNAC adduct is observed, though less has formed than in the absence of glutathione.

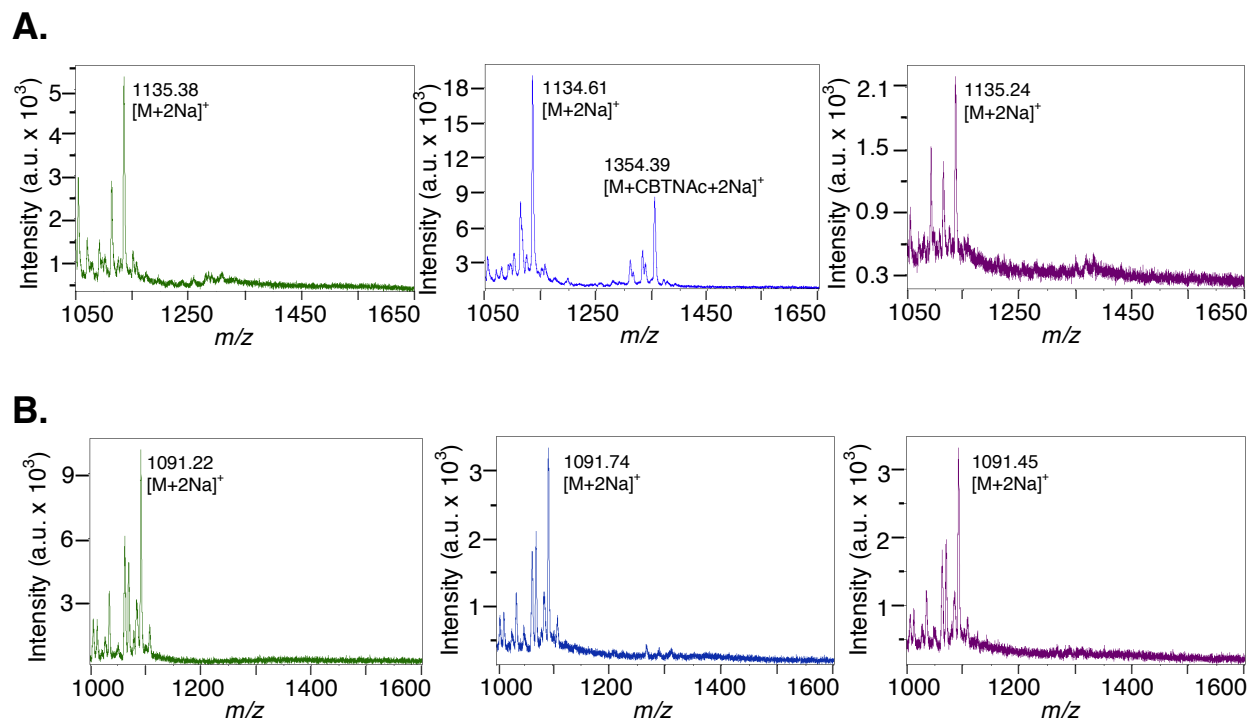
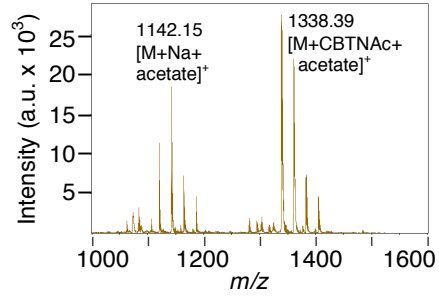
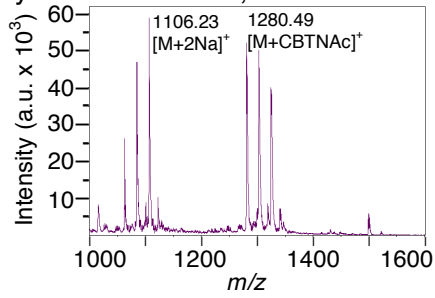
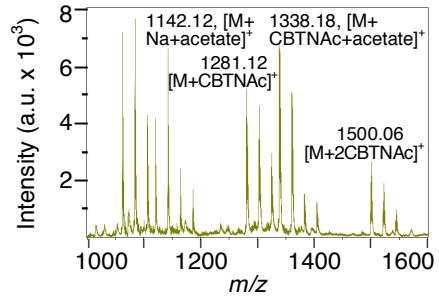
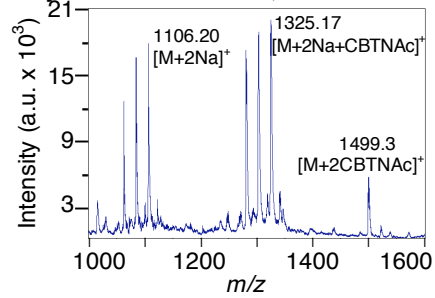


Figure S3. Results of binding experiment and cysteine competition assays for CBTag 1.0 (K9R) (**A.**) and CBTag 1.0 (C7S) (**B.**). Spectra are analogous to those in Figure 3. The first spectrum in each row corresponds to crude peptide, the second to the results of the binding assay, and the third to the results of the cysteine competition. In **A.**, CBTag 1.0 (K9R) is partially modified by one equivalent of CBTNAc, and that equivalent is removed by cysteine treatment, suggesting that, as expected, the modification is on the cysteine residue. In **B.**, CBTag 1.0 (C7S) is not at all modified by CBTNAc, implying that the cysteine residue is necessary for lysine modification.

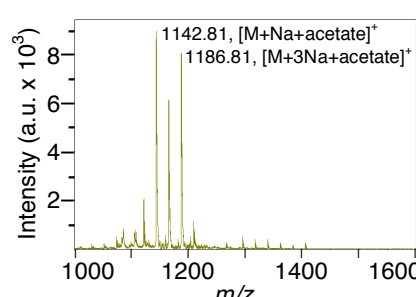
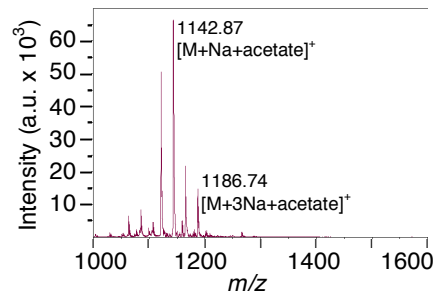
A. Cysteine treatment, +/- chloroacetate



B. No cysteine treatment, +/- chloroacetate

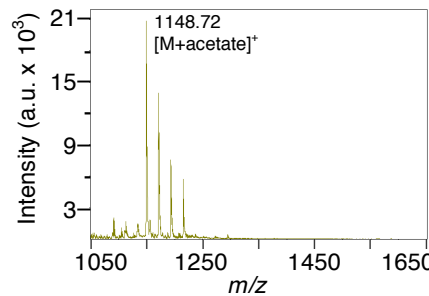
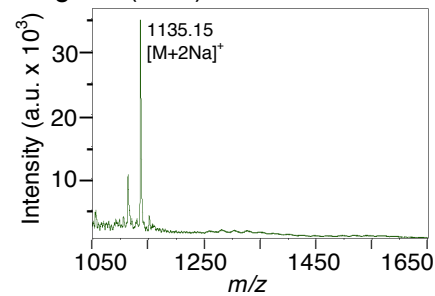


C. CBTAg 1.0 pretreated with chloroacetate, +/- CBTNAC



D.

CBTAg 1.0 (K9R) +/- chloroacetate



CBTAg 1.0 (C7S) +/- chloroacetate

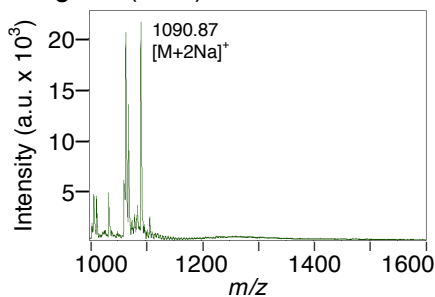
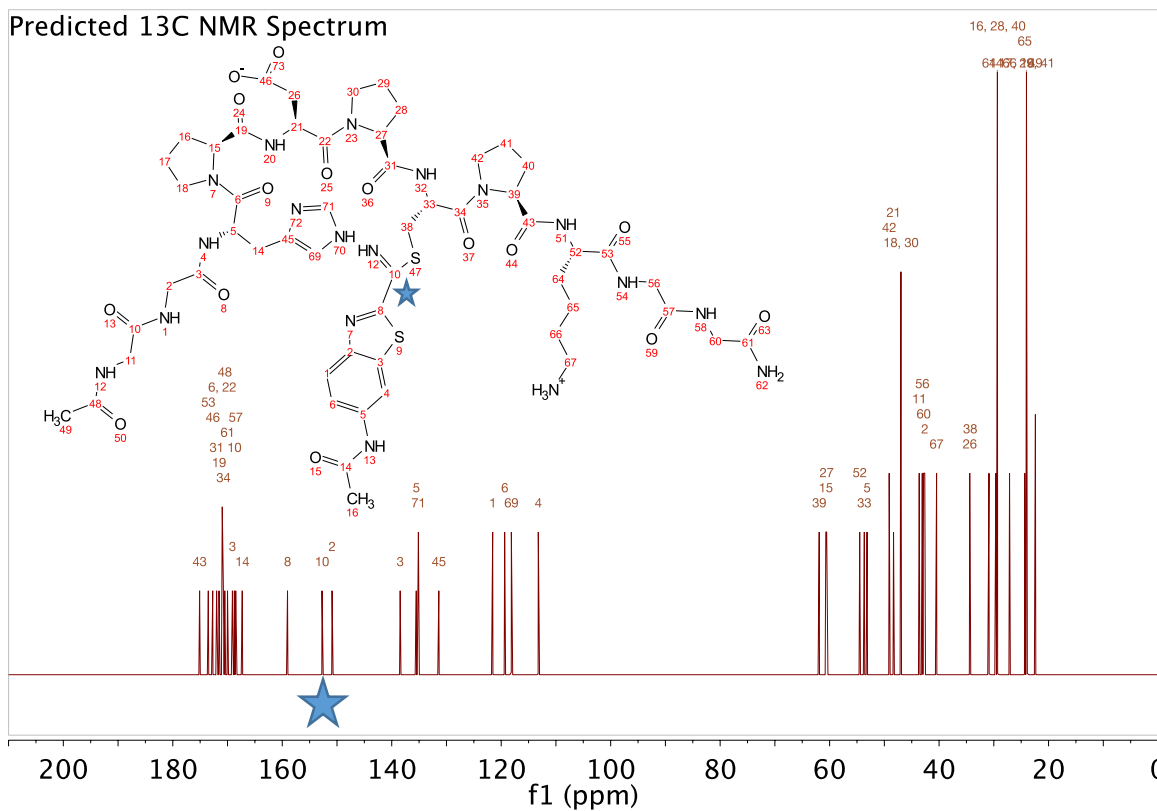
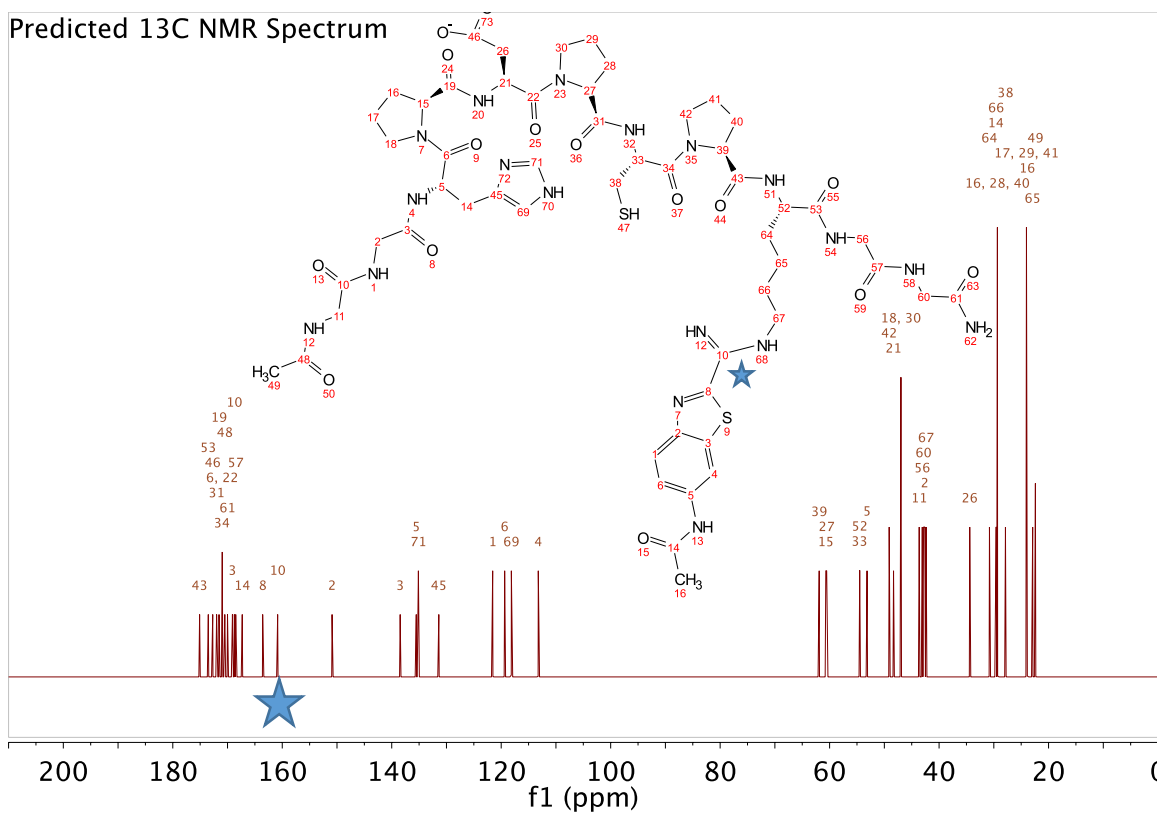


Figure S4. Results of chloroacetate labeling of thiols under various conditions. **A.** The left MALDI-TOF MS spectrum is after cysteine treatment of CBTag 1.0 that had been reacted with CBTNAc. The right spectrum are the results of treating the sample in the left spectrum with chloroacetate. The peaks shift by 57 m/z , indicating labeling of a thiol and suggesting CBTNAc is attached to the lysine residue. **B.** The left MALDI-TOF MS spectrum is after CBTag 1.0 was reacted with CBTNAc but before cysteine treatment. Chloroacetate treatment of this sample gave the spectrum on the right, where one population of the singly modified peptide was labeled (lysine adduct) and another was not (cysteine adduct). The peptide modified by two equivalents of CBTNAc was not labeled by chloroacetate. **C.** When CBTag 1.0 was pretreated with chloroacetate (left), no CBTNAc reacted with the resulting peptide (right). **D.** As a control to confirm chloroacetate thiol specificity, CBTag 1.0 (K9R) (top left) and CBTag 1.0 (C7S) (bottom left) were treated with chloroacetate. Only CBTag 1.0 (K9R) (top right) was labeled, confirming that lysine residues are not modified by chloroacetate.

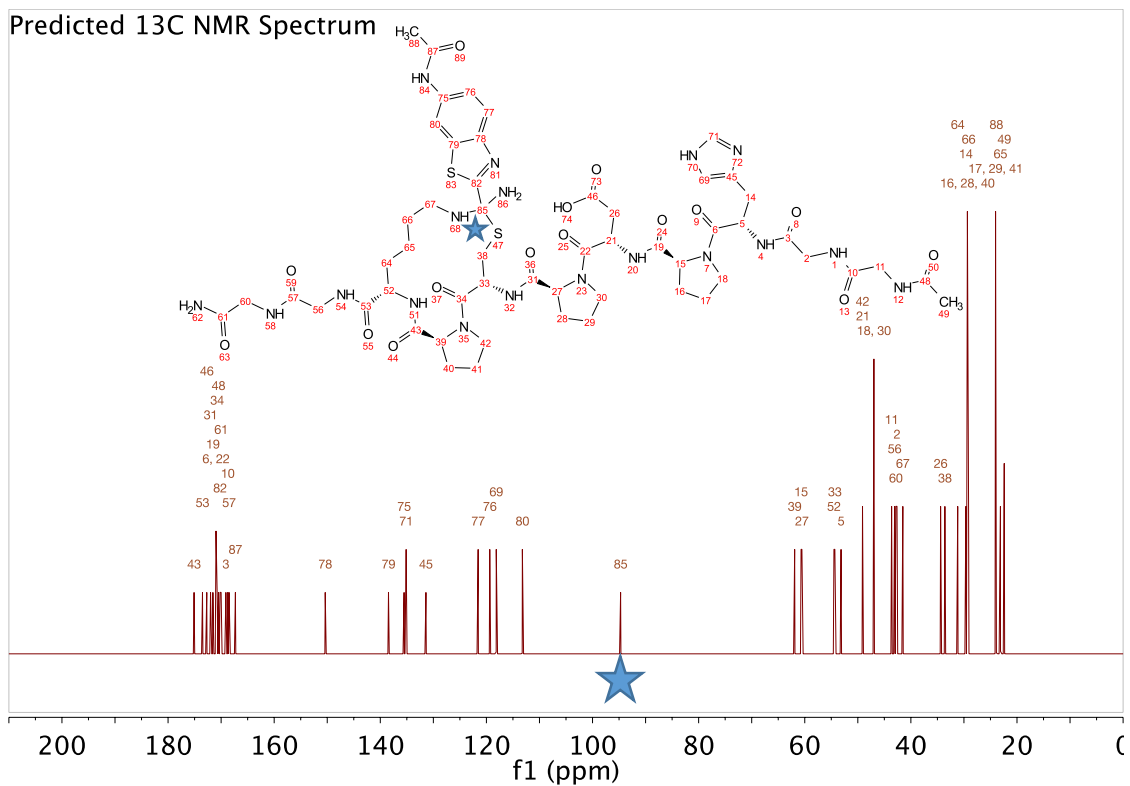
A. Predicted ¹³C NMR Spectrum



B. Predicted ¹³C NMR Spectrum



C.



D.

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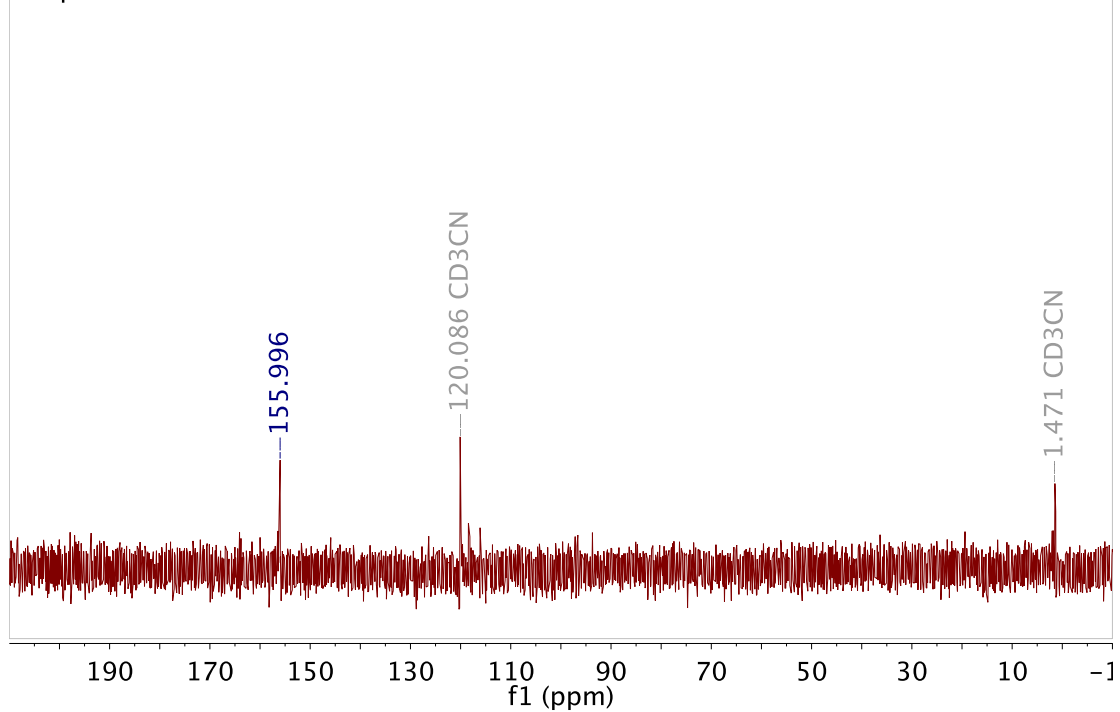


Figure S5. ^{13}C NMR confirms that the final CBTag 1.0-CBTNAc adduct is not the tetrahedral intermediate. **A.-C.**, Predicted spectra (MestreNova) for the cysteine adduct, the lysine adduct, and the tetrahedral intermediate. α -Carbon and corresponding peak are labelled with a blue star. **D.** ^{13}C NMR spectrum of (dilute) purified CBTag 1.0- ^{13}C BTNAc shows that the peak corresponding to the ^{13}C -labelled α -carbon is at 156 ppm (referenced to acetonitrile- d_3 methyl peak), which is similar to the predicted values for the lysine and cysteine adducts but significantly different from the predicted value for the tetrahedral intermediate.

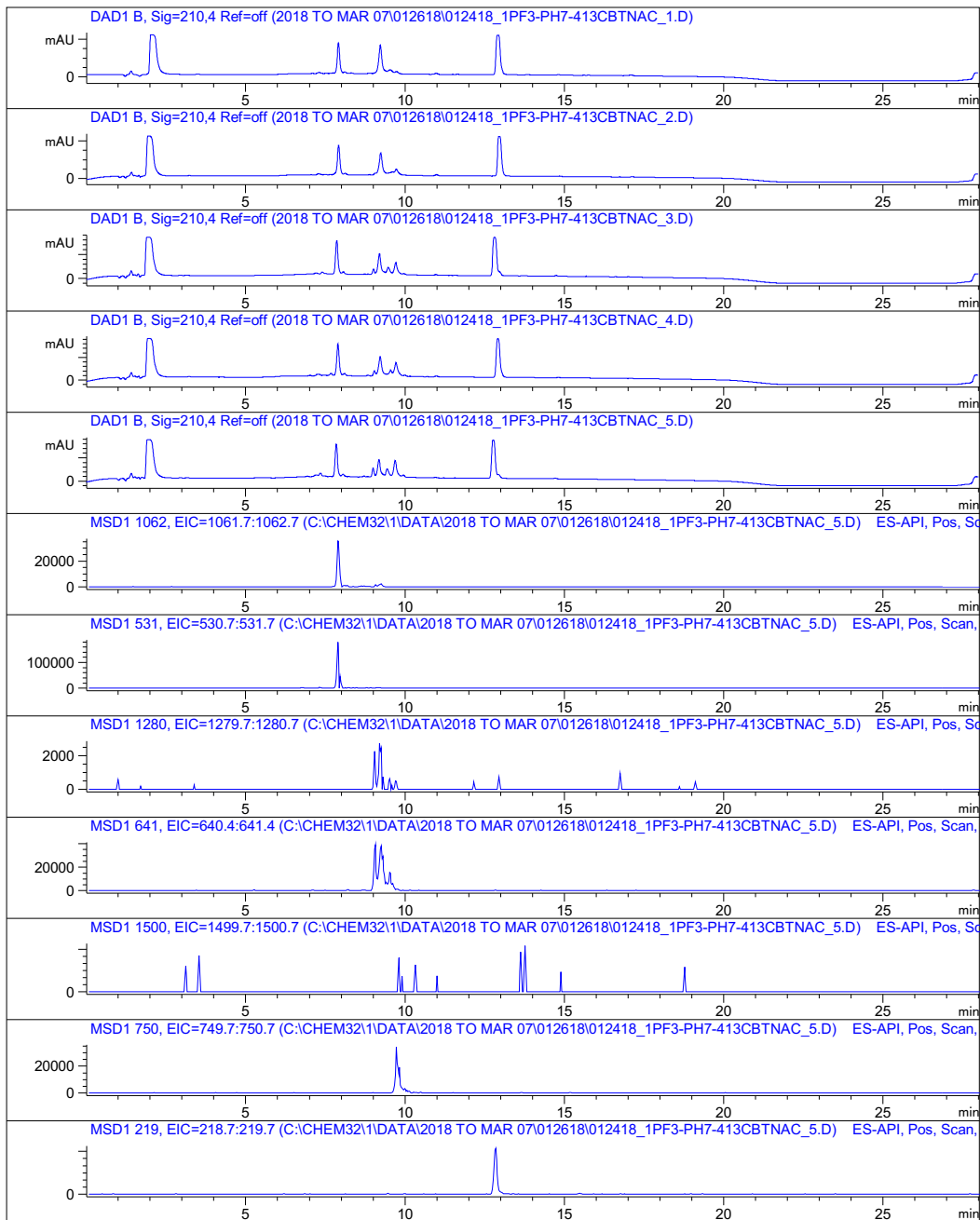


Figure S6. Overlay of LC-MS chromatographs for 1:4 CBTag 1.0/13CBTNAc over the time-course experiment and extracted mass ions. Identities of extracted mass ions: 1062 m/z, minute 7.9 – [CBTag 1.0 + H]⁺; 531 m/z, minute 7.9 – [CBTag 1.0 + 2H]²⁺; 1280 m/z, minutes 9 and 9.2 – [CBTag 1.0-13CBTNAc + H]⁺; 641 m/z, minutes 9 and 9.2 – [CBTag 1.0-13CBTNAc + 2H]²⁺; 1500 m/z, insignificant signal – [CBTag 1.0-2(13CBTNAc) + H]⁺; 750 m/z, minute 9.7 – [CBTag 1.0-2(13CBTNAc) + 2H]²⁺; 219 m/z, minute 12.9 – [13CBTNAc + H]⁺

Print of window 38: Current Chromatogram(s)

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Different Inj Volume from Sequence ! Actual Inj Volume : 10.000 µl

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Last changed : 3/8/18 8:51:08 AM

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Additional Info : Peak(s) manually integrated

Current Chromatogram(s)

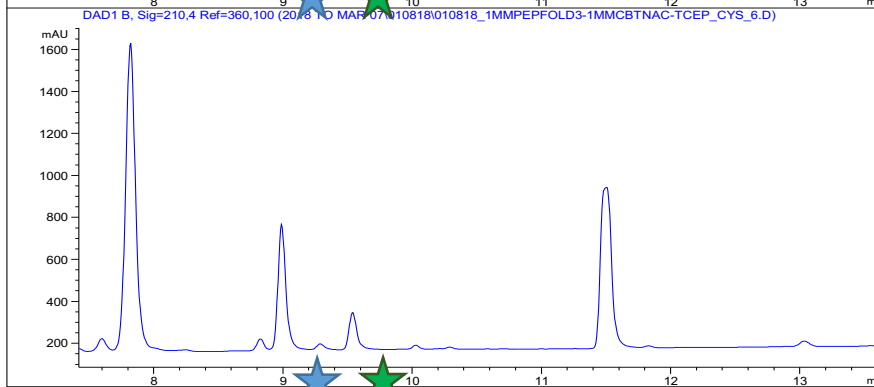
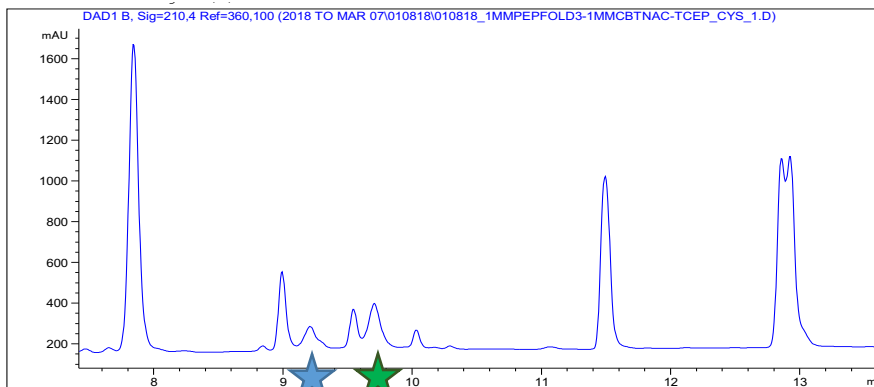
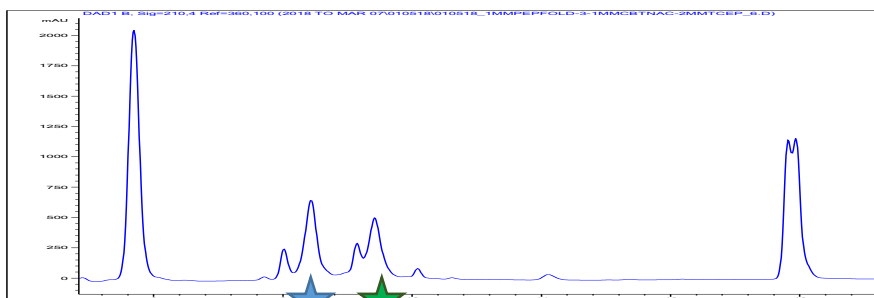


Figure S7. Cysteine treatment identifies peaks that contain cysteine adducts. Top spectrum was before cysteine treatment, middle was from an early time point during cysteine treatment, and bottom spectrum was at the end of the time-course assay. Based on these results and the mass spectrum in Figure S6, the blue star (minute 9.2) indicates the cysteine adduct, while the green star (minute 9.7) indicates the doubly modified peptide; the peak at minute 9 is the lysine adduct.

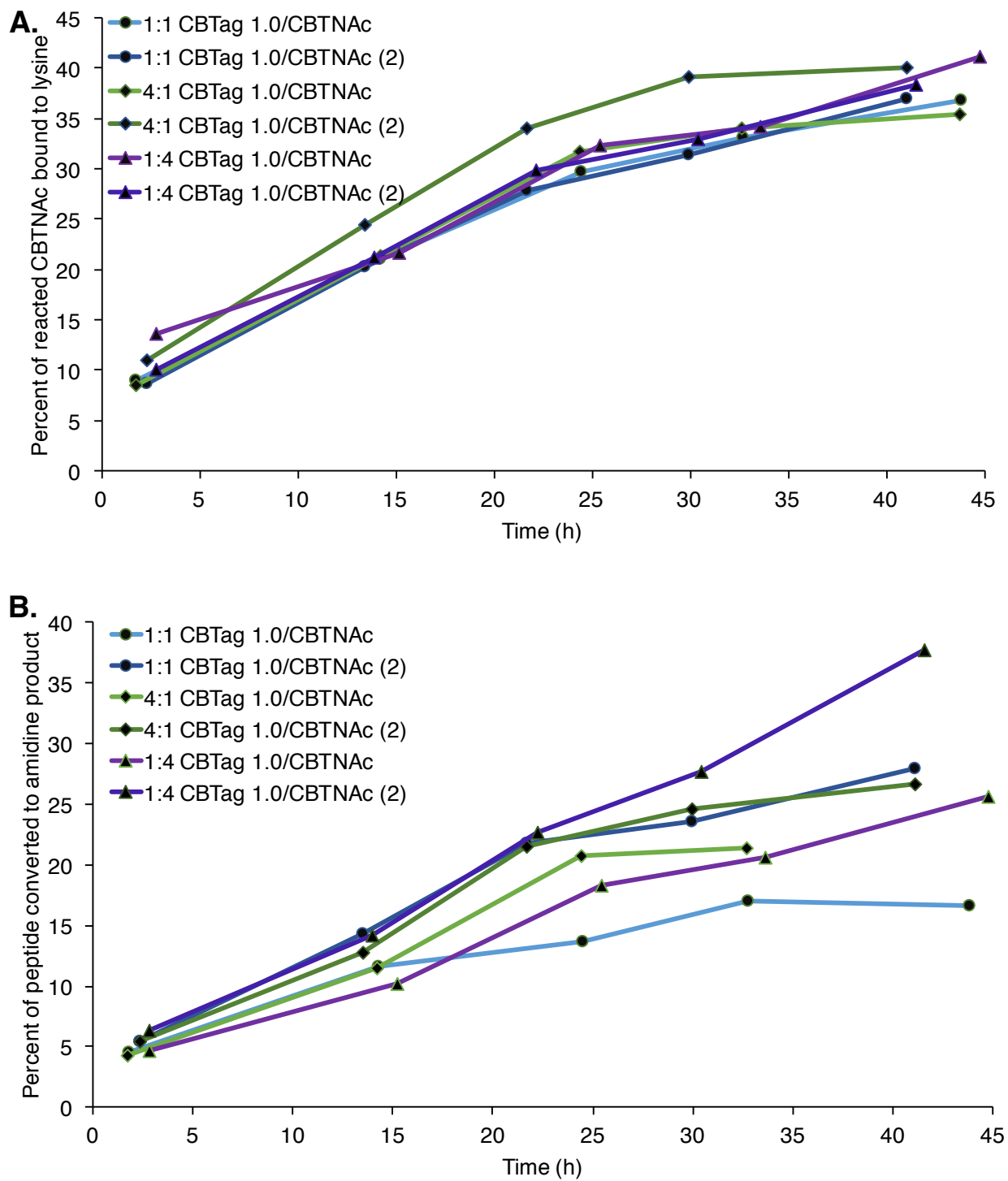


Figure S8. LC-MS-based time-course data for the reaction between CBTag 1.0 and CBTNAc. **A)** Percent of the CBTNAc bound to a peptide that is ligated through an amidine bond over time. **B)** Percent of the peptide that was converted to the amidine product over time. Blue lines and circular

markers represent two replicates of the reaction between CBTag 1.0 (22.5 mM) and CBTNAc (22.5 mM). Green lines and diamond markers represent two replicates of the reaction between CBTag 1.0 (22.5 mM) and CBTNAc (5.63 mM). The last time point of the first replicate is not shown because an instrument error during injection resulted in overall lower-than-expected signal. Purple lines and triangular markers represent two replicates of the reaction between CBTag 1.0 (5.63 mM) and CBTNAc (22.5 mM). Spreadsheets containing the corresponding calculations, LC-MS spectra, and LC-MS integration results are in Tables S2-S4 and the section following Figure S13.

Print of window 38: Current Chromatogram(s)
Data File : C:\CHEM32\...TA\2018 TO MAR 07\010518\010518_1MMPEPFOLD-3R-1MM13CBTNAC-2MMTCEP.D
Sample Name : 010518_1mMpepfold-3R-1mMcbtnac-2mMTCEP_1
=====

Acq. Operator : sglk	Seq. Line : 21
Acq. Instrument : Instrument 1	Location : Vial 31
Injection Date : 1/6/18 2:26:29 AM	Inj : 1
	Inj Volume : 15.000 µl
	Actual Inj Volume : 10.000 µl

Different Inj Volume from Sequence !
Acq. Method : D:\CHEM32\1\METHODS\AP_C18_INSERT.M
Last changed : 11/10/17 3:07:57 PM by Mason
Analysis Method : Z:\DESKTOP\BERTOZZI LAB\LCMS INFO\LCMS METHODS TO 112917\SLK_BERTOZZI_BPWITHINSERT.M
Last changed : 3/8/18 8:51:08 AM
(modified after loading)
Additional Info : Peak(s) manually integrated

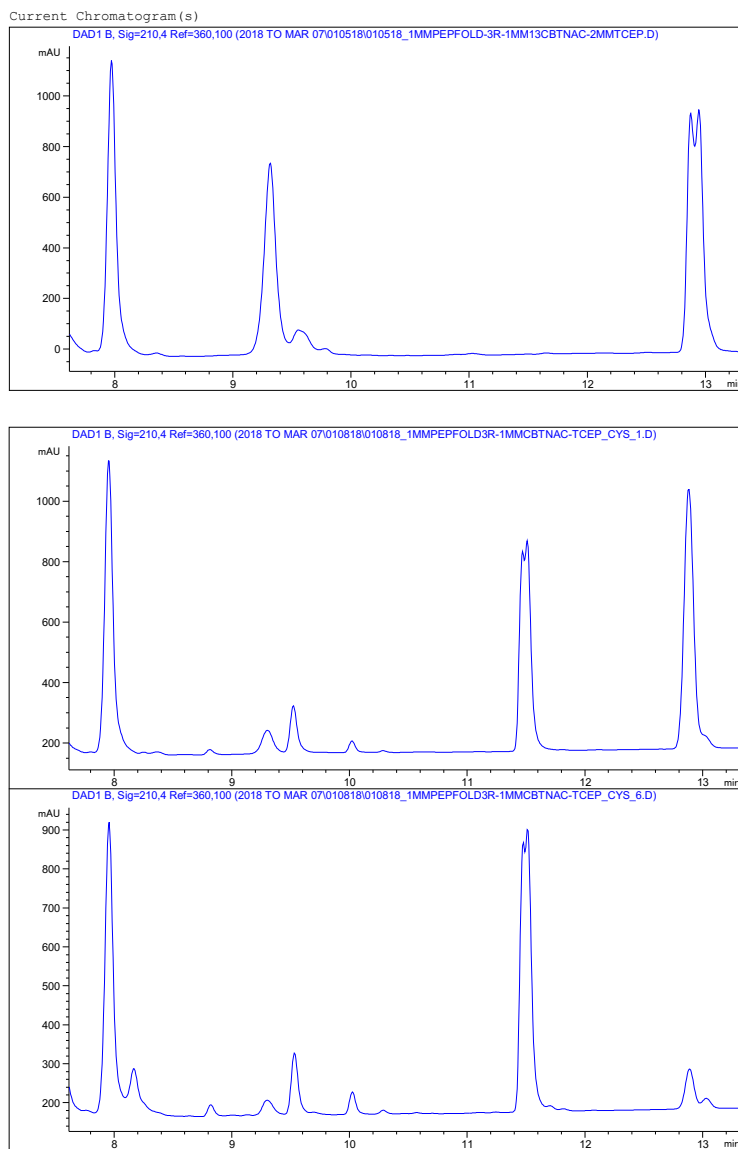


Figure S10. Cysteine treatment causes the minute 9.3 peak corresponding to the singly modified CBTAg 1.0 (K9R) to disappear.

Table S2. Calculations for 1:1 CBTAG 1.0/13CBTNAc LC-MS time-course assay (two replicates). Spectra and integration results used herein are included after Figure S13.

****Bolded columns were mentioned in text of paper or used in creation of graphs in Supporting Information**

Time 0 = 3:16 -		Time 0 = 3:16 -		Time 0 = 3:16 -		Time 0 = 3:16 -	
26-Jan		26-Jan		26-Jan		26-Jan	
0:05:30 =		0:05:30 =		0:05:30 =		0:05:30 =	
3:10:30		3:10:30		3:10:30		3:10:30	
		Actual time point		CBTAg 1.0-Lys-	CBTAg 1.0-Cys-	CBTAg 1.0-Cys-	
				13CBTNAc (min	13CBTNAc (min	13CBTNAc-Lys-	13CBTNAc (min
210 nm	Time of injection in file	(h)	CBTAg 1.0 (min 7.9)	8.99)	9.19)	9.7)	13CBTNAc (min 12.9)
012418_Pf3-PH7-13CBTNAc_1	4:58:31 p.m.	1.80	19072.5	875.5	20975.8	2091.6	19164.1
012418_Pf3-PH7-13CBTNAc_2	5:25:45 a.m.	14.25	21742.2	2265.4	20082	6531	16769.8
012418_Pf3-PH7-13CBTNAc_3	3:39:38 p.m.	24.48	31604.91	2944.3	13766.1	8471.9	13473.4
012418_Pf3-PH7-13CBTNAc_4	11:53:39 p.m.	32.72	28513.8	3432	13322.2	10263.3	14764.6
012418_Pf3-PH7-13CBTNAc_5	11:01:48 a.m.	43.85	25995.5	2775.6	8668.3	8322.7	13238.1
Time 0 = 3:16 -							
26-Jan		26-Jan		26-Jan		26-Jan	
0:05:30 =		0:05:30 =		0:05:30 =		0:05:30 =	
3:10:30		3:10:30		3:10:30		3:10:30	
		Actual time point		CBTAg 1.0-Lys-	CBTAg 1.0-Cys-	CBTAg 1.0-Cys-	
				13CBTNAc (min	13CBTNAc (min	13CBTNAc-Lys-	13CBTNAc (min
254 nm	Time of injection in file	(h)	CBTAg 1.0 (min 7.9)	8.99)	9.19)	9.7)	13CBTNAc (min 12.9)
012418_Pf3-PH7-13CBTNAc_1	4:58:31 p.m.	1.80	138.3	4066.1	583	16074.4	
012418_Pf3-PH7-13CBTNAc_2	5:25:45 a.m.	14.25	365.8	3527.3	1575.1	11460.9	
012418_Pf3-PH7-13CBTNAc_3	3:39:38 p.m.	24.48	579.3	2843.1	2145.2	11569.5	
012418_Pf3-PH7-13CBTNAc_4	11:53:39 p.m.	32.72	561	2454	2562.6	12511.7	
012418_Pf3-PH7-13CBTNAc_5	11:01:48 a.m.	43.85	445.7	1461.1	1937.3	9349.3	
Assumption: area under modified peptide peaks is proportional to number of modifications							
210 nm							
				All peptide: Sum		Percent of total	
				CBTAg 1.0-Lys-		peptide that has any	
				13CBTNAc, CBTAg		13CBTNAc	
Lysine-modified:	Any modification: Sum			1.0-Cys-	Percent of reacted	modification ((Any	
Sum CBTAg 1.0-Lys-	CBTAg 1.0-Lys-			13CBTNAc,	13CBTNAc bound	modification -	
13CBTNAc and	13CBTNAc, CBTAg 1.0-			1/2(CBTAg 1.0-Cys-	to a lysine (Lysine-	1/2(CBTAg 1.0-Cys-	
1/2(CBTAg 1.0-Cys-	Cys-13CBTNAc, CBTAg			13CBTNAc-Lys-	modified/Any	13CBTNAc-Lys-	
13CBTNAc-Lys-	1.0-Cys-13CBTNAc-Lys-			modification)	modification)	13CBTNAc)/All	
13CBTNAc)	13CBTNAc				modified/All peptide)	peptide)	
1921.3	23942.9			41969.6	8.024508309	54.5563932	
5530.9	28878.4			47355.1	19.15237686	54.08688821	
7180.25	25182.3			52551.26	28.5130826	39.85889206	
8563.65	27017.5			50399.65	31.69667808	43.42460712	
6936.95	19766.6			41600.75	35.09430049	37.5119439	
254 nm							
				Percent of		Percent of total	
				reacted		peptide that has any	
				13CBTNAc bound		13CBTNAc	
				to a lysine		modification ((Any	
				(Lysine-		modification -	
				modified/Any		1/2(CBTAg 1.0-Cys-	
				modification)		13CBTNAc-Lys-	
						13CBTNAc)/All	
						peptide)	
Lysine-modified:	Any modification: Sum			429.8	4787.4	8.977733216	
Sum CBTAg 1.0-Lys-	CBTAg 1.0-Lys-			1153.35	5468.2	21.09194982	
13CBTNAc and	13CBTNAc, CBTAg 1.0-			1651.9	5567.6	29.66987571	
1/2(CBTAg 1.0-Cys-	Cys-13CBTNAc, CBTAg			1842.3	5577.6	33.03033563	
13CBTNAc-Lys-	1.0-Cys-13CBTNAc-Lys-			1414.35	3844.1	36.79274733	
13CBTNAc)	13CBTNAc						

	Time 0 = 5:02 - 0:05:30 =	4:56:30			*a lot of these peaks were saturated	using 280 nm as control	13CBTNac 210 nm	*(Ratio of CBTAg 1.0- Cys 280	CBTag 1.0-Cys- 13CBTNac-Lys- 13CBTNac (min	13CBTNac (min 12.9)
		Actual time point (h)	CBTag 1.0 (min 7.9)	CBTag 1.0-Lys- 13CBTNac (min	CBTag 1.0-Cys- 13CBTNac (min	nm/13CBTNac 280	nm)	nm/13CBTNac 280	13CBTNac (min	
210 nm	Time of injection in file									
020218_Pf3-PH7-13CBTNac_1	6:47:32 p.m.	2.33	14758.6	8.99	9.19	20164.3	21027.50305	2894.9	8795.9	
020218_Pf3-PH7-13CBTNac_2	5:55:51 a.m.	13.47	15407.4	1732.7	24026.3	24579.91136	11859.8	11314.4		
020218_Pf3-PH7-13CBTNac_3	2:09:56 p.m.	21.71	11620.8	2901.1	16445.3	18346.71955	15010.7	9674.1		
020218_Pf3-PH7-13CBTNac_4	10:23:55 p.m.	29.94	11865.8	3692.2	17331.6	18916.25472	16845.4	4868.5		
020218_Pf3-PH7-13CBTNac_5	9:32:20 a.m.	41.08	8382.1	3265.7	12603.9	10621.54062	13433.9	4078.5		
280 nm				control for saturation	CBTag 1.0-Cys 280 nm	Ratio of CBTAg 1.0- Cys 280	nm/13CBTNac 280		13CBTNac 280 nm	
					4321.66	2.390602787		1807.77		
					4781.66	2.172444969		2201.05		
					4214.79	1.896478179		2222.43		
					3953.2	3.885437962		1017.44		
					1891.59	2.604276234		726.34		
254 nm	Time 0 = 5:02 - 0:05:30 =	4:56:30			*a lot of these peaks were saturated					
		Actual time point (h)	CBTag 1.0 (min 7.9)	CBTag 1.0-Lys- 13CBTNac (min	CBTag 1.0-Cys- 13CBTNac (min	CBTag 1.0-Cys- 13CBTNac (min	13CBTNac (min	13CBTNac (min 12.9)		
020218_Pf3-PH7-13CBTNac_1	6:47:32 p.m.	2.33		8.99	9.19	6653.1	1016	4049.4		
020218_Pf3-PH7-13CBTNac_2	5:55:51 a.m.	13.47		449.1	6981.6	3533.3	5390			
020218_Pf3-PH7-13CBTNac_3	2:09:56 p.m.	21.71		668.3	5847.8	5163.1	5270.8			
020218_Pf3-PH7-13CBTNac_4	10:23:55 p.m.	29.94		900.5	5806.4	6531.1	2182.5			
020218_Pf3-PH7-13CBTNac_5	9:32:20 a.m.	41.08		765.4	3172	5281	1729			

Assumption: area under modified peptide peaks is proportional to number of modifications
210 nm

Lysine-modified: Sum CBTAG 1.0-Lys- 13CBTNac and 1/2(CBTAG 1.0-Cys- 13CBTNac-Lys- 13CBTNac)	Any modification: Sum CBTAG 1.0-Lys- 13CBTNac, CBTAG 1.0- Cys-13CBTNac, CBTAG 1.0-Cys-13CBTNac-Lys- 13CBTNac	All peptide: Sum CBTAG 1.0-Lys- 13CBTNac, CBTAG 1.0-Cys- 13CBTNac, 1/2(CBTAG 1.0-Cys- 13CBTNac-Lys- 13CBTNac)	Percent of reacted 13CBTNac bound to a lysine (Lysine- modified/Any modification)	Percent of total peptide with a modification on lysine (Lysine-modified/All peptide)	Percent of total peptide that has any 13CBTNac modification ((Any modification - 1/2(CBTAG 1.0-Cys- 13CBTNac-Lys- 13CBTNac))/All peptide)
2115.15	23726.9	37038.05	8.914565325	5.710748811	60.15286982
7662.6	37618.8	47096.3	20.36907078	16.27006792	67.28532815
10406.45	34357.1	38472.55	30.28908144	27.04902586	69.79456782
12114.9	37869.2	41312.3	31.99143367	29.32516466	71.27780346
9982.65	29303.5	30968.65	34.06640845	32.23469541	72.93359575

Lysine-modified: Sum CBTAG 1.0-Lys- 13CBTNac and 1/2(CBTAG 1.0-Cys- 13CBTNac-Lys- 13CBTNac)	Any modification (adjusted for saturation): Sum CBTAG 1.0-Lys- 13CBTNac, CBTAG 1.0- Cys-13CBTNac, CBTAG 1.0-Cys-13CBTNac-Lys- 13CBTNac	All peptide (adjusted for saturation): Sum CBTAG 1.0-Lys- 13CBTNac, CBTAG 1.0-Cys- 13CBTNac, 1/2(CBTAG 1.0-Cys- 13CBTNac-Lys- 13CBTNac)	Percent of reacted 13CBTNac bound to a lysine (adjusted for saturation) (Lysine- modified/Any modification)	Percent of total peptide with a modification on lysine (adjusted for saturation) (Lysine- modified/All peptide)	Percent of total peptide that has any 13CBTNac modification (adjusted for saturation) ((Any modification - 1/2(CBTAG 1.0-Cys- 13CBTNac-Lys- 13CBTNac))/All peptide)
2115.15	24590.10305	39348.70305	8.601631296	5.375399533	58.81427152
7662.6	38172.41136	53579.81136	20.07365981	14.30128215	60.17660485
10406.45	36258.51955	47879.31955	28.70070297	21.73474915	60.05342144
12114.9	39453.85472	51319.65472	30.70650533	23.60674495	60.46641367
9982.65	27321.14062	35703.24062	36.53818901	27.960067	57.70958116

254 nm

Lysine-modified: Sum CBTAG 1.0-Lys- 13CBTNac and 1/2(CBTAG 1.0-Cys- 13CBTNac-Lys- 13CBTNac)	Any modification: Sum CBTAG 1.0-Lys- 13CBTNac, CBTAG 1.0- Cys-13CBTNac, CBTAG 1.0-Cys-13CBTNac-Lys- 13CBTNac	Percent of reacted 13CBTNac bound to a lysine (Lysine- modified/Any modification)
675.6	7836.7	8.620975666
2215.75	10964	20.20932142
3249.85	11679.2	27.82596411
4166.05	13238	31.47038828
3405.9	9218.4	36.94675866

Table S3. Calculations for 1:4 CBTAg 1.0/13CBTNAC LC-MS time-course assay (two replicates). Spectra and integration results

used herein are included after Figure S13.

26-Jan		Time 0 = 3:20 -		0:05:30 =		3:14:30	
						CBTag 1.0-Cys-13CBTNAC-Lys-13CBTNAC (min 9.7)	
210 nm	Time of injection in file	Actual time point (h)	CBTag 1.0 (min 7.9)	CBTag 1.0-Lys-13CBTNAC (min 8.99)	CBTag 1.0-Cys-13CBTNAC (min 9.19)	13CBTNAC (min 12.9)	
012418_1PF3-PH7-413CBTNAC_1	6:02:03 p.m.	2.81	9417	487.3	12127.8	1118.1	19788.9
012418_1PF3-PH7-413CBTNAC_2	6:23:53 a.m.	15.18	9138.3	748.6	8372.4	2478	18214.2
012418_1PF3-PH7-413CBTNAC_3	4:37:48 p.m.	25.41	7891.2	1164.3	5924.5	3880.2	14152.5
012418_1PF3-PH7-413CBTNAC_4	12:51:47 a.m.	33.64	8335.7	1270.6	6181.5	4995.1	13985.1
012418_1PF3-PH7-413CBTNAC_5	12:00:02 p.m.	44.78	7711.9	1694.7	4647.7	5140.1	13714.5
						CBTag 1.0-Cys-13CBTNAC-Lys-13CBTNAC (min 9.7)	
254 nm	Time of injection in file	Actual time point (h)		CBTag 1.0-Lys-13CBTNAC (min 8.99)	CBTag 1.0-Cys-13CBTNAC (min 9.19)	13CBTNAC (min 12.9)	
012418_1PF3-PH7-413CBTNAC_1	6:02:03 p.m.	2.81		142.4	1966.5	394.1	17591.7
012418_1PF3-PH7-413CBTNAC_2	6:23:53 a.m.	15.18		161.1	1543.8	735.6	13625.9
012418_1PF3-PH7-413CBTNAC_3	4:37:48 p.m.	25.41		203.3	1016.1	1075.1	10742.7
012418_1PF3-PH7-413CBTNAC_4	12:51:47 a.m.	33.64		248.6	1101.1	1343.8	10660
012418_1PF3-PH7-413CBTNAC_5	12:00:02 p.m.	44.78		337.4	775.4	1352.4	9645.9
						Any modification: Sum	
			Lysine-modified: Sum	CBTag 1.0-Lys-13CBTNAC, CBTag 1.0-1/2(CBTag 1.0-Cys-13CBTNAC-Lys-13CBTNAC)	All peptide: Sum CBTag 1.0-Lys-13CBTNAC, CBTag 1.0-Cys-13CBTNAC, 1/2(CBTag 1.0-Cys-13CBTNAC-Lys-13CBTNAC)	Percent of reacted 13CBTNAC bound to a lysine (Lysine-modified/Any modification)	Percent of total peptide with a modification on lysine (Lysine-modified/All peptide)
			1046.35	13733.2	22591.15	7.61912737	4.63168099
			1987.6	11599	19498.3	17.13596	10.1937092
			3104.4	10969	16920.1	28.30157717	18.34740929
			3768.15	12447.2	18285.35	30.27307346	20.60748085
			4264.75	11482.5	16624.35	37.14130198	25.65363458
				8912.45	16624.35		25.65363458
			339.45	2503		13.56172593	
			528.9	2440.5		21.67178857	
			740.85	2294.5		32.28808019	
			920.5	2693.5		34.17486542	
			1013.6	2465.2		41.11633945	

2-Feb Time 0 = 5:02 -
0:05:30 = 4:56:30

	Time of injection in file	Actual time point (h)	CBTag 1.0 (min 7.9)	CBTag 1.0-Lys-13CBTNac (min 8.99)	CBTag 1.0-Cys-13CBTNac (min 9.19)	CBTag 1.0-Cys-13CBTNac-Lys-13CBTNac (min 9.7)	13CBTNac (min 12.9)
210 nm							
020218_1PF3-PH7-413CBTNac_1	7:45:39 p.m.	2.82	4179.1	367.7	9649.2	1156.3	14850.1
020218_1PF3-PH7-413CBTNac_2	6:54:01 a.m.	13.96	3660.3	461.7	9230.7	3333.8	14882.8
020218_1PF3-PH7-413CBTNac_3	3:08:04 p.m.	22.19	3616.8	680.2	6993.7	4871.4	9454
020218_1PF3-PH7-413CBTNac_4	11:22:05 p.m.	30.42	3166.8	877	7026.9	6074.1	15707.4
020218_1PF3-PH7-413CBTNac_5	10:30:27 p.m.	41.56	2262.7	1027.3	4835.6	6570.6	11867
254 nm							
020218_1PF3-PH7-413CBTNac_1	7:45:39 p.m.	2.82		55.9	1641.7	286.4	10866.8
020218_1PF3-PH7-413CBTNac_2	6:54:01 a.m.	13.96		105.1	1616.7	902	8779.7
020218_1PF3-PH7-413CBTNac_3	3:08:04 p.m.	22.19		152.1	1291.4	1378.6	4896.6
020218_1PF3-PH7-413CBTNac_4	11:22:05 p.m.	30.42		196	1271.3	1673.5	14857.8
020218_1PF3-PH7-413CBTNac_5	10:30:27 p.m.	41.56		190	791.4	1595.7	7938.7

Any modification: Sum		Percent of total peptide with a lysine (Lysine-modified/Any modification)		Percent of total peptide that has any 13CBTNac modification ((Any modification - 1/2(CBTag 1.0-Cys-13CBTNac-Lys-13CBTNac))/All peptide)	
Lysine-modified: Sum CBTag 1.0-Lys-13CBTNac and 1/2(CBTag 1.0-Cys-13CBTNac-Lys-13CBTNac)	CBTag 1.0-Lys-13CBTNac, CBTag 1.0-Cys-13CBTNac-Lys-13CBTNac	All peptide: Sum CBTag 1.0-Lys-13CBTNac, CBTag 1.0-Cys-13CBTNac, 1/2(CBTag 1.0-Cys-13CBTNac-Lys-13CBTNac)	Percent of reacted a lysine (Lysine-modified/Any modification)	Percent of total peptide with a lysine (Lysine-modified/All peptide)	Percent of total peptide that has any 13CBTNac modification ((Any modification - 1/2(CBTag 1.0-Cys-13CBTNac-Lys-13CBTNac))/All peptide)
945.85	11173.2	14774.15	8.465345649	6.402060355	71.71343191
2128.6	13026.2	15019.6	16.34091293	14.17214839	75.62984367
3115.9	12545.3	13726.4	24.83719002	22.70005245	73.65077515
3914.05	13978	14107.75	28.00150236	27.74397051	77.55276355
4312.6	12433.5	11410.9	34.68532593	37.79368849	80.17071397
	9148.2	11410.9		37.79368849	80.17071397
199.1	1984		10.03528226		
556.1	2623.8		21.1944508		
841.4	2822.1		29.81467701		
1032.75	3140.8		32.88174987		
987.85	2577.1		38.33184587		

Table S4. Calculations for 4:1 CBTAg 1.0/13CBTNAC LC-MS time-course assay (two replicates). Spectra and integration results

used herein are included after Figure S13.

26-Jan		Time 0 = 3:18 - 0:05:30 =	3:12:30																																																																																																		
	Time of injection in file	Actual time point (h)	CBTAg 1.0 (min 7.9)	CBTAg 1.0-Lys-13CBTNAC (min 8.99)	CBTAg 1.0-Cys-13CBTNAC (min 9.19)	CBTAg 1.0-Cys-13CBTNAC-Lys-13CBTNAC (min 9.7)	13CBTNAC (min 12.9)																																																																																														
210 nm																																																																																																					
012418_4PF3-PH7-13CBTNAC_1	5:27:34 p.m.	1.75	18495	642.7	18527.5	2025.3	1810.4																																																																																														
012418_4PF3-PH7-13CBTNAC_2	5:54:47 a.m.	14.20	20626.2	2080.7	18970.2	6051.6	1533.2																																																																																														
012418_4PF3-PH7-13CBTNAC_3	4:08:40 p.m.	24.43	14191.8	3157.1	12107.1	7429.6	1474.9																																																																																														
012418_4PF3-PH7-13CBTNAC_4	12:22:42 a.m.	32.67	15650.7	3078.2	12270.4	9018.7	1438.8																																																																																														
012418_4PF3-PH7-13CBTNAC_5	11:30:54 a.m.	43.80	666.5	50.9	199.5	196.9	74.8																																																																																														
254 nm																																																																																																					
012418_4PF3-PH7-13CBTNAC_1	5:27:34 p.m.	1.75		109.5	3892.3	554	767																																																																																														
012418_4PF3-PH7-13CBTNAC_2	5:54:47 a.m.	14.20		369.2	3423.6	1544.3	589.1																																																																																														
012418_4PF3-PH7-13CBTNAC_3	4:08:40 p.m.	24.43		556.6	2360.1	2024.4	596.6																																																																																														
012418_4PF3-PH7-13CBTNAC_4	12:22:42 a.m.	32.67		612.5	2387.1	2560	623.7																																																																																														
012418_4PF3-PH7-13CBTNAC_5	11:30:54 a.m.	43.80		10.7	38.9	46.6	33																																																																																														
<table border="0" style="width:100%; border-collapse: collapse;"> <tr> <td style="width:30%;"></td> <td style="width:15%; text-align: right;">Any modification: Sum</td> <td style="width:15%; text-align: right;">All peptide: Sum</td> <td style="width:15%;"></td> <td style="width:15%;"></td> <td style="width:15%;"></td> <td style="width:15%;"></td> <td style="width:15%;"></td> </tr> <tr> <td></td> <td style="text-align: right;">CBTAg 1.0-Lys-13CBTNAC, CBTAg</td> <td style="text-align: right;">CBTAg 1.0-Lys-13CBTNAC, CBTAg</td> <td></td> <td></td> <td></td> <td></td> <td></td> </tr> <tr> <td style="text-align: right;">Lysine-modified: Sum</td> <td style="text-align: right;">CBTAg 1.0-Cys-13CBTNAC and 1/2(CBTAg 1.0-Cys-13CBTNAC-Lys-13CBTNAC)</td> <td style="text-align: right;">CBTAg 1.0-Cys-13CBTNAC-Lys-13CBTNAC</td> <td style="text-align: right;">1/2(CBTAg 1.0-Cys-13CBTNAC-Lys-13CBTNAC)</td> <td style="text-align: right;">Percent of reacted a lysine (Lysine-modified/Any modification)</td> <td style="text-align: right;">Percent of total peptide with a modification on lysine (Lysine-modified/All peptide)</td> <td colspan="2" style="text-align: right;">Percent of total peptide that has any 13CBTNAC modification ((Any modification - 1/2(CBTAg 1.0-Cys-13CBTNAC-Lys-13CBTNAC))/All peptide)</td> </tr> <tr> <td style="text-align: right;">1655.35</td> <td style="text-align: right;">21195.5</td> <td style="text-align: right;">38677.85</td> <td style="text-align: right;">7.809912481</td> <td style="text-align: right;">4.279839753</td> <td colspan="2" style="text-align: right;">52.18193359</td> </tr> <tr> <td style="text-align: right;">5106.5</td> <td style="text-align: right;">27102.5</td> <td style="text-align: right;">44702.9</td> <td style="text-align: right;">18.84143529</td> <td style="text-align: right;">11.42319626</td> <td colspan="2" style="text-align: right;">53.8593693</td> </tr> <tr> <td style="text-align: right;">6871.9</td> <td style="text-align: right;">22693.8</td> <td style="text-align: right;">33170.8</td> <td style="text-align: right;">30.28095779</td> <td style="text-align: right;">20.7167147</td> <td colspan="2" style="text-align: right;">57.21598514</td> </tr> <tr> <td style="text-align: right;">7587.55</td> <td style="text-align: right;">24367.3</td> <td style="text-align: right;">35508.65</td> <td style="text-align: right;">31.13824675</td> <td style="text-align: right;">21.36817367</td> <td colspan="2" style="text-align: right;">55.92426071</td> </tr> <tr> <td style="text-align: right;">149.35</td> <td style="text-align: right;">447.3</td> <td style="text-align: right;">1015.35</td> <td style="text-align: right;">33.38922423</td> <td style="text-align: right;">14.70921357</td> <td colspan="2" style="text-align: right;">34.35761068</td> </tr> <tr> <td style="text-align: right;">386.5</td> <td style="text-align: right;">4555.8</td> <td style="text-align: right;">8.483691119</td> <td></td> <td></td> <td colspan="2"></td> </tr> <tr> <td style="text-align: right;">1141.35</td> <td style="text-align: right;">5337.1</td> <td style="text-align: right;">21.3852092</td> <td></td> <td></td> <td colspan="2"></td> </tr> <tr> <td style="text-align: right;">1568.8</td> <td style="text-align: right;">4941.1</td> <td style="text-align: right;">31.75001518</td> <td></td> <td></td> <td colspan="2"></td> </tr> <tr> <td style="text-align: right;">1892.5</td> <td style="text-align: right;">5559.6</td> <td style="text-align: right;">34.04021872</td> <td></td> <td></td> <td colspan="2"></td> </tr> <tr> <td style="text-align: right;">34</td> <td style="text-align: right;">96.2</td> <td style="text-align: right;">35.34303534</td> <td></td> <td></td> <td colspan="2"></td> </tr> </table>									Any modification: Sum	All peptide: Sum							CBTAg 1.0-Lys-13CBTNAC, CBTAg	CBTAg 1.0-Lys-13CBTNAC, CBTAg						Lysine-modified: Sum	CBTAg 1.0-Cys-13CBTNAC and 1/2(CBTAg 1.0-Cys-13CBTNAC-Lys-13CBTNAC)	CBTAg 1.0-Cys-13CBTNAC-Lys-13CBTNAC	1/2(CBTAg 1.0-Cys-13CBTNAC-Lys-13CBTNAC)	Percent of reacted a lysine (Lysine-modified/Any modification)	Percent of total peptide with a modification on lysine (Lysine-modified/All peptide)	Percent of total peptide that has any 13CBTNAC modification ((Any modification - 1/2(CBTAg 1.0-Cys-13CBTNAC-Lys-13CBTNAC))/All peptide)		1655.35	21195.5	38677.85	7.809912481	4.279839753	52.18193359		5106.5	27102.5	44702.9	18.84143529	11.42319626	53.8593693		6871.9	22693.8	33170.8	30.28095779	20.7167147	57.21598514		7587.55	24367.3	35508.65	31.13824675	21.36817367	55.92426071		149.35	447.3	1015.35	33.38922423	14.70921357	34.35761068		386.5	4555.8	8.483691119					1141.35	5337.1	21.3852092					1568.8	4941.1	31.75001518					1892.5	5559.6	34.04021872					34	96.2	35.34303534				
	Any modification: Sum	All peptide: Sum																																																																																																			
	CBTAg 1.0-Lys-13CBTNAC, CBTAg	CBTAg 1.0-Lys-13CBTNAC, CBTAg																																																																																																			
Lysine-modified: Sum	CBTAg 1.0-Cys-13CBTNAC and 1/2(CBTAg 1.0-Cys-13CBTNAC-Lys-13CBTNAC)	CBTAg 1.0-Cys-13CBTNAC-Lys-13CBTNAC	1/2(CBTAg 1.0-Cys-13CBTNAC-Lys-13CBTNAC)	Percent of reacted a lysine (Lysine-modified/Any modification)	Percent of total peptide with a modification on lysine (Lysine-modified/All peptide)	Percent of total peptide that has any 13CBTNAC modification ((Any modification - 1/2(CBTAg 1.0-Cys-13CBTNAC-Lys-13CBTNAC))/All peptide)																																																																																															
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1892.5	5559.6	34.04021872																																																																																																			
34	96.2	35.34303534																																																																																																			

2-Feb Time 0 = 5:02 -
0:05:30 = 4:56:30

	Time of injection in file	Actual time point (h)	CBTag 1.0 (min 7.9)	CBTag 1.0-Lys-13CBTNAc (min 8.99)	CBTag 1.0-Cys-13CBTNAc (min 9.19)	CBTag 1.0-Cys-13CBTNAc-Lys-13CBTNAc (min 9.7)	13CBTNAc (min 12.9)
210 nm							
020218_4PF3-PH7-13CBTNAc_1	7:16:34 p.m.	2.33	17726.9	919.9	17143.3	2137.4	1670
020218_4PF3-PH7-13CBTNAc_2	6:24:55 a.m.	13.47	20687.5	2669.5	17836.4	5985.9	1109.5
020218_4PF3-PH7-13CBTNAc_3	2:38:58 p.m.	21.71	15967.8	4050.5	12346.2	7415	1010.4
020218_4PF3-PH7-13CBTNAc_4	10:52:58 p.m.	29.94	16438.6	4837.6	11770.2	8735.1	863.5
020218_4PF3-PH7-13CBTNAc_5	10:01:22 a.m.	41.08	13302.2	4184.8	10201	8778.2	998.1
254 nm							
020218_4PF3-PH7-13CBTNAc_1	7:16:34 p.m.	2.33		200.3	4234.3	737	729.3
020218_4PF3-PH7-13CBTNAc_2	6:24:55 a.m.	13.47		572.6	3598.4	1752.5	474.2
020218_4PF3-PH7-13CBTNAc_3	2:38:58 p.m.	21.71		871.5	2728.3	2236.7	454
020218_4PF3-PH7-13CBTNAc_4	10:52:58 p.m.	29.94		1078.5	2427.3	2653.7	379.6
020218_4PF3-PH7-13CBTNAc_5	10:01:22 a.m.	41.08		886.4	1947.9	2469.6	429.6

	Any modification: Sum CBTag 1.0-Lys-13CBTNAc, CBTag 1.0-Cys-13CBTNAc, CBTag 1.0-Cys-13CBTNAc-Lys-13CBTNAc	All peptide: Sum CBTag 1.0-Lys-13CBTNAc, CBTag 1.0-Cys-13CBTNAc, 1/2(CBTag 1.0-Cys-13CBTNAc-Lys-13CBTNAc)	Percent of reacted 13CBTNAc bound to a lysine (Lysine-modified/Any modification)	Percent of total peptide with a modification on lysine (Lysine-modified/All peptide)	Percent of total peptide that has any 13CBTNAc modification ((Any modification - 1/2(CBTag 1.0-Cys-13CBTNAc-Lys-13CBTNAc))/All peptide)
Lysine-modified: Sum CBTag 1.0-Lys-13CBTNAc and 1/2(CBTag 1.0-Cys-13CBTNAc-Lys-13CBTNAc)	1988.6 5662.45 7758 9205.15 8573.9	20200.6 26491.8 23811.7 25342.9 23164	36858.8 44186.35 36072 37413.95 32077.1	9.844262052 21.3743498 32.58062213 36.32240194 37.01390088	5.395183782 12.8149304 21.50698603 24.60352355 26.72903723
	568.8 1448.85 1989.85 2405.35 2121.2	5171.6 5923.5 5836.5 6159.5 5303.9		10.99853044 24.4593568 34.09320655 39.05105934 39.99321254	

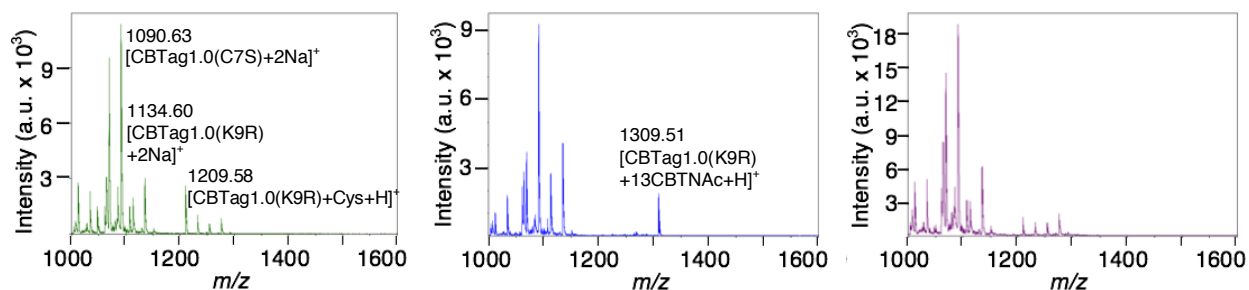


Figure S12. 13CBTNAC binding assay and cysteine treatment results for a 1:1 mixture of CBTag 1.0 (K9R) and CBTag 1.0 (C7S). The binding assay and cysteine competition were as follows: 40 μ L of a 10% DMF in PBS solution of 1:1 CBTag 1.0 (K9R)/CBTag 1.0 (C7S) (0.9 mM total peptide) with or without 13CBTNAC (1 mM) was incubated 48 h at r.t. Then, the negative control (without 13CBTNAC) and half (20 μ L) of the sample incubated with 13CBTNAC were each treated with an equal volume (20 μ L) of a solution of cysteine and DTT (10 and 15 mM, respectively) in PBS. The other half of the sample incubated with 13CBTNAC was treated with an equal volume of a solution of DTT (15 mM) in PBS. After 48 h at r.t., MALDI-TOF MS was used to analyze the negative control (left column, green spectra), the sample incubated with 13CBTNAC then DTT alone (middle column, blue spectra), and the sample incubated with 13CBTNAC then cysteine and DTT (right column, purple spectra). The CBTag 1.0 (K9R)-13CBTNAC adduct disappears on cysteine treatment; no CBTag 1.0 (C7S)-13CBTNAC adduct is apparent under any of these conditions.

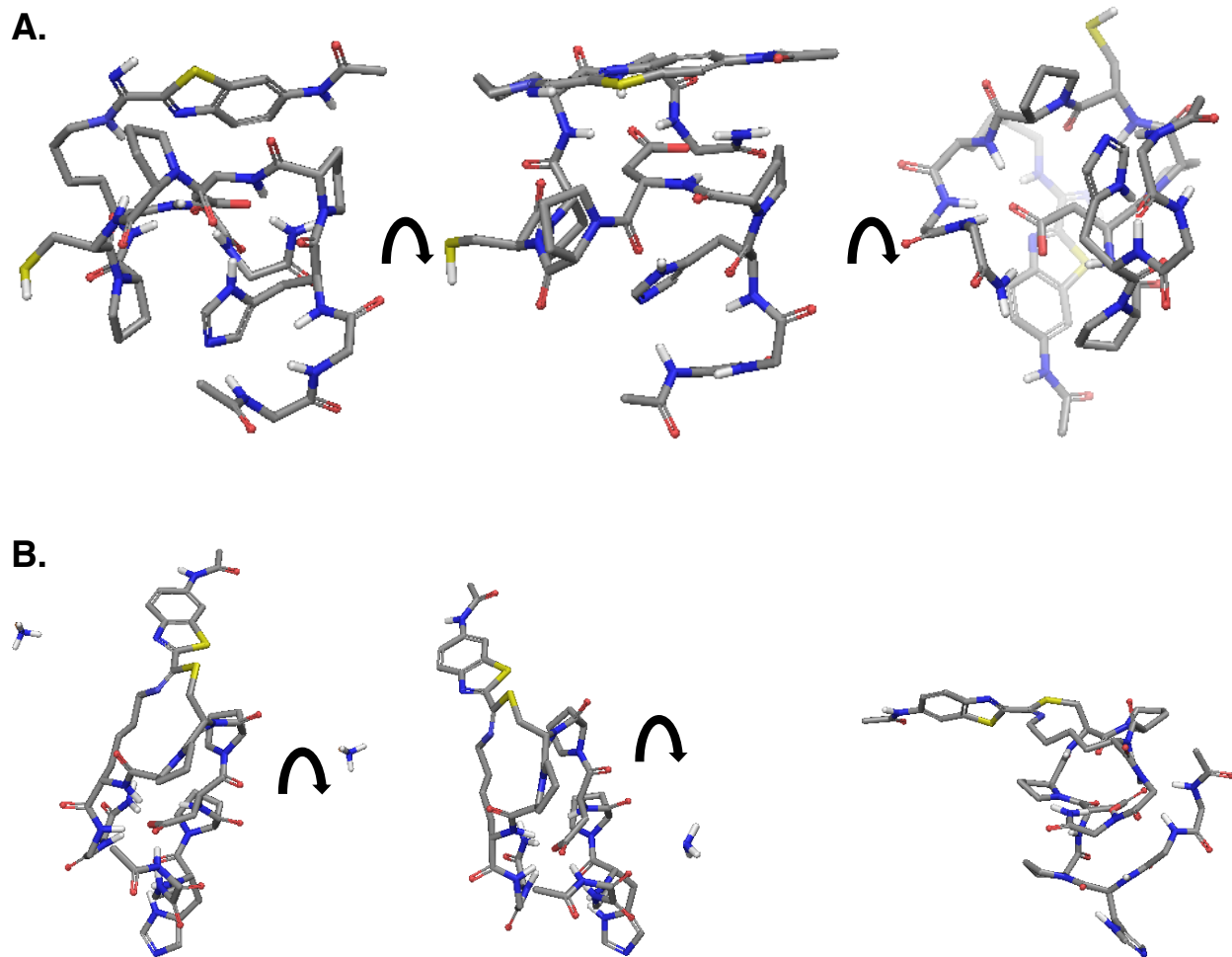


Figure S13. Lowest energy conformation of each potential final product (Maestro, Macromodel).

A. Rotated views of the amidine product (observed). The energy of this conformer was found to be -488 kcal/mol. **B.** Rotated views of the condensation reaction product, including ammonia (not observed). The energy of this conformer was found to be -456 kcal/mol.

LC-MS time-course spectra and integration results

Peak identification based on Figures S6-7:

CBTag 1.0 – minute 7.9

CBTag 1.0-13CBTNAc, lysine adduct – minute 9

CBTag 1.0-13CBTNAc, cysteine adduct – minute 9.2

CBTag 1.0-2(13CBTNAc) – minute 9.7

13CBTNAc – minute 12.9

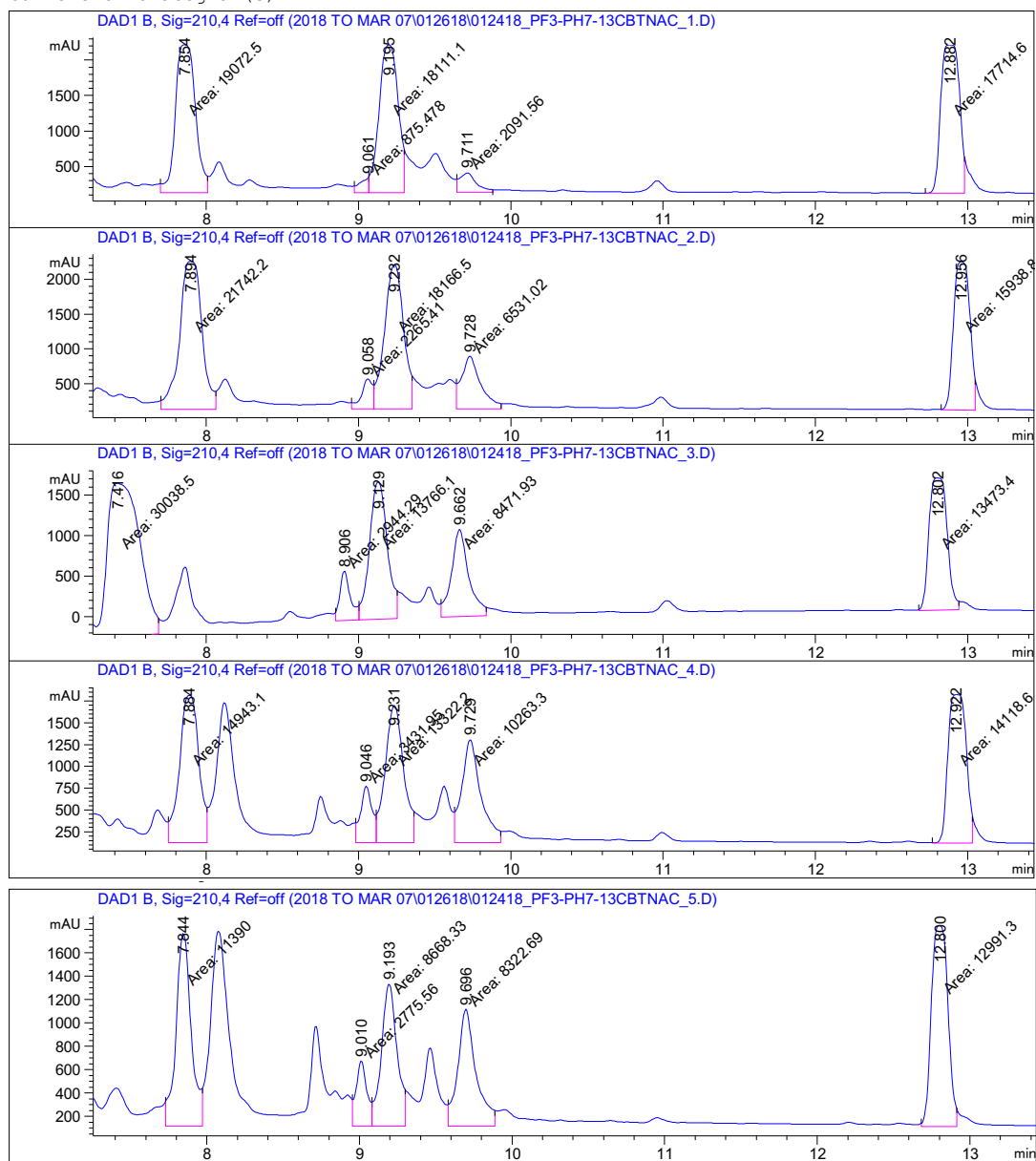
Integration results were consolidated previously in Tables S2-S4

Print of window 38: Current Chromatogram(s)
 Data File : C:\CHEM32\1\DATA\2018 TO MAR 07\012618\012418_PF3-PH7-13CBTNAC_1.D
 Sample Name : 012218_PF3-ph7-13cbtnac_1

=====
 Acq. Operator : SGLK Seq. Line : 5
 Acq. Instrument : Instrument 1 Location : Vial 5
 Injection Date : 1/26/18 4:58:31 PM Inj : 1
 Inj Volume : 1.000 µl

Acq. Method : D:\CHEM32\1\METHODS\AP_C18_INSERT.M
 Last changed : 1/22/18 3:04:38 PM by SGLK
 Analysis Method : Z:\DESKTOP\BERTOZZI LAB\LCMS INFO\LCMS METHODS TO 112917\SGLK_BERTOZZI_BP_WITHINSERT.M
 Last changed : 3/8/18 8:51:08 AM
 (modified after loading)
 Additional Info : Peak(s) manually integrated

Current Chromatogram(s)



Data File C:\CHEM32\1\DATA\2018 TO MAR 07\012618\012418_PF3-PH7-13CBTNAC_1.D
Sample Name: 012218_PF3-ph7-13cbtnac_1

=====
Integration Results
=====

Signal 1: DAD1 B, Sig=210,4 Ref=off (2018 TO MAR 07\012618\012418_PF3-PH7-13CBTNAC_1.D)

Peak #	Time [min]	Type	Area [mAU*s]	Height [mAU]	Width [min]	Start [min]	End [min]
1	7.854	FM	1.90725e4	2084.91626	0.1525	7.697	8.004
2	9.061	MF	875.47845	209.35365	0.0697	8.970	9.065
3	9.195	MF	1.81111e4	2078.43286	0.1452	9.065	9.298
4	9.711	FM	2091.56250	275.67270	0.1265	9.644	9.877
5	12.882	MF	1.77146e4	2086.62402	0.1415	12.720	12.976

Signal 2: DAD1 B, Sig=210,4 Ref=off (2018 TO MAR 07\012618\012418_PF3-PH7-13CBTNAC_2.D)

Peak #	Time [min]	Type	Area [mAU*s]	Height [mAU]	Width [min]	Start [min]	End [min]
1	7.894	FM	2.17422e4	2129.17847	0.1702	7.699	8.060
2	9.058	FM	2265.41406	433.72296	0.0871	8.952	9.098
3	9.232	MF	1.81665e4	2077.62915	0.1457	9.098	9.349
4	9.728	FM	6531.01660	759.14935	0.1434	9.640	9.934
5	12.956	MF	1.59388e4	2136.41089	0.1243	12.824	13.046

Signal 3: DAD1 B, Sig=210,4 Ref=off (2018 TO MAR 07\012618\012418_PF3-PH7-13CBTNAC_3.D)

Peak #	Time [min]	Type	Area [mAU*s]	Height [mAU]	Width [min]	Start [min]	End [min]
1	7.416	FM	3.00385e4	1894.61292	0.2642	7.077	7.685
2	8.906	MF	2944.28687	611.75421	0.0802	8.846	8.999
3	9.129	MF	1.37661e4	1695.87073	0.1353	8.999	9.250
4	9.662	MF	8471.92676	1076.19922	0.1312	9.538	9.835
5	12.802	MF	1.34734e4	1632.25354	0.1376	12.676	12.937

Signal 4: DAD1 B, Sig=210,4 Ref=off (2018 TO MAR 07\012618\012418_PF3-PH7-13CBTNAC_4.D)

Peak #	Time [min]	Type	Area [mAU*s]	Height [mAU]	Width [min]	Start [min]	End [min]
1	7.884	MF	1.49431e4	1688.32275	0.1475	7.747	8.001
2	9.010	FM	3431.95166	649.64691	0.0880	8.979	9.113
3	9.231	FM	1.33222e4	1571.53259	0.1413	9.113	9.360
4	9.729	FM	1.02633e4	1182.65515	0.1446	9.627	9.932
5	12.922	MF	1.41186e4	1700.74683	0.1384	12.764	13.027

Signal 5: DAD1 B, Sig=210,4 Ref=off (2018 TO MAR 07\012618\012418_PF3-PH7-13CBTNAC_5.D)

Peak #	Time [min]	Type	Area [mAU*s]	Height [mAU]	Width [min]	Start [min]	End [min]
1	7.844	MF	1.13900e4	1649.19177	0.1151	7.726	7.969
2	9.010	MF	2775.56274	557.69238	0.0829	8.951	9.081
3	9.193	MF	8668.32715	1219.24573	0.1185	9.081	9.297
4	9.696	MF	8322.69238	1001.90900	0.1384	9.578	9.886
5	12.800	MF	1.29913e4	1721.24487	0.1258	12.678	12.910

Data File C:\CHEM32\1\DATA\2018 TO MAR 07\012618\012418_PF3-PH7-13CBTNAC_1.D
Sample Name: 012218_PF3-ph7-13cbtnac_1

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Integration Results
=====

Signal 1: DAD1 A, Sig=254,4 Ref=off (2018 TO MAR 07\012618\012418_PF3-PH7-13CBTNAC_1.D)

Peak #	Time [min]	Type	Area [mAU*s]	Height [mAU]	Width [min]	Start [min]	End [min]
1	9.081	MF	455.95853	76.43199	0.0994	8.948	9.085
2	9.195	MF	4273.00830	647.51642	0.1100	9.085	9.285
3	9.713	FM	864.22162	103.05989	0.1398	9.631	9.836
4	12.880	MF	1.54454e4	2768.33911	0.0930	12.757	12.973
5	12.973	FM	383.86099	201.20613	0.0318	12.973	13.073

Signal 2: DAD1 A, Sig=254,4 Ref=off (2018 TO MAR 07\012618\012418_PF3-PH7-13CBTNAC_2.D)

Peak #	Time [min]	Type	Area [mAU*s]	Height [mAU]	Width [min]	Start [min]	End [min]
1	9.057	MF	416.94113	78.41770	0.0886	8.983	9.115
2	9.232	MF	3347.27686	497.54984	0.1121	9.115	9.320
3	9.728	MF	1268.26978	193.05396	0.1095	9.657	9.807
4	12.956	MM	1.15061e4	2109.27319	0.0909	12.842	13.088

Signal 3: DAD1 A, Sig=254,4 Ref=off (2018 TO MAR 07\012618\012418_PF3-PH7-13CBTNAC_3.D)

Peak #	Time [min]	Type	Area [mAU*s]	Height [mAU]	Width [min]	Start [min]	End [min]
1	8.906	MF	851.79407	162.02739	0.0876	8.852	8.984
2	9.129	FM	3439.48486	476.80533	0.1202	8.984	9.230
3	9.662	FM	2666.17871	344.44800	0.1290	9.541	9.762
4	12.803	MM	1.12936e4	2014.62061	0.0934	12.677	12.918

Signal 4: DAD1 A, Sig=254,4 Ref=off (2018 TO MAR 07\012618\012418_PF3-PH7-13CBTNAC_4.D)

Peak #	Time [min]	Type	Area [mAU*s]	Height [mAU]	Width [min]	Start [min]	End [min]
1	9.046	MF	906.43396	164.82642	0.0917	8.992	9.120
2	9.231	MF	2879.00098	392.18085	0.1224	9.120	9.325
3	9.730	MF	2489.67114	360.50821	0.1151	9.647	9.817
4	12.924	MM	1.27247e4	2235.55273	0.0949	12.818	13.074

Signal 5: DAD1 A, Sig=254,4 Ref=off (2018 TO MAR 07\012618\012418_PF3-PH7-13CBTNAC_5.D)

Peak #	Time [min]	Type	Area [mAU*s]	Height [mAU]	Width [min]	Start [min]	End [min]
1	9.011	MF	638.57806	124.45227	0.0855	8.962	9.095
2	9.193	FM	1658.48438	245.42241	0.1126	9.095	9.280
3	9.696	FM	2168.59033	286.15845	0.1263	9.591	9.827
4	12.800	MM	9266.77344	1678.98987	0.0920	12.687	12.978

Data File C:\CHEM32\1\DATA\2018 TO MAR 07\020218\013118_Pf3-PH7-13CBTNAC_1.D
Sample Name: 013118_Pf3-ph7-13cbtnac_1

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Integration Results
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Signal 1: DAD1 B, Sig=210,4 Ref=off (2018 TO MAR 07\020218\013118_Pf3-PH7-13CBTNAC_1.D)

Peak #	Time [min]	Type	Area [mAU*s]	Height [mAU]	Width [min]	Start [min]	End [min]
1	7.806	MF	1.47586e4	1877.88623	0.1310	7.677	7.947
2	9.011	MF	667.71442	192.94965	0.0577	8.939	9.012
3	9.169	MF	2.01643e4	1890.88965	0.1777	9.012	9.273
4	9.686	FM	2894.87231	414.46405	0.1164	9.622	9.956
5	12.862	MF	8795.91797	1592.83997	0.0920	12.740	12.963

Signal 2: DAD1 B, Sig=210,4 Ref=off (2018 TO MAR 07\020218\013118_Pf3-PH7-13CBTNAC_2.D)

Peak #	Time [min]	Type	Area [mAU*s]	Height [mAU]	Width [min]	Start [min]	End [min]
1	7.843	FM	1.54074e4	2173.26514	0.1182	7.740	7.976
2	9.014	MF	1732.66248	402.80444	0.0717	8.955	9.044
3	9.175	MF	2.40263e4	2183.97681	0.1834	9.044	9.314
4	9.695	MF	1.18598e4	1464.29858	0.1350	9.603	9.883
5	12.916	MF	1.13144e4	2036.28650	0.0926	12.788	13.007

Signal 3: DAD1 B, Sig=210,4 Ref=off (2018 TO MAR 07\020218\013118_Pf3-PH7-13CBTNAC_3.D)

Peak #	Time [min]	Type	Area [mAU*s]	Height [mAU]	Width [min]	Start [min]	End [min]
1	7.781	MF	1.16208e4	1624.52429	0.1192	7.661	7.925
2	8.956	MF	2901.13184	622.10889	0.0777	8.891	9.015
3	9.128	MF	1.64453e4	1625.91223	0.1686	9.015	9.254
4	9.651	MF	1.50107e4	1571.71680	0.1592	9.536	9.845
5	12.764	MF	9674.14648	1609.95398	0.1001	12.623	12.868

Signal 4: DAD1 B, Sig=210,4 Ref=off (2018 TO MAR 07\020218\013118_Pf3-PH7-13CBTNAC_4.D)

Peak #	Time [min]	Type	Area [mAU*s]	Height [mAU]	Width [min]	Start [min]	End [min]
1	7.826	FM	1.18658e4	1681.22424	0.1176	7.712	7.941
2	8.990	MF	3692.21680	820.23694	0.0750	8.929	9.047
3	9.171	MF	1.73316e4	1636.02942	0.1766	9.047	9.292
4	9.685	MF	1.68454e4	1617.40186	0.1736	9.587	9.896
5	12.862	MF	4868.47998	934.37787	0.0868	12.734	12.947

Signal 5: DAD1 B, Sig=210,4 Ref=off (2018 TO MAR 07\020218\013118_Pf3-PH7-13CBTNAC_5.D)

Peak #	Time [min]	Type	Area [mAU*s]	Height [mAU]	Width [min]	Start [min]	End [min]
1	7.804	FM	8382.09668	1519.23242	0.0920	7.725	7.928
2	8.959	MF	3265.69629	730.16943	0.0745	8.901	9.028
3	9.149	MF	1.26039e4	1678.56458	0.1251	9.028	9.219
4	9.658	MF	1.34339e4	1646.90576	0.1360	9.559	9.769
5	12.782	MF	4078.51001	775.32263	0.0877	12.664	12.883

Print of window 38: Current Chromatogram(s)

Data File : C:\CHEM32\1\DATA\2018 TO MAR 07\020218\013118_PF3-PH7-13CBTNAC_1.D

Sample Name : 013118_PF3-ph7-13cbtnac_1

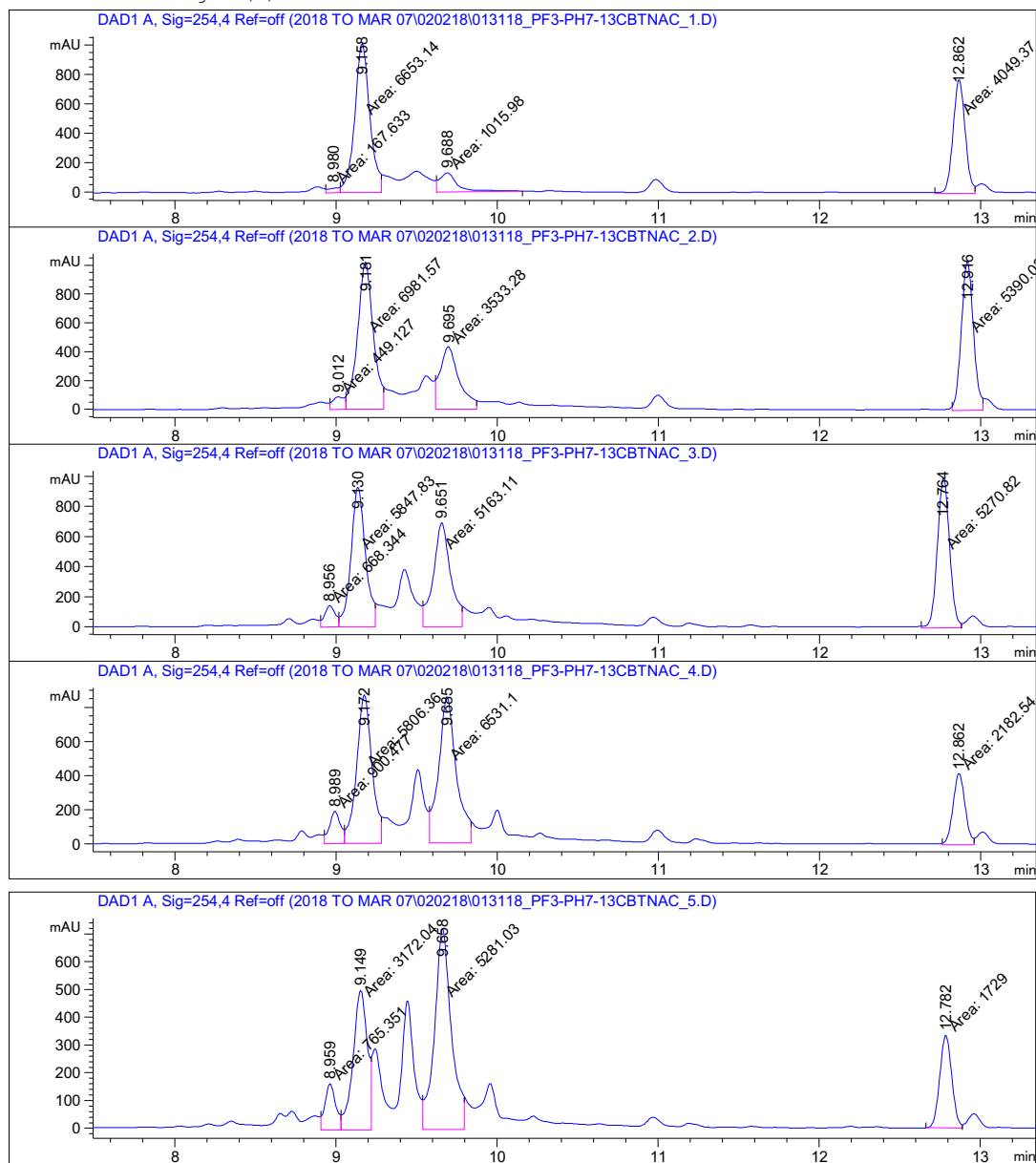
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Acq. Operator : SGLK Seq. Line : 5
Acq. Instrument : Instrument 1 Location : Vial 5
Injection Date : 2/2/18 6:47:32 PM Inj : 1
Inj Volume : 1.000 µl

Acq. Method : D:\CHEM32\1\METHODS\AP_C18_INSERT.M
Last changed : 1/22/18 3:04:38 PM by SGLK
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Last changed : 3/8/18 8:51:08 AM
(modified after loading)

Additional Info : Peak(s) manually integrated

Current Chromatogram(s)



Data File C:\CHEM32\1\DATA\2018 TO MAR 07\020218\013118_PF3-PH7-13CBTNAC_1.D
Sample Name: 013118_PF3-ph7-13cbtnac_1

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Integration Results
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Signal 1: DAD1 A, Sig=254,4 Ref=off (2018 TO MAR 07\020218\013118_PF3-PH7-13CBTNAC_1.D)

Peak #	Time [min]	Type	Area [mAU*s]	Height [mAU]	Width [min]	Start [min]	End [min]
1	8.980	MF	167.63275	40.41625	0.0691	8.935	9.025
2	9.158	MF	6653.14258	1013.87598	0.1094	9.025	9.279
3	9.688	FM	1015.97882	131.04523	0.1292	9.622	10.154
4	12.862	MF	4049.37402	772.72168	0.0873	12.714	12.963

Signal 2: DAD1 A, Sig=254,4 Ref=off (2018 TO MAR 07\020218\013118_PF3-PH7-13CBTNAC_2.D)

Peak #	Time [min]	Type	Area [mAU*s]	Height [mAU]	Width [min]	Start [min]	End [min]
1	9.012	FM	449.12659	88.06937	0.0850	8.959	9.058
2	9.181	FM	6981.57227	1022.56451	0.1138	9.058	9.295
3	9.695	FM	3533.27783	434.13306	0.1356	9.614	9.872
4	12.916	FM	5390.01611	1040.12830	0.0864	12.820	13.013

Signal 3: DAD1 A, Sig=254,4 Ref=off (2018 TO MAR 07\020218\013118_PF3-PH7-13CBTNAC_3.D)

Peak #	Time [min]	Type	Area [mAU*s]	Height [mAU]	Width [min]	Start [min]	End [min]
1	8.956	FM	668.34357	142.29138	0.0783	8.902	9.017
2	9.130	FM	5847.83105	930.69971	0.1047	9.017	9.242
3	9.651	FM	5163.11035	692.02686	0.1243	9.536	9.782
4	12.764	MF	5270.82471	997.93738	0.0880	12.628	12.878

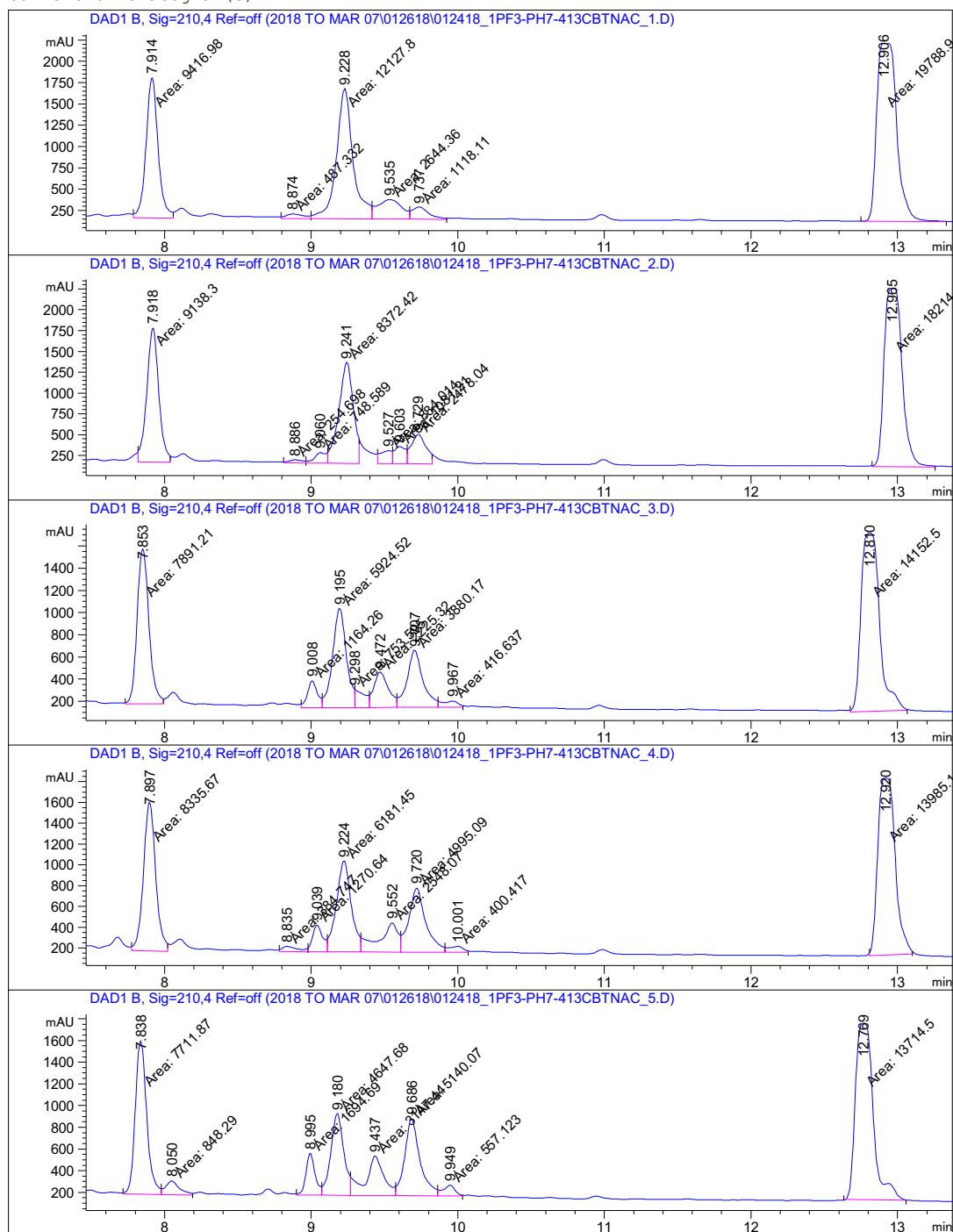
Signal 4: DAD1 A, Sig=254,4 Ref=off (2018 TO MAR 07\020218\013118_PF3-PH7-13CBTNAC_4.D)

Peak #	Time [min]	Type	Area [mAU*s]	Height [mAU]	Width [min]	Start [min]	End [min]
1	8.989	FM	900.47656	190.13754	0.0789	8.927	9.049
2	9.172	FM	5806.35840	870.80627	0.1111	9.049	9.279
3	9.685	FM	6531.10059	858.56616	0.1268	9.577	9.835
4	12.862	FM	2182.54004	418.45169	0.0869	12.759	12.955

Signal 5: DAD1 A, Sig=254,4 Ref=off (2018 TO MAR 07\020218\013118_PF3-PH7-13CBTNAC_5.D)

Peak #	Time [min]	Type	Area [mAU*s]	Height [mAU]	Width [min]	Start [min]	End [min]
1	8.959	FM	765.35132	166.98950	0.0764	8.906	9.029
2	9.149	FM	3172.03857	503.40402	0.1050	9.029	9.217
3	9.658	FM	5281.03174	725.90582	0.1213	9.536	9.794
4	12.782	MF	1728.99561	334.71692	0.0861	12.661	12.886

Current Chromatogram(s)



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Integration Results
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Signal 1: DAD1 B, Sig=210,4 Ref=off (2018 TO MAR 07\012618\012418_1PF3-PH7-413CBTNAC_1.D)

Peak #	Time [min]	Type	Area [mAU*s]	Height [mAU]	Width [min]	Start [min]	End [min]
1	7.914	MF	9416.98242	1647.93689	0.0952	7.787	8.060
2	8.874	FM	487.33218	54.21212	0.1498	8.795	8.999
3	9.228	FM	1.21278e4	1529.12659	0.1322	8.999	9.416
4	9.535	FM	2644.35767	228.19458	0.1931	9.416	9.674
5	9.737	FM	1118.11084	142.95132	0.1304	9.674	9.924
6	12.906	FM	1.97889e4	2092.50806	0.1576	12.750	13.333
7	17.096	MM	341.25854	47.20979	0.1205	16.977	17.244

Signal 2: DAD1 B, Sig=210,4 Ref=off (2018 TO MAR 07\012618\012418_1PF3-PH7-413CBTNAC_2.D)

Peak #	Time [min]	Type	Area [mAU*s]	Height [mAU]	Width [min]	Start [min]	End [min]
1	7.918	FM	9138.29590	1610.67407	0.0946	7.820	8.038
2	8.886	MF	254.69795	37.63269	0.1128	8.811	8.965
3	9.060	FM	748.58875	126.74625	0.0984	8.965	9.112
4	9.241	FM	8372.42285	1212.87939	0.1150	9.112	9.326
5	9.527	FM	884.01447	154.15724	0.0956	9.452	9.556
6	9.603	FM	1081.20557	205.80222	0.0876	9.556	9.654
7	9.729	FM	2478.03564	353.92752	0.1167	9.654	9.825
8	12.965	FM	1.82142e4	2143.19775	0.1416	12.826	13.256
9	17.135	FM	137.25032	18.79482	0.1217	17.041	17.286

Signal 3: DAD1 B, Sig=210,4 Ref=off (2018 TO MAR 07\012618\012418_1PF3-PH7-413CBTNAC_3.D)

Peak #	Time [min]	Type	Area [mAU*s]	Height [mAU]	Width [min]	Start [min]	End [min]
1	7.853	MF	7891.20898	1398.38062	0.0941	7.731	7.992
2	9.008	MF	1164.25757	244.43816	0.0794	8.933	9.075
3	9.195	MF	5924.52051	898.11829	0.1099	9.075	9.298
4	9.298	MF	753.59515	167.25101	0.0595	9.298	9.396
5	9.472	MF	2225.31738	319.45935	0.1161	9.396	9.586
6	9.707	MF	3880.17480	515.12500	0.1255	9.586	9.867
7	9.967	FM	416.63672	54.89103	0.1050	9.867	10.036
8	12.810	MM	1.41525e4	1605.68469	0.1469	12.676	13.068
9	17.018	FM	103.15417	13.08915	0.1313	16.907	17.166

Data File C:\CHEM32\1\DATA\2018 TO MAR 07\012618\012418_1PF3-PH7-413CBTNAC_1.D
Sample Name: 012418_1PF3-ph7-413CBTNac_1

Signal 4: DAD1 B, Sig=210,4 Ref=off (2018 TO MAR 07\012618\012418_1PF3-PH7-413CBTNAC_4.D)

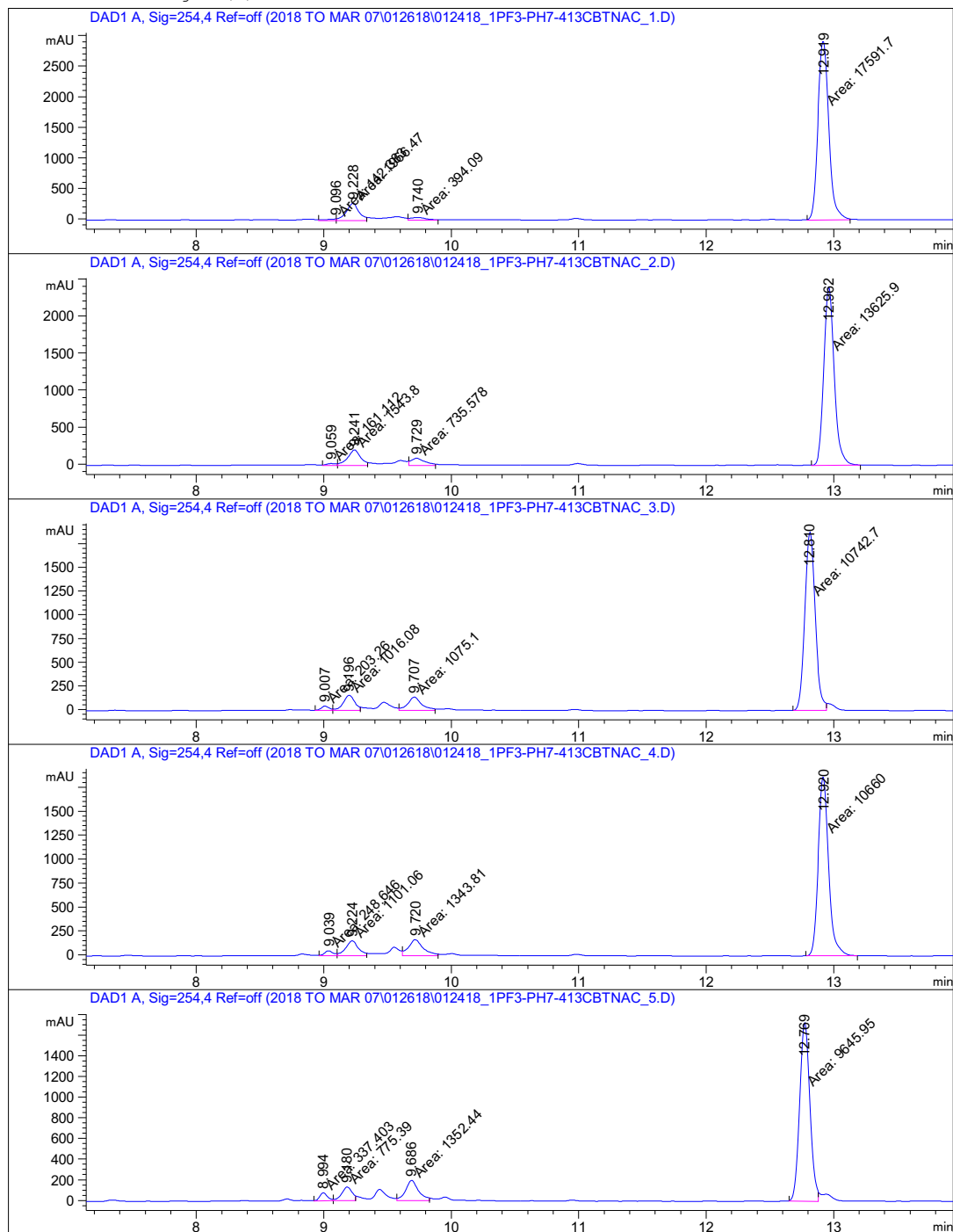
Peak #	Time [min]	Type	Area [mAU*s]	Height [mAU]	Width [min]	Start [min]	End [min]
1	7.897	MF	8335.66602	1429.31128	0.0972	7.776	8.022
2	8.835	MF	384.74734	50.63771	0.1266	8.782	8.979
3	9.039	FM	1270.64465	258.62827	0.0819	8.979	9.111
4	9.224	FM	6181.45459	876.76721	0.1175	9.111	9.339
5	9.552	FM	2548.07251	281.66565	0.1508	9.339	9.610
6	9.720	FM	4995.09375	616.77344	0.1350	9.610	9.914
7	10.001	FM	400.41724	57.92731	0.1152	9.914	10.071
8	12.920	MM	1.39851e4	1702.83252	0.1369	12.809	13.102
9	17.103	FM	84.47837	10.66243	0.1320	16.993	17.267

Signal 5: DAD1 B, Sig=210,4 Ref=off (2018 TO MAR 07\012618\012418_1PF3-PH7-413CBTNAC_5.D)

Peak #	Time [min]	Type	Area [mAU*s]	Height [mAU]	Width [min]	Start [min]	End [min]
1	7.838	MF	7711.86670	1410.79956	0.0911	7.715	7.976
2	8.050	FM	848.29047	127.37299	0.1110	7.976	8.190
3	8.995	MF	1694.69202	389.25287	0.0726	8.900	9.071
4	9.180	MF	4647.68359	753.63672	0.1028	9.071	9.268
5	9.437	MF	3147.43799	364.28168	0.1440	9.268	9.575
6	9.686	MF	5140.07275	710.37439	0.1206	9.575	9.864
7	9.949	FM	557.12329	97.50262	0.0952	9.864	10.032
8	12.769	MM	1.37145e4	1626.81152	0.1405	12.634	13.059
9	16.978	FM	75.99796	9.27865	0.1365	16.875	17.135

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Current Chromatogram(s)



Data File C:\CHEM32\1\DATA\2018 TO MAR 07\012618\012418_1PF3-PH7-413CBTNAC_1.D
Sample Name: 012418_1PF3-ph7-413CBTNAC_1

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Integration Results
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Signal 1: DAD1 A, Sig=254,4 Ref=off (2018 TO MAR 07\012618\012418_1PF3-PH7-413CBTNAC_1.D)

Peak #	Time [min]	Type	Area [mAU*s]	Height [mAU]	Width [min]	Start [min]	End [min]
1	9.096	MF	142.38287	26.04919	0.0911	8.961	9.097
2	9.228	FM	1966.46570	281.31848	0.1165	9.097	9.336
3	9.740	FM	394.09006	45.81873	0.1434	9.662	9.896
4	12.919	MM	1.75917e4	2931.18726	0.1000	12.792	13.128

Signal 2: DAD1 A, Sig=254,4 Ref=off (2018 TO MAR 07\012618\012418_1PF3-PH7-413CBTNAC_2.D)

Peak #	Time [min]	Type	Area [mAU*s]	Height [mAU]	Width [min]	Start [min]	End [min]
1	9.059	FM	161.11209	28.80318	0.0932	8.991	9.109
2	9.241	FM	1543.80066	213.12289	0.1207	9.109	9.346
3	9.729	FM	735.57843	97.84830	0.1253	9.668	9.876
4	12.962	MM	1.36259e4	2410.98779	0.0942	12.827	13.210

Signal 3: DAD1 A, Sig=254,4 Ref=off (2018 TO MAR 07\012618\012418_1PF3-PH7-413CBTNAC_3.D)

Peak #	Time [min]	Type	Area [mAU*s]	Height [mAU]	Width [min]	Start [min]	End [min]
1	9.007	FM	203.26022	46.58055	0.0727	8.934	9.072
2	9.196	FM	1016.08386	161.26431	0.1050	9.072	9.288
3	9.707	FM	1075.09631	142.35010	0.1259	9.590	9.875
4	12.810	MF	1.07427e4	1886.81433	0.0949	12.681	12.946

Signal 4: DAD1 A, Sig=254,4 Ref=off (2018 TO MAR 07\012618\012418_1PF3-PH7-413CBTNAC_4.D)

Peak #	Time [min]	Type	Area [mAU*s]	Height [mAU]	Width [min]	Start [min]	End [min]
1	9.039	FM	248.64555	52.22098	0.0794	8.962	9.105
2	9.224	FM	1101.06201	155.99211	0.1176	9.105	9.337
3	9.720	FM	1343.80579	168.67032	0.1328	9.618	9.895
4	12.920	MM	1.06600e4	1872.36560	0.0949	12.783	13.186

Signal 5: DAD1 A, Sig=254,4 Ref=off (2018 TO MAR 07\012618\012418_1PF3-PH7-413CBTNAC_5.D)

1	8.994	MF	337.40302	79.62730	0.0706	8.922	9.075
2	9.180	MF	775.38977	133.16174	0.0970	9.075	9.250
3	9.686	MF	1352.44153	195.07692	0.1155	9.573	9.831
4	12.769	MF	9645.94922	1733.51257	0.0927	12.652	12.880

Print of window 38: Current Chromatogram(s)

Data File : C:\CHEM32\1\DATA\2018 TO MAR 07\020218\013118_1PF3-PH7-413CBTNAC_1.D

Sample Name : 013118_1PF3-ph7-413CBTNac_1

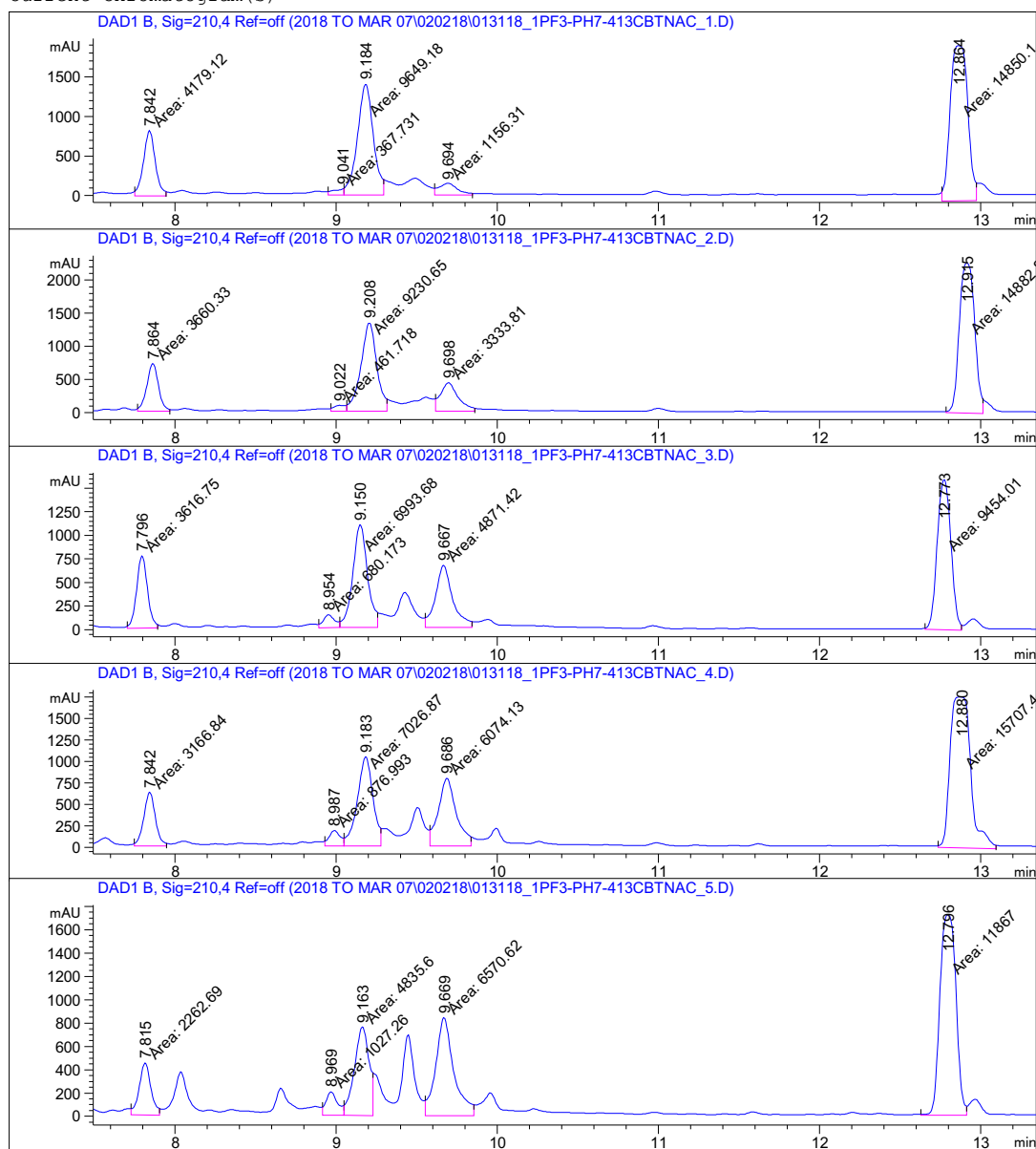
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Injection Date : 2/2/18 7:45:39 PM Inj : 1
Inj Volume : 1.000 µl

Acq. Method : D:\CHEM32\1\METHODS\AP_C18_INSERT.M
Last changed : 1/22/18 3:04:38 PM by SGLK
Analysis Method : Z:\DESKTOP\BERTOZZI LAB\LCMS INFO\LCMS METHODS TO 112917\SGLK_BERTOZZI_BP_WITHINSERT.M

Last changed : 3/8/18 8:51:08 AM
(modified after loading)

Additional Info : Peak(s) manually integrated

Current Chromatogram(s)



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Integration Results
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Signal 1: DAD1 B, Sig=210,4 Ref=off (2018 TO MAR 07\020218\013118_1PF3-PH7-413CBTNAC_1.D)

Peak #	Time [min]	Type	Area [mAU*s]	Height [mAU]	Width [min]	Start [min]	End [min]
1	7.842	FM	4179.11914	821.41675	0.0848	7.749	7.942
2	9.041	FM	367.73087	78.21339	0.0784	8.950	9.047
3	9.184	FM	9649.18066	1400.78040	0.1148	9.047	9.293
4	9.694	FM	1156.30530	145.55722	0.1324	9.609	9.843
5	12.864	FM	1.48501e4	1956.26233	0.1265	12.758	12.970

Signal 2: DAD1 B, Sig=210,4 Ref=off (2018 TO MAR 07\020218\013118_1PF3-PH7-413CBTNAC_2.D)

Peak #	Time [min]	Type	Area [mAU*s]	Height [mAU]	Width [min]	Start [min]	End [min]
1	7.864	FM	3660.32935	723.93250	0.0843	7.767	7.966
2	9.022	FM	461.71805	91.62712	0.0840	8.968	9.064
3	9.208	FM	9230.65137	1339.48608	0.1149	9.064	9.313
4	9.698	FM	3333.80762	432.63248	0.1284	9.615	9.858
5	12.915	MF	1.48828e4	2264.37549	0.1095	12.782	13.012

Signal 3: DAD1 B, Sig=210,4 Ref=off (2018 TO MAR 07\020218\013118_1PF3-PH7-413CBTNAC_3.D)

Peak #	Time [min]	Type	Area [mAU*s]	Height [mAU]	Width [min]	Start [min]	End [min]
1	7.796	FM	3616.75317	768.20435	0.0785	7.702	7.893
2	8.954	FM	680.17310	138.71642	0.0817	8.891	9.020
3	9.150	FM	6993.68018	1092.80615	0.1067	9.020	9.257
4	9.667	FM	4871.42480	657.31110	0.1235	9.550	9.840
5	12.773	FM	9454.00977	1592.20349	0.0990	12.652	12.879

Signal 4: DAD1 B, Sig=210,4 Ref=off (2018 TO MAR 07\020218\013118_1PF3-PH7-413CBTNAC_4.D)

Peak #	Time [min]	Type	Area [mAU*s]	Height [mAU]	Width [min]	Start [min]	End [min]
1	7.842	FM	3166.83960	631.48499	0.0836	7.746	7.945
2	8.987	FM	876.99335	181.88477	0.0804	8.929	9.047
3	9.183	FM	7026.86963	1040.78650	0.1125	9.047	9.275
4	9.686	FM	6074.12842	789.74097	0.1282	9.580	9.835
5	12.880	MM	1.57074e4	1758.29065	0.1489	12.735	13.092

Signal 5: DAD1 B, Sig=210,4 Ref=off (2018 TO MAR 07\020218\013118_1PF3-PH7-413CBTNAC_5.D)

Peak #	Time [min]	Type	Area [mAU*s]	Height [mAU]	Width [min]	Start [min]	End [min]
1	7.815	FM	2262.69141	448.04358	0.0842	7.726	7.901
2	8.969	FM	1027.25977	204.35941	0.0838	8.915	9.047
3	9.163	FM	4835.60400	760.72070	0.1059	9.047	9.228
4	9.669	FM	6570.62402	840.52429	0.1303	9.550	9.852
5	12.796	MF	1.18670e4	1718.16589	0.1151	12.625	12.910

Print of window 38: Current Chromatogram(s)

Data File : C:\CHEM32\1\DATA\2018 TO MAR 07\020218\013118_1PF3-PH7-413CBTNAC_1.D

Sample Name : 013118_1PF3-ph7-413CBTNac_1

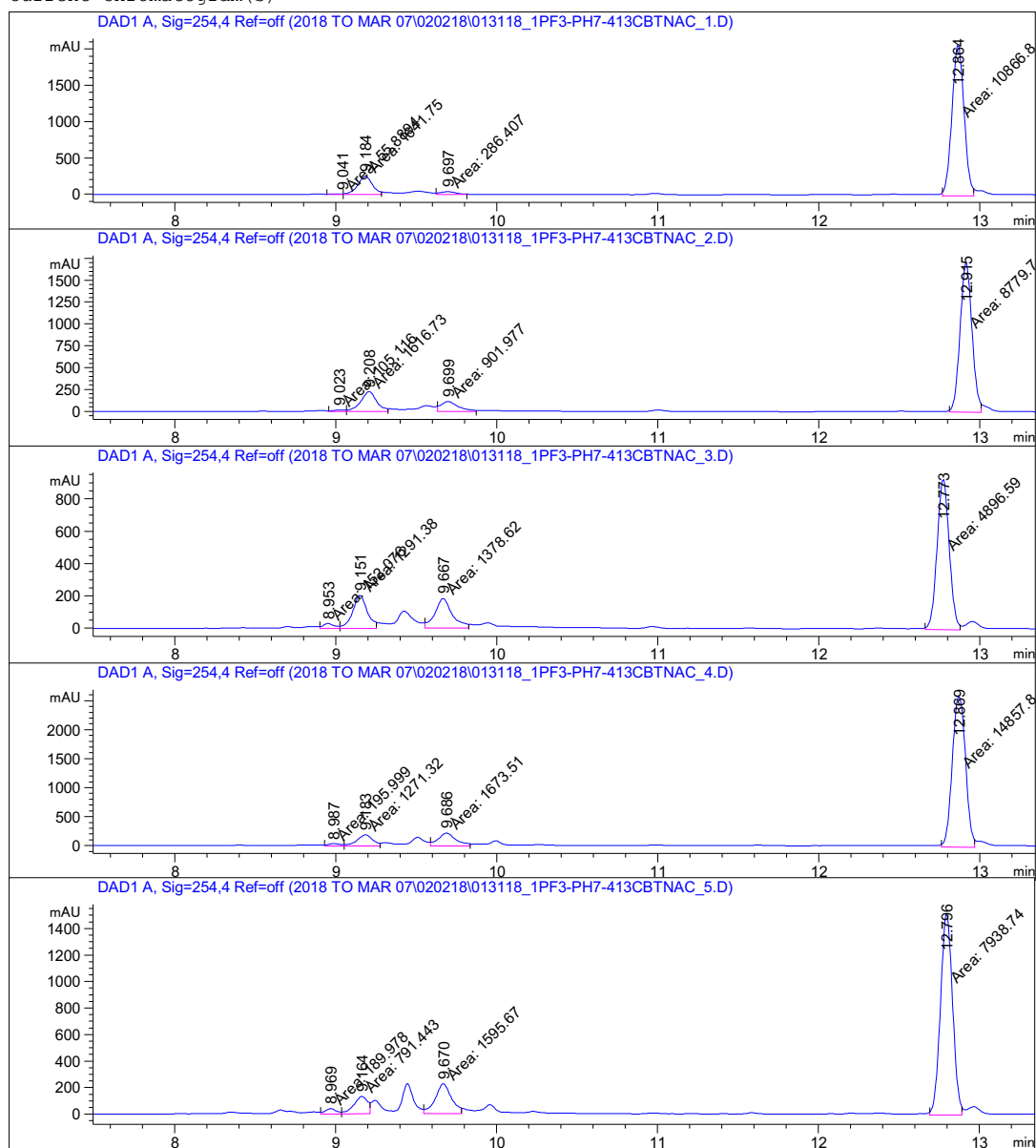
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Acq. Operator : SGLK Seq. Line : 7
Acq. Instrument : Instrument 1 Location : Vial 7
Injection Date : 2/2/18 7:45:39 PM Inj : 1
Inj Volume : 1.000 µl

Acq. Method : D:\CHEM32\1\METHODS\AP_C18_INSERT.M
Last changed : 1/22/18 3:04:38 PM by SGLK
Analysis Method : Z:\DESKTOP\BERTOZZI LAB\LCMS INFO\LCMS METHODS TO 112917\SGLK_BERTOZZI_BP_WITHINSERT.M

Last changed : 3/8/18 8:51:08 AM
(modified after loading)

Additional Info : Peak(s) manually integrated

Current Chromatogram(s)



Data File C:\CHEM32\1\DATA\2018 TO MAR 07\020218\013118_1PF3-PH7-413CBTNAC_1.D
 Sample Name: 013118_1PF3-ph7-413CBTNac_1

=====
 Integration Results
 =====

Signal 1: DAD1 A, Sig=254,4 Ref=off (2018 TO MAR 07\020218\013118_1PF3-PH7-413CBTNAC_1.D)

Peak #	Time [min]	Type	Area [mAU*s]	Height [mAU]	Width [min]	Start [min]	End [min]
1	9.041	FM	55.88944	11.06242	0.0842	8.942	9.044
2	9.184	FM	1641.74548	253.71167	0.1078	9.044	9.283
3	9.697	FM	286.40692	40.31698	0.1184	9.622	9.811
4	12.864	FM	1.08668e4	2075.80518	0.0872	12.765	12.958

Signal 2: DAD1 A, Sig=254,4 Ref=off (2018 TO MAR 07\020218\013118_1PF3-PH7-413CBTNAC_2.D)

Peak #	Time [min]	Type	Area [mAU*s]	Height [mAU]	Width [min]	Start [min]	End [min]
1	9.023	FM	105.11598	19.44548	0.0901	8.956	9.064
2	9.208	FM	1616.72717	230.14301	0.1171	9.064	9.324
3	9.699	FM	901.97675	117.54403	0.1279	9.631	9.870
4	12.915	FM	8779.70313	1712.29663	0.0855	12.808	13.006

Signal 3: DAD1 A, Sig=254,4 Ref=off (2018 TO MAR 07\020218\013118_1PF3-PH7-413CBTNAC_3.D)

Peak #	Time [min]	Type	Area [mAU*s]	Height [mAU]	Width [min]	Start [min]	End [min]
1	8.953	FM	152.07585	30.38887	0.0834	8.899	9.024
2	9.151	FM	1291.37805	203.47014	0.1058	9.024	9.252
3	9.667	FM	1378.61804	184.58427	0.1245	9.552	9.823
4	12.773	FM	4896.59473	931.85321	0.0876	12.659	12.874

Signal 4: DAD1 A, Sig=254,4 Ref=off (2018 TO MAR 07\020218\013118_1PF3-PH7-413CBTNAC_4.D)

Peak #	Time [min]	Type	Area [mAU*s]	Height [mAU]	Width [min]	Start [min]	End [min]
1	8.987	FM	195.99939	38.38641	0.0851	8.929	9.051
2	9.183	FM	1271.32251	188.63309	0.1123	9.051	9.274
3	9.686	FM	1673.51196	218.45514	0.1277	9.586	9.832
4	12.869	MF	1.48578e4	2598.30322	0.0953	12.759	12.964

Signal 5: DAD1 A, Sig=254,4 Ref=off (2018 TO MAR 07\020218\013118_1PF3-PH7-413CBTNAC_5.D)

Peak #	Time [min]	Type	Area [mAU*s]	Height [mAU]	Width [min]	Start [min]	End [min]
1	0.980	BB	31.18398	7.66578e-1	0.4986	1.45e-3	1.063
2	8.969	FM	189.97842	40.02207	0.0791	8.906	9.035
3	9.164	FM	791.44257	130.94086	0.1007	9.035	9.213
4	9.670	FM	1595.67419	225.92827	0.1177	9.545	9.782
5	12.796	FM	7938.74023	1519.81384	0.0871	12.690	12.891

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 Integration Results
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Signal 1: DAD1 B, Sig=210,4 Ref=off (2018 TO MAR 07\012618\012418_4PF3-PH7-13CBTNAC_1.D)

Peak #	Time [min]	Type	Area [mAU*s]	Height [mAU]	Width [min]	Start [min]	End [min]
1	7.860	MF	1.84950e4	2050.75513	0.1503	7.720	8.024
2	8.089	MF	2392.83325	382.49109	0.1043	8.024	8.210
3	8.870	MF	765.58057	85.67575	0.1489	8.776	8.971
4	9.060	MF	642.70343	166.08194	0.0645	8.971	9.062
5	9.208	MF	1.85275e4	2048.39893	0.1507	9.062	9.343
6	9.715	MF	2025.30261	257.27994	0.1312	9.638	9.885
7	12.896	MF	1810.43713	333.72260	0.0904	12.793	12.981
8	17.091	MM	3022.47485	399.32254	0.1262	16.939	17.285

Signal 2: DAD1 B, Sig=210,4 Ref=off (2018 TO MAR 07\012618\012418_4PF3-PH7-13CBTNAC_2.D)

Peak #	Time [min]	Type	Area [mAU*s]	Height [mAU]	Width [min]	Start [min]	End [min]
1	7.894	FM	2.06262e4	2095.16553	0.1641	7.694	8.040
2	8.117	FM	2581.28320	382.76730	0.1124	8.040	8.218
3	9.056	FM	2080.65186	425.99606	0.0814	8.969	9.100
4	9.232	FM	1.89702e4	2035.62708	0.1553	9.100	9.433
5	9.726	FM	6051.60547	719.79962	0.1401	9.636	9.945
6	12.955	MM	1533.16333	254.23740	0.1005	12.864	13.138
7	17.131	MM	1801.86560	237.32285	0.1265	16.935	17.304
8	27.940	BBA	1001.94745	111.75077	0.1494	27.807	28.000

Signal 3: DAD1 B, Sig=210,4 Ref=off (2018 TO MAR 07\012618\012418_4PF3-PH7-13CBTNAC_3.D)

Peak #	Time [min]	Type	Area [mAU*s]	Height [mAU]	Width [min]	Start [min]	End [min]
1	7.386	MF	7936.72314	765.12000	0.1729	7.089	7.572
2	7.842	MF	1.41918e4	1574.01428	0.1503	7.712	7.979
3	8.066	MF	2933.36401	388.90378	0.1257	7.979	8.220
4	9.008	MF	3157.13452	698.73083	0.0753	8.918	9.071
5	9.190	MF	1.21071e4	1499.39441	0.1346	9.071	9.325
6	9.704	MF	7429.56299	972.61151	0.1273	9.604	9.896
7	12.807	MF	1474.88635	268.96881	0.0914	12.678	12.932
8	17.020	MM	1165.90271	149.83099	0.1297	16.844	17.177
9	27.049	HH	38.29931	3.93957	0.1554	26.843	27.199
10	27.931	BBA	964.60730	97.13586	0.1655	27.769	27.996

Data File C:\CHEM32\1\DATA\2018 TO MAR 07\012618\012418_4PF3-PH7-13CBTNAC_1.D
Sample Name: 012218_Pf3-ph8-azidoCBTNac_1

Signal 4: DAD1 B, Sig=210,4 Ref=off (2018 TO MAR 07\012618\012418_4PF3-PH7-13CBTNAC_4.D)

Peak #	Time [min]	Type	Area [mAU*s]	Height [mAU]	Width [min]	Start [min]	End [min]
1	7.681	FM	3636.06616	680.77594	0.0890	7.600	7.738
2	7.881	FM	1.56507e4	1654.62610	0.1576	7.738	8.014
3	8.118	FM	9029.92383	1248.92078	0.1205	8.014	8.327
4	9.038	FM	3078.17871	652.84564	0.0786	8.975	9.099
5	9.219	FM	1.22704e4	1517.02673	0.1348	9.099	9.339
6	9.714	FM	9018.74121	1109.87085	0.1354	9.616	9.914
7	12.914	MF	1438.77722	274.10233	0.0875	12.795	12.995
8	17.100	MM	878.28180	117.26001	0.1248	16.955	17.257
9	27.939	HBA	5135.85693	416.95944	0.2053	27.132	27.999

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Integration Results
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Signal 1: DAD1 A, Sig=254,4 Ref=off (2018 TO MAR 07\012618\012418_4PF3-PH7-13CBTNAC_1.D)

Peak #	Time [min]	Type	Area [mAU*s]	Height [mAU]	Width [min]	Start [min]	End [min]
1	9.073	FM	109.53465	26.67127	0.0684	8.975	9.077
2	9.208	FM	3892.34985	579.80493	0.1119	9.077	9.332
3	9.718	FM	553.98206	74.16487	0.1245	9.638	9.879
4	12.896	MF	767.04785	139.52420	0.0916	12.774	12.987

Signal 2: DAD1 A, Sig=254,4 Ref=off (2018 TO MAR 07\012618\012418_4PF3-PH7-13CBTNAC_2.D)

Peak #	Time [min]	Type	Area [mAU*s]	Height [mAU]	Width [min]	Start [min]	End [min]
1	9.055	FM	369.18109	77.76151	0.0791	8.970	9.104
2	9.232	FM	3423.59888	478.64450	0.1192	9.104	9.360
3	9.726	FM	1544.29590	191.12616	0.1347	9.642	9.902
4	12.955	MF	589.09991	108.67957	0.0903	12.857	13.029

Signal 3: DAD1 A, Sig=254,4 Ref=off (2018 TO MAR 07\012618\012418_4PF3-PH7-13CBTNAC_3.D)

Peak #	Time [min]	Type	Area [mAU*s]	Height [mAU]	Width [min]	Start [min]	End [min]
1	9.008	MF	556.58862	136.95667	0.0677	8.942	9.077
2	9.191	FM	2360.06812	378.14111	0.1040	9.077	9.295
3	9.703	FM	2024.40527	277.56799	0.1216	9.582	9.879
4	12.807	MF	596.59241	112.93456	0.0880	12.713	12.913

Signal 4: DAD1 A, Sig=254,4 Ref=off (2018 TO MAR 07\012618\012418_4PF3-PH7-13CBTNAC_4.D)

Peak #	Time [min]	Type	Area [mAU*s]	Height [mAU]	Width [min]	Start [min]	End [min]
1	9.038	FM	612.48633	130.93390	0.0780	8.951	9.104
2	9.219	FM	2387.05029	345.88968	0.1150	9.104	9.322
3	9.715	FM	2560.03564	324.88141	0.1313	9.615	9.893
4	12.914	MF	623.71161	117.50446	0.0885	12.825	13.001

Print of window 38: Current Chromatogram(s)

Data File : C:\CHEM32\1\DATA\2018 TO MAR 07\020218\013118_4PF3-PH7-13CBTNAC_1.D

Sample Name : 013118_4PF3-ph7-13CBTNAC_1

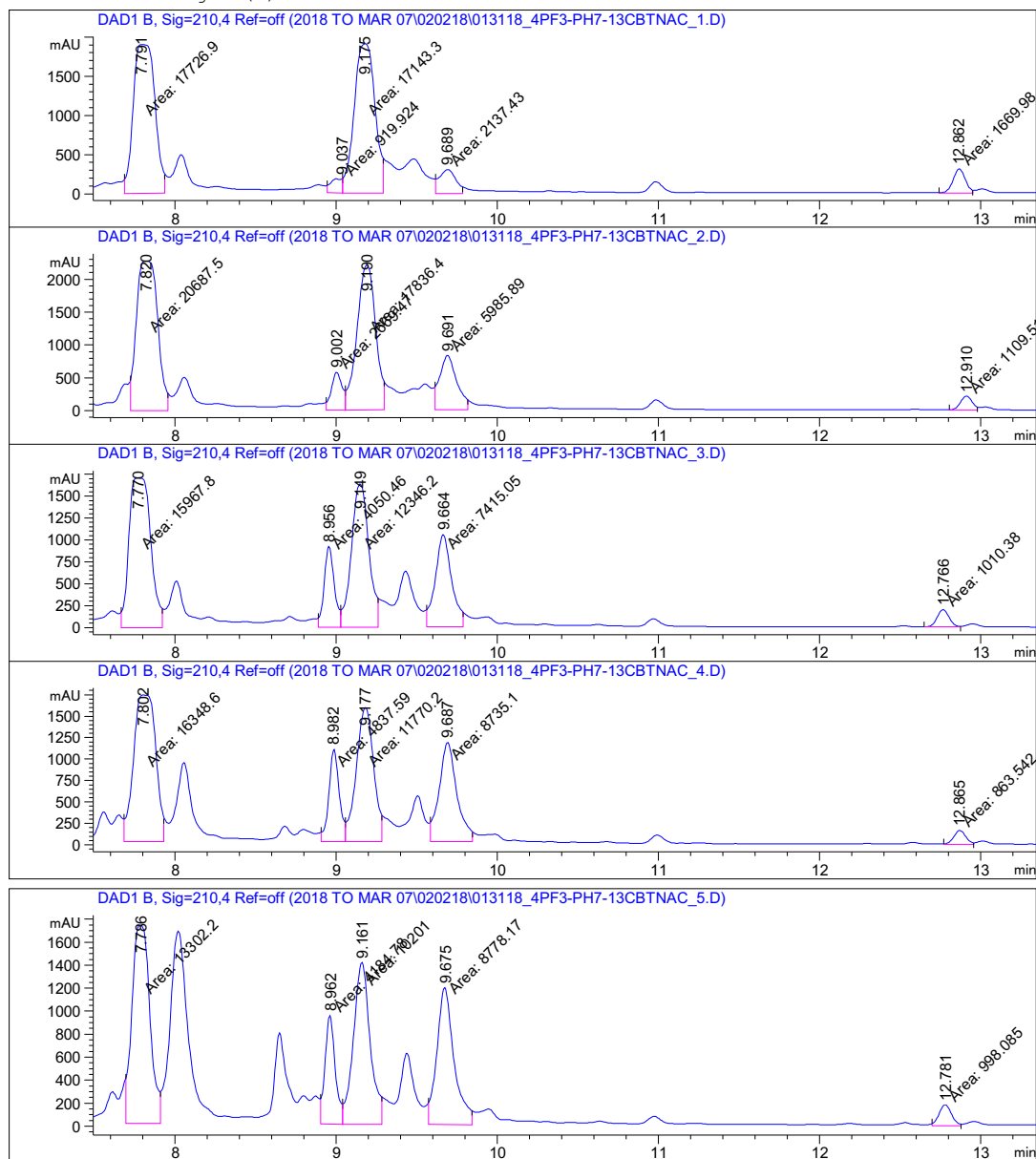
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Acq. Operator : SGLK Seq. Line : 6
Acq. Instrument : Instrument 1 Location : Vial 6
Injection Date : 2/2/18 7:16:34 PM Inj : 1
Inj Volume : 1.000 µl

Acq. Method : D:\CHEM32\1\METHODS\AP_C18_INSERT.M
Last changed : 1/22/18 3:04:38 PM by SGLK
Analysis Method : Z:\DESKTOP\BERTOZZI LAB\LCMS INFO\LCMS METHODS TO 112917\SGLK_BERTOZZI_BP_WITHINSERT.M

Last changed : 3/8/18 8:51:08 AM
(modified after loading)

Additional Info : Peak(s) manually integrated

Current Chromatogram(s)



Data File C:\CHEM32\1\DATA\2018 TO MAR 07\020218\013118_4PF3-PH7-13CBTNAC_1.D
Sample Name: 013118_4PF3-ph7-13CBTNAC_1

=====
Integration Results
=====

Signal 1: DAD1 B, Sig=210,4 Ref=off (2018 TO MAR 07\020218\013118_4PF3-PH7-13CBTNAC_1.D)

Peak #	Time [min]	Type	Area [mAU*s]	Height [mAU]	Width [min]	Start [min]	End [min]
1	7.791	FM	1.77269e4	1896.11926	0.1558	7.684	7.935
2	9.037	FM	919.92407	184.64258	0.0830	8.943	9.039
3	9.175	FM	1.71433e4	1902.55383	0.1502	9.039	9.290
4	9.689	FM	2137.42554	306.13031	0.1164	9.615	9.783
5	12.862	MF	1669.97876	311.27527	0.0894	12.740	12.947

Signal 2: DAD1 B, Sig=210,4 Ref=off (2018 TO MAR 07\020218\013118_4PF3-PH7-13CBTNAC_2.D)

Peak #	Time [min]	Type	Area [mAU*s]	Height [mAU]	Width [min]	Start [min]	End [min]
1	7.820	MF	2.06875e4	2273.26367	0.1517	7.722	7.955
2	9.002	MF	2669.47339	576.34473	0.0772	8.938	9.056
3	9.190	MF	1.78364e4	2205.12256	0.1348	9.056	9.297
4	9.691	MF	5985.88770	826.99255	0.1206	9.614	9.815
5	12.910	MF	1109.50574	216.23482	0.0855	12.802	12.978

Signal 3: DAD1 B, Sig=210,4 Ref=off (2018 TO MAR 07\020218\013118_4PF3-PH7-13CBTNAC_3.D)

Peak #	Time [min]	Type	Area [mAU*s]	Height [mAU]	Width [min]	Start [min]	End [min]
1	7.770	MF	1.59678e4	1708.92773	0.1557	7.666	7.921
2	8.956	MF	4050.46216	925.19824	0.0730	8.888	9.028
3	9.149	MF	1.23462e4	1635.00671	0.1259	9.028	9.260
4	9.664	MF	7415.04932	1055.82605	0.1170	9.561	9.787
5	12.766	MF	1010.38171	196.10500	0.0859	12.645	12.871

Signal 4: DAD1 B, Sig=210,4 Ref=off (2018 TO MAR 07\020218\013118_4PF3-PH7-13CBTNAC_4.D)

Peak #	Time [min]	Type	Area [mAU*s]	Height [mAU]	Width [min]	Start [min]	End [min]
1	7.802	FM	1.63486e4	1706.57397	0.1597	7.682	7.930
2	8.982	FM	4837.59375	1077.47766	0.0748	8.907	9.056
3	9.177	FM	1.17702e4	1562.65039	0.1255	9.056	9.282
4	9.687	FM	8735.09570	1156.13318	0.1259	9.583	9.843
5	12.865	FM	863.54230	162.56932	0.0885	12.768	12.954

Signal 5: DAD1 B, Sig=210,4 Ref=off (2018 TO MAR 07\020218\013118_4PF3-PH7-13CBTNAC_5.D)

Peak #	Time [min]	Type	Area [mAU*s]	Height [mAU]	Width [min]	Start [min]	End [min]
1	7.786	MF	1.33022e4	1725.83533	0.1285	7.694	7.908
2	8.962	MF	4184.78467	947.06653	0.0736	8.904	9.040
3	9.161	MF	1.02010e4	1408.12524	0.1207	9.040	9.282
4	9.675	MF	8778.17090	1192.27075	0.1227	9.573	9.840
5	12.781	MF	998.08514	184.60497	0.0901	12.695	12.875

Print of window 38: Current Chromatogram(s)

Data File : C:\CHEM32\1\DATA\2018 TO MAR 07\020218\013118_4PF3-PH7-13CBTNAC_1.D

Sample Name : 013118_4PF3-ph7-13CBTNAC_1

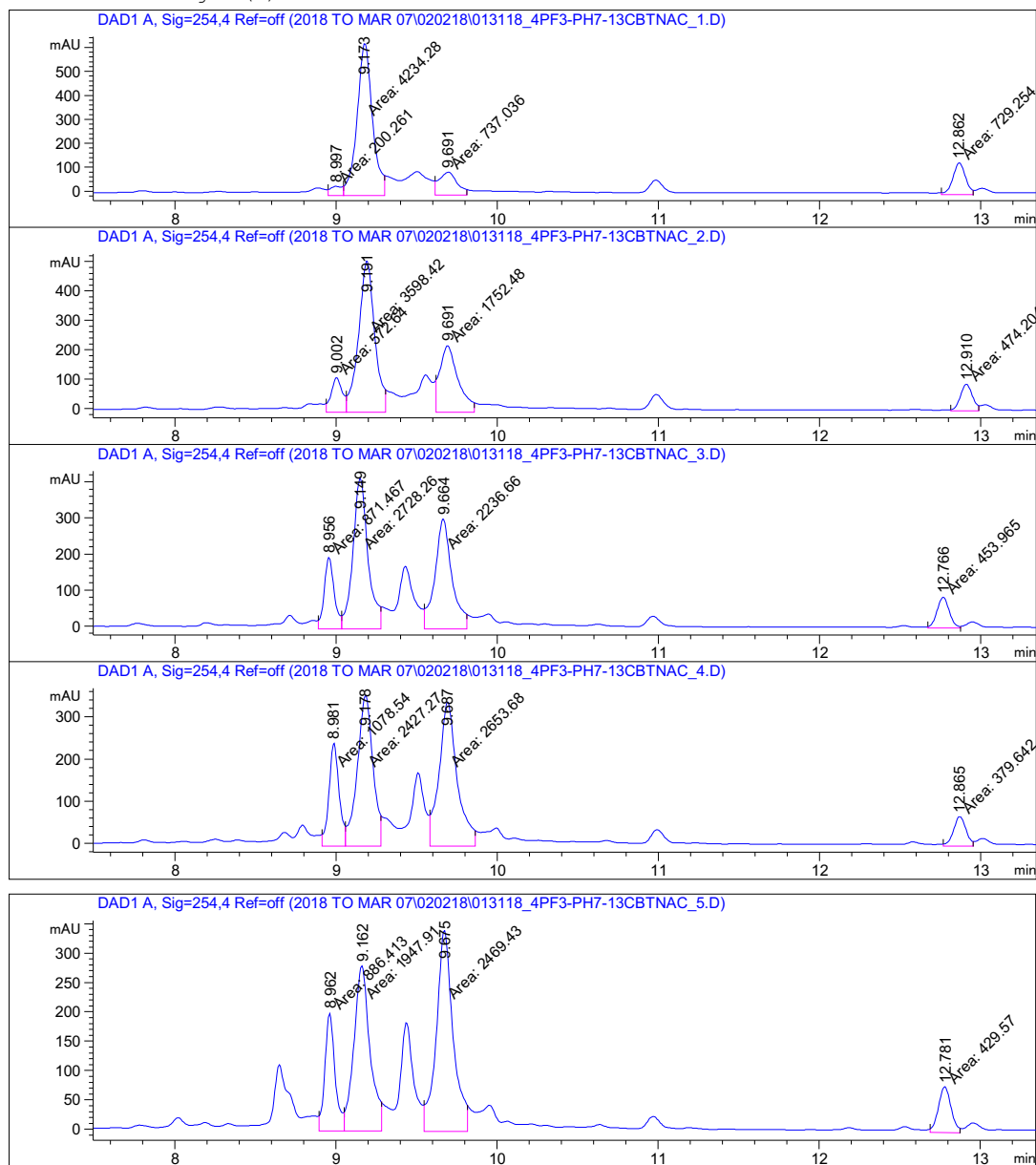
=====
Acq. Operator : SGLK Seq. Line : 6
Acq. Instrument : Instrument 1 Location : Vial 6
Injection Date : 2/2/18 7:16:34 PM Inj : 1
Inj Volume : 1.000 µl

Acq. Method : D:\CHEM32\1\METHODS\AP_C18_INSERT.M
Last changed : 1/22/18 3:04:38 PM by SGLK
Analysis Method : Z:\DESKTOP\BERTOZZI LAB\LCMS INFO\LCMS METHODS TO 112917\SGLK_BERTOZZI_BP_WITHINSERT.M

Last changed : 3/8/18 8:51:08 AM
(modified after loading)

Additional Info : Peak(s) manually integrated

Current Chromatogram(s)



Data File C:\CHEM32\1\DATA\2018 TO MAR 07\020218\013118_4PF3-PH7-13CBTNAC_1.D
 Sample Name: 013118_4PF3-ph7-13CBTNac_1

=====
 Integration Results
 =====

Signal 1: DAD1 A, Sig=254,4 Ref=off (2018 TO MAR 07\020218\013118_4PF3-PH7-13CBTNAC_1.D)

Peak #	Time [min]	Type	Area [mAU*s]	Height [mAU]	Width [min]	Start [min]	End [min]
1	8.997	MF	200.26137	38.45741	0.0868	8.950	9.045
2	9.173	MF	4234.27588	634.43121	0.1112	9.045	9.299
3	9.691	MF	737.03558	96.44783	0.1274	9.614	9.811
4	12.862	MF	729.25427	132.65248	0.0916	12.754	12.951

Signal 2: DAD1 A, Sig=254,4 Ref=off (2018 TO MAR 07\020218\013118_4PF3-PH7-13CBTNAC_2.D)

Peak #	Time [min]	Type	Area [mAU*s]	Height [mAU]	Width [min]	Start [min]	End [min]
1	9.002	FM	572.63983	118.38261	0.0806	8.938	9.062
2	9.191	FM	3598.41650	516.68695	0.1161	9.062	9.304
3	9.691	FM	1752.47876	226.24167	0.1291	9.619	9.856
4	12.910	MF	474.20395	90.58943	0.0872	12.811	12.985

Signal 3: DAD1 A, Sig=254,4 Ref=off (2018 TO MAR 07\020218\013118_4PF3-PH7-13CBTNAC_3.D)

Peak #	Time [min]	Type	Area [mAU*s]	Height [mAU]	Width [min]	Start [min]	End [min]
1	8.956	FM	871.46686	199.60472	0.0728	8.888	9.034
2	9.149	FM	2728.26025	419.56812	0.1084	9.034	9.276
3	9.664	FM	2236.65991	306.16095	0.1218	9.546	9.811
4	12.766	FM	453.96454	85.18710	0.0888	12.670	12.873

Signal 4: DAD1 A, Sig=254,4 Ref=off (2018 TO MAR 07\020218\013118_4PF3-PH7-13CBTNAC_4.D)

Peak #	Time [min]	Type	Area [mAU*s]	Height [mAU]	Width [min]	Start [min]	End [min]
1	8.981	FM	1078.54163	244.56328	0.0735	8.910	9.057
2	9.178	FM	2427.26831	358.23096	0.1129	9.057	9.276
3	9.687	FM	2653.67725	342.92633	0.1290	9.580	9.861
4	12.865	FM	379.64224	70.02226	0.0904	12.766	12.951

Signal 5: DAD1 A, Sig=254,4 Ref=off (2018 TO MAR 07\020218\013118_4PF3-PH7-13CBTNAC_5.D)

Peak #	Time [min]	Type	Area [mAU*s]	Height [mAU]	Width [min]	Start [min]	End [min]
1	8.962	MF	886.41290	200.69423	0.0736	8.893	9.051
2	9.162	MF	1947.91333	281.73981	0.1152	9.051	9.282
3	9.675	MF	2469.42773	342.71152	0.1201	9.546	9.816
4	12.781	MF	429.56952	78.42221	0.0913	12.687	12.873

LC-MS spectra (compound purity)

All extracted mass ions correspond to $[M + H]^+$ or $[M - H]^-$ for the given compound unless labeled otherwise.

S63-S64	CBTNAc (1)
S65-S66	CIBTNAc (2)
S67-S68	¹³ CBTNAc (3)
S69-S70	CBTag 1.0 (4)
S71-S72	PEP-FOLD-4 (5)
S73	Blank (no injection) – background noise (MS+) in spectra for compounds 6-21
S74-S105	PEP-FOLD-1, -2, -5, -6, -7, -8, -9, -11, -12, -13, -14, -15, -16, -17, -18, -19 (6-21)
S106-S107	CBTag 1.0 (K9R) (22)
S108-S109	CBTag 1.0 (C7S) (23)
S110-S111	CBTag 1.0- ¹³ CBTNAc (amidine) (24)

CBTNAc (1)

Data File C:\CHEM32\1\DATA\2018 TO MAR 07\030718_CBTNAC_LC.D

Sample Name: 030718_CBTNAC_LC

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Acq. Operator : SGLK	Seq. Line : 5
Acq. Instrument : Instrument 1	Location : Vial 13
Injection Date : 3/7/18 3:16:46 PM	Inj : 1
	Inj Volume : 1.000 µl

Different Inj Volume from Sequence ! Actual Inj Volume : 5.000 µl

Acq. Method : D:\CHEM32\1\METHODS\AP_C18_INSERT.M

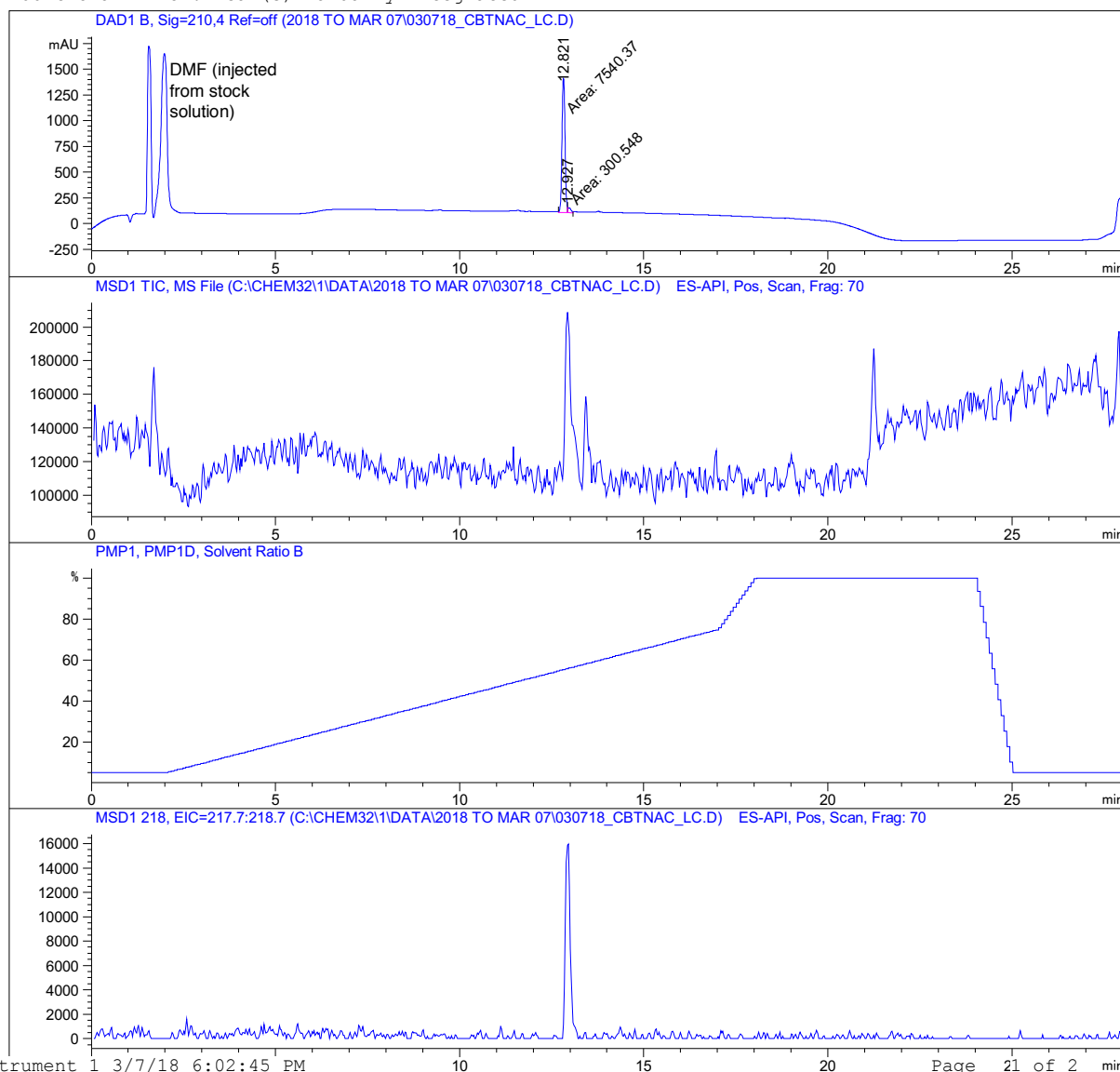
Last changed : 3/2/18 3:32:17 PM by CLM

Analysis Method : Z:\DESKTOP\BERTOZZI LAB\LCMS INFO\LCMS METHODS TO 112917\SGLK_BERTOZZIBP_WITHINSERT.M

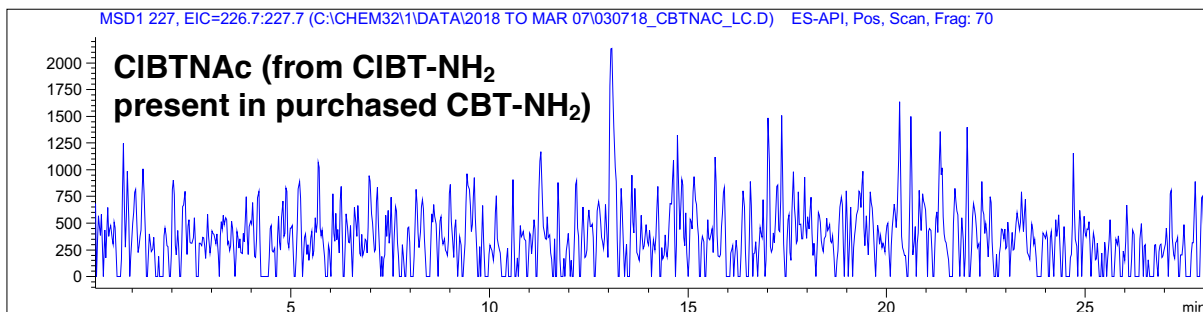
Last changed : 3/6/18 6:13:20 PM

(modified after loading)

Additional Info : Peak(s) manually integrated



Data File C:\CHEM32\1\DATA\2018 TO MAR 07\030718_CBTNAC_LC.D
Sample Name: 030718_CBTNac_LC



=====
Area Percent Report
=====

Sorted By : Signal
Multiplier: : 1.0000
Dilution: : 1.0000
Do not use Multiplier & Dilution Factor with ISTDs

Signal 1: DAD1 B, Sig=210,4 Ref=off

Peak #	RetTime [min]	Type	Width [min]	Area [mAU*s]	Height [mAU]	Area %
1	12.821	MF	0.0964	7540.36719	1303.94641	96.1669
2	12.927	FM	0.0870	300.54807	49.86433	3.8331

Totals : 7840.91525 1353.81074

Signal 2: MSD1 TIC, MS File

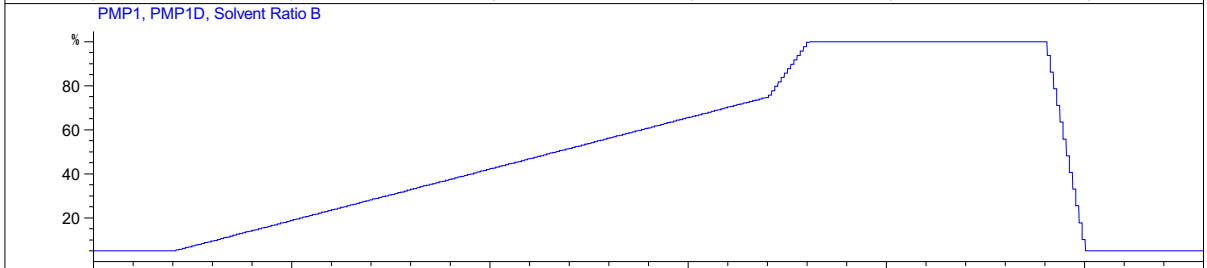
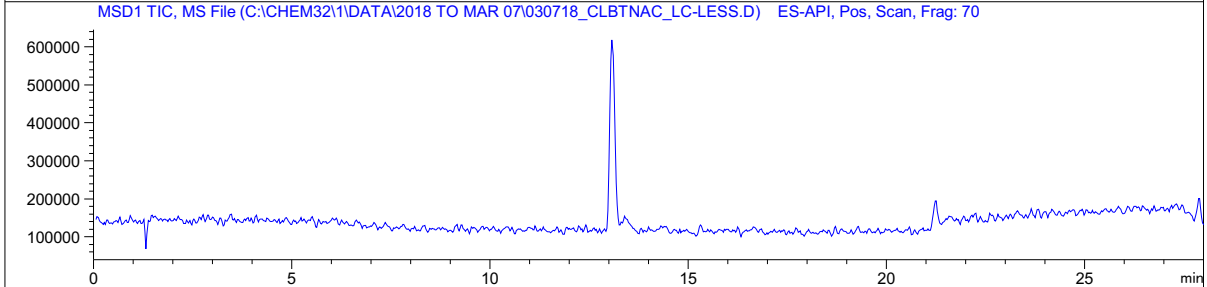
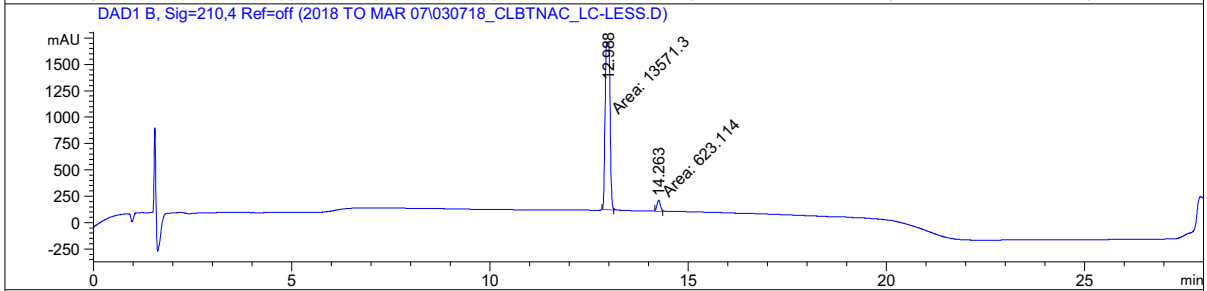
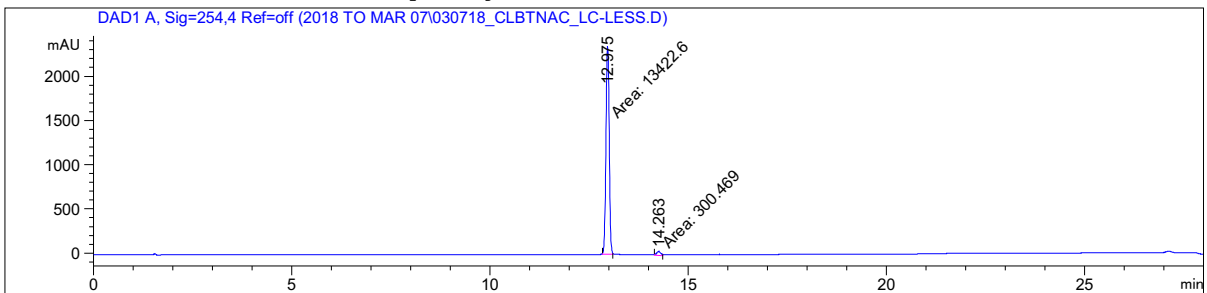
=====
*** End of Report ***

CIBTNAC (2)

Data File C:\CHEM32\1\DATA\2018 TO MAR 07\030718_CLBTNAC_LC-LESS.D

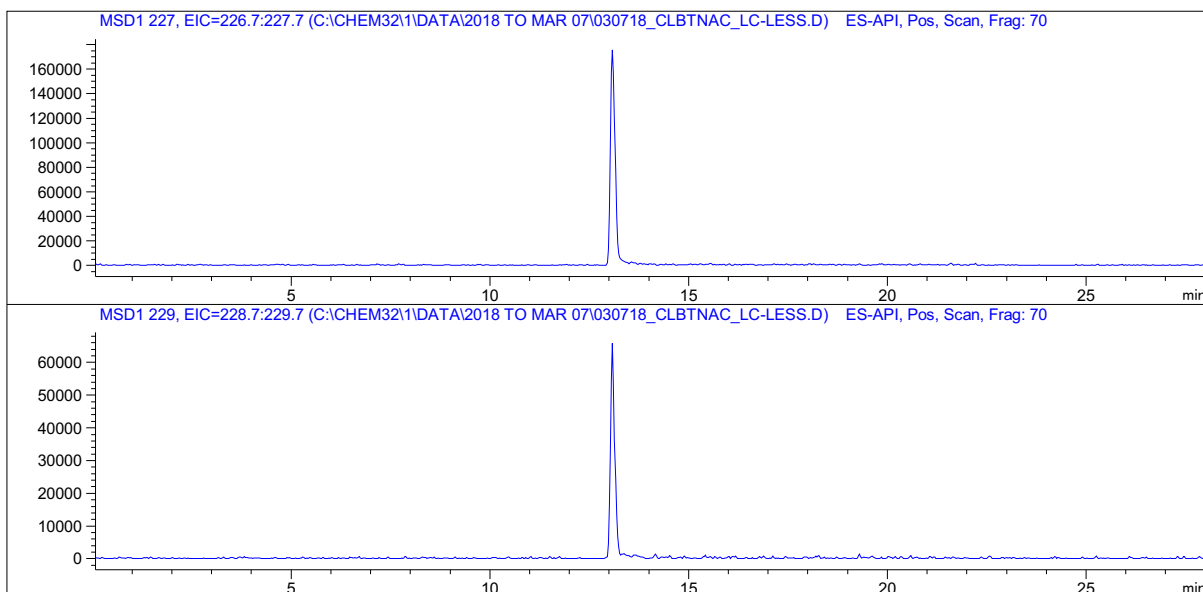
Sample Name: 030718_C1BTNAC_LC-less

```
=====
Acq. Operator   : SGLK                               Seq. Line :    4
Acq. Instrument : Instrument 1                       Location  : Vial 11
Injection Date  : 3/7/18 2:47:36 PM                 Inj       :    1
                                                    Inj Volume: 1.000 µl
Different Inj Volume from Sequence !   Actual Inj Volume : 5.000 µl
Acq. Method    : D:\CHEM32\1\METHODS\AP_C18_INSERT.M
Last changed   : 3/2/18 3:32:17 PM by CLM
Analysis Method : Z:\DESKTOP\BERTOZZI LAB\LCMS INFO\LCMS METHODS TO 112917\SGLK_BERTOZZIBP_
                WITHINSERT.M
Last changed   : 3/6/18 6:13:20 PM
                (modified after loading)
Additional Info : Peak(s) manually integrated
=====
```



Instrument 1 3/7/18 5:48:01 PM Page 21 of 3 min

Data File C:\CHEM32\1\DATA\2018 TO MAR 07\030718_CLBTNAC_LC-LESS.D
 Sample Name: 030718_ClBTNac_LC-less



=====
 Area Percent Report
 =====

Sorted By : Signal
 Multiplier: : 1.0000
 Dilution: : 1.0000
 Do not use Multiplier & Dilution Factor with ISTDs

Signal 1: DAD1 A, Sig=254,4 Ref=off

Peak #	RetTime [min]	Type	Width [min]	Area [mAU*s]	Height [mAU]	Area %
1	12.975	MM	0.0949	1.34226e4	2356.18262	97.8105
2	14.263	MM	0.1172	300.46902	42.71576	2.1895

Totals : 1.37231e4 2398.89838

Signal 2: DAD1 B, Sig=210,4 Ref=off

Peak #	RetTime [min]	Type	Width [min]	Area [mAU*s]	Height [mAU]	Area %
1	12.988	MM	0.1422	1.35713e4	1591.18579	95.6102
2	14.263	MM	0.0988	623.11401	105.09184	4.3898

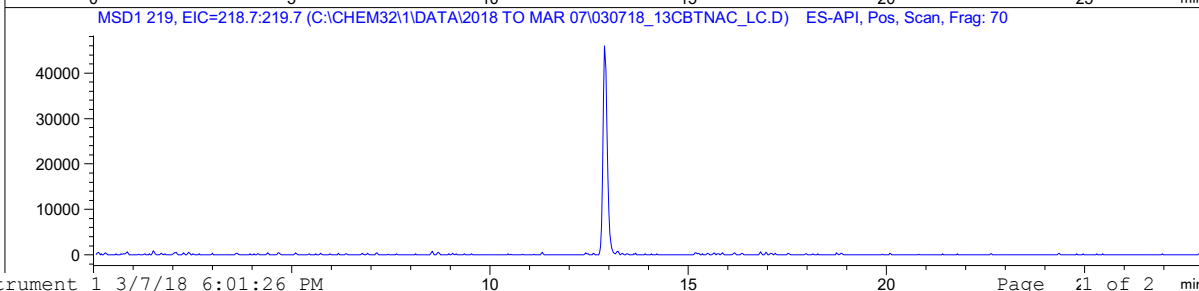
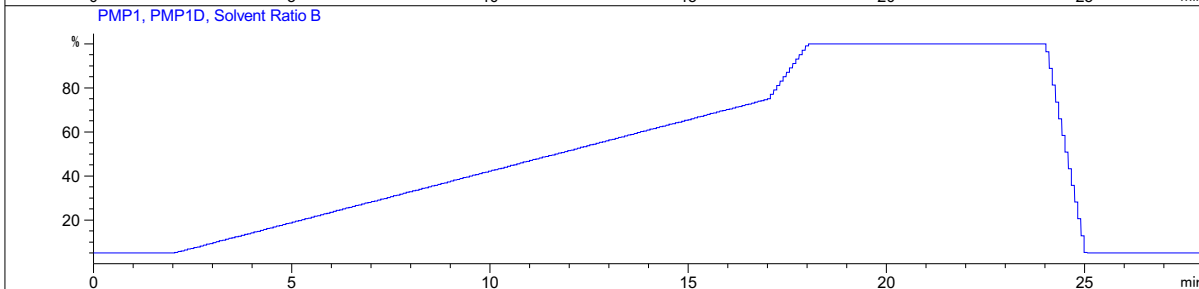
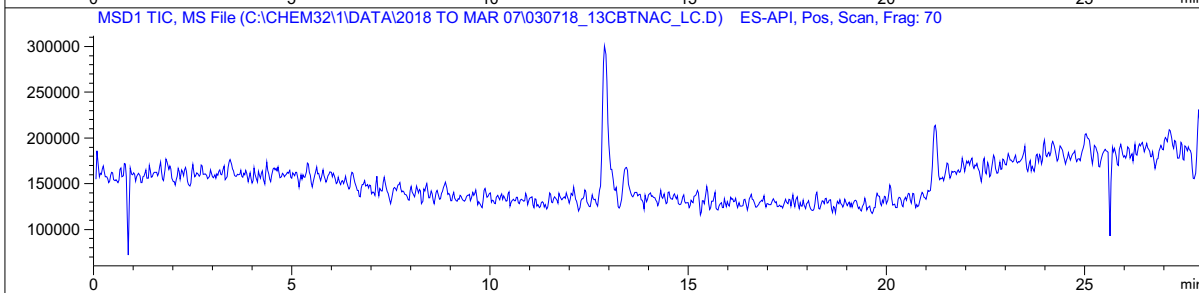
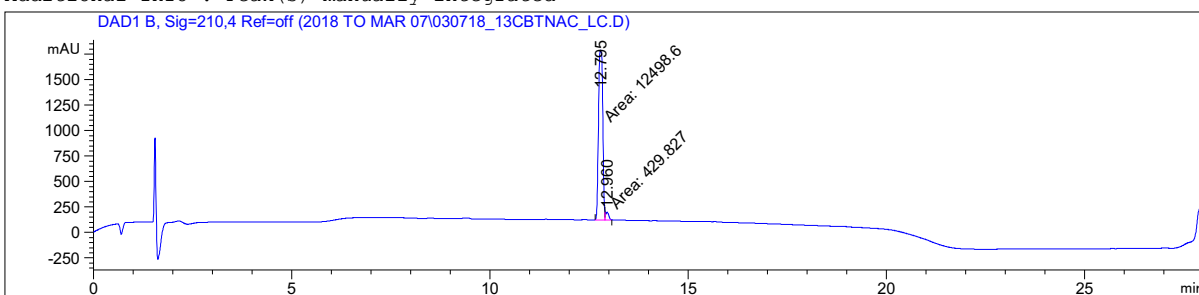
Totals : 1.41944e4 1696.27763

Signal 3: MSD1 TIC, MS File

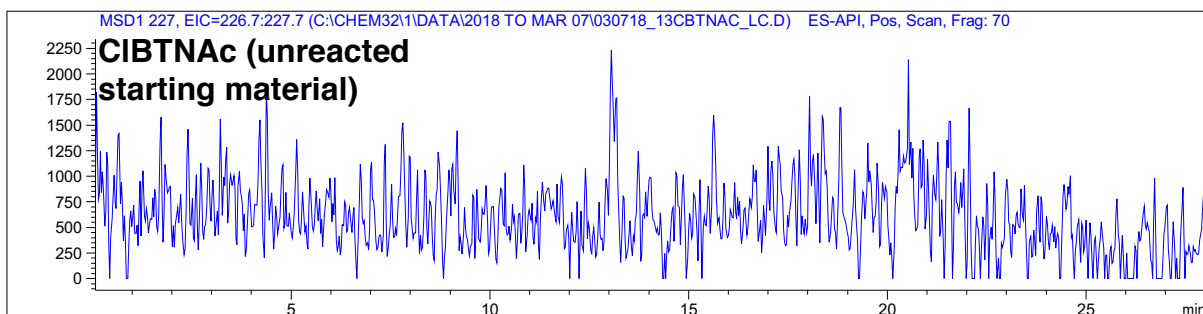
13CBTNAC (3)

Data File C:\CHEM32\1\DATA\2018 TO MAR 07\030718_13CBTNAC_LC.D
Sample Name: 030718_13CBTNAC_LC

```
=====
Acq. Operator   : SGLK                      Seq. Line :    2
Acq. Instrument : INSTRUMENT 1              Location  : Vial 12
Injection Date  : 3/7/18 1:49:08 PM         Inj       :    1
                                                Inj Volume: 1.000 µl
Different Inj Volume from Sequence !      Actual Inj Volume : 5.000 µl
Acq. Method     : D:\CHEM32\1\METHODS\AP_C18_INSERT.M
Last changed    : 3/2/18 3:32:17 PM by CLM
Analysis Method : Z:\DESKTOP\BERTOZZI LAB\LCMS INFO\LCMS METHODS TO 112917\SGLK_BERTOZZIBP_
                WITHINSERT.M
Last changed    : 3/6/18 6:13:20 PM
                (modified after loading)
Additional Info  : Peak(s) manually integrated
=====
```



Data File C:\CHEM32\1\DATA\2018 TO MAR 07\030718_13CBTNAC_LC.D
Sample Name: 030718_13CBTNAC_LC



=====
Area Percent Report
=====

Sorted By : Signal
Multiplier: : 1.0000
Dilution: : 1.0000
Do not use Multiplier & Dilution Factor with ISTDs

Signal 1: DAD1 B, Sig=210,4 Ref=off

Peak #	RetTime [min]	Type	Width [min]	Area [mAU*s]	Height [mAU]	Area %
1	12.795	MF	0.1249	1.24986e4	1667.93628	96.6753
2	12.960	FM	0.0927	429.82697	77.28518	3.3247

Totals : 1.29285e4 1745.22146

Signal 2: MSD1 TIC, MS File

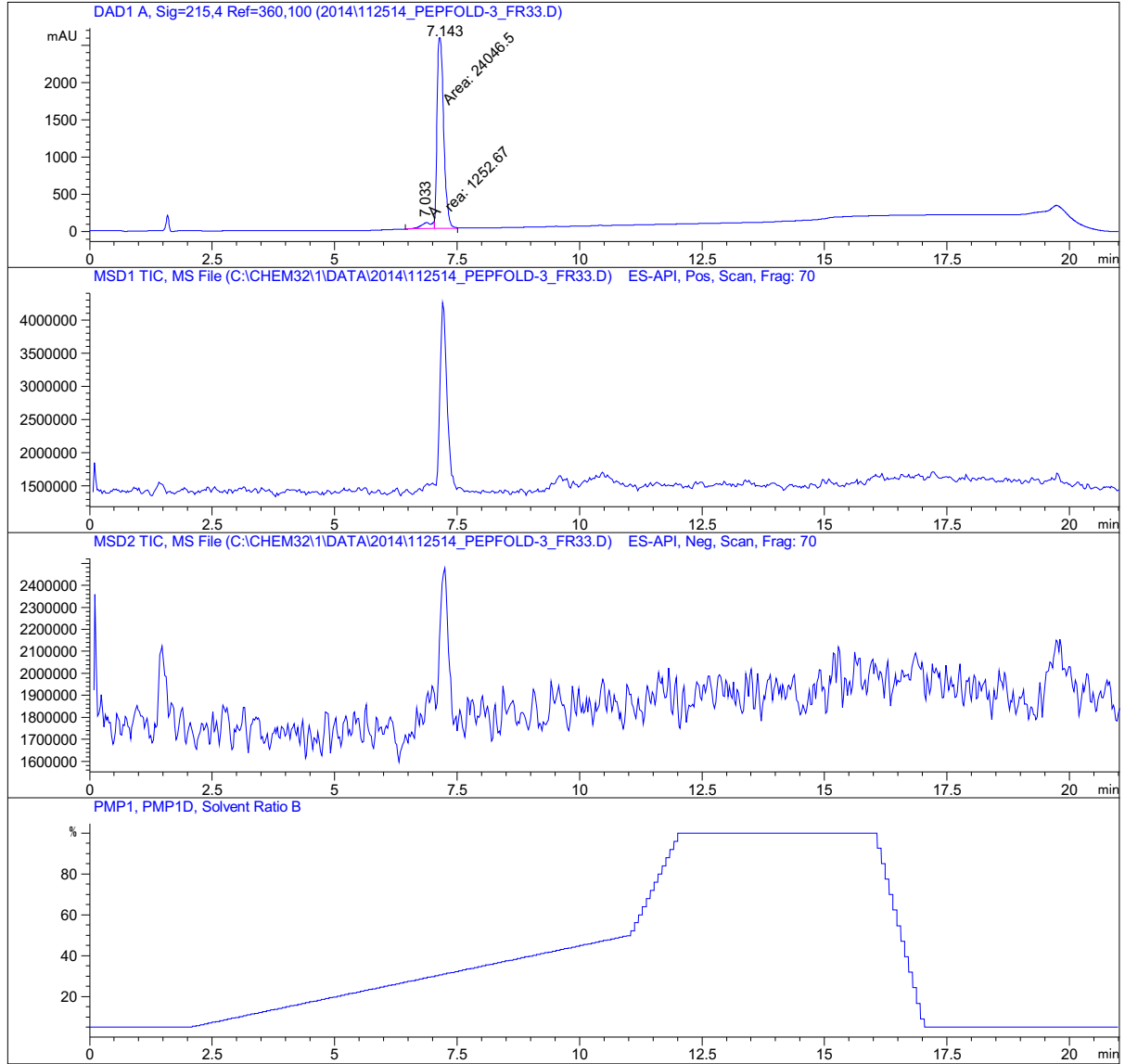
=====
*** End of Report ***

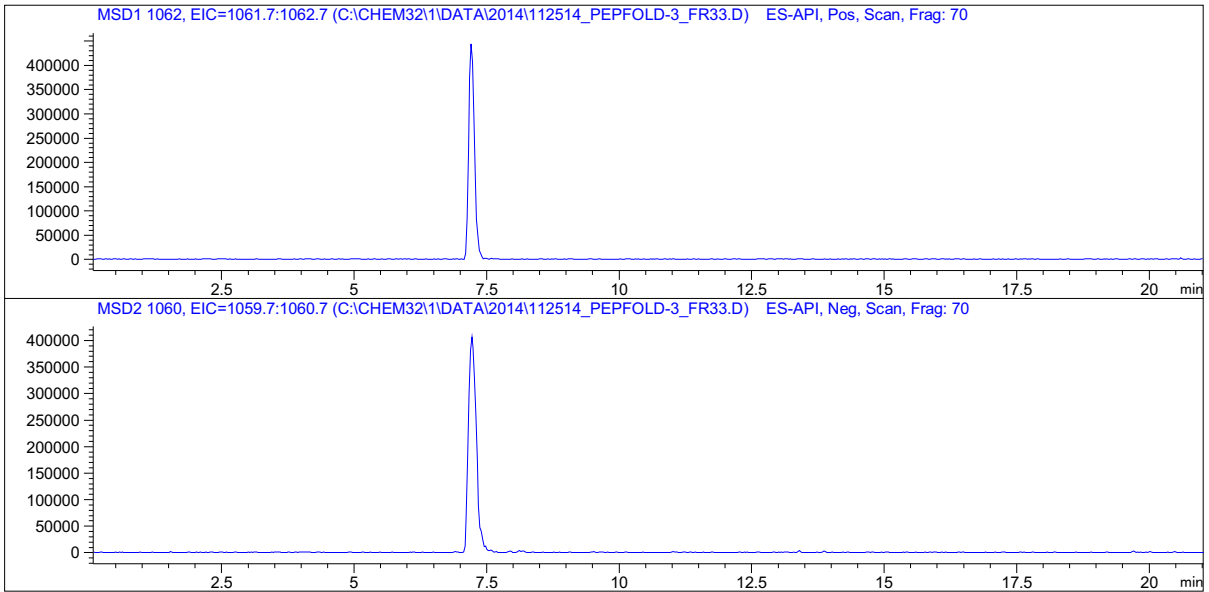
CBTag 1.0, Ac-GGHPDPCPKGG-NH₂ (4)

Acq. Method : D:\CHEM32\1\METHODS\SGLK_BERTOZZILC_PEP

Inj Volume : 25.000 µl

Additional Info : Peak(s) manually integrated





=====
 Area Percent Report
 =====

Signal 1: DAD1 A, Sig=215,4 Ref=360,100

Peak #	RetTime [min]	Type	Width [min]	Area [mAU*s]	Height [mAU]	Area %
1	7.033	MF	0.2265	1252.66980	92.18911	4.9514
2	7.143	FM	0.1564	2.40465e4	2562.40234	95.0486

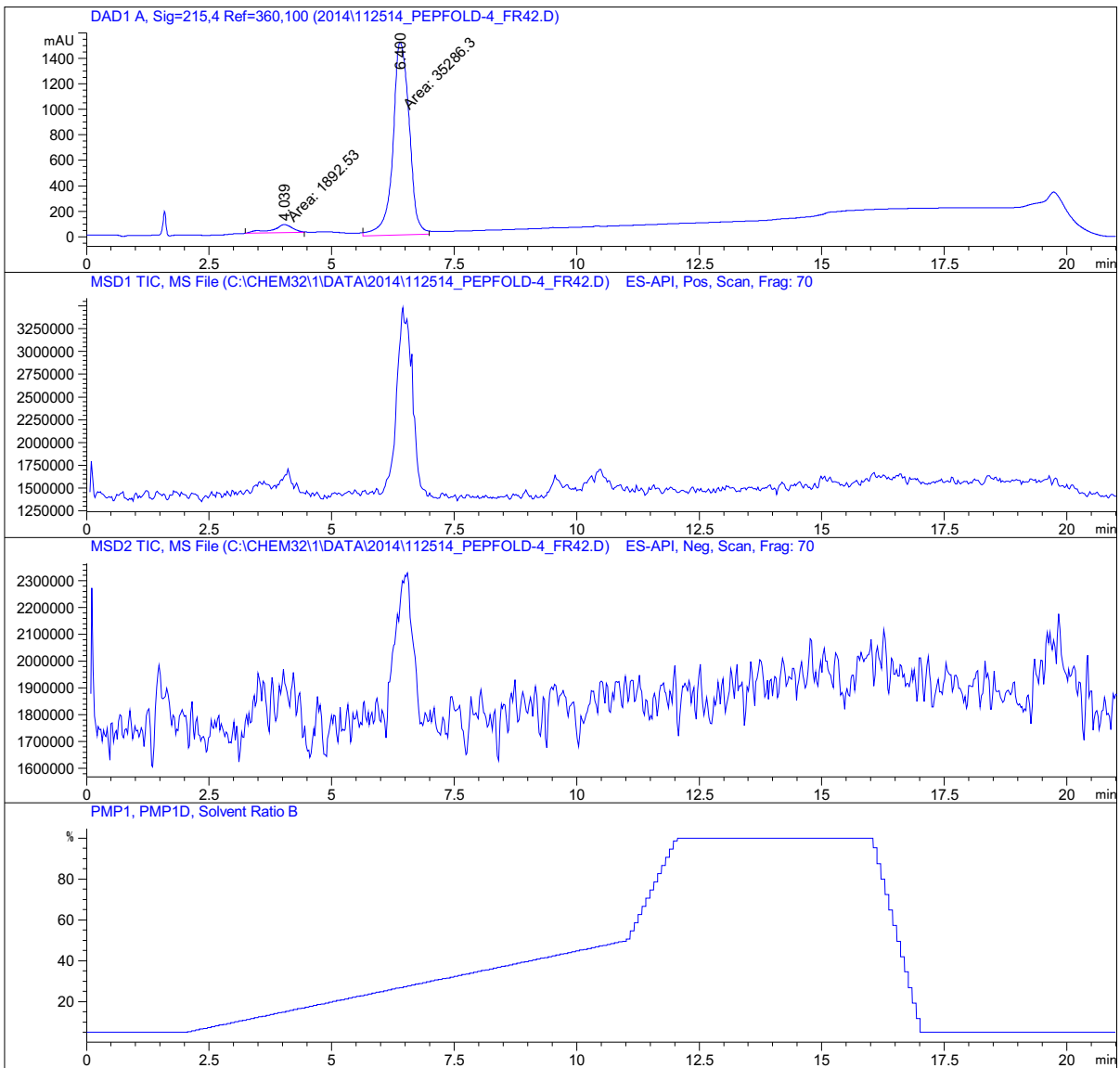
Totals : 2.52992e4 2654.59145

PEP-FOLD-4, Ac-GGDPHPCKGG-NH₂ (5)

Data File C:\CHEM32\1\DATA\2014\112514_PEPFOLD-4_FR42.D
Sample Name: 112514_PEPFOLD-4_fr42

```
=====
Acq. Operator   : EM                               Seq. Line :    4
Acq. Instrument : Instrument 1                     Location  : Vial 77
Injection Date  : 11/25/14 4:55:14 PM             Inj       :    1
                                                    Inj Volume: 25.000 µl

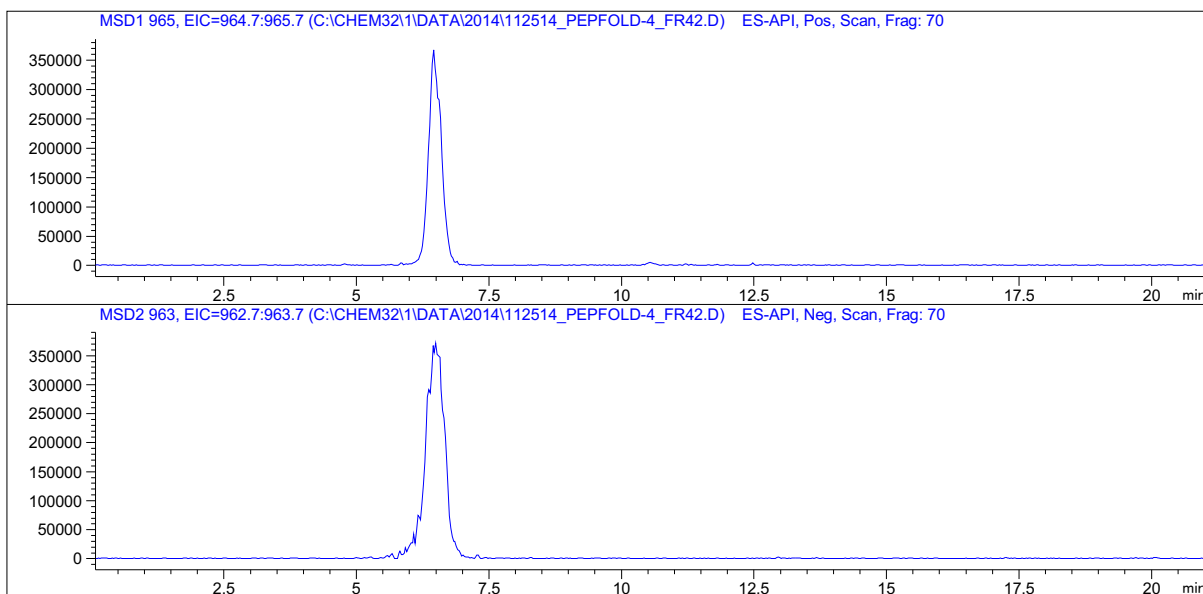
Acq. Method     : D:\CHEM32\1\METHODS\SGLK_BERTOZZILC_PEP
Last changed    : 11/25/14 3:41:49 PM by EM
Analysis Method : Z:\DESKTOP\BERTOZZI LAB\LCMS INFO\LCMS METHODS TO 112917\SGLK_BERTOZZIBP_
                WITHINSERT.M
Last changed    : 2/7/18 7:43:15 PM
                (modified after loading)
Additional Info : Peak(s) manually integrated
=====
```



Instrument 1 2/7/18 7:51:10 PM

Page 1 of 3

Data File C:\CHEM32\1\DATA\2014\112514_PEPFOLD-4_FR42.D
Sample Name: 112514_PEPFOLD-4_fr42



=====
Area Percent Report
=====

Sorted By : Signal
Multiplier: : 1.0000
Dilution: : 1.0000
Do not use Multiplier & Dilution Factor with ISTDs

Signal 1: DAD1 A, Sig=215,4 Ref=360,100

Peak #	RetTime [min]	Type	Width [min]	Area [mAU*s]	Height [mAU]	Area %
1	4.039	MM	0.4972	1892.52612	63.43561	5.0903
2	6.400	MM	0.3892	3.52863e4	1511.20435	94.9097

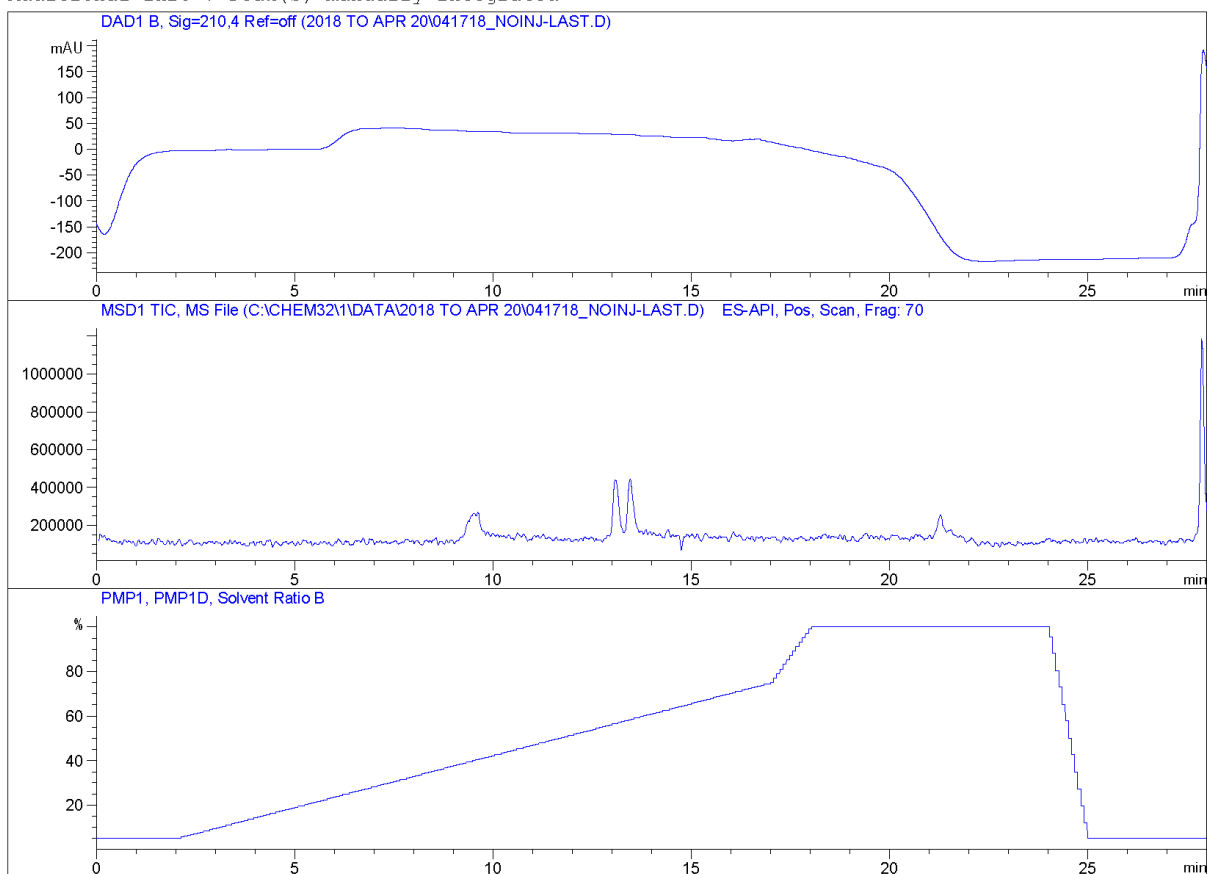
Totals : 3.71788e4 1574.63995

Signal 2: MSD1 TIC, MS File

Blank (no injection) – background MS peaks for compounds 6-21

Data File C:\CHEM32\1\DATA\2018 TO APR 20\041718_NOINJ-LAST.D
Sample Name: 041718_noinj-last

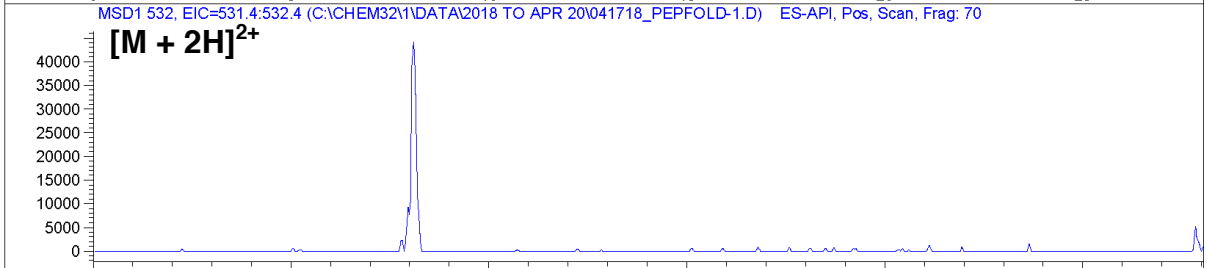
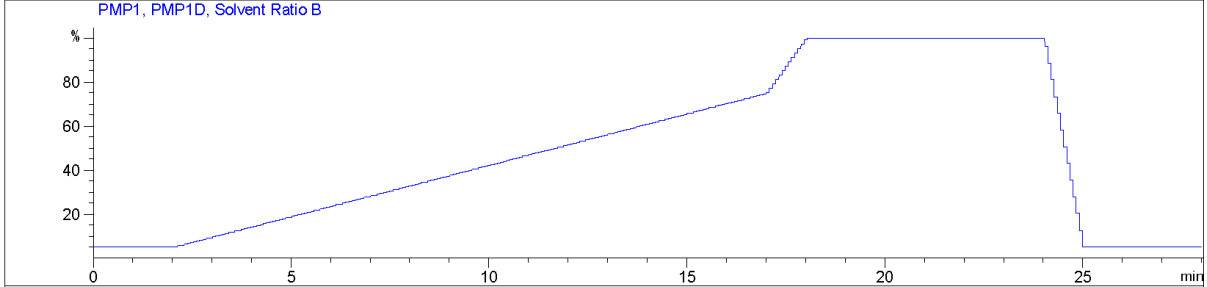
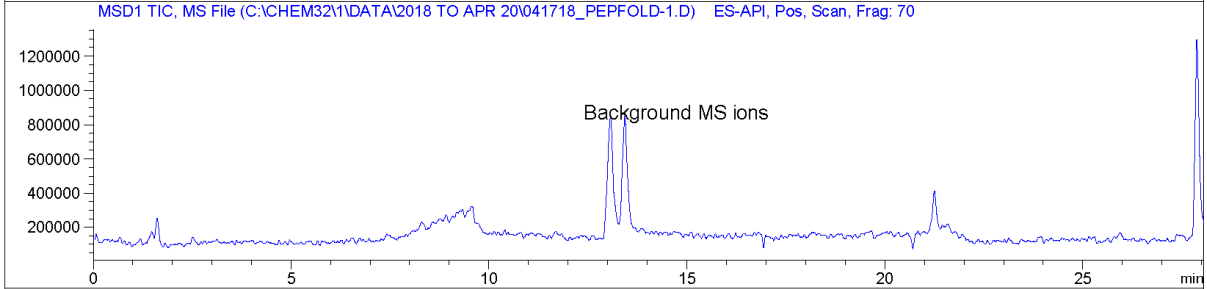
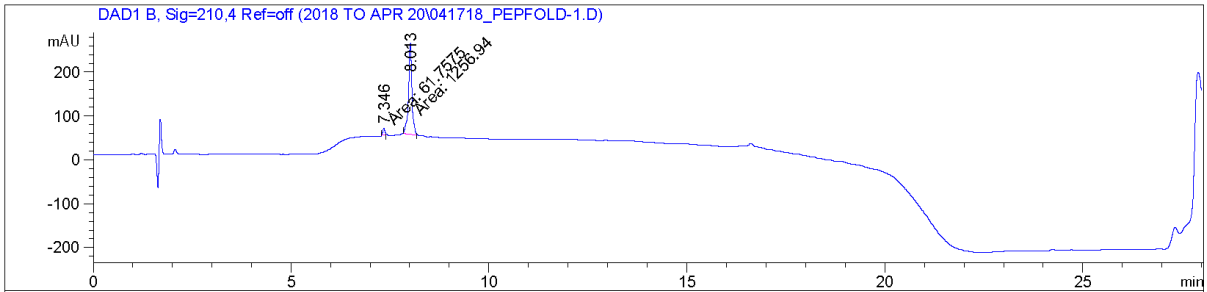
```
=====
Acq. Operator   : SGLK                               Seq. Line : 21
Acq. Instrument : Instrument 1                       Location  : Vial 80
Injection Date  : 4/17/18 9:15:18 PM                Inj       : 1
                                                    Inj Volume: 1.000 µl
Different Inj Volume from Sequence !   Actual Inj Volume : 0.000 µl
Acq. Method     : D:\CHEM32\1\METHODS\AP_C18_INSERT.M
Last changed    : 4/17/18 11:25:09 AM by SGLK
Analysis Method : Z:\DESKTOP\BERTOZZI LAB\LCMS INFO\LCMS METHODS TO 112917\SGLK_BERTOZZIBP_
                WITHINSERT.M
Last changed    : 4/26/18 12:19:51 PM
                (modified after loading)
Additional Info : Peak(s) manually integrated
=====
```



PEP-FOLD-1, Ac-GGDPCPHPKGG-NH₂ (6)

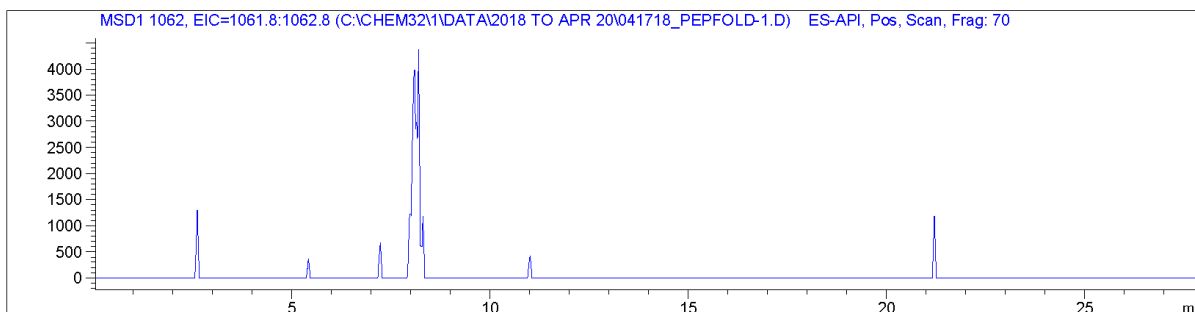
Data File C:\CHEM32\1\DATA\2018 TO APR 20\041718_PEPFOLD-1.D
Sample Name: 041718_pepfold-1

```
=====
Acq. Operator   : SGLK                      Seq. Line :    1
Acq. Instrument : Instrument 1              Location  : Vial 61
Injection Date  : 4/17/18 11:30:06 AM      Inj       :    1
                                                Inj Volume: 1.000 µl
Different Inj Volume from Sequence !      Actual Inj Volume : 2.000 µl
Acq. Method     : D:\CHEM32\1\METHODS\AP_C18_INSERT.M
Last changed    : 4/17/18 11:25:09 AM by SGLK
Analysis Method : Z:\DESKTOP\BERTOZZI LAB\LCMS INFO\LCMS METHODS TO 112917\SGLK_BERTOZZIBP_
                WITHINSERT.M
Last changed    : 4/26/18 11:40:30 AM
                (modified after loading)
Additional Info : Peak(s) manually integrated
=====
```



Instrument 1 4/26/18 11:48:23 AM Page 21 of 2

Data File C:\CHEM32\1\DATA\2018 TO APR 20\041718_PEPFOLD-1.D
Sample Name: 041718_pepfold-1



=====
Area Percent Report
=====

Sorted By : Signal
Multiplier: : 1.0000
Dilution: : 1.0000
Do not use Multiplier & Dilution Factor with ISTDs

Signal 1: DAD1 B, Sig=210,4 Ref=off

Peak #	RetTime [min]	Type	Width [min]	Area [mAU*s]	Height [mAU]	Area %
1	7.346	MM	0.0631	61.75753	16.30812	4.6832
2	8.013	MM	0.1000	1256.93677	209.44200	95.3168

Totals : 1318.69430 225.75012

Signal 2: MSD1 TIC, MS File

Signal 3: MSD1 532, EIC=531.4:532.4

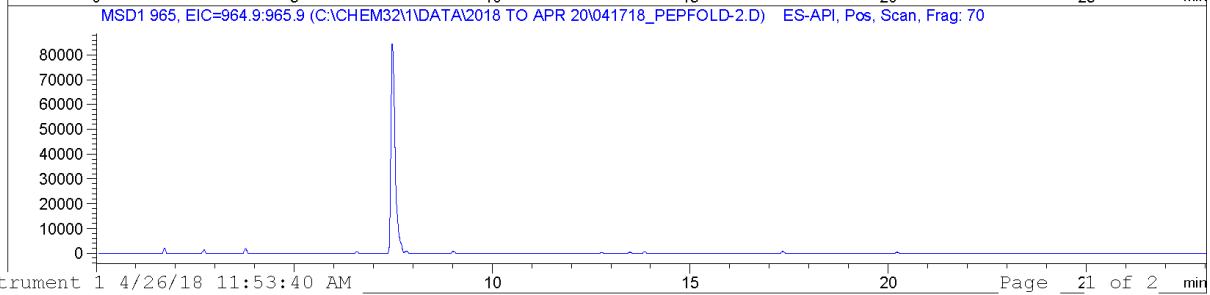
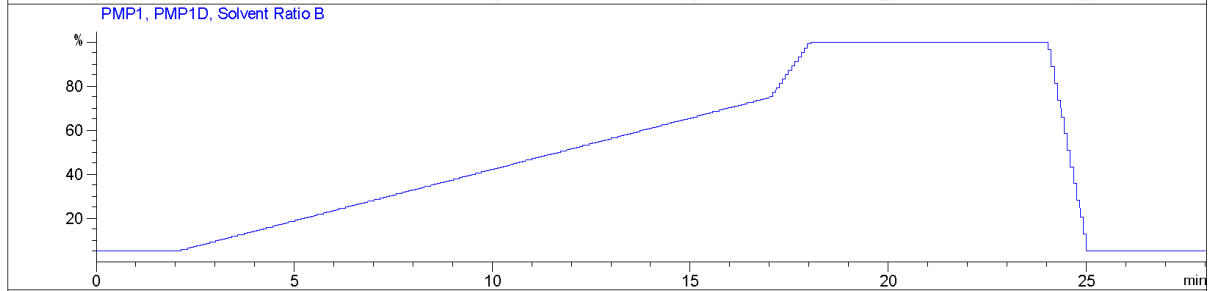
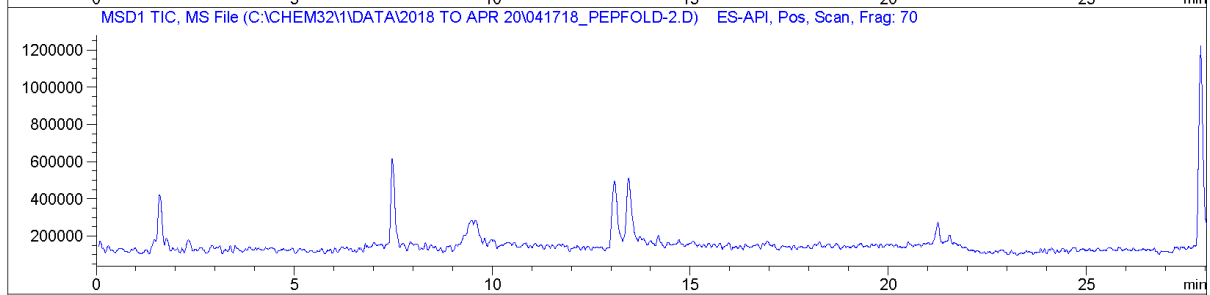
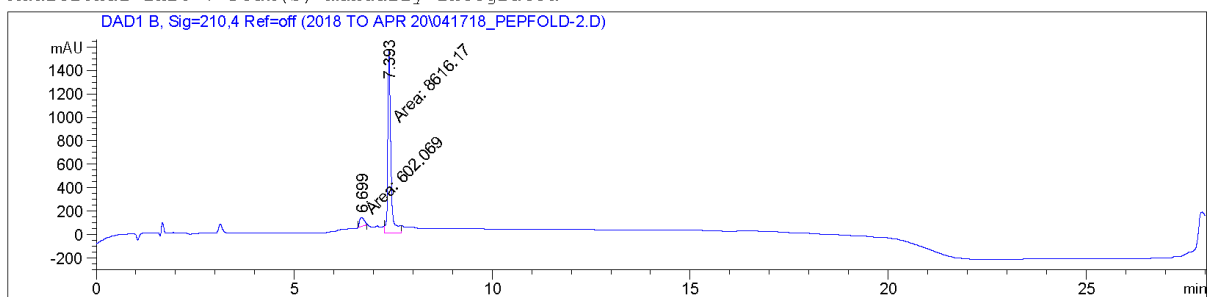
Signal 4: MSD1 1062, EIC=1061.8:1062.8

=====
*** End of Report ***

PEP-FOLD-2, Ac-GGHPDCPKGG-NH₂ (7)

Data File C:\CHEM32\1\DATA\2018 TO APR 20\041718_PEPFOLD-2.D
Sample Name: 041718_pepfold-2

```
=====
Acq. Operator   : SGLK                      Seq. Line :    2
Acq. Instrument : Instrument 1              Location  : Vial 62
Injection Date  : 4/17/18 11:59:24 AM      Inj       :    1
                                                Inj Volume: 1.000 µl
Different Inj Volume from Sequence !      Actual Inj Volume : 2.000 µl
Acq. Method     : D:\CHEM32\1\METHODS\AP_C18_INSERT.M
Last changed    : 4/17/18 11:25:09 AM by SGLK
Analysis Method : Z:\DESKTOP\BERTOZZI LAB\LCMS INFO\LCMS METHODS TO 112917\SGLK_BERTOZZIBP_
                WITHINSERT.M
Last changed    : 4/26/18 11:40:30 AM
                (modified after loading)
Additional Info : Peak(s) manually integrated
=====
```



Instrument 1 4/26/18 11:53:40 AM Page 21 of 2 min

Data File C:\CHEM32\1\DATA\2018 TO APR 20\041718_PEPFOLD-2.D
Sample Name: 041718_pepfold-2

=====
Area Percent Report
=====

Sorted By : Signal
Multiplier: : 1.0000
Dilution: : 1.0000
Do not use Multiplier & Dilution Factor with ISTDs

Signal 1: DAD1 B, Sig=210,4 Ref=off

Peak #	RetTime [min]	Type	Width [min]	Area [mAU*s]	Height [mAU]	Area %
1	6.699	MM	0.1309	602.06927	76.66061	6.5313
2	7.393	MM	0.0916	8616.17383	1568.30005	93.4687

Totals : 9218.24310 1644.96066

Signal 2: MSD1 TIC, MS File

Signal 3: MSD1 965, EIC=964.9:965.9

=====
*** End of Report ***

PEP-FOLD-5, Ac-GGHPEPCPKGG-NH₂ (8)

Data File C:\CHEM32\1\DATA\2018 TO APR 20\041718_PEPFOLD-5.D
Sample Name: 041718_pepfold-5

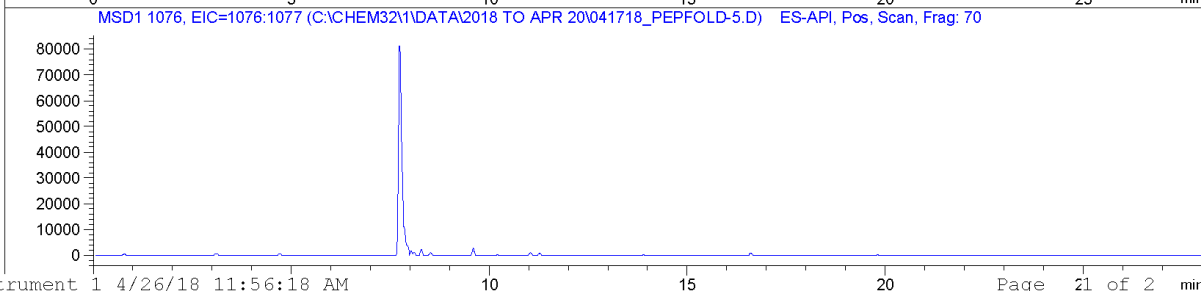
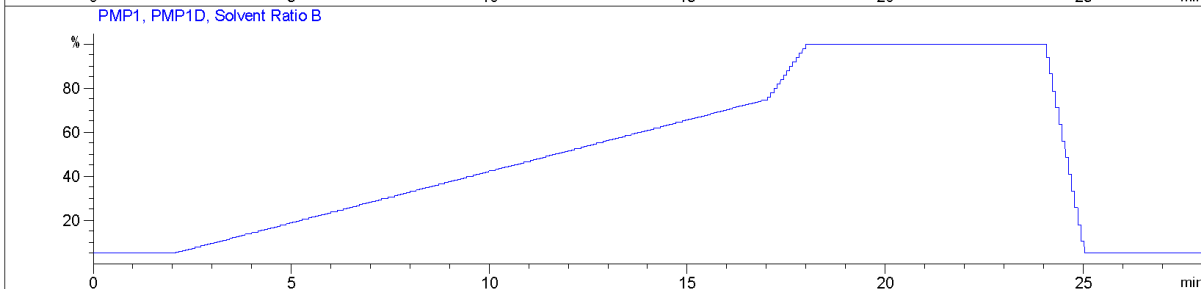
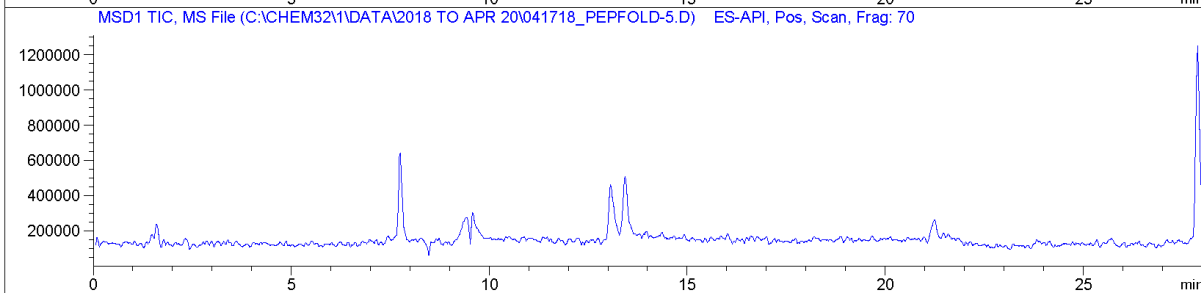
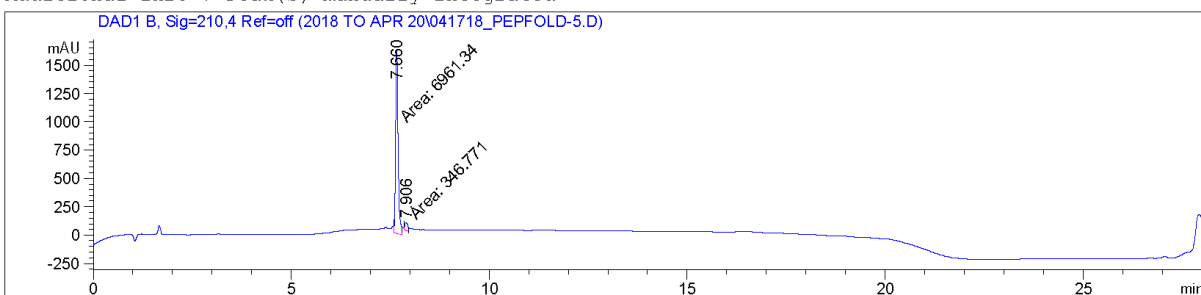
=====

Acq. Operator	: SGLK	Seq. Line	: 5
Acq. Instrument	: Instrument 1	Location	: Vial 65
Injection Date	: 4/17/18 1:27:08 PM	Inj	: 1
		Inj Volume	: 1.000 µl

Different Inj Volume from Sequence ! Actual Inj Volume : 2.000 µl

Acq. Method	: D:\CHEM32\1\METHODS\AP_C18_INSERT.M
Last changed	: 4/17/18 11:25:09 AM by SGLK
Analysis Method	: Z:\DESKTOP\BERTOZZI LAB\LCMS INFO\LCMS METHODS TO 112917\SGLK_BERTOZZIBP_WITHINSERT.M
Last changed	: 4/26/18 11:40:30 AM (modified after loading)

Additional Info : Peak(s) manually integrated



Data File C:\CHEM32\1\DATA\2018 TO APR 20\041718_PEPFOLD-5.D
Sample Name: 041718_pepfold-5

=====
Area Percent Report
=====

Sorted By : Signal
Multiplier: : 1.0000
Dilution: : 1.0000
Do not use Multiplier & Dilution Factor with ISTDs

Signal 1: DAD1 B, Sig=210,4 Ref=off

Peak #	RetTime [min]	Type	Width [min]	Area [mAU*s]	Height [mAU]	Area %
1	7.660	MM	0.0715	6961.34277	1623.41699	95.2550
2	7.906	MM	0.0808	346.77087	71.53614	4.7450

Totals : 7308.11365 1694.95313

Signal 2: MSD1 TIC, MS File

Signal 3: MSD1 1076, EIC=1076:1077

=====
*** End of Report ***

PEP-FOLD-6, Ac-GGHPECPKGG-NH₂ (9)

Data File C:\CHEM32\1\DATA\2018 TO APR 20\041718_PEPFOLD-6.D
Sample Name: 041718_pepfold-6

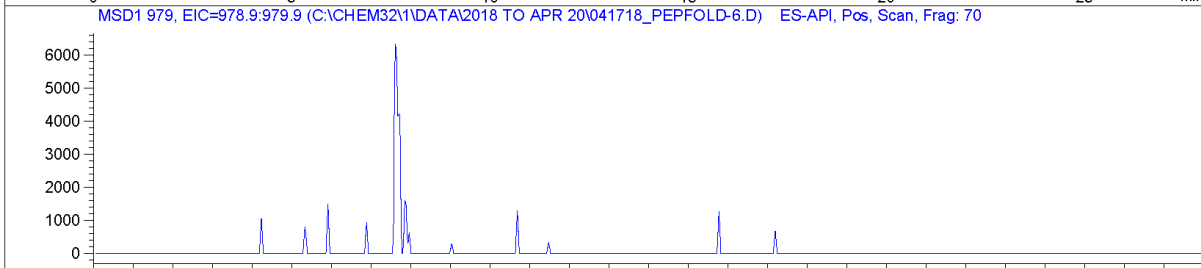
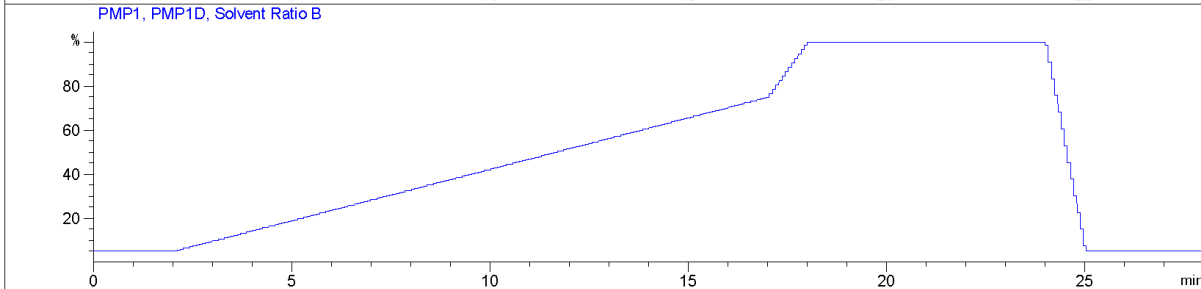
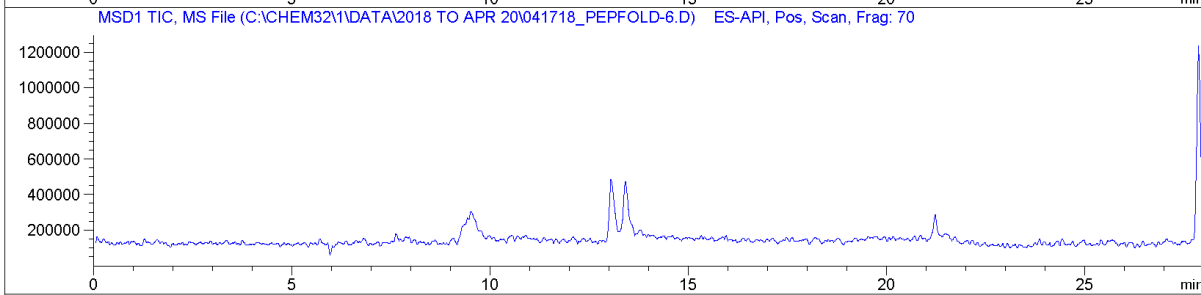
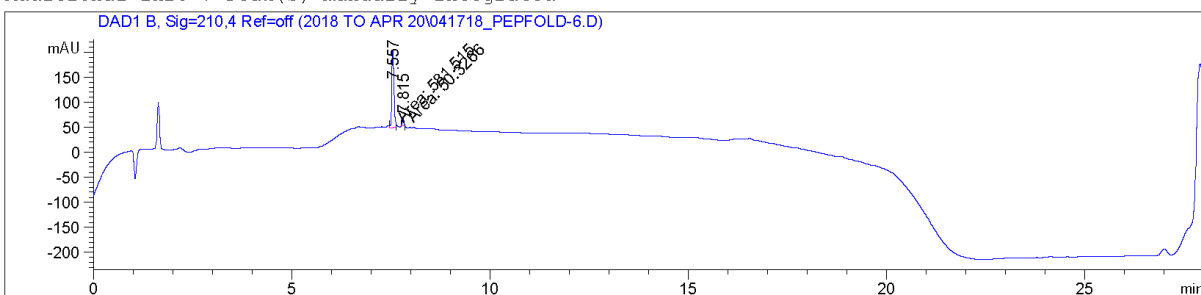
=====

Acq. Operator	: SGLK	Seq. Line	: 6
Acq. Instrument	: Instrument 1	Location	: Vial 66
Injection Date	: 4/17/18 1:56:26 PM	Inj	: 1
		Inj Volume	: 1.000 µl

Different Inj Volume from Sequence ! Actual Inj Volume : 2.000 µl

Acq. Method	: D:\CHEM32\1\METHODS\AP_C18_INSERT.M
Last changed	: 4/17/18 11:25:09 AM by SGLK
Analysis Method	: Z:\DESKTOP\BERTOZZI LAB\LCMS INFO\LCMS METHODS TO 112917\SGLK_BERTOZZIBP_WITHINSERT.M
Last changed	: 4/26/18 11:40:30 AM (modified after loading)

Additional Info : Peak(s) manually integrated



Data File C:\CHEM32\1\DATA\2018 TO APR 20\041718_PEPFOLD-6.D
Sample Name: 041718_pepfold-6

=====
Area Percent Report
=====

Sorted By : Signal
Multiplier: : 1.0000
Dilution: : 1.0000
Do not use Multiplier & Dilution Factor with ISTDs

Signal 1: DAD1 B, Sig=210,4 Ref=off

Peak #	RetTime [min]	Type	Width [min]	Area [mAU*s]	Height [mAU]	Area %
1	7.557	MM	0.0617	581.51514	157.19263	92.0349
2	7.815	MM	0.0495	50.32655	16.94779	7.9651

Totals : 631.84169 174.14042

Signal 2: MSD1 TIC, MS File

=====
*** End of Report ***

PEP-FOLD-7, Ac-GGEPHPCPKGG-NH₂ (10)

Data File C:\CHEM32\1\DATA\2018 TO APR 20\041718_PEPFOLD-7.D
Sample Name: 041718_pepfold-7

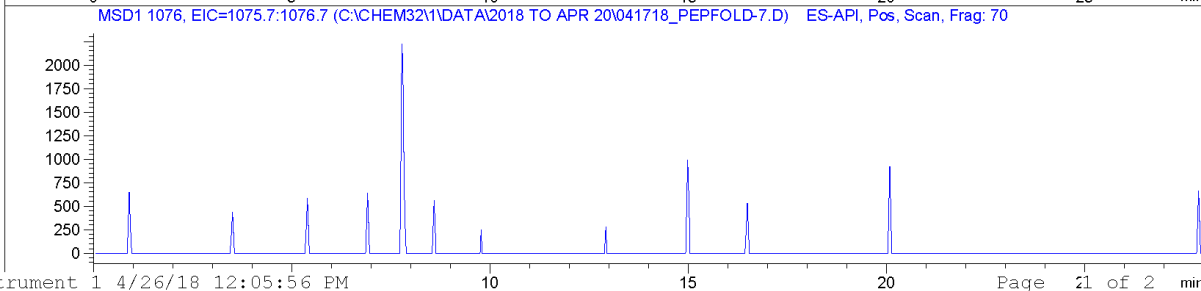
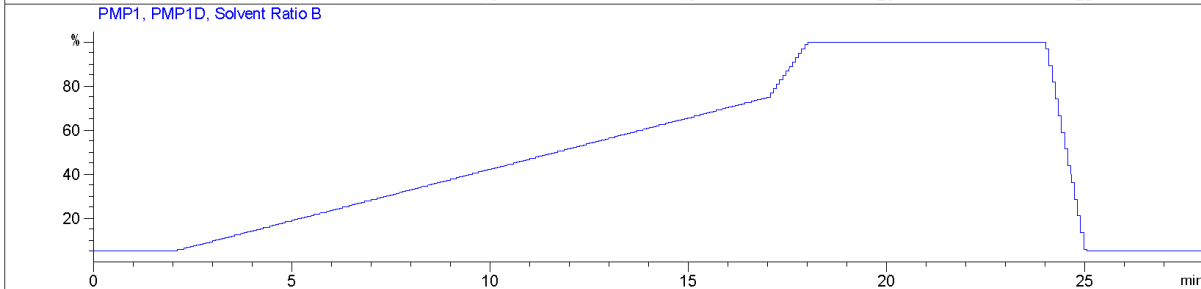
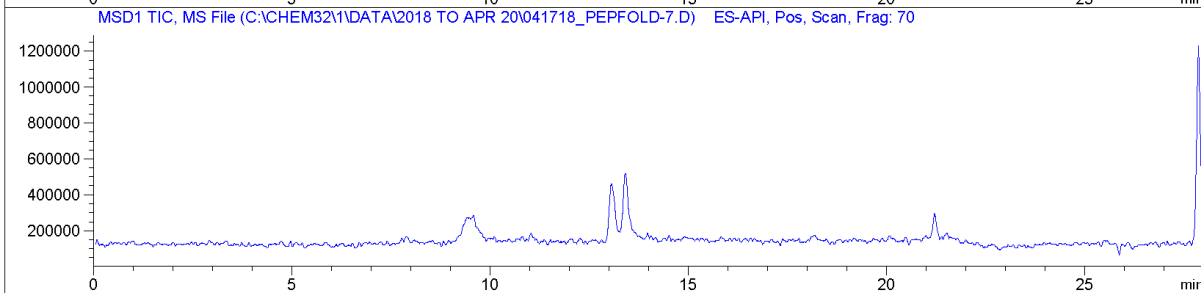
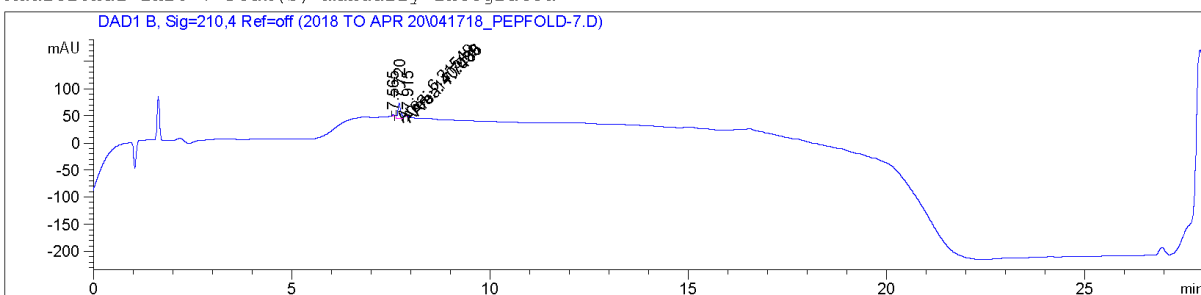
=====

Acq. Operator	: SGLK	Seq. Line	: 7
Acq. Instrument	: Instrument 1	Location	: Vial 67
Injection Date	: 4/17/18 2:25:44 PM	Inj	: 1
		Inj Volume	: 1.000 µl

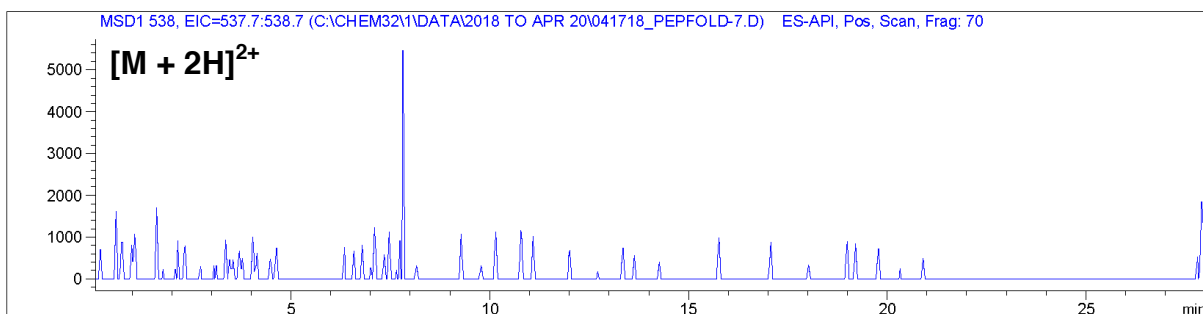
Different Inj Volume from Sequence ! Actual Inj Volume : 2.000 µl

Acq. Method	: D:\CHEM32\1\METHODS\AP_C18_INSERT.M
Last changed	: 4/17/18 11:25:09 AM by SGLK
Analysis Method	: Z:\DESKTOP\BERTOZZI LAB\LCMS INFO\LCMS METHODS TO 112917\SGLK_BERTOZZIBP_WITHINSERT.M
Last changed	: 4/26/18 11:40:30 AM (modified after loading)

Additional Info : Peak(s) manually integrated



Data File C:\CHEM32\1\DATA\2018 TO APR 20\041718_PEPFOLD-7.D
Sample Name: 041718_pepfold-7



=====
Area Percent Report
=====

Sorted By : Signal
Multiplier: : 1.0000
Dilution: : 1.0000
Do not use Multiplier & Dilution Factor with ISTDs

Signal 1: DAD1 B, Sig=210,4 Ref=off

Peak #	RetTime [min]	Type	Width [min]	Area [mAU*s]	Height [mAU]	Area %
1	7.565	MM	0.0488	6.21549	2.12108	4.0360
2	7.720	FM	0.0823	140.03857	28.36635	90.9326
3	7.915	MM	0.0409	7.74860	3.15911	5.0315

Totals : 154.00266 33.64654

Signal 2: MSD1 TIC, MS File

Signal 3: MSD1 1076, EIC=1075.7:1076.7

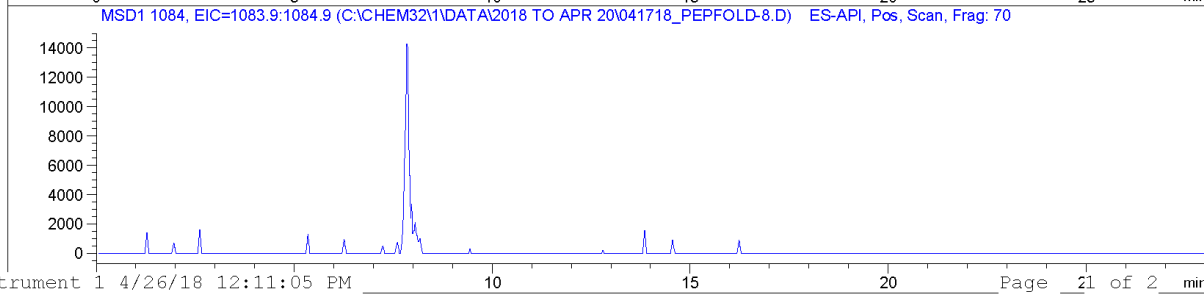
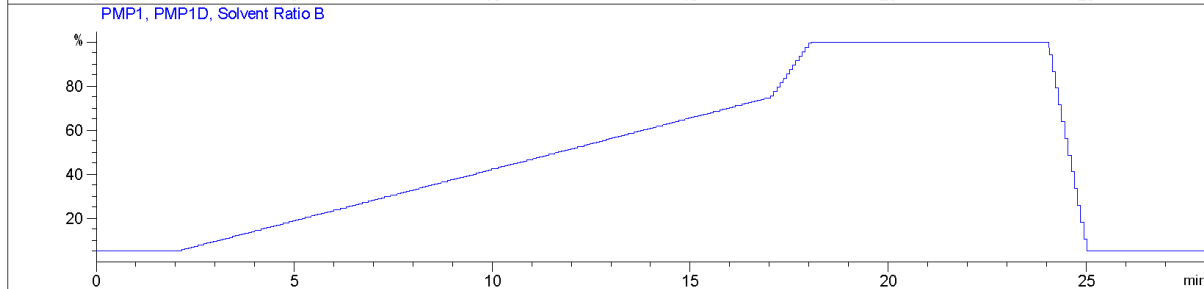
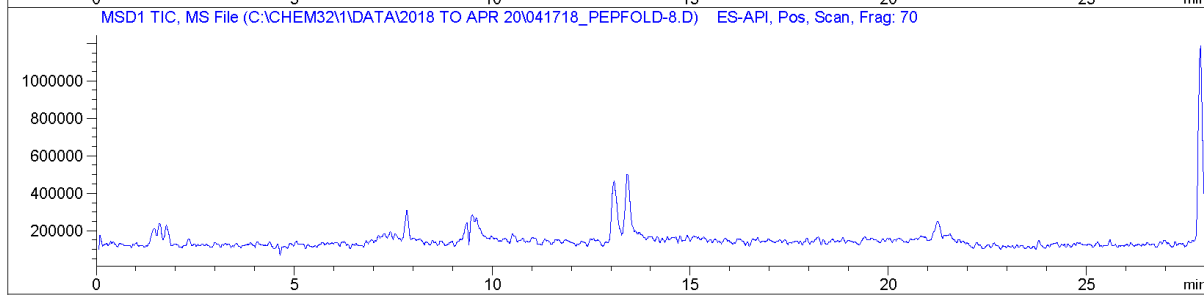
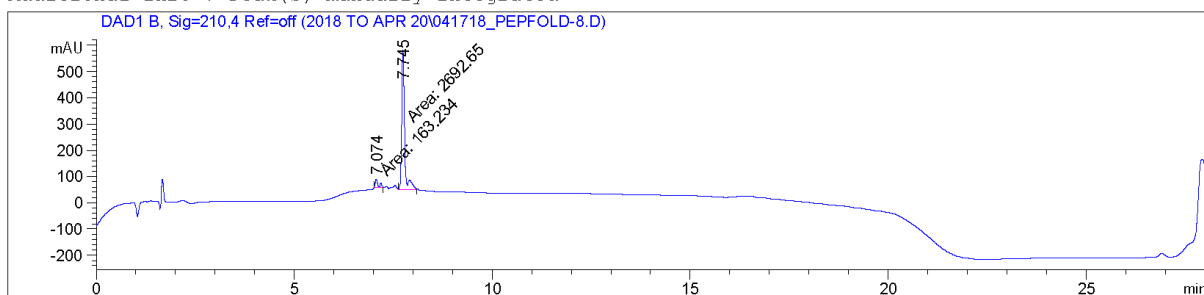
Signal 4: MSD1 538, EIC=537.7:538.7

=====
*** End of Report ***

PEP-FOLD-8, Ac-GGCPKPHPHGG-NH₂ (11)

Data File C:\CHEM32\1\DATA\2018 TO APR 20\041718_PEPFOLD-8.D
Sample Name: 041718_pepfold-8

```
=====
Acq. Operator   : SGLK                      Seq. Line :    8
Acq. Instrument : Instrument 1              Location  : Vial 68
Injection Date  : 4/17/18 2:55:02 PM       Inj       :    1
                                                Inj Volume: 1.000 µl
Different Inj Volume from Sequence !      Actual Inj Volume : 2.000 µl
Acq. Method     : D:\CHEM32\1\METHODS\AP_C18_INSERT.M
Last changed    : 4/17/18 11:25:09 AM by SGLK
Analysis Method : Z:\DESKTOP\BERTOZZI LAB\LCMS INFO\LCMS METHODS TO 112917\SGLK_BERTOZZIBP_
                WITHINSERT.M
Last changed    : 4/26/18 11:40:30 AM
                (modified after loading)
Additional Info  : Peak(s) manually integrated
=====
```



Data File C:\CHEM32\1\DATA\2018 TO APR 20\041718_PEPFOLD-8.D
Sample Name: 041718_pepfold-8

=====
Area Percent Report
=====

Sorted By : Signal
Multiplier: : 1.0000
Dilution: : 1.0000
Do not use Multiplier & Dilution Factor with ISTDs

Signal 1: DAD1 B, Sig=210,4 Ref=off

Peak #	RetTime [min]	Type	Width [min]	Area [mAU*s]	Height [mAU]	Area %
1	7.074	MM	0.0863	163.23375	31.52087	5.7157
2	7.745	MM	0.0839	2692.64893	534.70697	94.2843

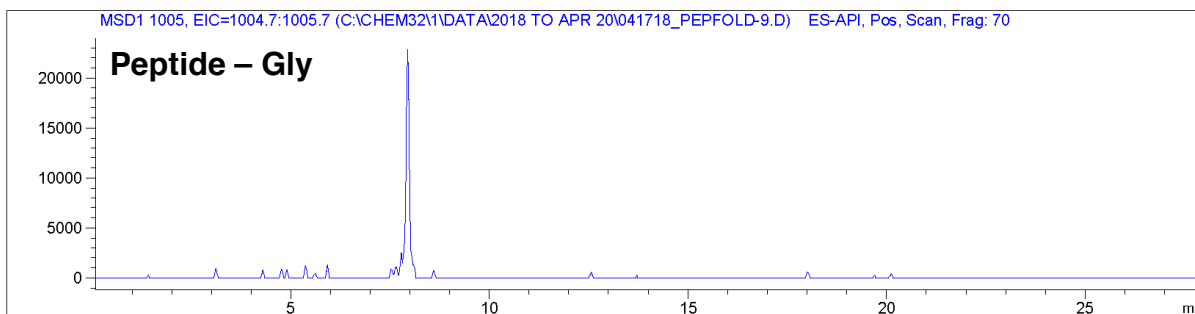
Totals : 2855.88268 566.22784

Signal 2: MSD1 TIC, MS File

Signal 3: MSD1 1084, EIC=1083.9:1084.9

=====
*** End of Report ***

Data File C:\CHEM32\1\DATA\2018 TO APR 20\041718_PEPFOLD-9.D
Sample Name: 041718_pepfold-9



=====
Area Percent Report
=====

Sorted By : Signal
Multiplier: : 1.0000
Dilution: : 1.0000
Do not use Multiplier & Dilution Factor with ISTDs

Signal 1: DAD1 B, Sig=210,4 Ref=off

Peak #	RetTime [min]	Type	Width [min]	Area [mAU*s]	Height [mAU]	Area %
1	7.837	MM	0.0960	5536.45996	960.84705	94.9663
2	7.991	MM	0.0538	293.46121	90.87576	5.0337

Totals : 5829.92117 1051.72280

Signal 2: MSD1 TIC, MS File

Signal 3: MSD1 1062, EIC=1061.7:1062.7

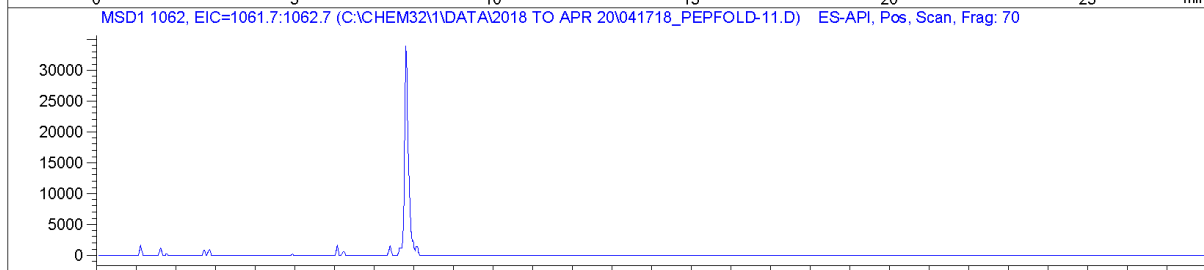
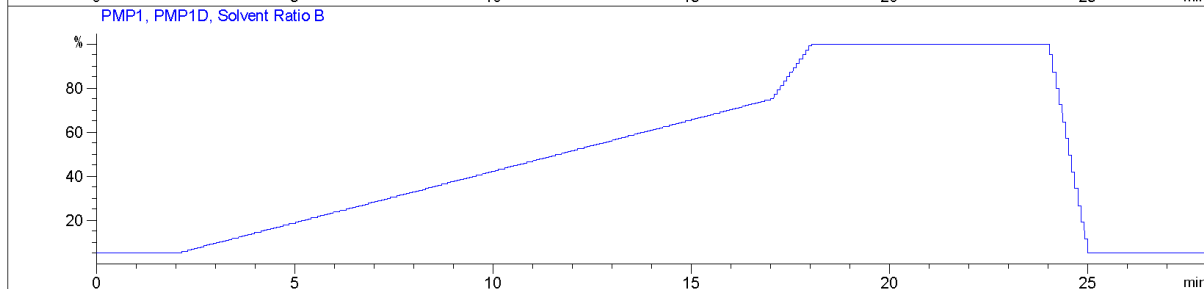
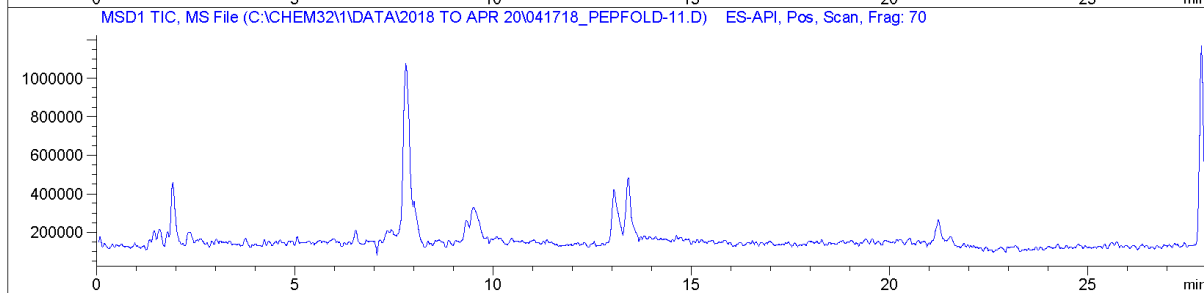
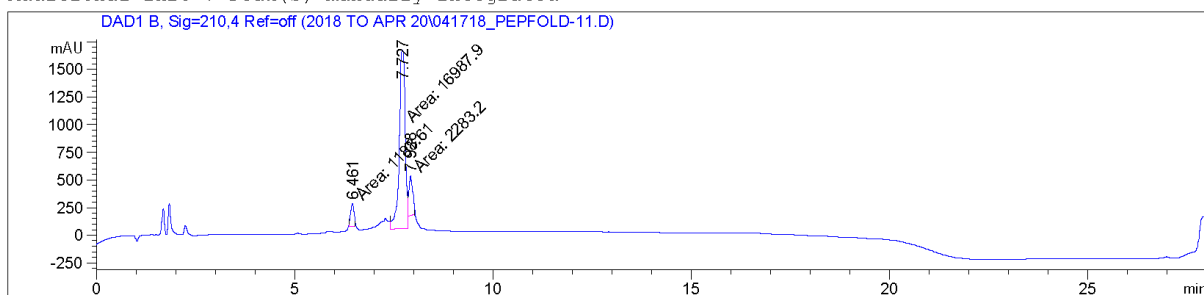
Signal 4: MSD1 1005, EIC=1004.7:1005.7

=====
*** End of Report ***

PEP-FOLD-11, Ac-GGCPDPHPKGG-NH₂ (13)

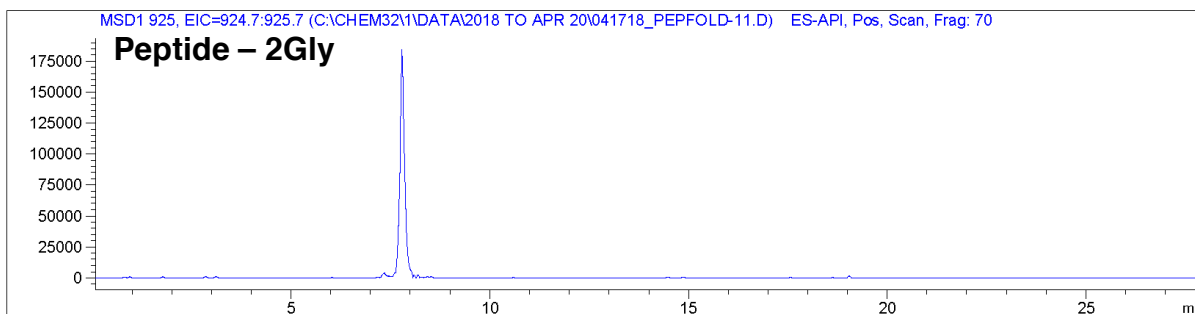
Data File C:\CHEM32\1\DATA\2018 TO APR 20\041718_PEPFOLD-11.D
Sample Name: 041718_pepfold-11

```
=====
Acq. Operator   : SGLK                      Seq. Line : 10
Acq. Instrument : Instrument 1              Location  : Vial 70
Injection Date  : 4/17/18 3:53:42 PM      Inj       : 1
                                                Inj Volume: 1.000 µl
Different Inj Volume from Sequence !      Actual Inj Volume : 2.000 µl
Acq. Method     : D:\CHEM32\1\METHODS\AP_C18_INSERT.M
Last changed    : 4/17/18 11:25:09 AM by SGLK
Analysis Method : Z:\DESKTOP\BERTOZZI LAB\LCMS INFO\LCMS METHODS TO 112917\SGLK_BERTOZZIBP_
                WITHINSERT.M
Last changed    : 4/26/18 12:19:51 PM
                (modified after loading)
Additional Info : Peak(s) manually integrated
=====
```



Instrument 1 4/26/18 12:21:49 PM Page 21 of 2 min

Data File C:\CHEM32\1\DATA\2018 TO APR 20\041718_PEPFOLD-11.D
Sample Name: 041718_pepfold-11



=====
Area Percent Report
=====

Sorted By : Signal
Multiplier: : 1.0000
Dilution: : 1.0000
Do not use Multiplier & Dilution Factor with ISTDs

Signal 1: DAD1 B, Sig=210,4 Ref=off

Peak #	RetTime [min]	Type	Width [min]	Area [mAU*s]	Height [mAU]	Area %
1	6.461	MM	0.0969	1188.60876	204.49396	5.8095
2	7.727	MM	0.1756	1.69879e4	1612.37292	83.0310
3	7.928	MM	0.1060	2283.19775	358.82666	11.1595

Totals : 2.04597e4 2175.69354

Signal 2: MSD1 TIC, MS File

Signal 3: MSD1 1062, EIC=1061.7:1062.7

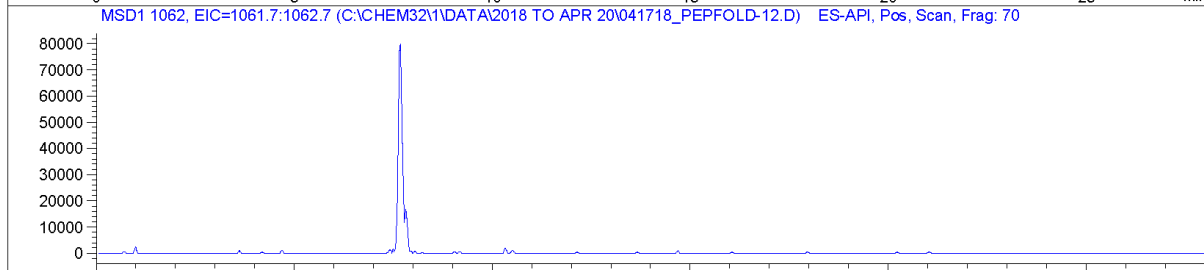
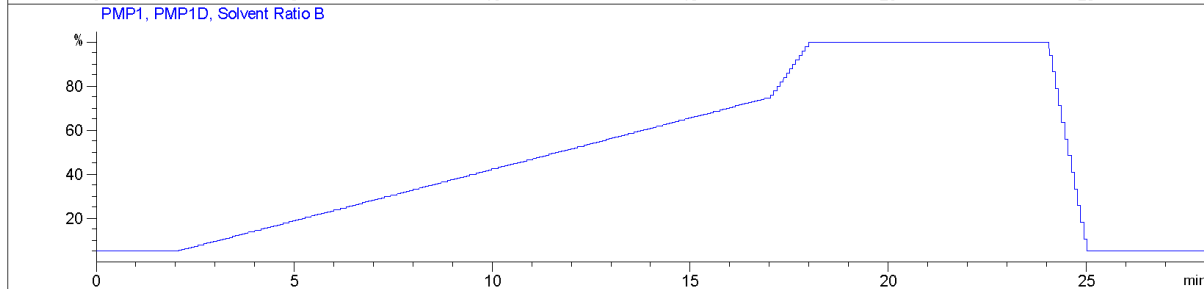
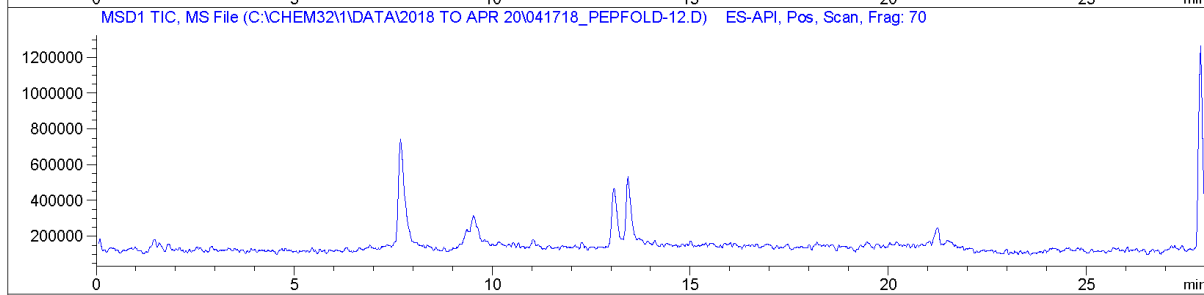
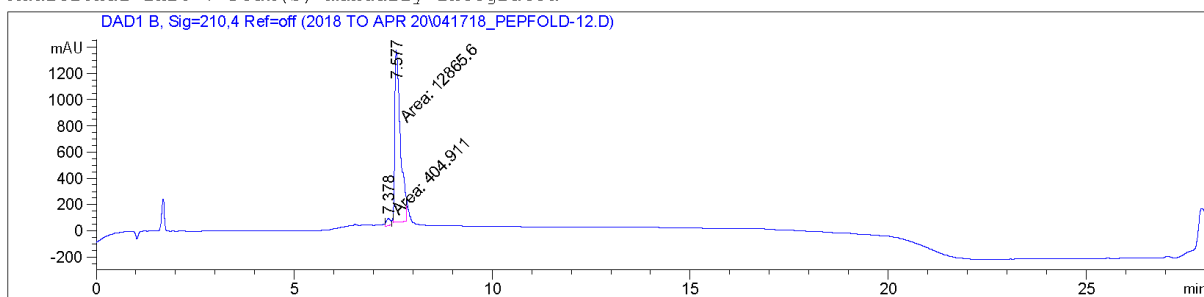
Signal 4: MSD1 925, EIC=924.7:925.7

=====
*** End of Report ***

PEP-FOLD-12, Ac-GGKPCPHPDGG-NH₂ (14)

Data File C:\CHEM32\1\DATA\2018 TO APR 20\041718_PEPFOLD-12.D
Sample Name: 041718_pepfold-12

```
=====
Acq. Operator   : SGLK                               Seq. Line : 11
Acq. Instrument : Instrument 1                       Location  : Vial 71
Injection Date  : 4/17/18 4:23:01 PM                Inj       : 1
                                                    Inj Volume: 1.000 µl
Different Inj Volume from Sequence !   Actual Inj Volume : 2.000 µl
Acq. Method    : D:\CHEM32\1\METHODS\AP_C18_INSERT.M
Last changed   : 4/17/18 11:25:09 AM by SGLK
Analysis Method : Z:\DESKTOP\BERTOZZI LAB\LCMS INFO\LCMS METHODS TO 112917\SGLK_BERTOZZIBP_
                WITHINSERT.M
Last changed   : 4/26/18 12:19:51 PM
                (modified after loading)
Additional Info : Peak(s) manually integrated
=====
```



Data File C:\CHEM32\1\DATA\2018 TO APR 20\041718_PEPFOLD-12.D
Sample Name: 041718_pepfold-12

=====
Area Percent Report
=====

Sorted By : Signal
Multiplier: : 1.0000
Dilution: : 1.0000
Do not use Multiplier & Dilution Factor with ISTDs

Signal 1: DAD1 B, Sig=210,4 Ref=off

Peak #	RetTime [min]	Type	Width [min]	Area [mAU*s]	Height [mAU]	Area %
1	7.378	MF	0.1246	404.91074	54.17891	3.0512
2	7.577	MM	0.1629	1.28656e4	1316.29163	96.9488

Totals : 1.32706e4 1370.47054

Signal 2: MSD1 TIC, MS File

Signal 3: MSD1 1062, EIC=1061.7:1062.7

=====
*** End of Report ***

Data File C:\CHEM32\1\DATA\2018 TO APR 20\041718_PEPFOLD-13.D
Sample Name: 041718_pepfold-13

=====
Area Percent Report
=====

Sorted By : Signal
Multiplier: : 1.0000
Dilution: : 1.0000
Do not use Multiplier & Dilution Factor with ISTDs

Signal 1: DAD1 B, Sig=210,4 Ref=off

Peak #	RetTime [min]	Type	Width [min]	Area [mAU*s]	Height [mAU]	Area %
1	9.429	MM	0.0862	513.55121	99.34387	4.8848
2	9.634	FM	0.1434	9999.78418	1161.94617	95.1152

Totals : 1.05133e4 1261.29004

Signal 2: MSD1 TIC, MS File

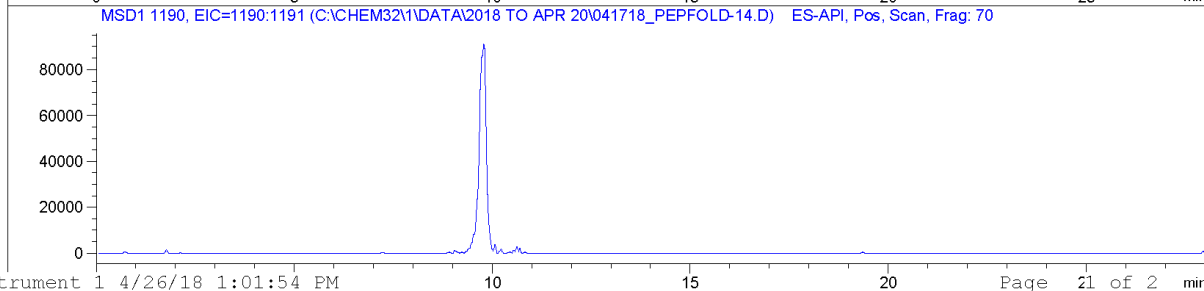
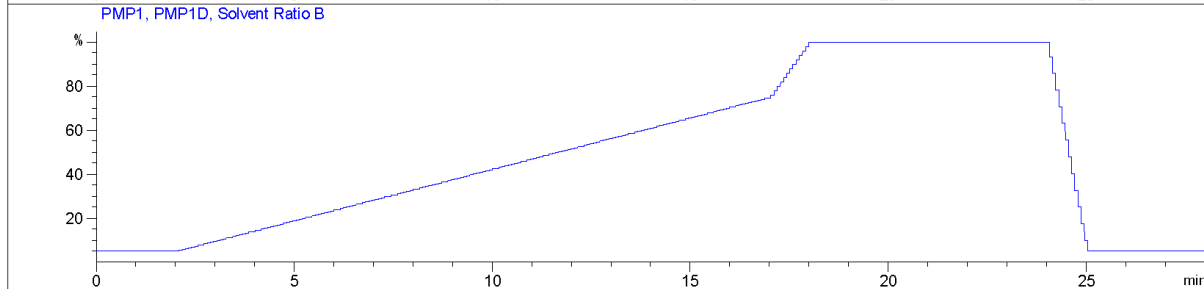
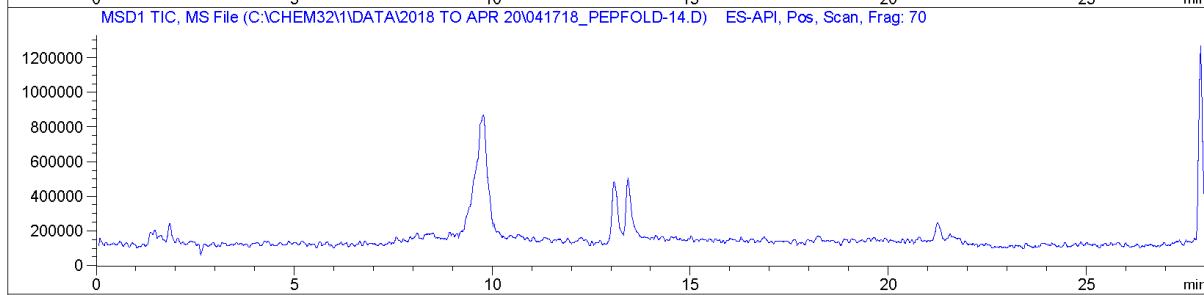
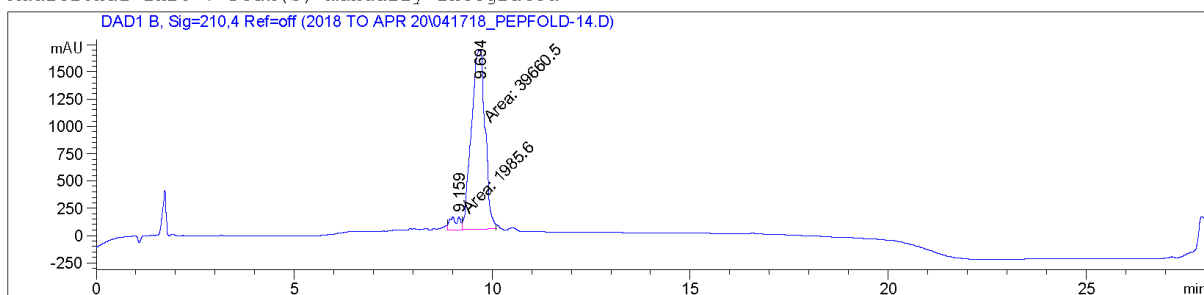
Signal 3: MSD1 1133, EIC=1132.7:1133.7

=====
*** End of Report ***

PEP-FOLD-14, Ac-GGWPHPGCPKGG-NH₂ (16)

Data File C:\CHEM32\1\DATA\2018 TO APR 20\041718_PEPFOLD-14.D
Sample Name: 041718_pepfold-14

```
=====
Acq. Operator   : SGLK                      Seq. Line : 13
Acq. Instrument : Instrument 1                Location  : Vial 73
Injection Date  : 4/17/18 5:21:31 PM        Inj       : 1
                                                Inj Volume: 1.000 µl
Different Inj Volume from Sequence !      Actual Inj Volume : 2.000 µl
Acq. Method     : D:\CHEM32\1\METHODS\AP_C18_INSERT.M
Last changed    : 4/17/18 11:25:09 AM by SGLK
Analysis Method : Z:\DESKTOP\BERTOZZI LAB\LCMS INFO\LCMS METHODS TO 112917\SGLK_BERTOZZIBP_
                WITHINSERT.M
Last changed    : 4/26/18 12:19:51 PM
                (modified after loading)
Additional Info : Peak(s) manually integrated
=====
```



Data File C:\CHEM32\1\DATA\2018 TO APR 20\041718_PEPFOLD-14.D
Sample Name: 041718_pepfold-14

=====
Area Percent Report
=====

Sorted By : Signal
Multiplier: : 1.0000
Dilution: : 1.0000
Do not use Multiplier & Dilution Factor with ISTDs

Signal 1: DAD1 B, Sig=210,4 Ref=off

Peak #	RetTime [min]	Type	Width [min]	Area [mAU*s]	Height [mAU]	Area %
1	9.159	MF	0.2637	1985.60120	125.47730	4.7678
2	9.694	FM	0.4020	3.96605e4	1644.22729	95.2322

Totals : 4.16461e4 1769.70460

Signal 2: MSD1 TIC, MS File

=====
*** End of Report ***

Data File C:\CHEM32\1\DATA\2018 TO APR 20\041718_PEPFOLD-15.D
Sample Name: 041718_pepfold-15

=====
Area Percent Report
=====

Sorted By : Signal
Multiplier: : 1.0000
Dilution: : 1.0000
Do not use Multiplier & Dilution Factor with ISTDs

Signal 1: DAD1 B, Sig=210,4 Ref=off

Peak #	RetTime [min]	Type	Width [min]	Area [mAU*s]	Height [mAU]	Area %
1	8.910	MM	0.0731	96.39982	21.96997	0.7900
2	9.523	MM	0.1717	1.16448e4	1130.44336	95.4322
3	9.708	MM	0.0727	460.96796	105.69280	3.7777

Totals : 1.22022e4 1258.10614

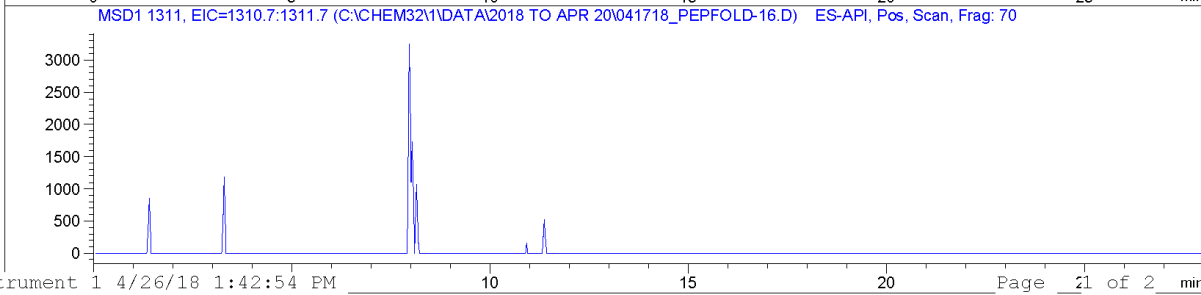
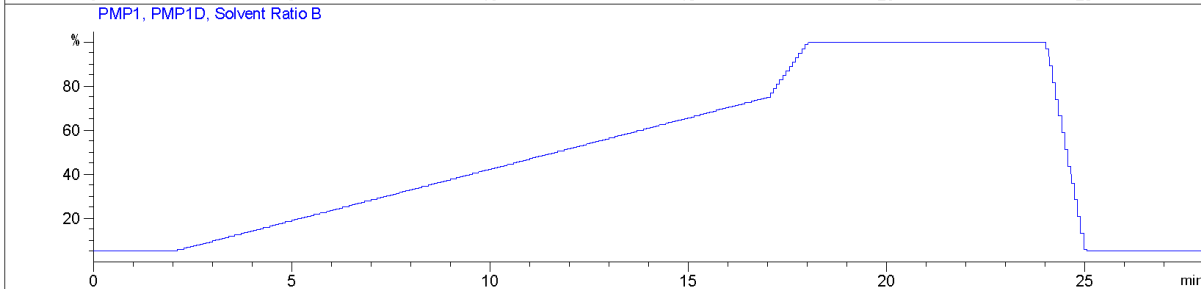
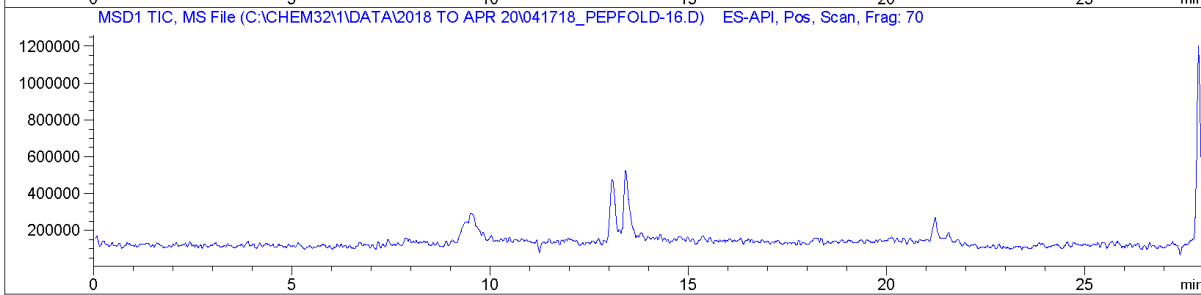
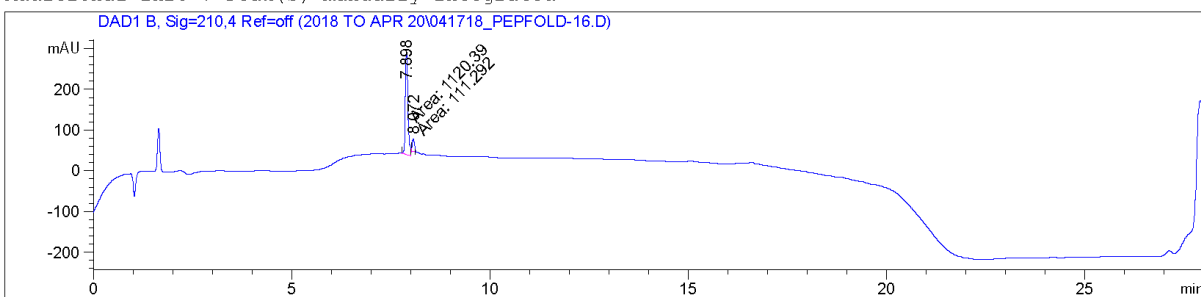
Signal 2: MSD1 TIC, MS File

=====
*** End of Report ***

PEP-FOLD-16, Ac-GGHPHPKPCPEGG-NH₂ (18)

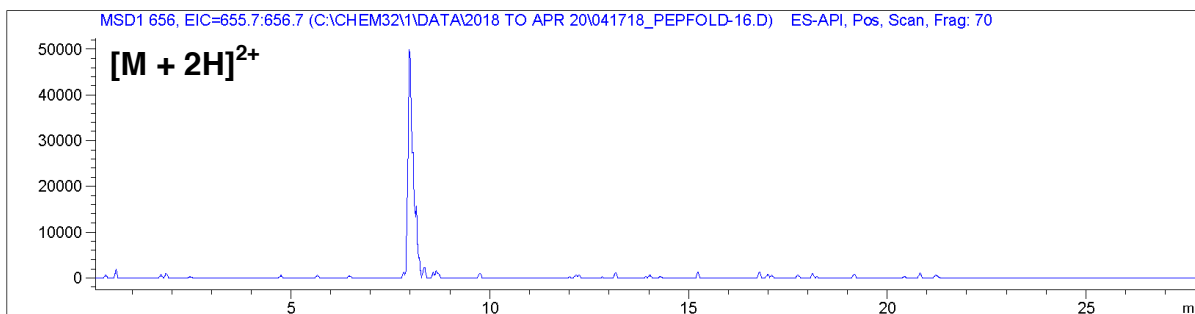
Data File C:\CHEM32\1\DATA\2018 TO APR 20\041718_PEPFOLD-16.D
Sample Name: 041718_pepfold-16

```
=====
Acq. Operator   : SGLK                      Seq. Line : 15
Acq. Instrument : Instrument 1              Location  : Vial 75
Injection Date  : 4/17/18 6:20:08 PM      Inj       : 1
                                                Inj Volume: 1.000 µl
Different Inj Volume from Sequence !      Actual Inj Volume : 2.000 µl
Acq. Method    : D:\CHEM32\1\METHODS\AP_C18_INSERT.M
Last changed   : 4/17/18 11:25:09 AM by SGLK
Analysis Method : Z:\DESKTOP\BERTOZZI LAB\LCMS INFO\LCMS METHODS TO 112917\SGLK_BERTOZZIBP_
                WITHINSERT.M
Last changed   : 4/26/18 12:19:51 PM
                (modified after loading)
Additional Info : Peak(s) manually integrated
=====
```



Instrument 1 4/26/18 1:42:54 PM Page 21 of 2 min

Data File C:\CHEM32\1\DATA\2018 TO APR 20\041718_PEPFOLD-16.D
Sample Name: 041718_pepfold-16



=====
Area Percent Report
=====

Sorted By : Signal
Multiplier: : 1.0000
Dilution: : 1.0000
Do not use Multiplier & Dilution Factor with ISTDs

Signal 1: DAD1 B, Sig=210,4 Ref=off

Peak #	RetTime [min]	Type	Width [min]	Area [mAU*s]	Height [mAU]	Area %
1	7.898	MM	0.0726	1120.38989	257.31540	90.9642
2	8.072	MM	0.0570	111.29197	32.53252	9.0358

Totals : 1231.68186 289.84792

Signal 2: MSD1 TIC, MS File

=====
*** End of Report ***

Data File C:\CHEM32\1\DATA\2018 TO APR 20\041718_PEPFOLD-17.D
Sample Name: 041718_pepfold-17

=====
Area Percent Report
=====

Sorted By : Signal
Multiplier: : 1.0000
Dilution: : 1.0000
Do not use Multiplier & Dilution Factor with ISTDs

Signal 1: DAD1 B, Sig=210,4 Ref=off

Peak #	RetTime [min]	Type	Width [min]	Area [mAU*s]	Height [mAU]	Area %
1	9.423	MF	0.0528	685.16229	216.40576	4.3872
2	9.535	FM	0.1557	1.49320e4	1598.33960	95.6128

Totals : 1.56172e4 1814.74536

Signal 2: MSD1 TIC, MS File

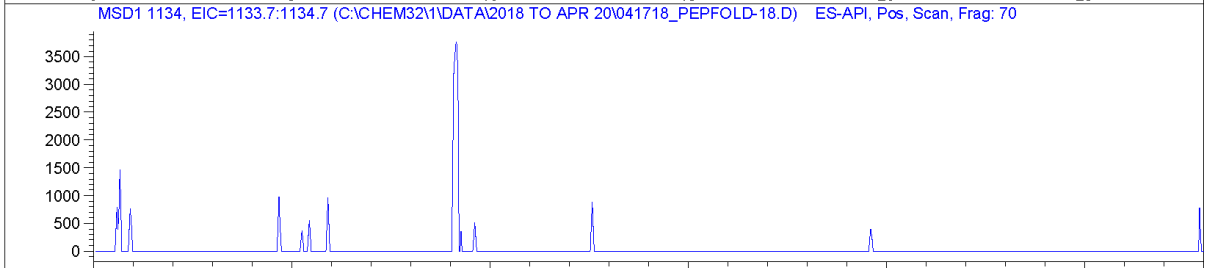
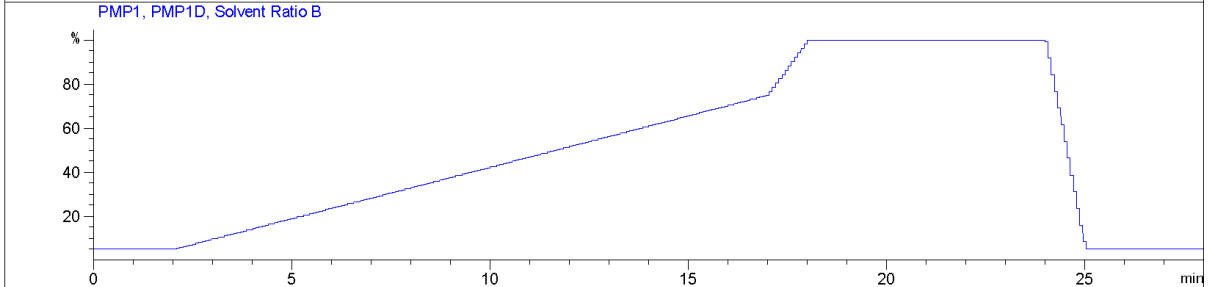
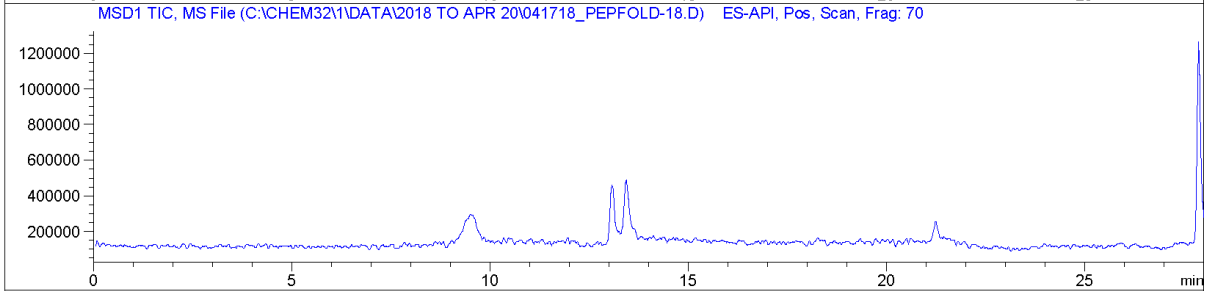
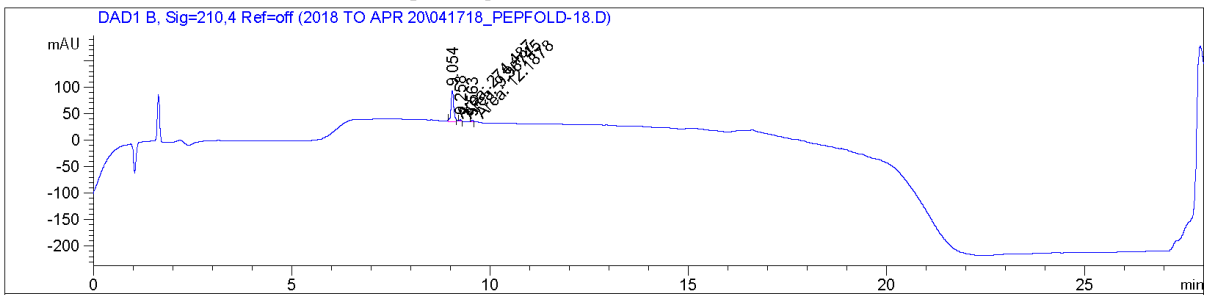
Signal 3: MSD1 1362, EIC=1361.1:1362.1

=====
*** End of Report ***

PEP-FOLD-18, Ac-GGHPKPGCGFGG-NH₂ (20)

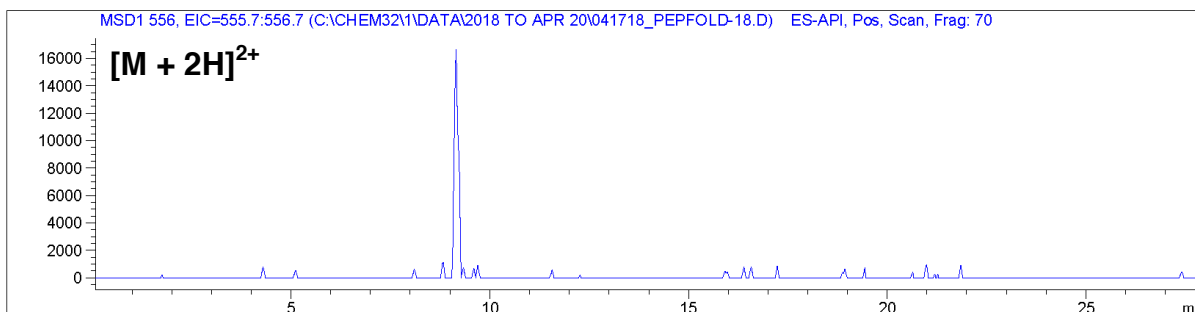
Data File C:\CHEM32\1\DATA\2018 TO APR 20\041718_PEPFOLD-18.D
Sample Name: 041718_pepfold-18

```
=====
Acq. Operator   : SGLK                      Seq. Line : 17
Acq. Instrument : Instrument 1              Location  : Vial 77
Injection Date  : 4/17/18 7:18:44 PM      Inj       : 1
                                                Inj Volume: 1.000 µl
Different Inj Volume from Sequence !      Actual Inj Volume : 2.000 µl
Acq. Method    : D:\CHEM32\1\METHODS\AP_C18_INSERT.M
Last changed   : 4/17/18 11:25:09 AM by SGLK
Analysis Method : Z:\DESKTOP\BERTOZZI LAB\LCMS INFO\LCMS METHODS TO 112917\SGLK_BERTOZZIBP_
                WITHINSERT.M
Last changed   : 4/26/18 12:19:51 PM
                (modified after loading)
Additional Info : Peak(s) manually integrated
=====
```



Instrument 1 4/26/18 1:51:04 PM Page 21 of 2 min

Data File C:\CHEM32\1\DATA\2018 TO APR 20\041718_PEPFOLD-18.D
Sample Name: 041718_pepfold-18



=====
Area Percent Report
=====

Sorted By : Signal
Multiplier: : 1.0000
Dilution: : 1.0000
Do not use Multiplier & Dilution Factor with ISTDs

Signal 1: DAD1 B, Sig=210,4 Ref=off

Peak #	RetTime [min]	Type	Width [min]	Area [mAU*s]	Height [mAU]	Area %
1	9.054	MM	0.0770	274.48676	59.39601	92.5251
2	9.258	MM	0.0569	9.98745	2.92673	3.3666
3	9.563	MM	0.0678	12.18780	2.99629	4.1083

Totals : 296.66201 65.31904

Signal 2: MSD1 TIC, MS File

=====
*** End of Report ***

PEP-FOLD-19, Ac-GGHPKPCGFGG-NH₂ (21)

Data File C:\CHEM32\1\DATA\2018 TO APR 20\041718_PEPFOLD-19.D
Sample Name: 041718_pepfold-19

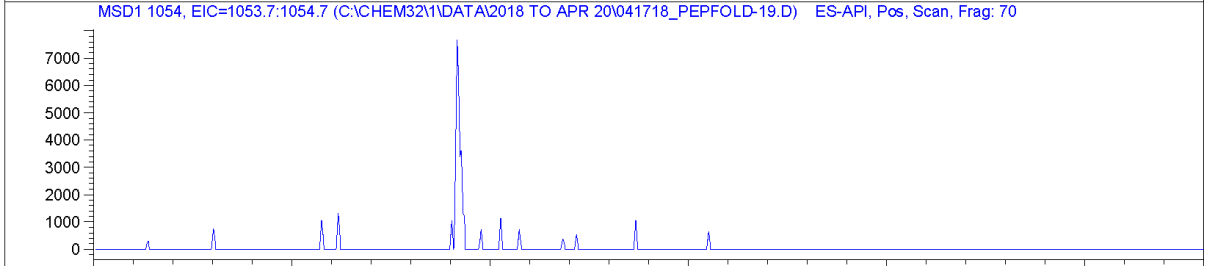
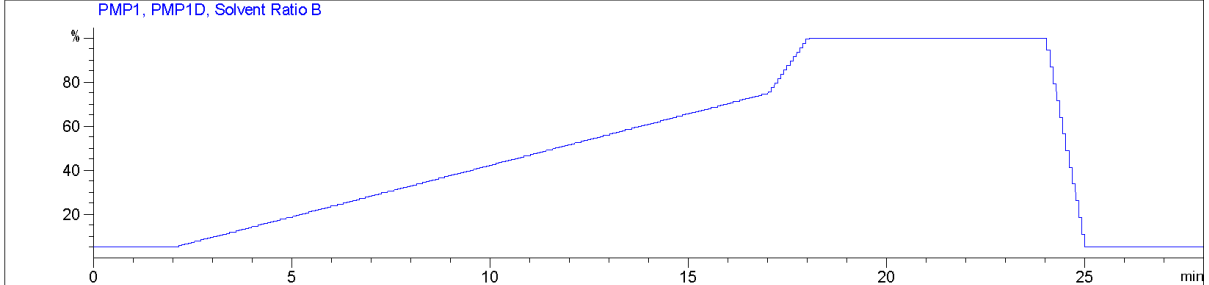
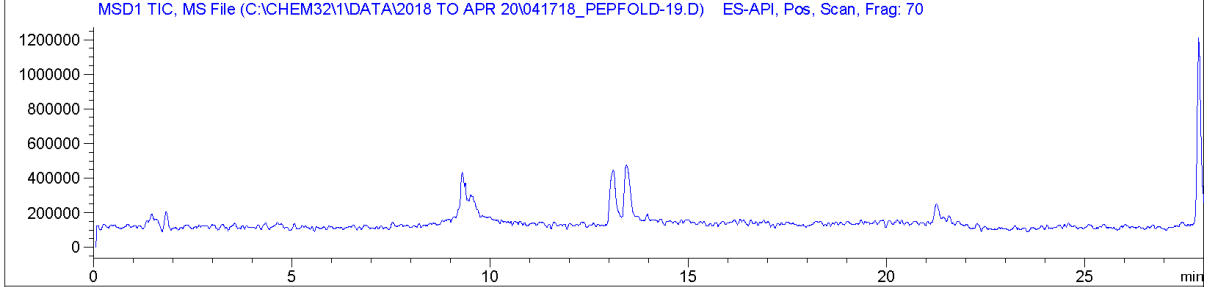
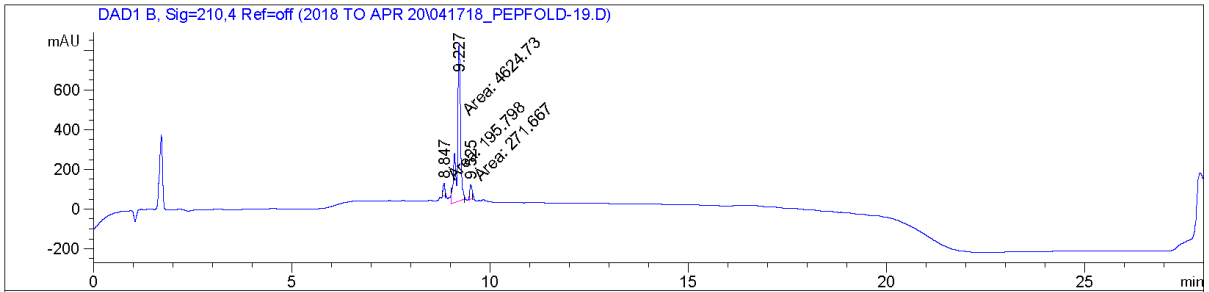
=====

Acq. Operator	: SGLK	Seq. Line	: 18
Acq. Instrument	: Instrument 1	Location	: Vial 78
Injection Date	: 4/17/18 7:48:01 PM	Inj	: 1
		Inj Volume	: 1.000 µl

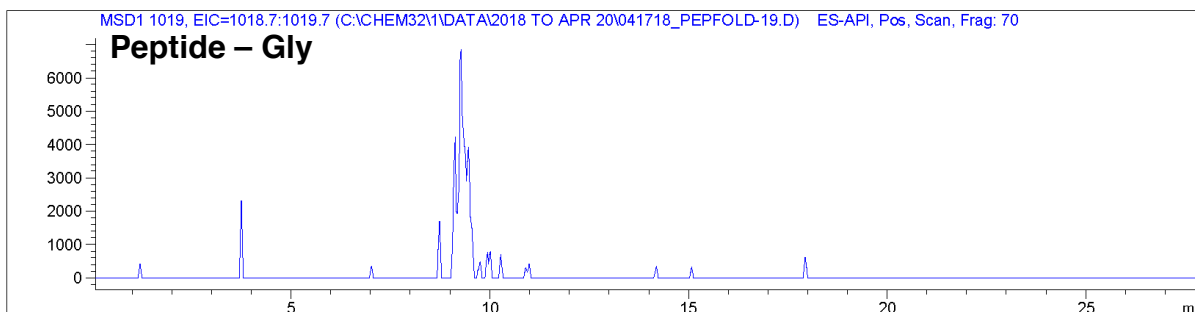
Different Inj Volume from Sequence ! Actual Inj Volume : 2.000 µl

Acq. Method	: D:\CHEM32\1\METHODS\AP_C18_INSERT.M
Last changed	: 4/17/18 11:25:09 AM by SGLK
Analysis Method	: Z:\DESKTOP\BERTOZZI LAB\LCMS INFO\LCMS METHODS TO 112917\SGLK_BERTOZZIBP_WITHINSERT.M
Last changed	: 4/26/18 12:19:51 PM (modified after loading)

Additional Info : Peak(s) manually integrated



Data File C:\CHEM32\1\DATA\2018 TO APR 20\041718_PEPFOLD-19.D
Sample Name: 041718_pepfold-19



=====
Area Percent Report
=====

Sorted By : Signal
Multiplier: : 1.0000
Dilution: : 1.0000
Do not use Multiplier & Dilution Factor with ISTDs

Signal 1: DAD1 B, Sig=210,4 Ref=off

Peak #	RetTime [min]	Type	Width [min]	Area [mAU*s]	Height [mAU]	Area %
1	8.847	MM	0.0498	195.79842	65.58862	3.8451
2	9.227	MM	0.0964	4624.72705	799.44141	90.8199
3	9.525	MM	0.0609	271.66748	74.33782	5.3350

Totals : 5092.19295 939.36784

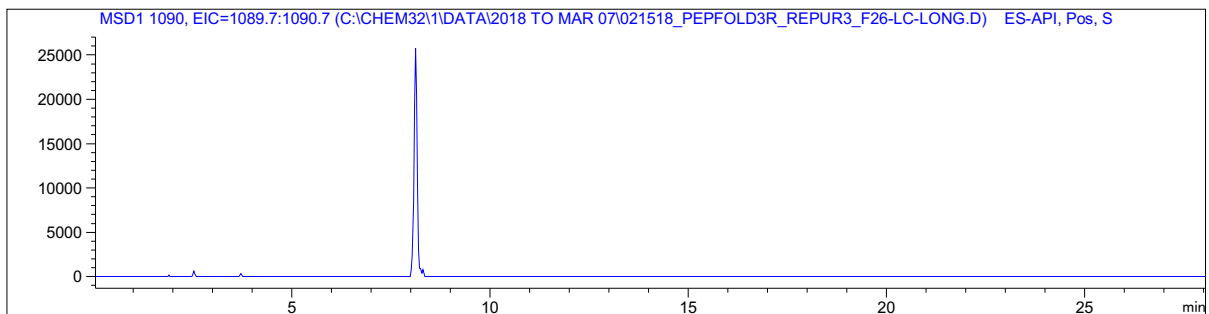
Signal 2: MSD1 TIC, MS File

Signal 3: MSD1 1054, EIC=1053.7:1054.7

Signal 4: MSD1 1019, EIC=1018.7:1019.7

=====
*** End of Report ***

Data File C:\CHEM32\1\DATA\2018 TO MAR 07\021518_PEPFOLD3R_REPUR3_F26-LC-LONG.D
Sample Name: 021518_pepfold3r_repur3_f26-lc-long



=====
Area Percent Report
=====

Sorted By : Signal
Multiplier: : 1.0000
Dilution: : 1.0000
Do not use Multiplier & Dilution Factor with ISTDs

Signal 1: DAD1 B, Sig=210,4 Ref=off

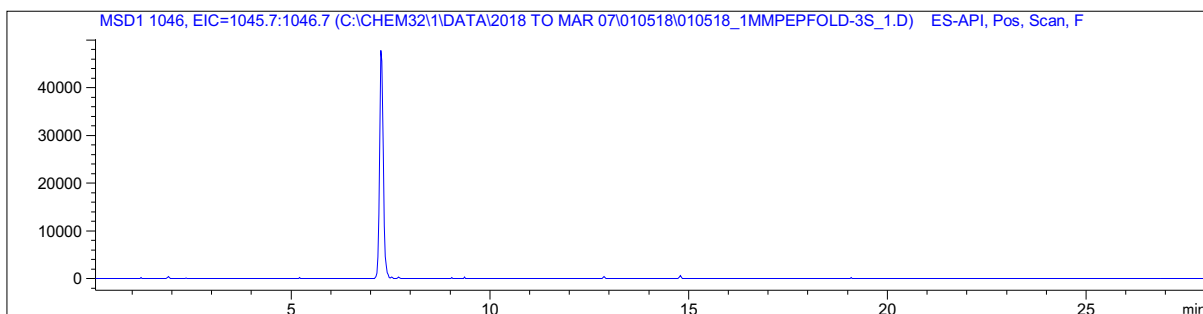
Peak #	RetTime [min]	Type	Width [min]	Area [mAU*s]	Height [mAU]	Area %
1	7.853	MF	0.0853	58.17865	11.36420	0.7518
2	8.051	FM	0.0776	7507.59863	1611.58948	97.0185
3	8.274	FM	0.1097	138.12289	20.97552	1.7849
4	9.266	MM	0.0639	34.41899	8.97556	0.4448

Totals : 7738.31917 1652.90476

Signal 2: MSD1 TIC, MS File

=====
*** End of Report ***

Data File C:\CHEM32\1\DATA\2018 TO MAR 07\010518\010518_1MMPEPFOLD-3S_1.D
Sample Name: 010518_lmMpepfold-3S_1



=====
Area Percent Report
=====

Sorted By : Signal
Multiplier: : 1.0000
Dilution: : 1.0000
Do not use Multiplier & Dilution Factor with ISTDs

Signal 1: DAD1 B, Sig=210,4 Ref=360,100

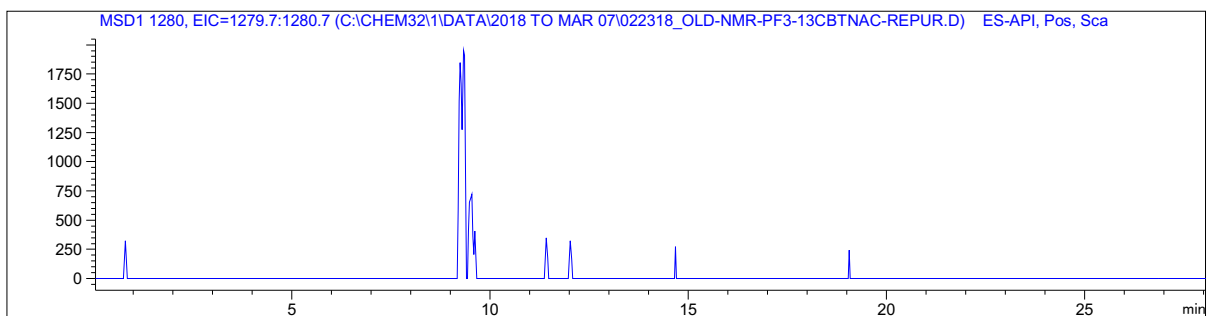
Peak #	RetTime [min]	Type	Width [min]	Area [mAU*s]	Height [mAU]	Area %
1	7.201	MF	0.1101	1.22979e4	1862.15747	94.9863
2	7.419	FM	0.1554	649.12140	69.64057	5.0137

Totals : 1.29470e4 1931.79804

Signal 2: MSD1 TIC, MS File

=====
*** End of Report ***

Data File C:\CHEM32\1\DATA\2018 TO MAR 07\022318_OLD-NMR-PF3-13CBTNAC-REPUR.D
Sample Name: 022318_old-nmr-pf3-13cbtnac-repur



=====
Area Percent Report
=====

Sorted By : Signal
Multiplier: : 1.0000
Dilution: : 1.0000
Do not use Multiplier & Dilution Factor with ISTDs

Signal 1: DAD1 F, Sig=200,4 Ref=off

Peak #	RetTime [min]	Type	Width [min]	Area [mAU*s]	Height [mAU]	Area %
1	9.162	MM	0.0911	4624.47559	846.48572	95.5475
2	17.466	MM	0.0596	215.49754	60.21696	4.4525

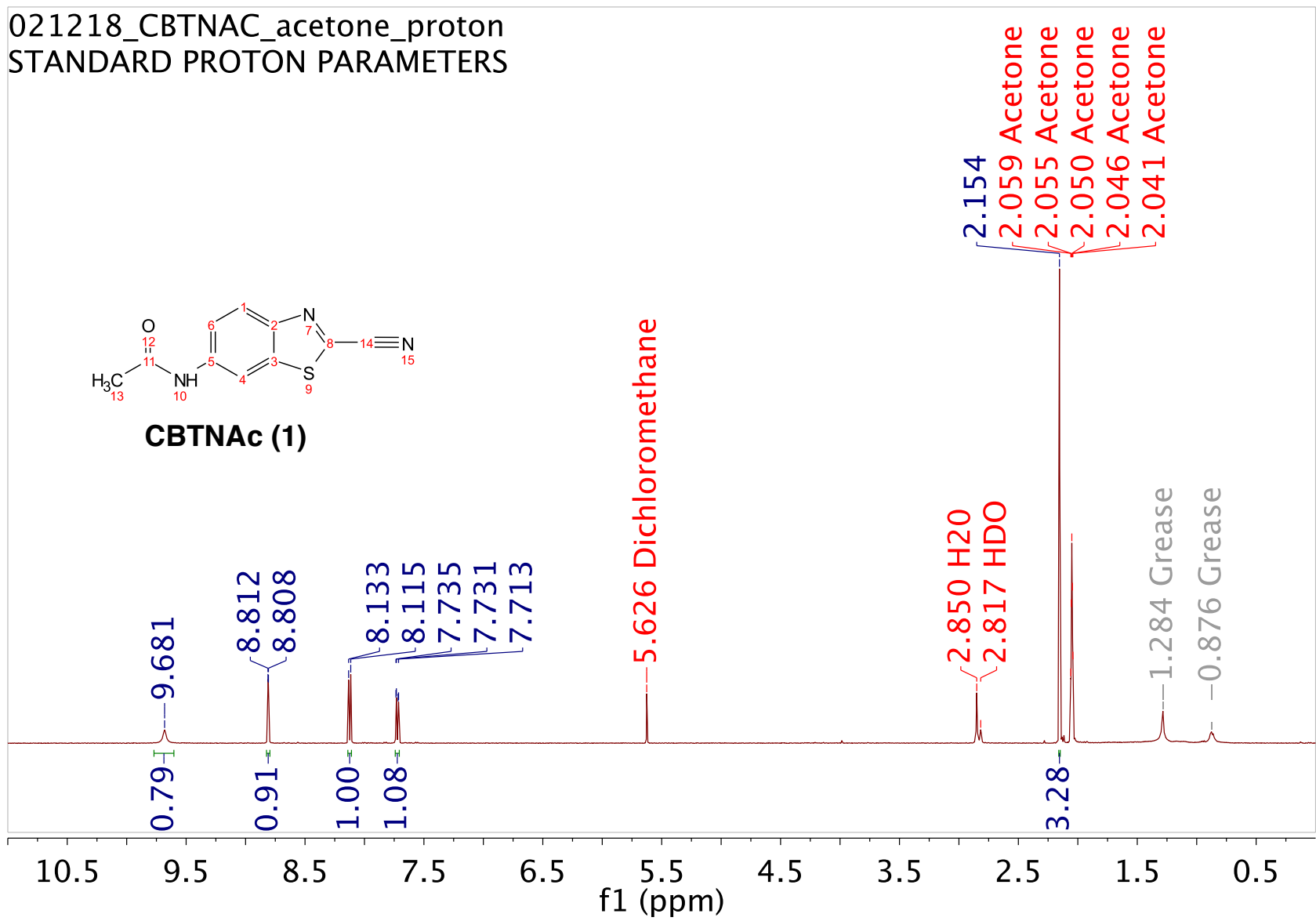
Totals : 4839.97313 906.70268

Signal 2: MSD1 TIC, MS File

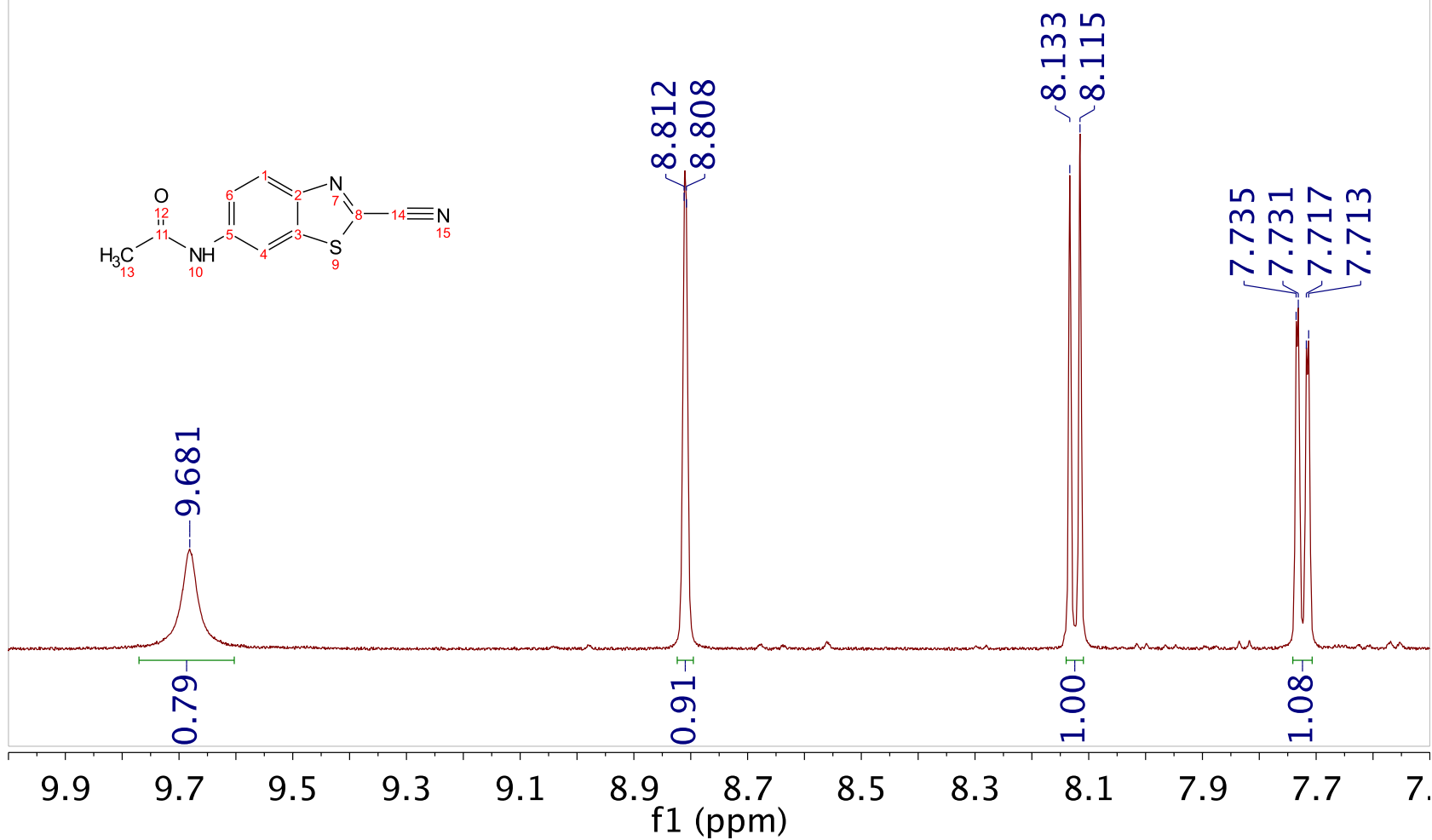
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*** End of Report ***

NMR Spectra

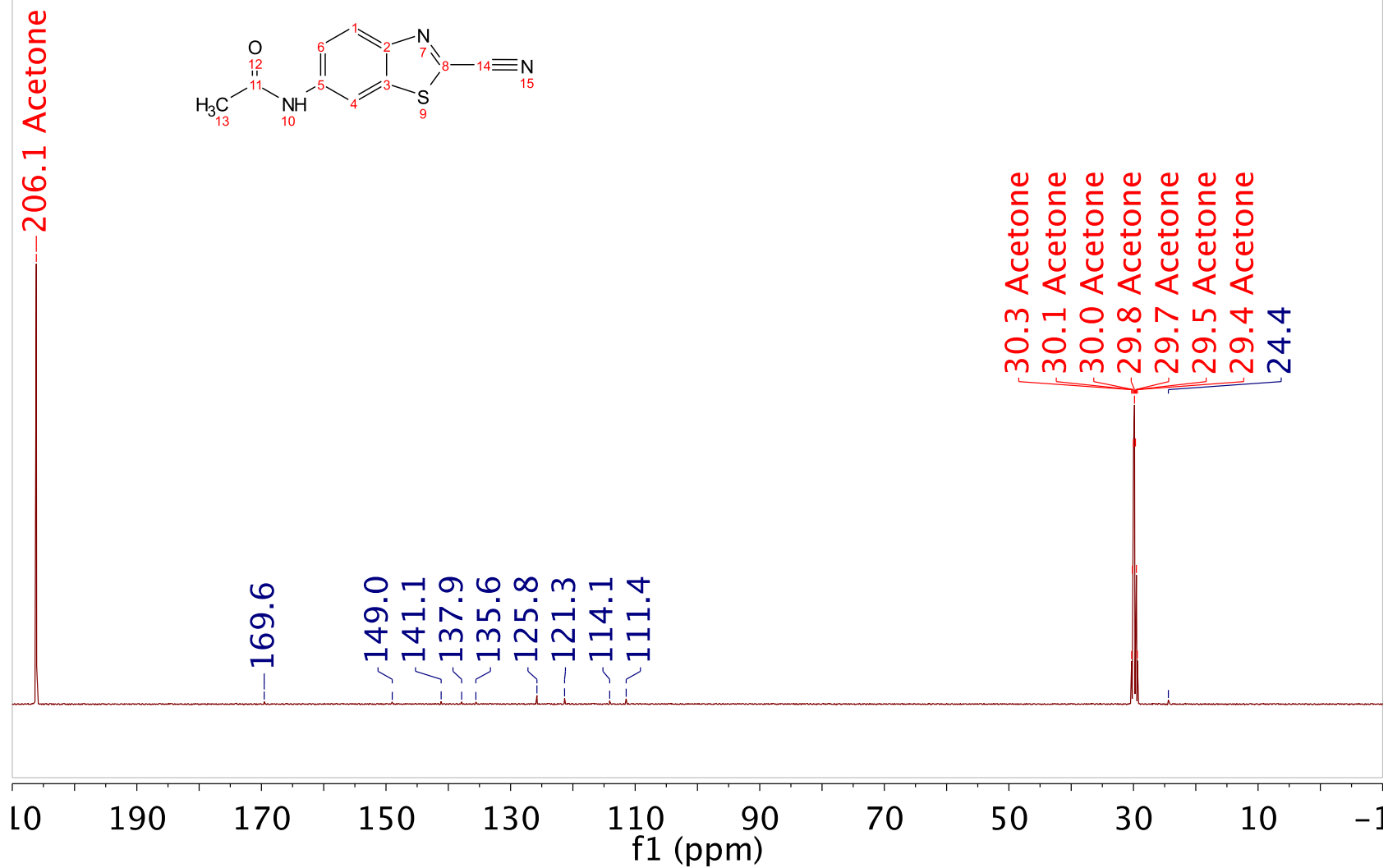
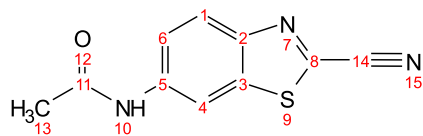
021218_CBTNAC_acetone_proton
STANDARD PROTON PARAMETERS



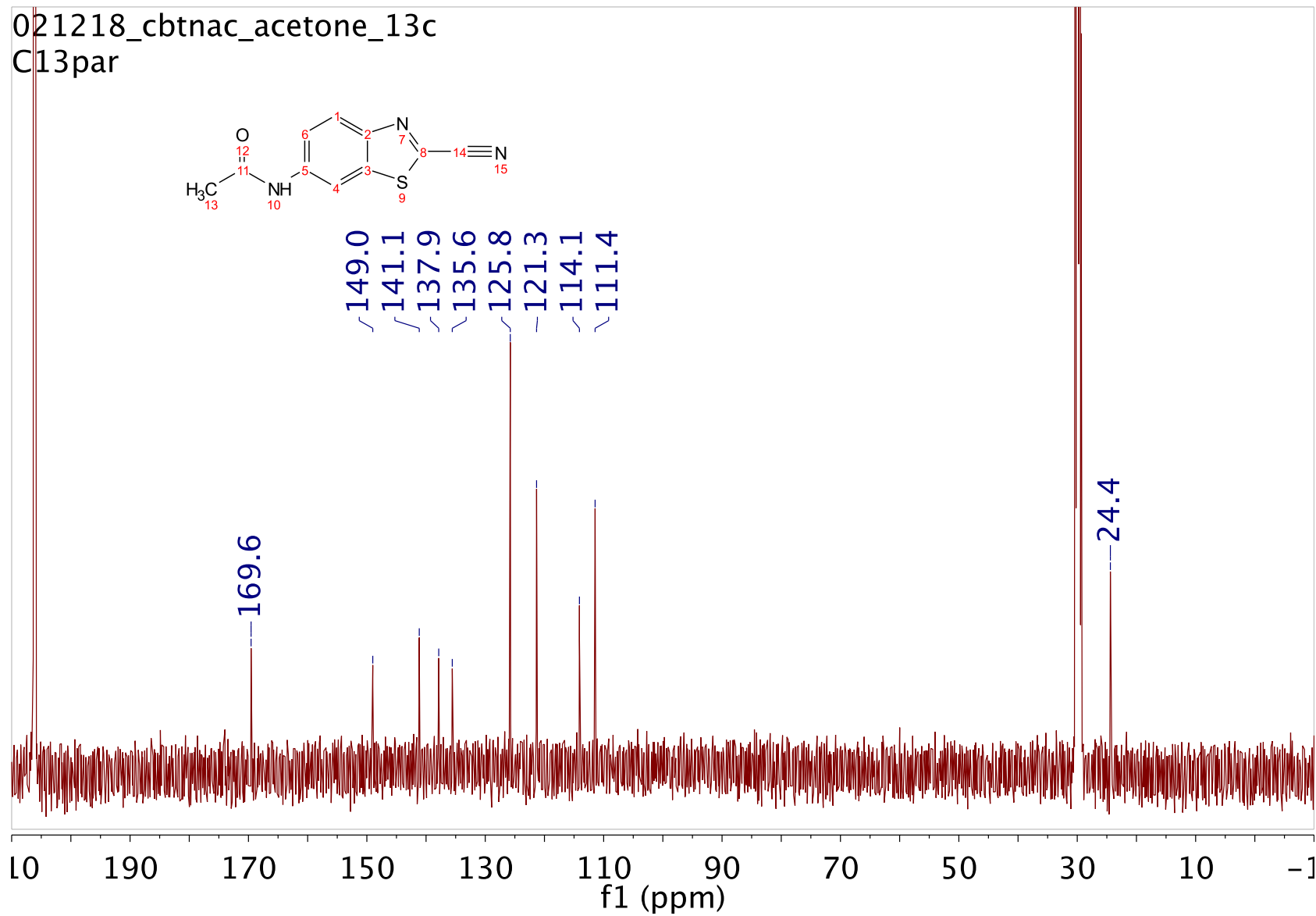
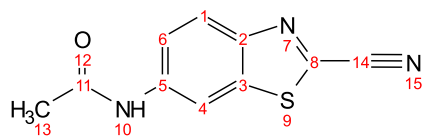
021218_CBTNAC_acetone_proton
STANDARD PROTON PARAMETERS



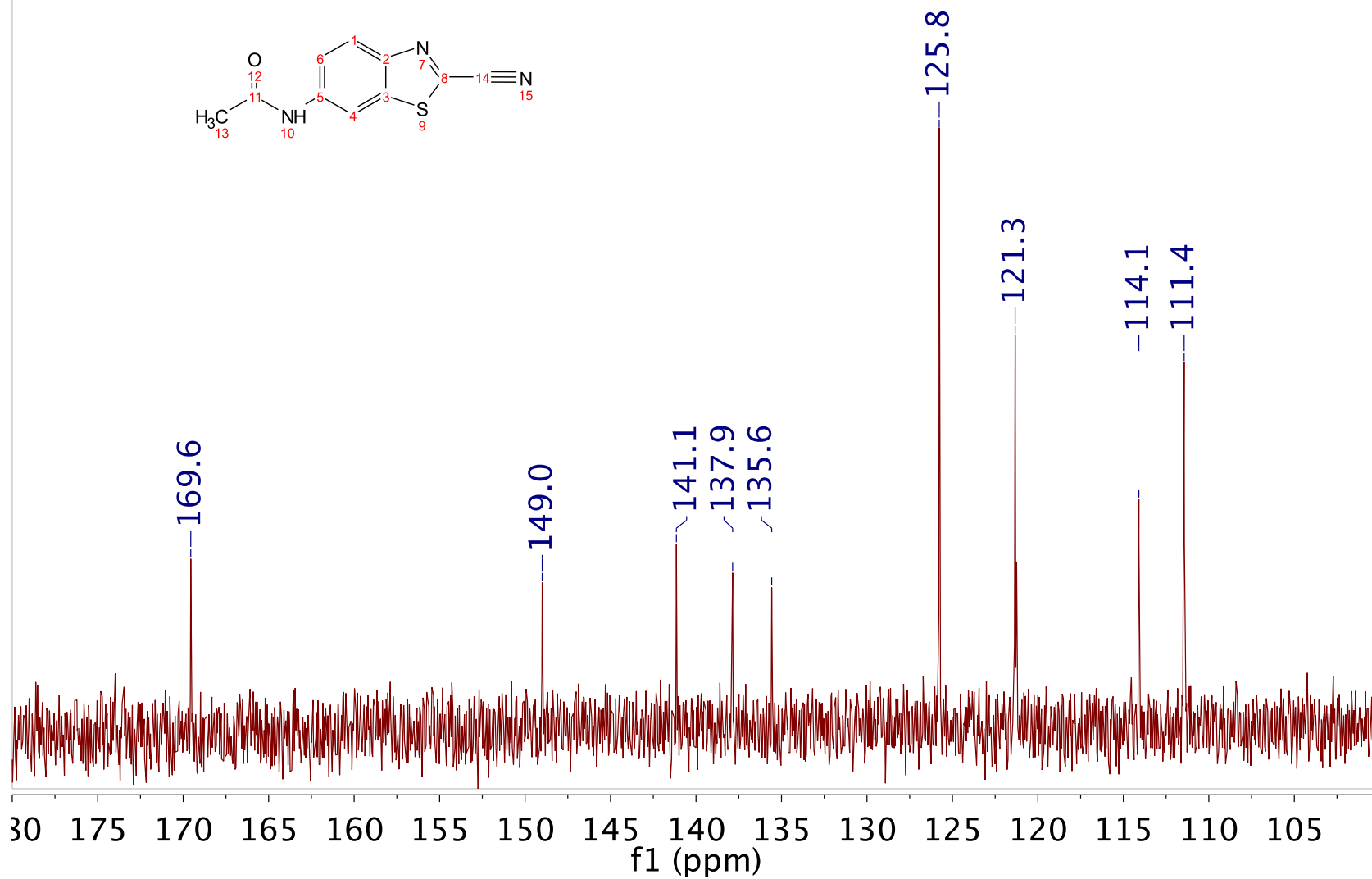
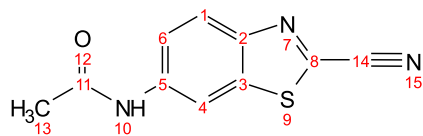
021218_cbtnac_acetone_13c
C13par



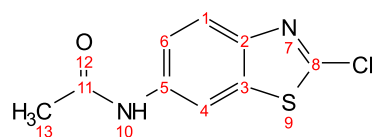
021218_cbtnac_acetone_13c
C13par



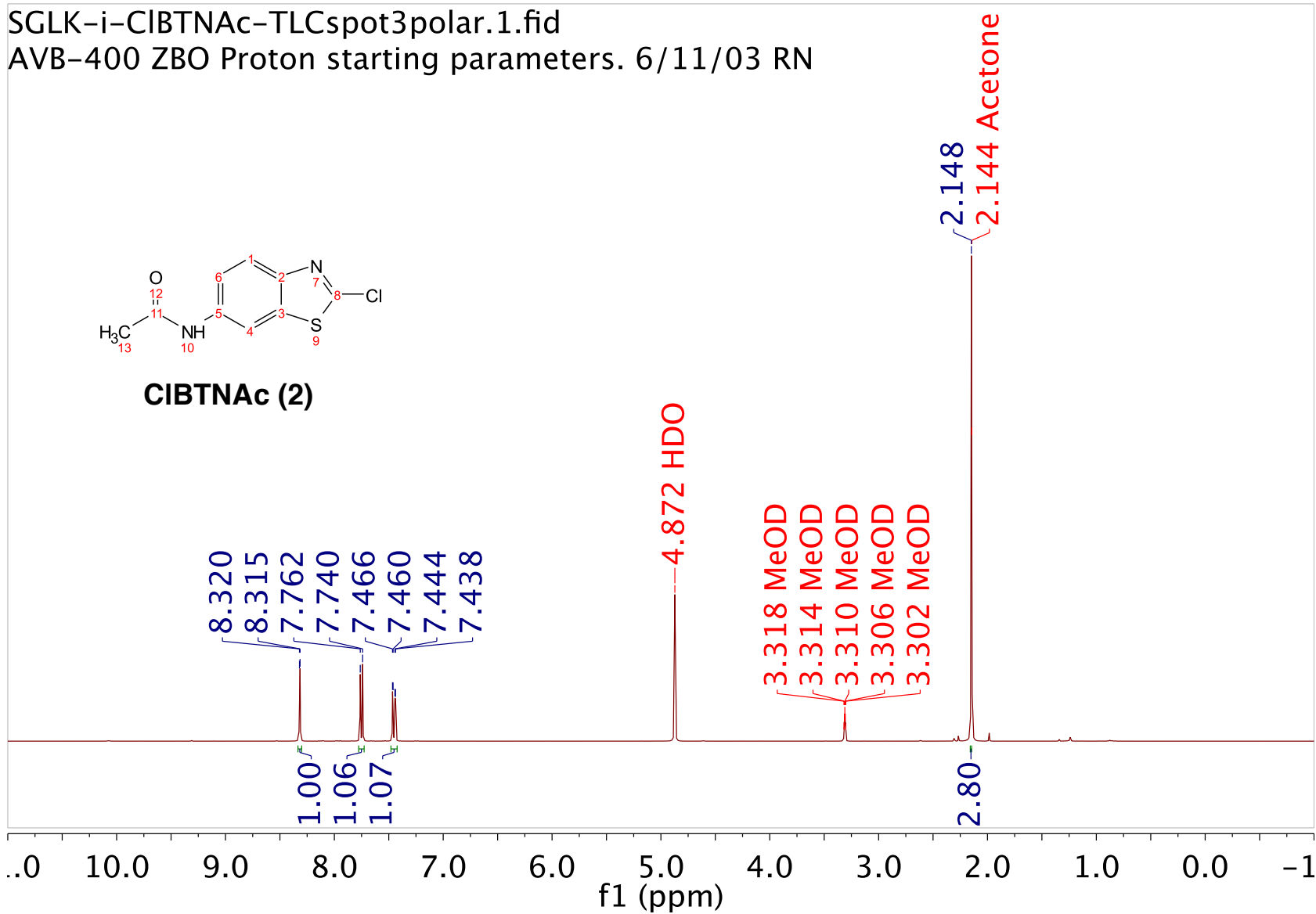
021218_cbtnac_acetone_13c
C13par



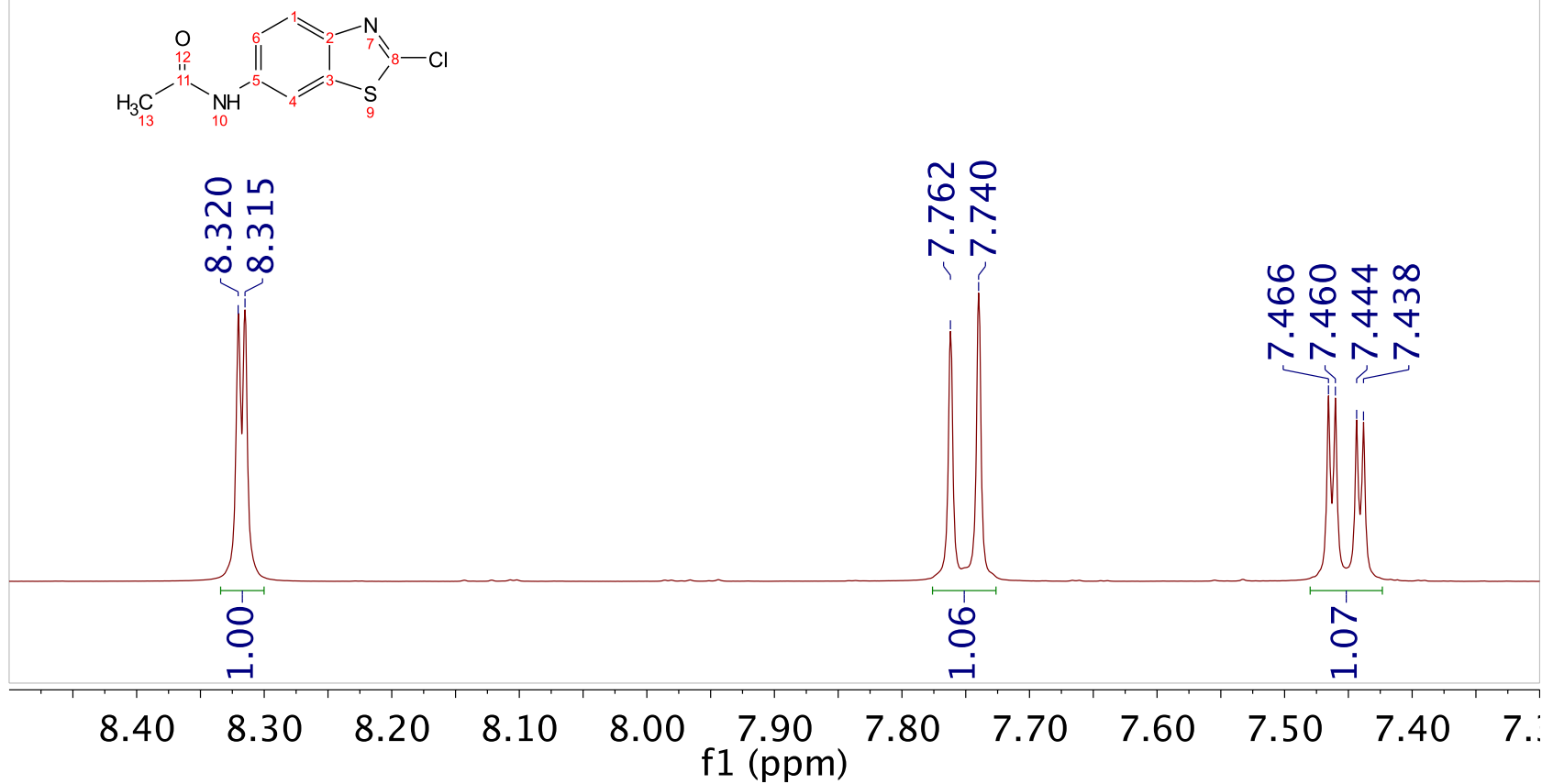
SGLK-i-CIBTNAc-TLCspot3polar.1.fid
AVB-400 ZBO Proton starting parameters. 6/11/03 RN



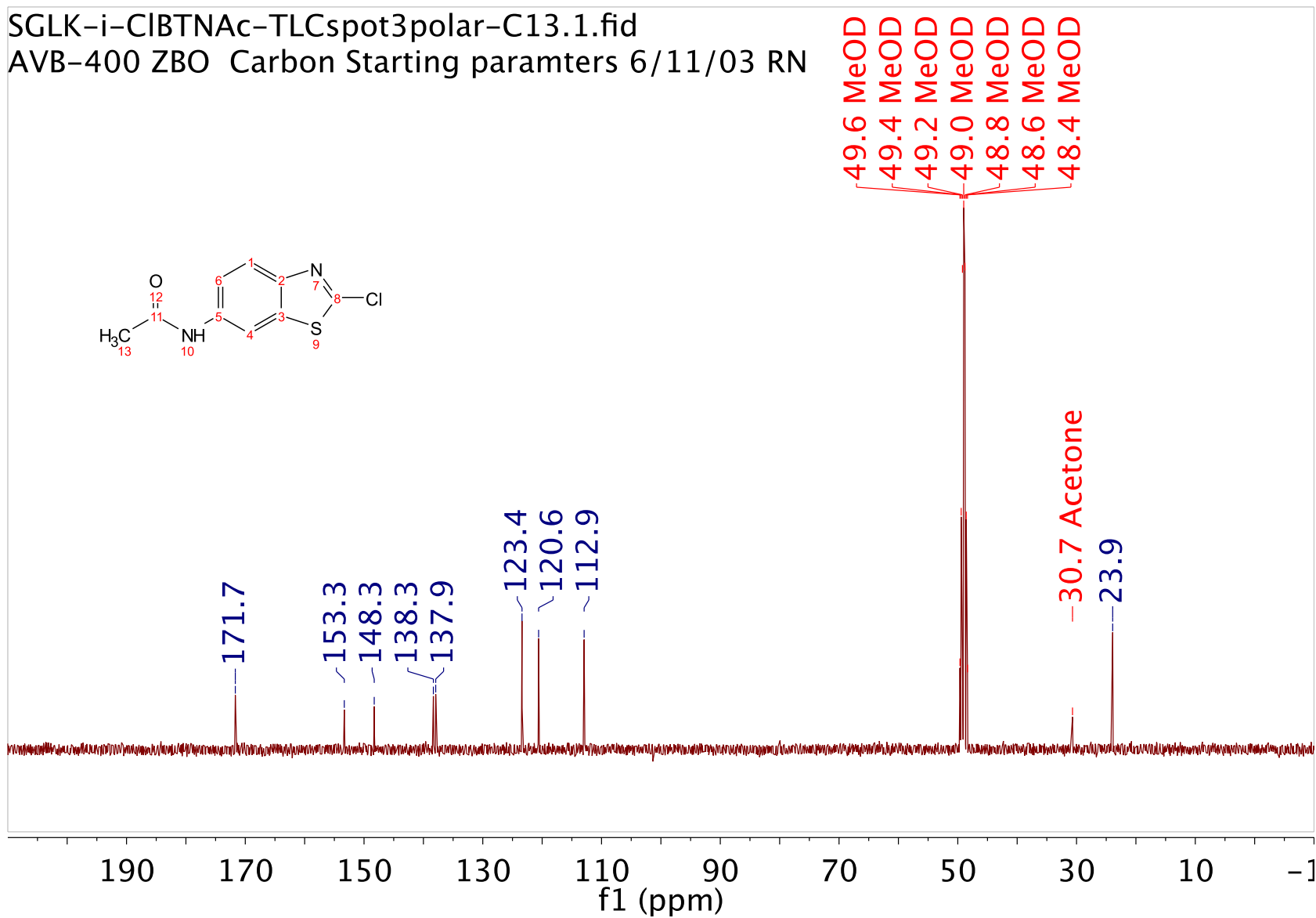
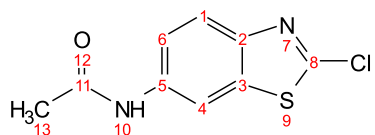
CIBTNAc (2)



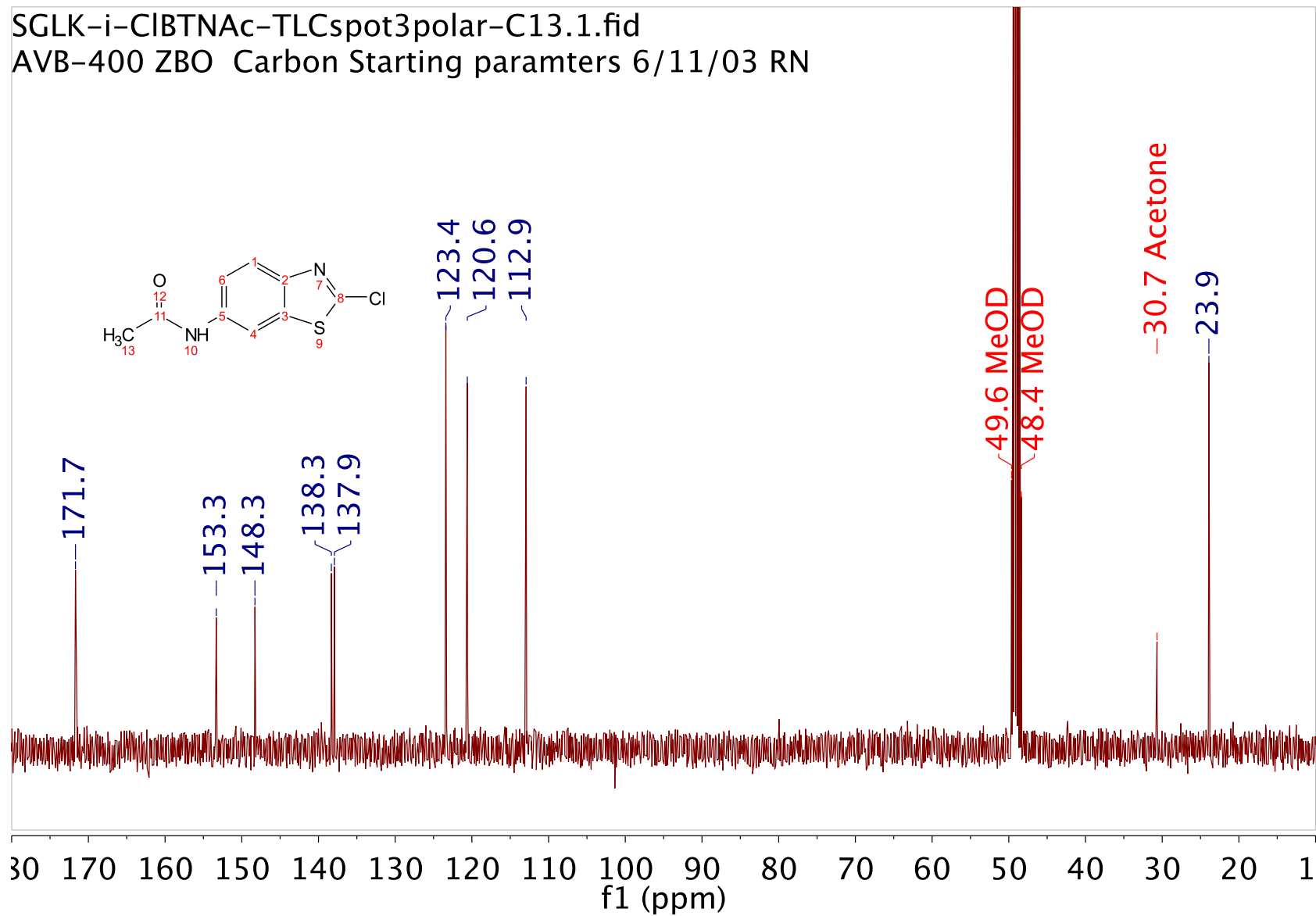
SGLK-i-CIBTNAc-TLCspot3polar.1.fid
AVB-400 ZBO Proton starting parameters. 6/11/03 RN



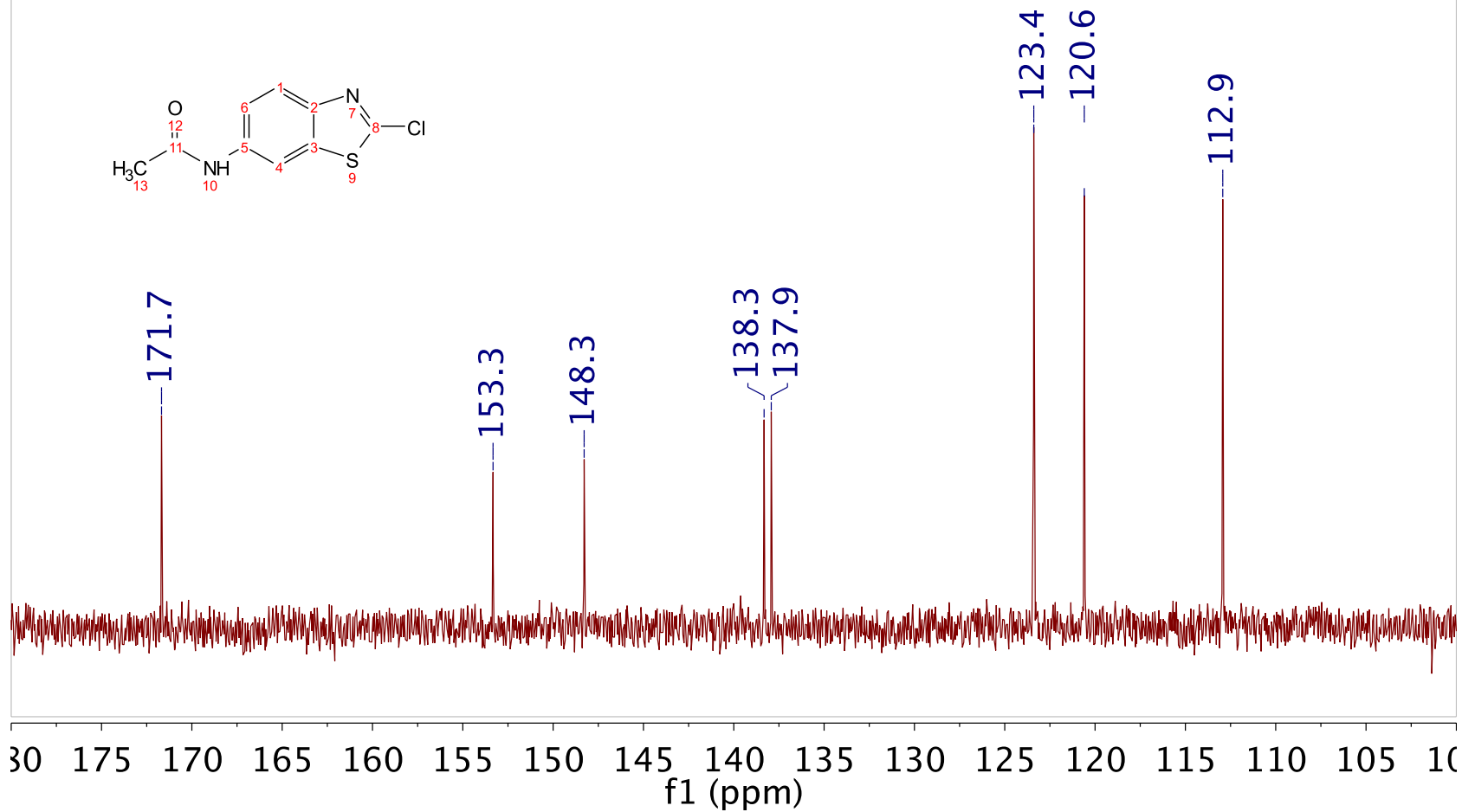
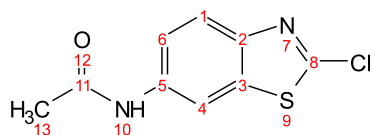
SGLK-i-CIBTNAc-TLCspot3polar-C13.1.fid
AVB-400 ZBO Carbon Starting paramters 6/11/03 RN



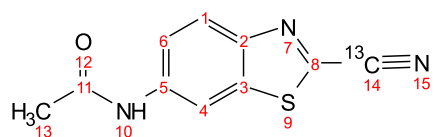
SGLK-i-CIBTNAc-TLCspot3polar-C13.1.fid
AVB-400 ZBO Carbon Starting paramters 6/11/03 RN



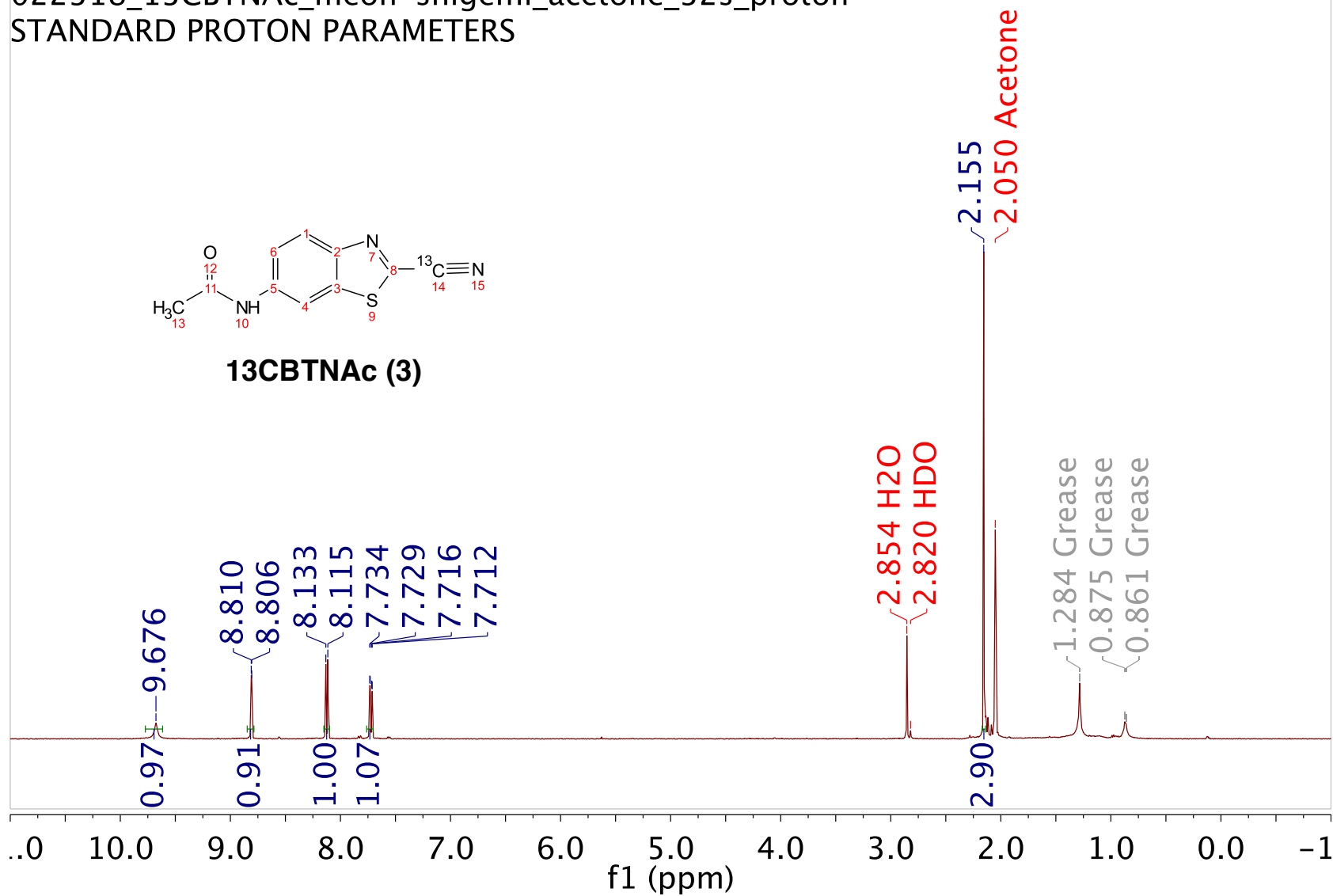
SGLK-i-CIBTNAc-TLCspot3polar-C13.1.fid
AVB-400 ZBO Carbon Starting paramters 6/11/03 RN



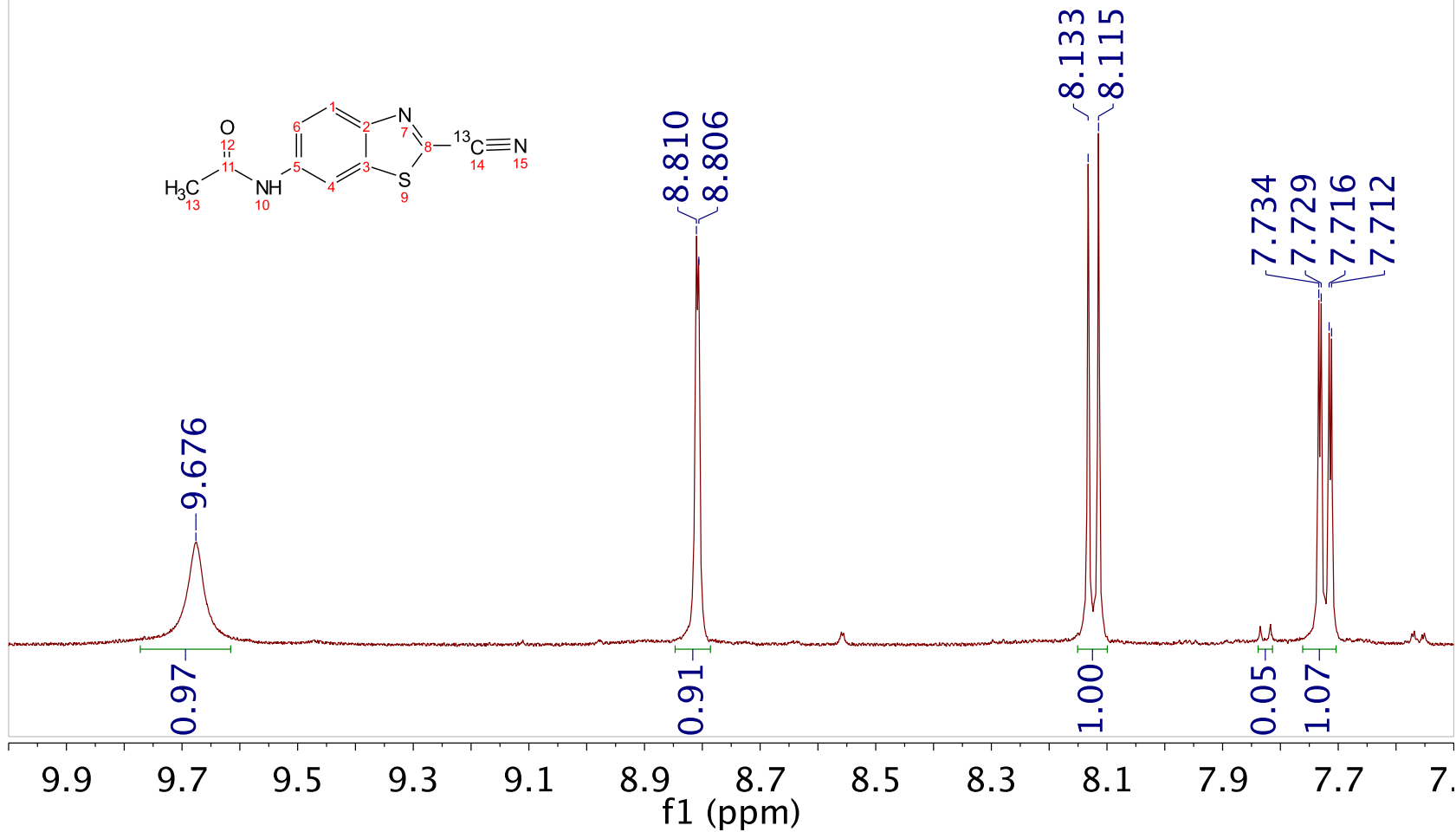
022318_13CBTNAc_meoh-shigemi_acetone_32s_proton
STANDARD PROTON PARAMETERS



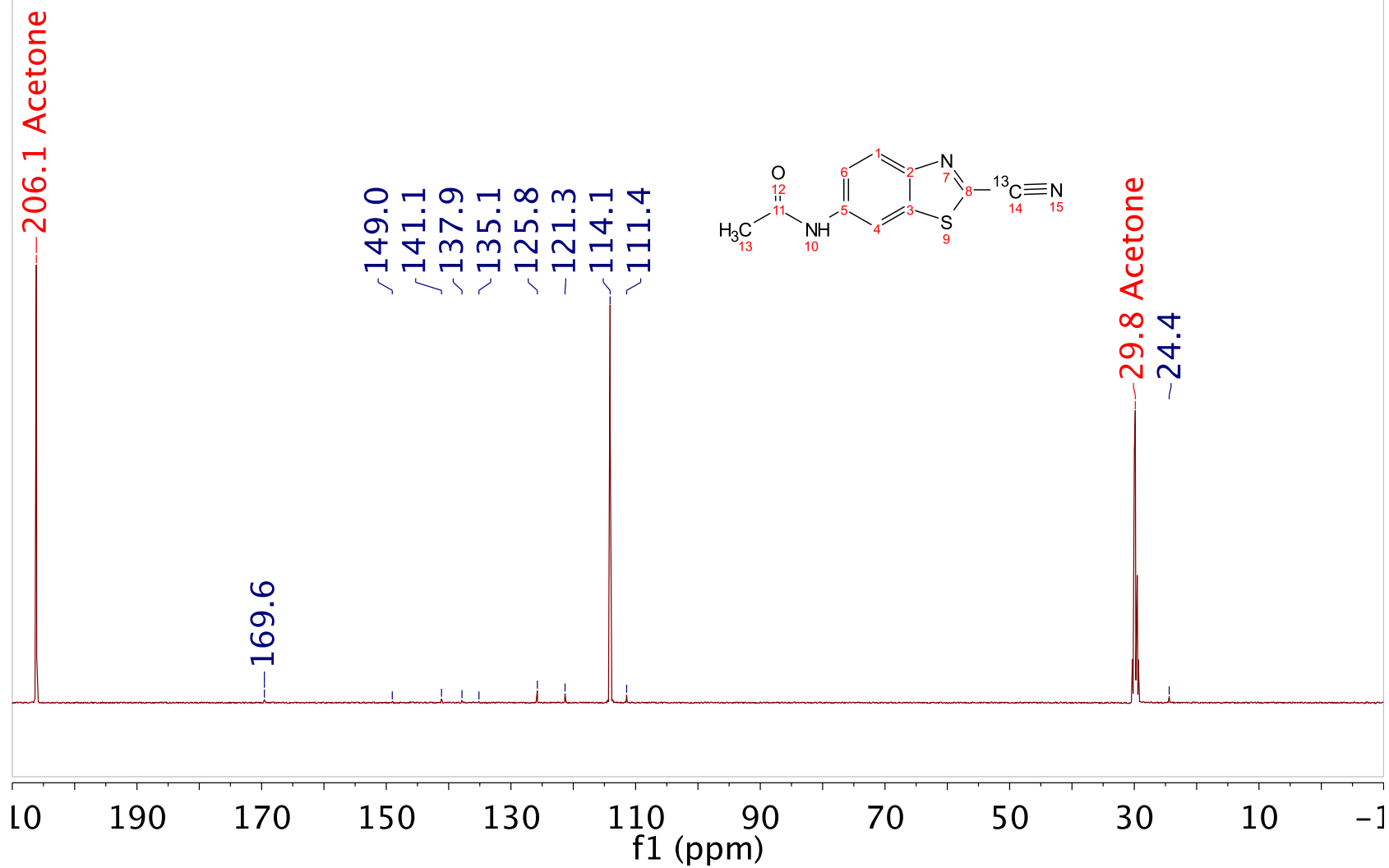
13CBTNAc (3)



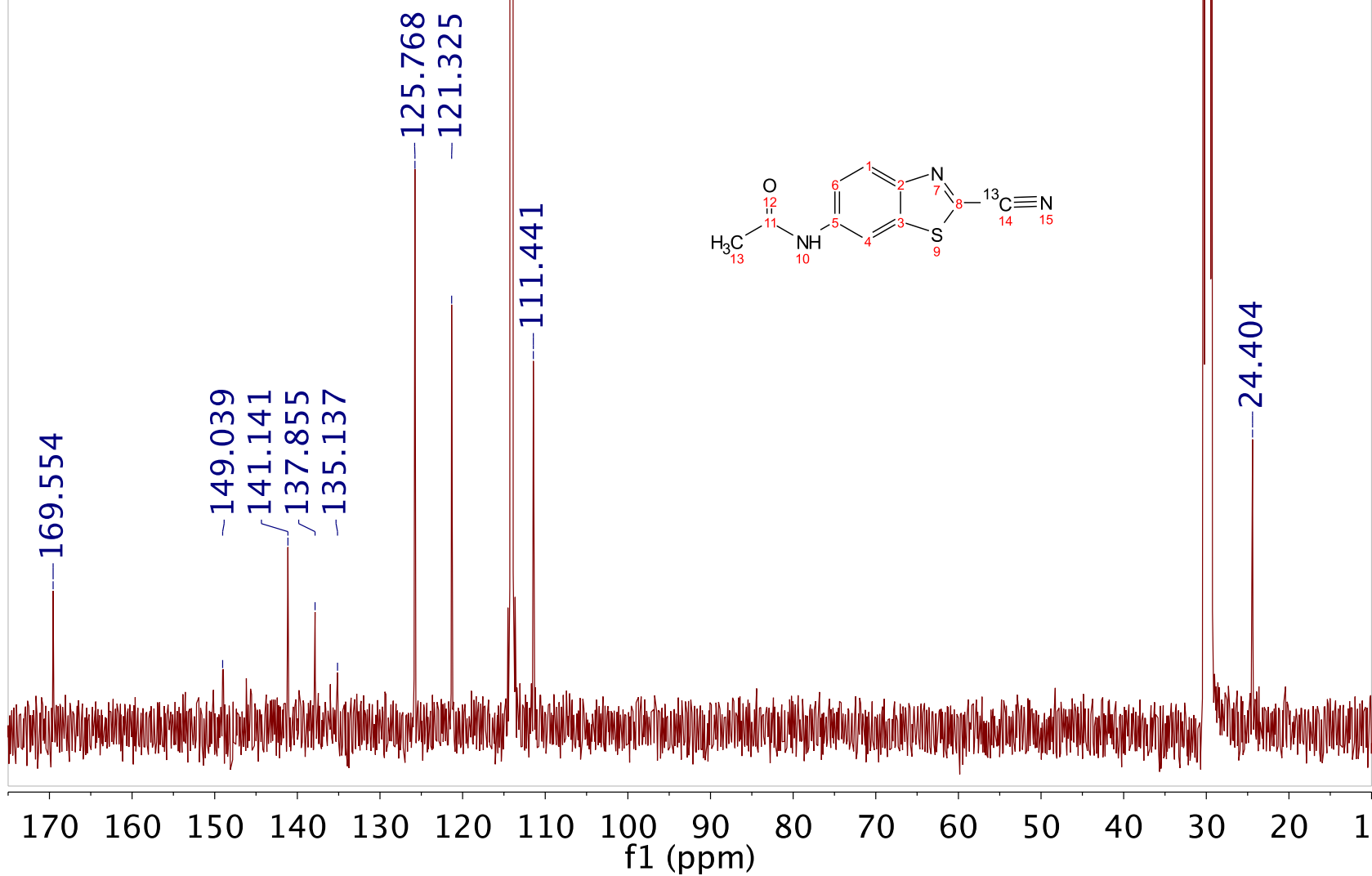
022318_13CBTNAc_meoh-shigemi_acetone_32s_proton
STANDARD PROTON PARAMETERS



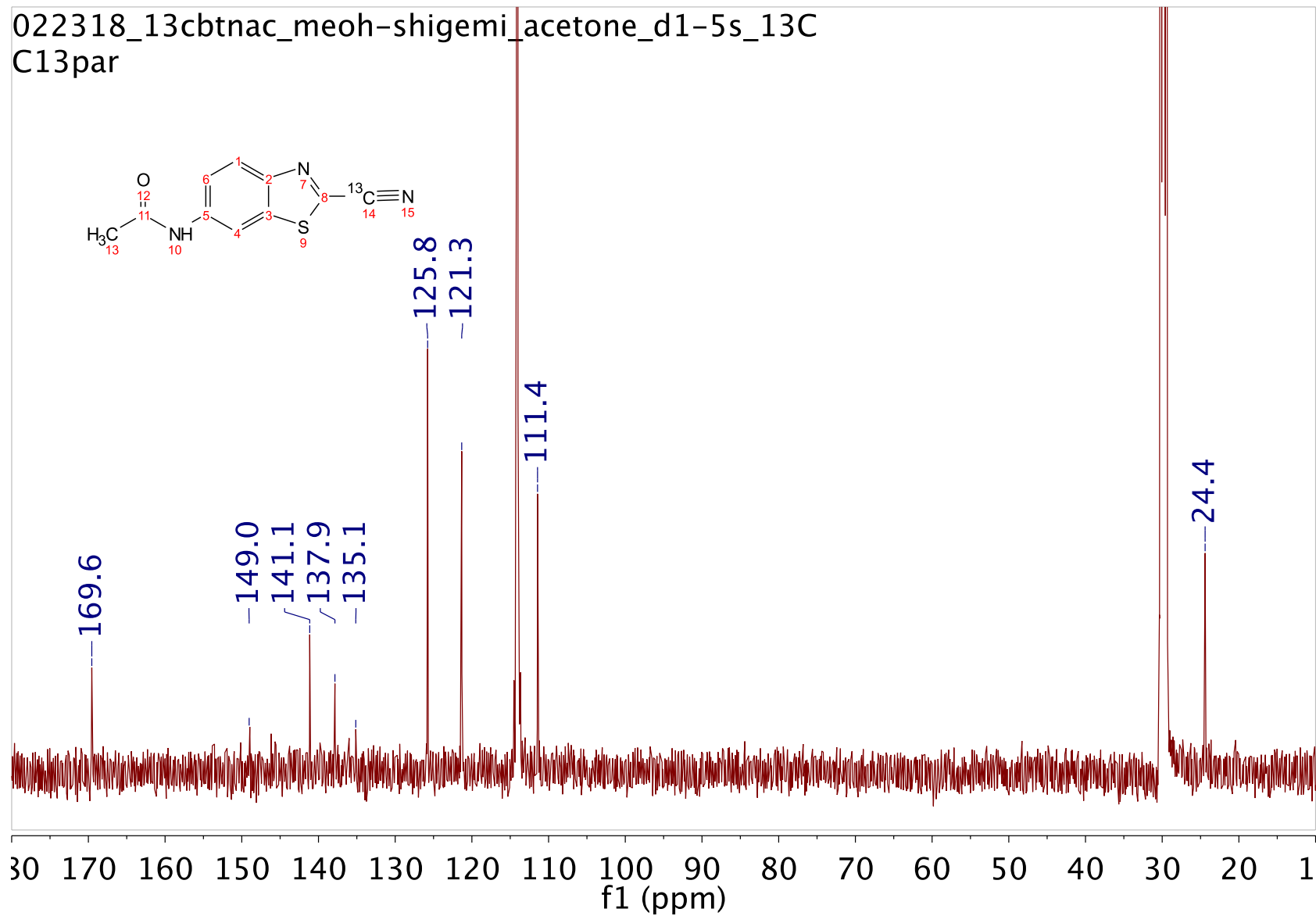
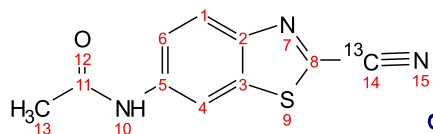
022318_13cbtnac_meoh-shigemi_acetone_d1-5s_13C
C13par



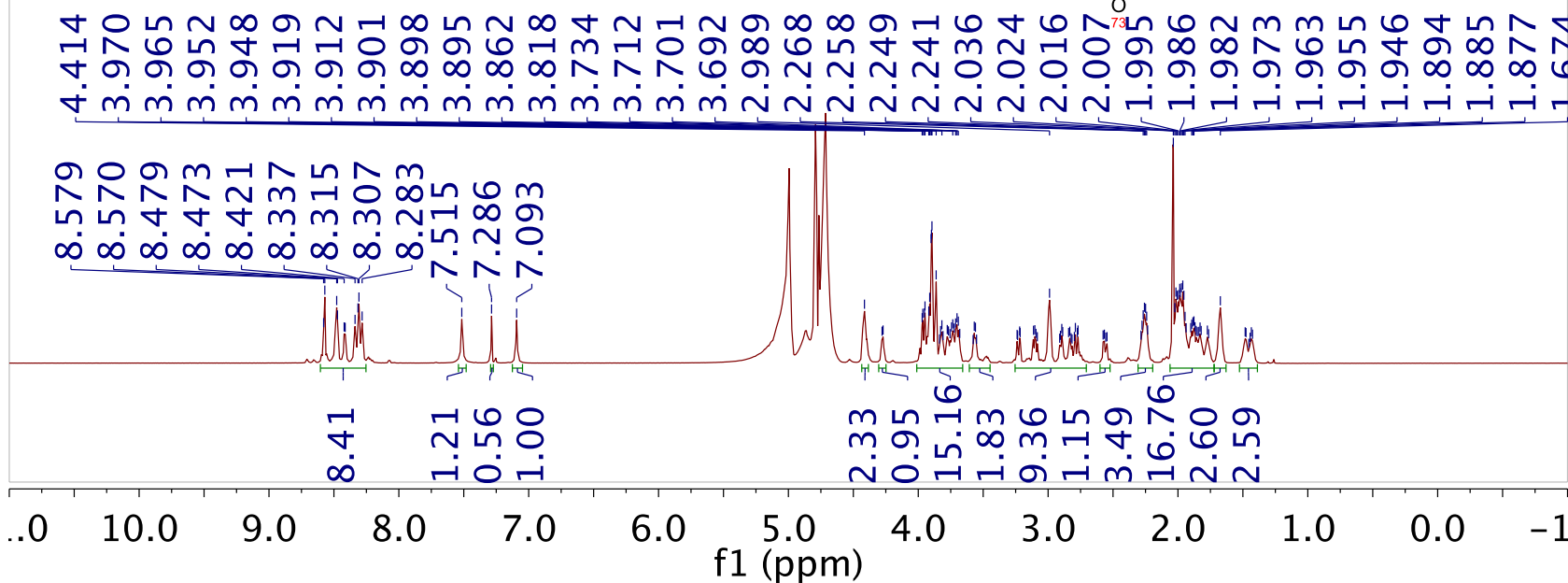
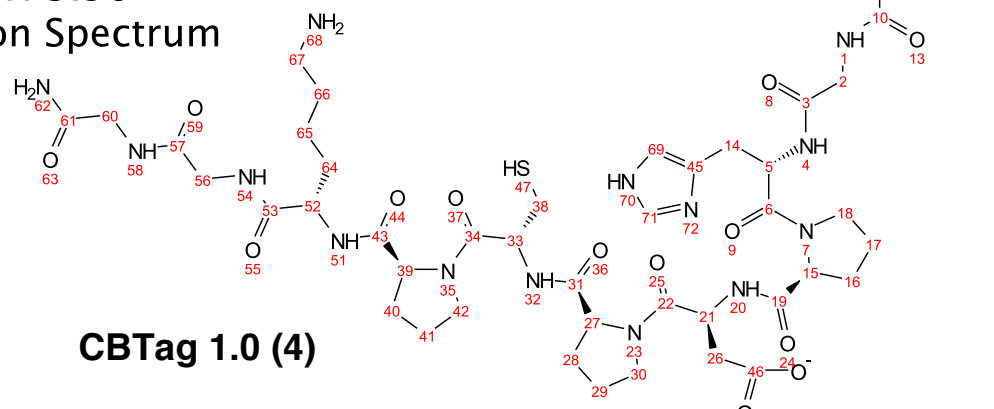
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C13par



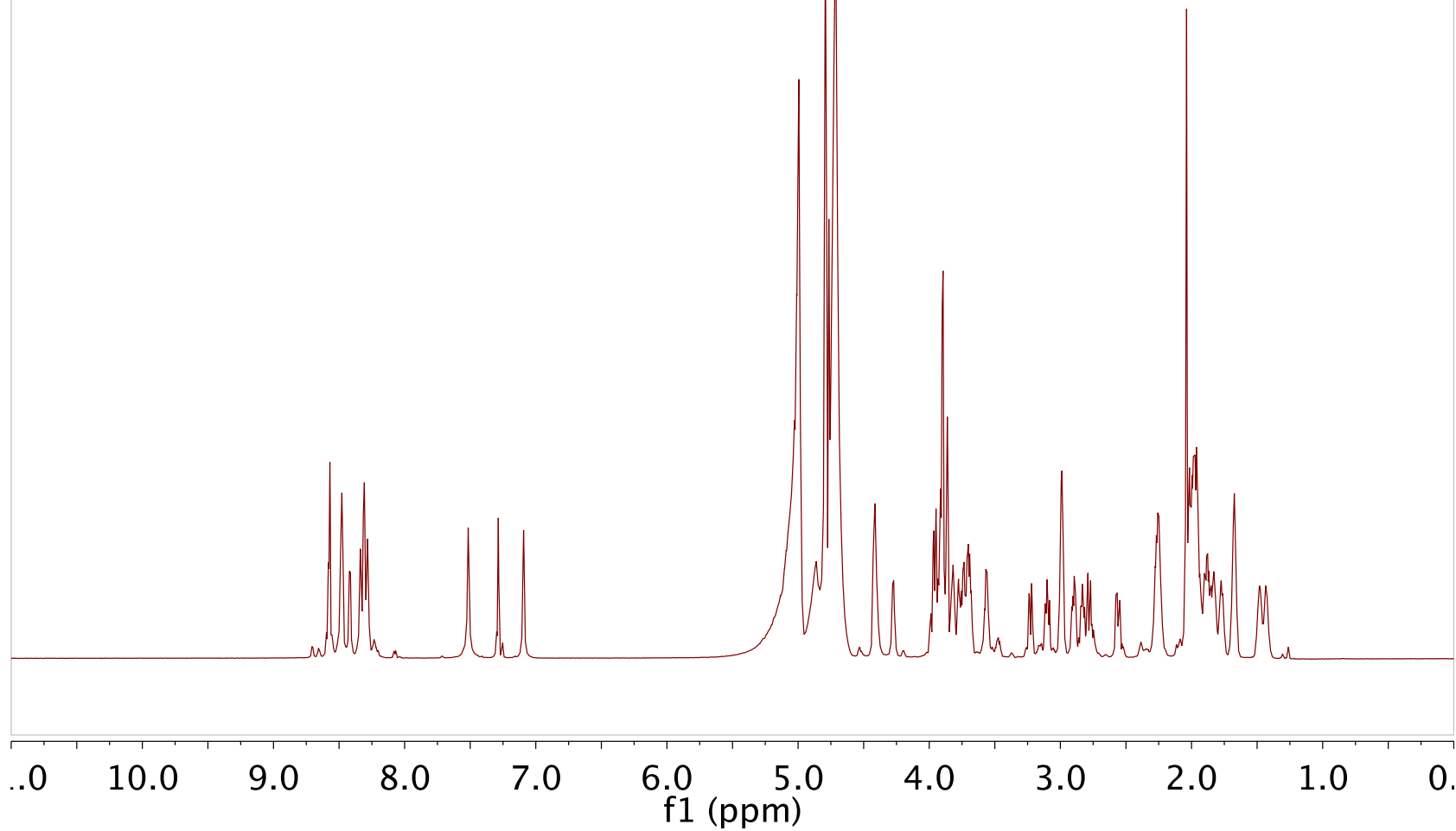
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C13par



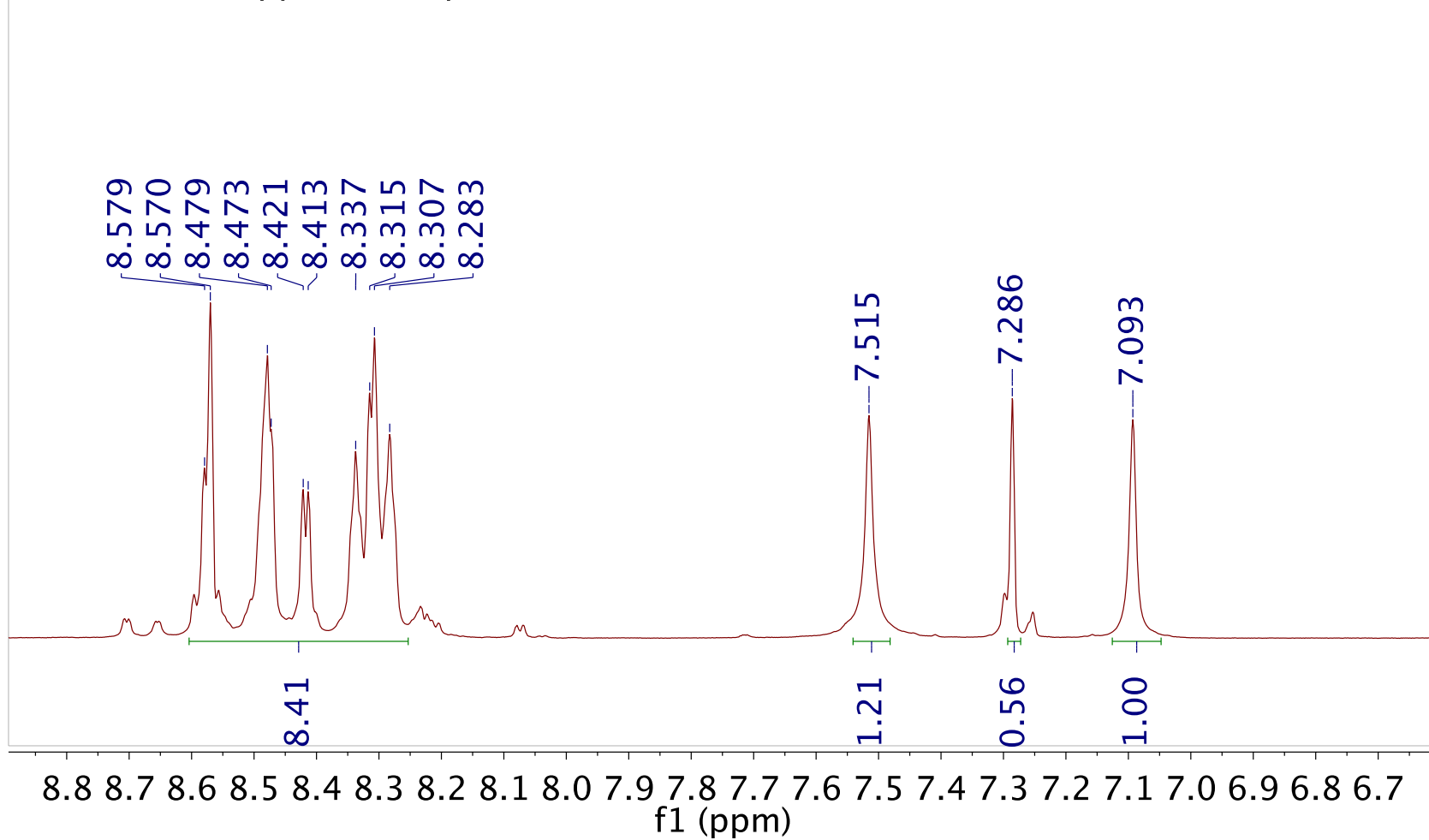
160622_PEPFOLD-3_1H1Dpr_25C
 PEPFOLD-3 (acetyl-GGHPDPCPKGG=amide) - 6/22/16
 ~7.4 mM in 10% D2O, pH 3.98
 Presat Water Suppression Spectrum



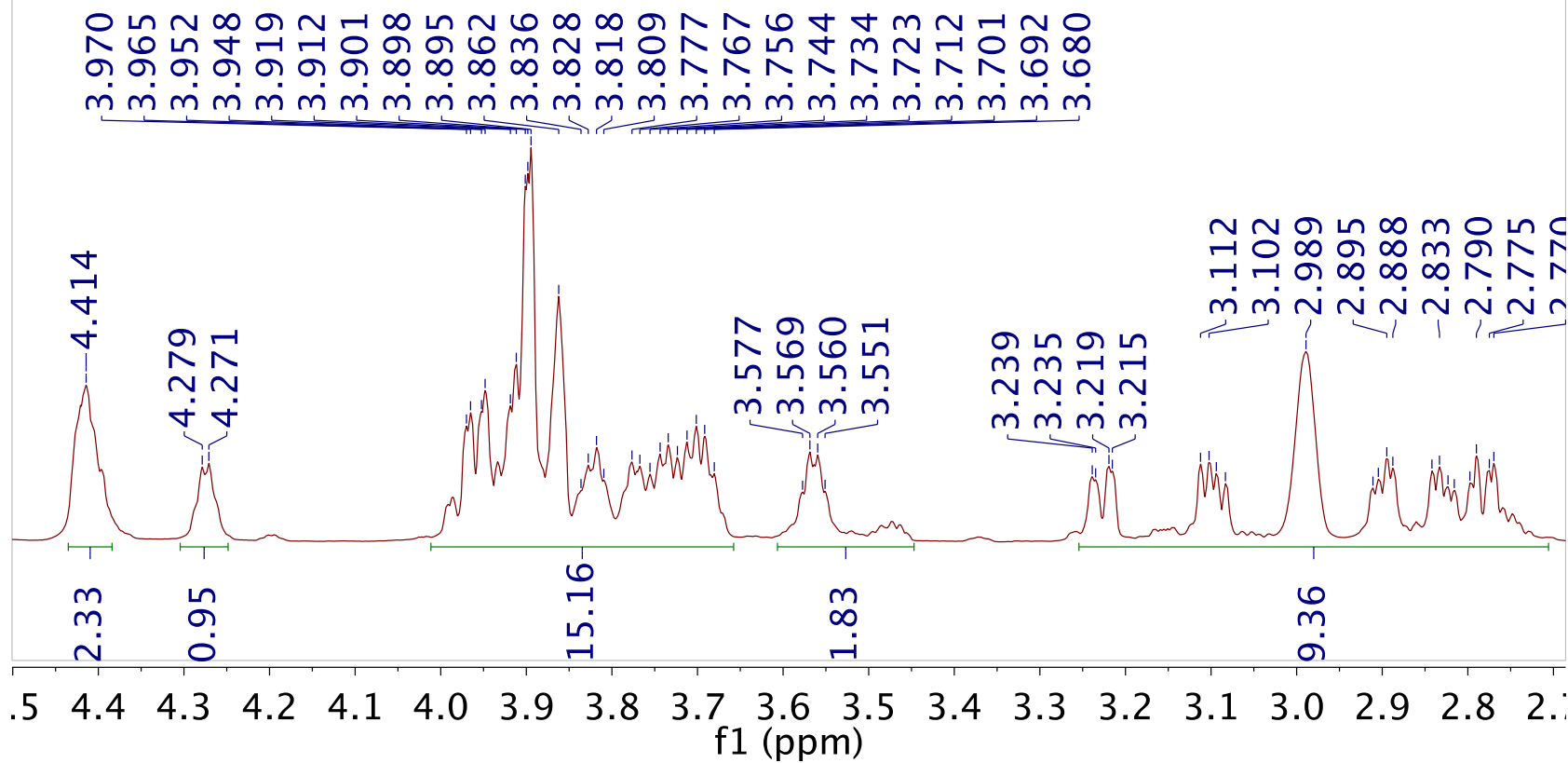
160622_PEPFOLD-3_1H1Dpr_25C
PEPFOLD-3 (acetyl-GGHPDPCPKGG=amide) - 6/22/16
~7.4 mM in 10% D2O, pH 3.98
Presat Water Suppression Spectrum



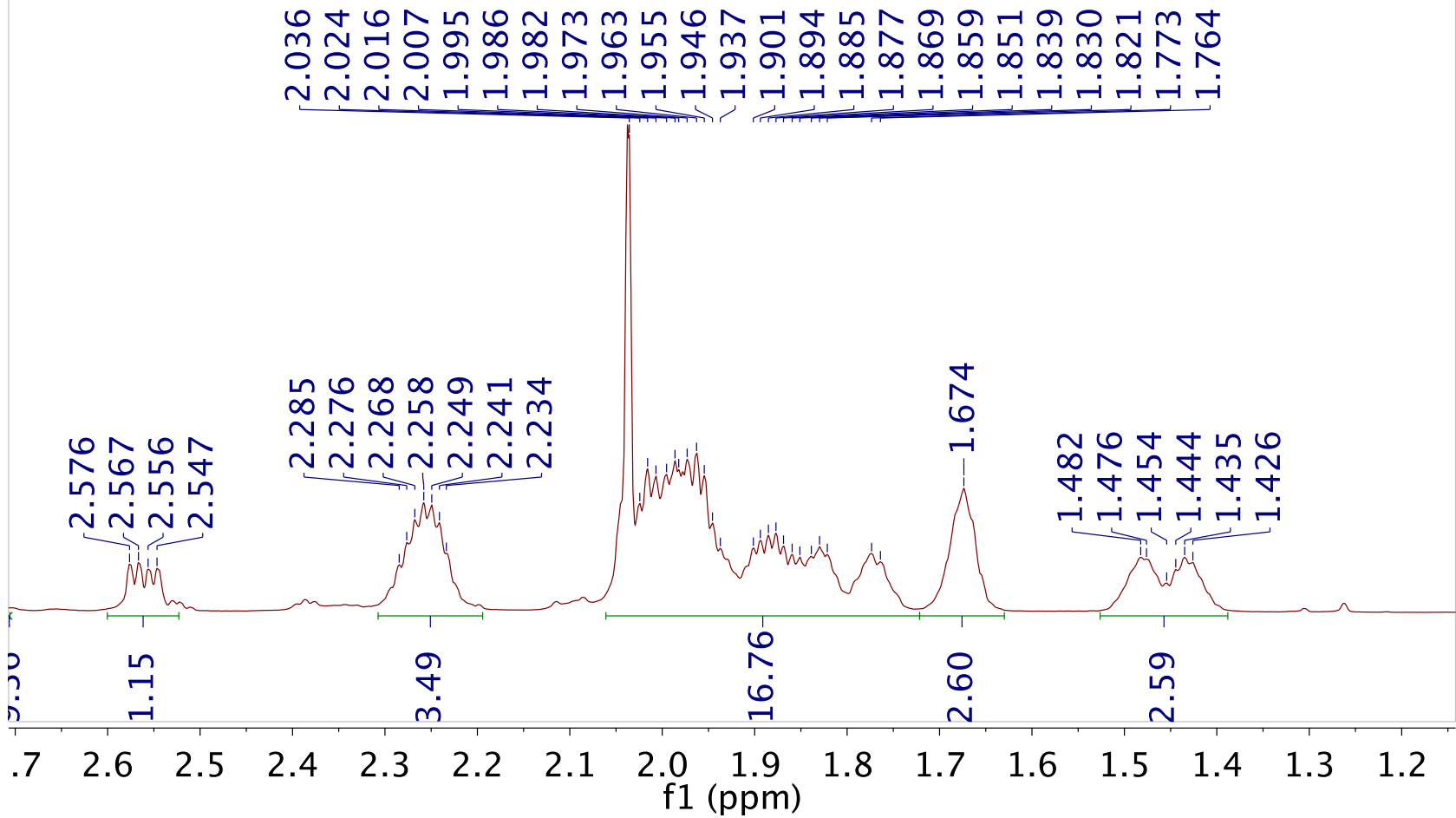
160622_PEPFOLD-3_1H1Dpr_25C
PEPFOLD-3 (acetyl-GGHPDPCPKGG=amide) - 6/22/16
~7.4 mM in 10% D2O, pH 3.98
Presat Water Suppression Spectrum



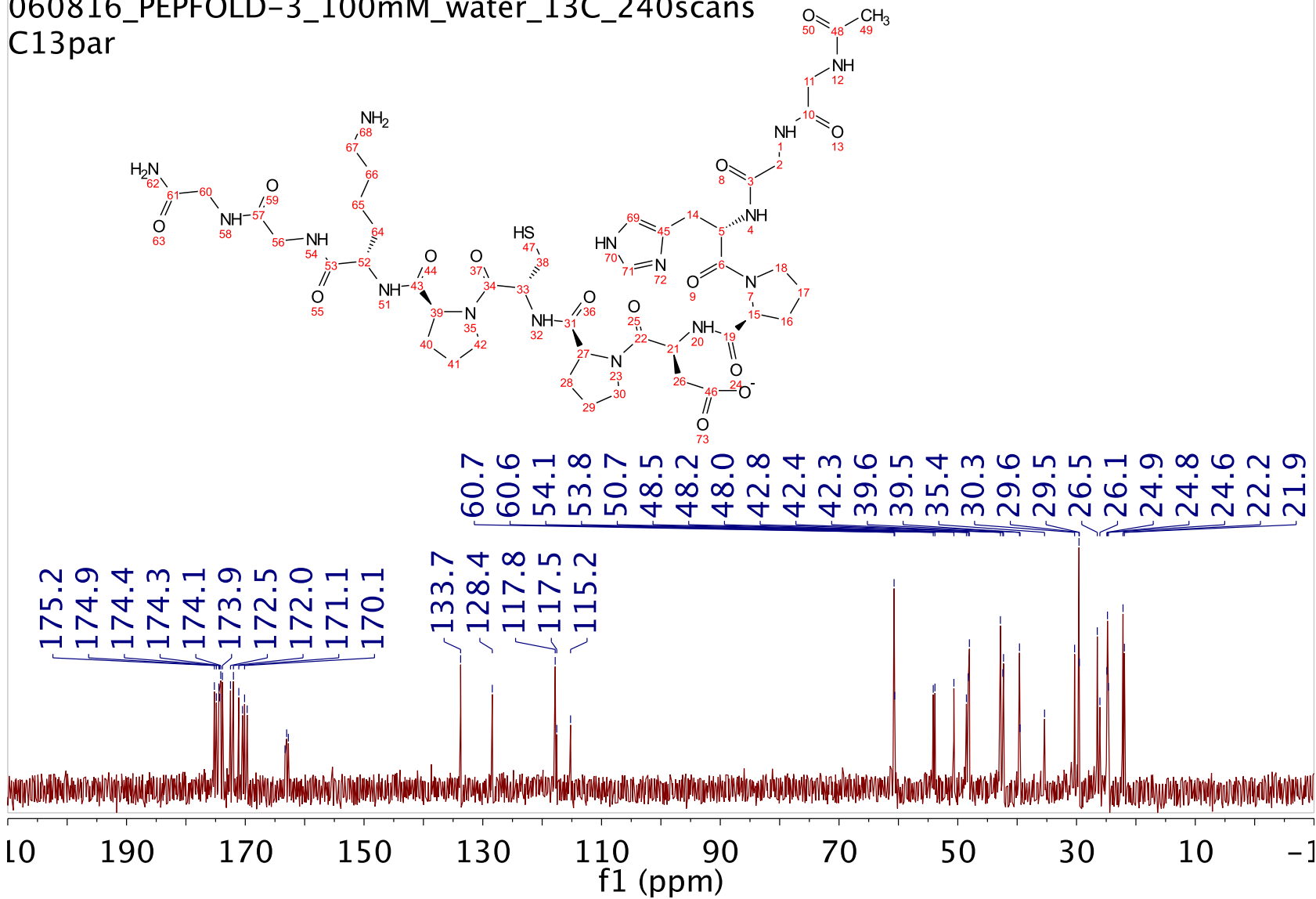
160622_PEPFOLD-3_1H1Dpr_25C
PEPFOLD-3 (acetyl-GGHPDPCPKGG=amide) - 6/22/16
~7.4 mM in 10% D2O, pH 3.98
Presat Water Suppression Spectrum



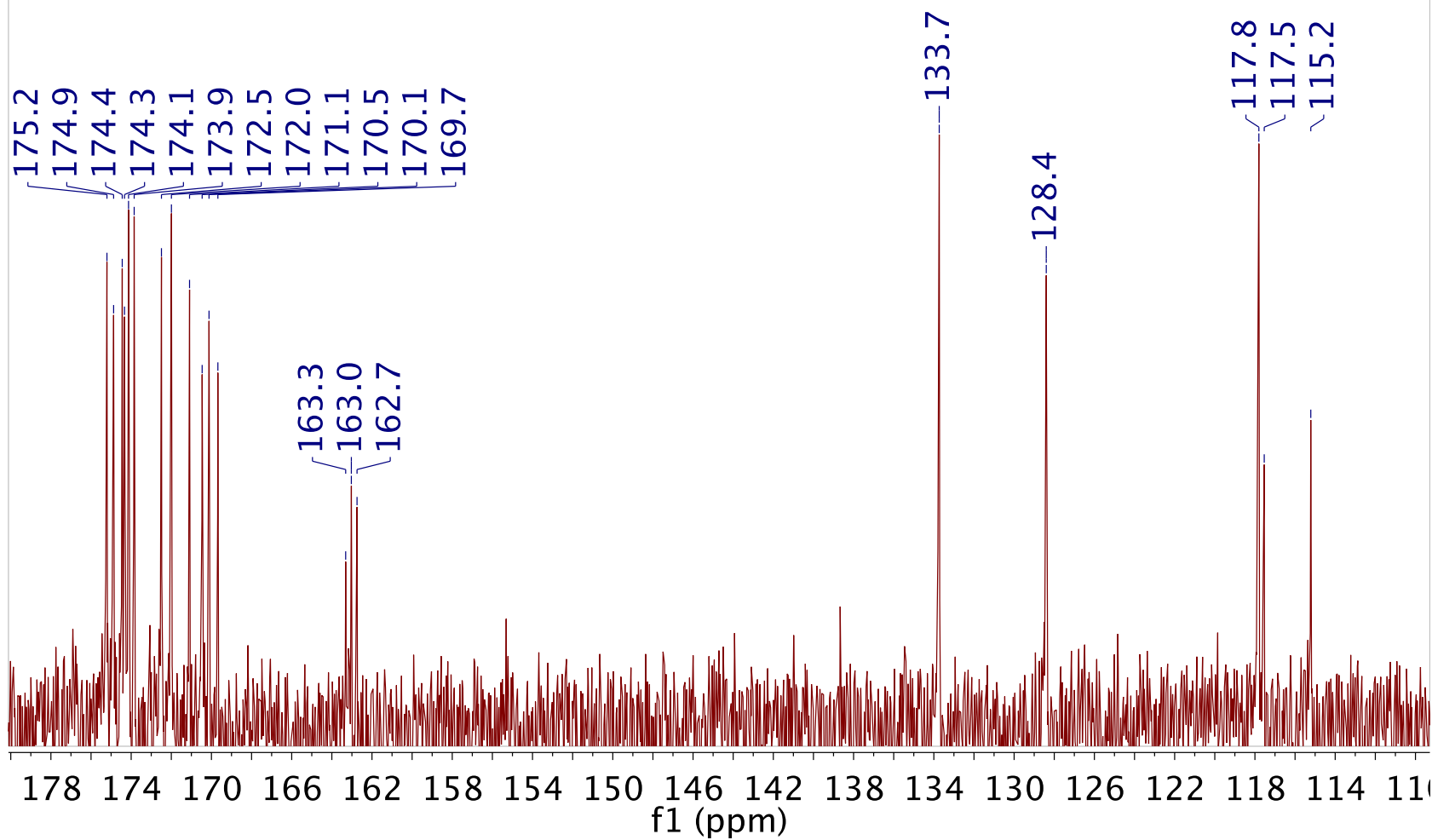
160622_PEPFOLD-3_1H1Dpr_25C
 PEPFOLD-3 (acetyl-GGHPDPCPKGG=amide) - 6/22/16
 ~7.4 mM in 10% D2O, pH 3.98
 Presat Water Suppression Spectrum



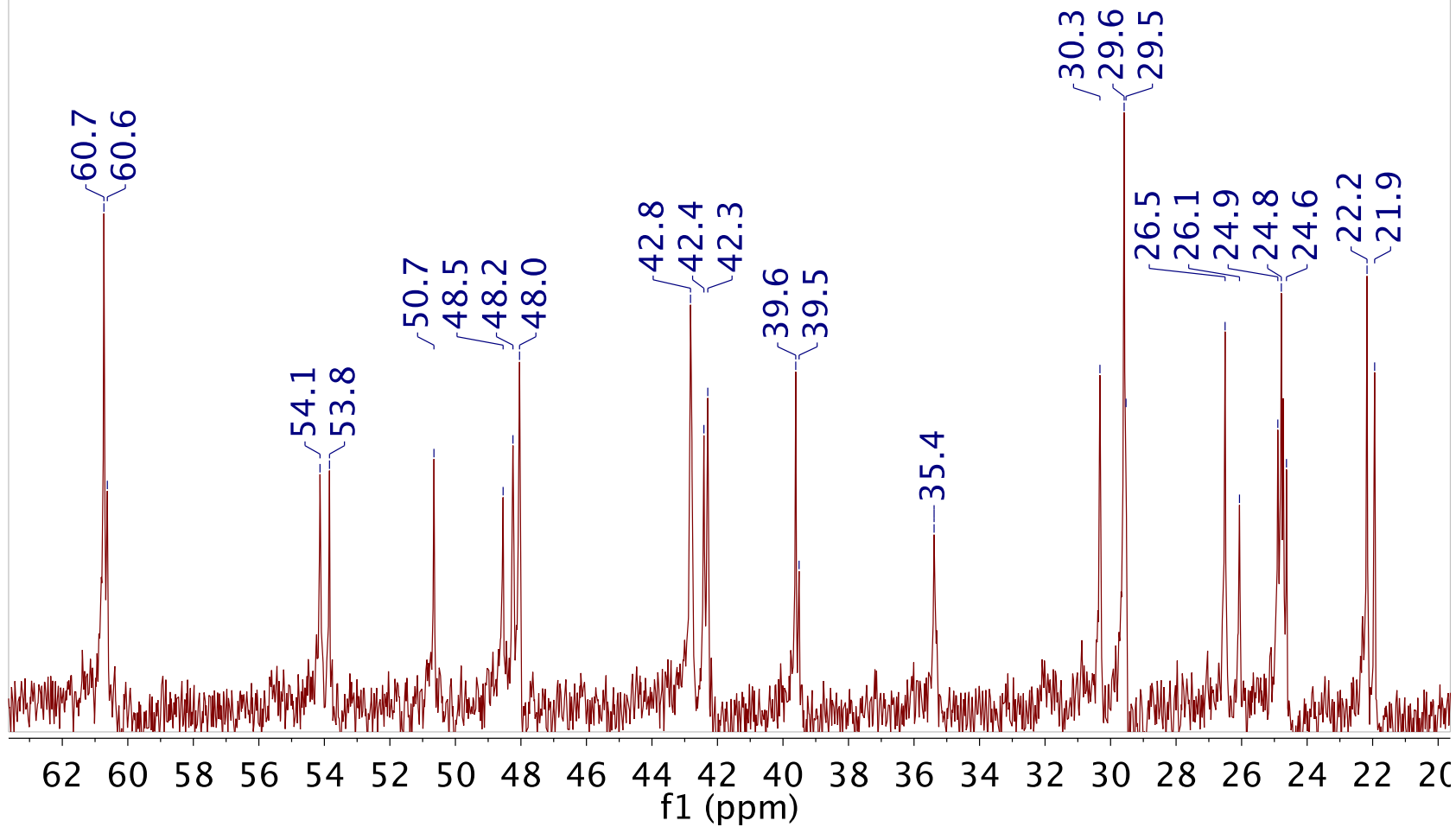
060816_PEPFOLD-3_100mM_water_13C_240scans
C13par



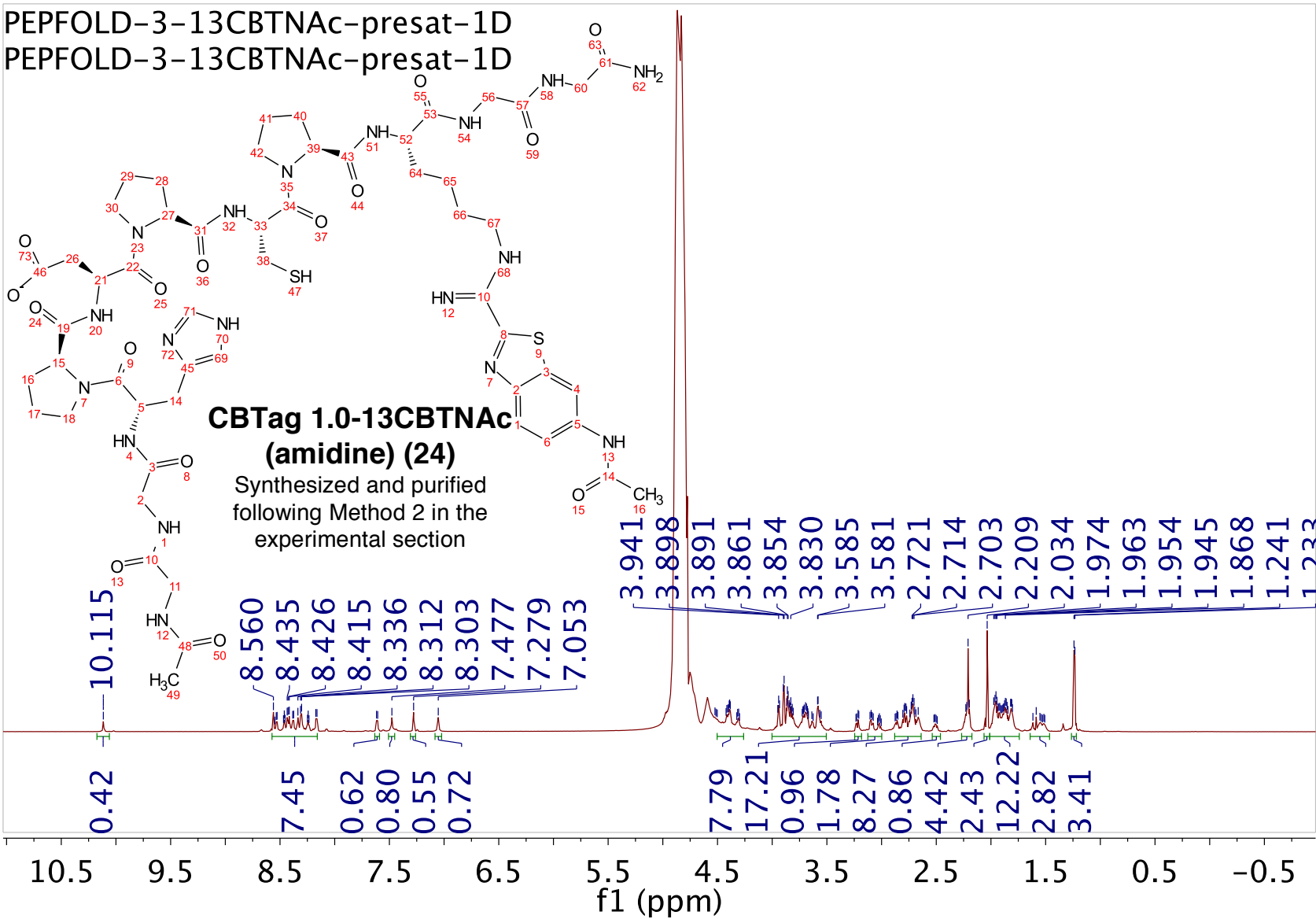
060816_PEPFOLD-3_100mM_water_13C_240scans
C13par



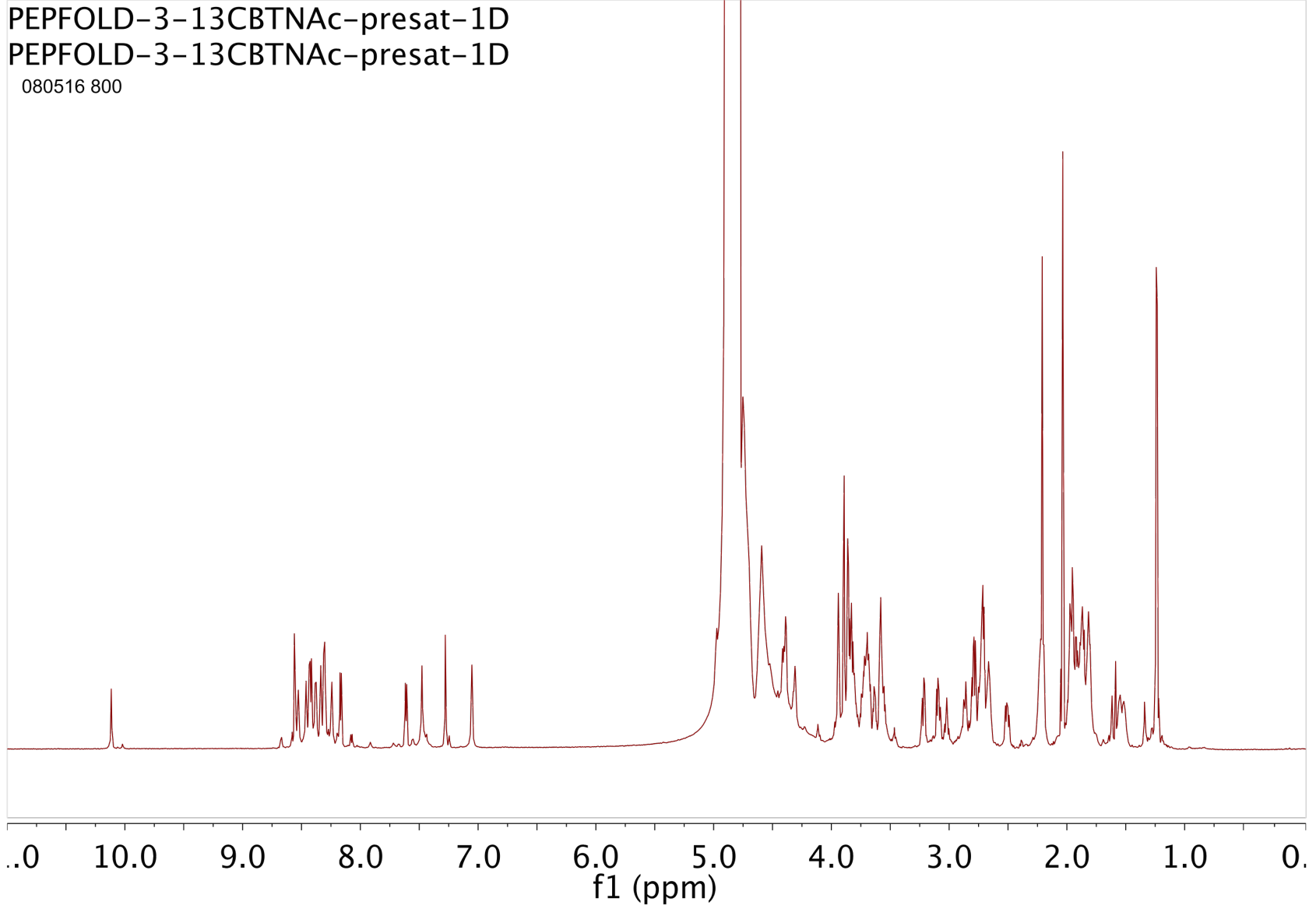
060816_PEPFOLD-3_100mM_water_13C_240scans
C13par



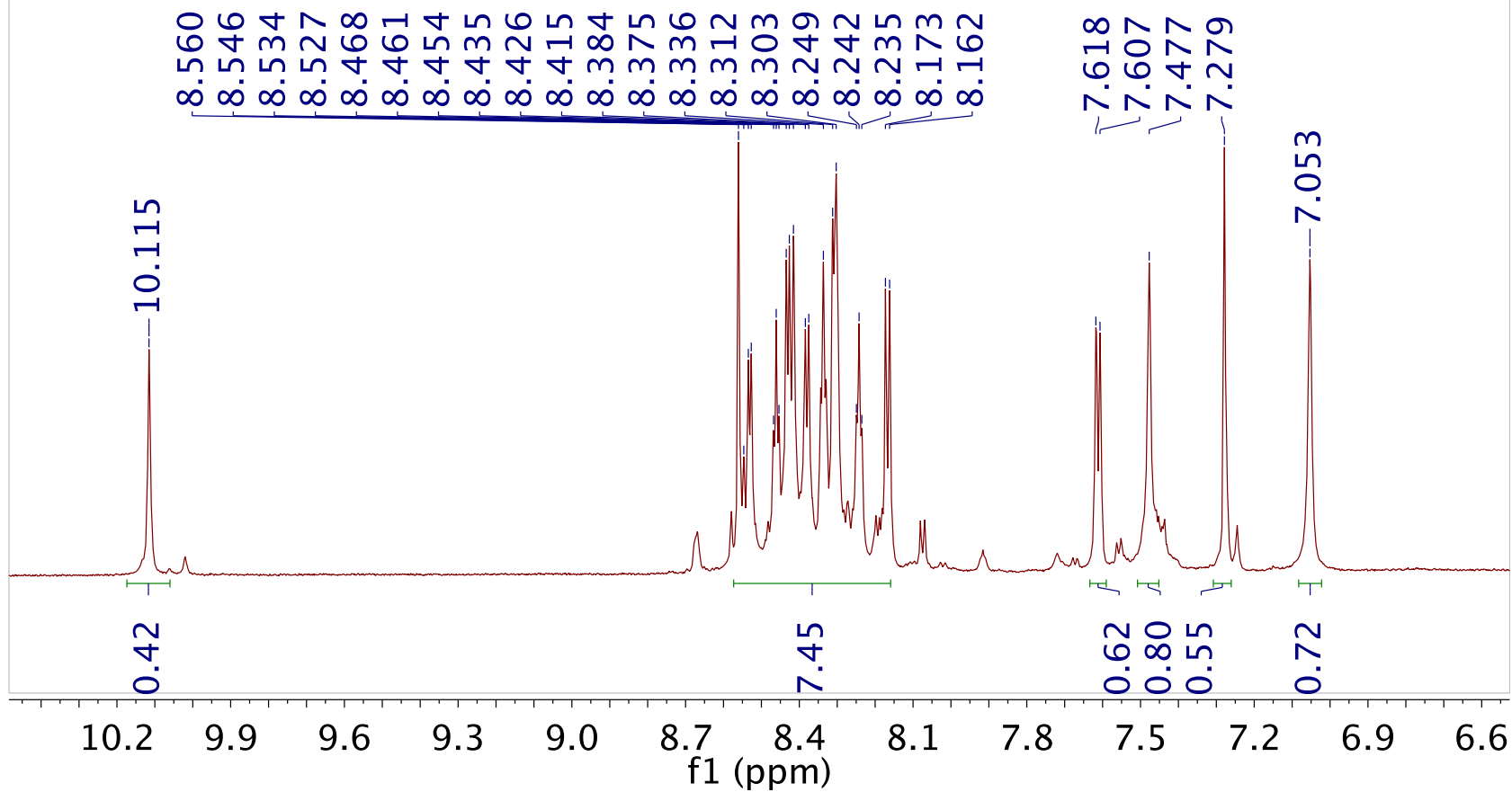
PEPFOLD-3-13CBTNAc-presat-1D
PEPFOLD-3-13CBTNAc-presat-1D



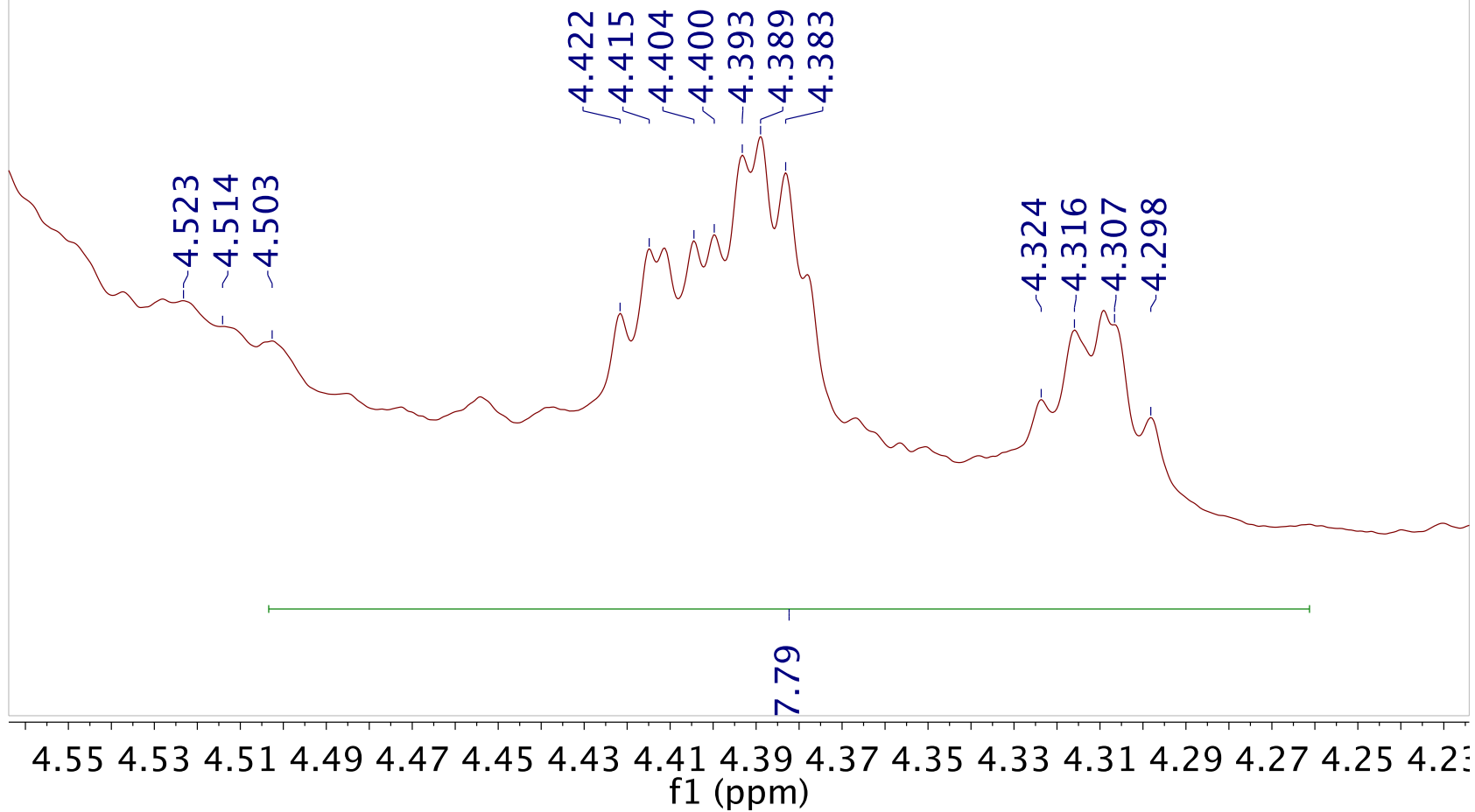
PEPFOLD-3-13CBTNAc-presat-1D
PEPFOLD-3-13CBTNAc-presat-1D
080516 800



PEPFOLD-3-13CBTNAC-presat-1D
PEPFOLD-3-13CBTNAC-presat-1D

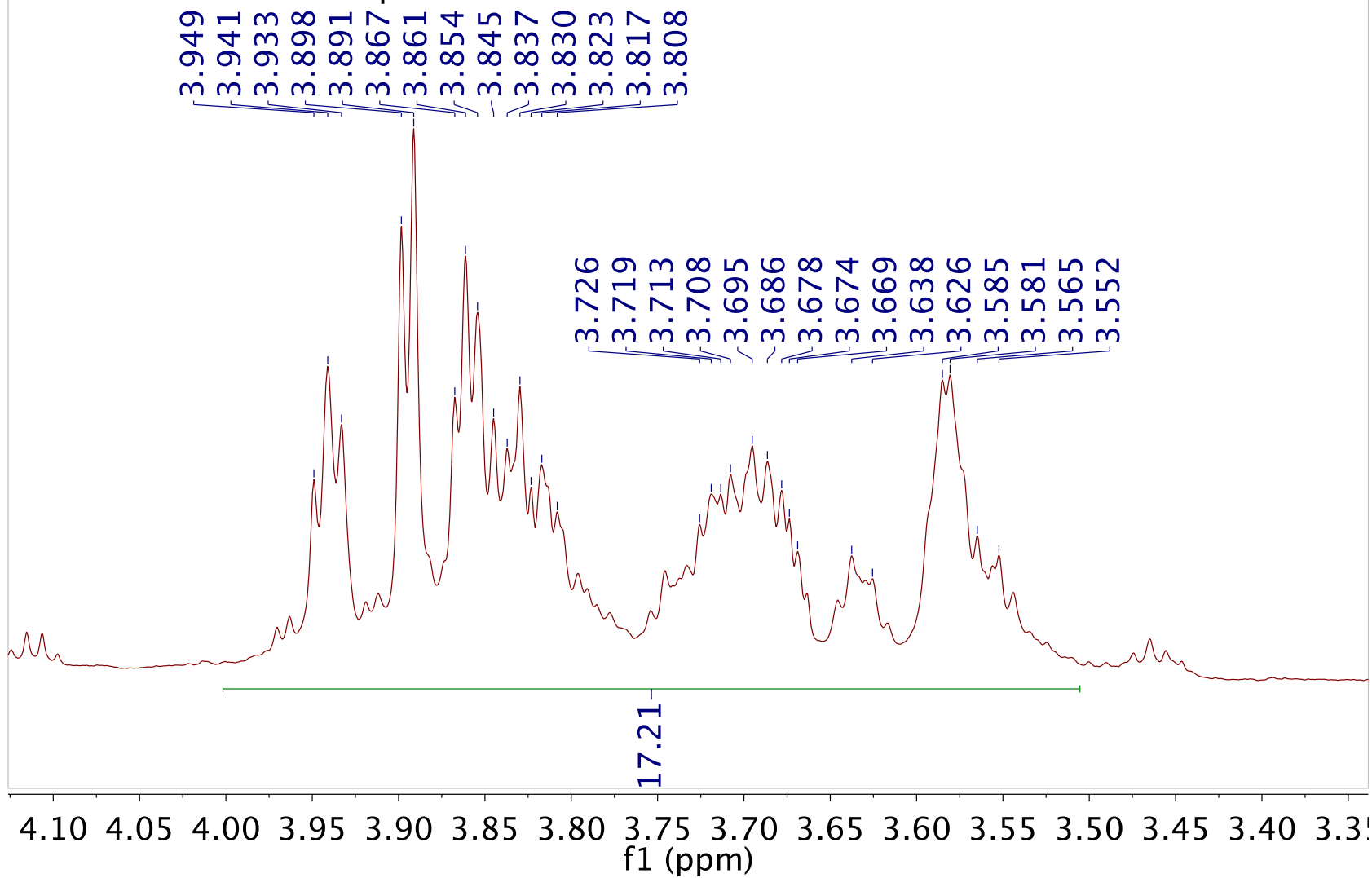


PEPFOLD-3-13CBTNAc-presat-1D
PEPFOLD-3-13CBTNAc-presat-1D

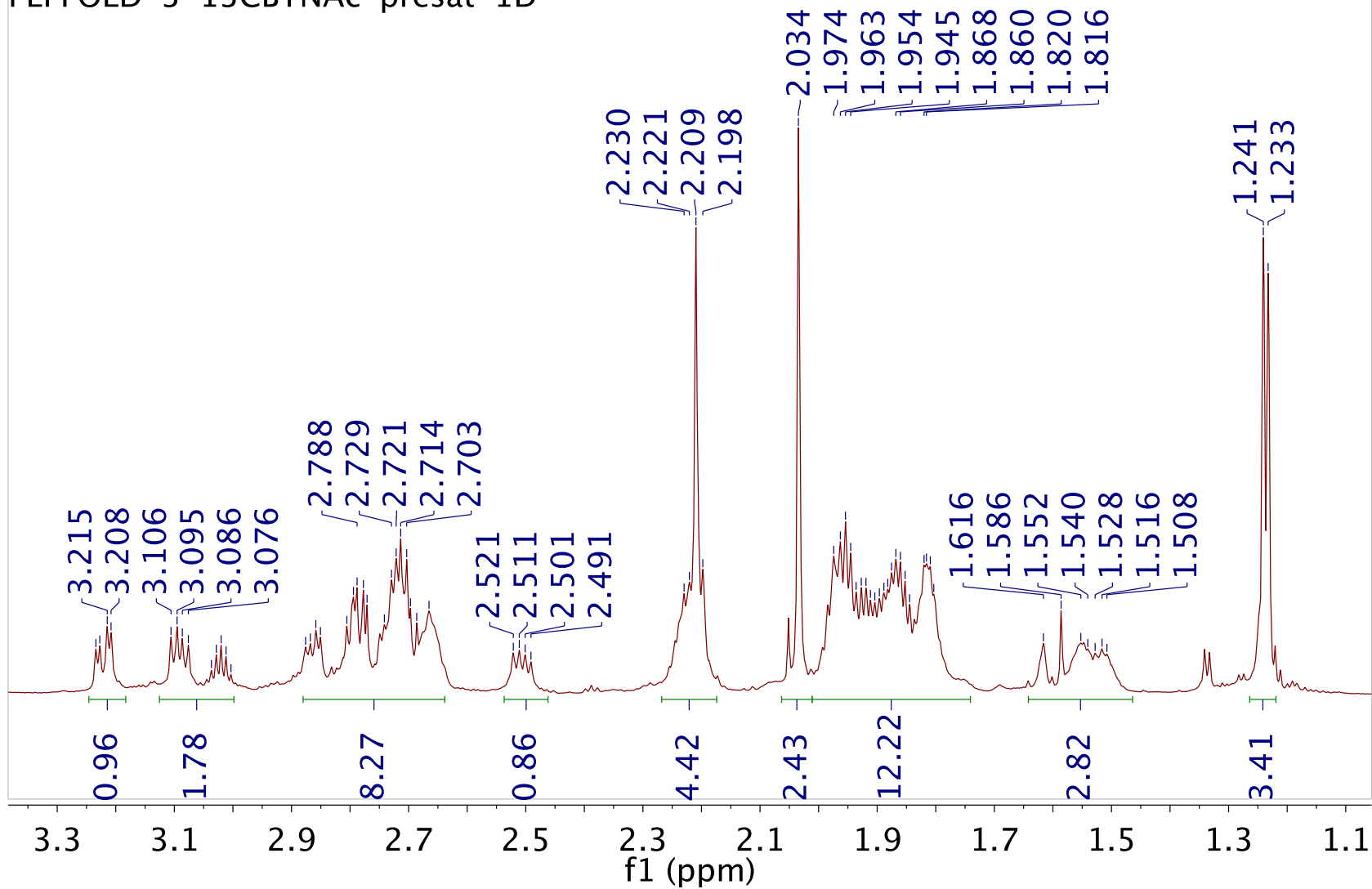


PEPFOLD-3-13CBTNAc-presat-1D

PEPFOLD-3-13CBTNAc-presat-1D



PEPFOLD-3-13CBTNAc-presat-1D
PEPFOLD-3-13CBTNAc-presat-1D



030118_PEPFOLD-3-13CBTNAc_pure_90-10-2uL-H2O-D2O-CD3CN_12000s_d1-2_13C
C13par

