

Supporting Information

Distributed Drug Discovery, Part 2: Rehearsal of Alkylating Agents for the Synthesis of Resin-Bound Unnatural Amino Acids and Virtual D³ Library Construction

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Tutorial for Using the Distributed Drug Discovery (D³) Database on the Collaborative Drug Discovery (CDD) Website

The Distributed Drug Discovery (D³) database is a virtual catalog of 48,608 unique acylated unnatural amino acid derivatives obtained from a combinatorial enumeration. For access to this database, register for a free read-download account with Collaborative Drug Discovery (CDD) at <http://www.collaborativedrug.com/register/iupui-d3> (accessed November 2, 2008).

The following discussion is divided into three parts:

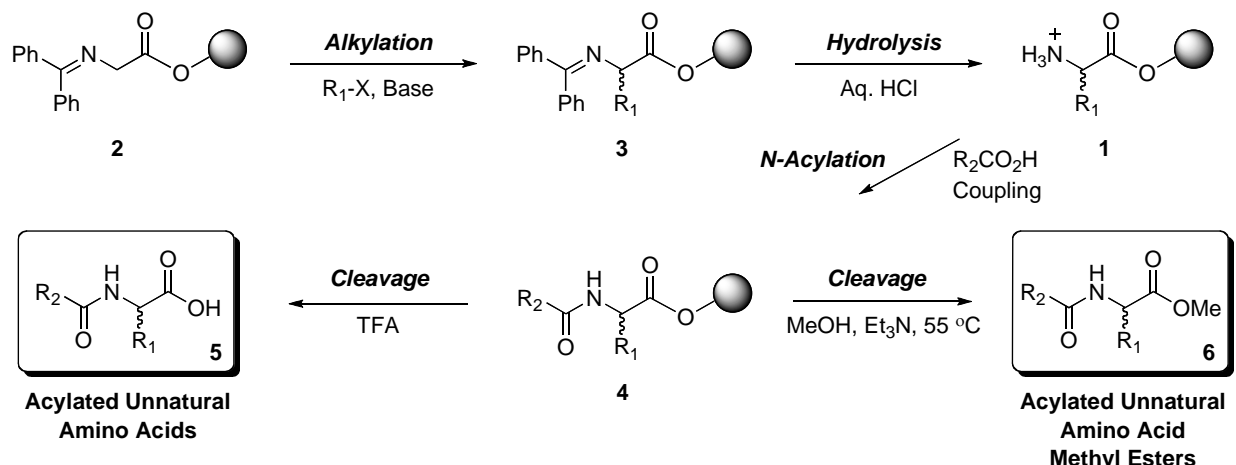
1) Synthesis

2) Enumeration

3) Tutorial

Compound identifiers are those described in the accompanying *Journal of Combinatorial Chemistry* papers [Scott, W. L.; O'Donnell, M. J. et al. *J. Comb. Chem.* DOI: 10.1021/cc800184v (<http://dx.doi.org/10.1021/cc800184v>) and DOI: 10.1021/cc800185z (<http://dx.doi.org/10.1021/cc800185z>) and DOI: 10.1021/cc800183m (<http://dx.doi.org/10.1021/cc800183m>)]. The user is referred to these papers for an in-depth discussion of the D³ project.

Synthesis. Scheme 1 describes the chemistry involved in the combinatorial enumeration to prepare a virtual catalog of 48,608 unique acylated unnatural amino acids **5** or their methyl esters **6**. The starting material is the Wang resin-bound benzophenone imine of glycine (**2**). The first diversity element (R₁) is attached to the glycine scaffold by reaction of an alkyl halide or Michael acceptor (both abbreviated as "R₁-X") in the presence of base to give **3** in an alkylation or conjugate addition reaction. The imine activating group is removed by hydrolysis and then the second diversity element is added by N-acylation using a standard coupling reaction. Cleavage from the resin is accomplished with either trifluoroacetic acid to give the acylated unnatural amino acid (**5**) or by transesterification with methanol to yield the acylated unnatural amino acid methyl ester (**6**).



Scheme 1. Synthetic Routes to Acylated Unnatural Amino Acids **5** and Methyl Esters **6**.

A total of 100 commercially available electrophiles (R₁X = alkyl halide or Michael acceptor) and 100 commercially available carboxylic acids (R₂CO₂H) were used in an enumeration creating all the possible combinations of R₁ and R₂ for **5** and **6**.

Enumeration. Enumeration with the 100 electrophiles (alkyl halides and Michael acceptors) and 100 carboxylic acids gave 24,416 acylated amino acids **5** and 24,192 acylated amino acid methyl esters **6**. The reason these numbers exceed 10,000 in each case is discussed below.

Issues of stereochemistry were addressed in this enumeration. Examples illustrating the possibilities for the amino acid products **5** are shown (Table 1). The products are identified in three ways: row/column (e.g. **A1**), number in D³ database (e.g. DDD-000002150), or number from *J. Comb. Chem.* paper [e.g. (**R**)-**5**{9,119}]. The diversity elements, reactants R₁X and R₂CO₂H, include achiral (**1** and **A**), optically pure (**B**), racemic (**2** and **C**) and prochiral (**3**) examples. Only one of the possible stereoisomers for each product is shown in this table, designed to illustrate three main points.

(1) When achiral or optically pure reactants (R₁X and R₂CO₂H) were used, racemic products (2 stereoisomers) resulted, e.g. **A1** and its enantiomer or **B1** and its diastereomer at the α carbon. The database contains 15,308 unique molecules **5** (7,654 pairs) of this class.

(2) When one of the reactants (R₁X and R₂CO₂H) was racemic or, in the case of Michael acceptors, prochiral, 4 stereoisomers were obtained, e.g. **A2** or **A3** and their stereoisomers. The database contains 8,068 unique molecules **5** (2,017 sets of four stereoisomers) of this class.

(3) When both reactants (R₁X and R₂CO₂H) were racemic or prochiral and racemic, 8 stereoisomers were formed. Examples: **C2** or **C3** and their stereoisomers. The database contains 1,040 such unique molecules **5** (130 sets of eight stereoisomers) of this class.

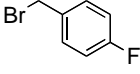

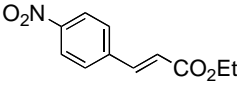
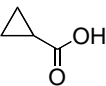
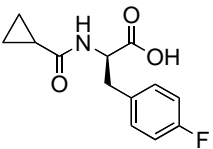
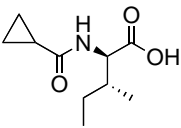
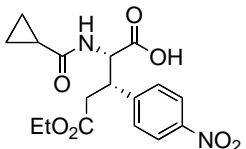
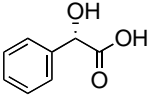
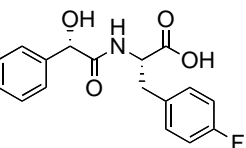
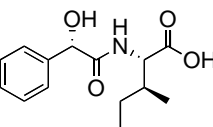
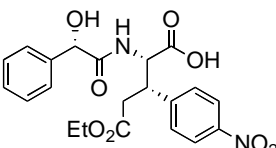
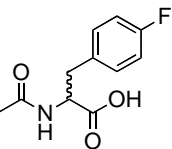
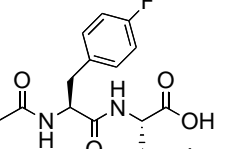
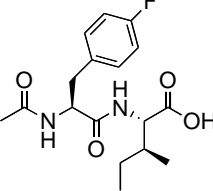
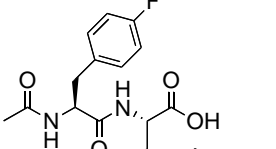
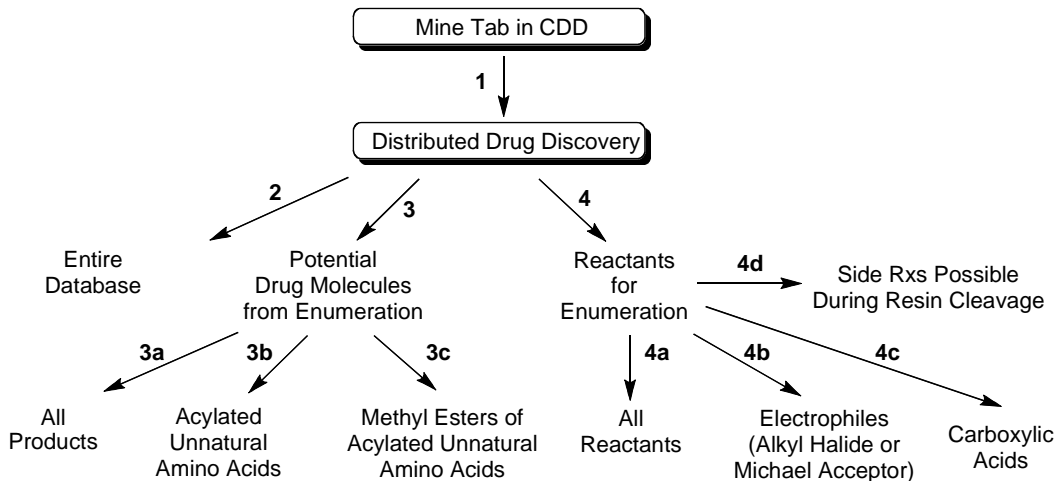
	"R ₁ X"			
		1	2	3
R ₂ CO ₂ H				
A		 DDD-000002150 (R)- 5 {9,119} (1 of 2 Stereoisomers)	 DDD-000002127 (R,R)- 5 {47,119} (1 of 4 Stereoisomers)	 DDD-000014763 (S,S)- 5 {108,119} (1 of 4 Stereoisomers)
B		 DDD-000020243 (S,S)- 5 {9,163} (1 of 2 Stereoisomers)	 DDD-000020219 (S,S)- 5 {47,163} (1 of 4 Stereoisomers)	 DDD-000020313 (S,S,S)- 5 {108,163} (1 of 4 Stereoisomers)
C		 DDD-000023240 (S,S)- 5 {9,184} (1 of 4 Stereoisomers)	 DDD-000023216 (S,S,S)- 5 {47,184} (1 of 8 Stereoisomers)	 DDD-000023310 (S,S,S)- 5 {108,184} (1 of 8 Stereoisomers)

Table 1. Sample 3 x 3 Enumeration Representative of 48,608 Member D³ Catalog.

Tutorial. This tutorial is a guide to using the IUPUI Distributed Drug Discovery (D³) database residing on the Collaborative Drug Discovery (CDD) website. The tutorial is accessible from: a) the Supporting Information in Scott, W. L.; O'Donnell, M. J. et al. *J. Comb. Chem.* DOI: 10.1021/cc800184v (<http://dx.doi.org/10.1021/cc800184v>) and DOI: 10.1021/cc800185z (<http://dx.doi.org/10.1021/cc800185z>) b) the CDD website; or c) the IUPUI Department of Chemistry and Chemical Biology website [<http://chem.iupui.edu/> (accessed November 2, 2008)] under faculty & staff directory for O'Donnell or Scott. The tutorial available at (ii) and (iii) will be updated periodically.

- 1) To Obtain Username and Password for the IUPUI Distributed Drug Discovery (D³) database.
For access to the IUPUI - Distributed Drug Discovery (D³) database, register for a free read-download account with Collaborative Drug Discovery (CDD) at <https://www.collaborativedrug.com/register/iupui-d3> (accessed November 2, 2008) by completing the "Sign up for IUPUI – Distributed Drug Discovery (D3)" information.
- 2) Login to the IUPUI Distributed Drug Discovery (D³) database.
URL: <http://www.collaborativedrug.com/> (accessed November 2, 2008)
Username: Your Username
Password: Your Password
Select: "Mine" on the Dashboard page (upper right-hand corner)
- 3) Mining.
Allows quick searching of the entire D³ database (or a subset thereof) using "protocols". Searches can be further refined with Structures, Chemical Properties and/or Molecule Keywords. Scheme 2 outlines the D³ database organization and protocol structure:



1. Select: Distributed Drug Discovery from pull-down "protocol" -> Distributed Drug Discovery Work Site
2. Select: (any Distributed Drug Discovery protocol) -> Entire Distributed Drug Discovery Database
3. Select: Potential Drug Molecules from Enumeration
 - 3a. Option: (any readout) -> All Enumerated Products
 - 3b. Option: Acylated Unnatural Amino Acids -> All Enumerated Acylated Unnatural Amino Acids
 - 3c. Option: Methyl Esters of Acylated Unnatural Amino Acids -> All Enumerated Methyl Esters
4. Select: Reactants for Enumeration
 - 4a. Option: (any readout) -> All Reactants
 - 4b. Option: Electrophiles (Alkyl Halide or Michael Acceptor) -> All Electrophile Reactants
 - 4c. Option: Carboxylic Acids -> All Carboxylic Acid Reactants
 - 4d. Option: Side Rxs Possible During Resin Cleavage -> Reactant Functionality Transformed During Cleavage

Scheme 2. D³ Database Organization and Protocol Structure.

From the Mine tab, “any protocol type”, “any protocol”, and “any readout” pull-down menus can be specified. One or more selections lead to all possible search results within the chosen category. Table 2 lists the results obtained from searches in the indicated categories (numbers in parentheses refer to steps in Scheme 2):

<u>Protocols</u>	<u>Search Results</u> ^a
(any protocol type)	
(any protocol)	Default
Distributed Drug Discovery (1)	
(any Distributed Drug Discovery protocol) (2)	48,818
Potential Drug Molecules from Enumeration (3)	
(any readout) (3a)	48,608
Acylated Unnatural Amino Acids (3b)	24,416
Methyl Esters of Acylated Unnatural Amino Acids (3c)	24,192
Reactants for Enumeration (4)	
(any readout) (4a)	212
Electrophiles (Alkyl Halide or Michael Acceptor) (4b)	112
Carboxylic Acids (4c)	100
Side Rx Possible During Resin Cleavage (4d)	22

^a “Add a term” to modify a search by: Structures, Chemical Properties and/or Molecule Keywords

Table 2. Results Obtained from Different Protocol Searches.

Example 1: All Products Search

Select: Mine tab

Select: New Query

Select the following from the pull-down protocol menus:

Distributed Drug Discovery

Potential Drug Molecules from Enumeration

(any readout)

Note: “*(any readout)*” means the default has been automatically chosen.

Select: Search Molecules

Result: Displays first 100 of 48,608 acylated unnatural amino acids and methyl esters from enumeration.

Select: Third molecule (DDD-000001000) in list of products. Note that the first two products in the list are both reactant carboxylic acids (DDD-0000000267 and DDD-0000000274) and enumeration products (DDD-000001010 and DDD-000013558, respectively).

Result: Left column – information about the product and the reactants used for its preparation in the enumeration; right column – CDD-generated product information (see Appendices 1 and 2 for a listing of product and reactant information).

4) File Downloads

The three files described below are available for download at several locations in the database. The most direct route to these downloads follows:

Select: Archive tab

Select: Protocols

Select: "Potential Drug Molecules from Enumeration"

Select (under Associated Files): Filename

- "IUPUI D3 Enumerated Products.sdf": The SD File of the 48,608 enumerated products. This file contains the fields described in Appendix 3.
- "IUPUI D3 Tutorial.pdf": The tutorial will be updated periodically and be available through CDD at this site and also on the IUPUI Department of Chemistry and Chemical Biology website [<http://chem.iupui.edu/> (accessed November 2, 2008)] under the faculty & staff directory for O'Donnell or Scott.
- "IUPUI D3 Refs Rxs Electrophiles.pdf": This file contains selected lead references, cited in Scott, W. L.; O'Donnell, M. J. et al. *J. Comb. Chem.* DOI: 10.1021/cc800184v (<http://dx.doi.org/10.1021/cc800184v>) for reaction of each electrophile (alkyl halide or Michael acceptor) with Schiff bases of amino acid derivatives under a variety of basic conditions.

5) Substructure or Full Structure Searches

Select: Mine tab

Select: New Query

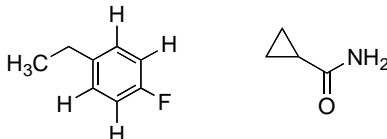
Select: Structures – by substructure

Select: "Launch the editor" to build a structure for this search (opens MarvinSketch applet)

Note: A dialog box may appear with information about a certificate or digital signature. If this happens, select "Trust" or "Run."

a) Example 2: Substructure Search

Draw the following search query in MarvinSketch (see Appendix 4 for detailed drawing instructions).



Select: Use This Structure

Result: Structures in Mine Protocols and Molecules structure box.

Note: Sometimes a "?" appears in the resulting structure box, indicating the image did not load but the structure is still stored and one can continue.

Select the following from the pull-down protocol menus:

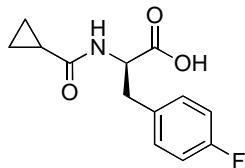
Distributed Drug Discovery

Potential Drug Molecules from Enumeration

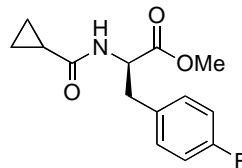
(any readout)

Select: Search Molecules

Result: 4 matching compounds from the 48,606 enumerated products; the two enantiomeric carboxylic acids and their two enantiomeric methyl esters:



A1
DDD-000002150
ent-A1
DDD-000014693



A1 (Methyl Ester)
DDD-000102150
ent-A1 (Methyl Ester)
DDD-000114693

b) Example 3: Substructure Search

Select: Mine tab

Select: New Query

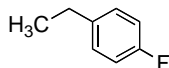
Select the following from the pull-down protocol menus:

Distributed Drug Discovery

Potential Drug Molecules from Enumeration

Acylated Unnatural Amino Acids

Draw the following search query in MarvinSketch (see Appendix 4 for detailed drawing instructions):



Select: Use This Structure

Select: Search Molecules

Result: 1518 hits from the database of 24,416 amino acid products (Table 3).

The 24 hits from Table 1 are summarized below:

<u>Structure in Table 1</u>	<u>Number of Stereoisomers</u>
A1	2
B1	2
C1	4
C2	8
C3	8

Table 3. Stereochemical Results from Example 3.

c) Example 4: Substructure Search Demonstrating Stereochemistry and Side Reactions

Select: Mine tab

Select: New Query

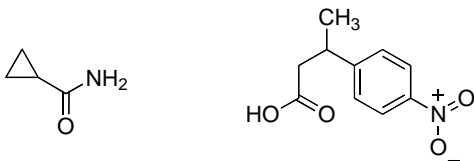
Select the following from the pull-down protocol menus:

Distributed Drug Discovery

Potential Drug Molecules from Enumeration

(any readout)

Draw the following search query in MarvinSketch (see Appendix 4 for detailed drawing instructions):

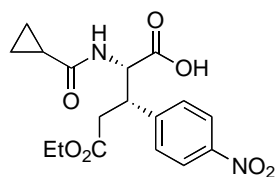


Select: Use This Structure

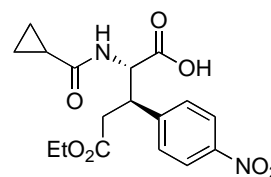
Select: Search Molecules

Result: 8 matching results from the database of 48,608 amino acid and methyl ester products (Table 4). The 4 stereoisomers of the acylated unnatural amino acids (**5**) are represented in the top row while the 4 stereoisomers of the methyl esters (**6**)

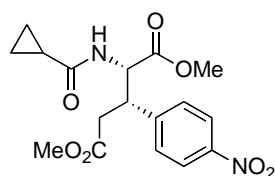
are in the bottom row. For the methyl ester products a possible side reaction during resin cleavage (transesterification of the ethyl ester in the Michael acceptor) has been carried out. Notation of this side reaction plus a lead reference are obtained by searching for the electrophile used in this preparation (Michael acceptor DDD-000000121).



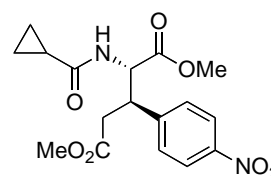
A3
 DDD-000014763
ent-A3
 DDD-000002219



diast-A3
 DDD-000014762
ent-(diast-A3)
 DDD-000002220



A3 (di-Methyl Ester)
 DDD-000114763
ent-A3 (di-Methyl Ester)
 DDD-000102219



diast-A3 (di-Methyl Ester)
 DDD-000114762
ent-(diast-A3) (di-Methyl Ester)
 DDD-000102220

Table 4. Results from Example 4.

6) Obtaining Information About a Particular Molecule

a) Example 5: Product Information Search

- From a Search:

Under Search Results, select structure or DDD number

- Using a D³ Number:

From the original Mine page:

Select: New Query

In Molecule Keywords type: DDD-000002150 (shortcut: DDD 2150)

Select: Search Molecules

Result: 11 hits. The CDD search strategy returns molecules that begin with “2150”: DDD-000002150 and the 10 molecules DDD-000021500 through DDD-000021509. Lower DDD registry numbers appear first in the search results, so DDD-000002150 is the first entry.

b) Example 6: Reactant Information Search (see Appendix 2 for a listing of reactant information)

Select: Mine tab

Select: New Query

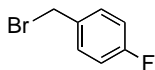
Select the following from the pull-down protocol menus:

Distributed Drug Discovery

Reactants for Enumeration

(any readout)

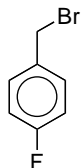
Draw the following search query in MarvinSketch (see Appendix 4 for detailed drawing instructions). To insert the Br: Position the cursor over the H₃C and type Br or select “More”, choose Br, Close, Click on H₃C.



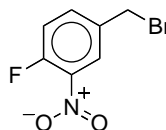
Select: Use This Structure

Select: Search Molecules

Result: 2 hits



1-(bromomethyl)-
4-fluorobenzene
DDD-00000048



4-(bromomethyl)-
1-fluoro-2-nitrobenzene
DDD-00000049

Select: Structure or name [1-(bromomethyl)-4-fluorobenzene], to obtain information about this reactant (see Appendix 2 for a listing of reactant information)

7) Selecting Other Public Data Sets

Other public data sets besides the Distributed Drug Discovery (D3) database are available as follows:

Select: Collaborate tab

Select: Data Sets

Select: Select all or make individual selection(s)

Select: Save selections

Select: Mine tab and proceed with search

Appendix 1

Information about Individual Enumeration Products

- 1) Information about the enumeration product and the reactants used for its generation (left column).

Definition (category content):

Name (DDD Number)

Synonyms

Description (Blank)

Structure (SMILES or InChI or InChIKey)

Molecular Formula

Product Type

Reactant: Electrophile (Chemical Name)

Reactant: Electrophile DDD No.

Reactant: Carboxylic Acid (Chemical Name)

Reactant: Carboxylic Acid DDD No.

- 2) CDD-generated information about the enumeration product (right column).

Structure

Lipinski properties

Molecular weight

log P

H-bond donors

H-bond acceptors

Lipinski Rule of 5

Additional properties

Formula

pKa

Exact mass

Atom count

Composition

Topological polar surface area (PSA)

Appendix 2

Information about Individual Reactants

1) Information about the reactant (left column).

Definition (category content):

Name (DDD Number)

Synonyms (Chemical Name(s))

Description (Blank)

Structure (SMILES or InChI or InChIKey)

Reactant Type

Molecular Formula

*Reference No. for Rxns with Schiff Bases of Amino Acid Derivatives

*Side Rxns Possible During Resin Cleavage

*These categories are only shown when an entry is present.

2) CDD-generated information about the reactant (right column).

Structure

Lipinski properties

Molecular weight

log P

H-bond donors

H-bond acceptors

Lipinski Rule of 5

Additional properties

Formula

pKa

Exact mass

Atom count

Composition

Topological polar surface area (PSA)

Appendix 3

Information Available for Enumeration Products in SD File Download

Structure

SMILES

Name (DDD Number)

Product Type (Acylated Unnatural Amino Acid or Methyl Esters of Unnatural Amino Acids)

Molecular weight

log P

H-bond donors

H-bond acceptors

Lipinski Rule of 5

Formula

pKa

Exact mass

Atom count

Composition

Topological polar surface area (PSA)

Reactant: Electrophile (Chemical Name)

Reactant: Electrophile DDD No.

Reactant: Carboxylic Acid (Chemical Name)

Reactant: Carboxylic Acid DDD No.

Appendix 4

Detailed Instructions for Drawing Structures for Example 2 (page 5)

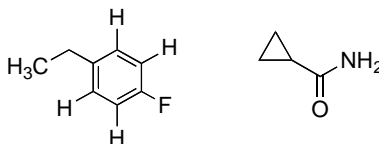
Repeat Login Procedure

Select the following from the pull-down protocol menus:

Distributed Drug Discovery
Potential Drug Molecules from Enumeration
(any readout)

Note: “(any readout)” means the default has been automatically chosen.

Target Substructures to Draw in Marvin Sketch:



From within the CDD Database:

Select: Mine tab

Select: New Query

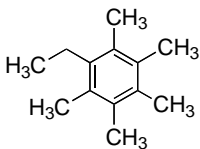
Select: Structures – by substructure

Select: “Launch the editor” to build a structure for this search (opens MarvinSketch applet)

Note: A dialog box may appear with information about a certificate or digital signature. If this happens, select “Trust” or “Run.”

From within the Structure Editor of MarvinSketch:

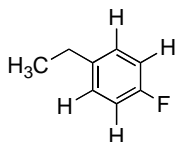
- (1) Select the benzene ring from the structure palate.
- (2) Move the cursor to position the benzene ring on the left side of the drawing surface then click.
- (3) Select the bond tool (below “Help”).
- (4) Position the cursor above one of the carbons so that a blue circle appears then click. Alternatively, you can click/drag/release to position the bond.
- (5) Repeat step 4 for all benzene ring carbons.
- (6) Position the cursor above one of the CH₃ groups then click.



Intermediate
Structure A

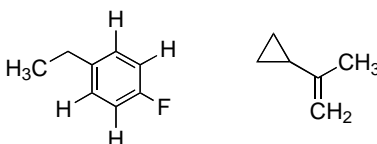
- (7) The hydrogens and fluorine on the benzene ring can be added in one of two ways:
 - (a) Position the cursor above a CH₃ group so that a blue circle appears then type the atom symbol or
 - (b) Select the atom (“H” or “F”) in the palate then click above each CH₃ to be changed. If the atom symbol is not in the palate, select “More” for a complete list.

- (8) Since not explicitly designated otherwise, the chain H₃C remaining is assumed to be a carbon with 0-3 hydrogens attached.



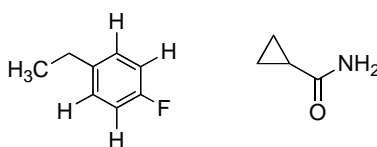
Intermediate
Structure B

- (9) Select the bond tool and click in the open space to the right of the previously drawn structure.
- (10) Build the carbon framework of the right-hand structure as before. Click/drag/release to complete the final bond of the cyclopropane ring. To create the second bond of the double bond, position the cursor over the center of the single bond (parentheses will appear) then click.



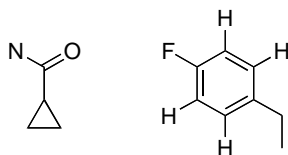
Intermediate Structures C

- (11) The heteroatoms can be added to the right-hand structure in one of two ways:
- Select the atom (“O” or “N”) in the palate then click above the appropriate atom to be changed.
 - Position the cursor above the CH₂ or CH₃ group (a circle will appear) then type either an O or an N, respectively.
- (12) As before, since not explicitly designated otherwise, the NH₂ is assumed to be a nitrogen with 0-2 hydrogens attached.



Final Search Structures D
(in Structure Editor of MarvinSketch)

- (13) Select “Use This Structure”.
- From within the CDD Database:
Result: Structures in Mine Protocols and Molecules structure box.

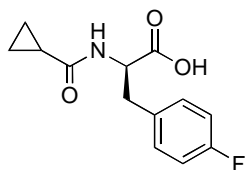


Final Search Structures E
(in CDD Search Window)

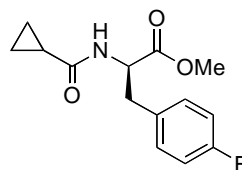
Note: Sometimes a “?” appears in the resulting structure box, indicating the image did not load but the structure is still stored and one can continue.

Select: Search Molecules

Result: 4 matching results from the 48,606 enumerated products; the two enantiomeric carboxylic acids and their two enantiomeric methyl esters:



A1
DDD-000002150
ent-A1
DDD-000014693



A1 (Methyl Ester)
DDD-000102150
ent-A1 (Methyl Ester)
DDD-000114693

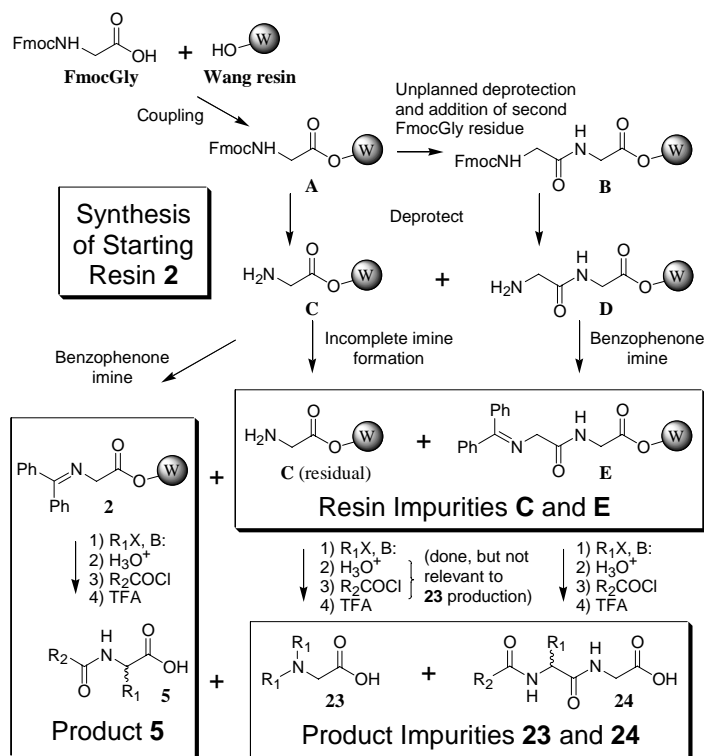
Supporting Information

II. Analysis of Resins from Sources I and II, and Interpretation of Results.

The formation of **23** and **24** in A1 products produced from resin source **I** can be explained by assuming the starting material, resin-bound imine **2**, is contaminated with impurities **C** and **E** (Scheme). Resin-bound **C** arises from incomplete transimination with benzophenone imine in the step producing **2** (see text). The presence of **E** in the starting resin has a somewhat more complicated origin. As shown in the scheme, the commercial synthesis of **2** begins with the coupling of FmocGly to a Wang linker attached to a polystyrene polymer. It is well documented in the peptide literature¹ that this coupling process can lead to double coupling product **B** when small amounts of the desired product **A** undergo *in situ* deprotection, and subsequent coupling of a second molecule of FmocGly. When the desired synthesis of imine **2** is completed (by removal of the Fmoc group on **A** to form **C** followed by transimination to **2** with benzophenone imine) the parallel undesired transformation occurs on **B** to give the impurity **E**.

Given the presence of these two impurities, **C** and **E**, in the starting resin **I**, compound **23** is then formed by dialkylation of the primary amine on **C**, and compound **24** (FmocPheGly, R₁ = CH₂Ph) formed when **E** undergoes the same alkylation and acylation chemistry that converts **2** to **5**. Ironically, this FmocPheGly impurity **24** (~11%) also represents successful alkylation, but now on the terminal glycine of a GlyGly residue. Consistent with this interpretation, for almost all the other R₁X alkylations with resin **I** the parallel alkylation impurities **23** and **24** were observed, in addition to desired product **5**. Finally, the third impurity in A1 products from both resins (at 5.3 min, M+1 = 494) is consistent with structure **25**. This would arise from successful alkylation, but subsequent cleavage of product from the resin with the Wang linker still attached.

This byproduct of Wang chemistry, although not often noted in the peptide literature, has been documented.²



Scheme. Source of Impurities in Resin I Leading to Impurities 23 and 24.

As can be seen in Figure 2 (see text), there were no significant amounts of either 23 or 24 in products from resin supplier II. The only byproduct in A1 samples (at 5.3 min) from resin II was 25. It was present in seven out of eight replicate A1's from teams #18-25. Since this material (with Wang linker attached) also represented successful alkylation, the resin is of high quality and commercial source II was used in all the subsequent labs at IUPUI, along with labs conducted in Spain, Russia and Poland.

III. Selected LC/MS and/or NMR analytical data included in Supporting Information.

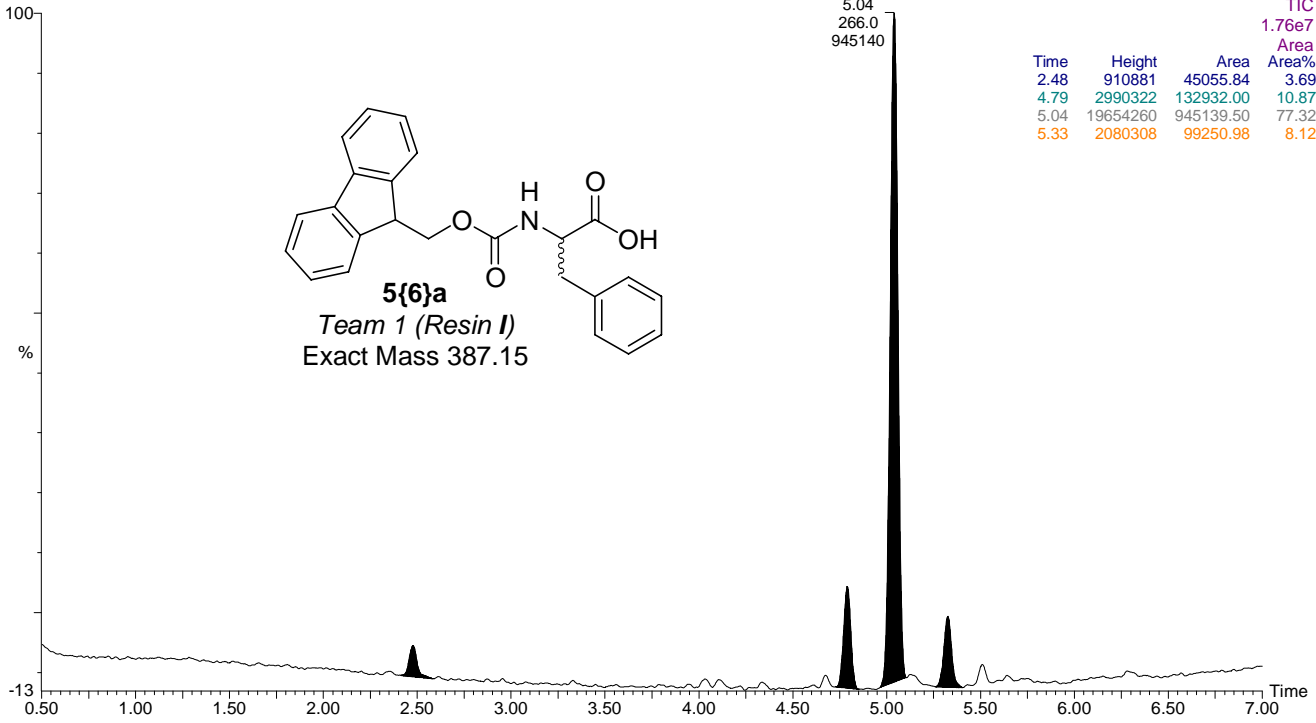
The following Supporting Information provides selected LC/MS and/or NMR data (grouped together by compound) to permit more detailed assessment of:

1. The quality and consistency of replicated synthesis, both within a laboratory and globally. For this purpose we provide copies of the LC/MS for all the Fmoc derivatives (the “a” series) of unnatural/natural amino acids prepared at IUPUI, Lublin (Poland) and Moscow (Russia).
2. The identity, as assessed by NMR, of all the final, purified derivatives prepared in the “a” series.
3. The divergent quality, as assessed by LC/MS, of the various preparations of compounds **5{15}b** and **5{17}b** (see pages 104-107 and 108-111, respectively). The syntheses of these compounds represented the rare example where one of the teams (in this case team 28) obtained radically different results from the other replicated samples. As discussed in the text, team 28 obtained none of the expected products **5{15}b** or **5{17}b**, whereas three other teams (teams 12,13, 29 and 11,12, 27 respectively) were successful and had similar results (63% \pm 3% and 80% \pm 8%, respectively) for each of these compounds in the appropriate Bill-Board positions.^{FN -}

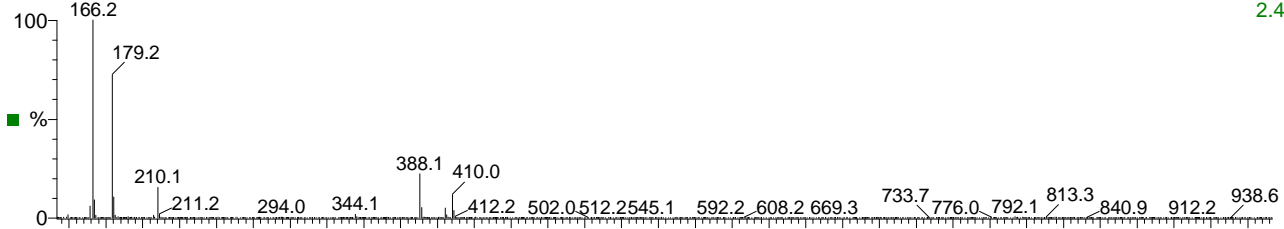
After FN22

5{6}a

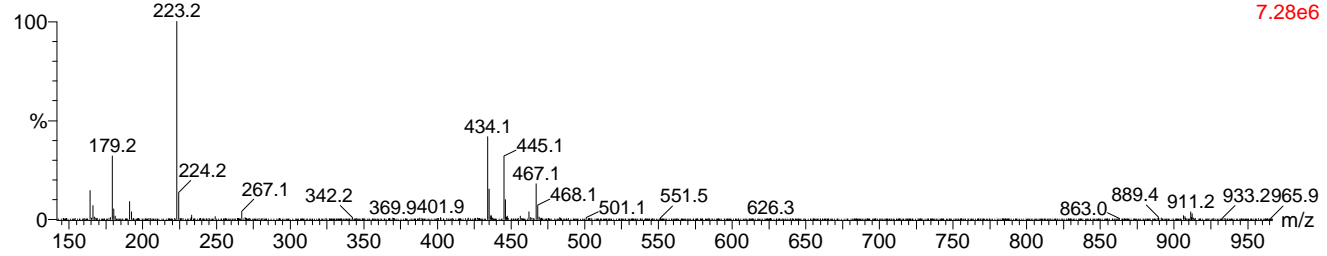
T1-A1 Sm (Mn, 1x1)



T1-A1 191 (5.112)

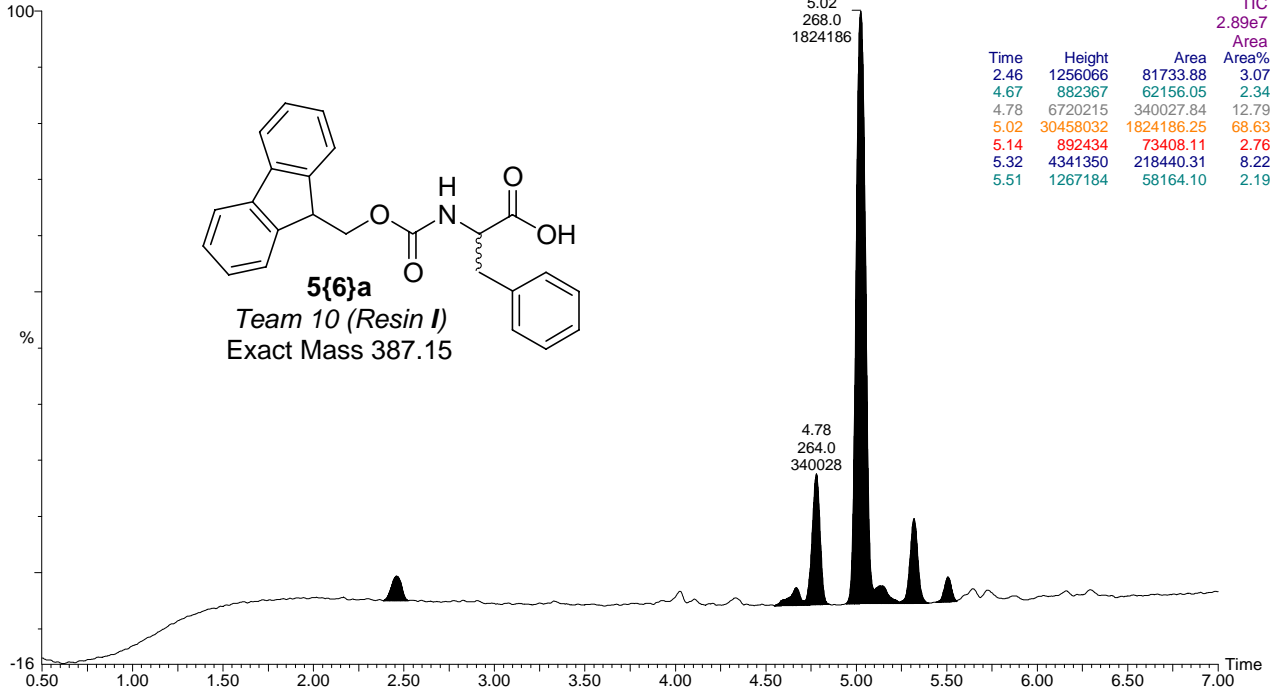


T1-A1 181 (4.843)

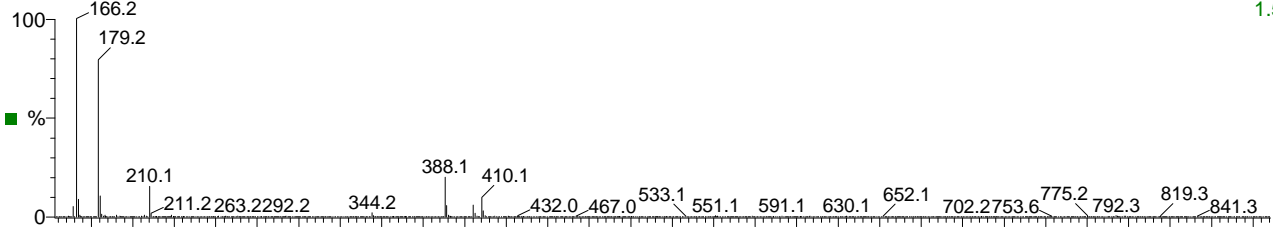


5{6}a

T10-A1 Sm (Mn, 1x1)

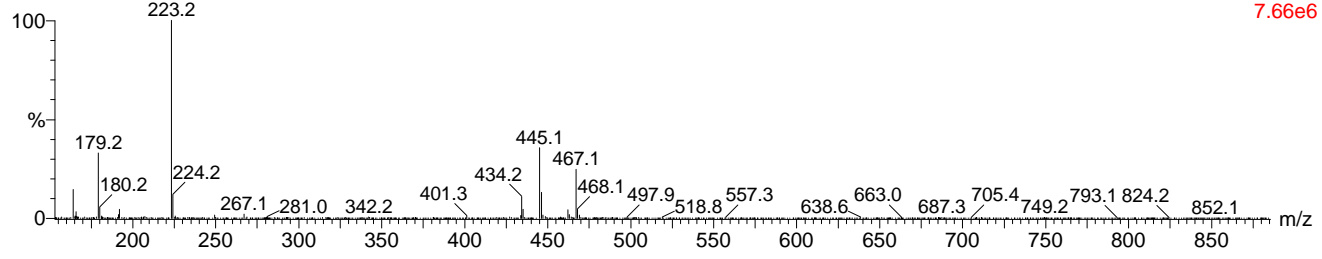


T10-A1 190 (5.085) Cm (188:193)



1: Scan ES+
1.57e7

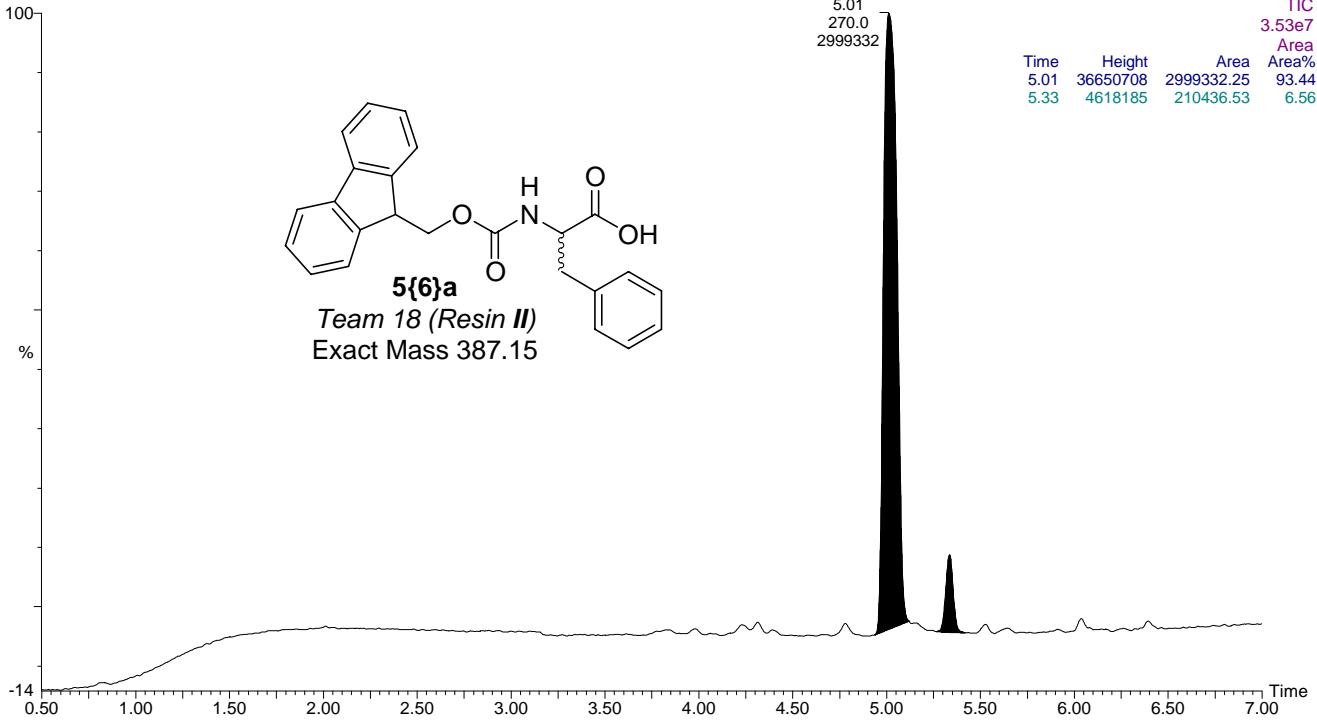
T10-A1 180 (4.816)



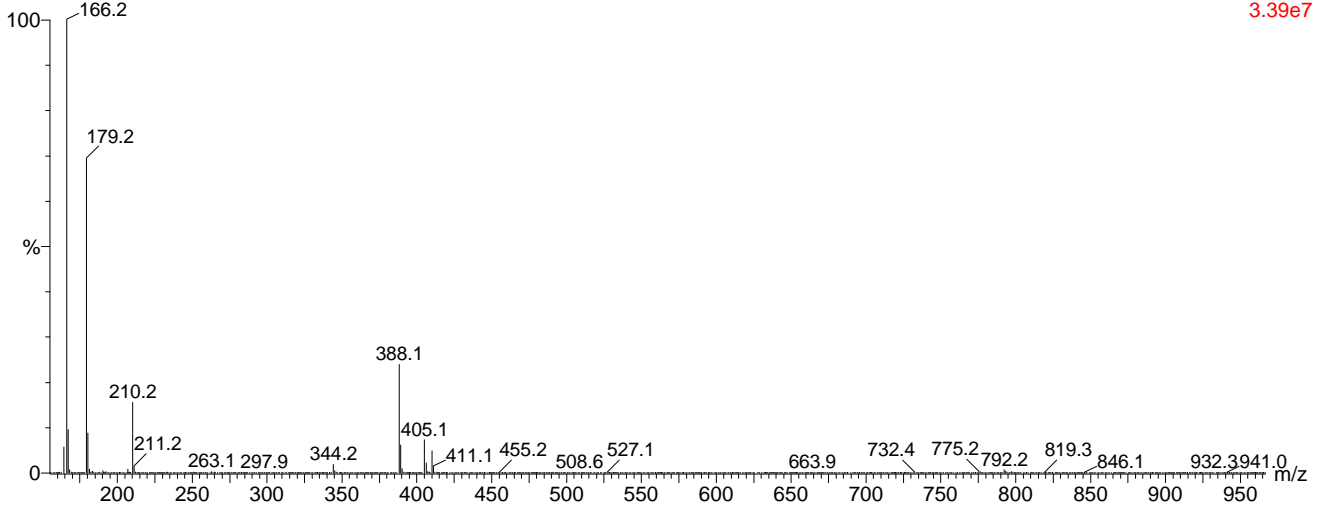
1: Scan ES+
7.66e6

5{6}a

T18-A1 Sm (Mn, 1x1)



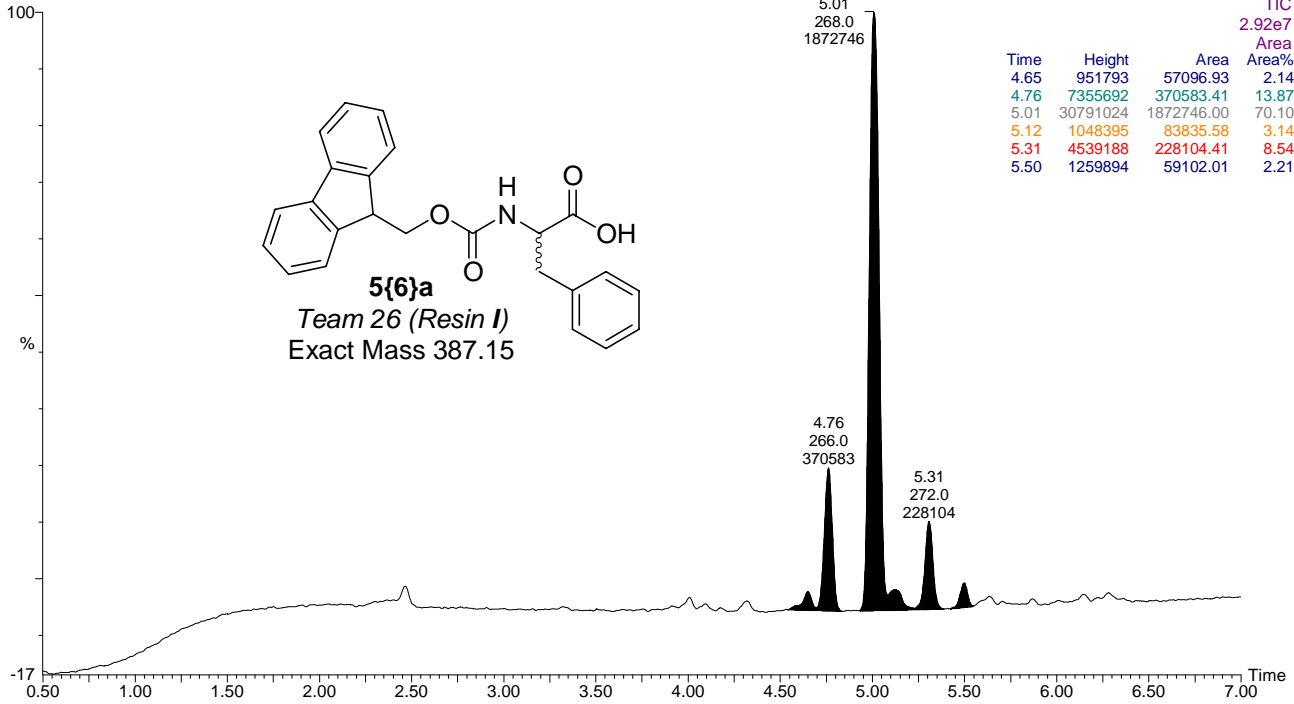
T18-A1 189 (5.058) Cm (189:192)



5{6}a

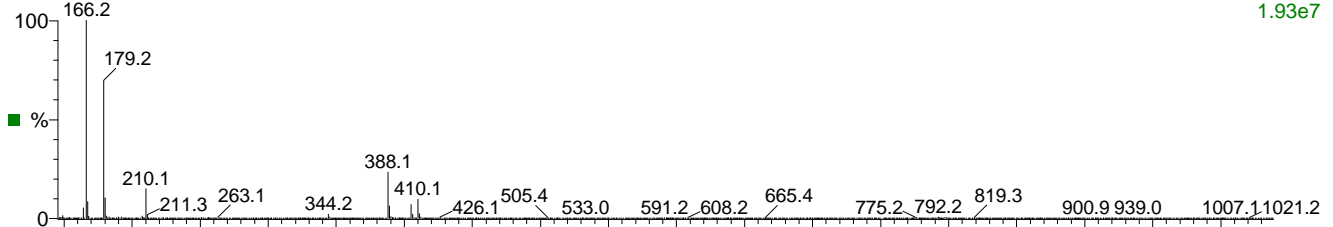
T26-A1 Sm (Mn, 1x1)

3: Diode Array
TIC
2.92e7



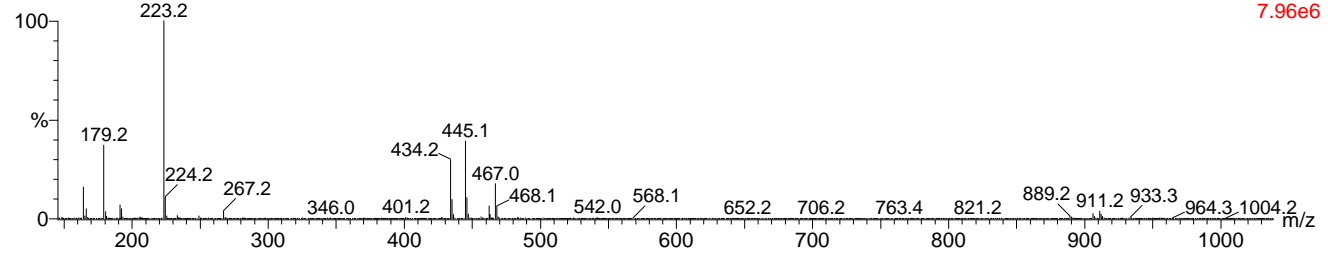
T26-A1 189 (5.058) Cm (187:191)

1: Scan ES+
1.93e7



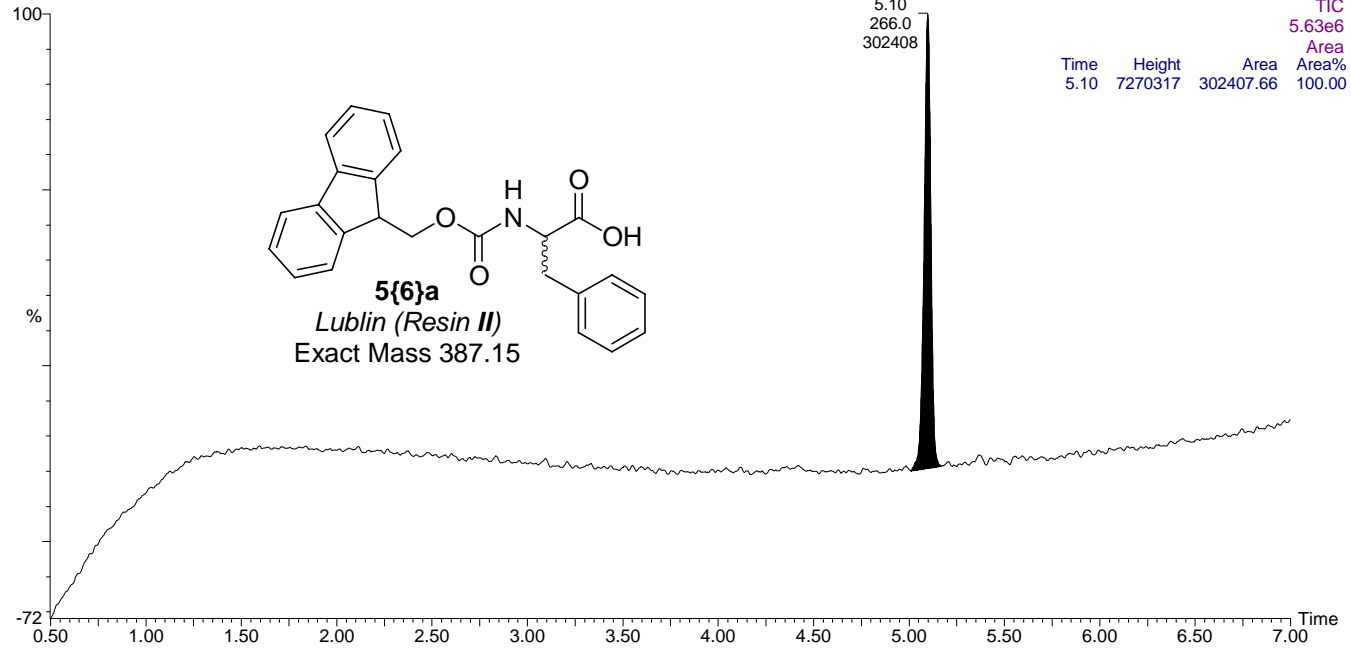
T26-A1 180 (4.816) Cm (179:182)

1: Scan ES+
7.96e6

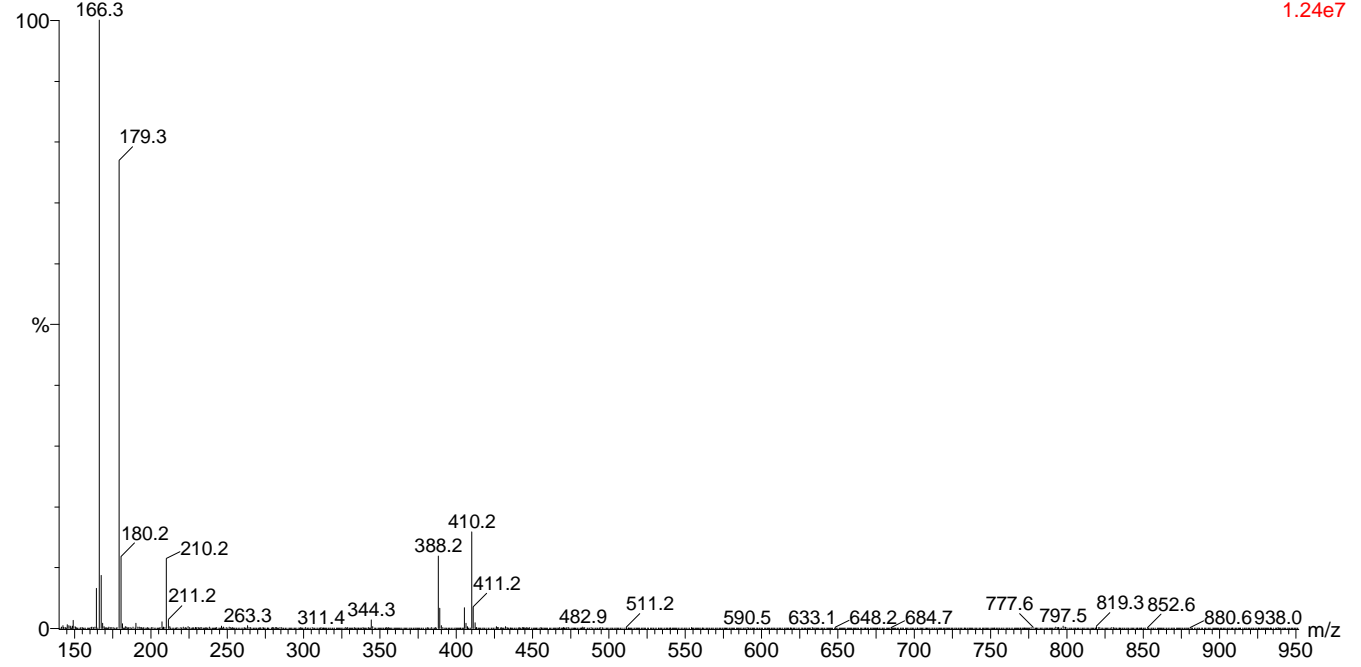


5{6}a

Lublin-Poland-A1 Sm (Mn, 1x1)

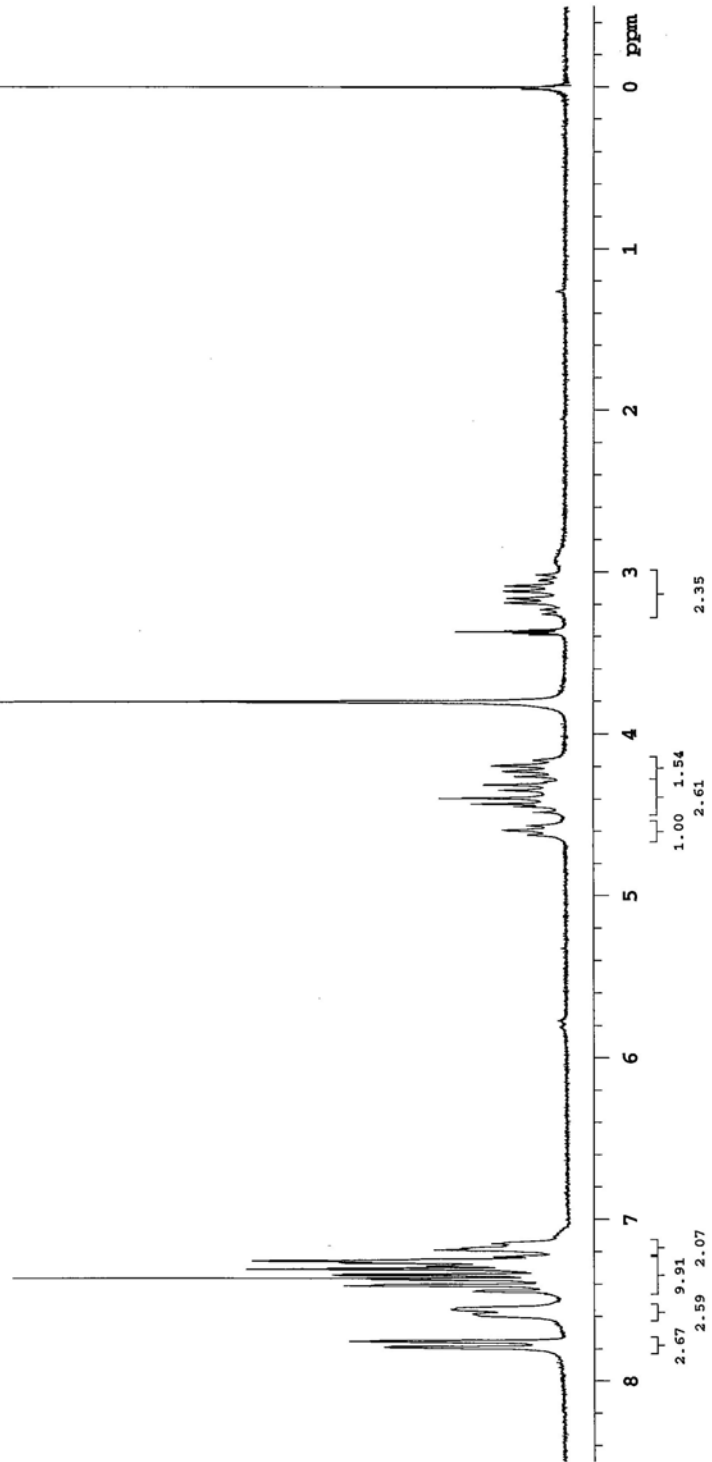
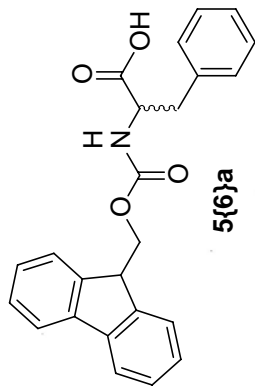


Lublin-Poland-A1 192 (5.138) Cm (190:194)



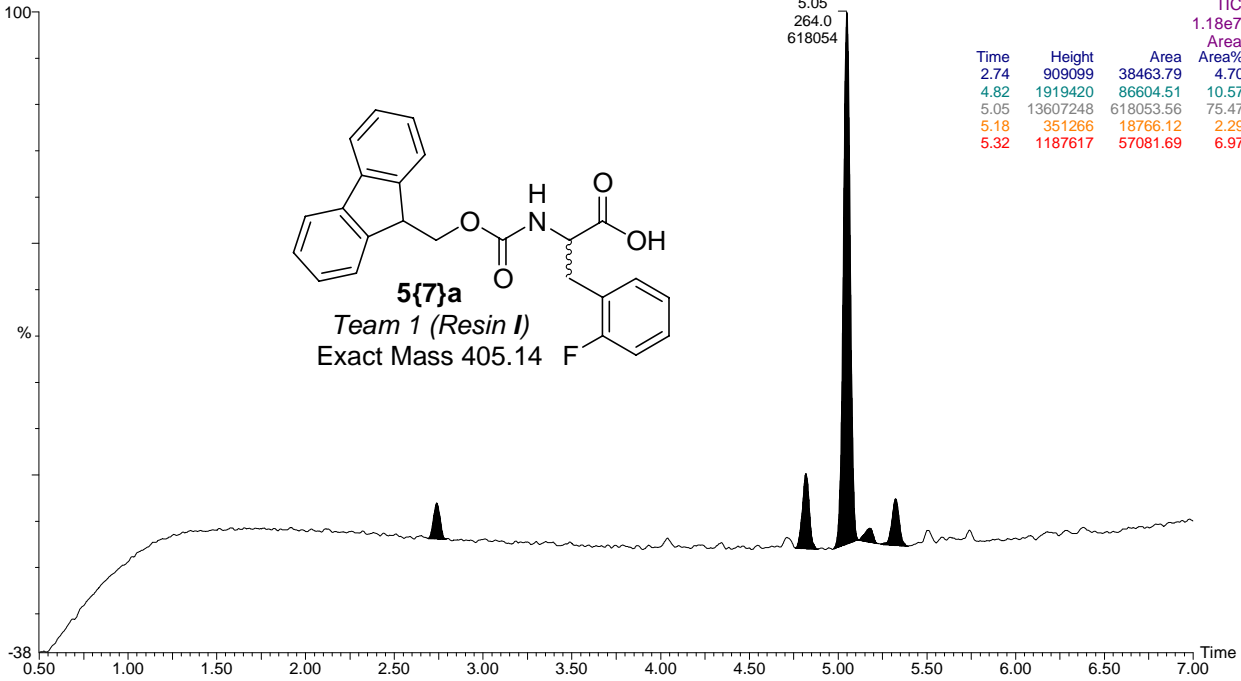
1H_BB#27_A1_CD3ODinCDCl3_02_07

Pulse Sequence: s2pul

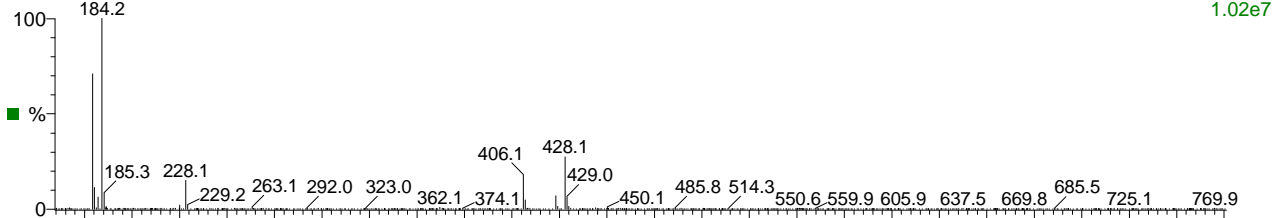


5{7}a

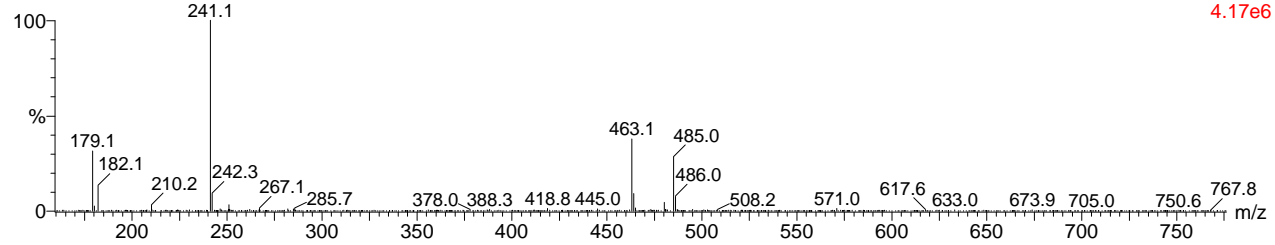
T1-A2 Sm (Mn, 1x1)



T1-A2 190 (5.085)

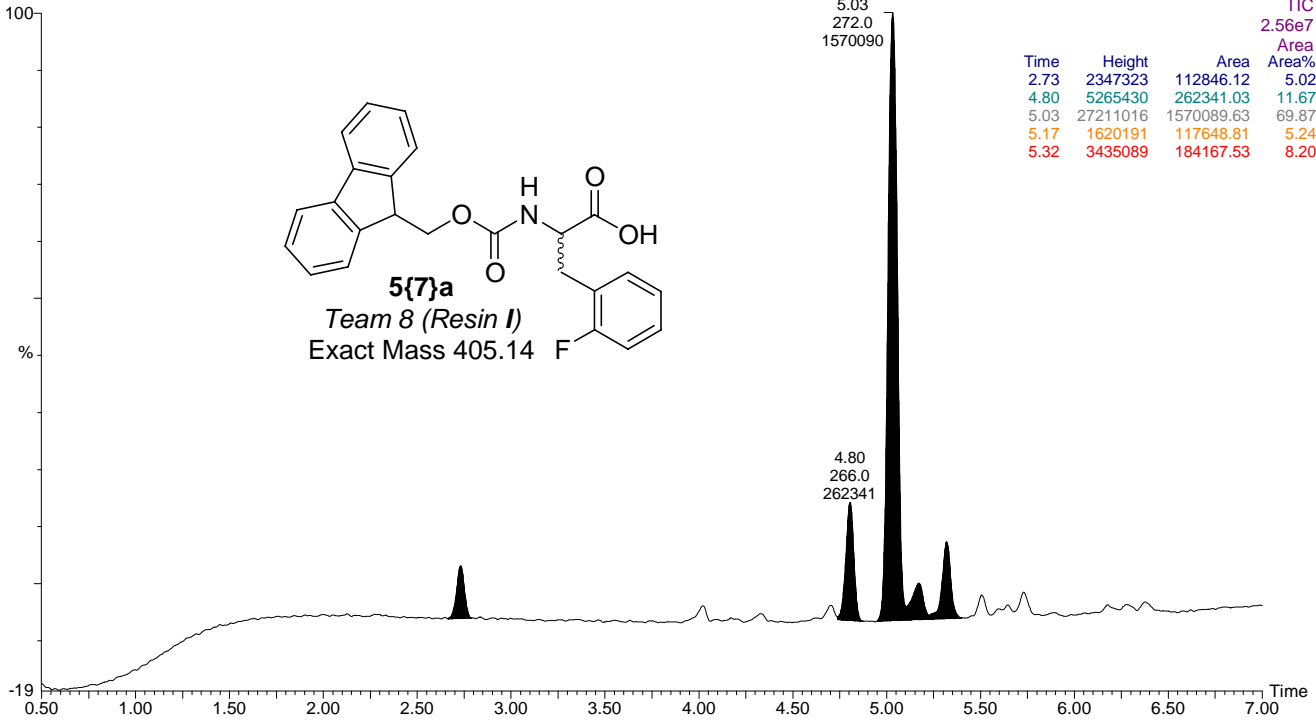


T1-A2 182 (4.870)

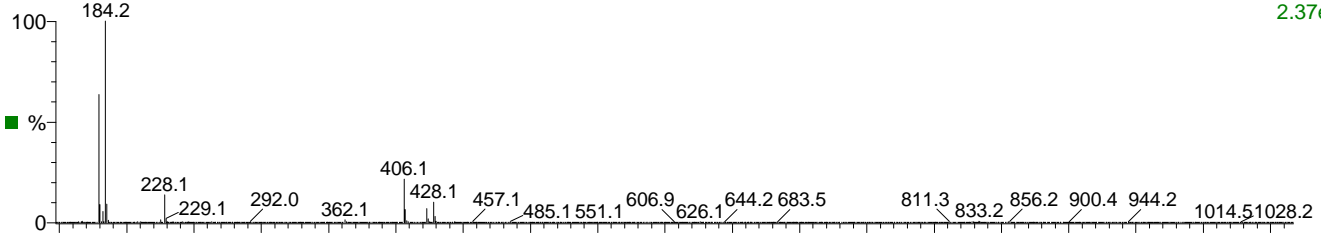


5{7}a

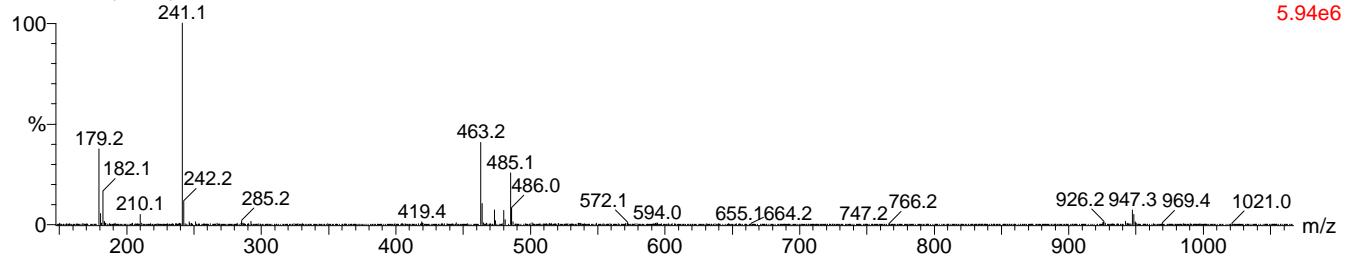
T8-A3 Sm (Mn, 1x1)



T8-A3 191 (5.112) Cm (189:192)

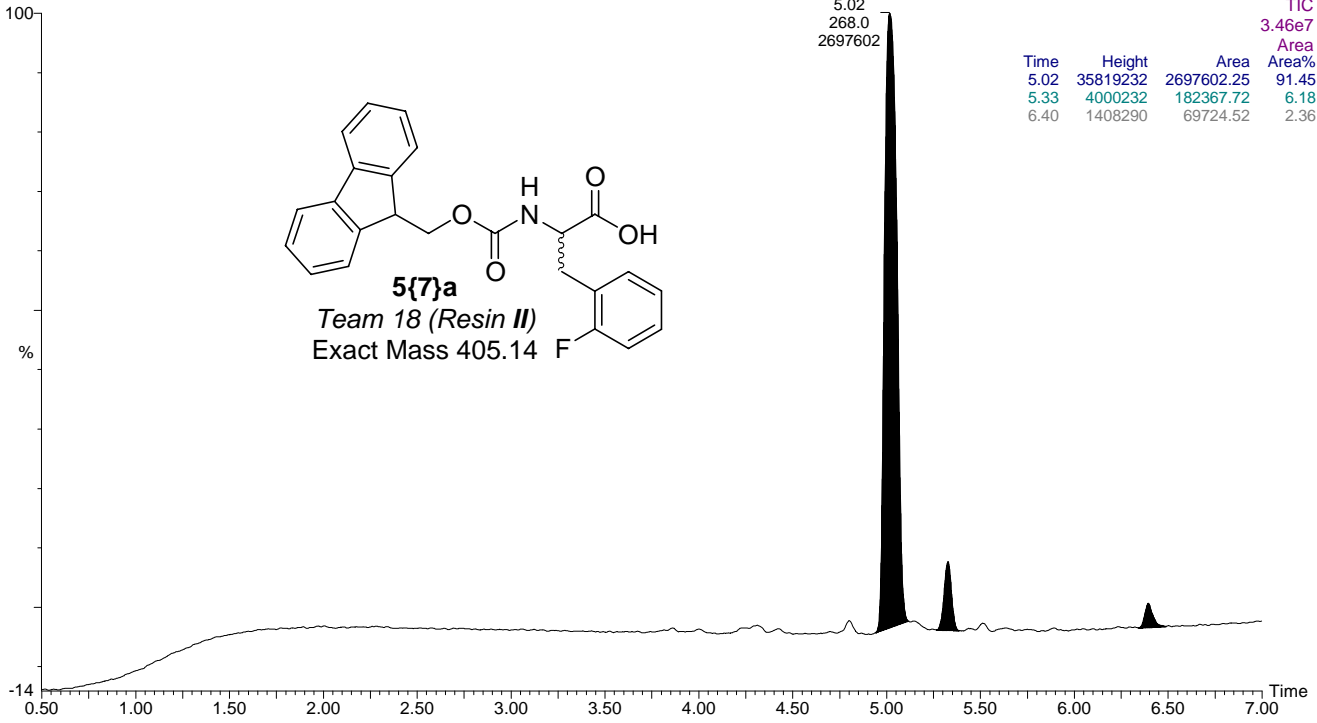


T8-A3 181 (4.843)

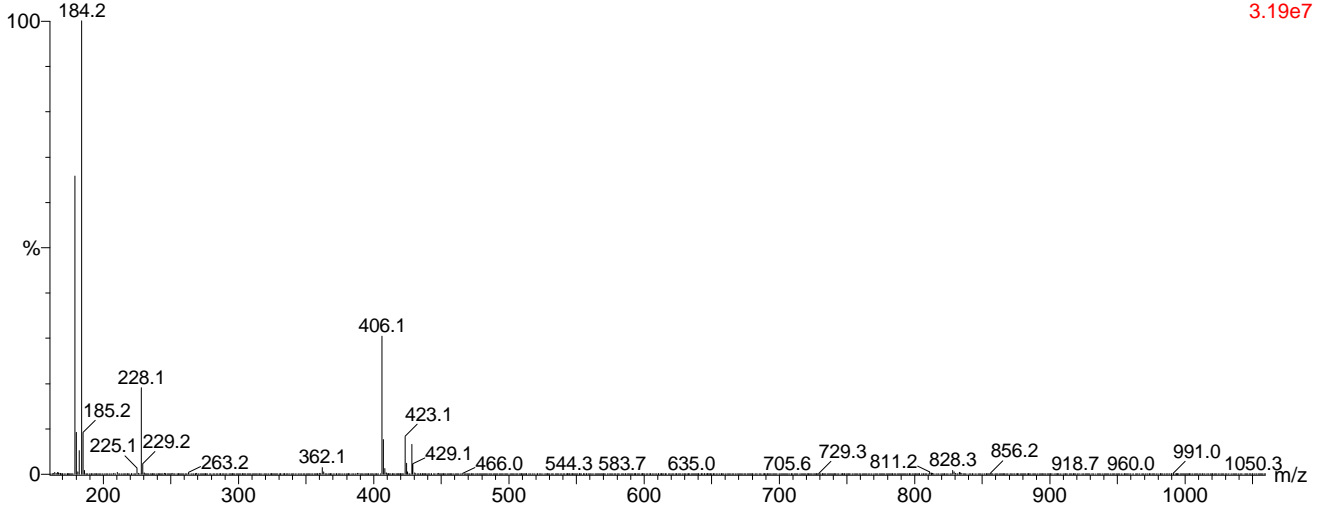


5{7}a

T18-A2 Sm (Mn, 1x1)



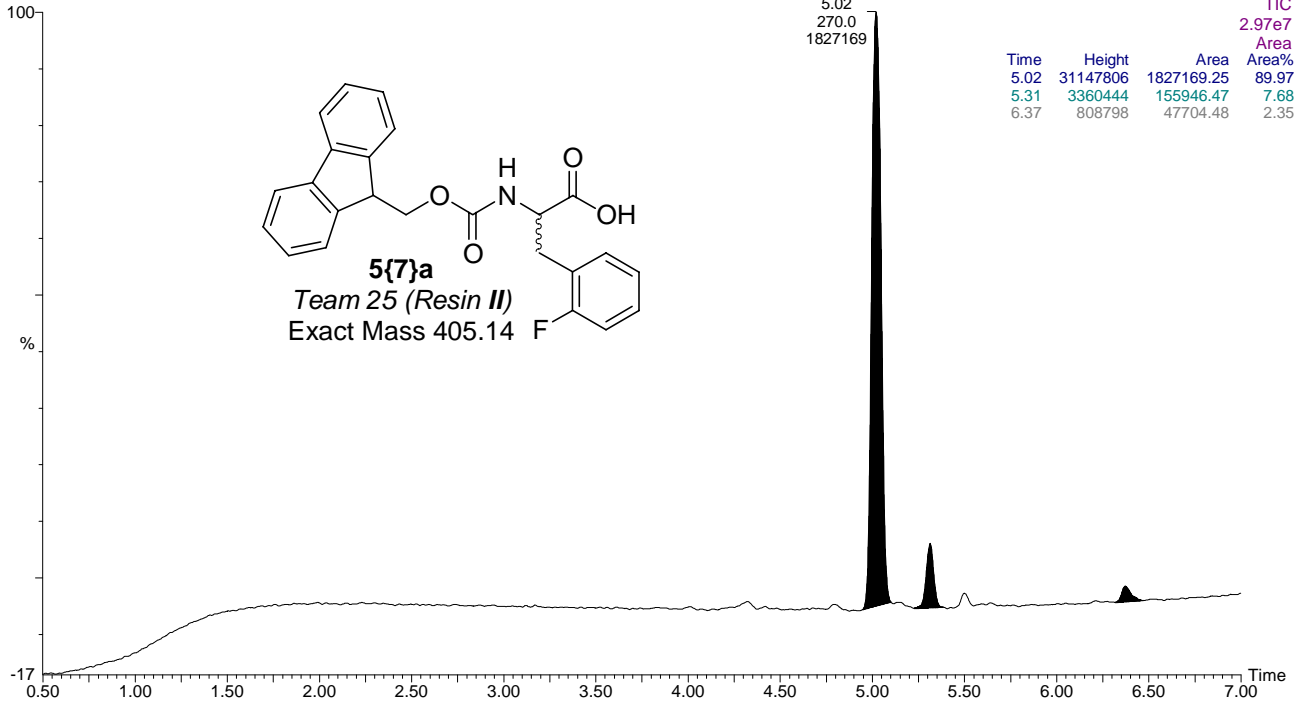
T18-A2 190 (5.085) Cm (189:192)



5{7}a

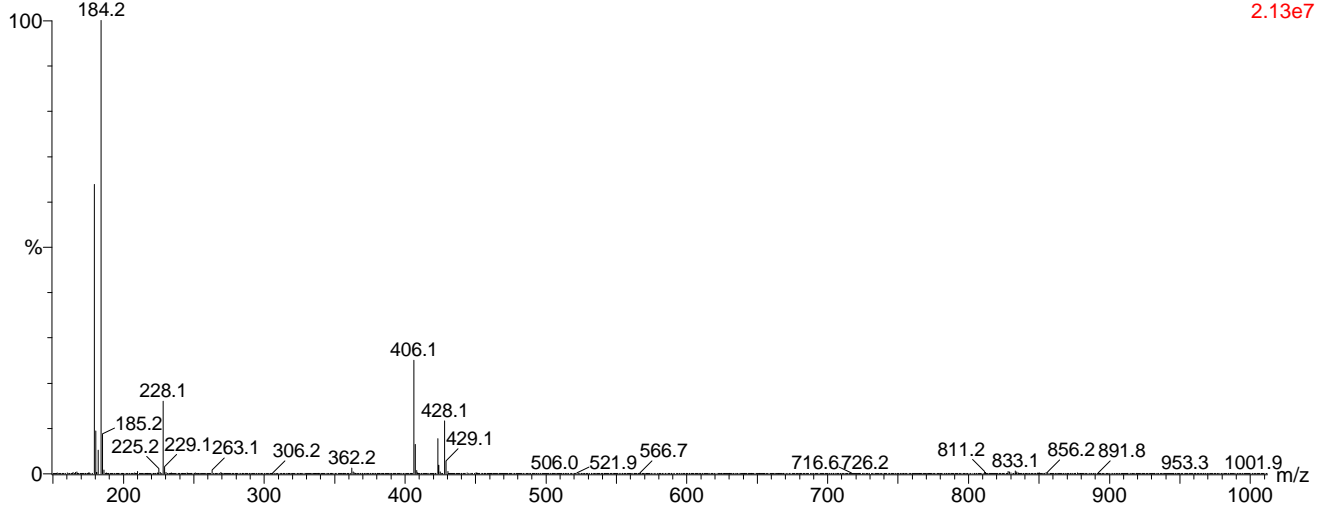
T25-A3 Sm (Mn, 1x1)

3: Diode Array
TIC
2.97e7



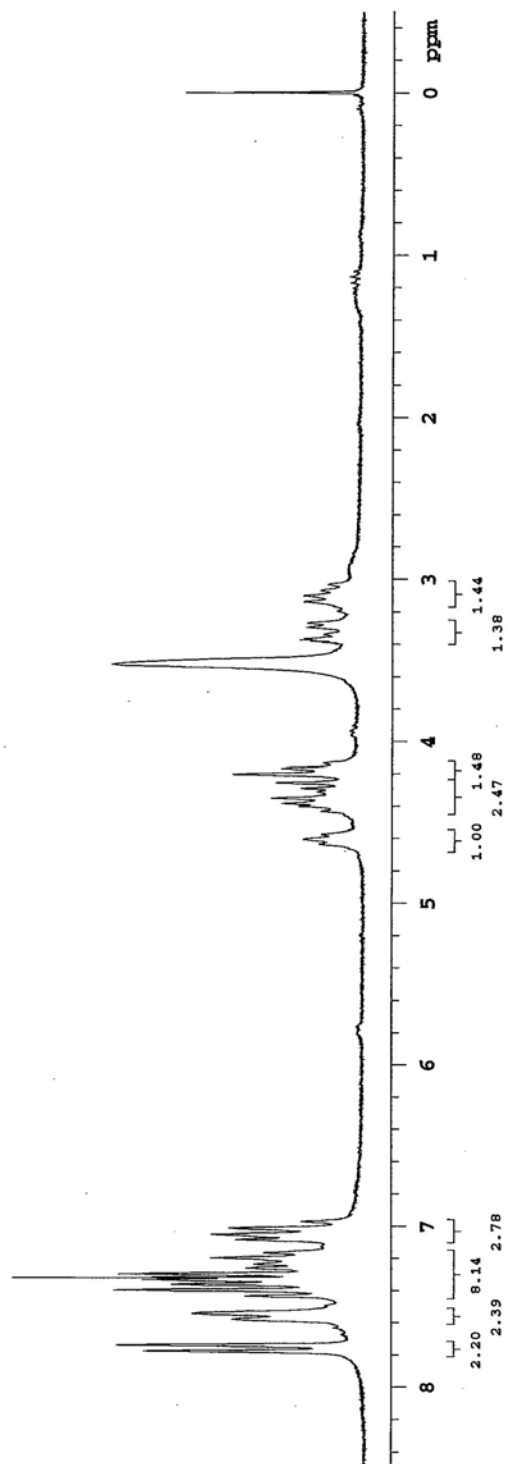
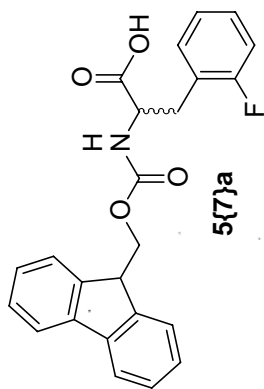
T25-A3 190 (5.085) Cm (188:192)

1: Scan ES+
2.13e7



1H_RR#27_A2_CD3ODinCDCl3_02_18_07

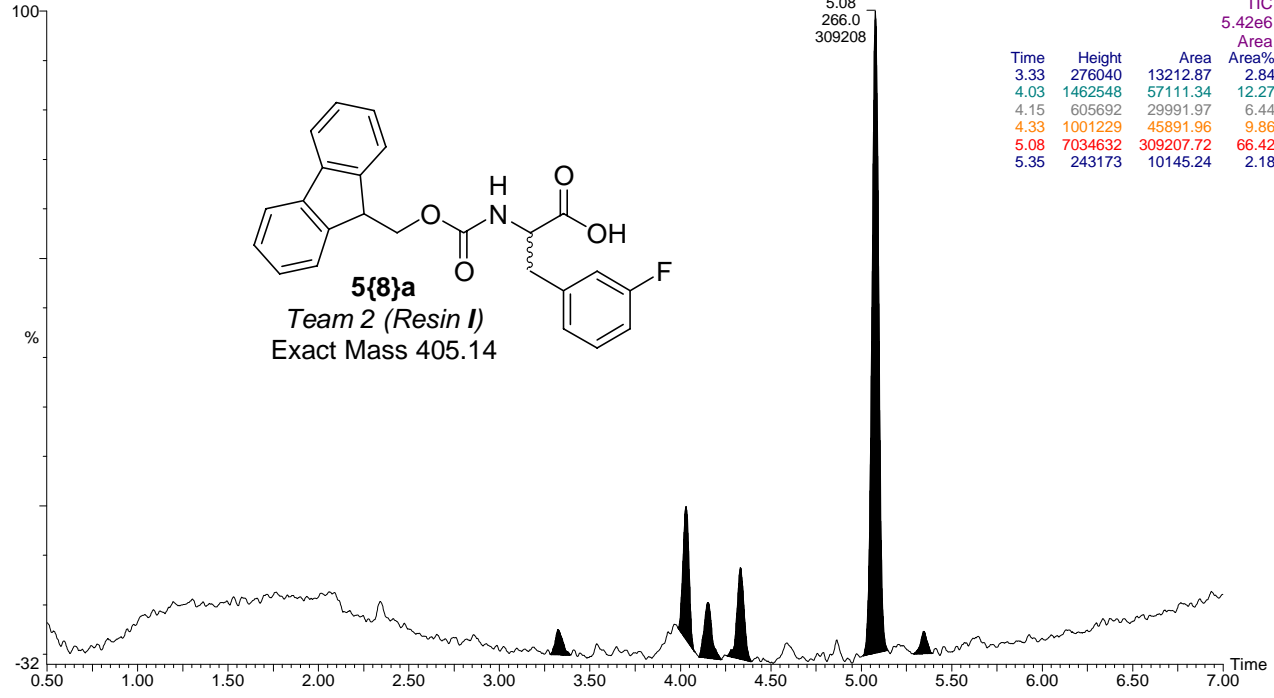
Pulse Sequence: s2pul



5{8}a

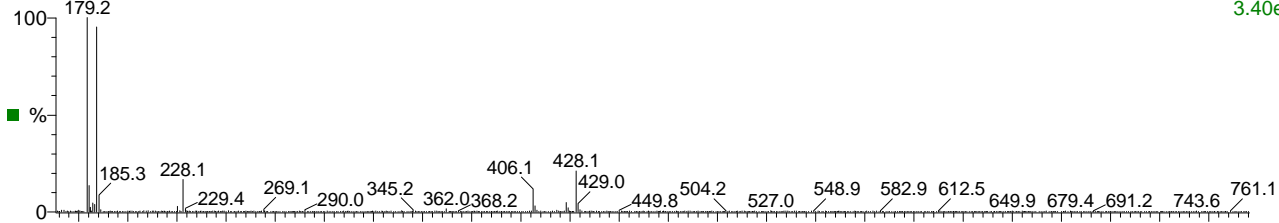
T2-A3 Sm (Mn, 1x1)

3: Diode Array



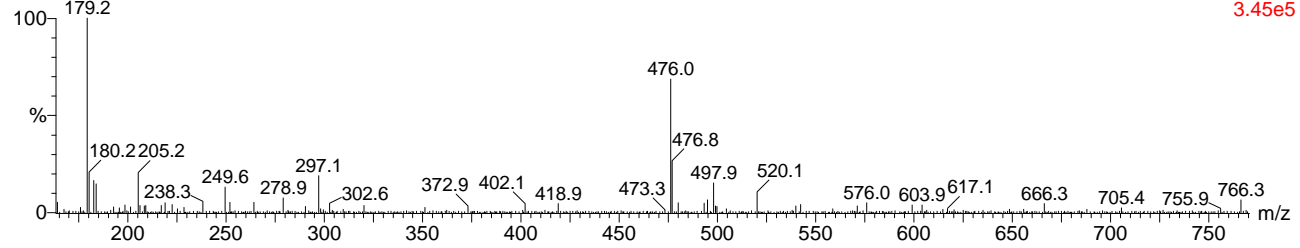
T2-A3 192 (5.138) Cm (191:193)

1: Scan ES+
3.40e6



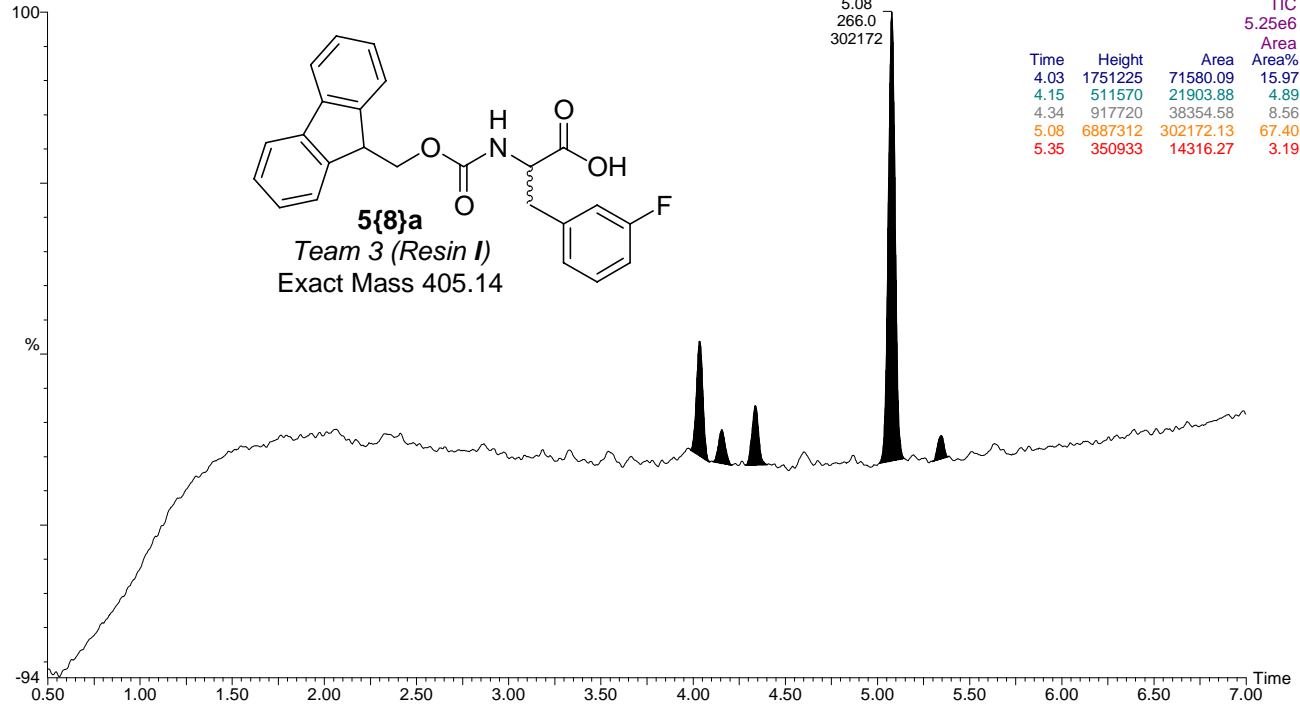
T2-A3 152 (4.065) Cm (152)

1: Scan ES+
3.45e5

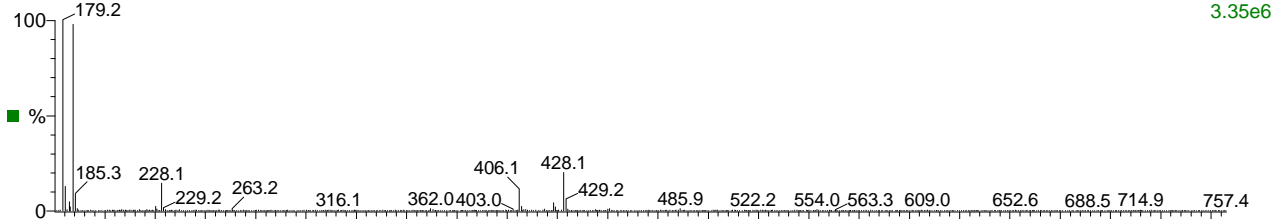


5{8}a

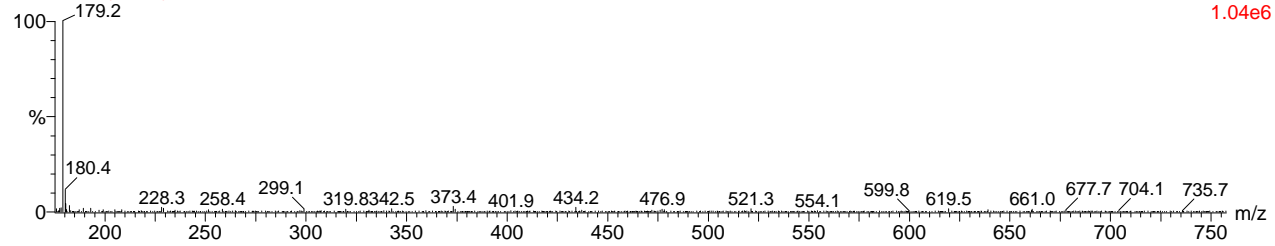
T3-A2 Sm (Mn, 1x1)



T3-A2 192 (5.138) Cm (191:193)



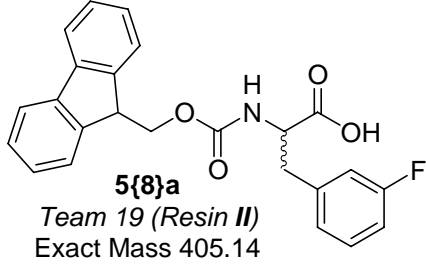
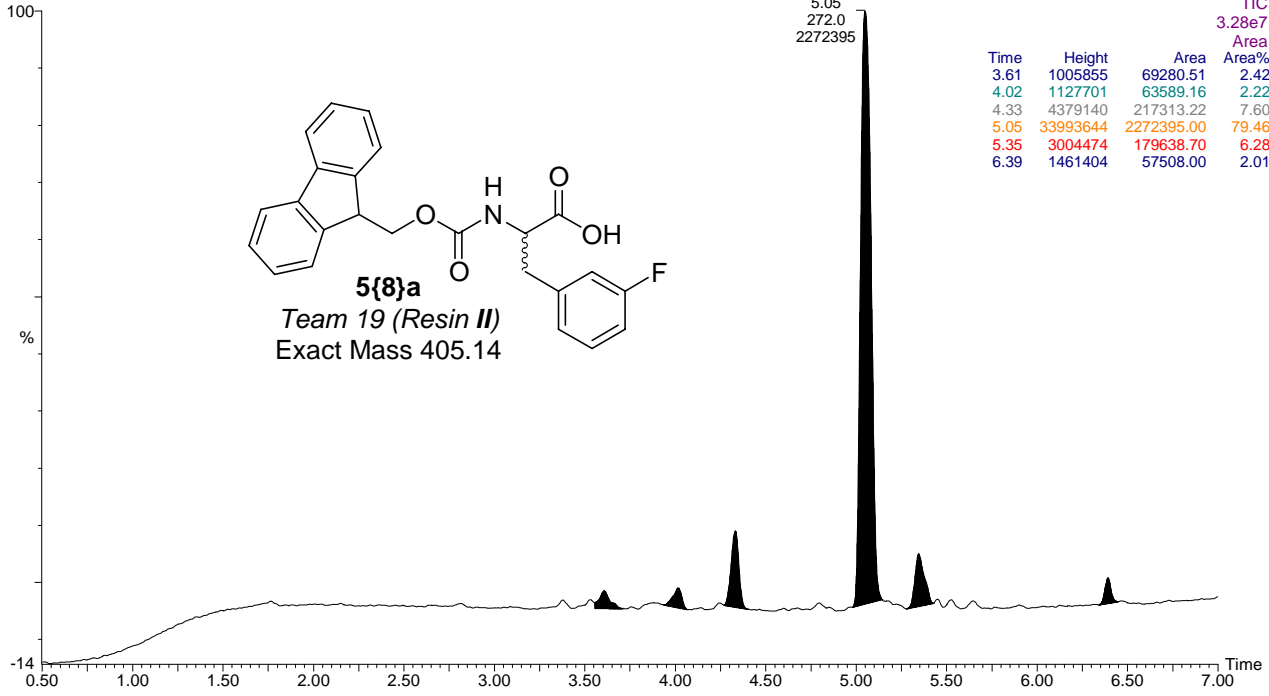
T3-A2 153 (4.092)



5{8}a

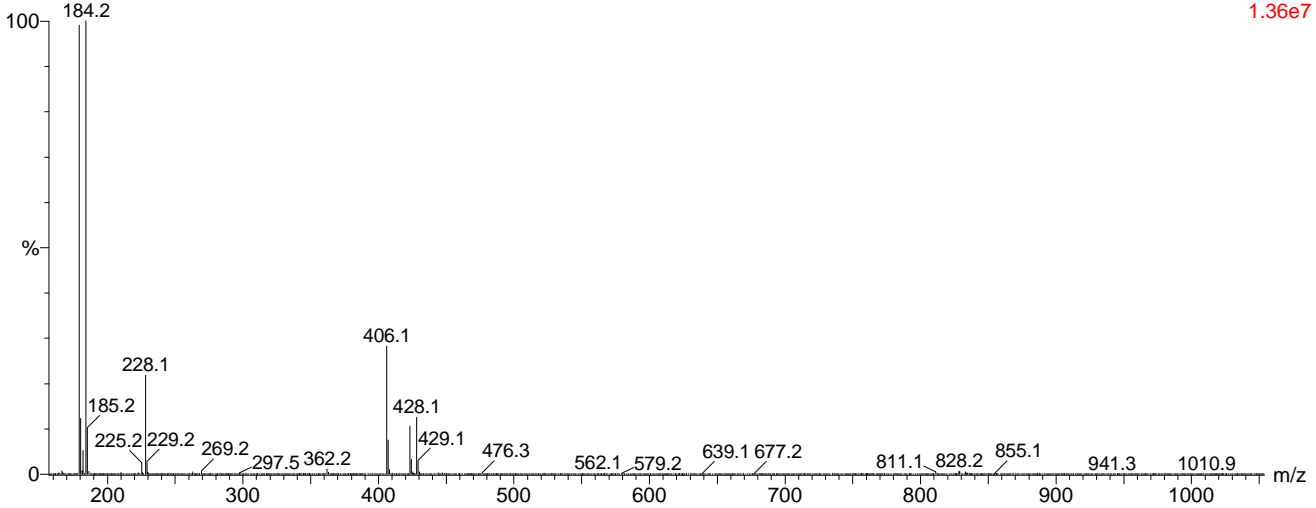
T19-A3 Sm (Mn, 1x1)

3: Diode Array
TIC
3.28e7



T19-A3 191 (5.112) Cm (190:193)

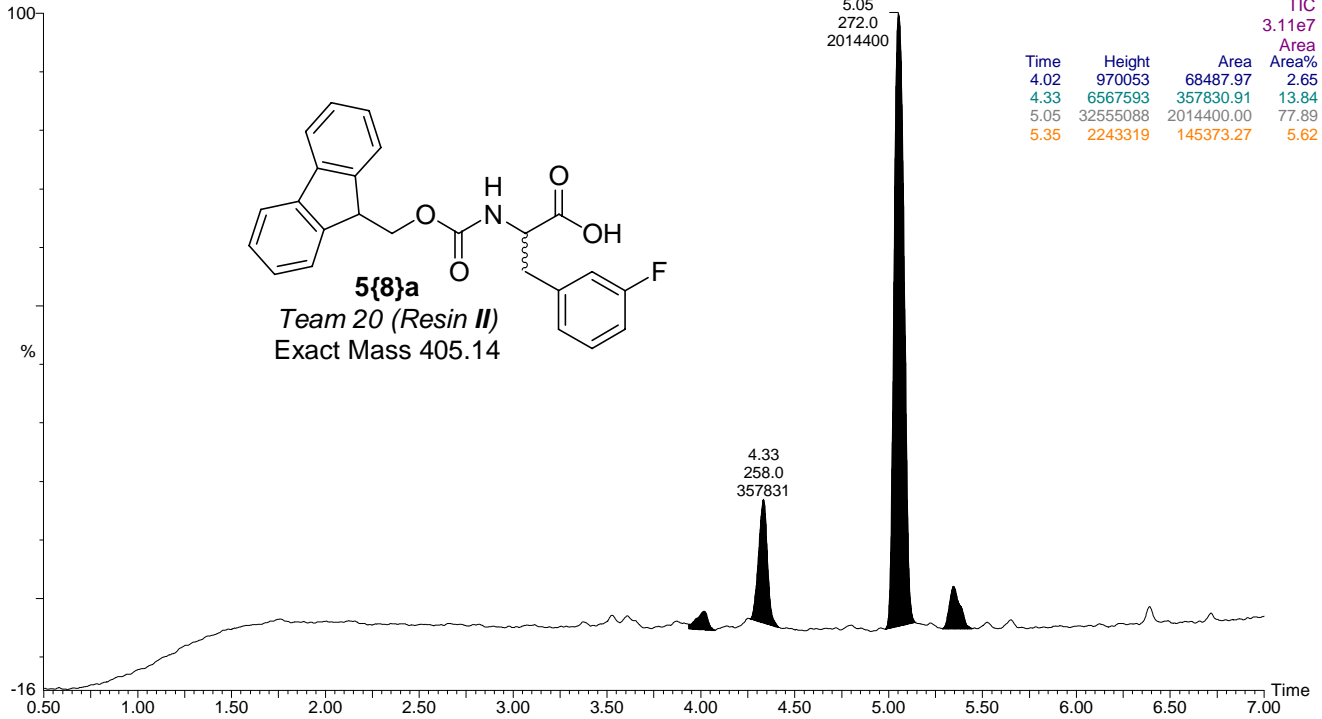
1: Scan ES+
1.36e7



5{8}a

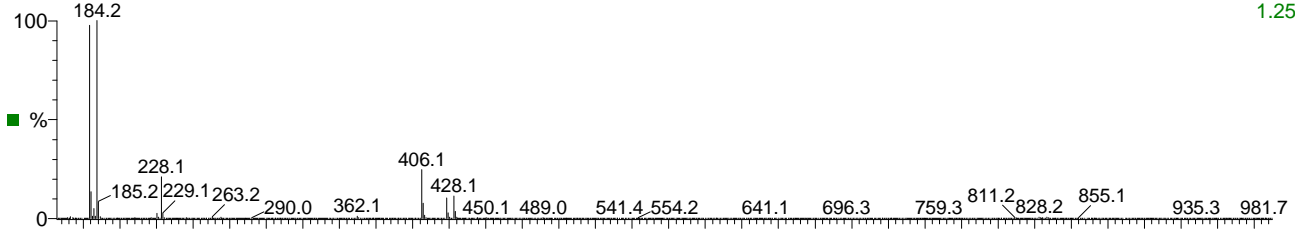
T20-A2 Sm (Mn, 1x1)

3: Diode Array



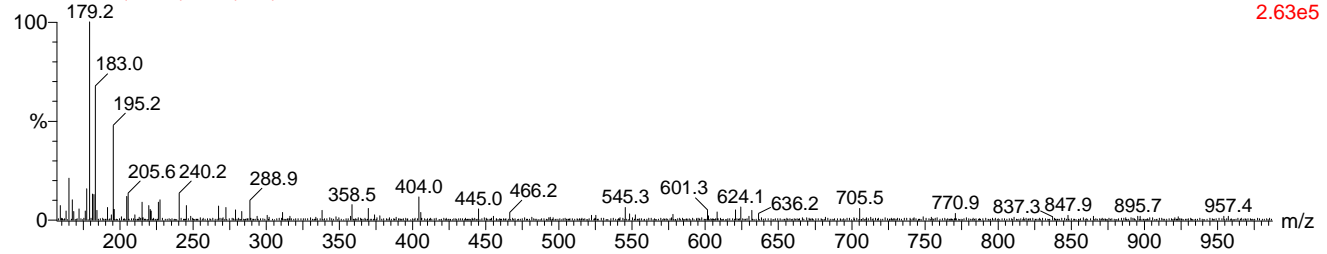
T20-A2 191 (5.112) Cm (190:193)

1: Scan ES+
1.25e7



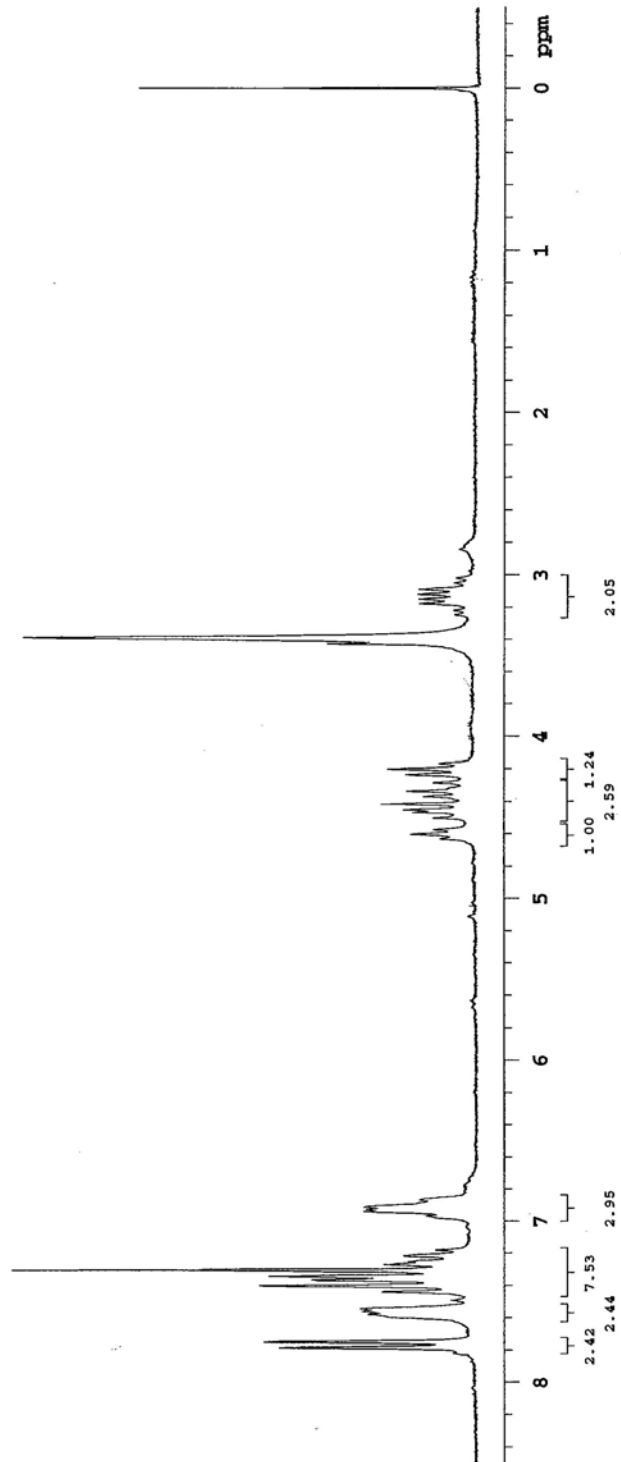
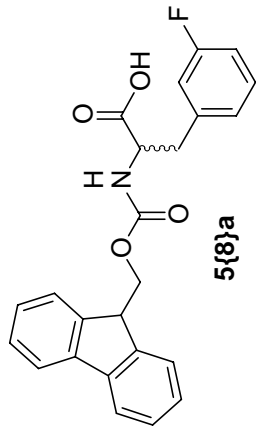
T20-A2 164 (4.387) Cm (164)

1: Scan ES+
2.63e5



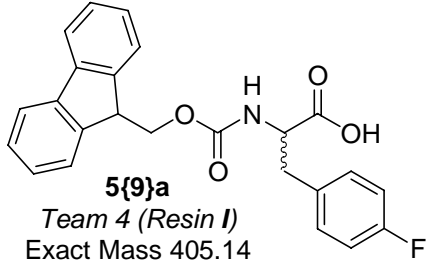
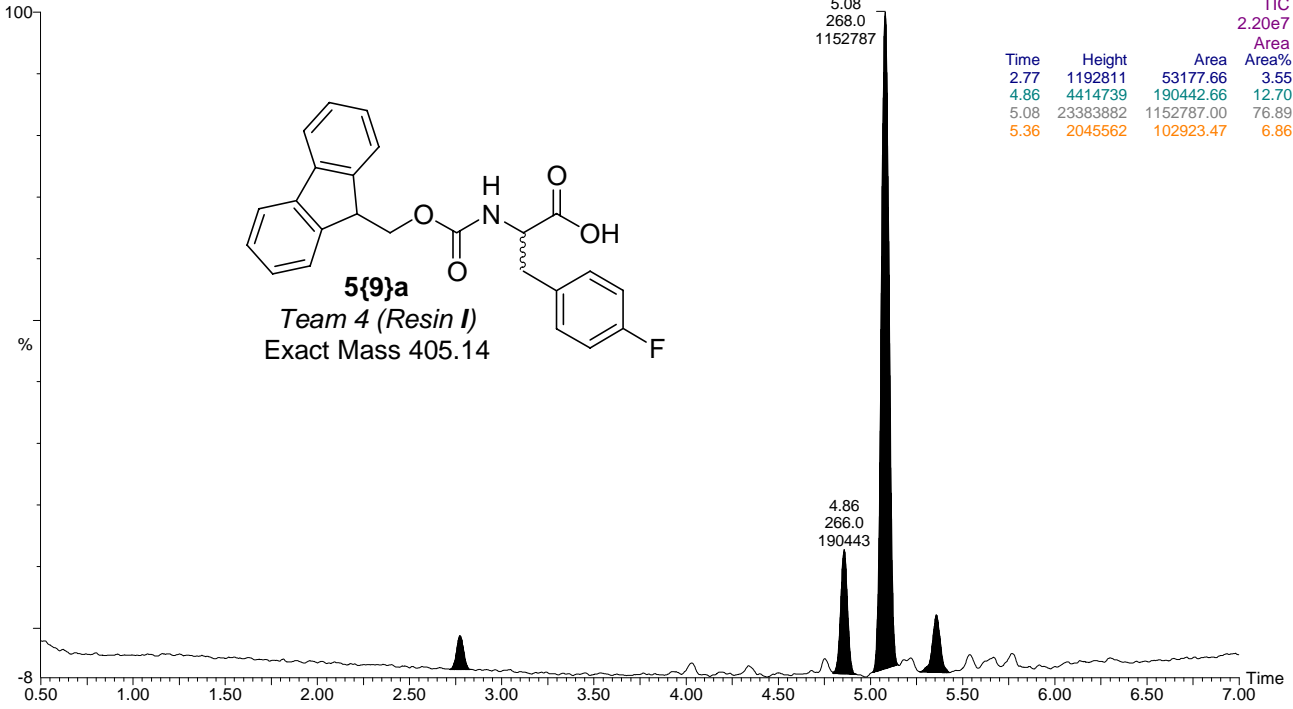
1H_RF#40_A1_CD3ODinCDCl3_03_07

Pulse Sequence: s2pul

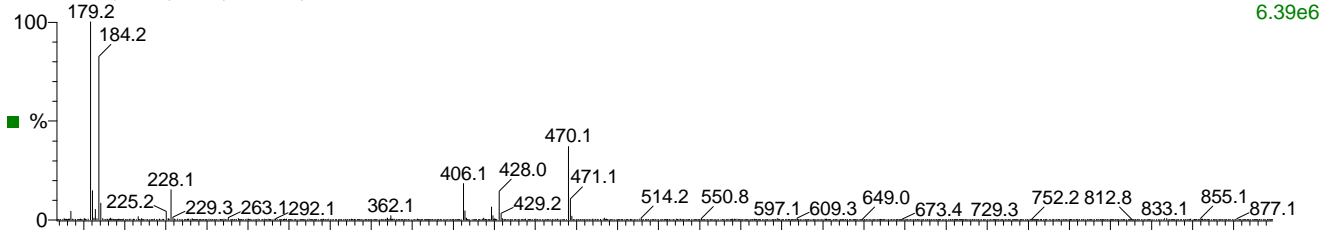


5{9}a

T4-A3 Sm (Mn, 1x1)

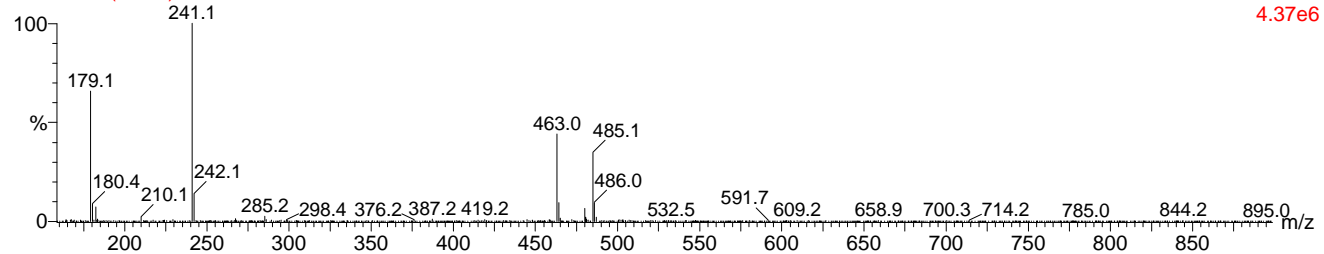


T4-A3 192 (5.138) Cm (191:194)



1: Scan ES+
6.39e6

T4-A3 183 (4.897)

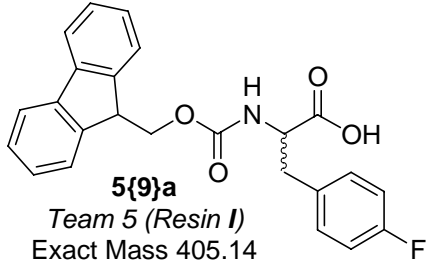
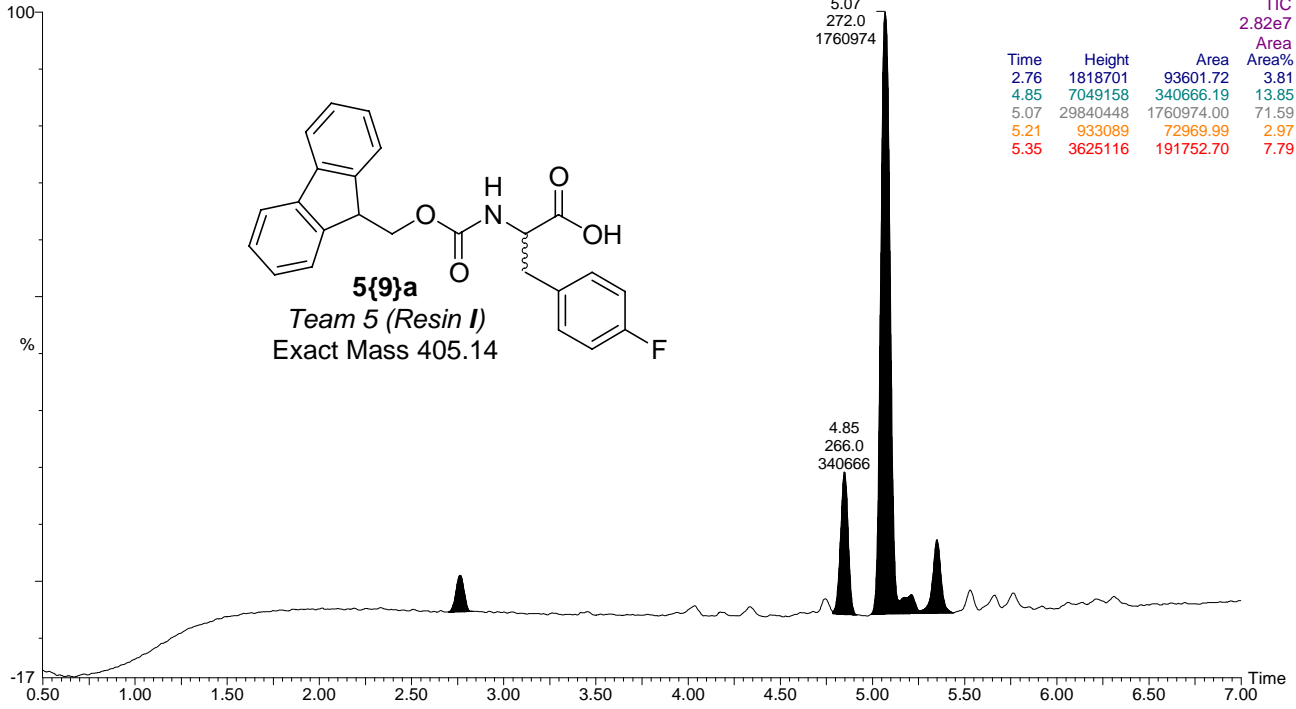


1: Scan ES+
4.37e6

5{9}a

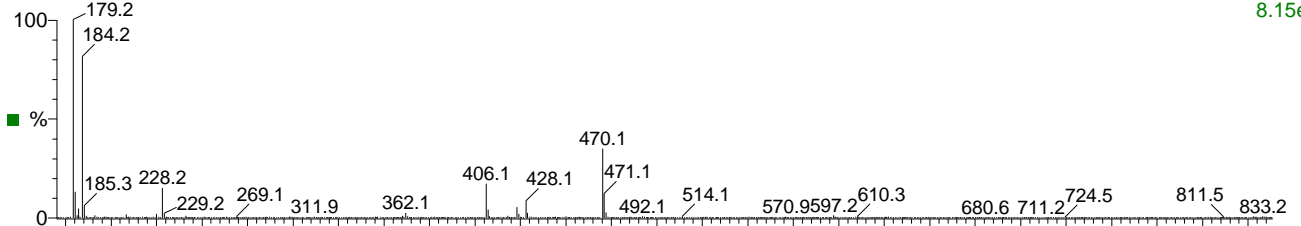
T5-A2 Sm (Mn, 1x1)

3: Diode Array
TIC
2.82e7



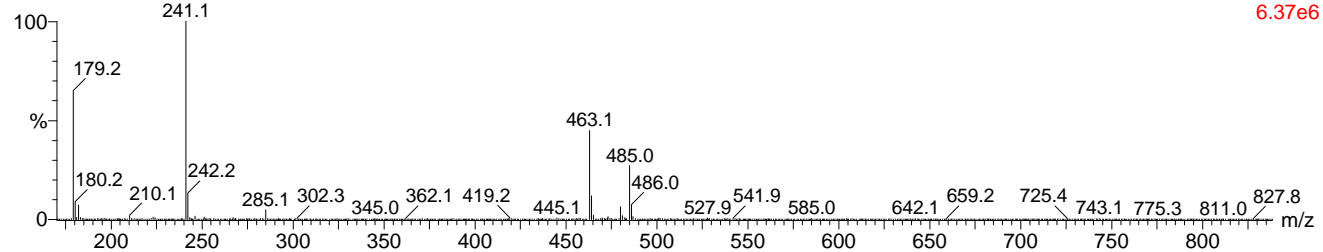
T5-A2 192 (5.138) Cm (191:194)

1: Scan ES+
8.15e6



T5-A2 183 (4.897) Cm (182:184)

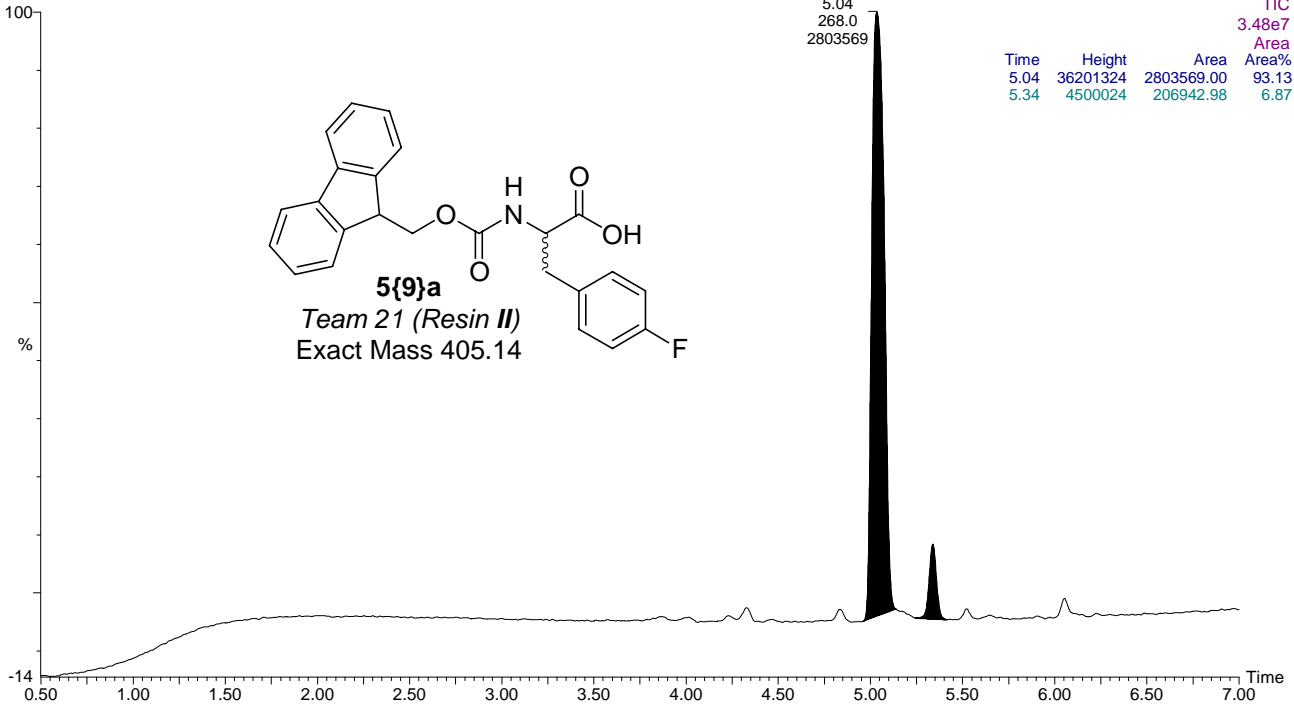
1: Scan ES+
6.37e6



5{9}a

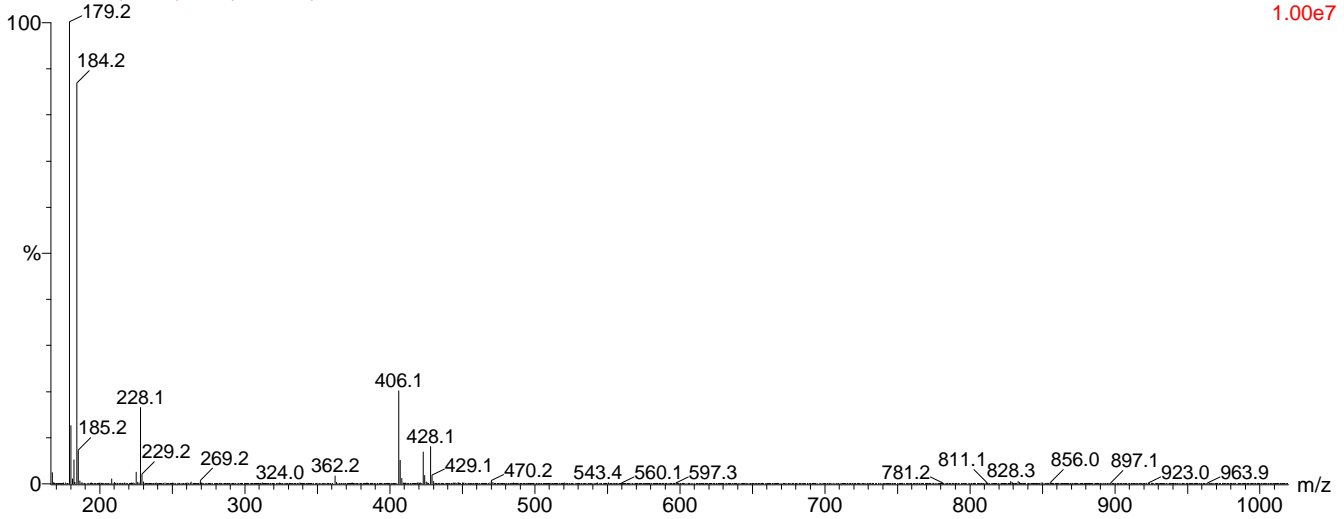
T21-A3 Sm (Mn, 1x1)

3: Diode Array



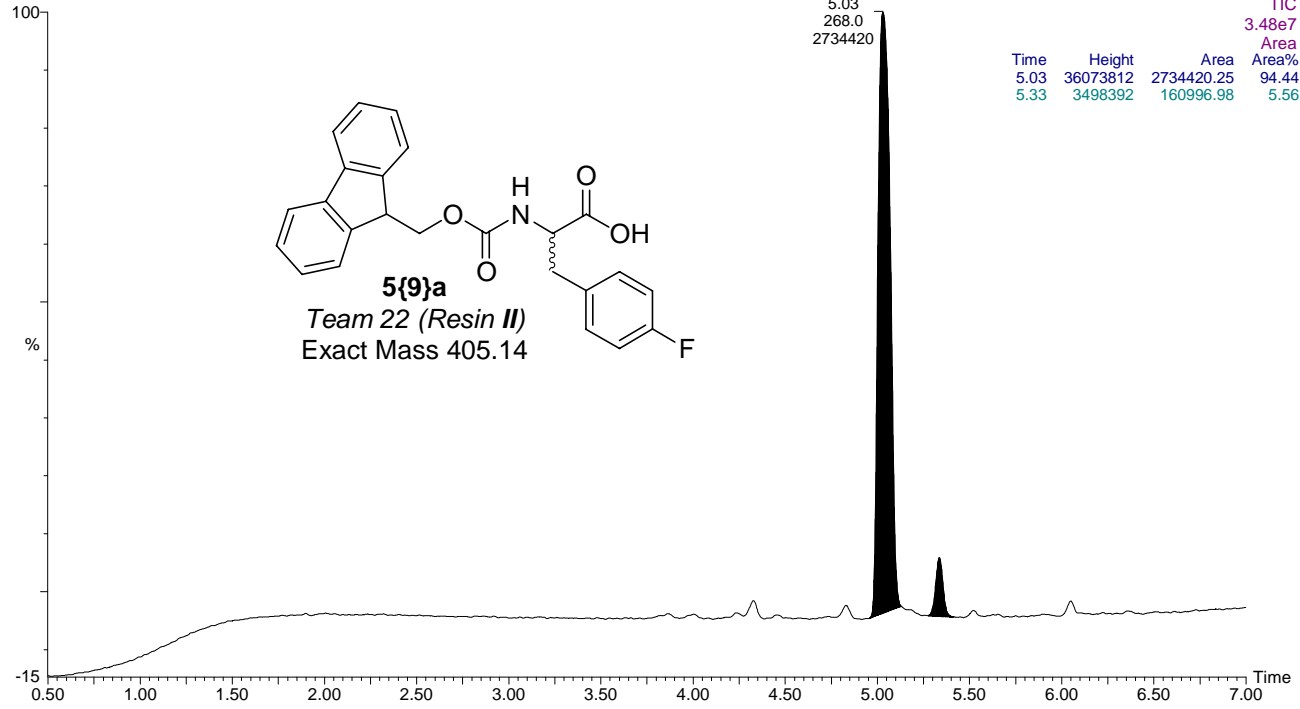
T21-A3 190 (5.085) Cm (189:193)

1: Scan ES+
1.00e7

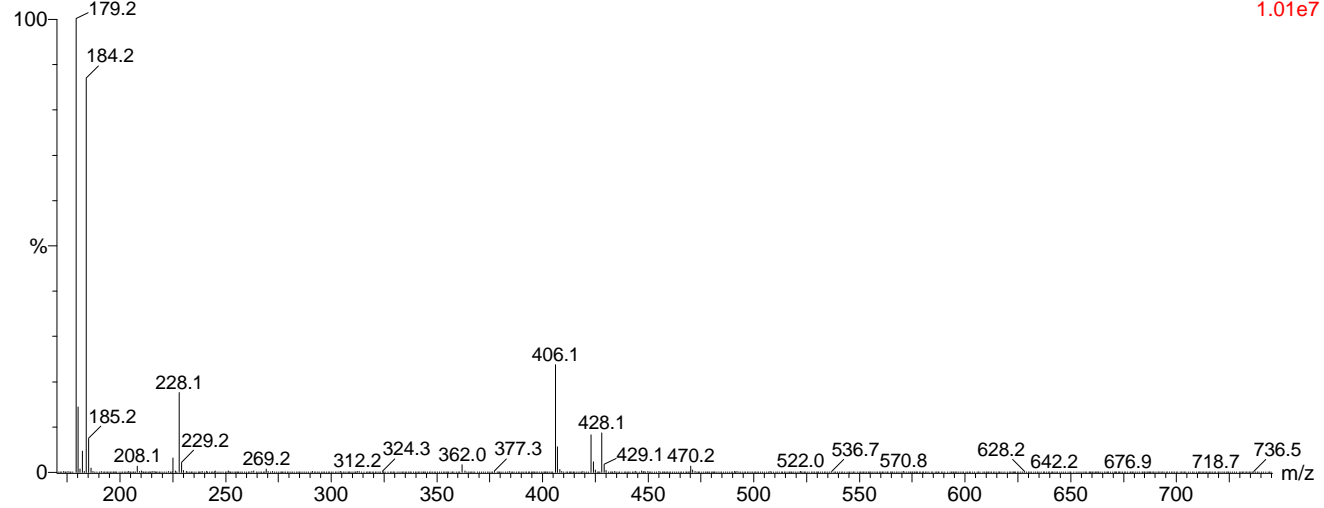


5{9}a

T22-A2 Sm (Mn, 1x1)

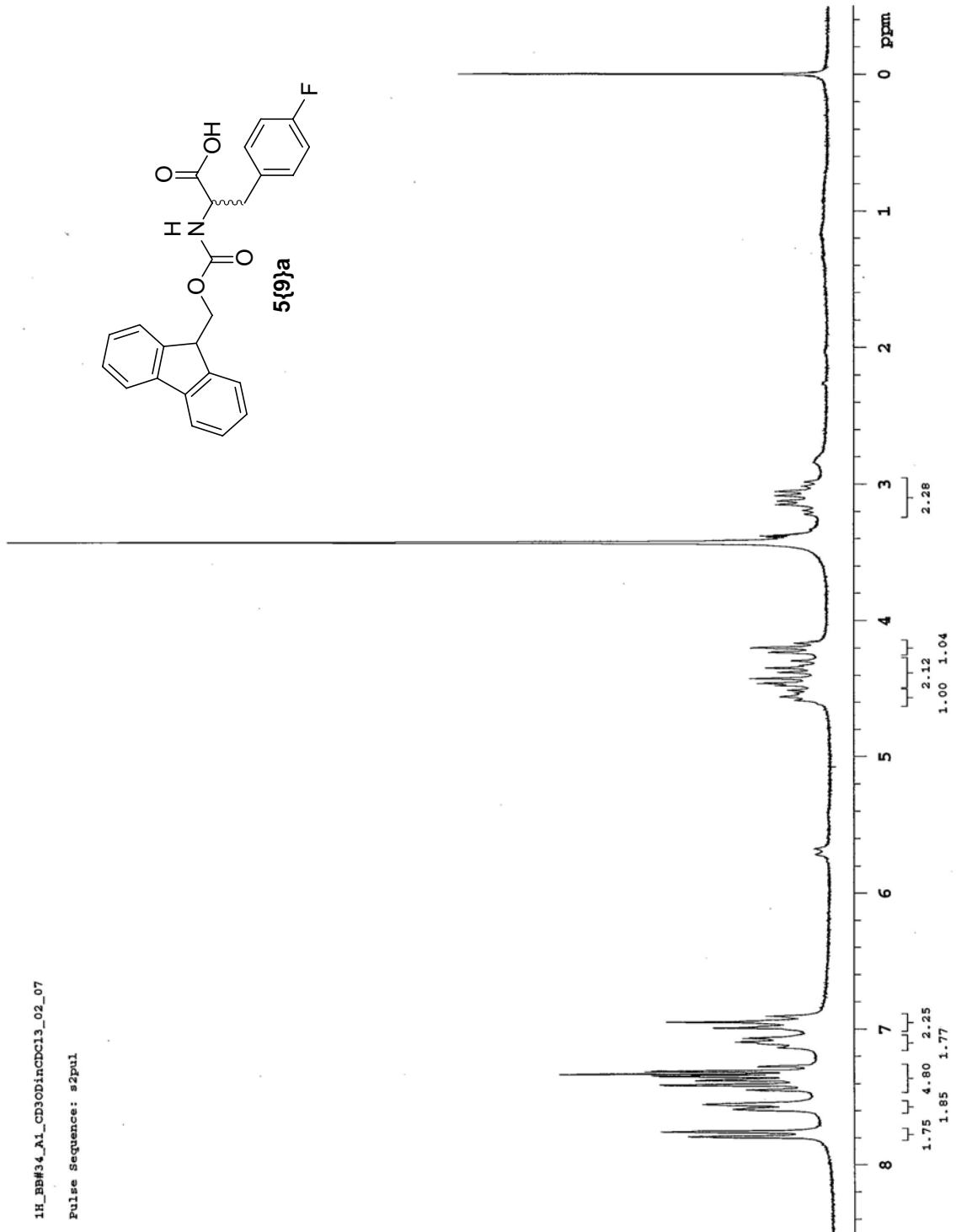
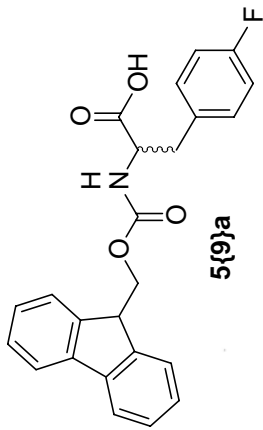


T22-A2 190 (5.085) Cm (190:193)



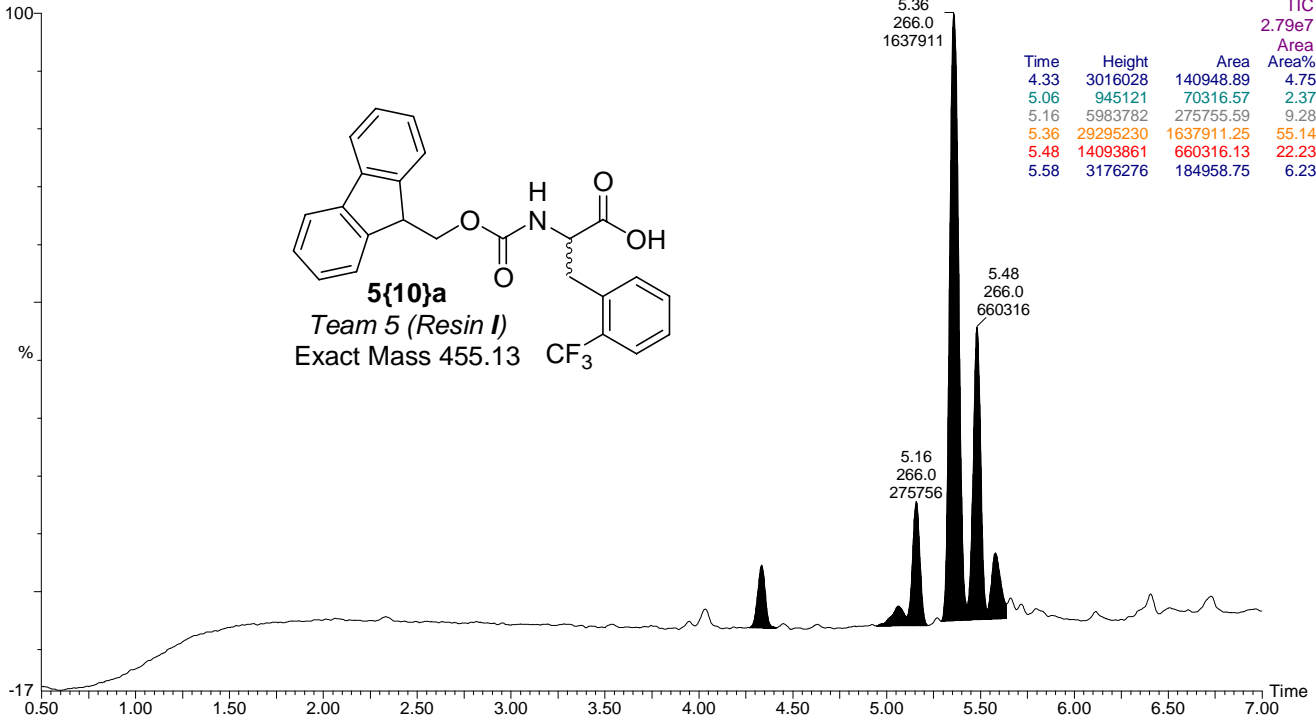
1H_BB#34_A1_CD3ODinCDC13_02_07

Pulse Sequence: s2pul



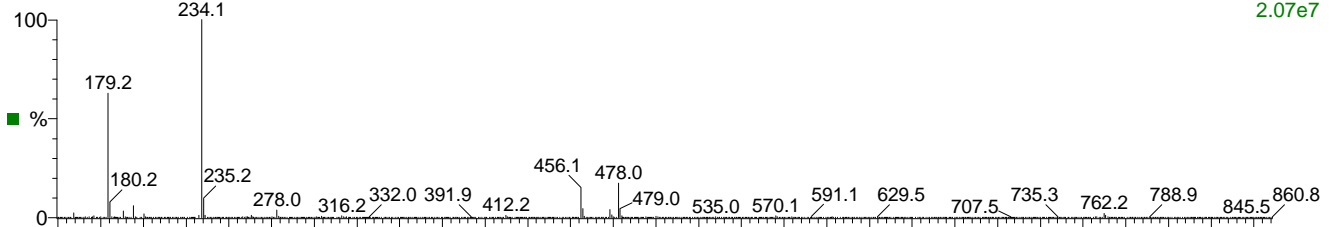
5{10}a

T5-A3 Sm (Mn, 1x1)



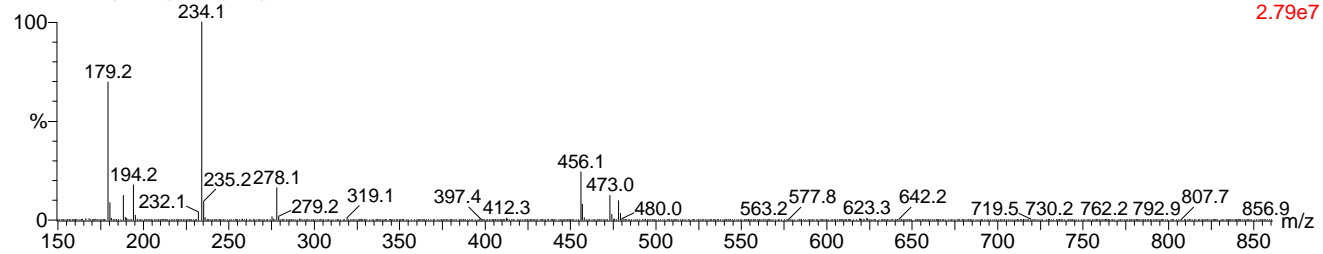
T5-A3 207 (5.541) Cm (207:208)

1: Scan ES+
2.07e7



T5-A3 203 (5.434) Cm (203)

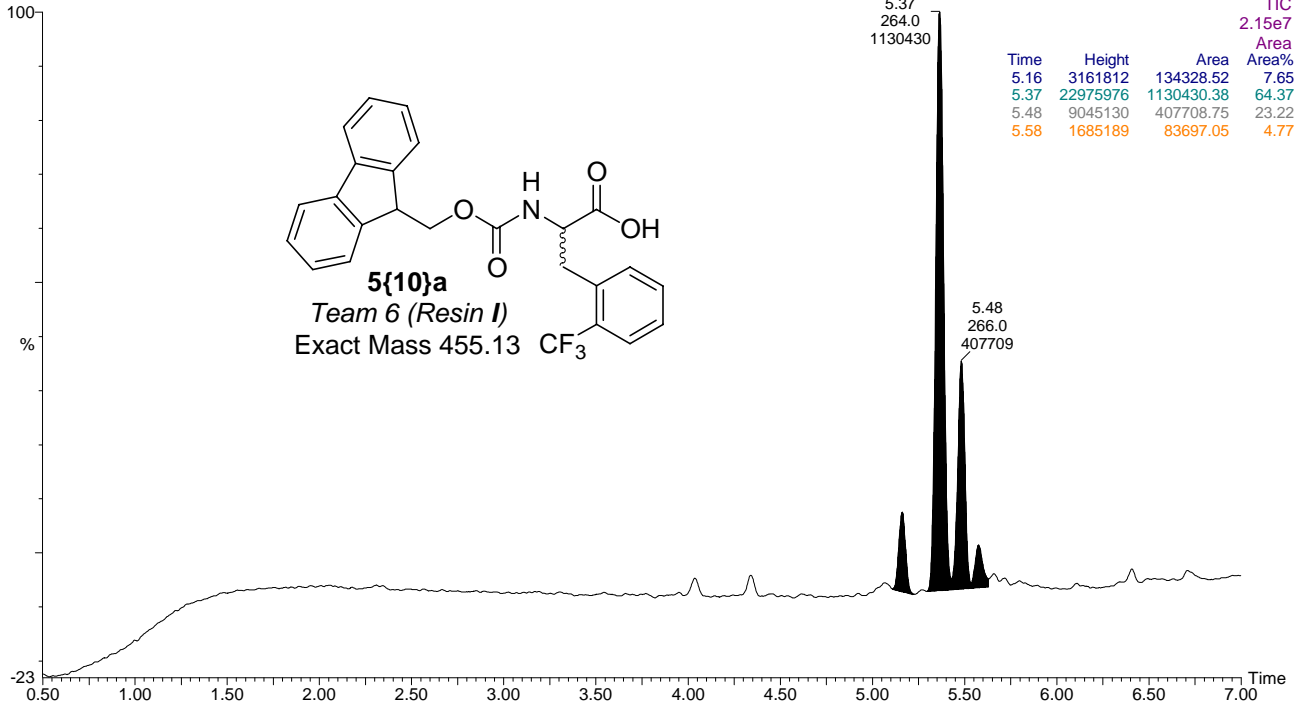
1: Scan ES+
2.79e7



5{10}a

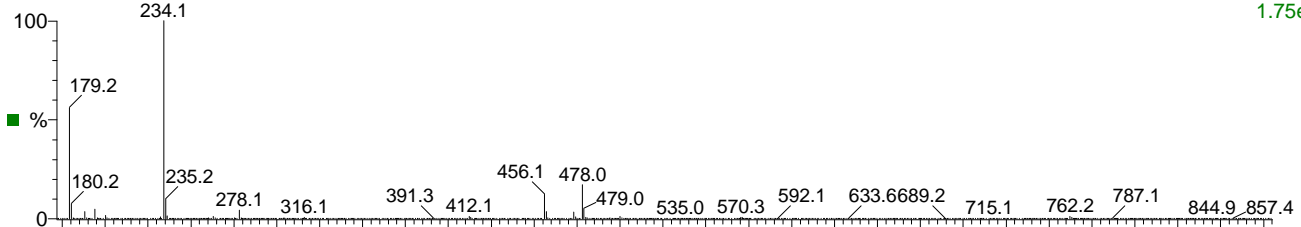
T6-A2 Sm (Mn, 1x1)

3: Diode Array
TIC
2.15e7



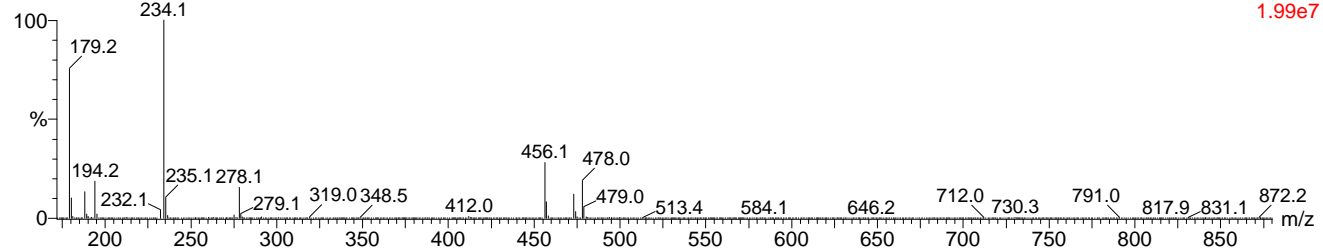
T6-A2 207 (5.541) Cm (207:208)

1: Scan ES+
1.75e7



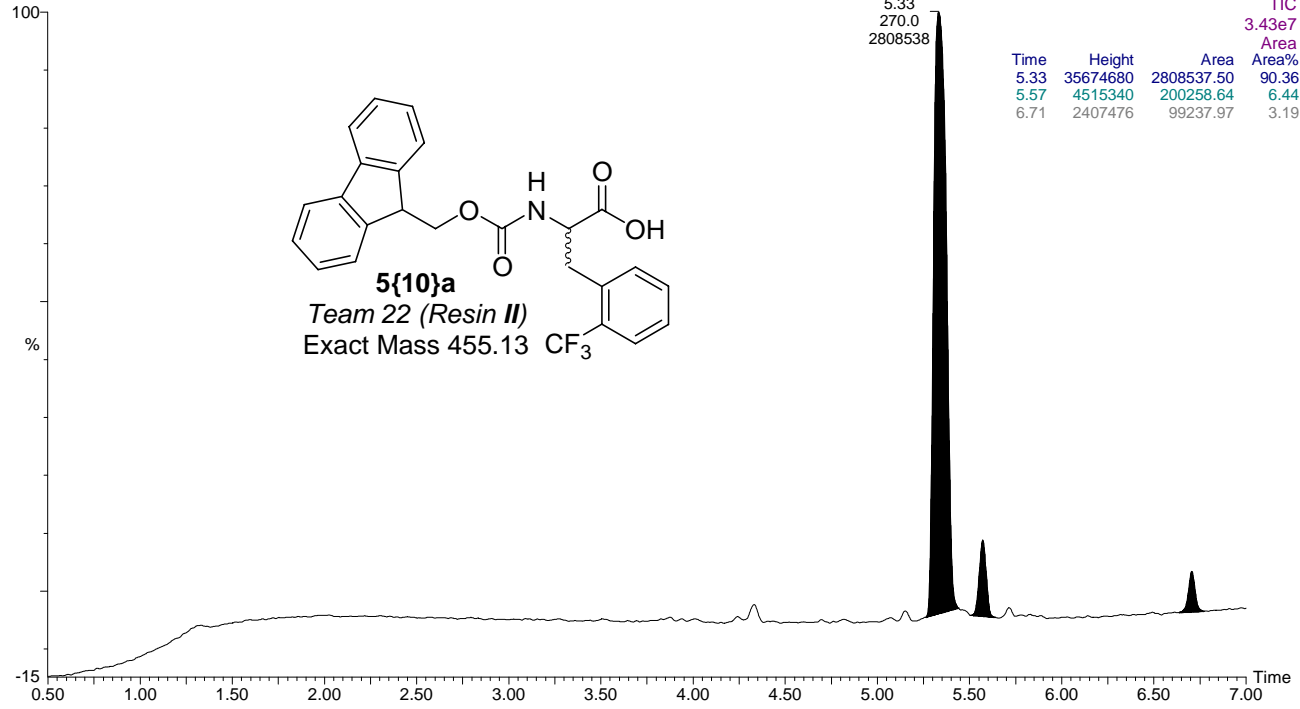
T6-A2 203 (5.434) Cm (202:203)

1: Scan ES+
1.99e7

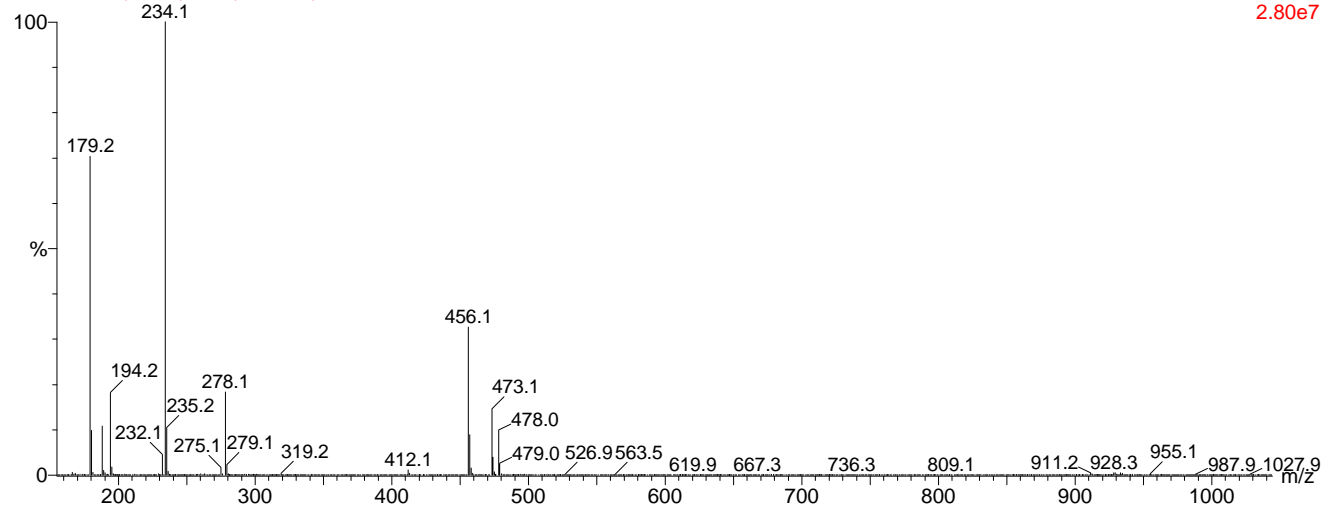


5{10}a

T22-A3 Sm (Mn, 1x1)

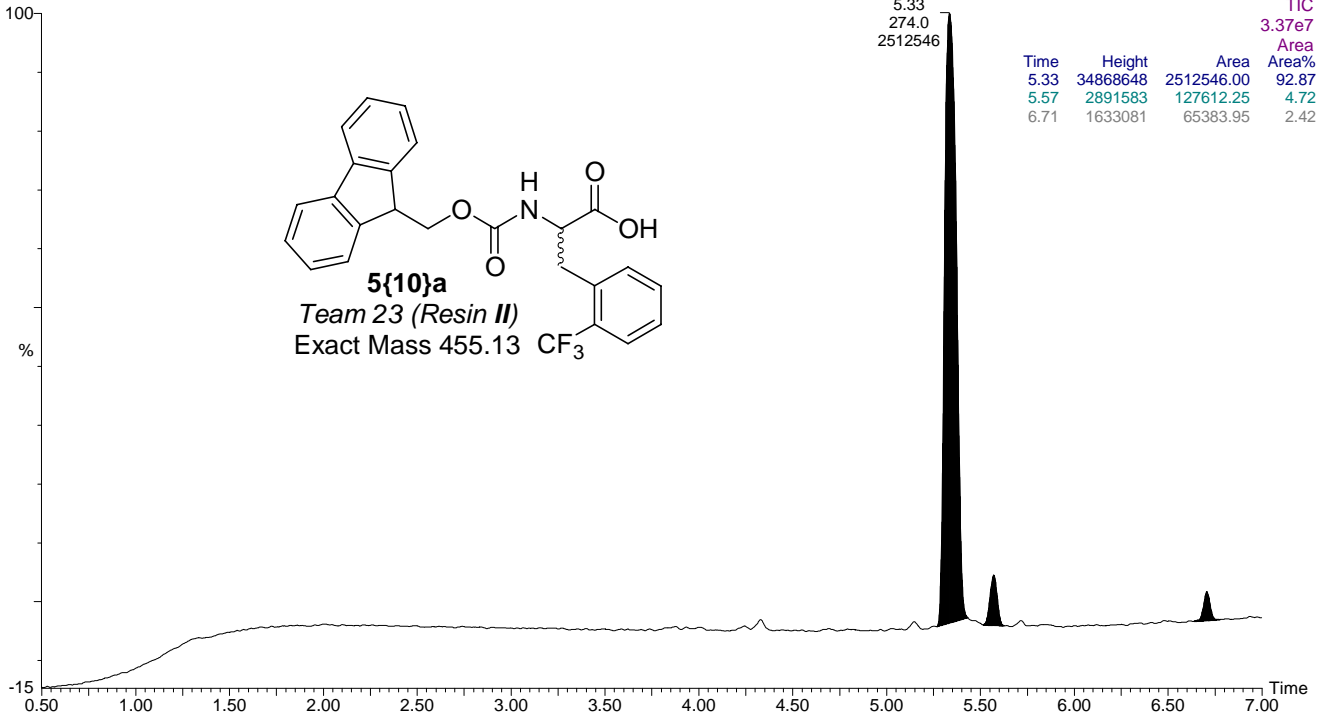


T22-A3 201 (5.380) Cm (201:204)

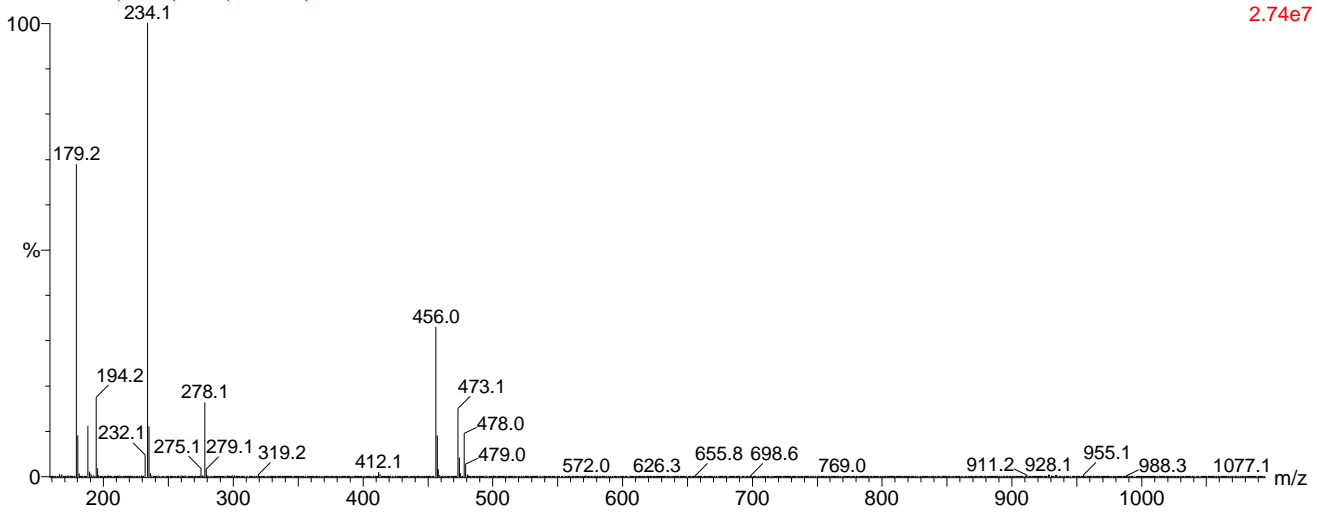


5{10}a

T23-A2 Sm (Mn, 1x1)

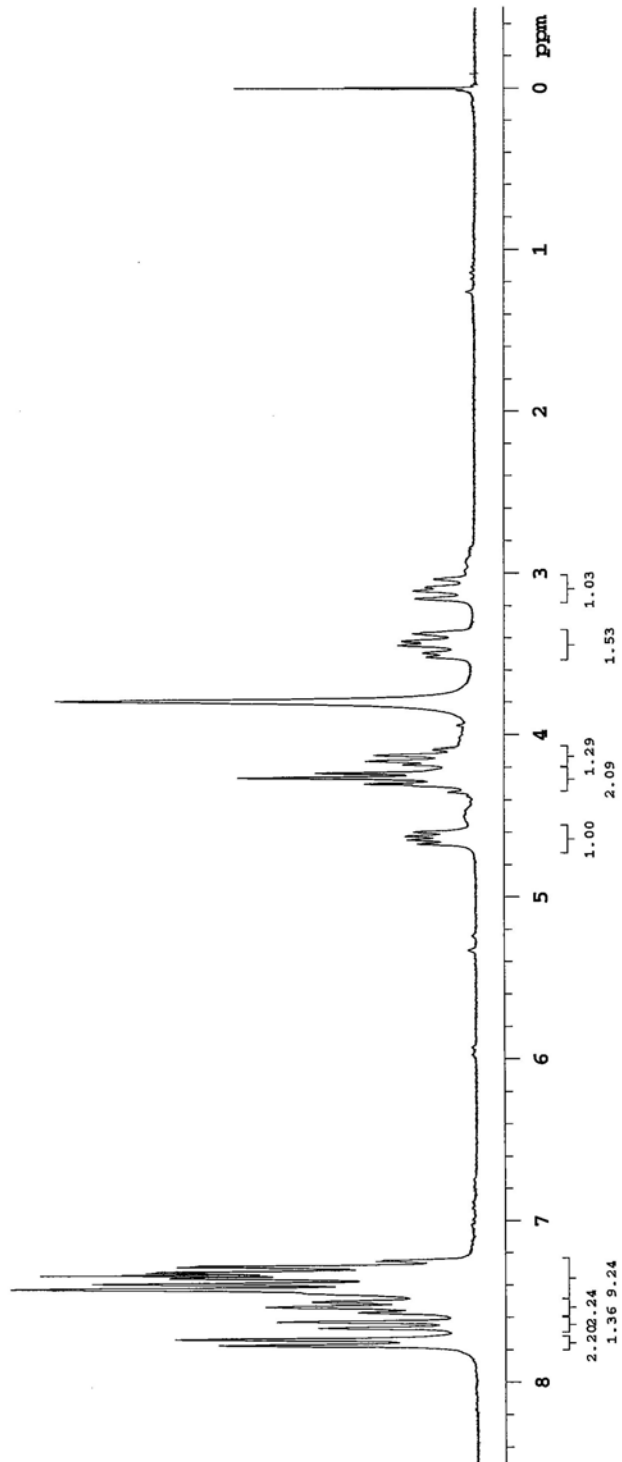
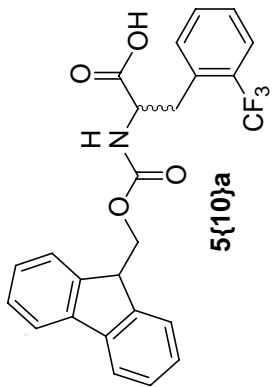


T23-A2 201 (5.380) Cm (201:204)



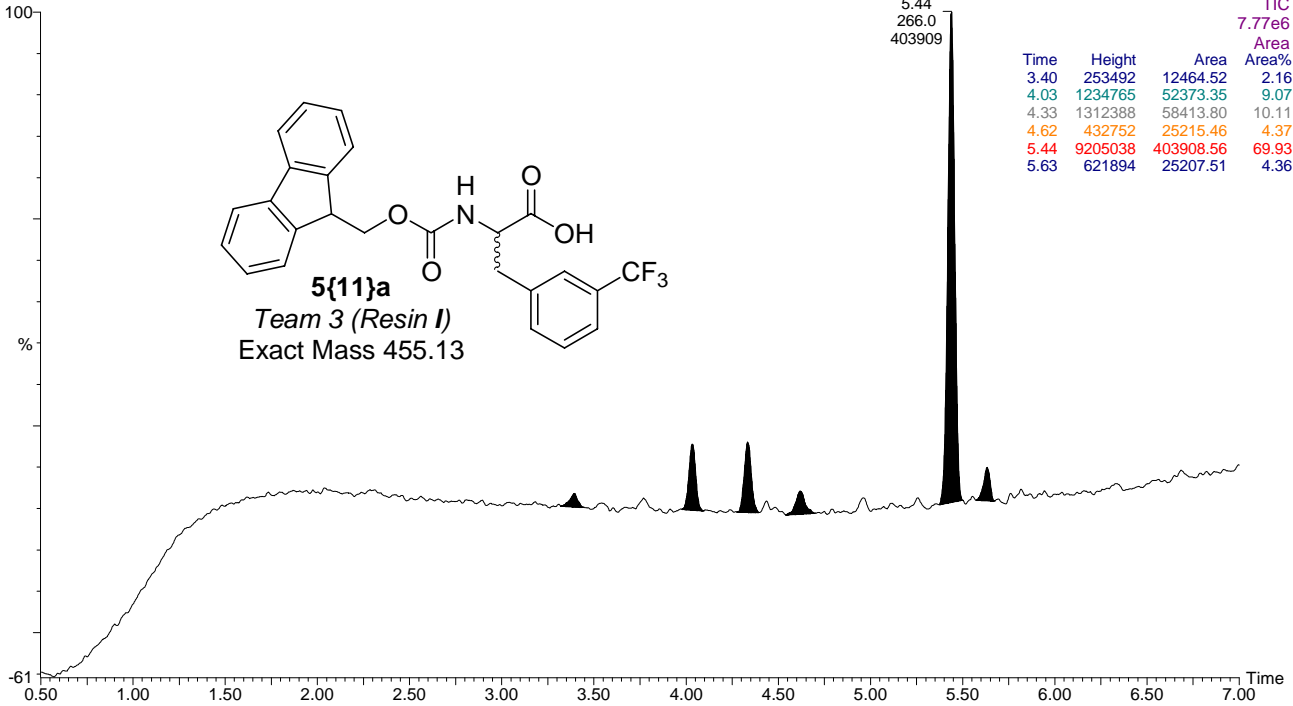
1H_RF#27_B3_leastCD3ODinCDCl3_02_17_02_17_07

Pulse Sequence: s2pul

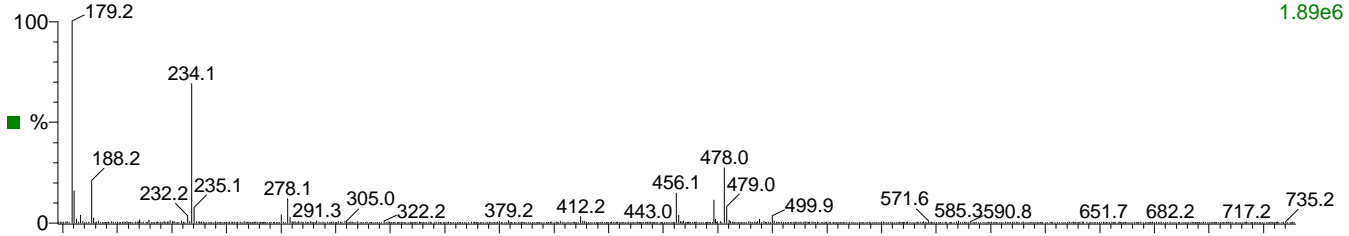


5{11}a

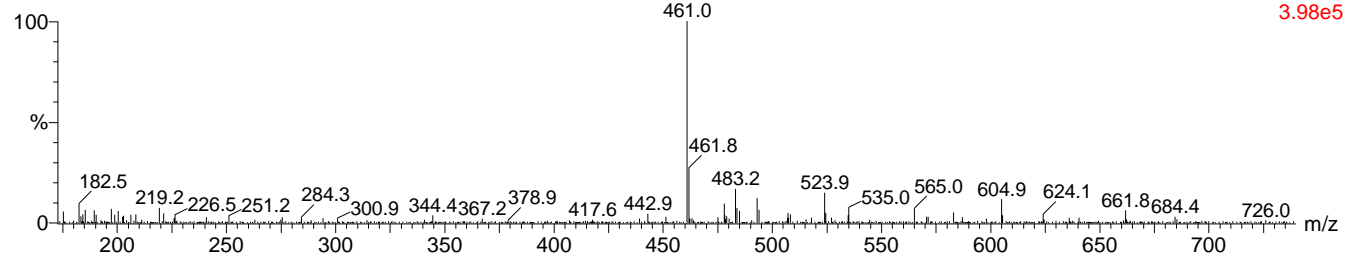
T3-A3 Sm (Mn, 1x1)



T3-A3 206 (5.514) Cm (204:207)

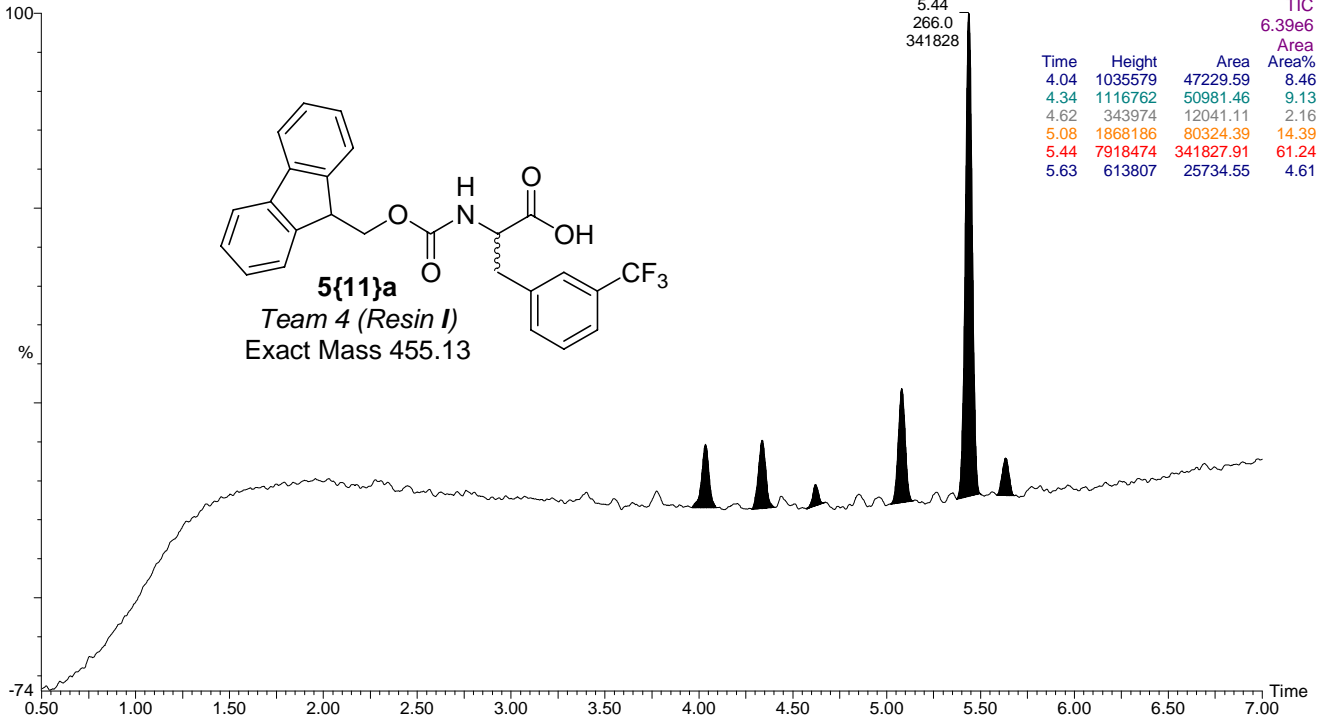


T3-A3 164 (4.387)

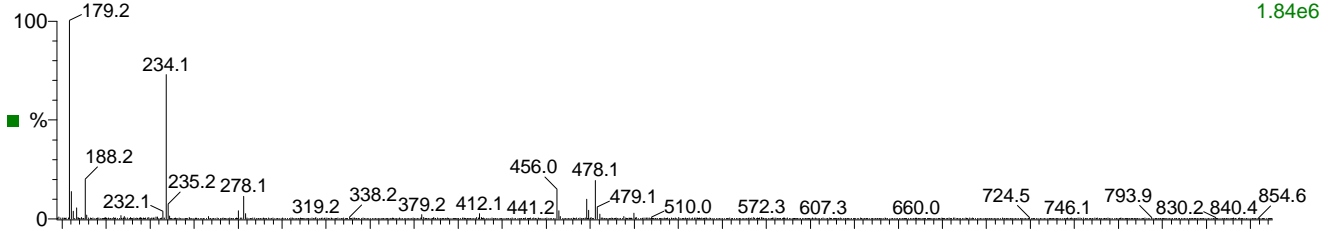


5{11}a

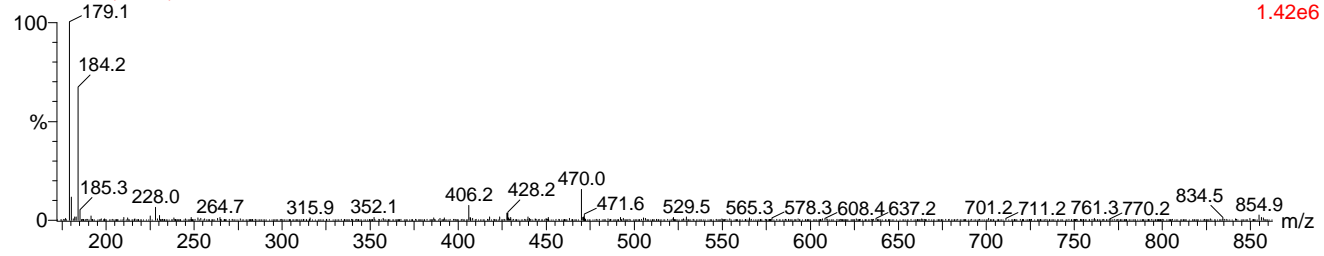
T4-A2 Sm (Mn, 1x1)



T4-A2 205 (5.487) Cm (204:207)



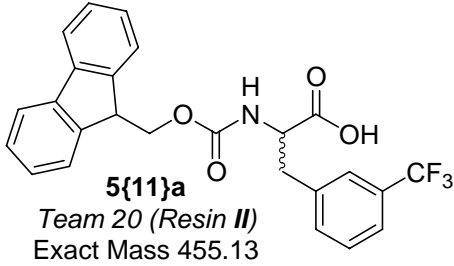
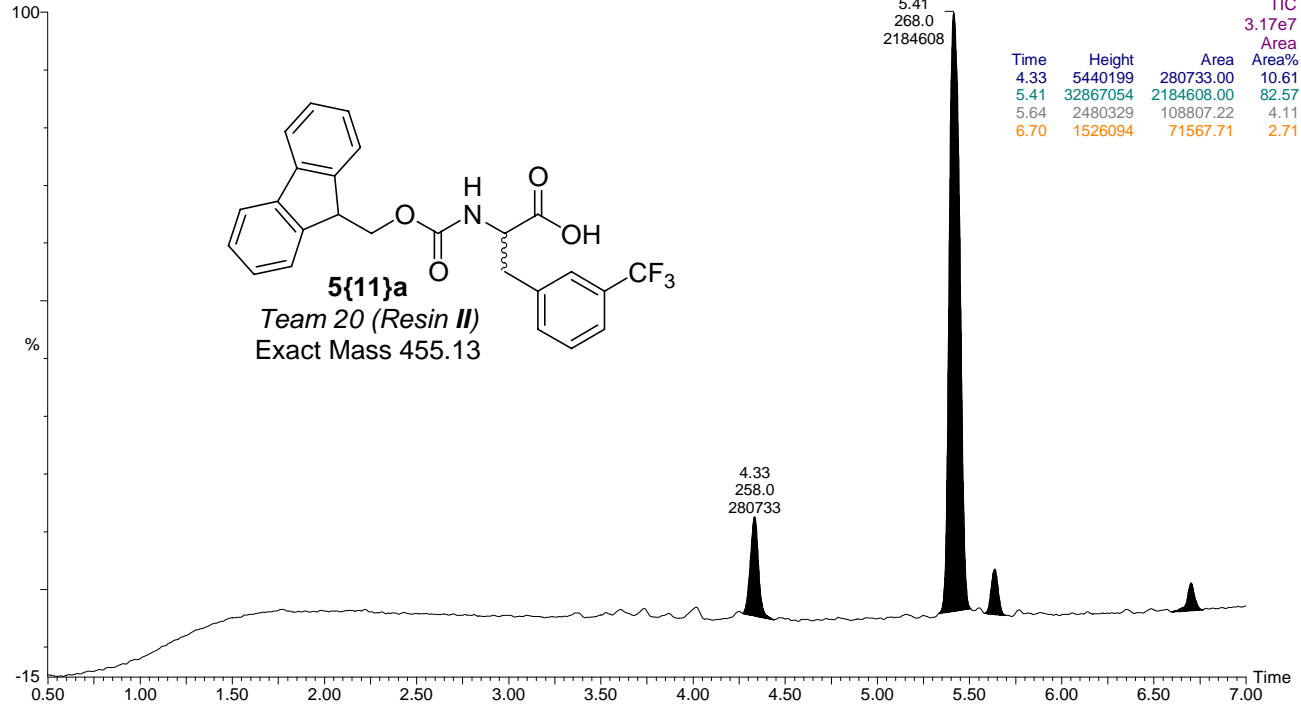
T4-A2 192 (5.138)



5{11}a

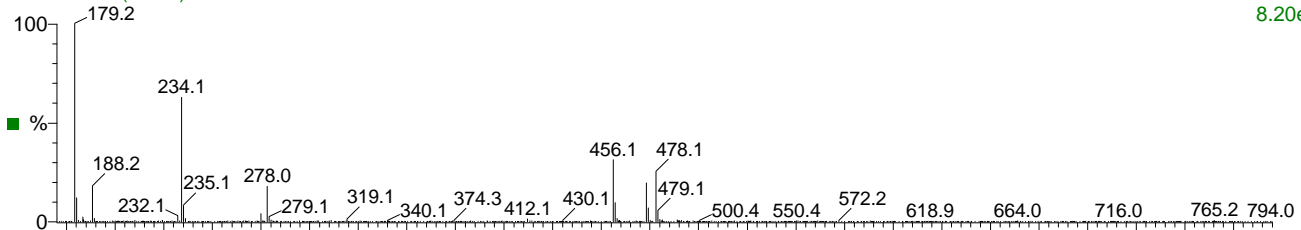
T20-A3 Sm (Mn, 1x1)

3: Diode Array
TIC



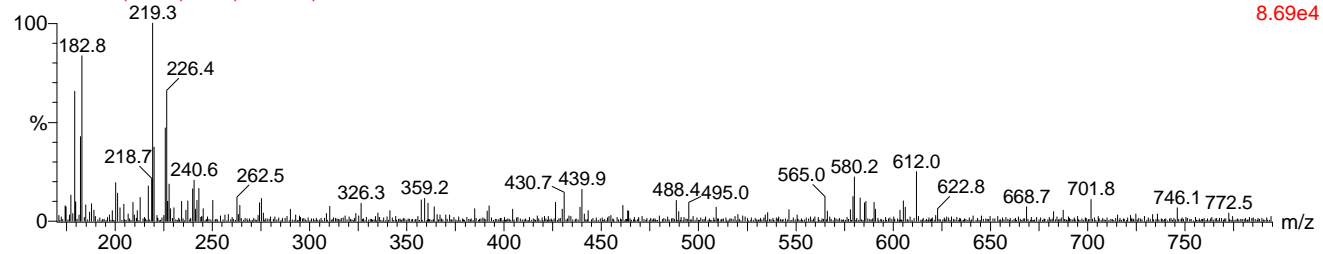
T20-A3 206 (5.514)

1: Scan ES+
8.20e6



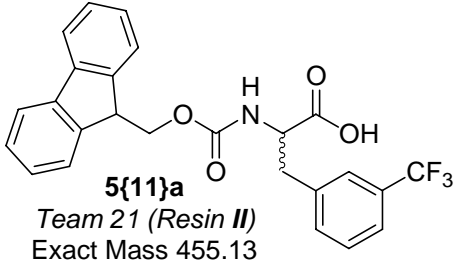
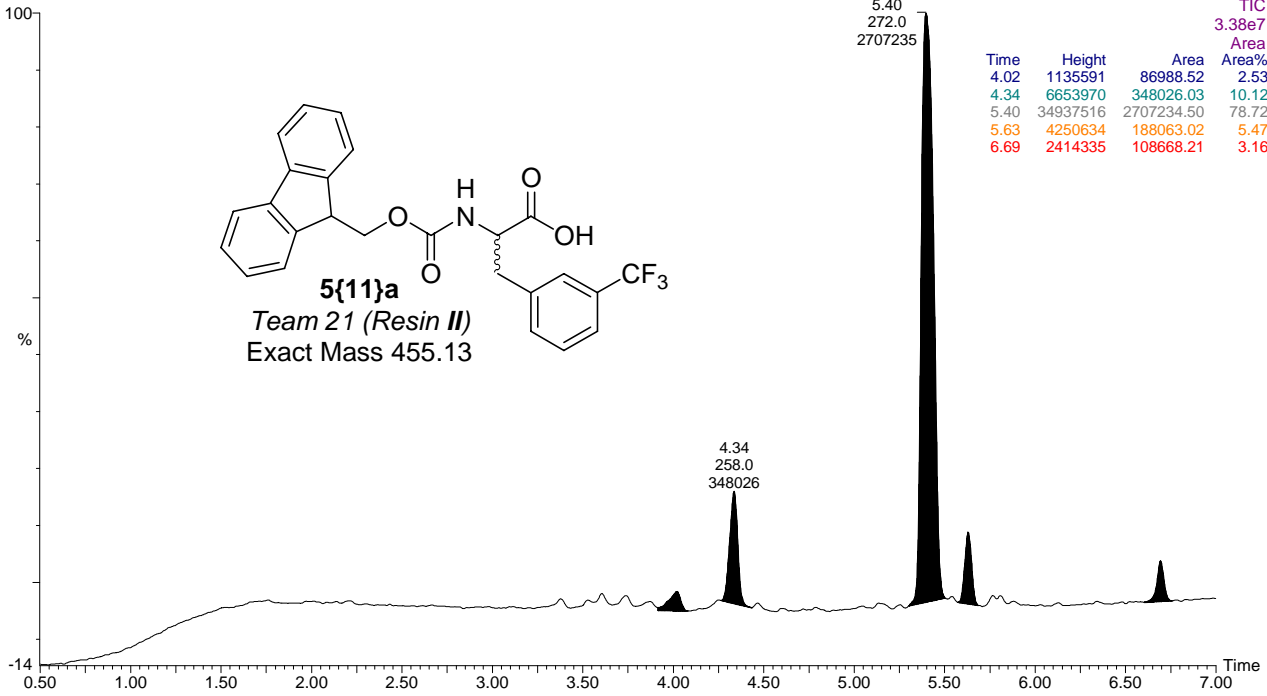
T20-A3 163 (4.360) Cm (163:164)

1: Scan ES+
8.69e4

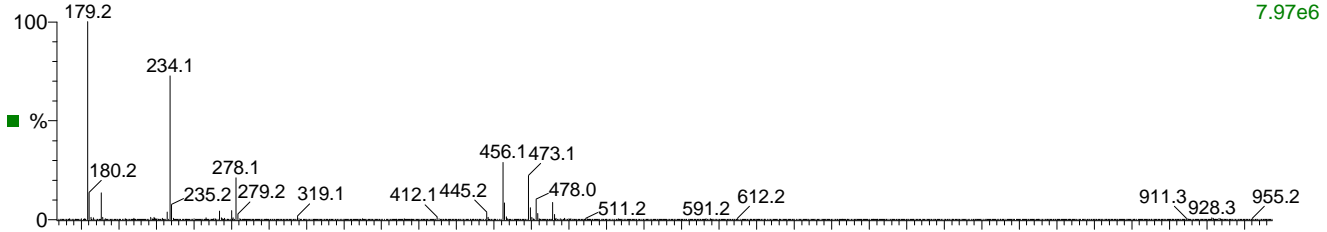


5{11}a

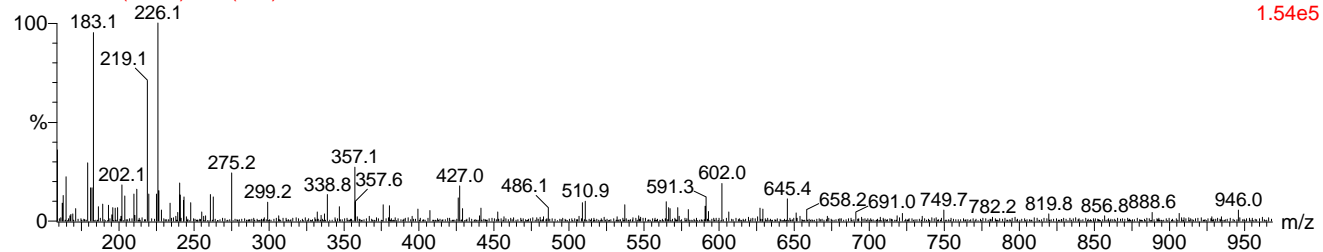
T21-A2 Sm (Mn, 1x1)



T21-A2 204 (5.460) Cm (202:207)

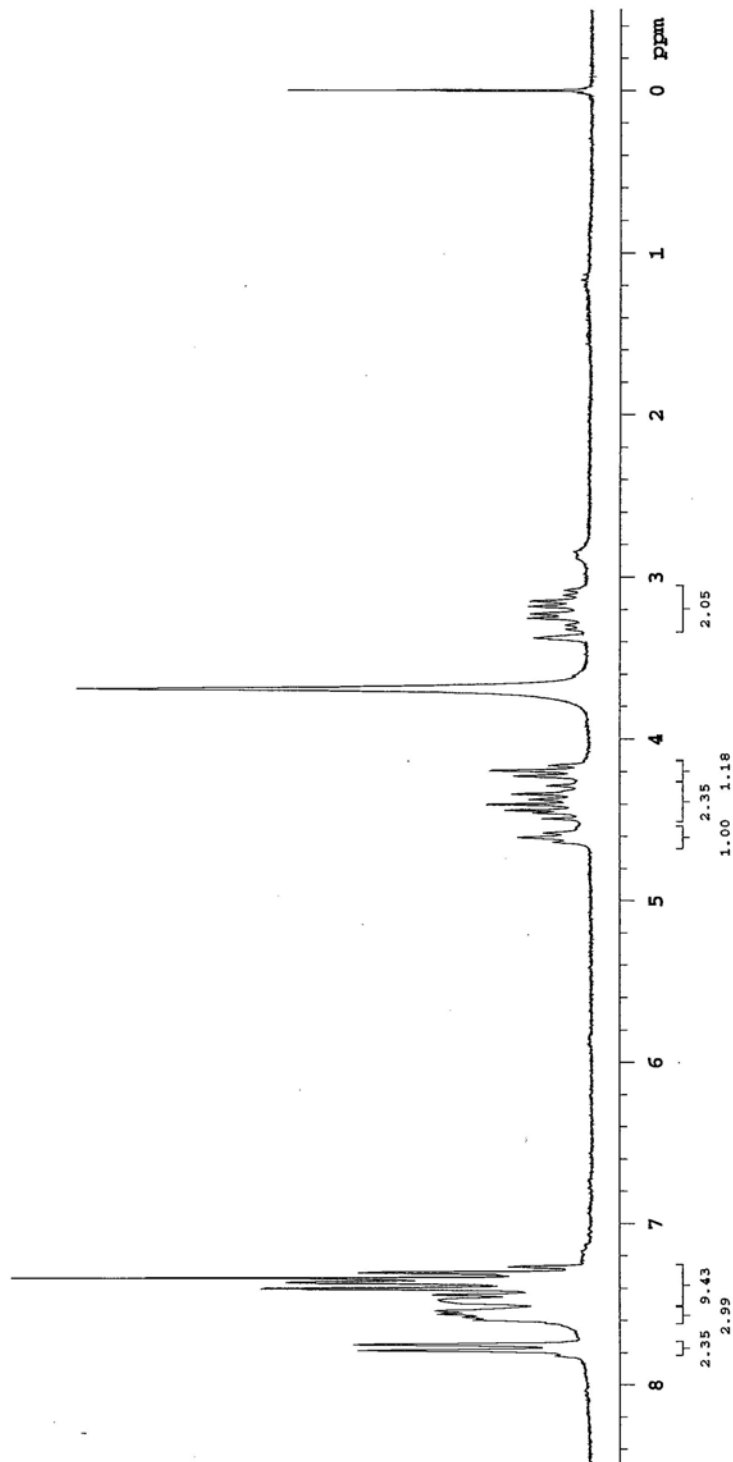
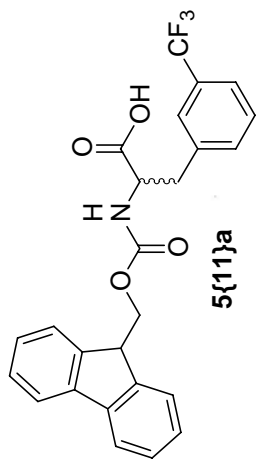


T21-A2 164 (4.387) Cm (164)



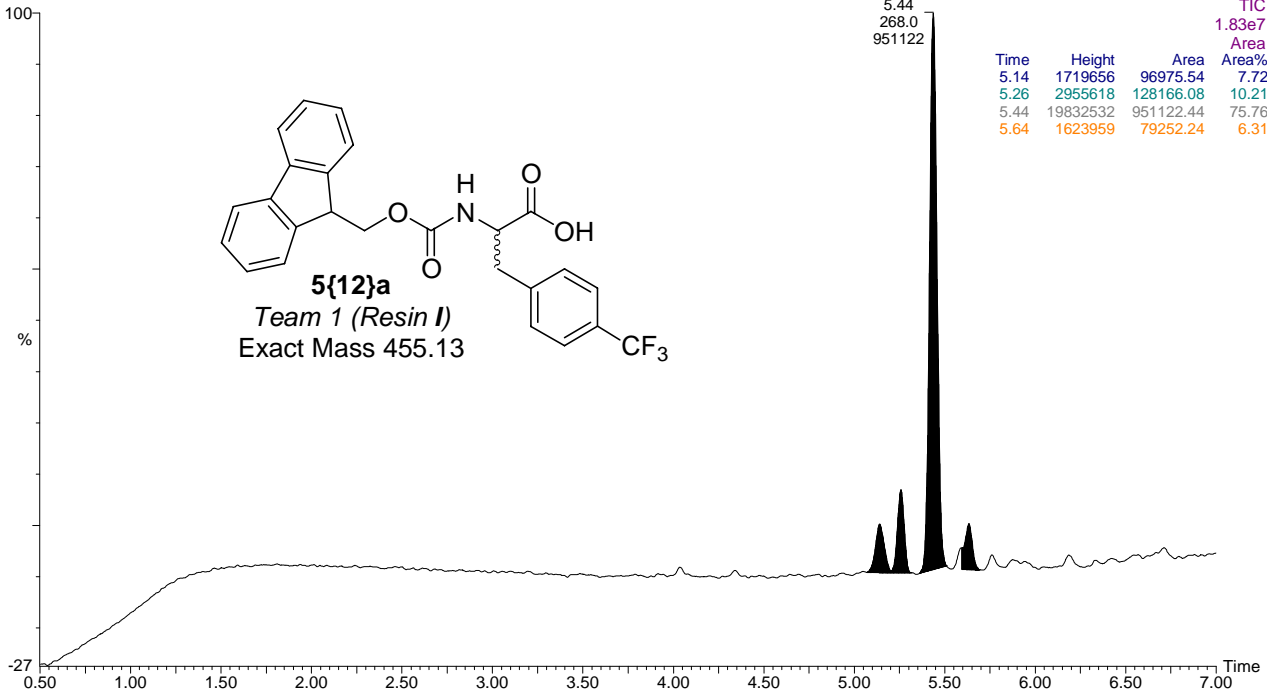
1H_NMR#40_A2_CD3ODINCD13_03_07

Pulse Sequence: s2pul

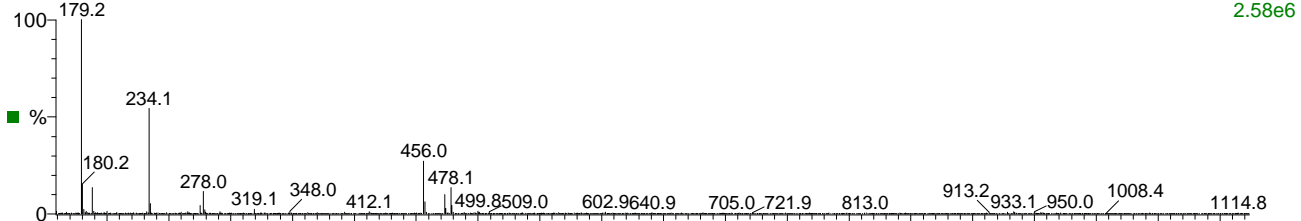


5{12}a

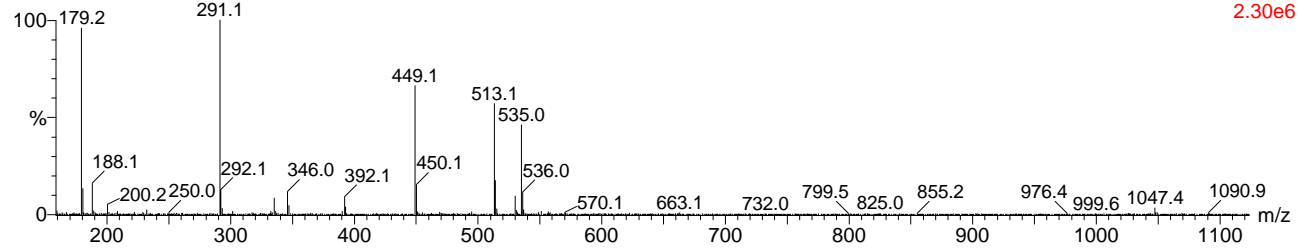
T1-A3 Sm (Mn, 1x1)



T1-A3 206 (5.514) Cm (205:206)



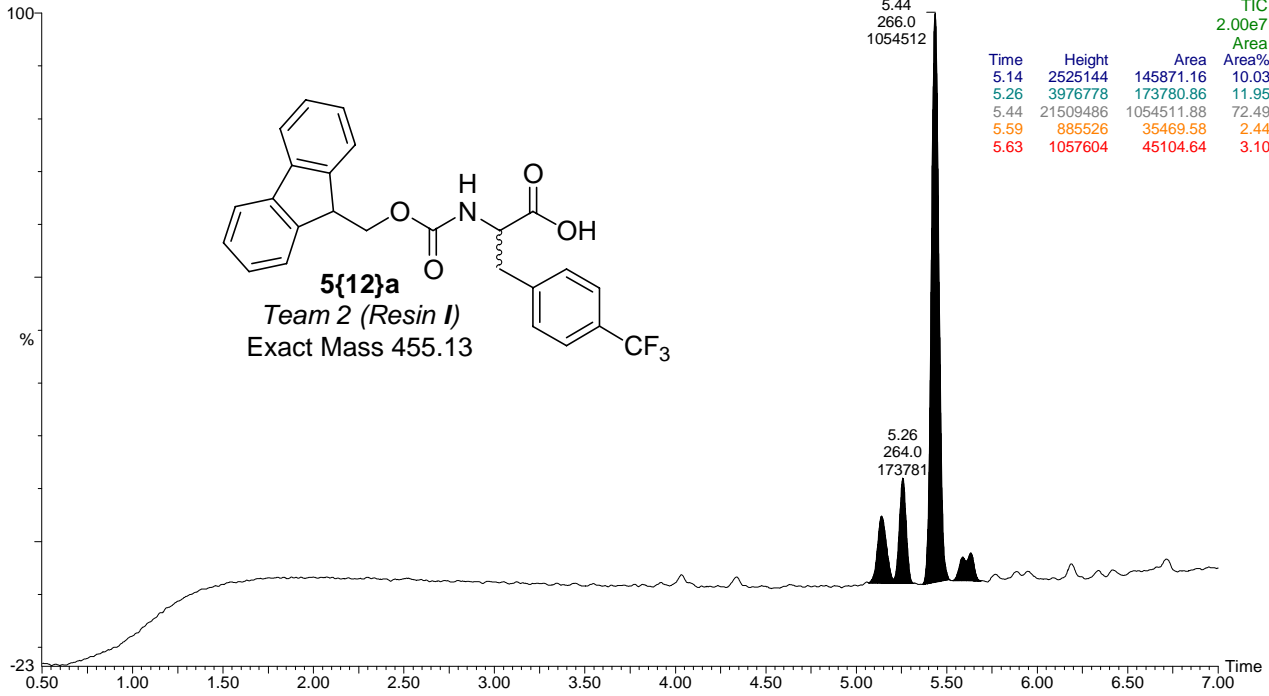
T1-A3 199 (5.326) Cm (198:199)



5{12}a

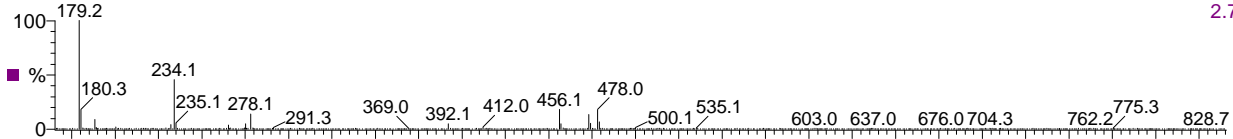
T2-A2 Sm (Mn, 1x1)

3: Diode Array



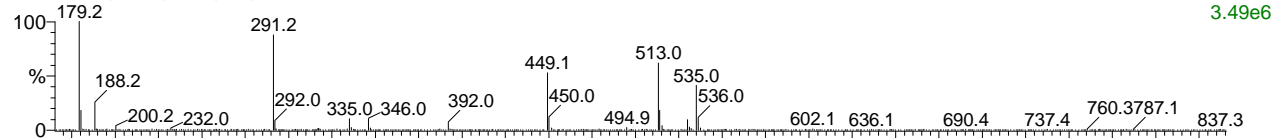
T2-A2 205 (5.487) Cm (205:206)

1: Scan ES+
2.75e6



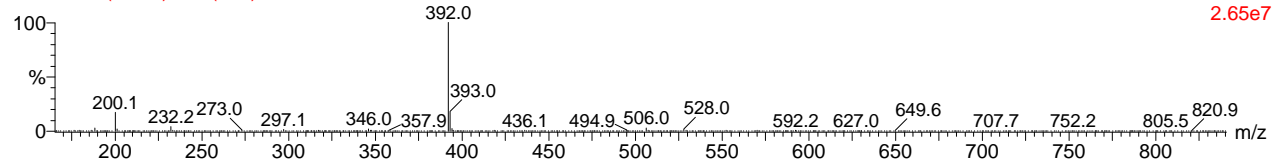
T2-A2 199 (5.326) Cm (199)

1: Scan ES+
3.49e6



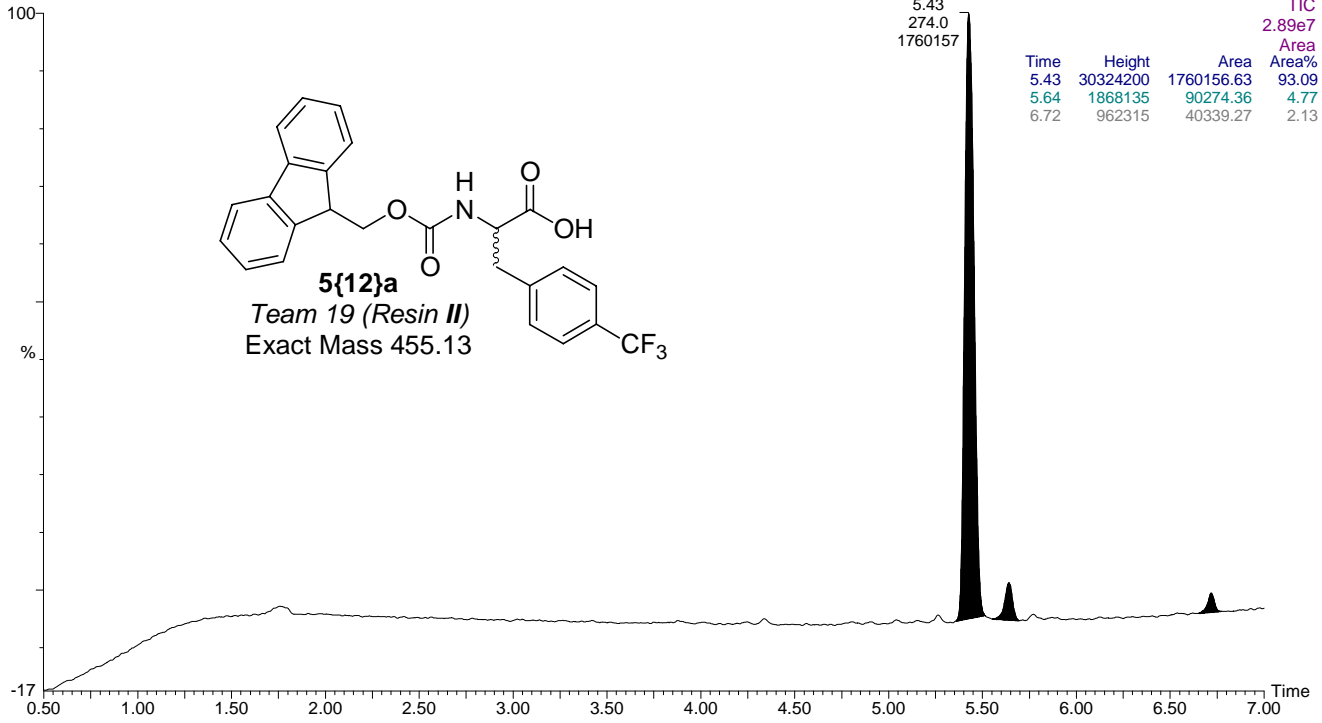
T2-A2 194 (5.192) Cm (194)

1: Scan ES+
2.65e7

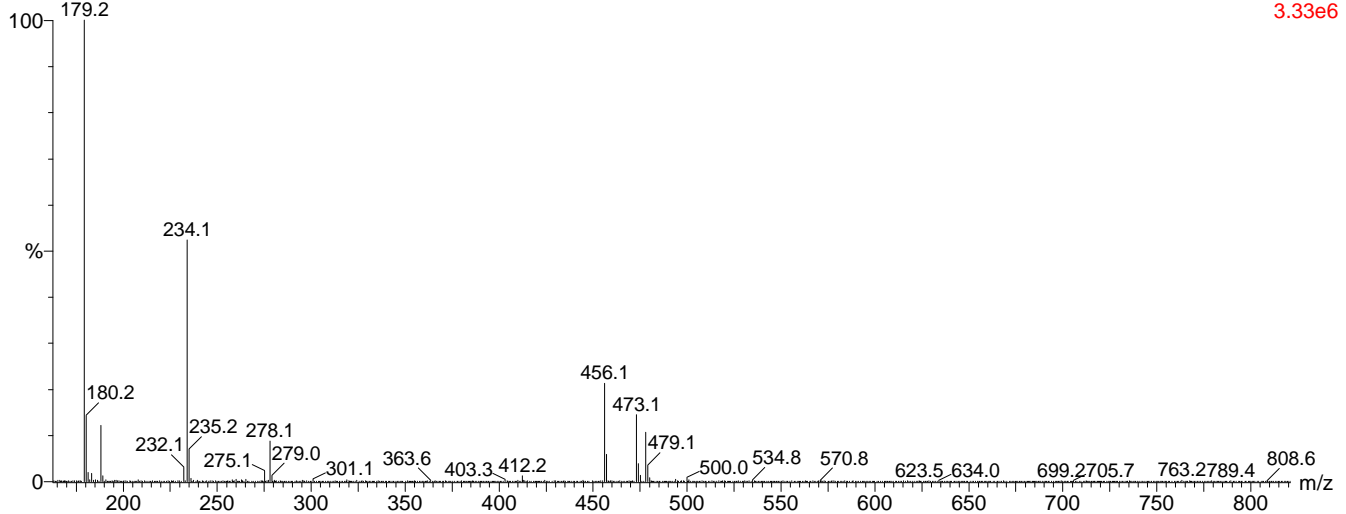


5{12}a

T19-A2 Sm (Mn, 1x1)

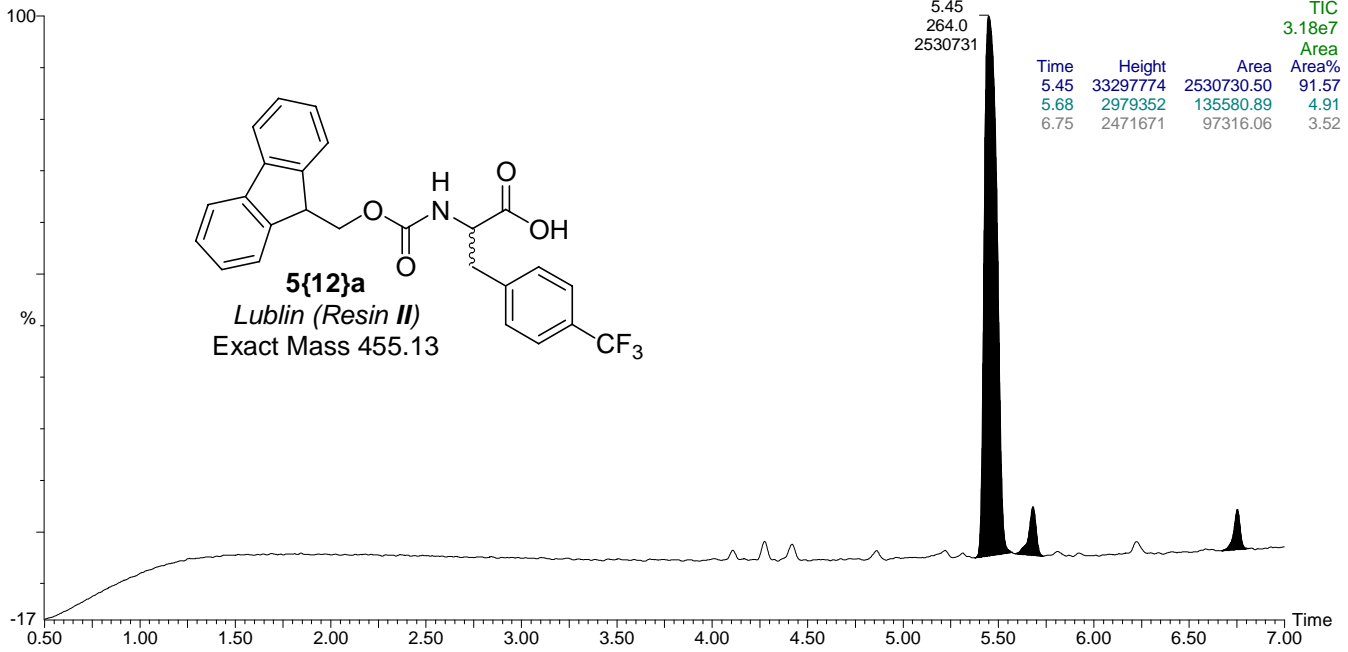


T19-A2 205 (5.487) Cm (204:207)



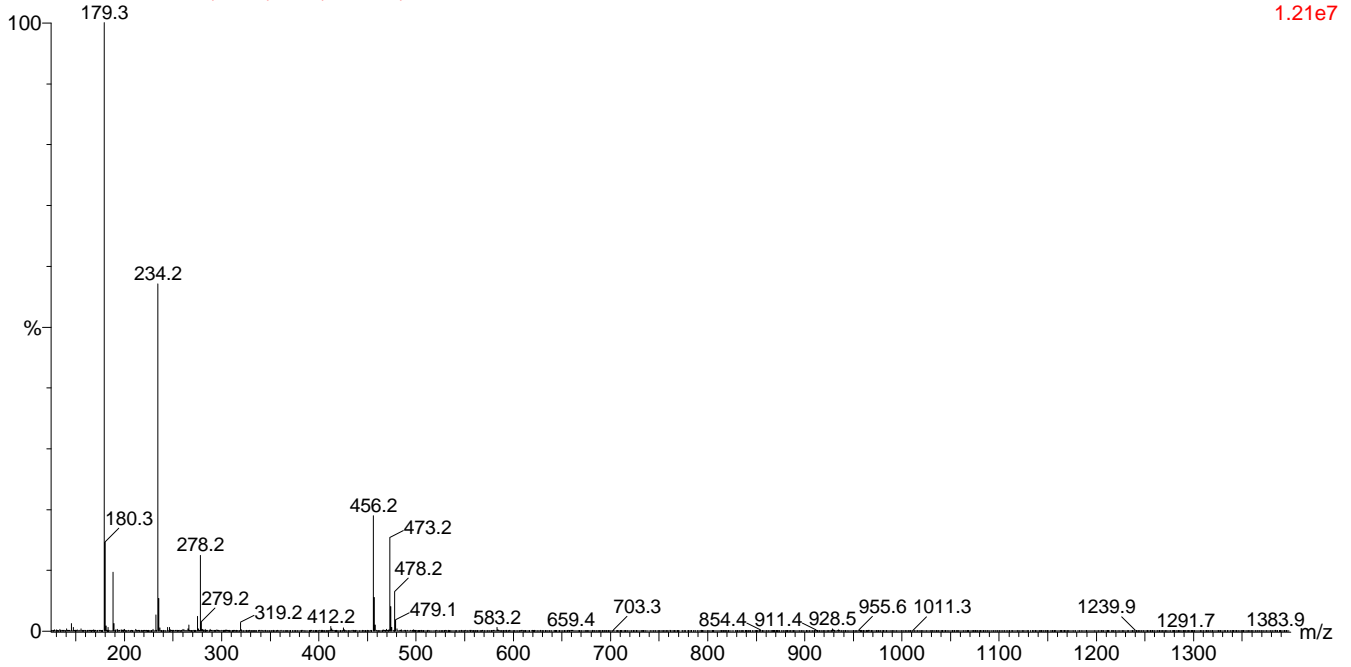
5{12}a

Lublin-Poland-A3 Sm (Mn, 1x1)



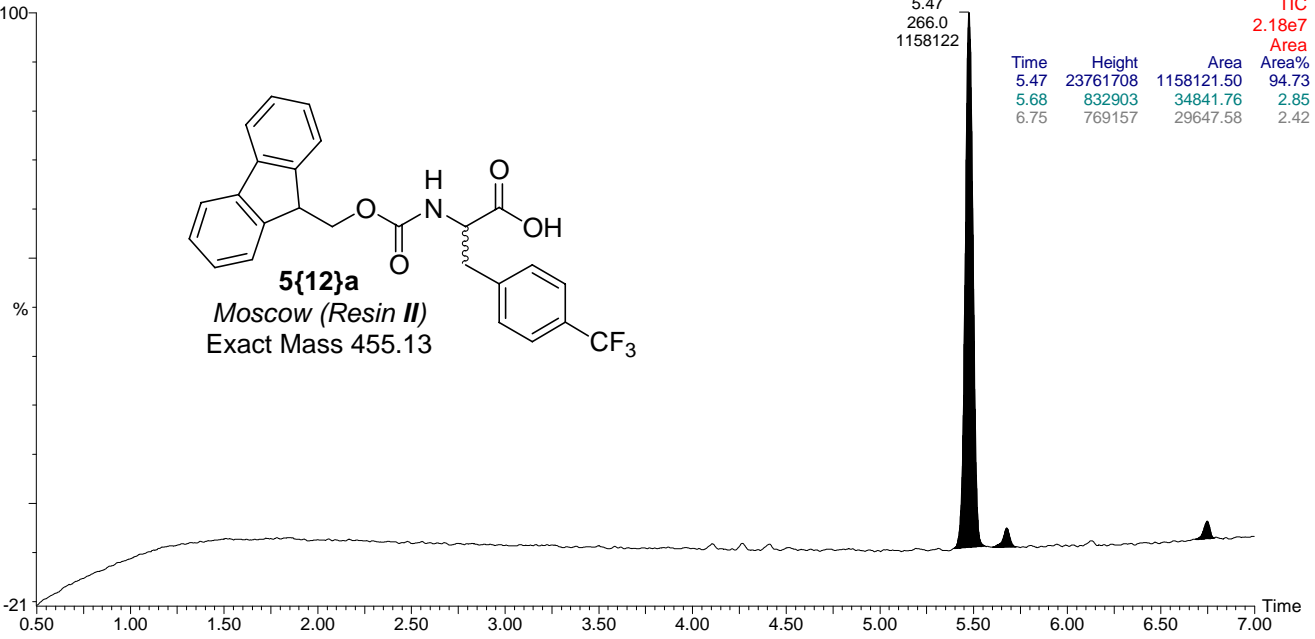
Lublin-Poland-A3 205 (5.487) Cm (204:208)

1: Scan ES+
1.21e7



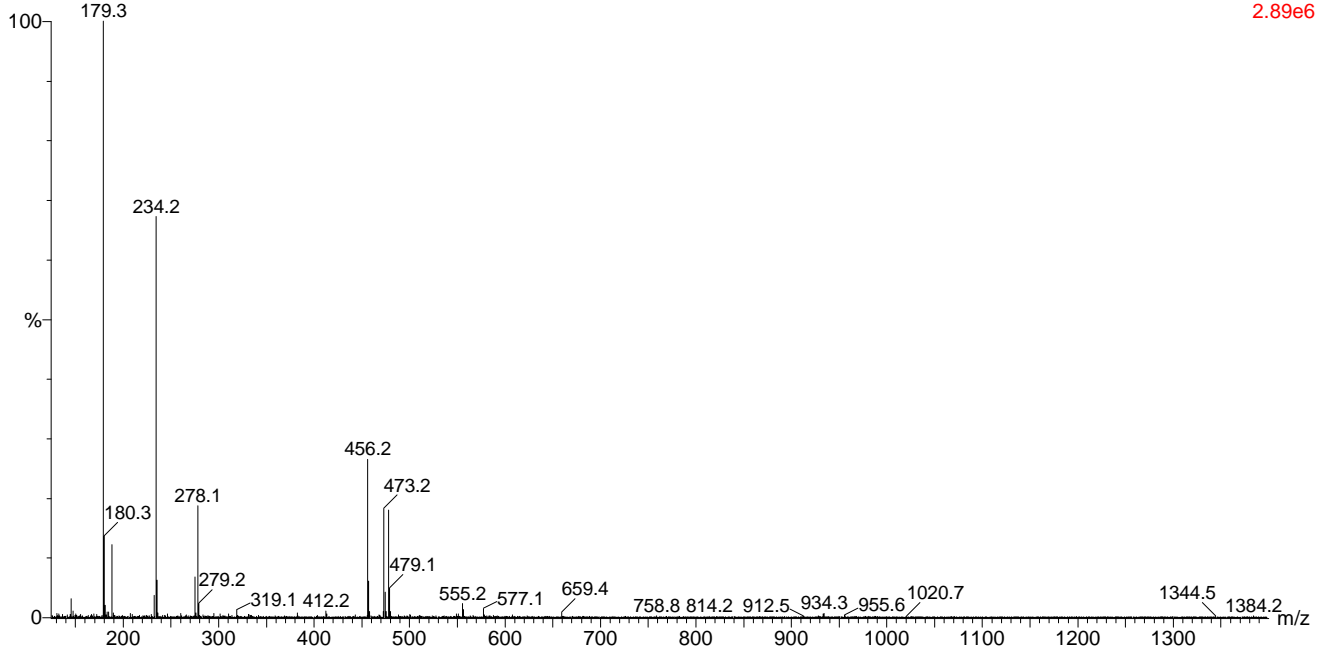
5{12}a

Moscow-A1 Sm (Mn, 1x1)



3: Diode Array
TIC
2.18e7

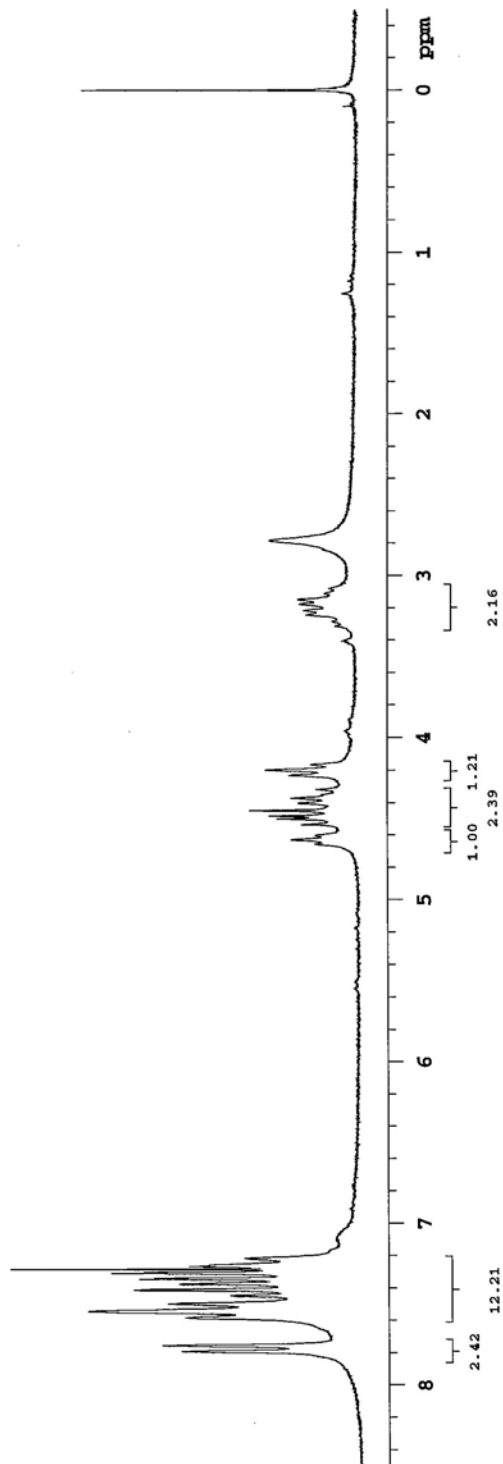
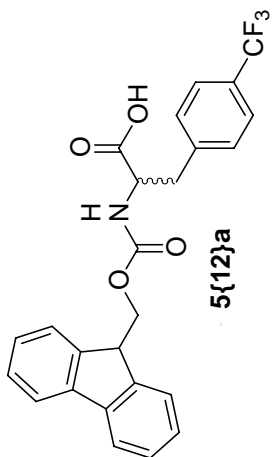
Moscow-A1 206 (5.514) Cm (204:209)



1: Scan ES+
2.89e6

1H_BB#27_A3_P_CDC13withCD3OD_02_01_07

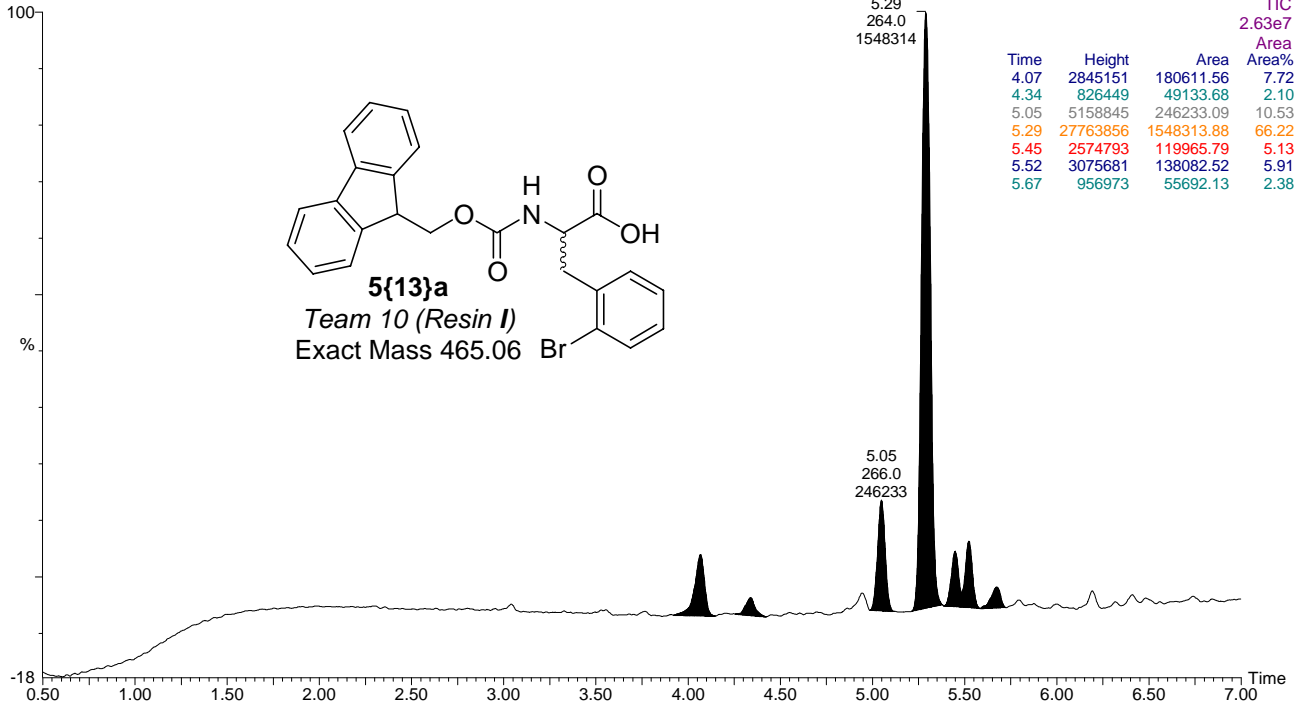
Pulse Sequence: s2pul



5{13}a

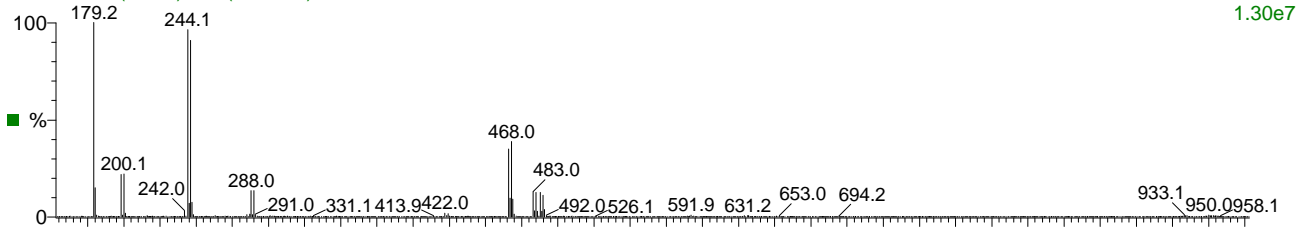
T10-A3 Sm (Mn, 1x1)

3: Diode Array
TIC
2.63e7



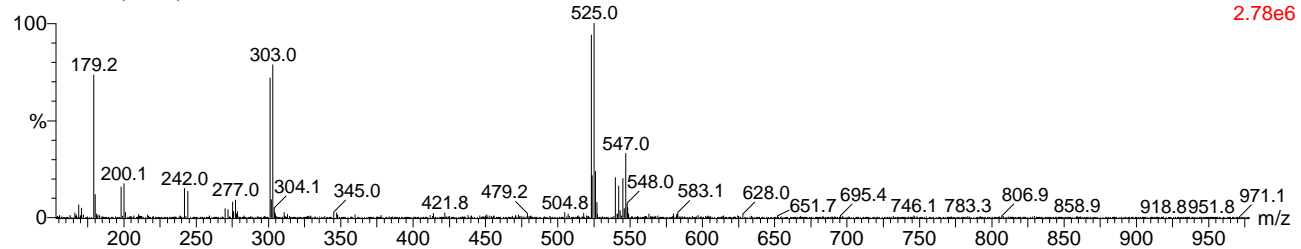
T10-A3 199 (5.326) Cm (199:201)

1: Scan ES+
1.30e7



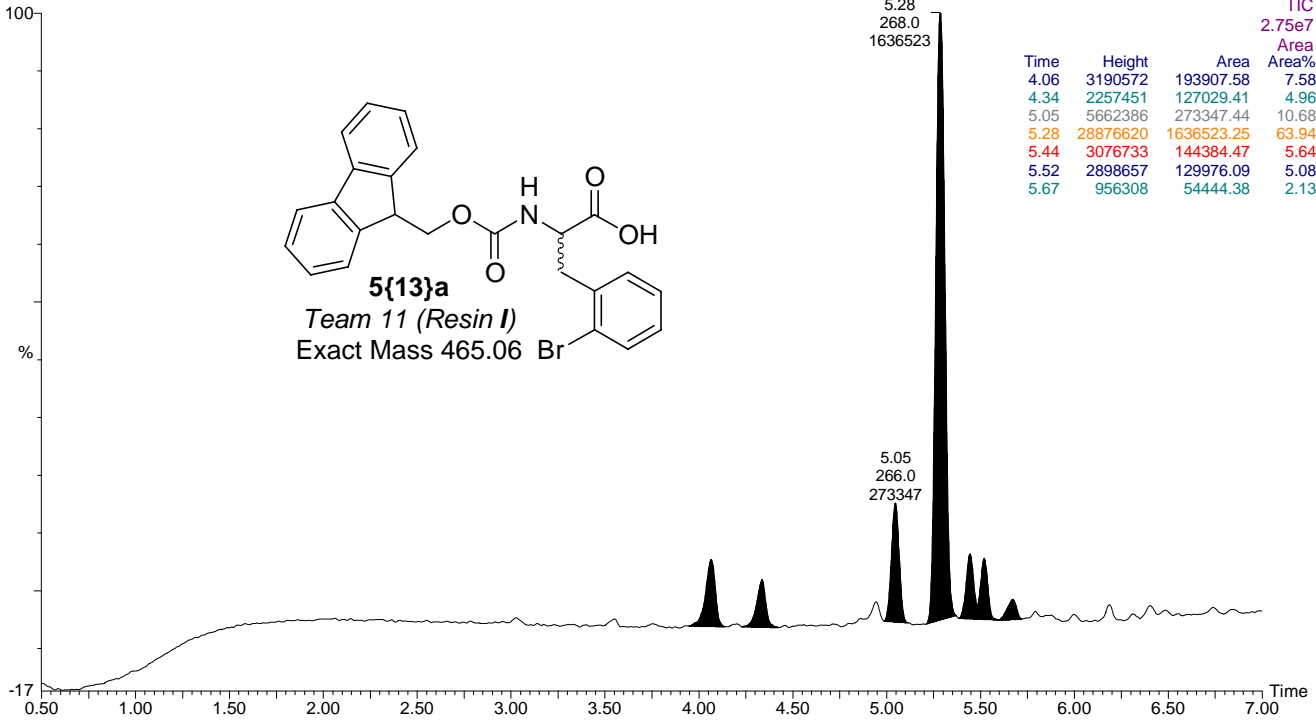
T10-A3 190 (5.085)

1: Scan ES+
2.78e6

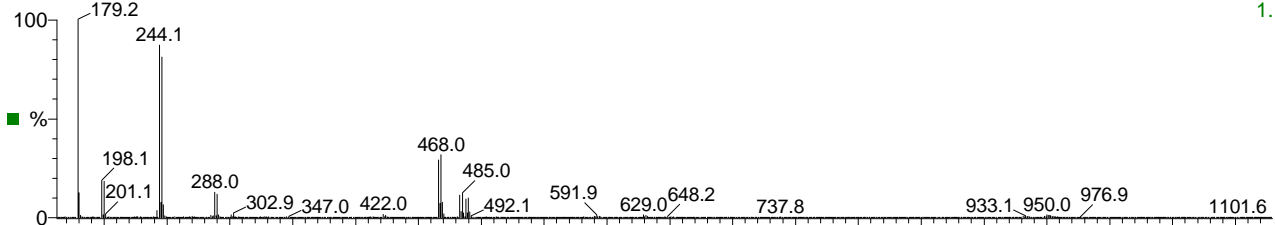


5{13}a

T11-A2 Sm (Mn, 1x1)

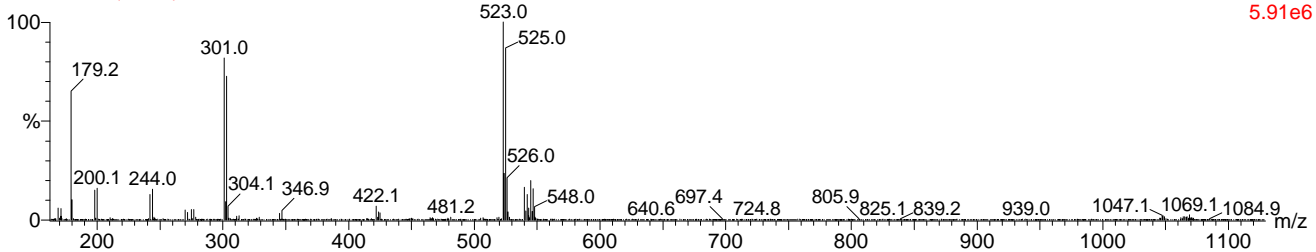


T11-A2 200 (5.353) Cm (199:202)



1: Scan ES+
1.18e7

T11-A2 191 (5.112)

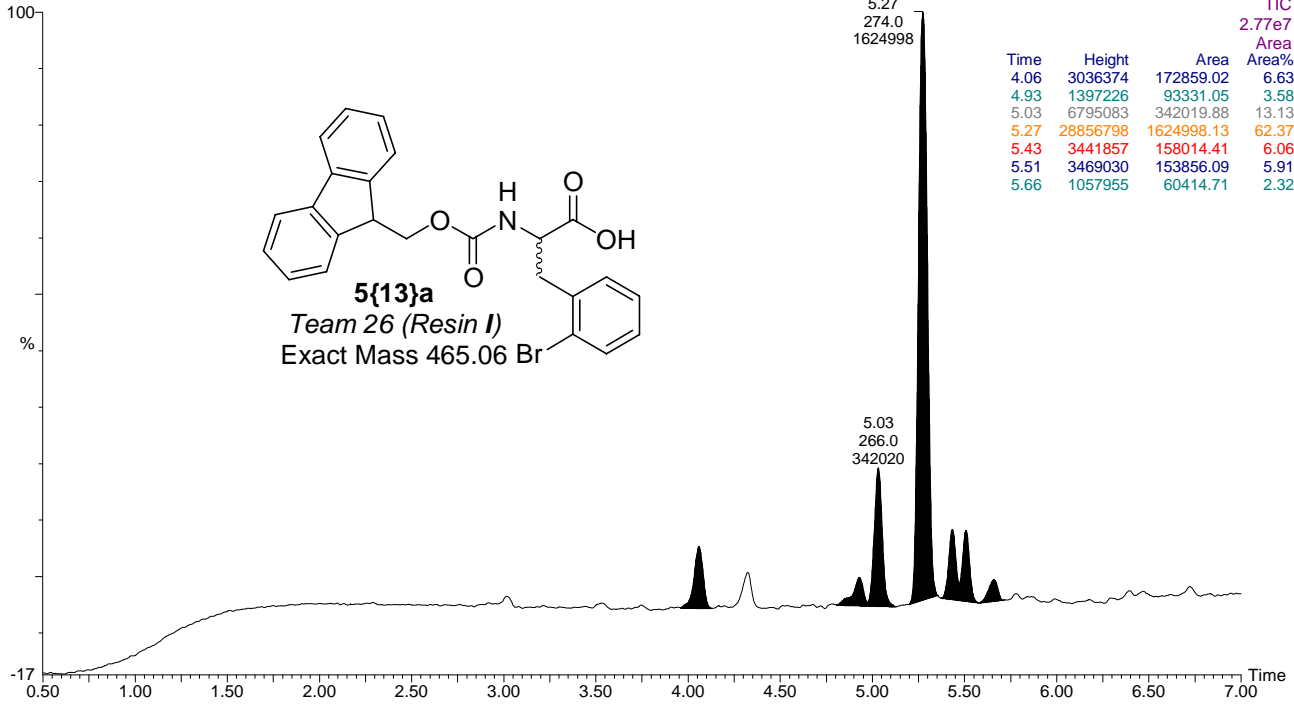


1: Scan ES+
5.91e6

5{13}a

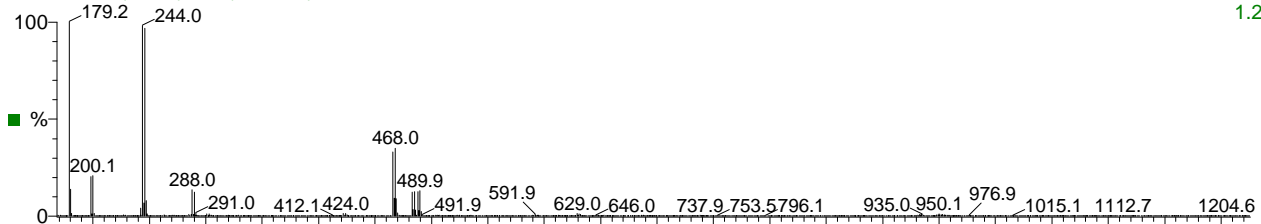
T26-A3 Sm (Mn, 1x1)

3: Diode Array
TIC
2.77e7



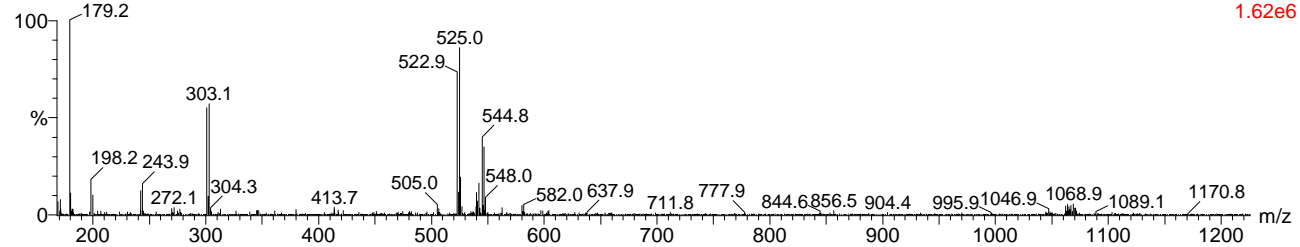
T26-A3 199 (5.326) Cm (198:201)

1: Scan ES+
1.22e7



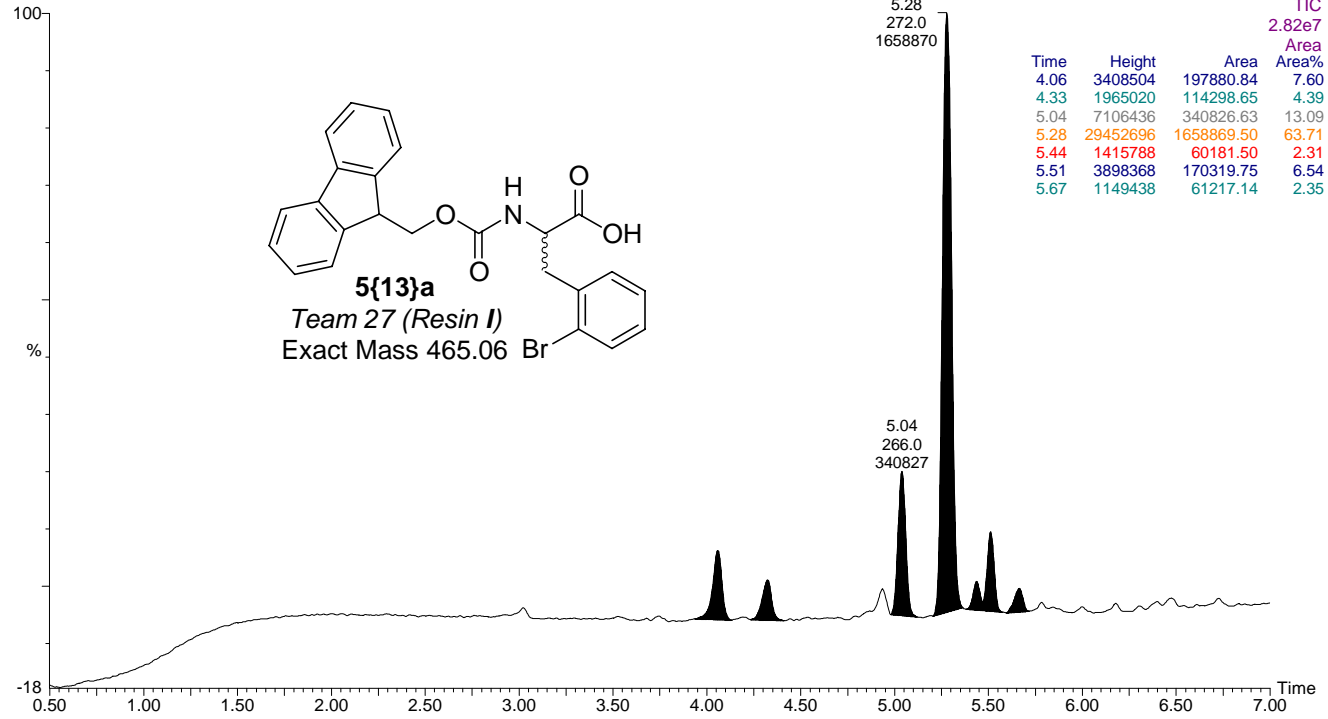
T26-A3 189 (5.058)

1: Scan ES+
1.62e6

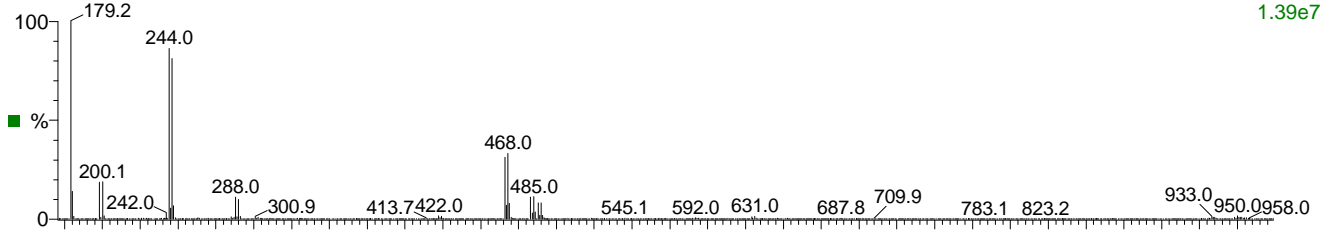


5{13}a

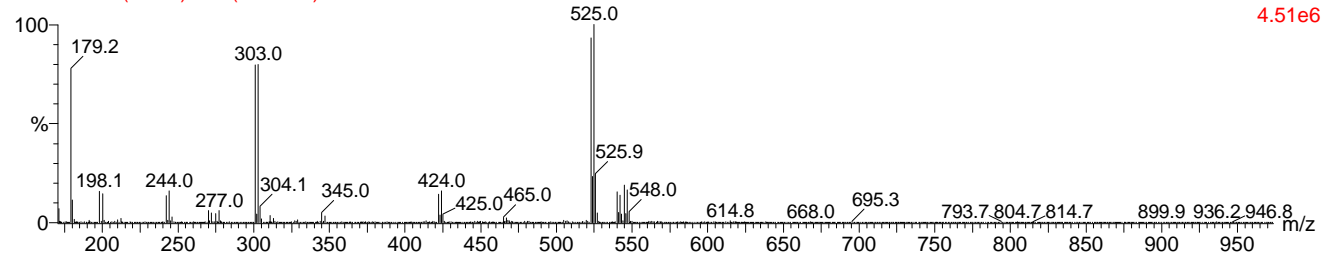
T27-A2 Sm (Mn, 1x1)



T27-A2 200 (5.353) Cm (198:201)

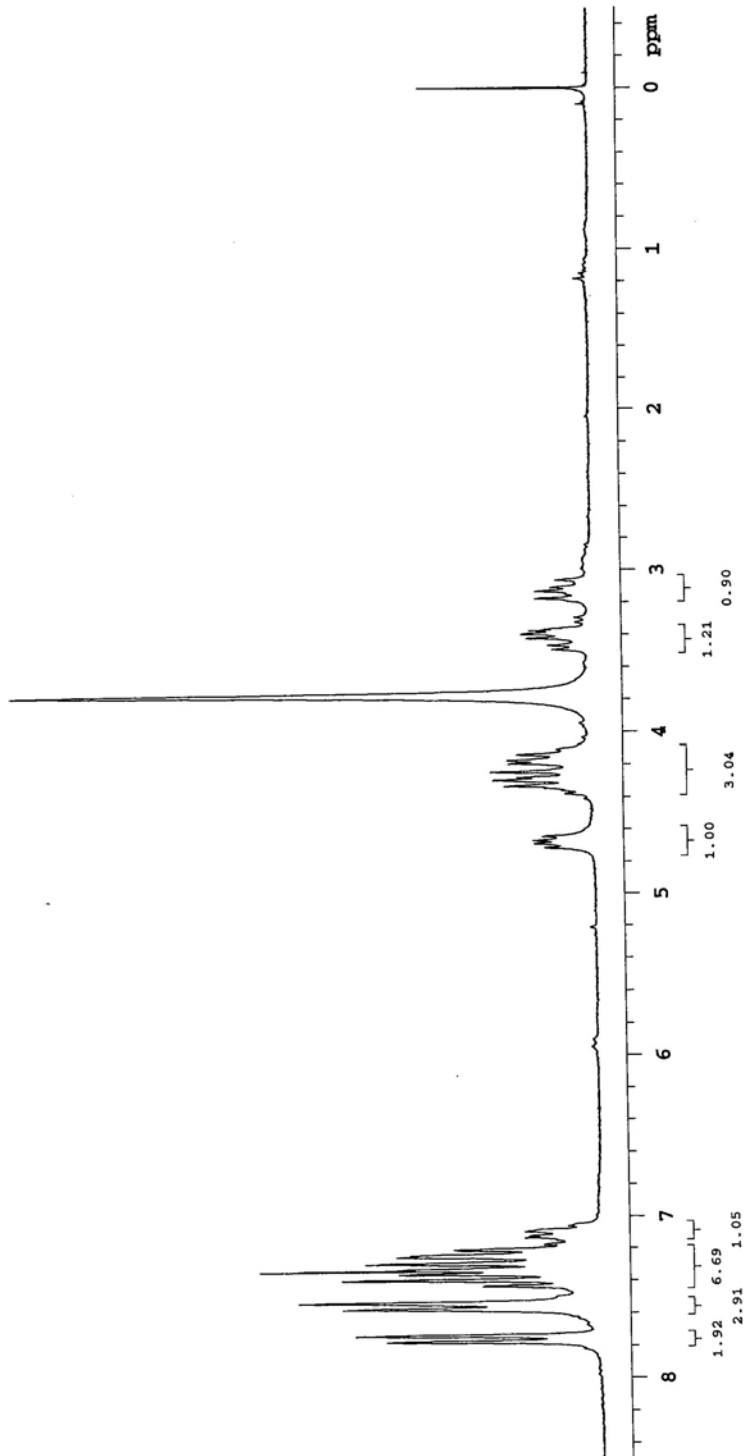
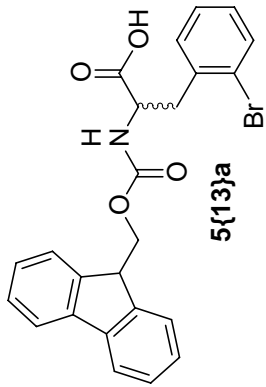


T27-A2 191 (5.112) Cm (190:192)



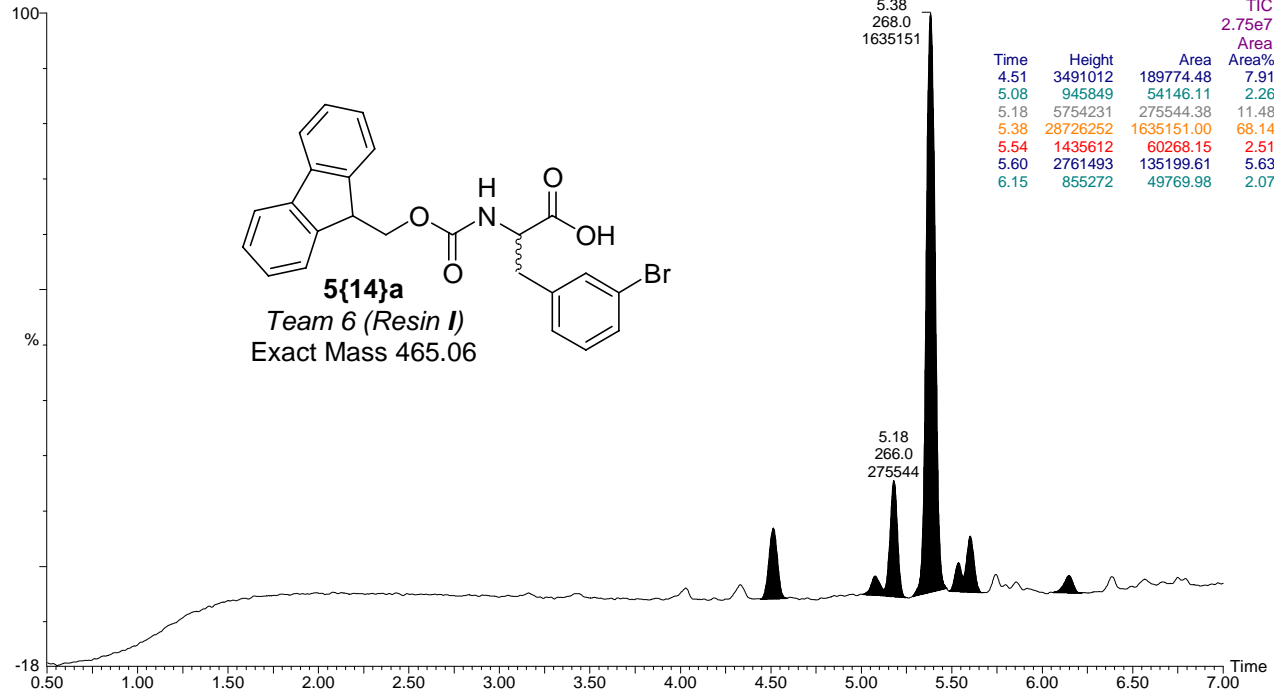
1H_NMR#40_A3_CD3ODINCD13_02_22_07

Pulse Sequence: s2pul

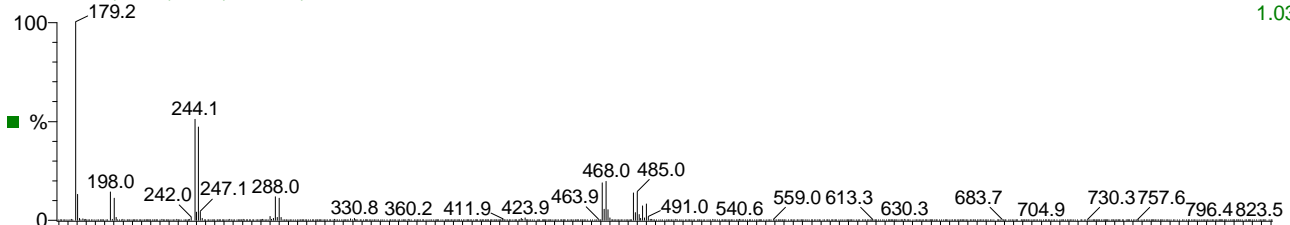


5{14}a

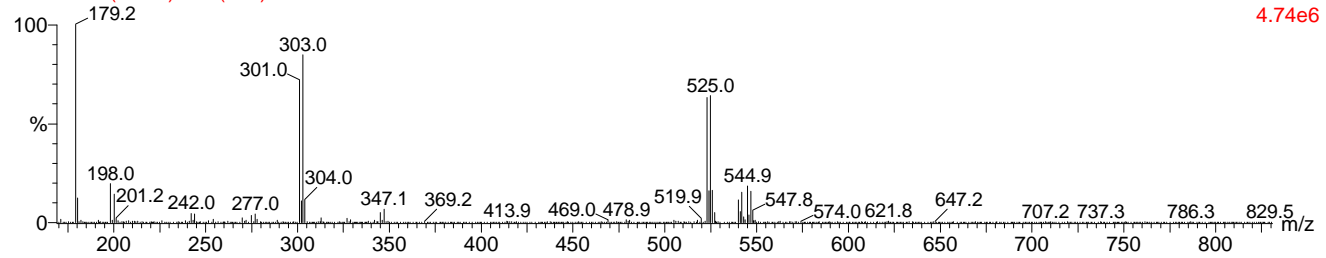
T6-A3 Sm (Mn, 1x1)



T6-A3 203 (5.434) Cm (203:204)

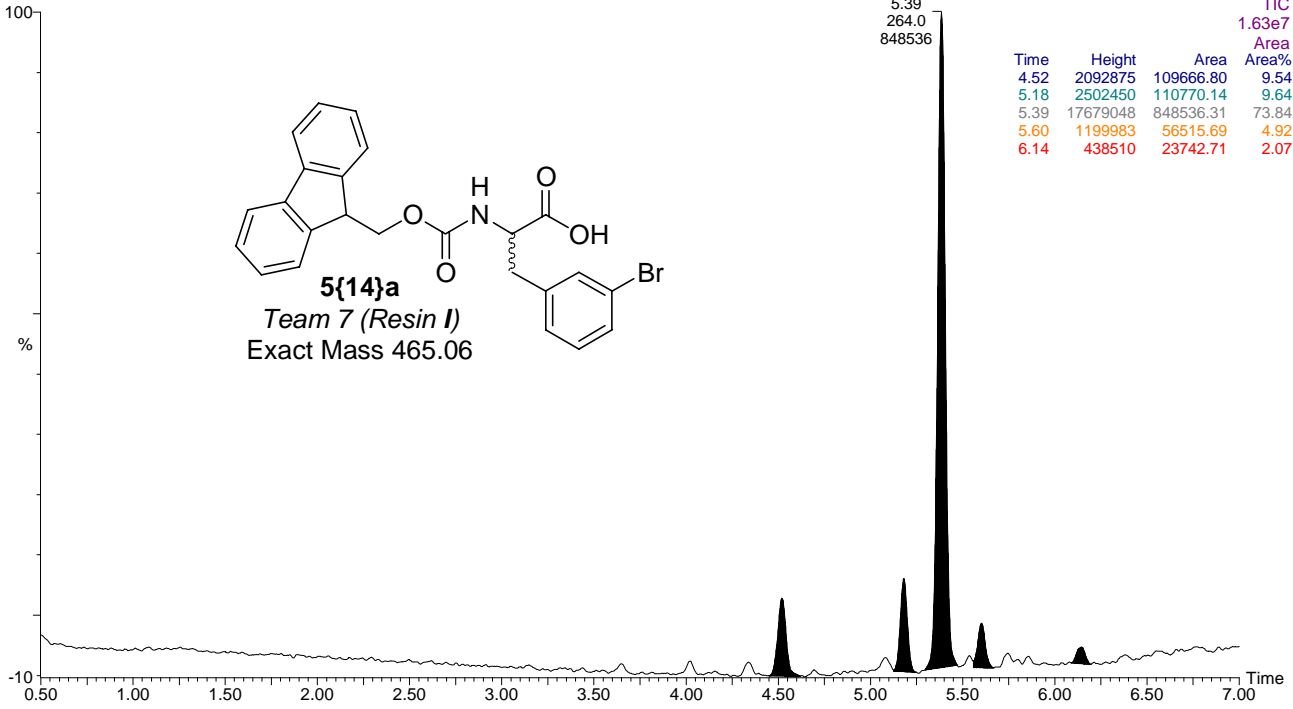


T6-A3 196 (5.246) Cm (196)

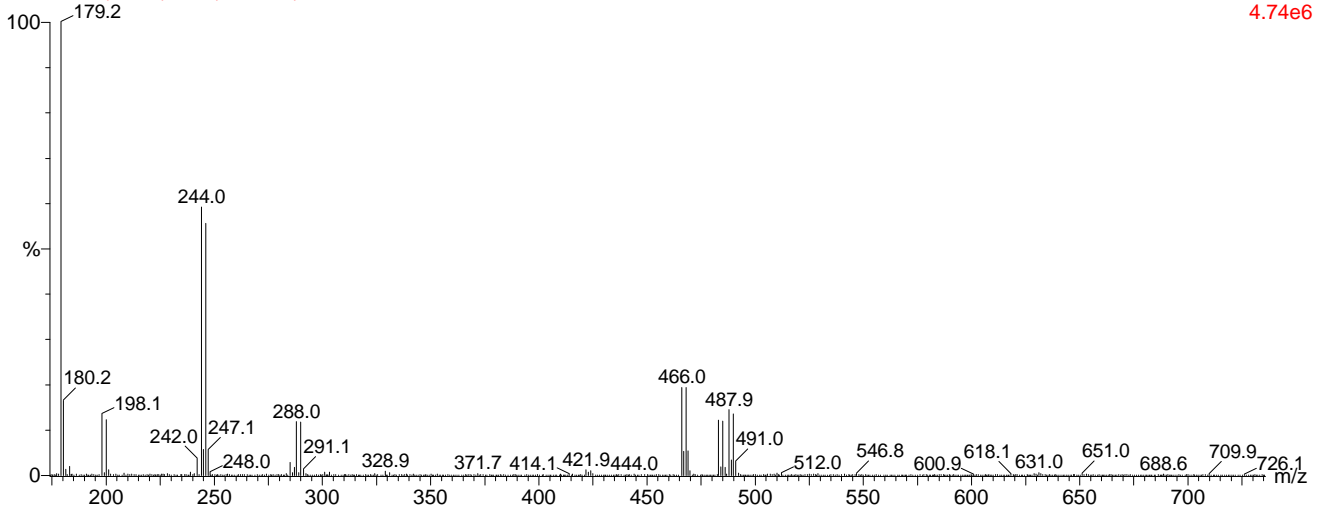


5{14}a

T7-A2 Sm (Mn, 1x1)



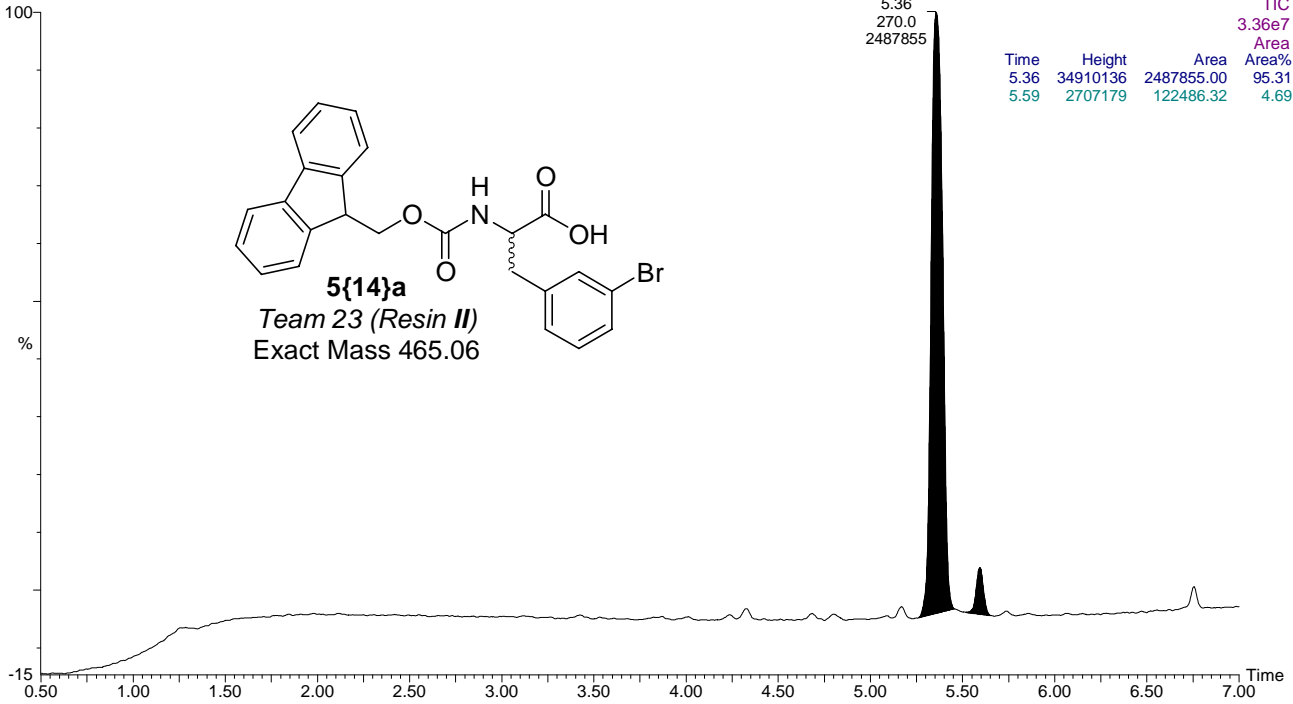
T7-A2 204 (5.460) Cm (202:205)



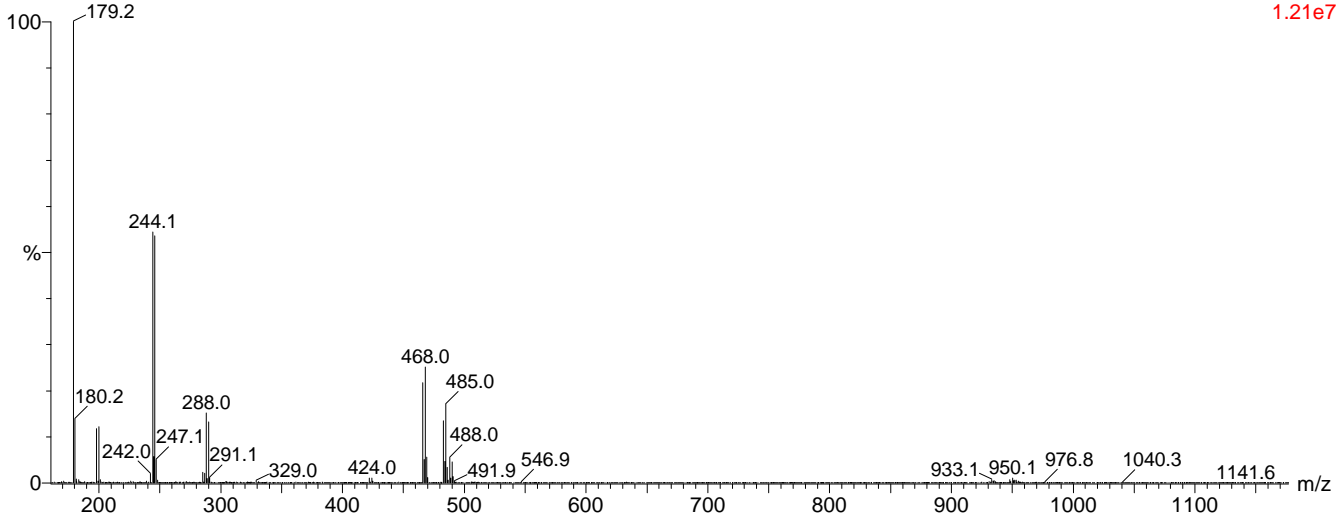
1: Scan ES+
4.74e6

5{14}a

T23-A3 Sm (Mn, 1x1)

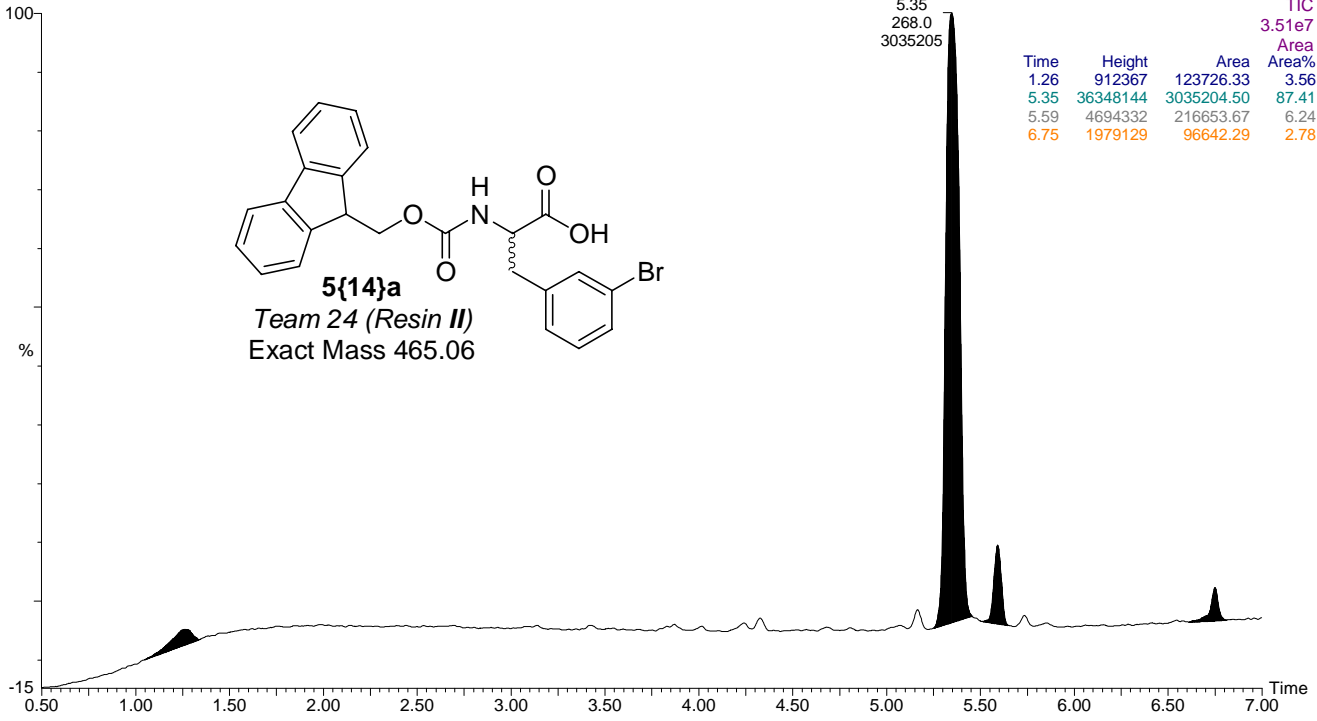


T23-A3 203 (5.434) Cm (202:204)

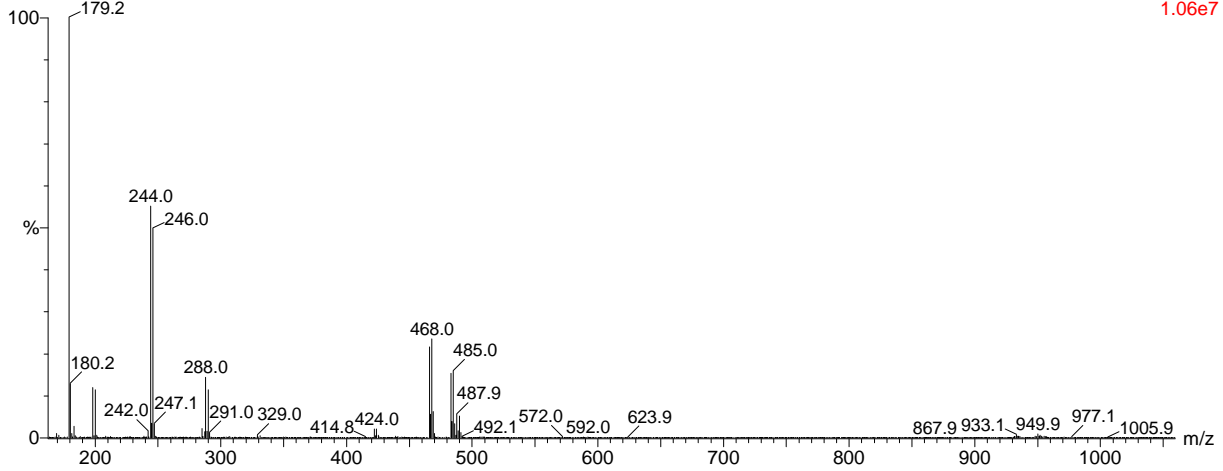


5{14}a

T24-A2 Sm (Mn, 1x1)

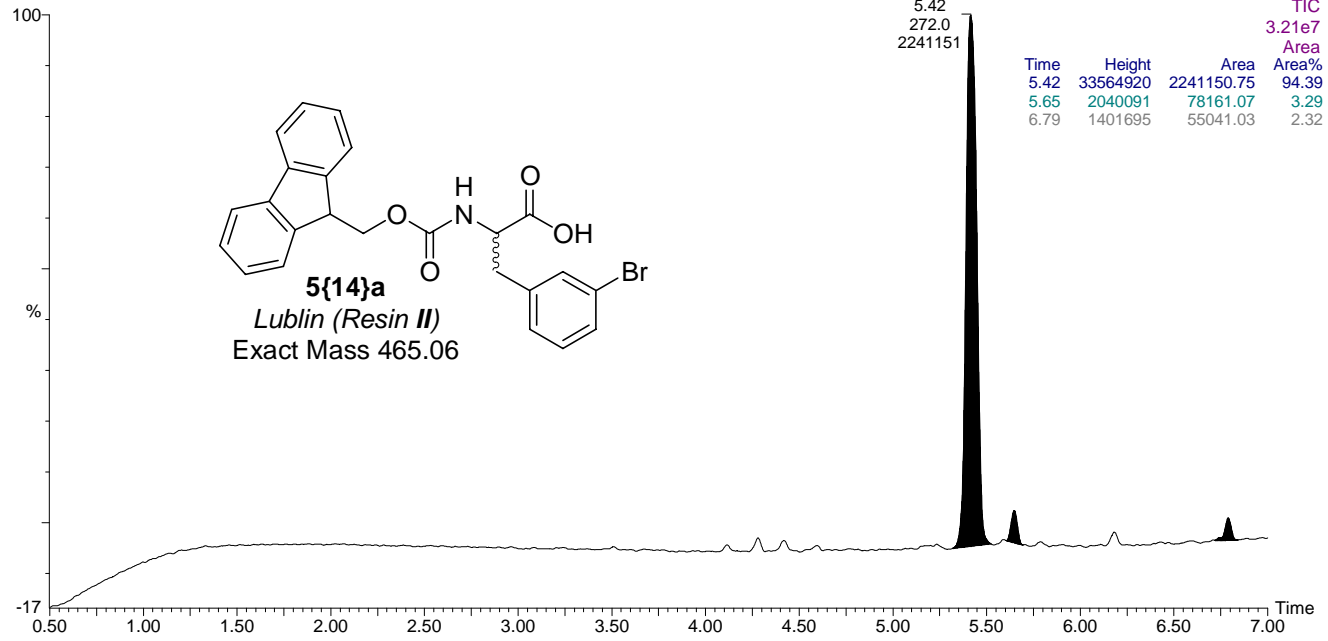


T24-A2 202 (5.407) Cm (201:205)



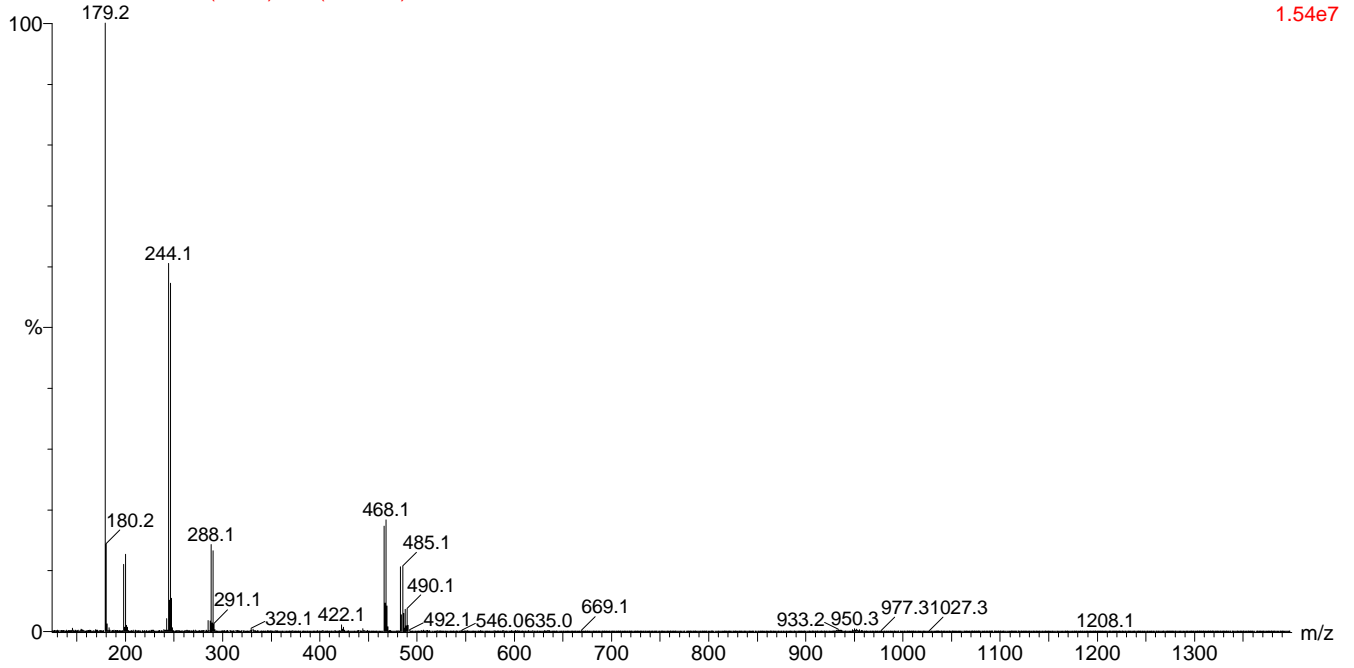
5{14}a

Lublin-Poland-A2 Sm (Mn, 1x1)



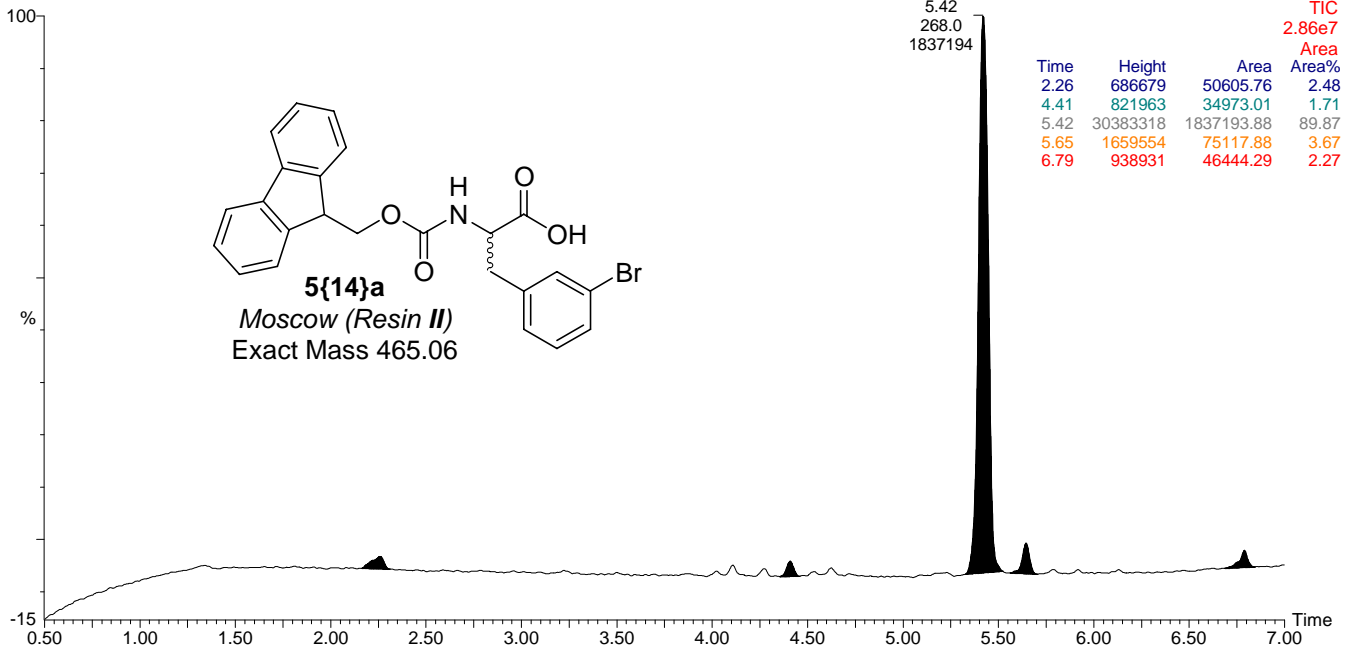
Lublin-Poland-A2 204 (5.460) Cm (201:208)

1: Scan ES+
1.54e7

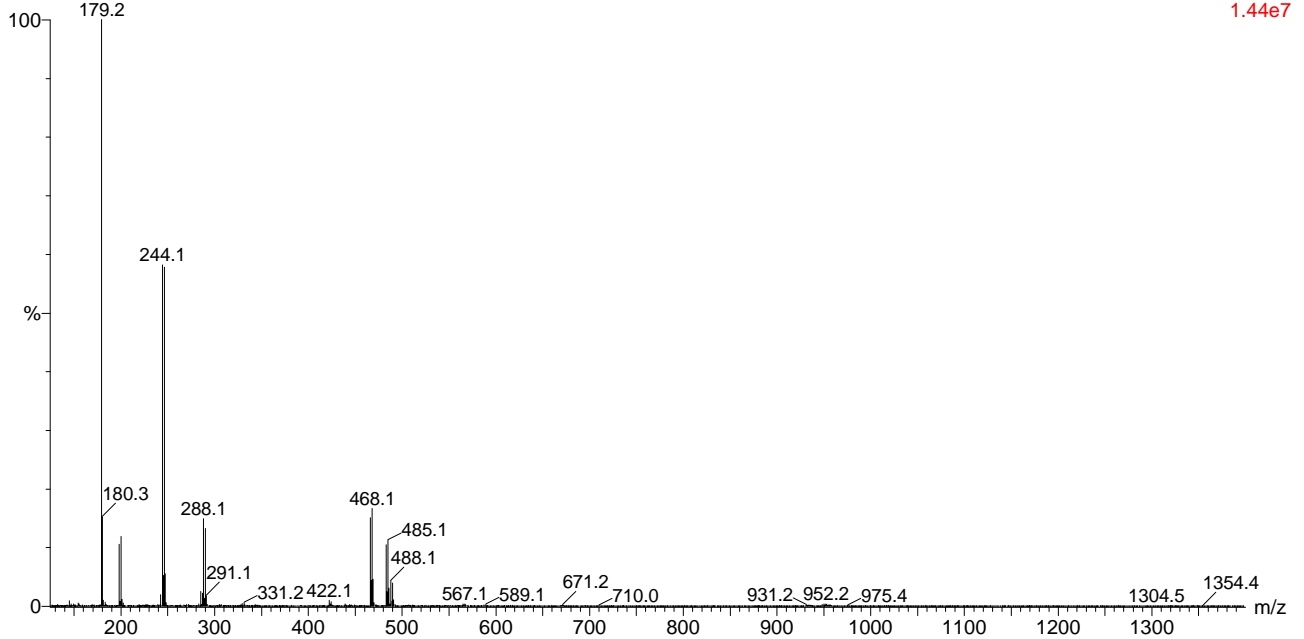


5{14}a

Moscow-A2 Sm (Mn, 1x1)



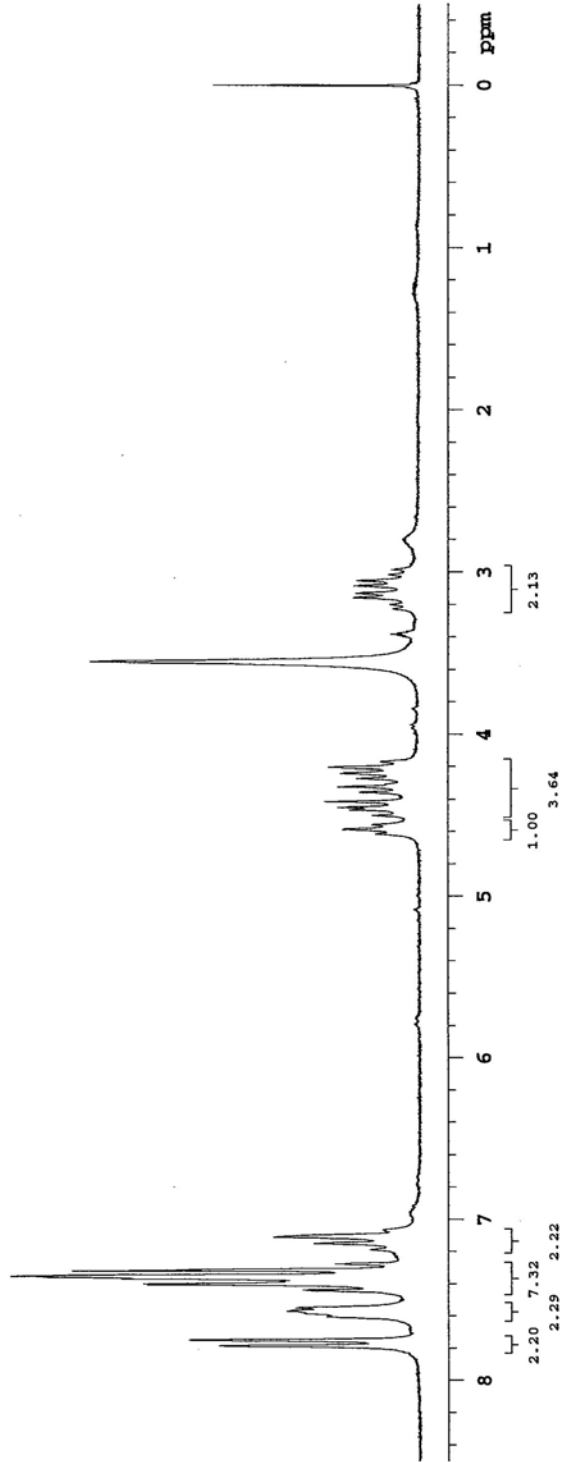
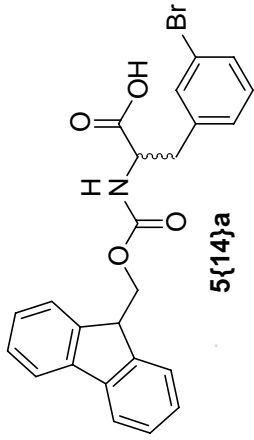
Moscow-A2 204 (5.460) Cm (202:208)



1: Scan ES+
1.44e7

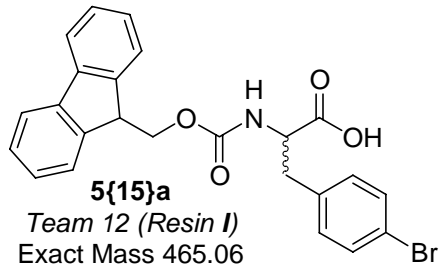
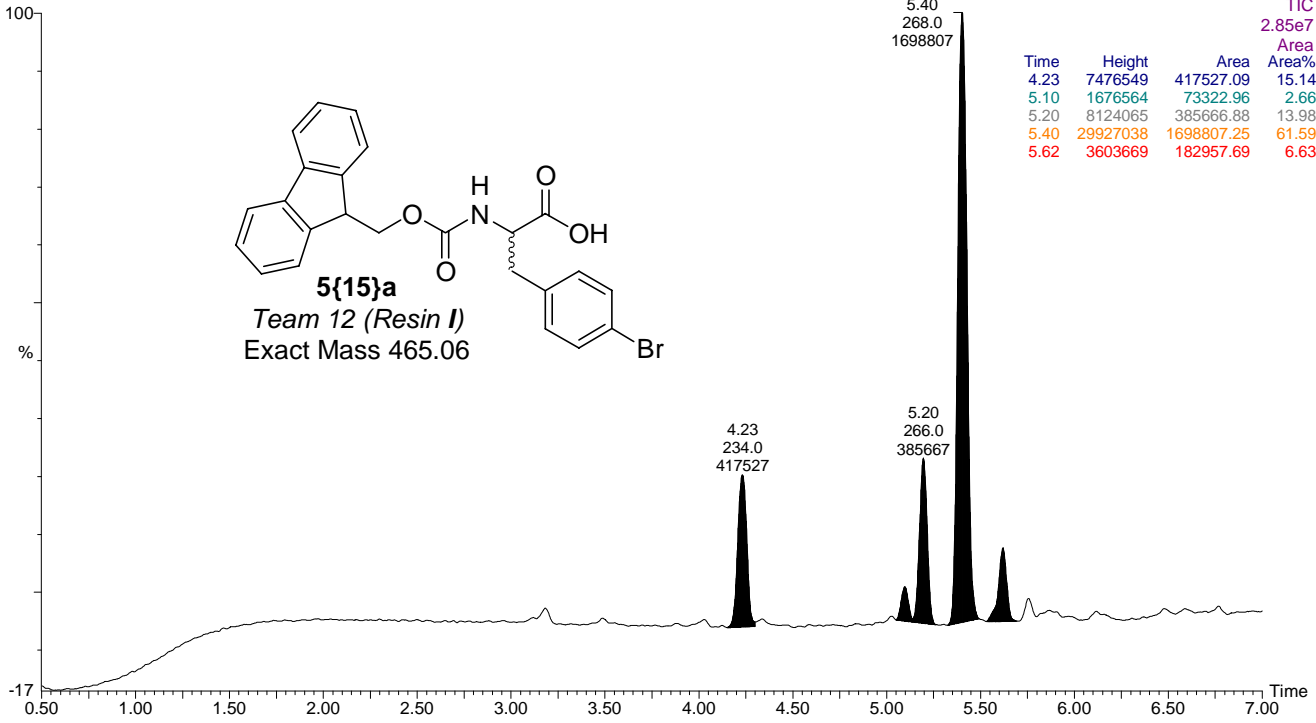
1H_BB#40_B1_CD3ODincDCI3_02_07

Pulse Sequence: s2pul



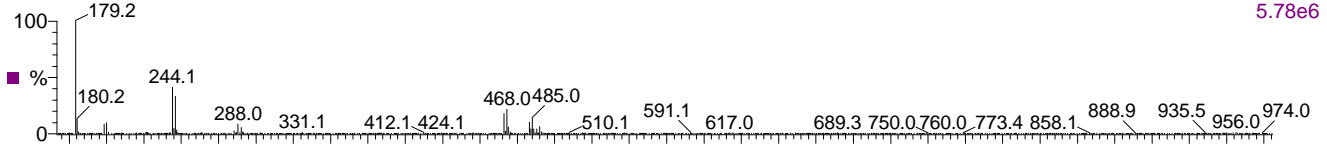
5{15}a

T12-A3 Sm (Mn, 1x1)

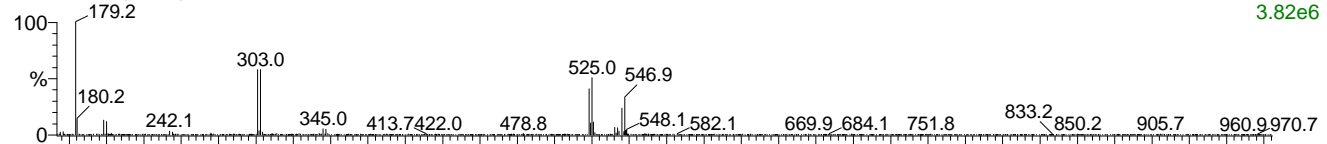


3: Diode Array
TIC
2.85e7

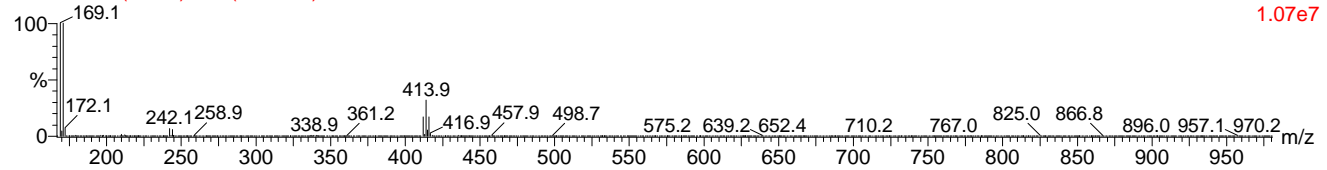
T12-A3 204 (5.460)



T12-A3 197 (5.273)



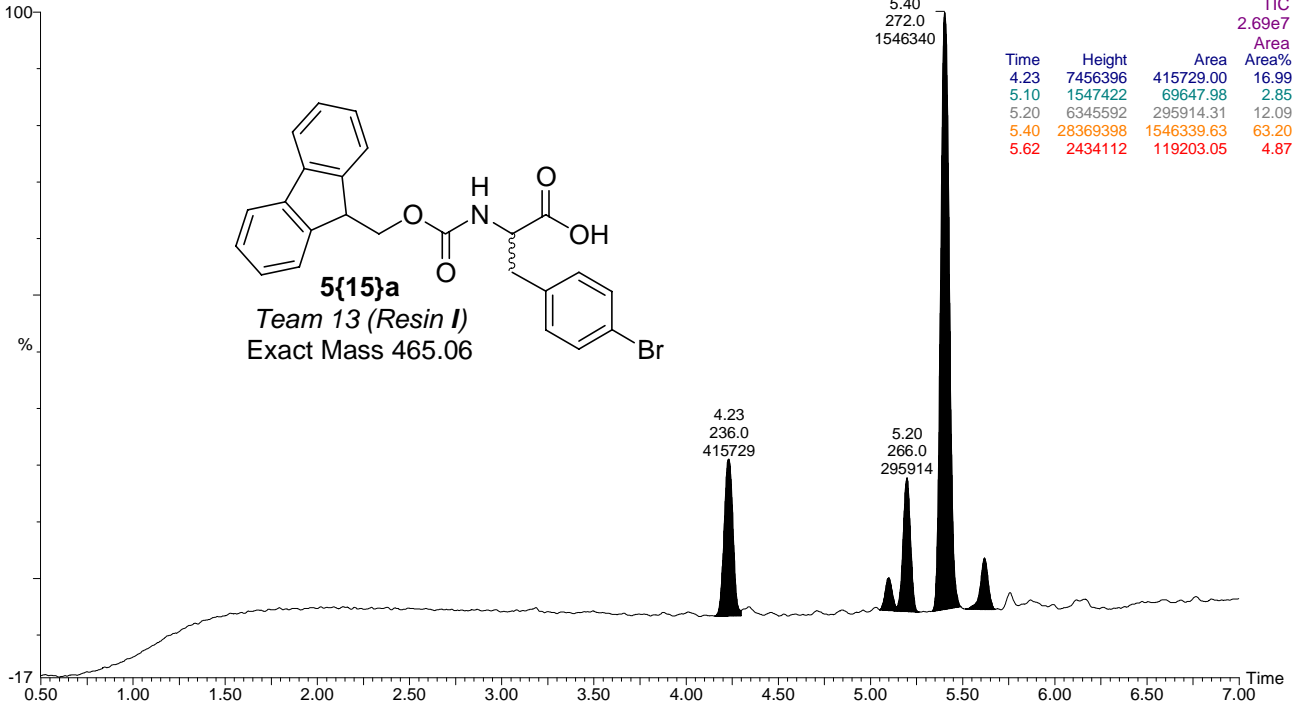
T12-A3 160 (4.280) Cm (159:164)



5{15}a

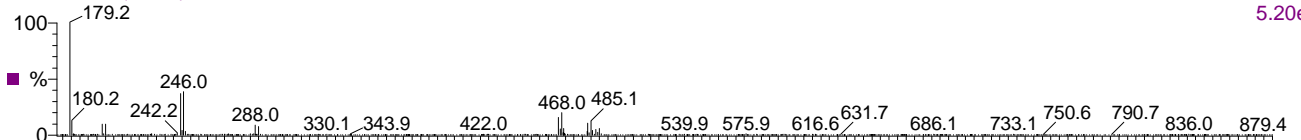
T13-A2 Sm (Mn, 1x1)

3: Diode Array



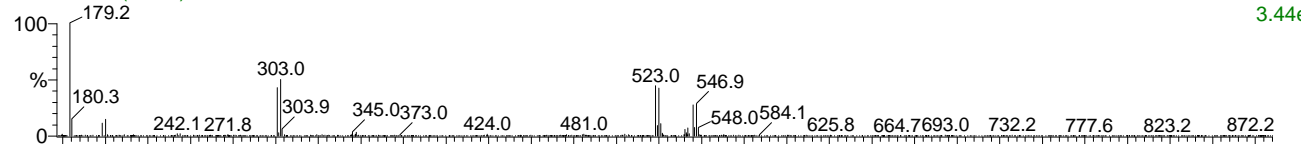
T13-A2 204 (5.460)

1: Scan ES+
5.20e6



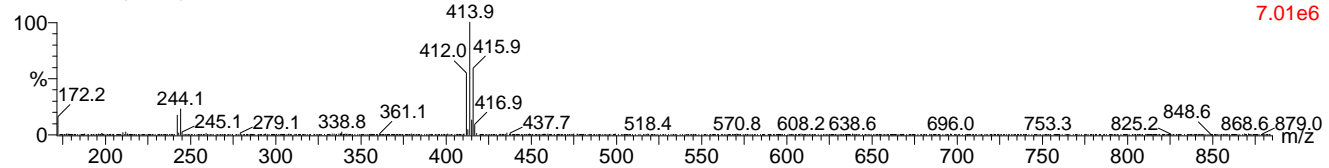
T13-A2 196 (5.246)

1: Scan ES+
3.44e6



T13-A2 160 (4.280)

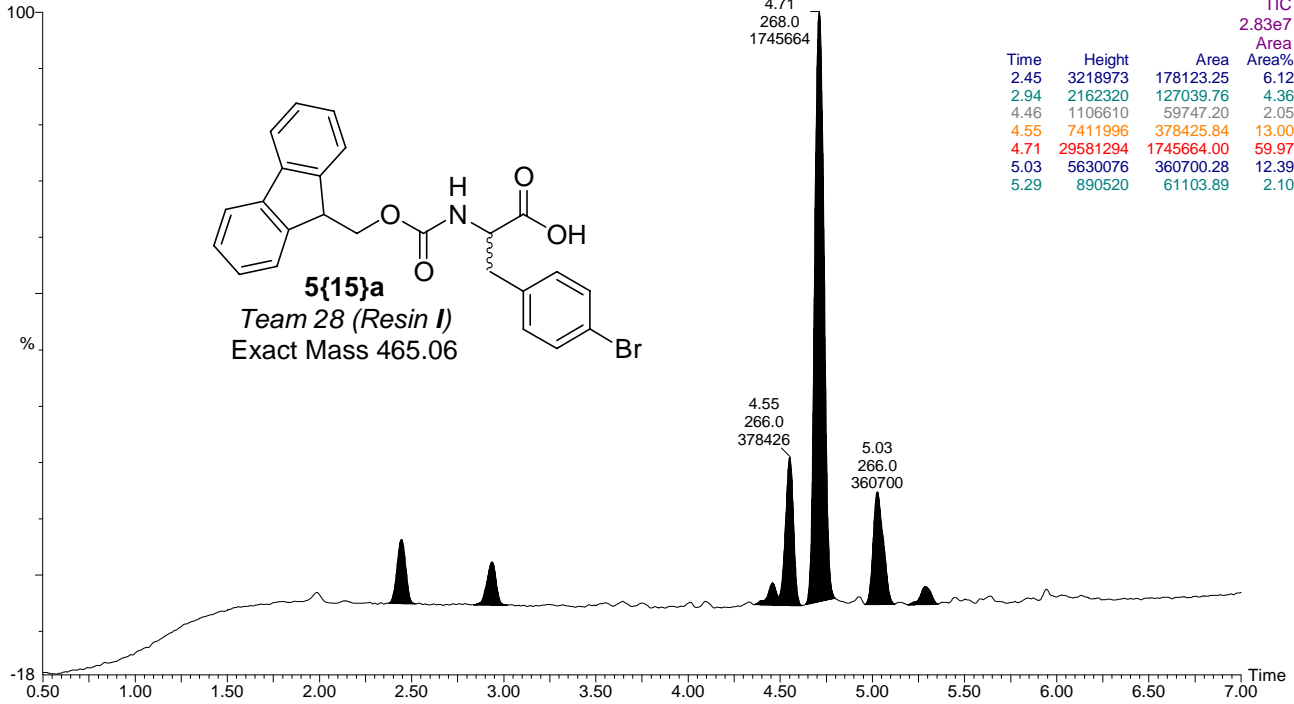
1: Scan ES+
7.01e6



5{15}a

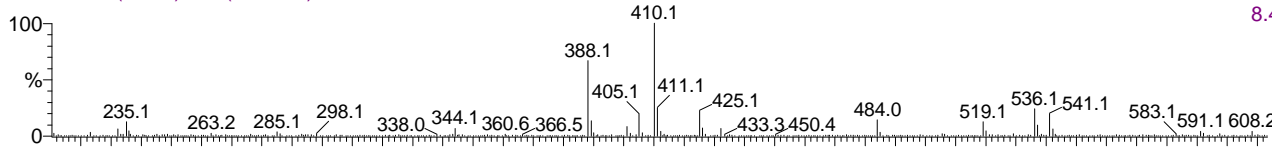
T28-A3 Sm (Mn, 1x1)

3: Diode Array
TIC
2.83e7



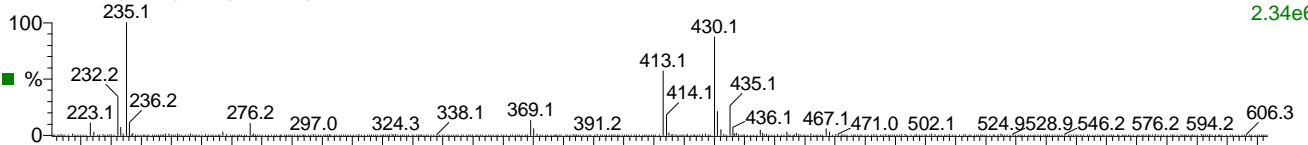
T28-A3 190 (5.085) Cm (189:191)

1: Scan ES+
8.44e5



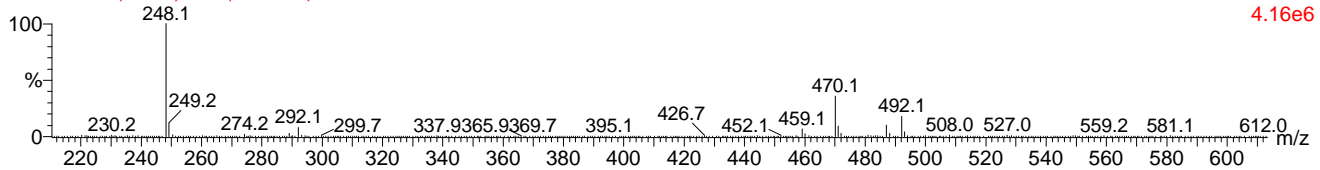
T28-A3 178 (4.763) Cm (177:180)

1: Scan ES+
2.34e6



T28-A3 172 (4.602) Cm (171:173)

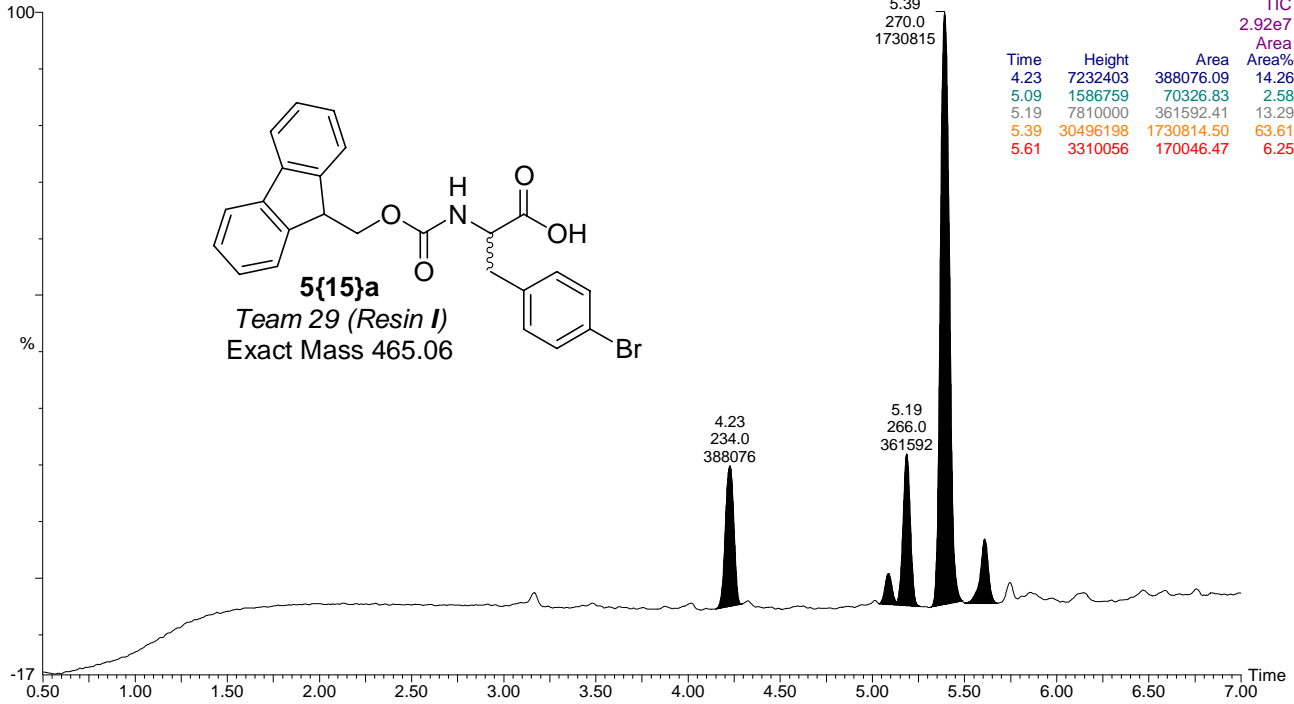
1: Scan ES+
4.16e6



5{15}a

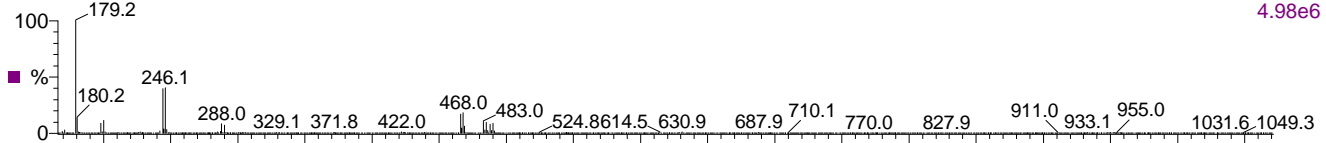
T29-A2 Sm (Mn, 1x1)

3: Diode Array
TIC
2.92e7



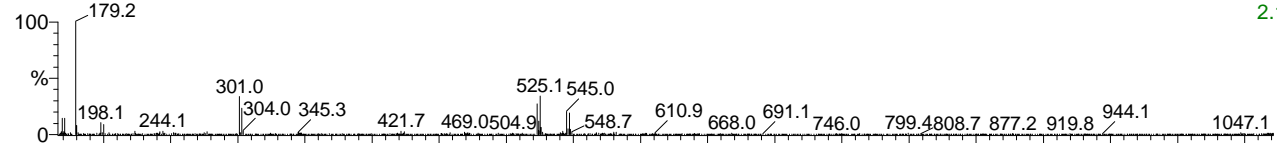
T29-A2 204 (5.460) Cm (203:205)

1: Scan ES+
4.98e6



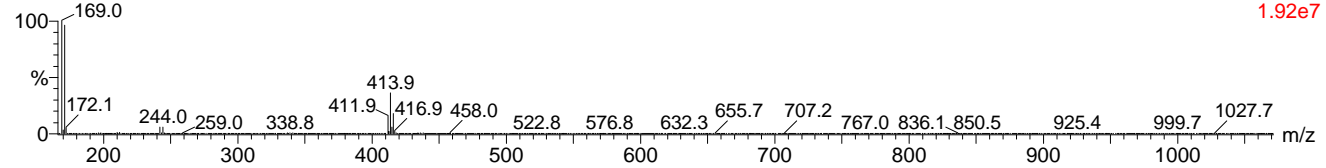
T29-A2 195 (5.219)

1: Scan ES+
2.14e6



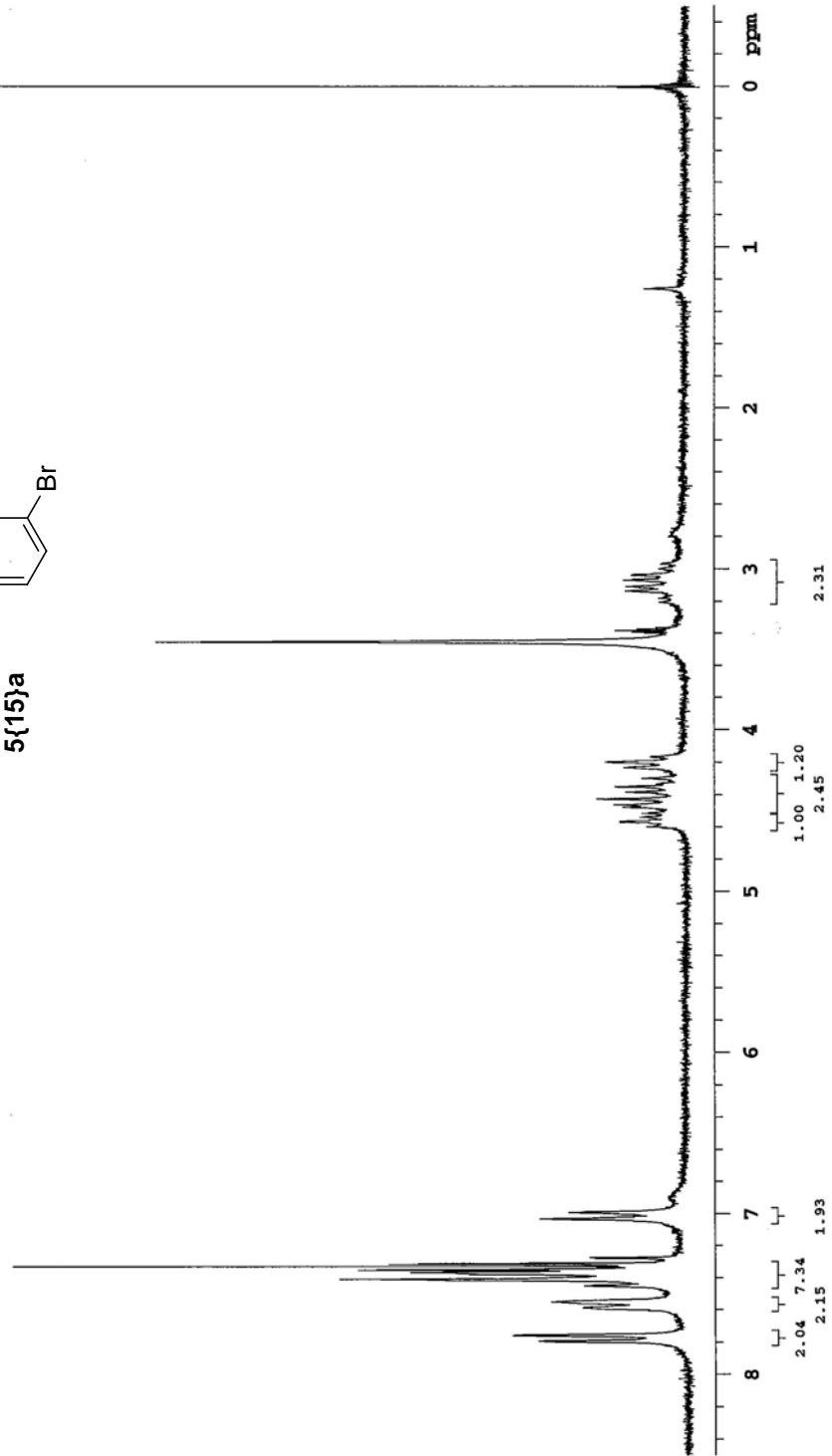
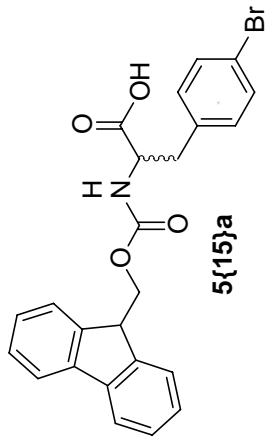
T29-A2 161 (4.307) Cm (159:161)

1: Scan ES+
1.92e7



1H_BB#34_B1_CD3OD1nDC13_02_07

Pulse Sequence: s2pul

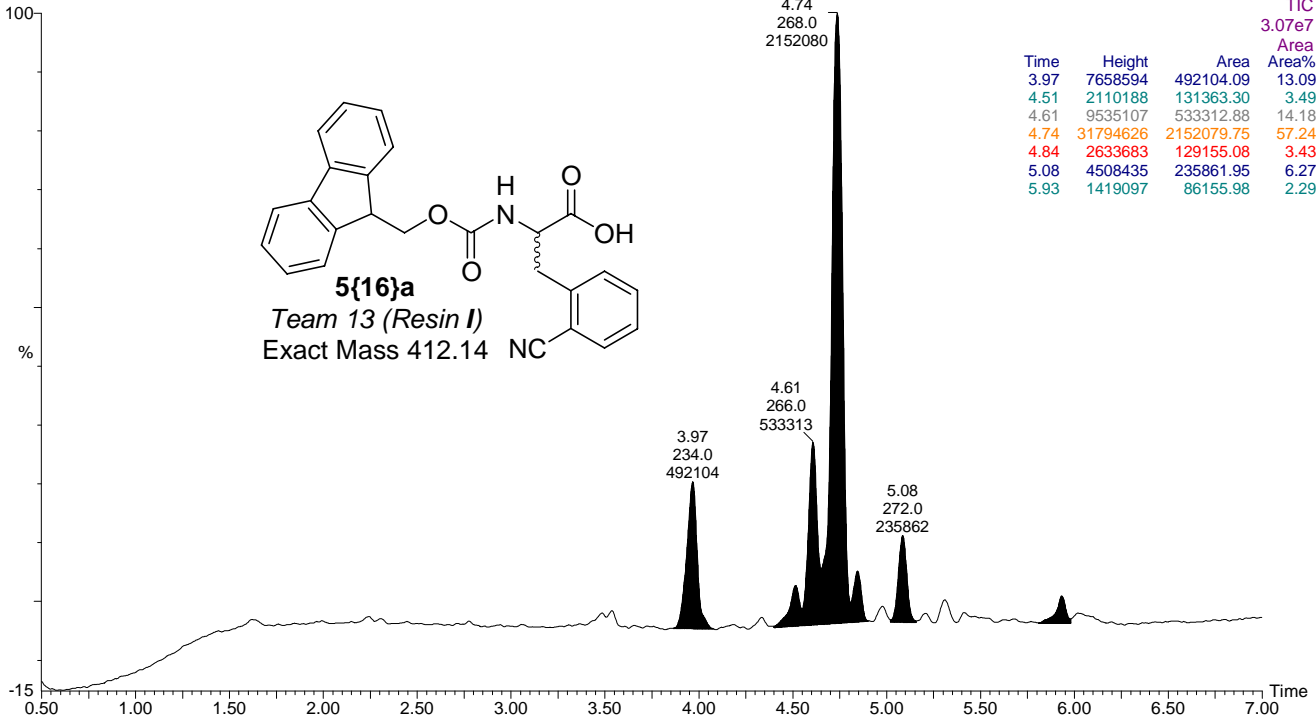
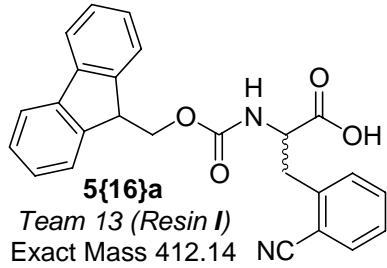


5{16}a

T13-A3 Sm (Mn, 1x1)

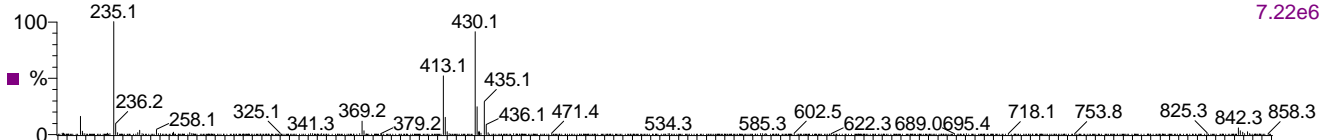
3: Diode Array
TIC
3.07e7

Time	Height	Area	Area%
3.97	7658594	492104.09	13.09
4.51	2110188	131363.30	3.49
4.61	9535107	533312.88	14.18
4.74	31794626	2152079.75	57.24
4.84	2633683	129155.08	3.43
5.08	4508435	235861.95	6.27
5.93	1419097	86155.98	2.29



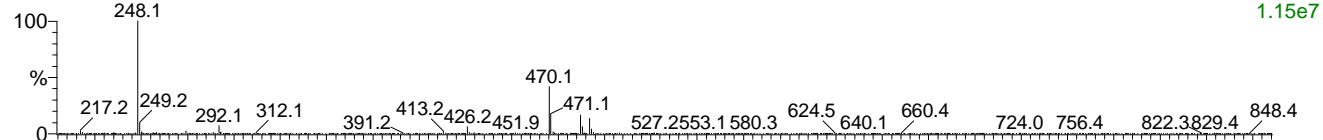
T13-A3 180 (4.816)

1: Scan ES+
7.22e6



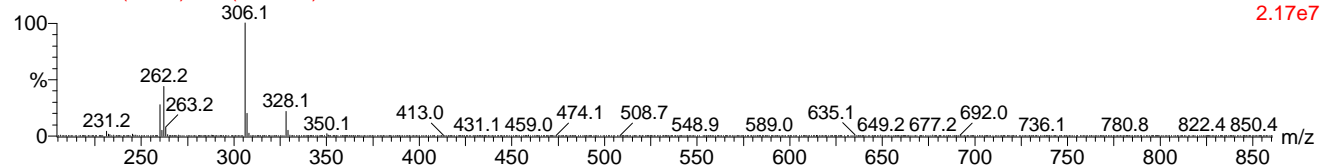
T13-A3 174 (4.655)

1: Scan ES+
1.15e7



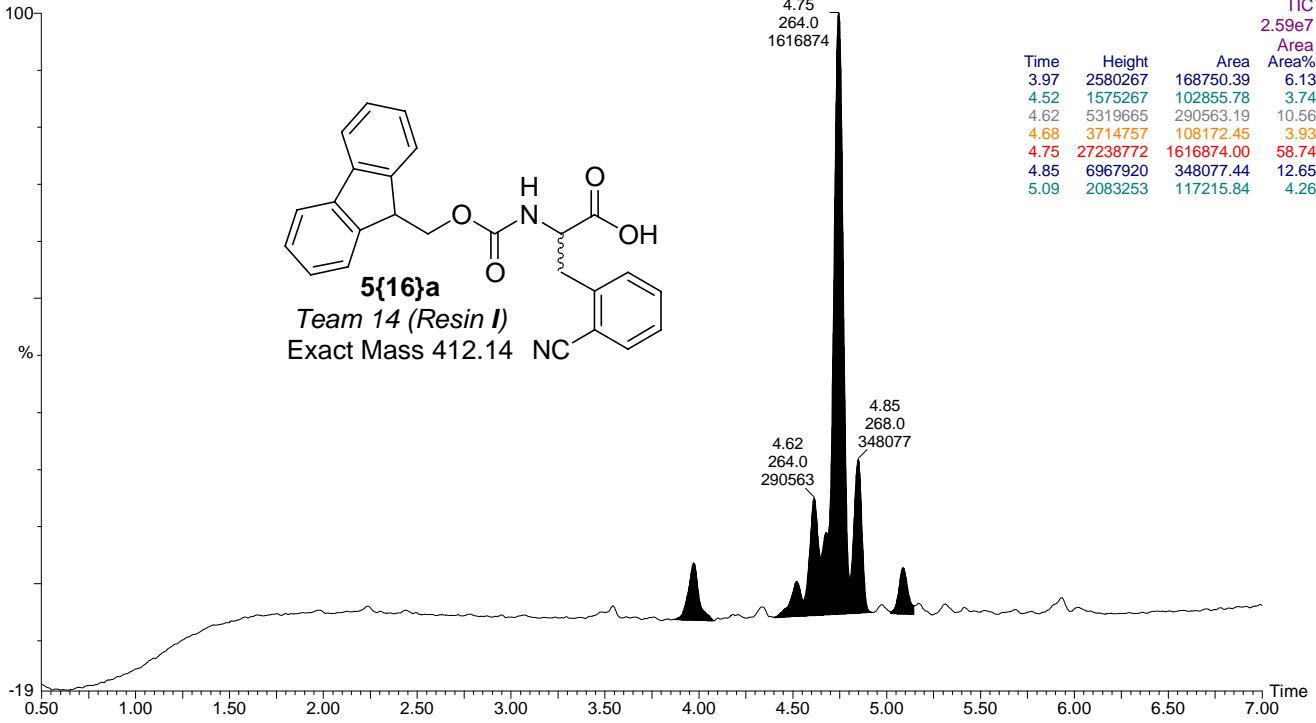
T13-A3 151 (4.038) Cm (149:151)

1: Scan ES+
2.17e7

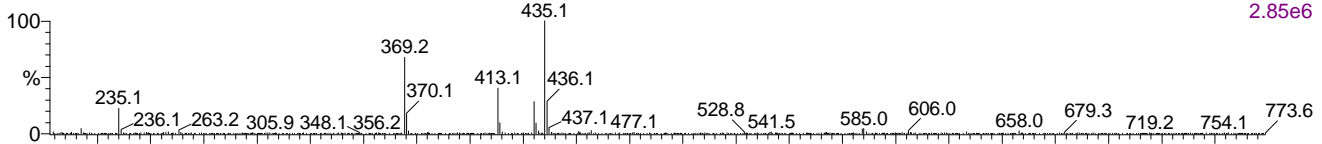


5{16}a

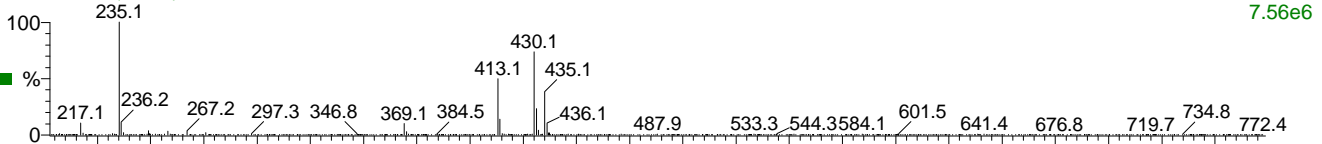
T14-A2 Sm (Mn, 1x1)



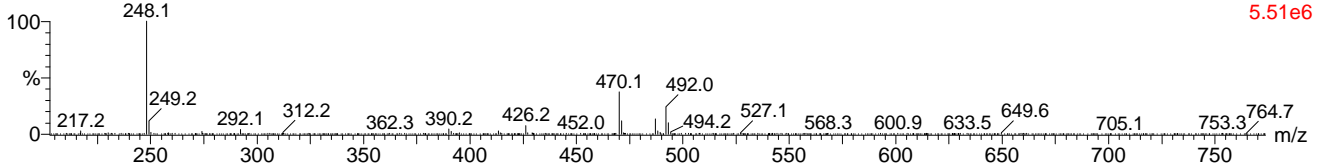
T14-A2 184 (4.924)



T14-A2 180 (4.816)



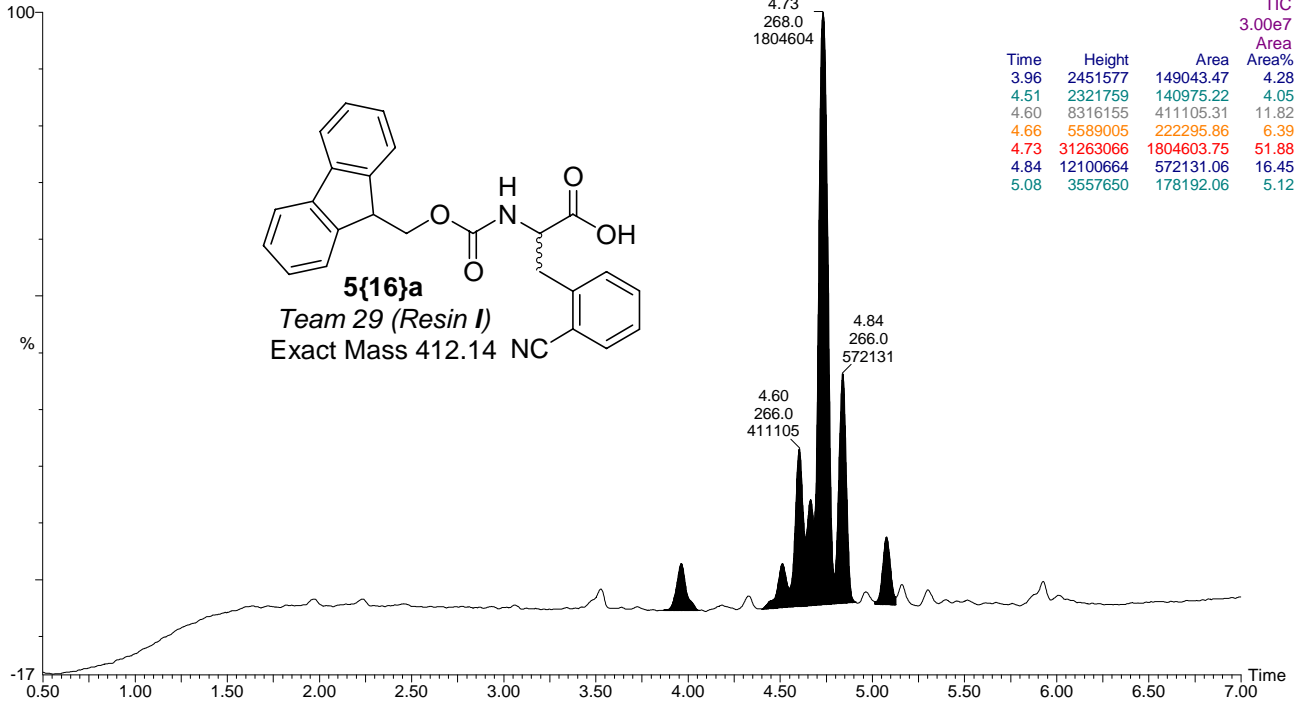
T14-A2 174 (4.655)



5{16}a

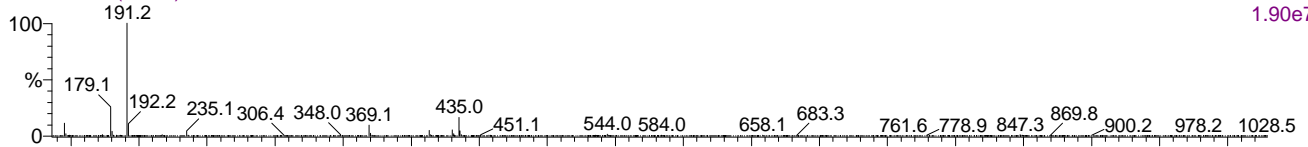
T29-A3 Sm (Mn, 1x1)

3: Diode Array
TIC
3.00e7



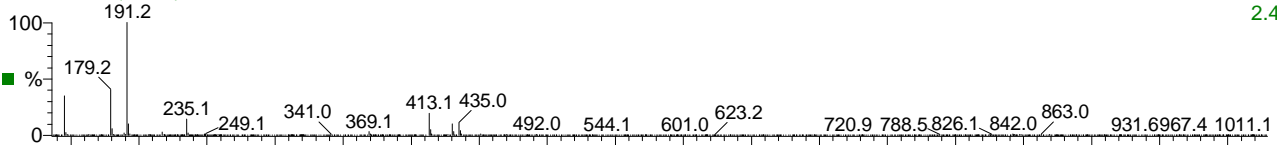
T29-A3 182 (4.870)

1: Scan ES+
1.90e7



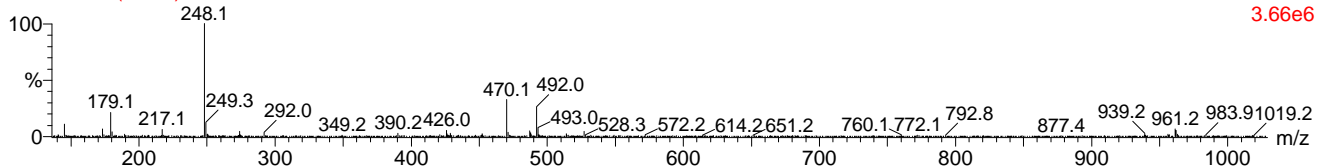
T29-A3 178 (4.763)

1: Scan ES+
2.44e7



T29-A3 173 (4.629)

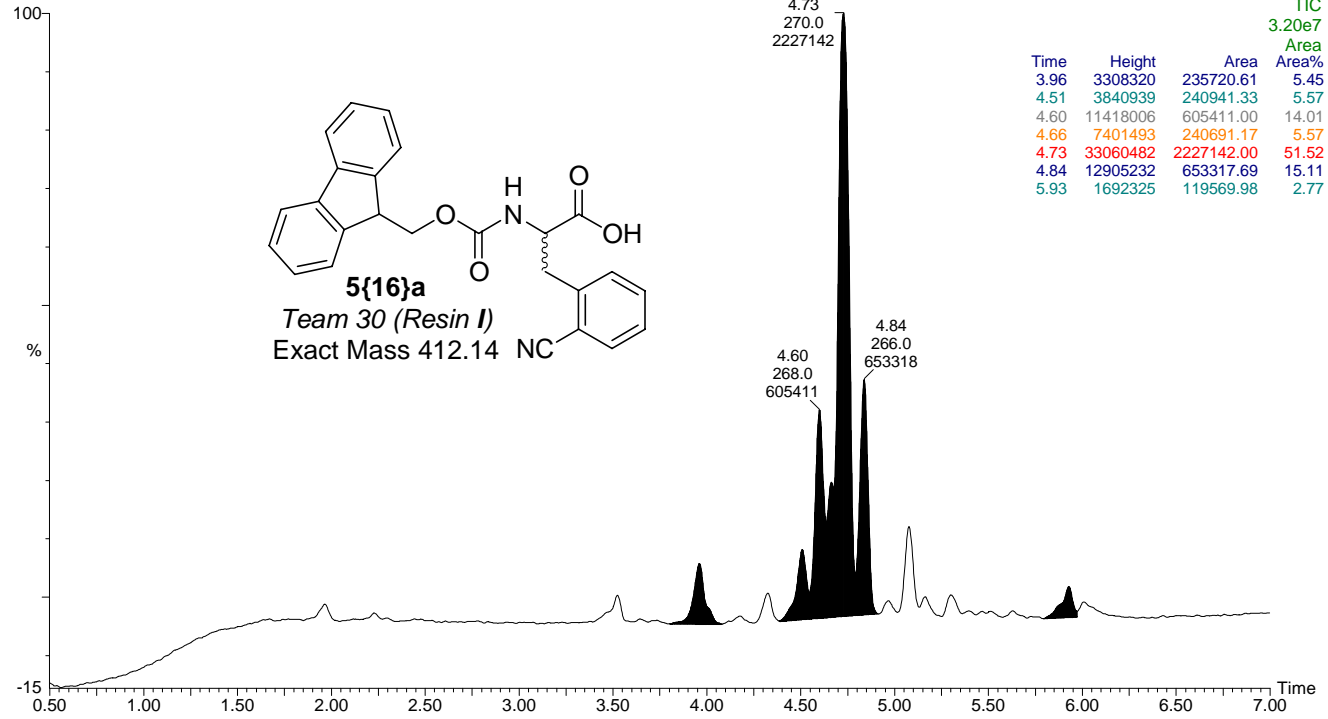
1: Scan ES+
3.66e6



5{16}a

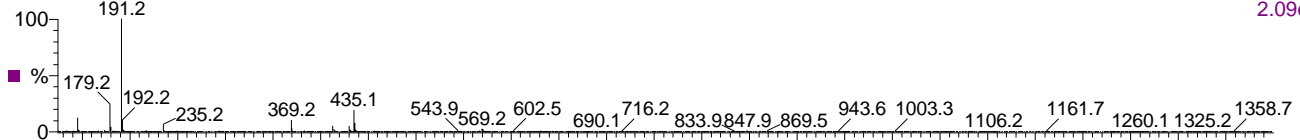
T30-A2 Sm (Mn, 1x1)

3: Diode Array



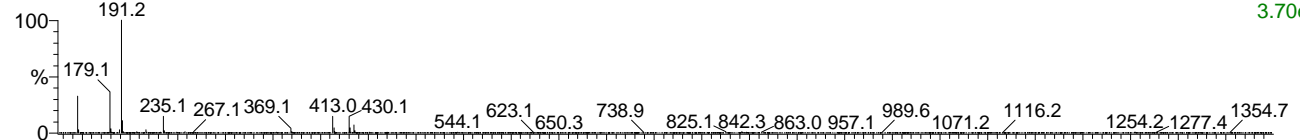
T30-A2 182 (4.870)

1: Scan ES+
2.09e7



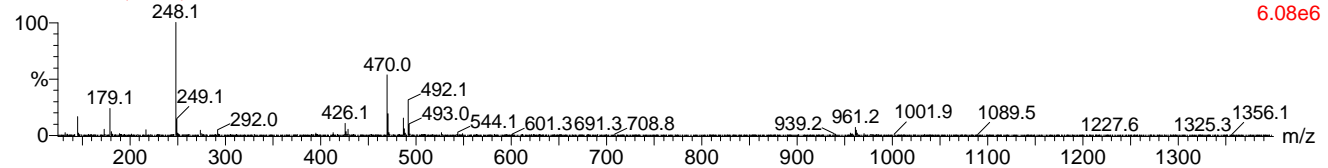
T30-A2 178 (4.763)

1: Scan ES+
3.70e7



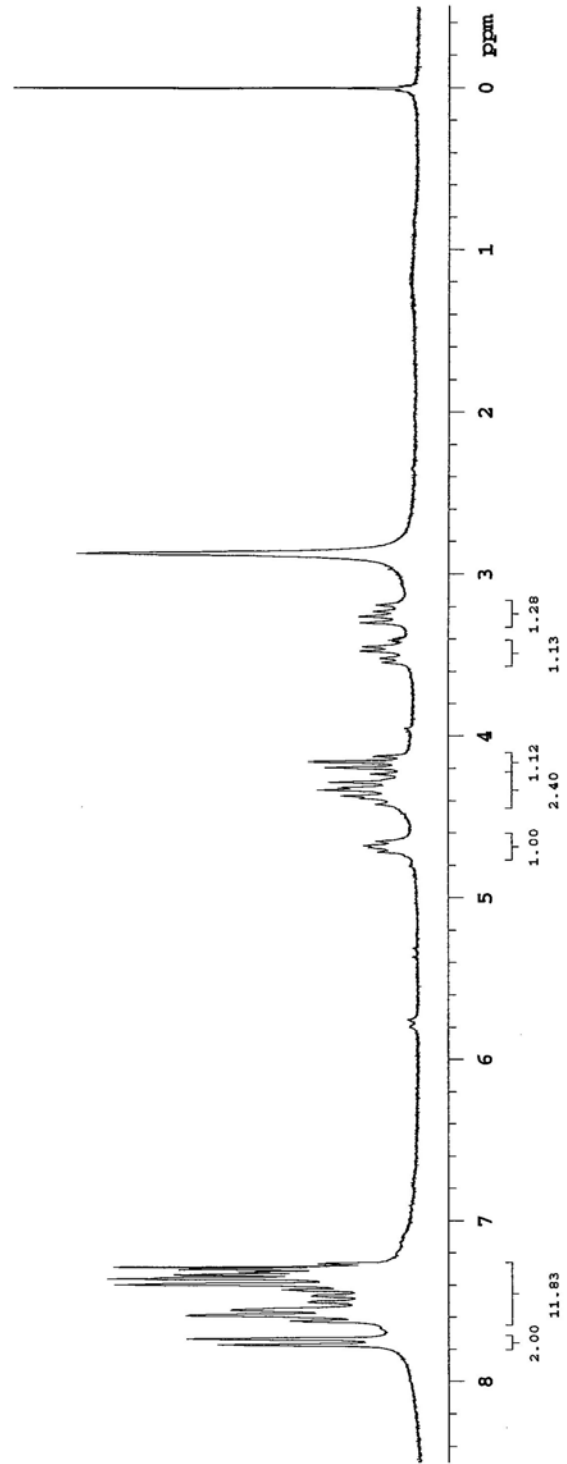
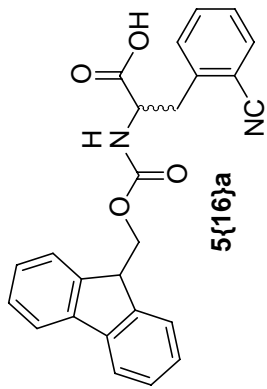
T30-A2 173 (4.629)

1: Scan ES+
6.08e6



1H_BE#34_A2_CD3ODinDC13_02_07

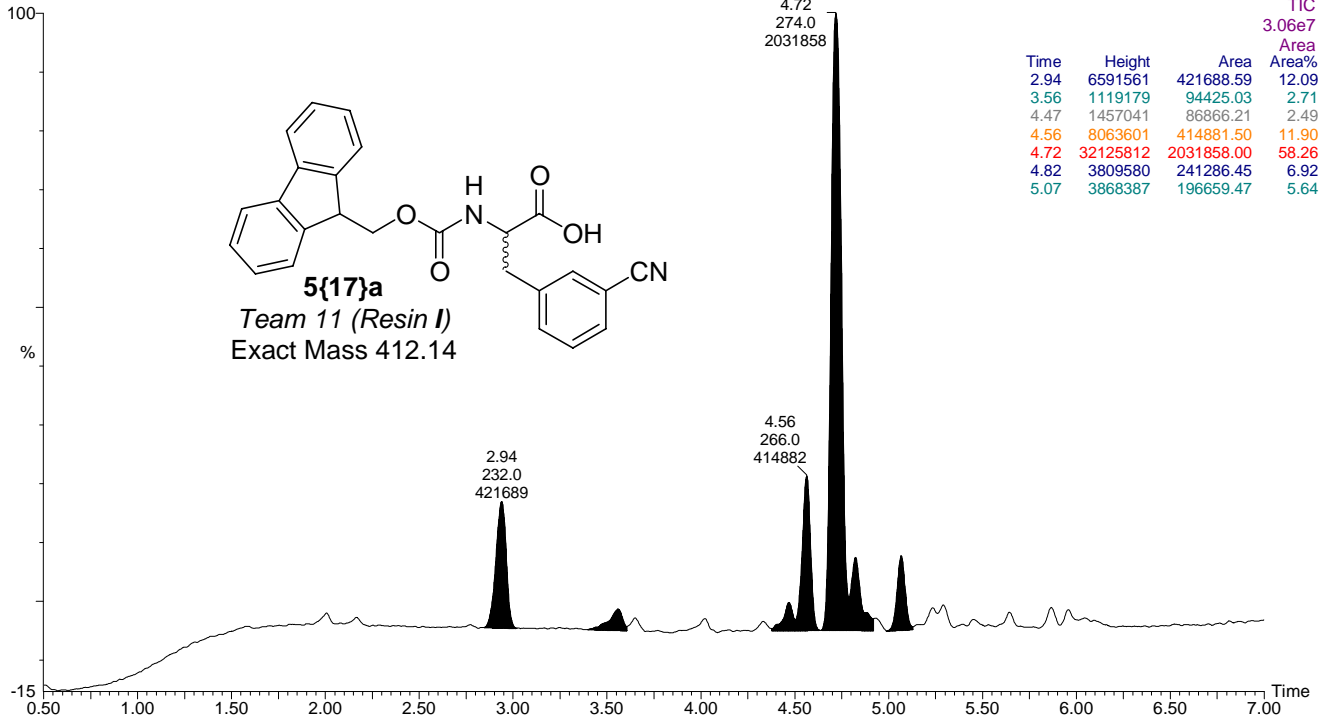
Pulse Sequence: s2pul



5{17}a

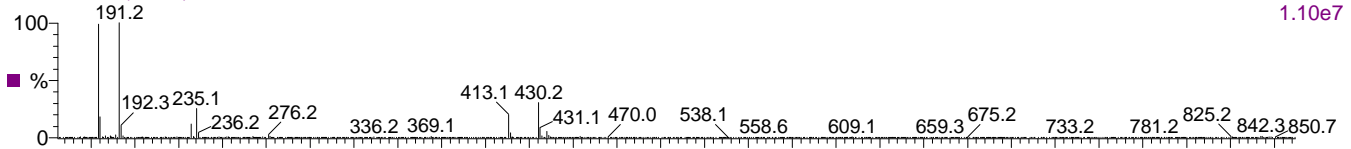
T11-A3 Sm (Mn, 1x1)

3: Diode Array



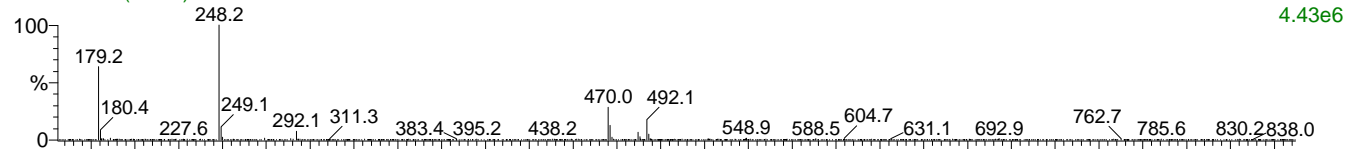
T11-A3 178 (4.763)

1: Scan ES+
1.10e7



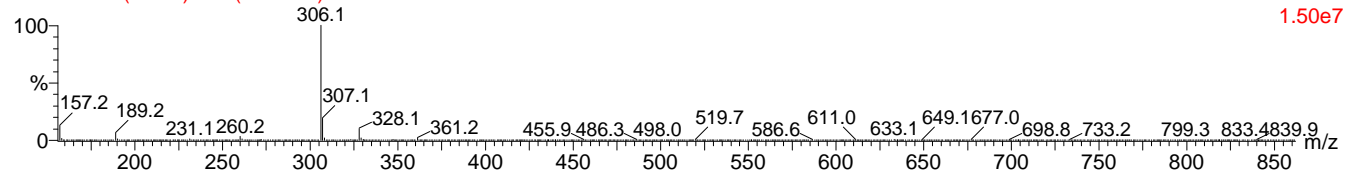
T11-A3 172 (4.602)

1: Scan ES+
4.43e6



T11-A3 112 (2.992) Cm (111:113)

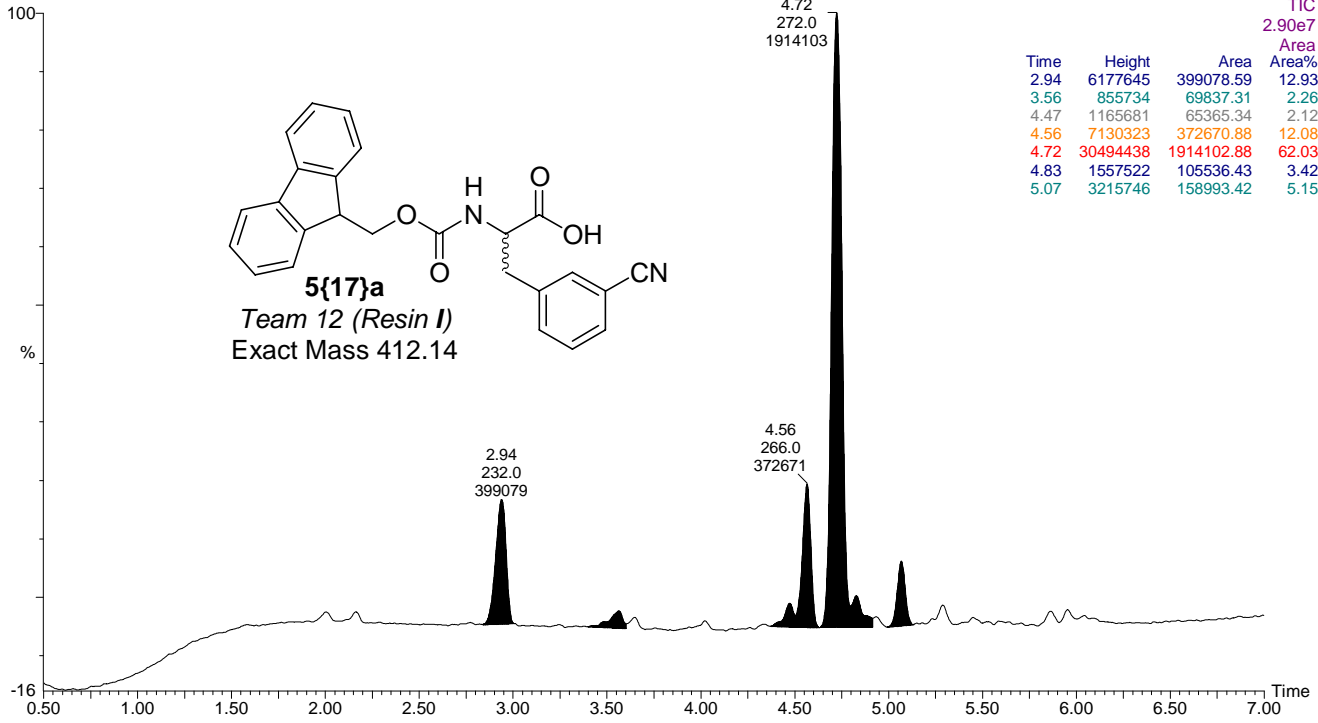
1: Scan ES+
1.50e7



5{17}a

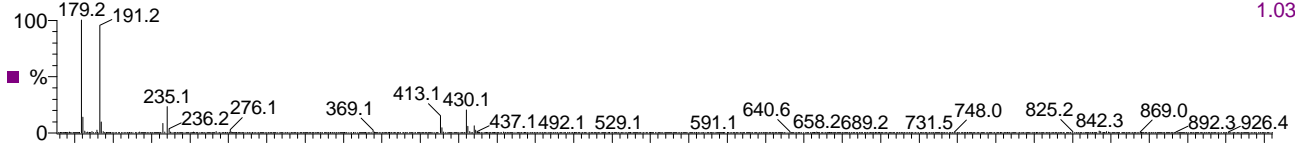
T12-A2 Sm (Mn, 1x1)

3: Diode Array
TIC
2.90e7



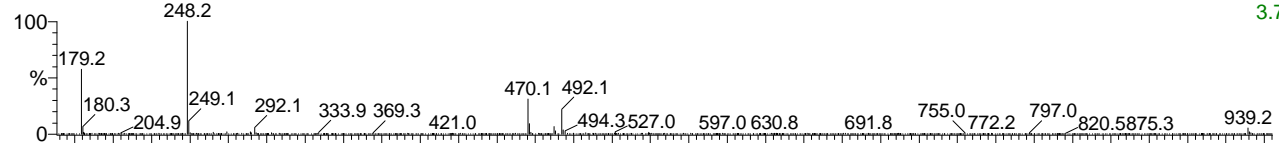
T12-A2 179 (4.790) Cm (178:181)

1: Scan ES+
1.03e7



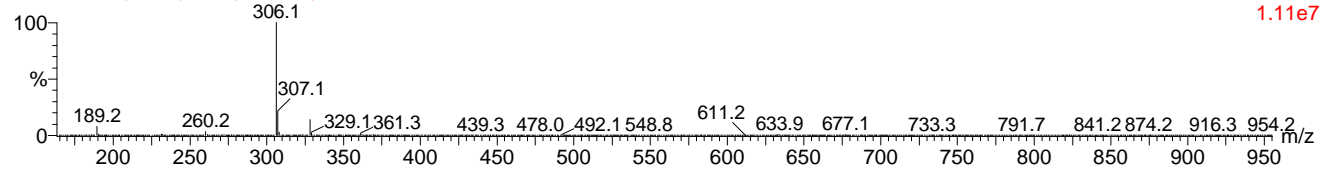
T12-A2 172 (4.602)

1: Scan ES+
3.74e6



T12-A2 112 (2.992) Cm (111:114)

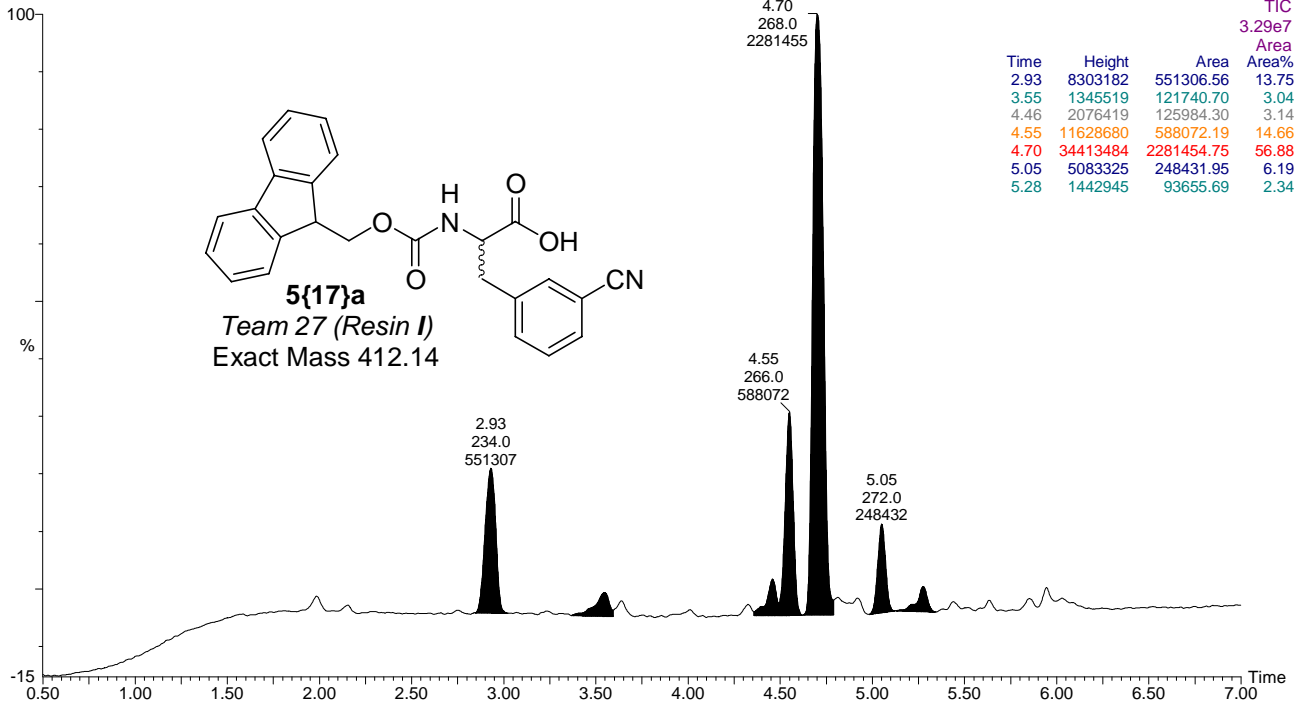
1: Scan ES+
1.11e7



5{17}a

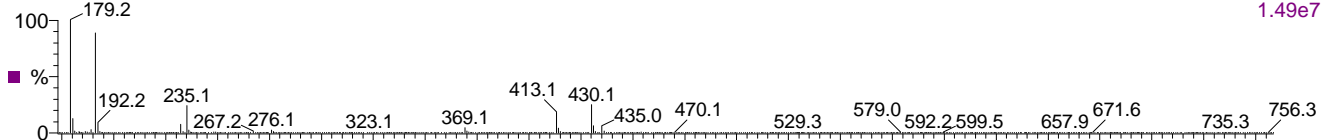
T27-A3 Sm (Mn, 1x1)

3: Diode Array
TIC
3.29e7



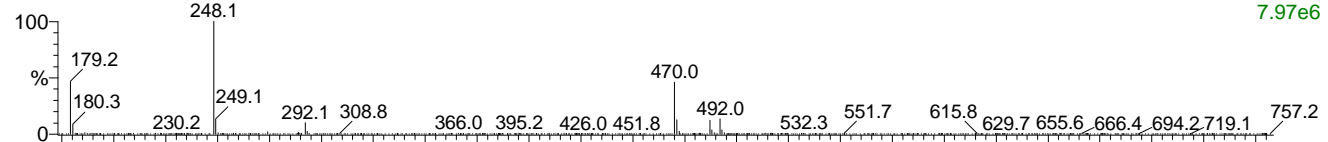
T27-A3 178 (4.763) Cm (177:179)

1: Scan ES+
1.49e7



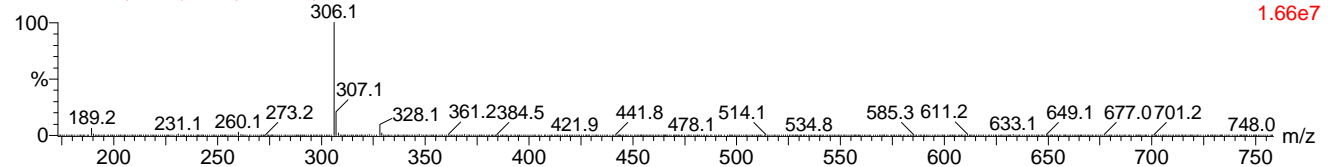
T27-A3 172 (4.602)

1: Scan ES+
7.97e6



T27-A3 112 (2.992) Cm (110:113)

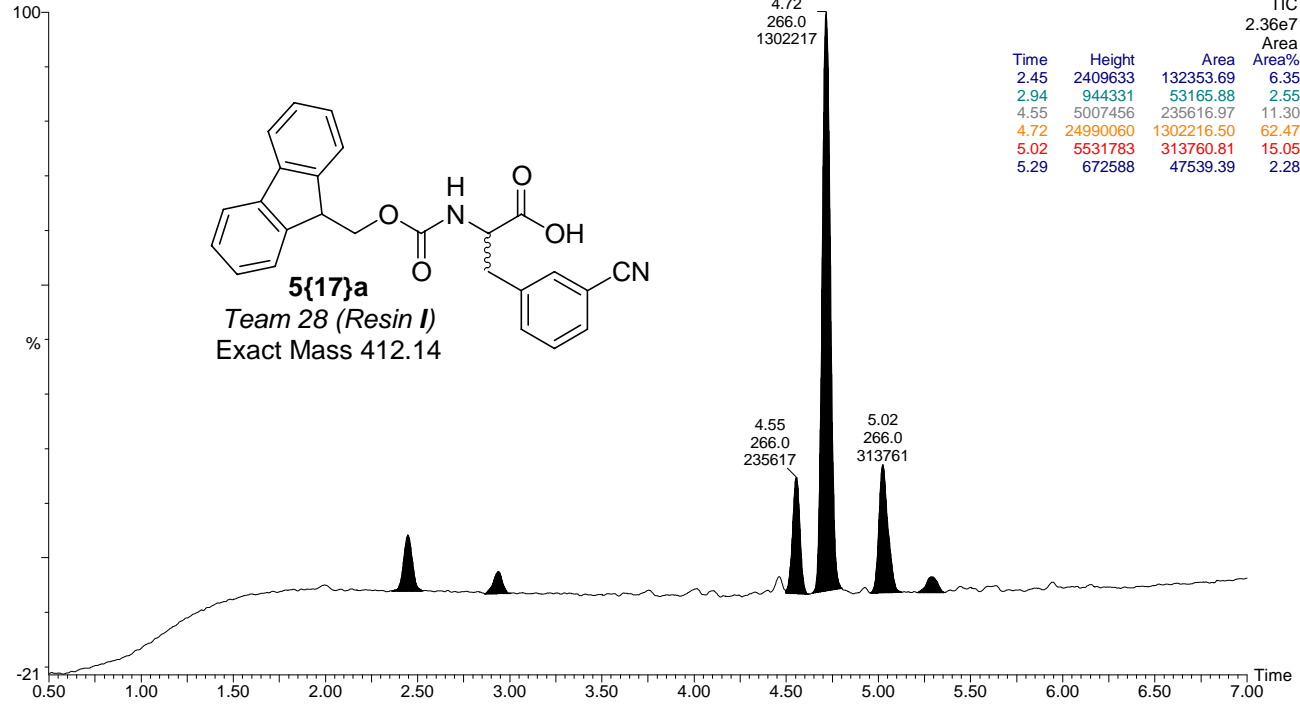
1: Scan ES+
1.66e7



5{17}a

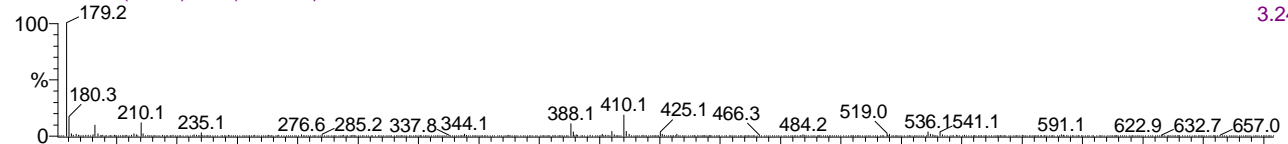
T28-A2 Sm (Mn, 1x1)

3: Diode Array
TIC
2.36e7



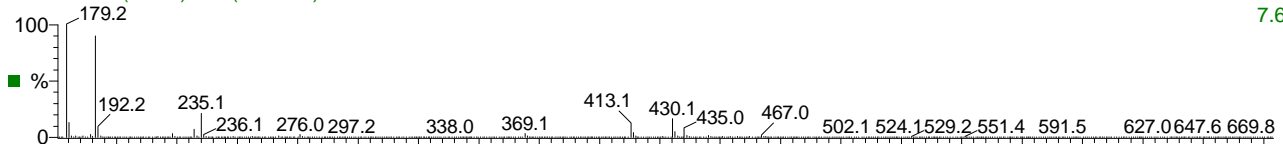
T28-A2 190 (5.085) Cm (189:192)

1: Scan ES+
3.24e6



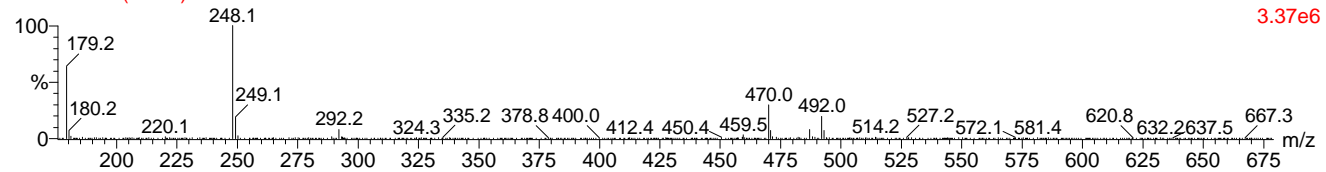
T28-A2 179 (4.790) Cm (177:180)

1: Scan ES+
7.60e6



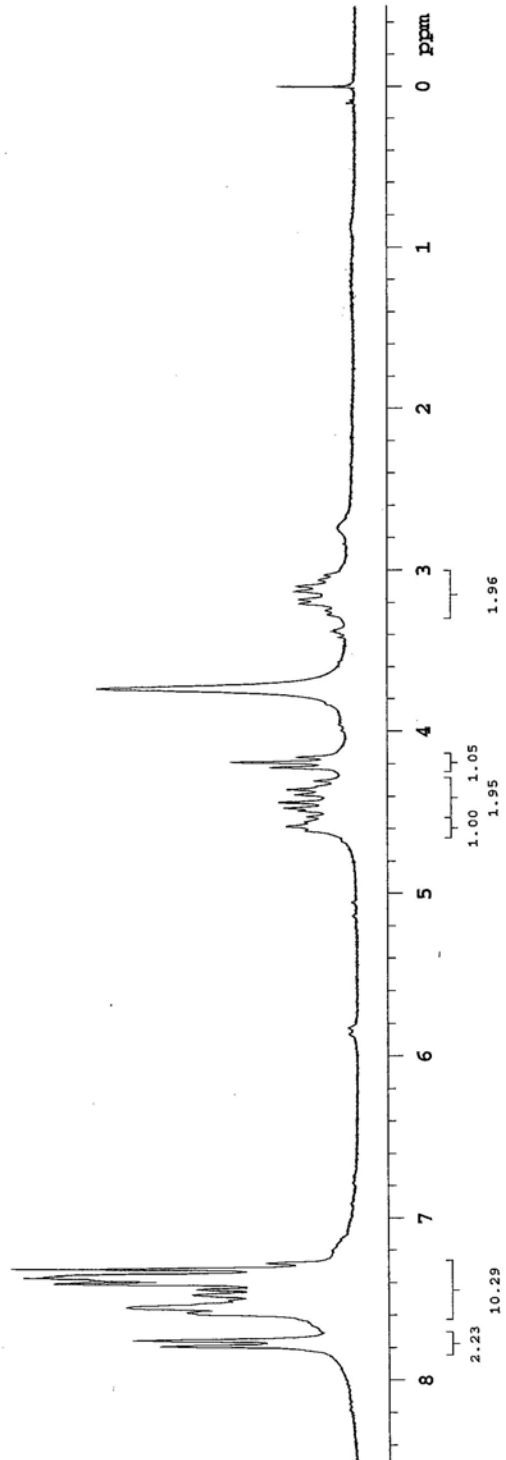
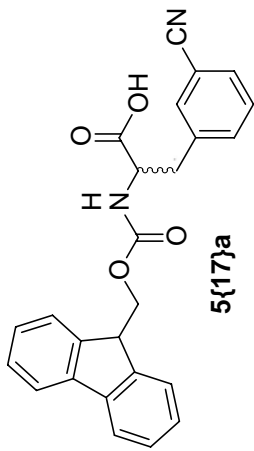
T28-A2 172 (4.602)

1: Scan ES+
3.37e6



1H_BE#27_B1_CD30DfncDC13_02_20_07

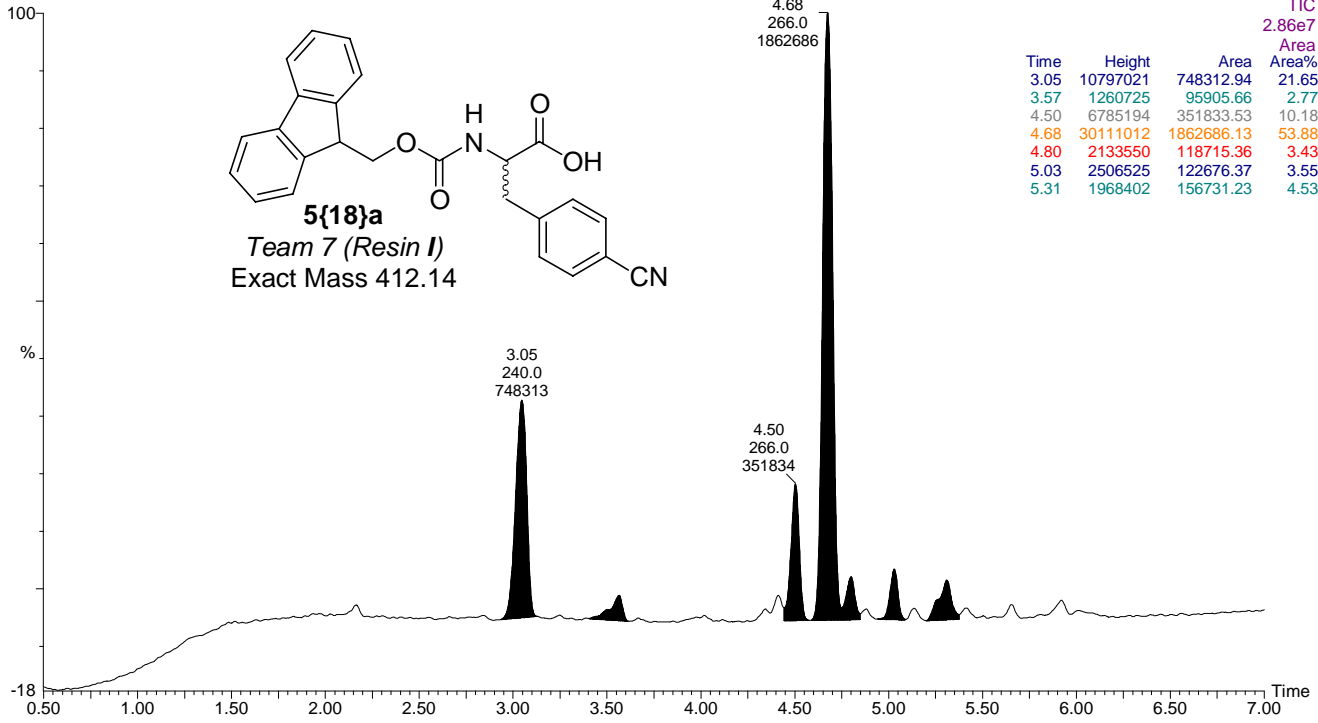
Pulse Sequence: s2pul



5{18}a

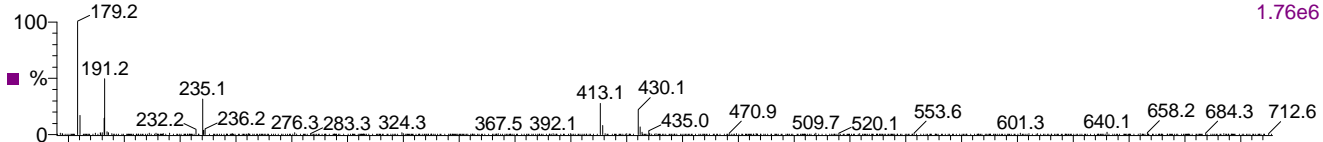
T7-A3 Sm (Mn, 1x1)

3: Diode Array
TIC
2.86e7



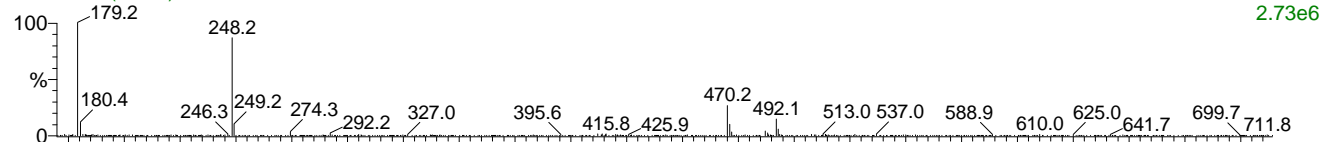
T7-A3 177 (4.736)

1: Scan ES+
1.76e6



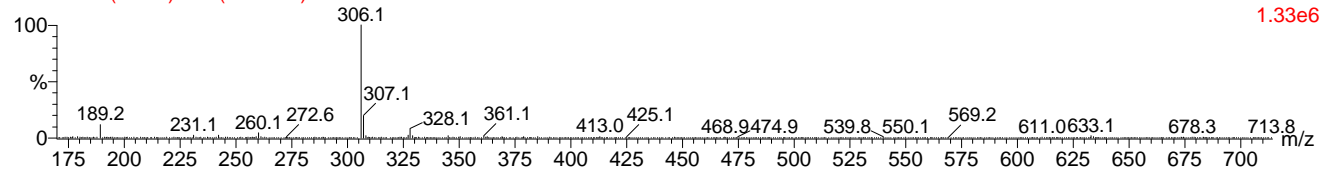
T7-A3 170 (4.548)

1: Scan ES+
2.73e6



T7-A3 116 (3.099) Cm (114:118)

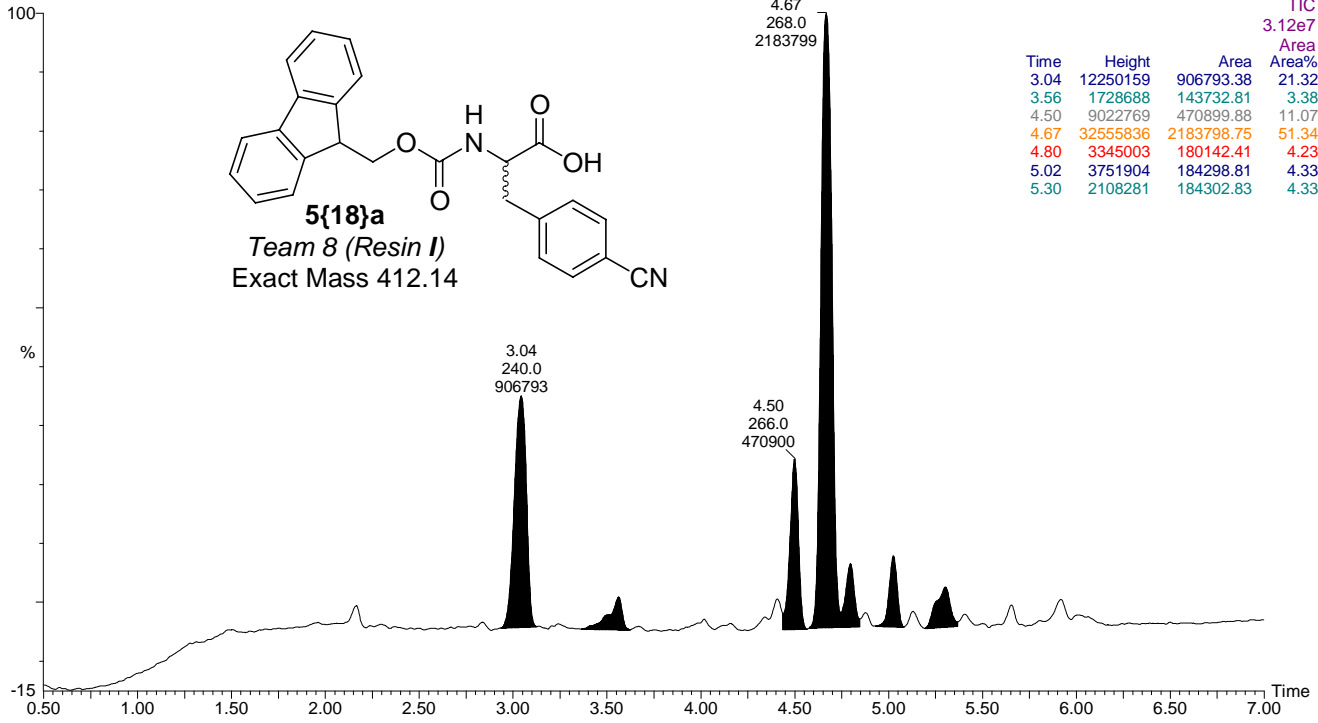
1: Scan ES+
1.33e6



5{18}a

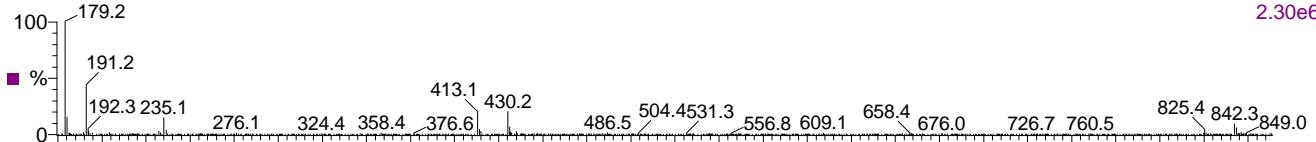
T8-A2 Sm (Mn, 1x1)

3: Diode Array
TIC
3.12e7



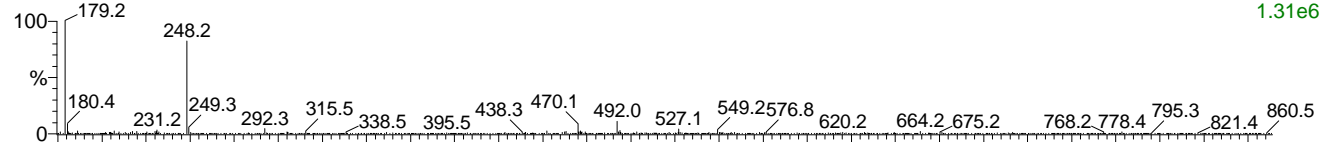
T8-A2 177 (4.736)

1: Scan ES+
2.30e6



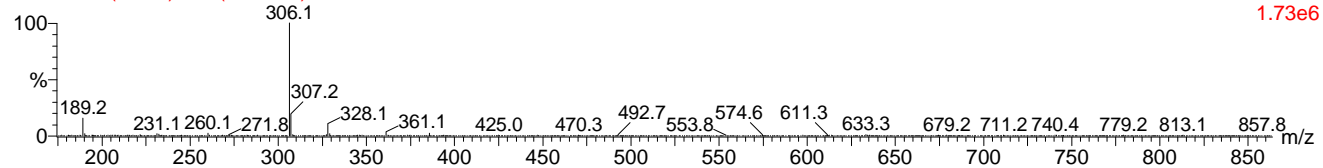
T8-A2 169 (4.521)

1: Scan ES+
1.31e6



T8-A2 117 (3.126) Cm (114:117)

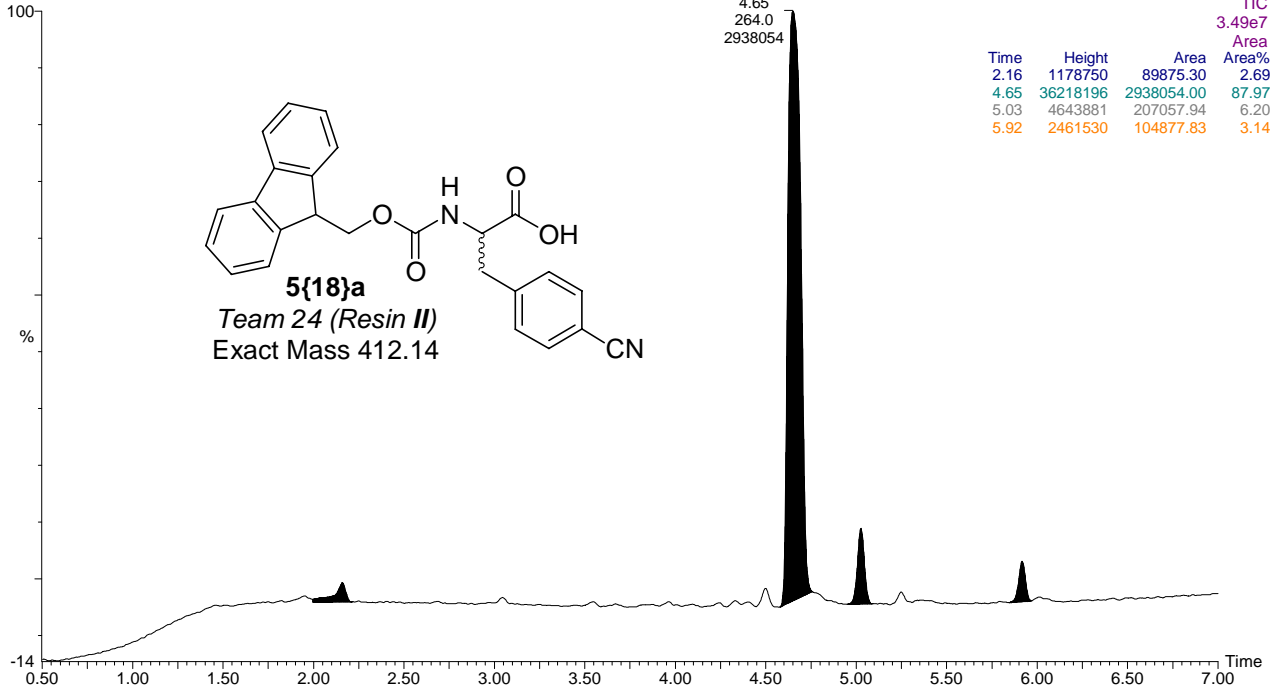
1: Scan ES+
1.73e6



5{18}a

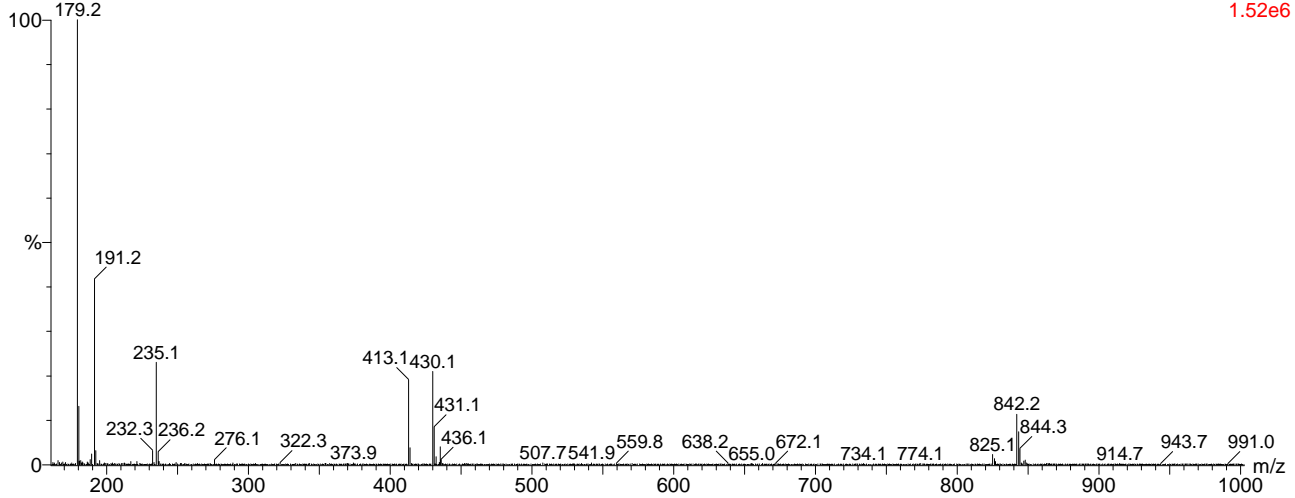
T24-A3 Sm (Mn, 1x1)

3: Diode Array



T24-A3 177 (4.736) Cm (174:179)

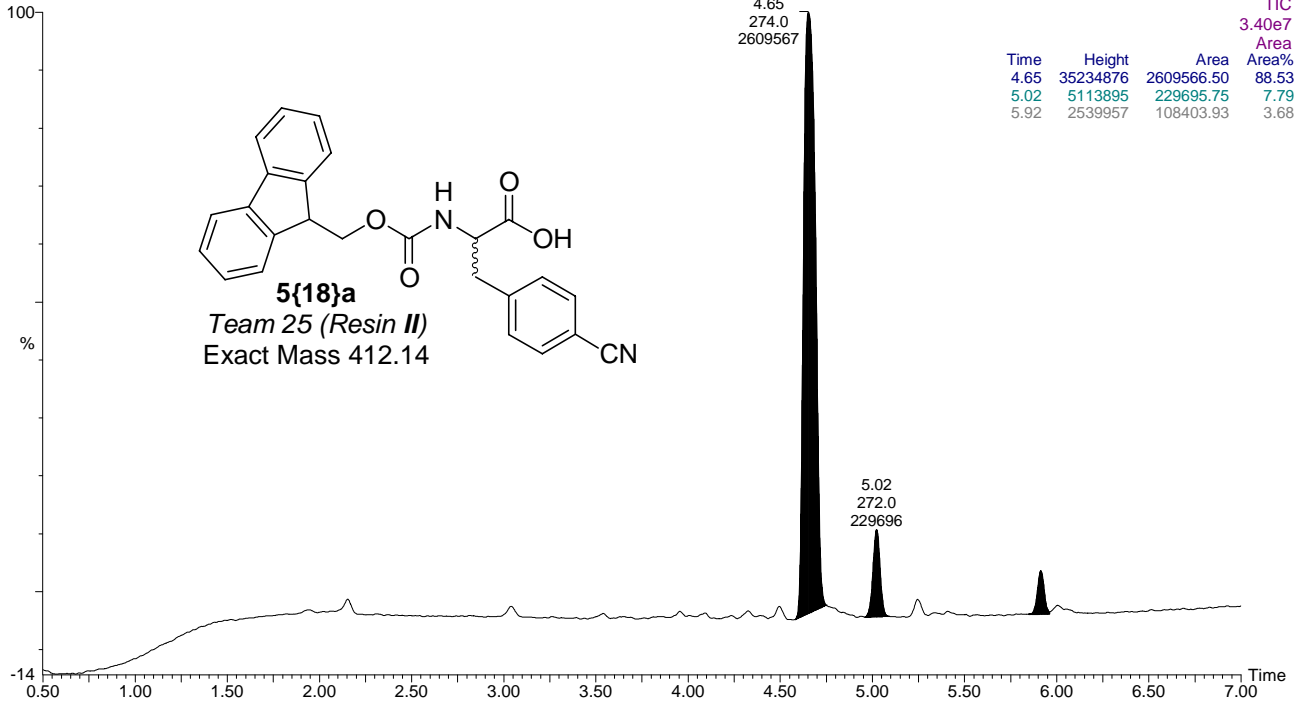
1: Scan ES+
1.52e6



5{18}a

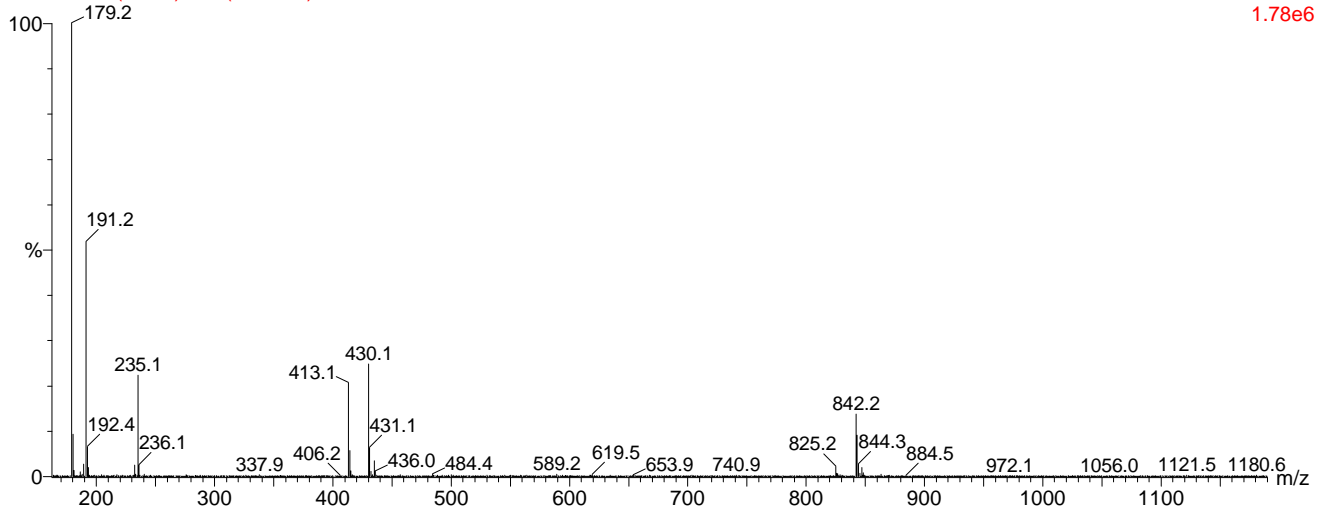
T25-A2 Sm (Mn, 1x1)

3: Diode Array
TIC
3.40e7



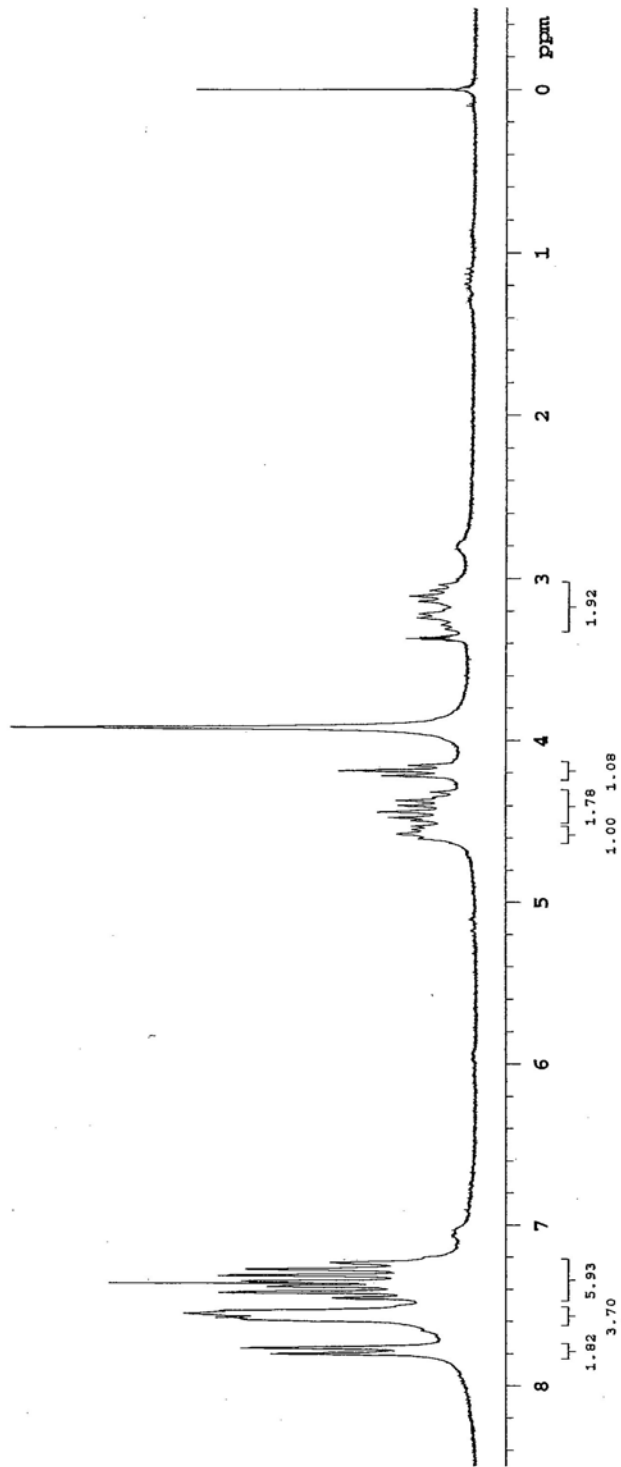
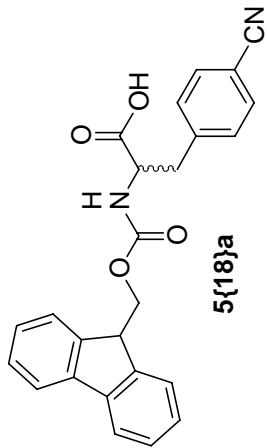
T25-A2 176 (4.709) Cm (175:178)

1: Scan ES+
1.78e6



1H_BE#34_A3_CD3ODinCDCl3_02_07

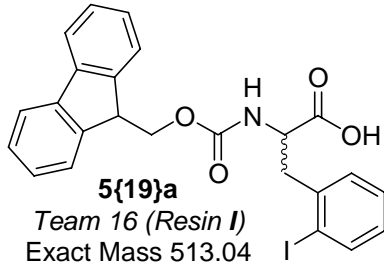
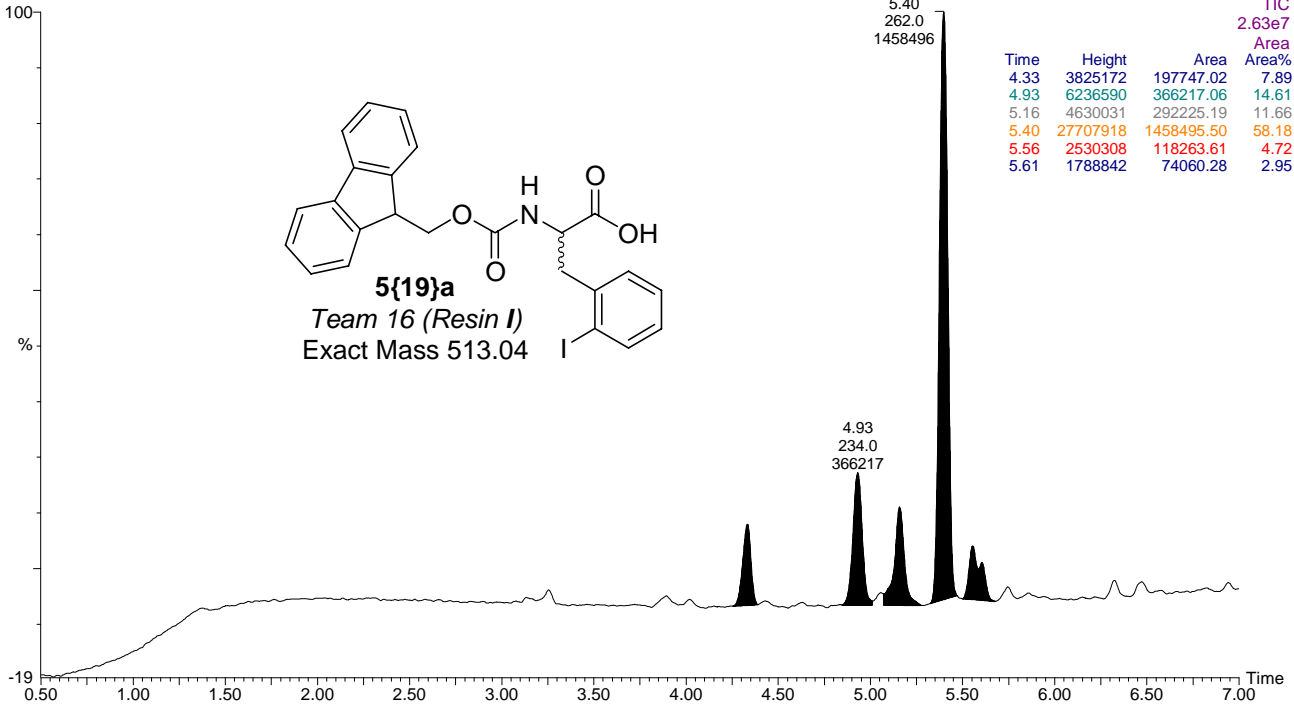
Pulse Sequence: s2pul



5{19}a

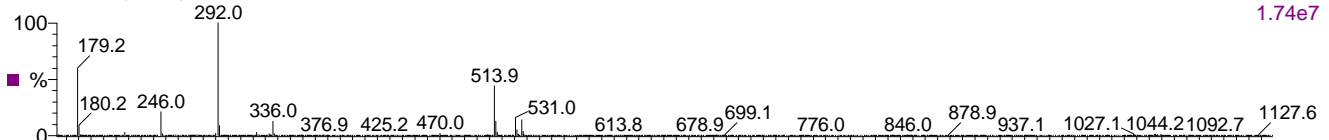
T16-A3 Sm (Mn, 1x1)

3: Diode Array



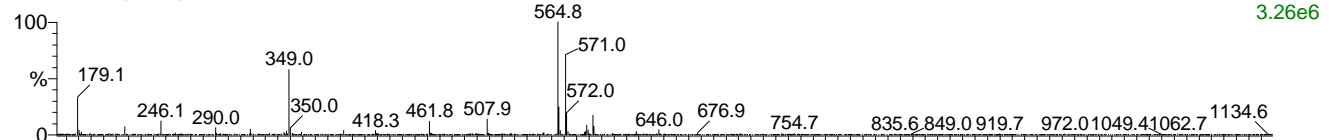
T16-A3 203 (5.434)

1: Scan ES+
1.74e7



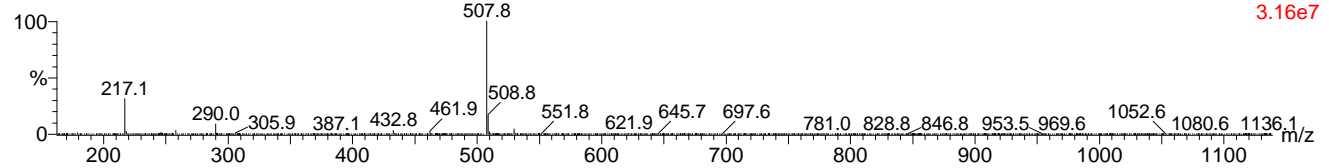
T16-A3 194 (5.192)

1: Scan ES+
3.26e6



T16-A3 186 (4.977)

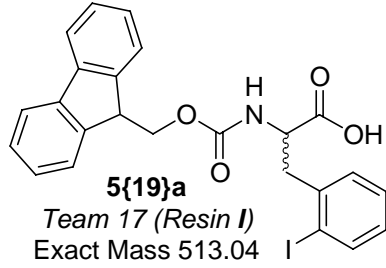
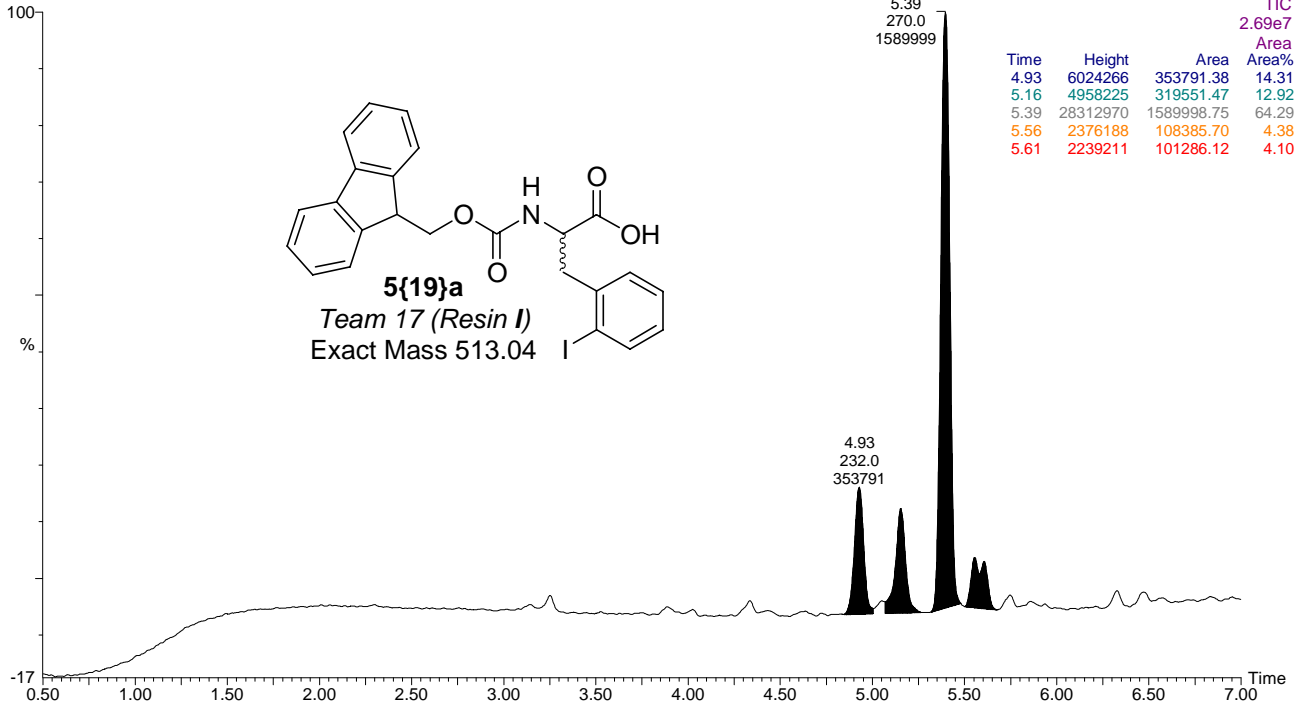
1: Scan ES+
3.16e7



5{19}a

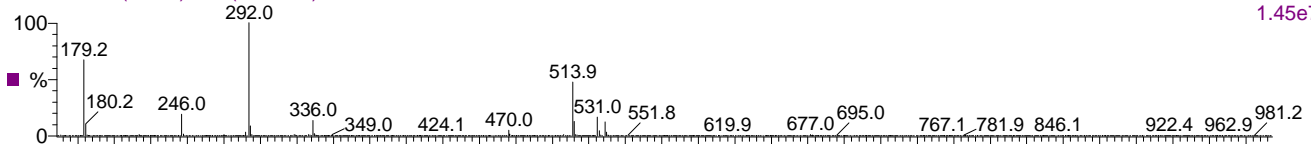
T17-A2 Sm (Mn, 1x1)

3: Diode Array
TIC
2.69e7



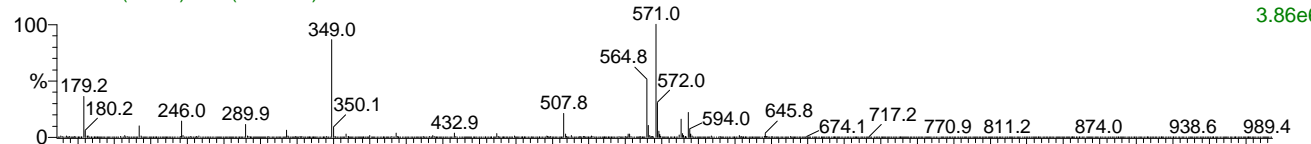
T17-A2 204 (5.460) Cm (203:206)

1: Scan ES+
1.45e7



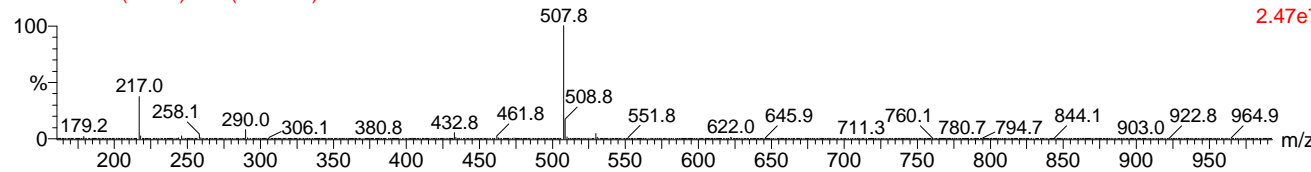
T17-A2 195 (5.219) Cm (193:196)

1: Scan ES+
3.86e6



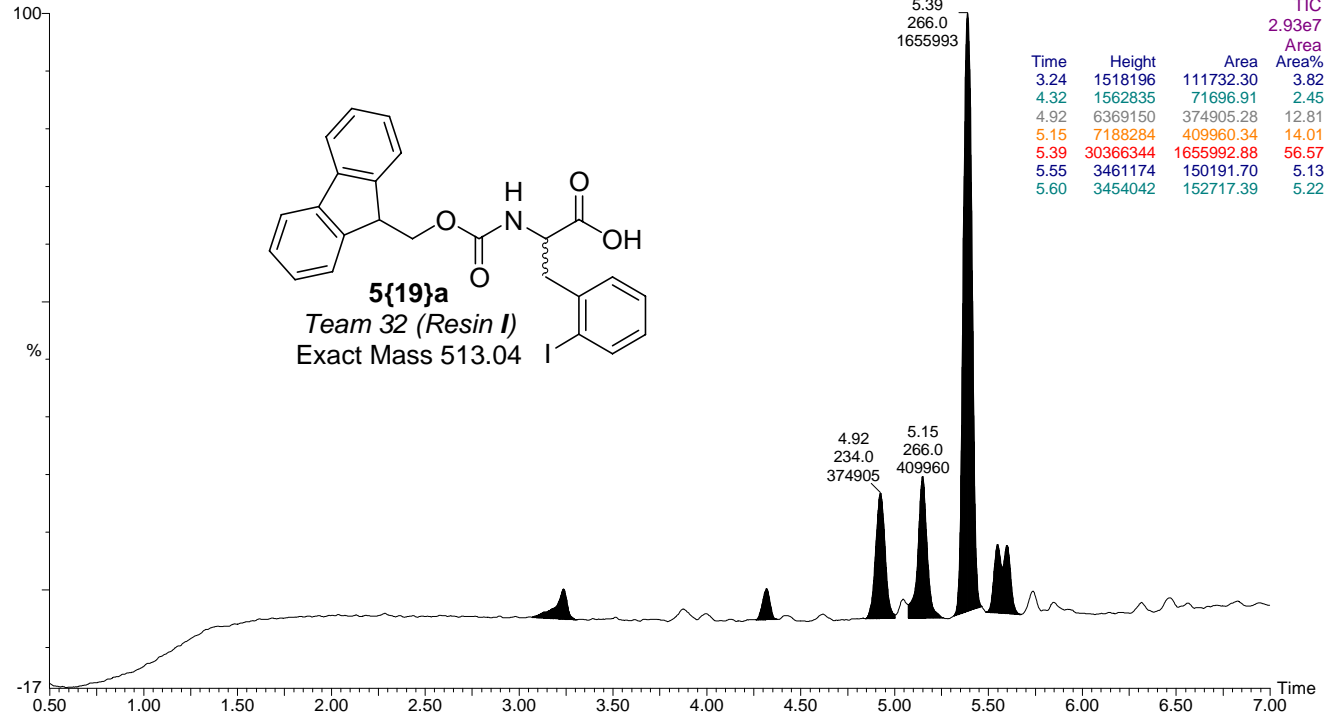
T17-A2 186 (4.977) Cm (185:187)

1: Scan ES+
2.47e7

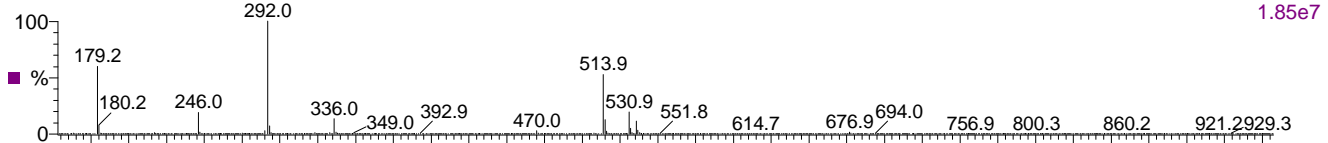


5{19}a

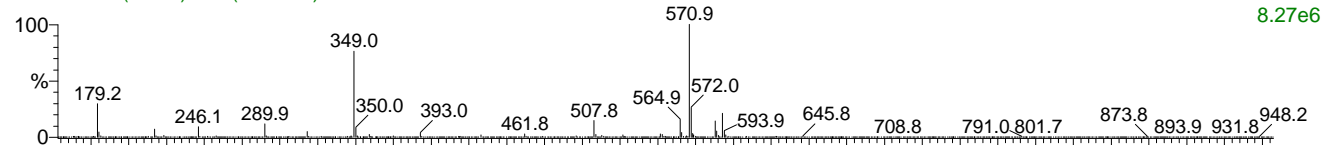
T32-A3 Sm (Mn, 1x1)



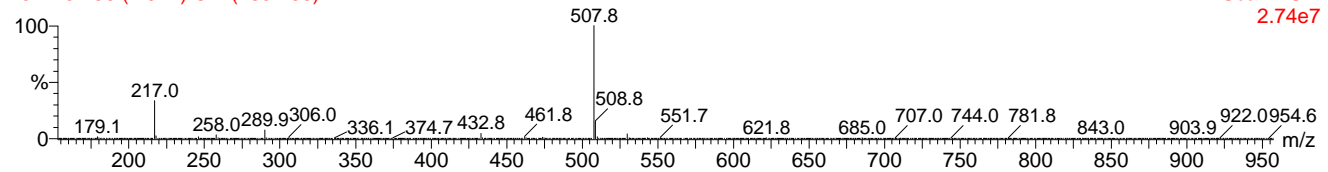
T32-A3 204 (5.460) Cm (203:205)



T32-A3 195 (5.219) Cm (194:196)

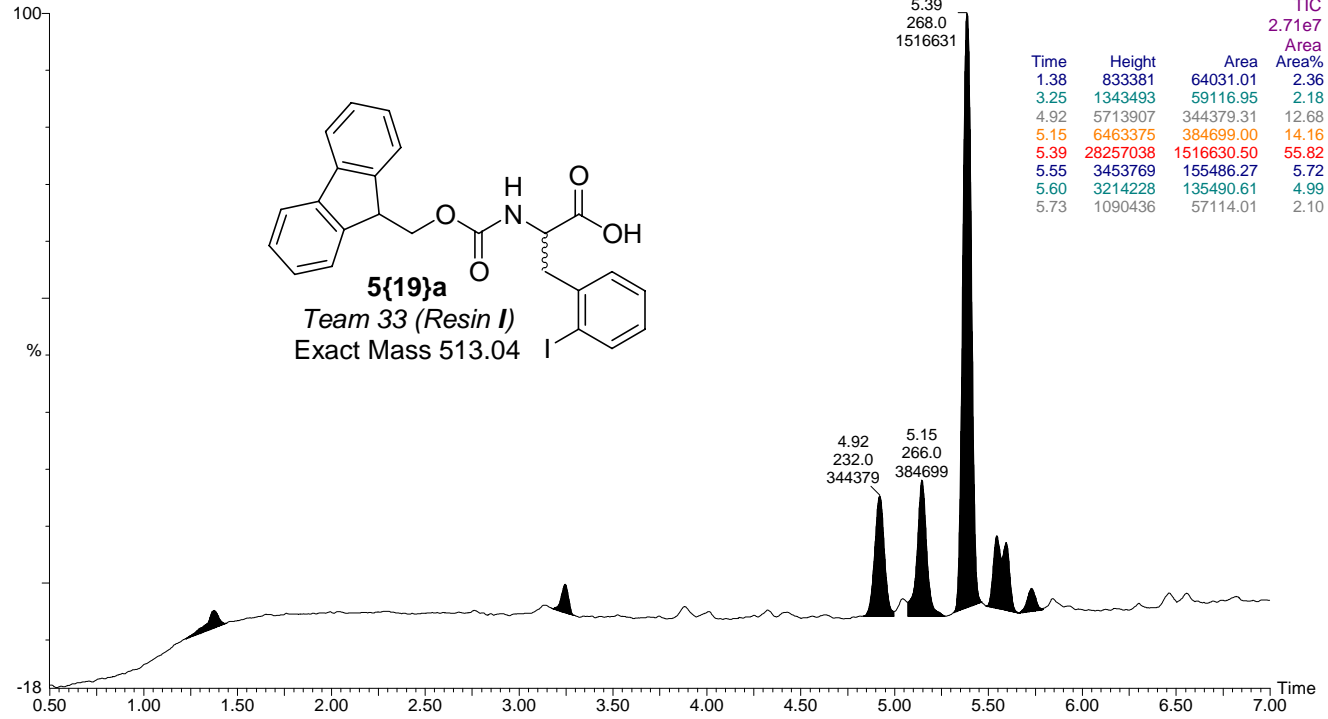


T32-A3 186 (4.977) Cm (185:188)

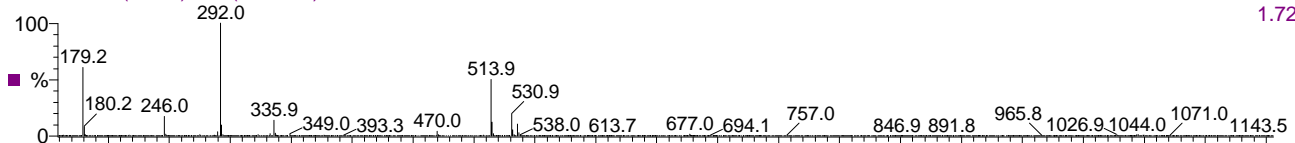


5{19}a

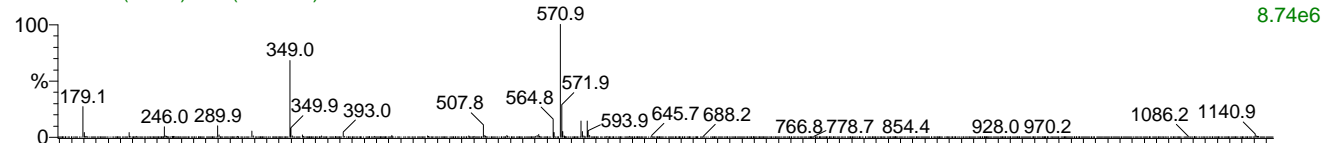
T33-A2 Sm (Mn, 1x1)



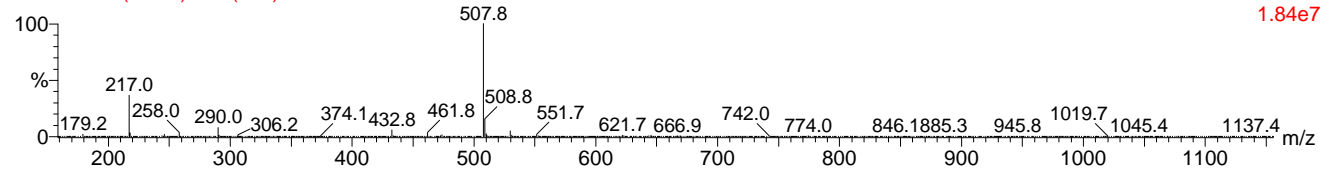
T33-A2 203 (5.434) Cm (203:205)



T33-A2 195 (5.219) Cm (194:195)

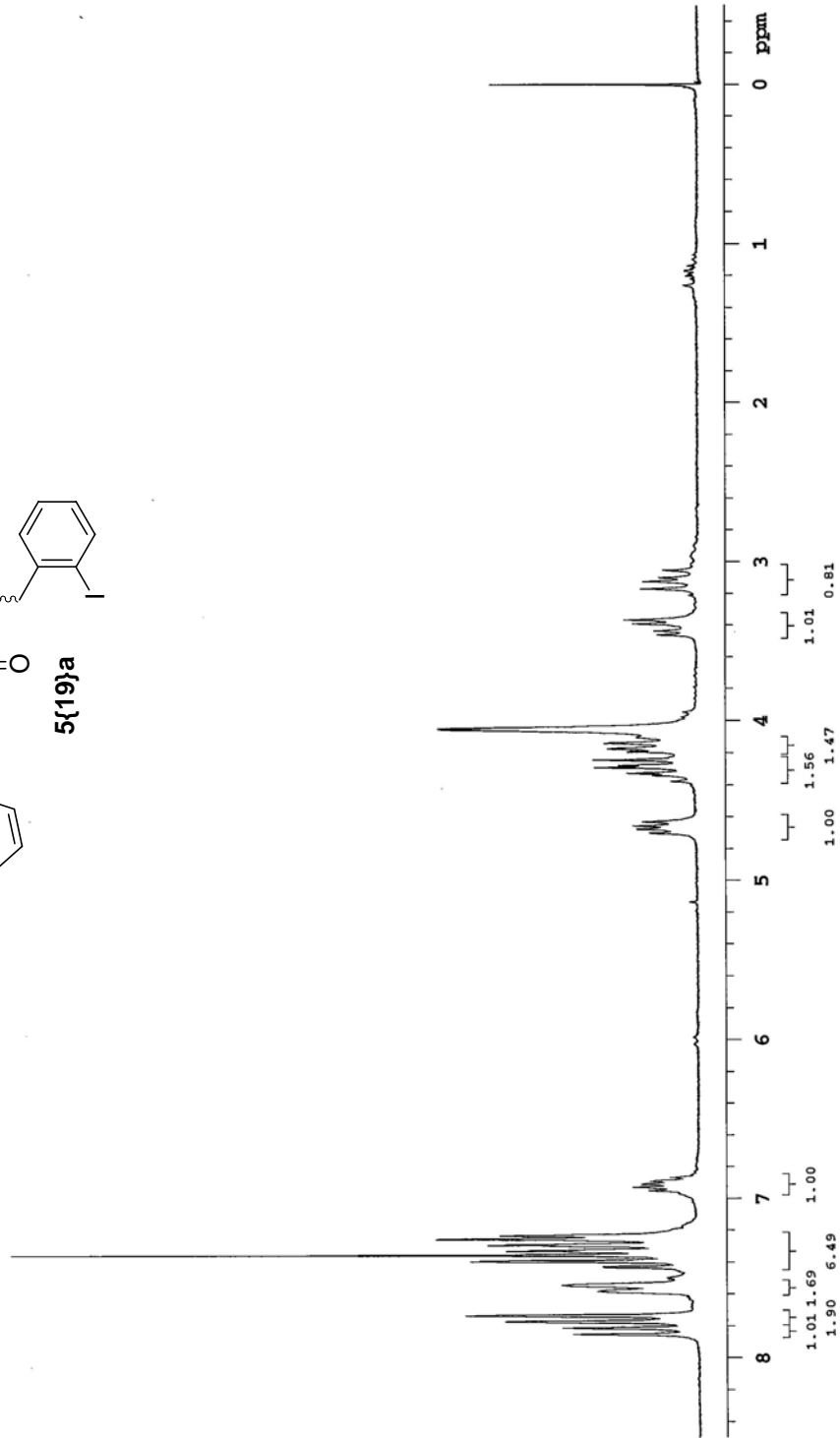
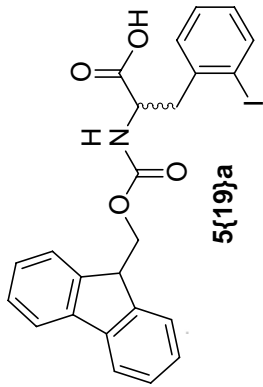


T33-A2 185 (4.951) Cm (185)



BB#34_B3_02_07_07

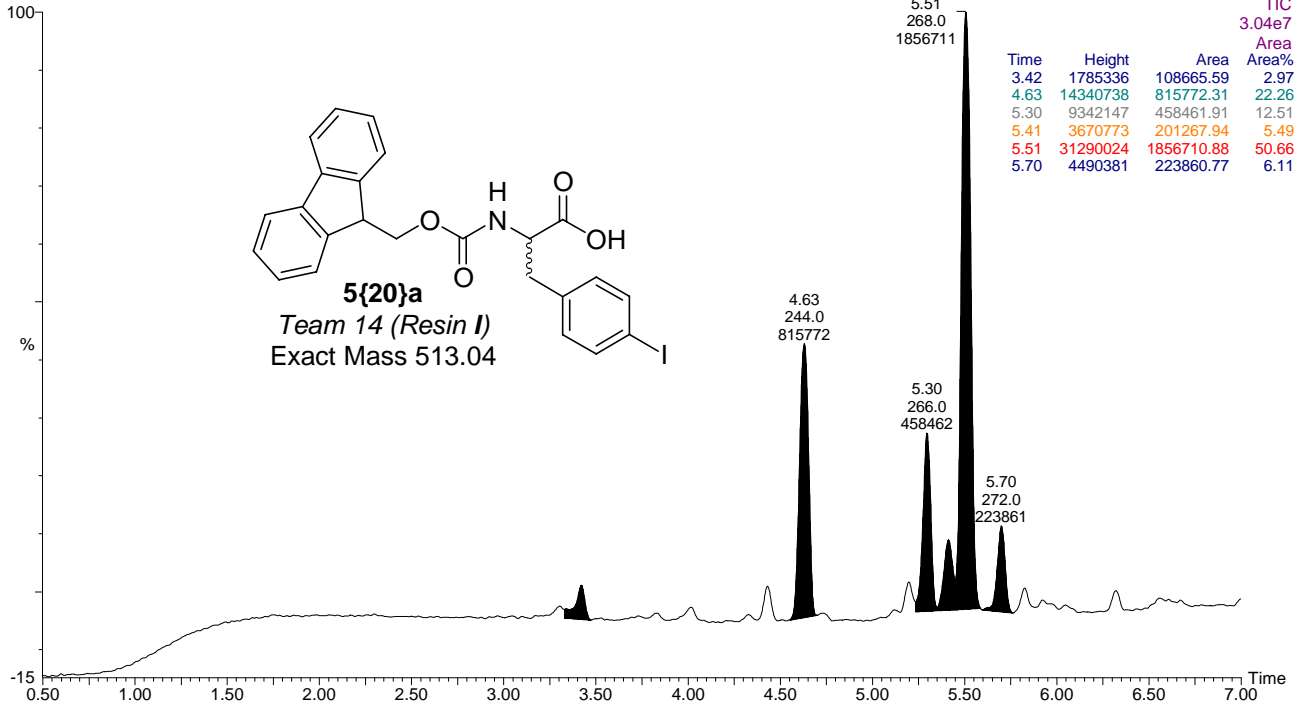
Pulse Sequence: s2pul



5{20}a

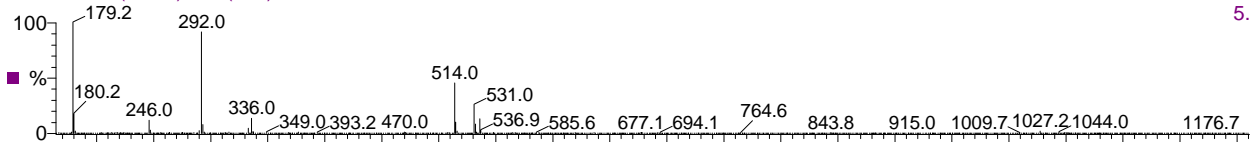
T14-A3 Sm (Mn, 1x1)

3: Diode Array



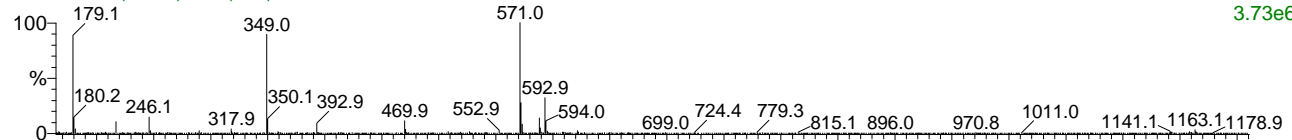
T14-A3 208 (5.568) Cm (208)

1: Scan ES+
5.12e6



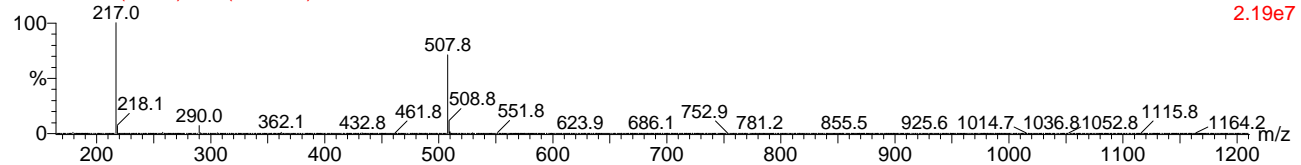
T14-A3 200 (5.353) Cm (200)

1: Scan ES+
3.73e6



T14-A3 175 (4.682) Cm (174:177)

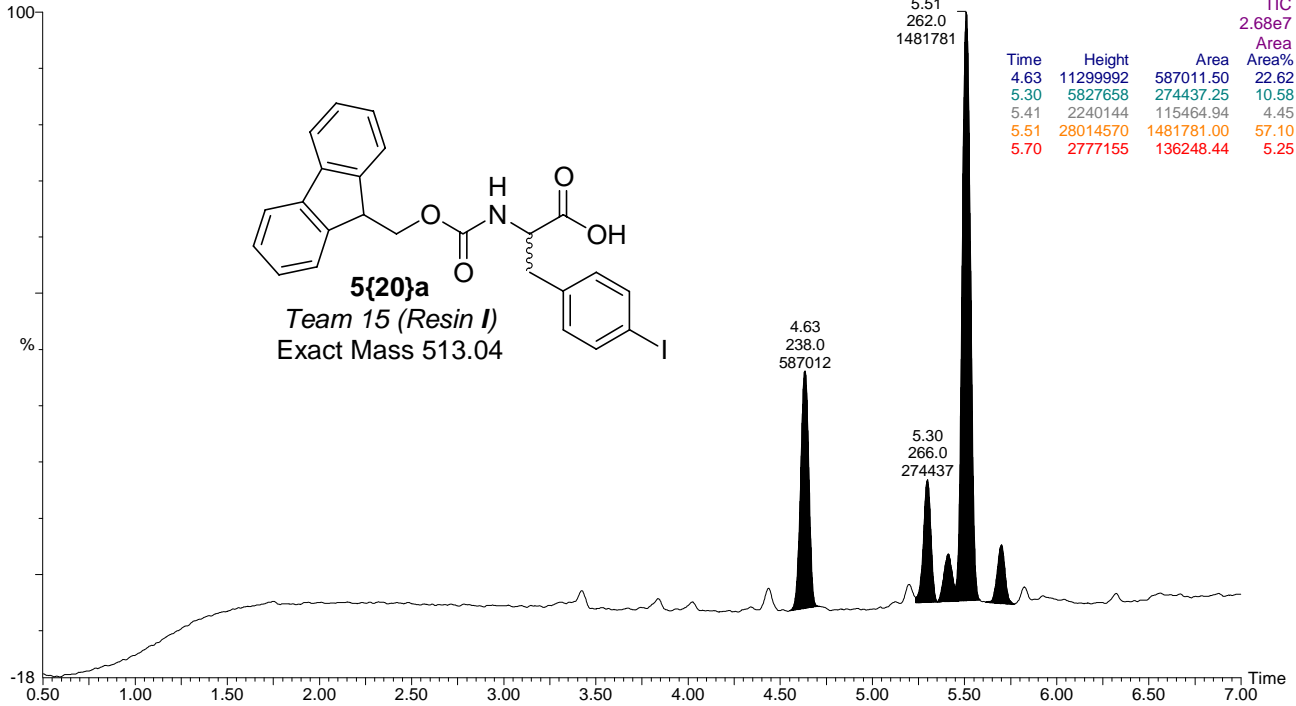
1: Scan ES+
2.19e7



5{20}a

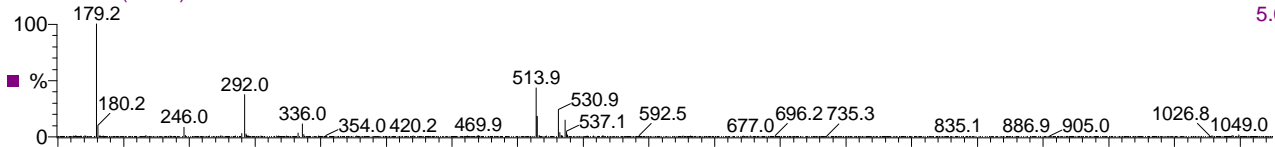
T15-A2 Sm (Mn, 1x1)

3: Diode Array



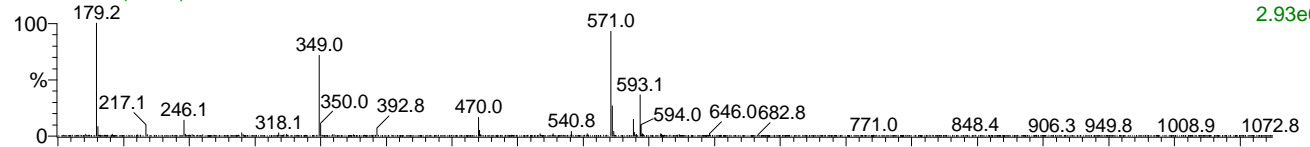
T15-A2 208 (5.568)

1: Scan ES+
5.08e6



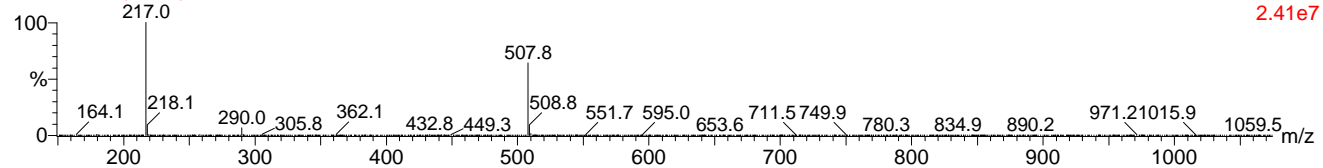
T15-A2 200 (5.353)

1: Scan ES+
2.93e6



T15-A2 175 (4.682)

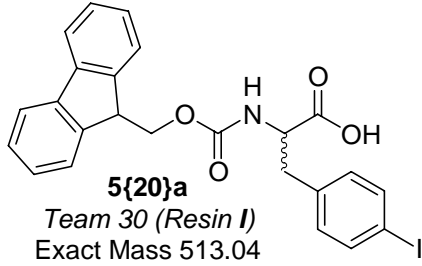
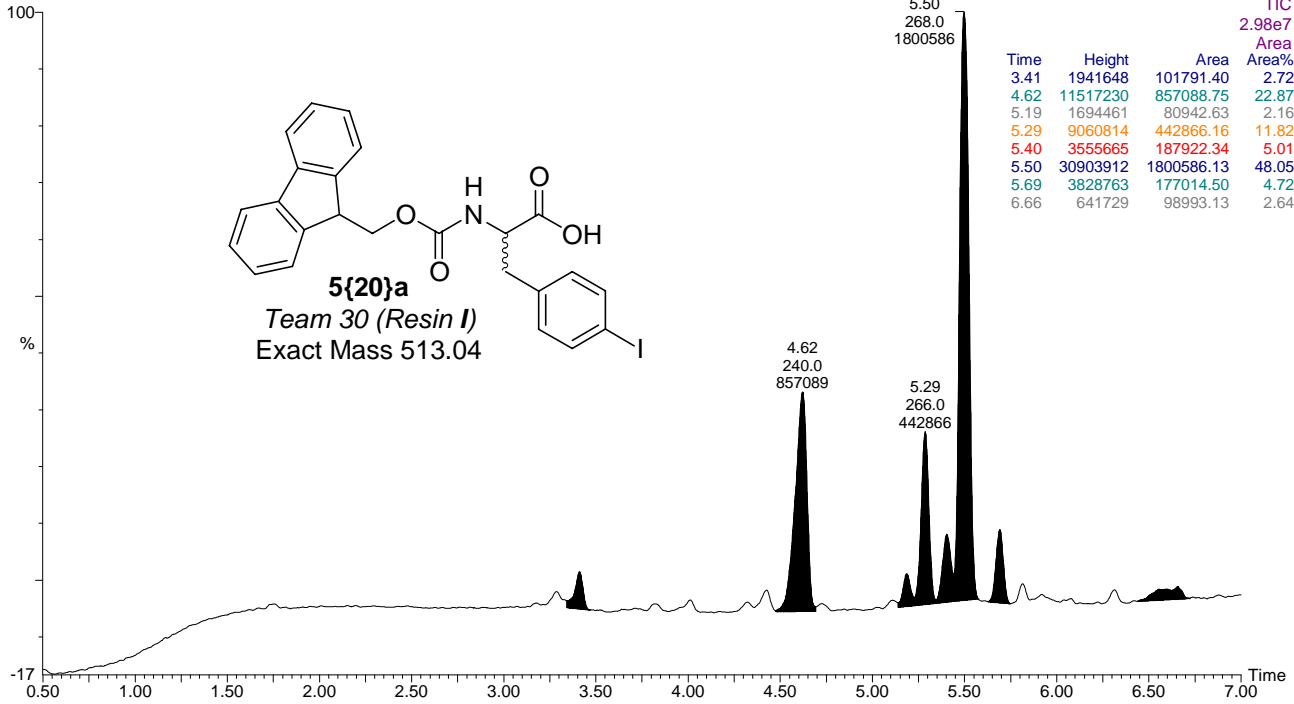
1: Scan ES+
2.41e7



5{20}a

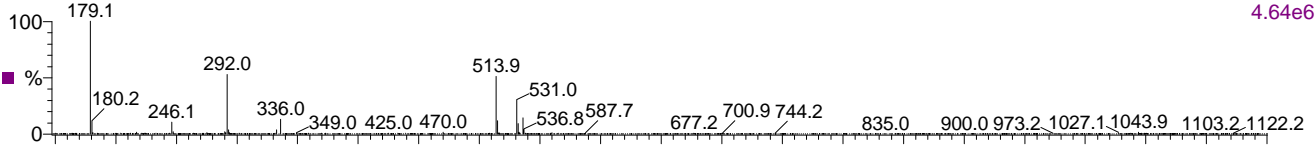
T30-A3 Sm (Mn, 1x1)

3: Diode Array
TIC
2.98e7



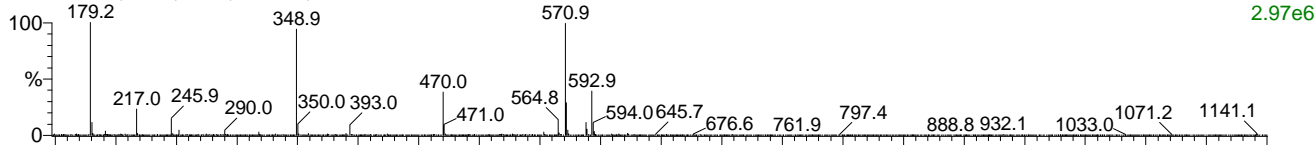
T30-A3 207 (5.541)

1: Scan ES+
4.64e6



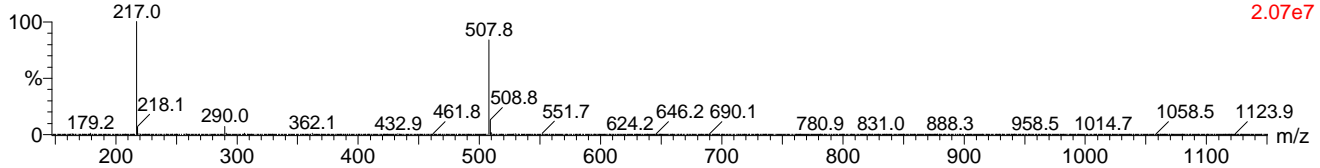
T30-A3 200 (5.353) Cm (199:201)

1: Scan ES+
2.97e6



T30-A3 175 (4.682) Cm (173:175)

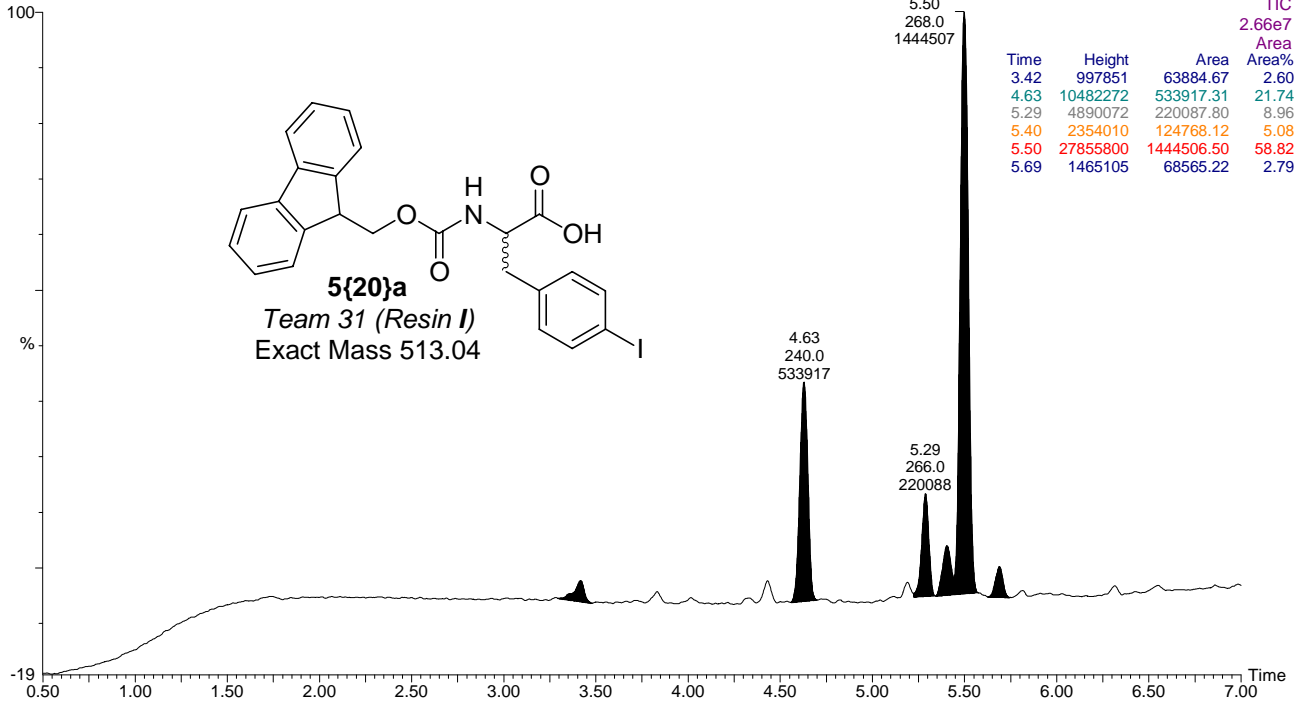
1: Scan ES+
2.07e7



5{20}a

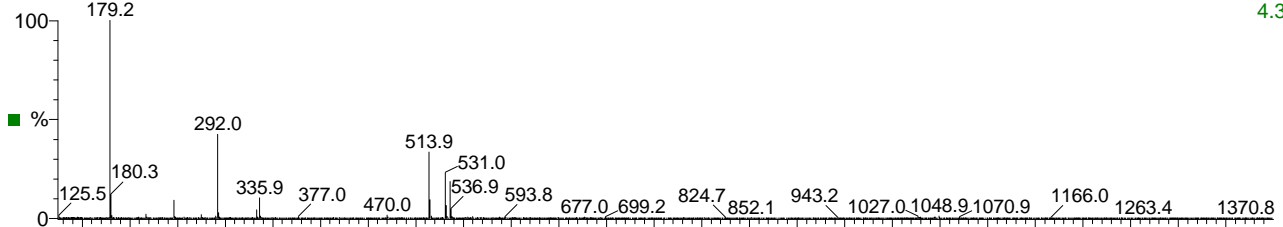
T31-A2 Sm (Mn, 1x1)

3: Diode Array
TIC
2.66e7



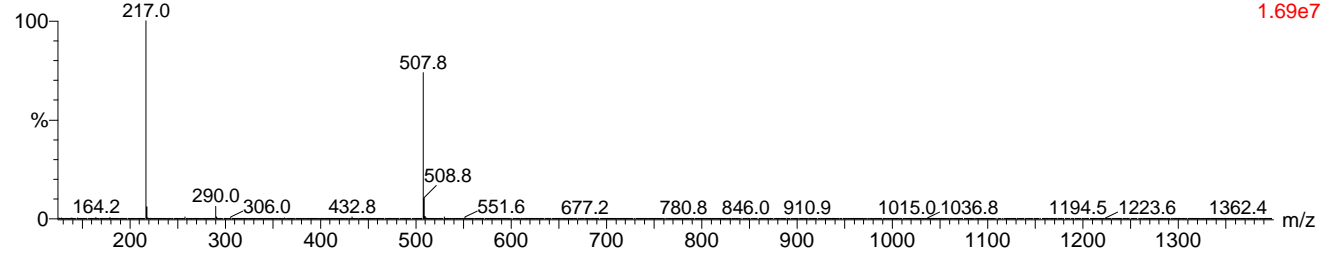
T31-A2 208 (5.568) Cm (207:209)

1: Scan ES+
4.31e6



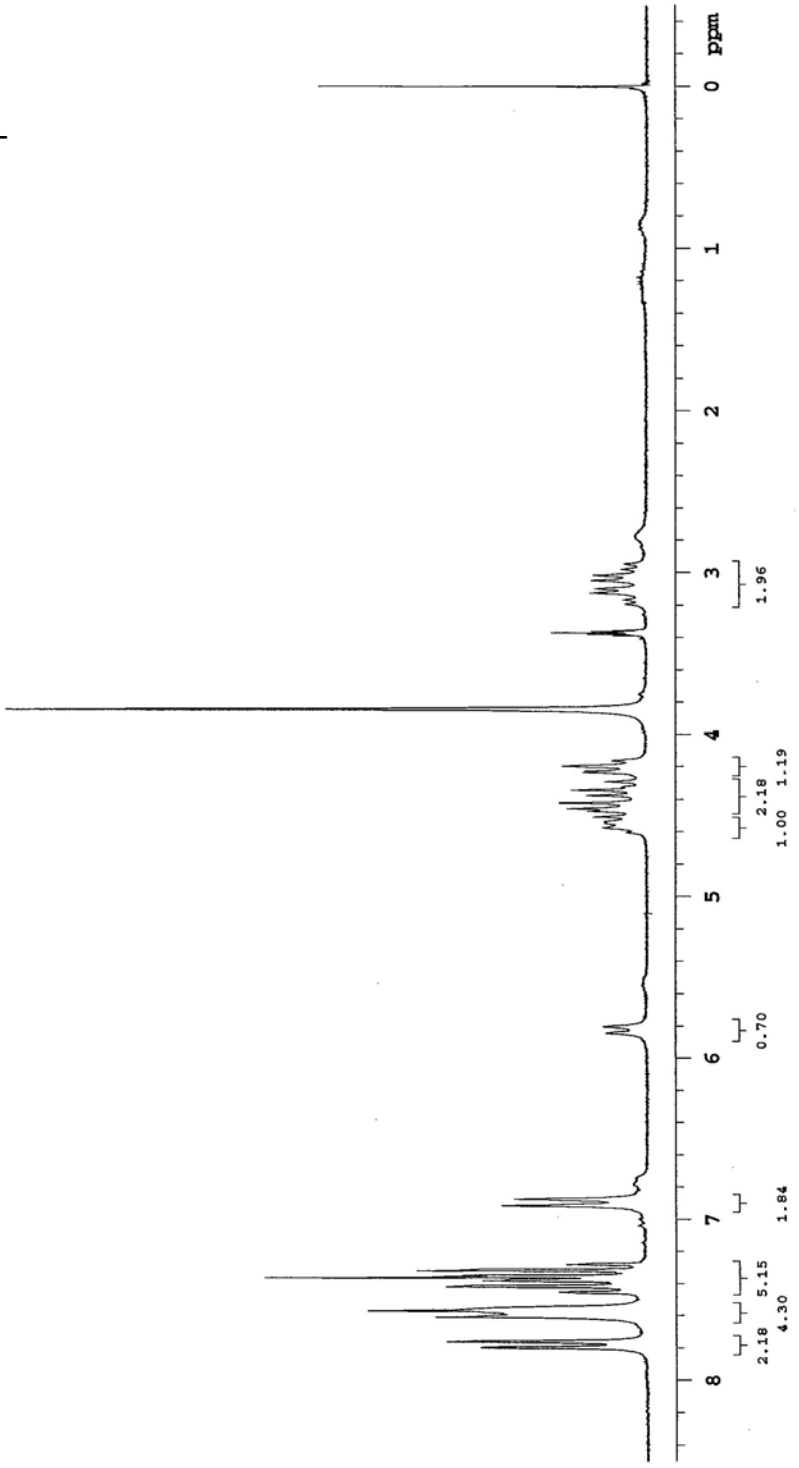
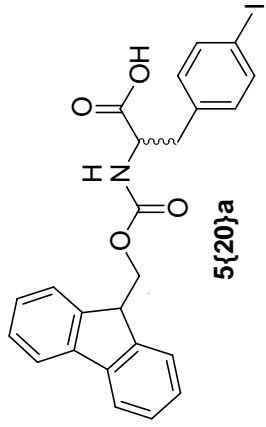
T31-A2 175 (4.682) Cm (174:177)

1: Scan ES+
1.69e7



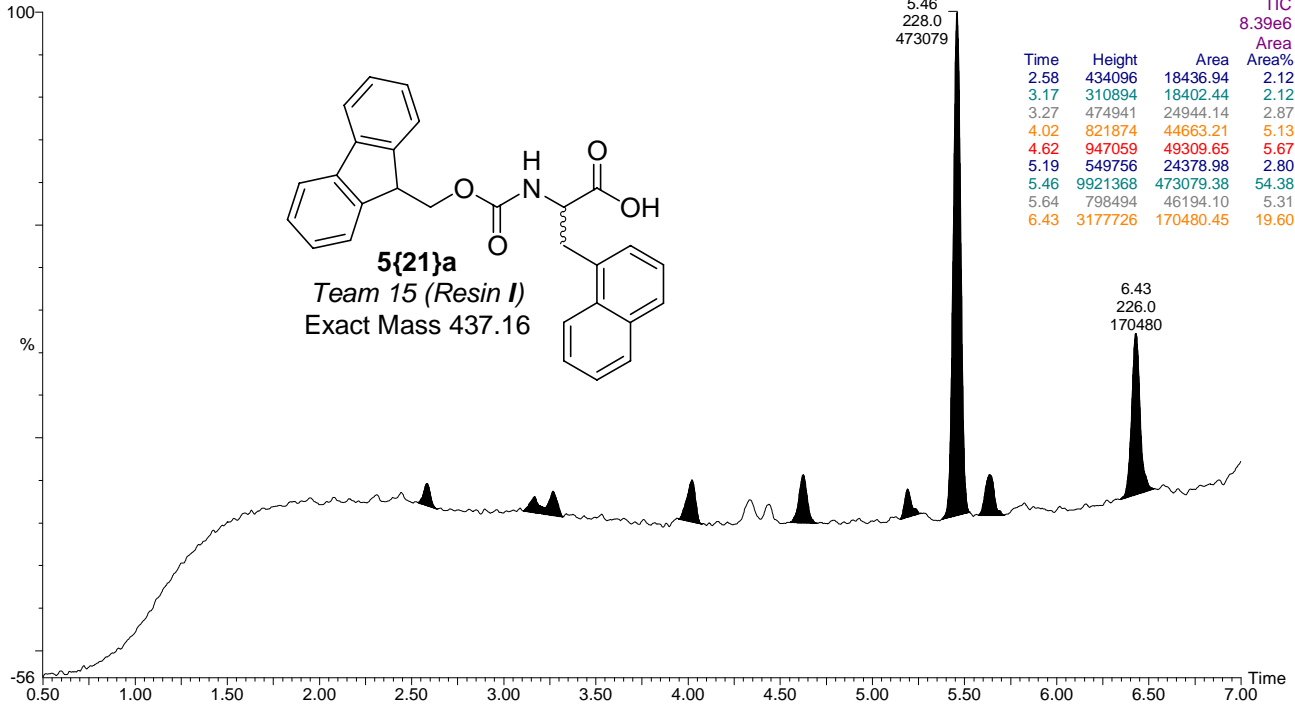
1H_BB#34_B2_CD3ODinCDCl3_02_07

Pulse Sequence: s2pul

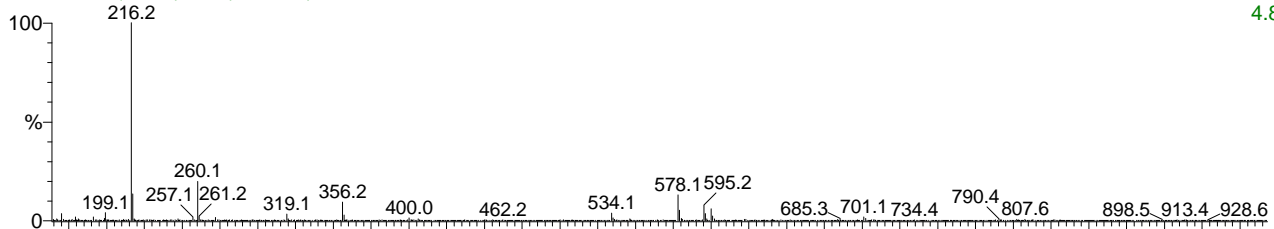


5{21}a

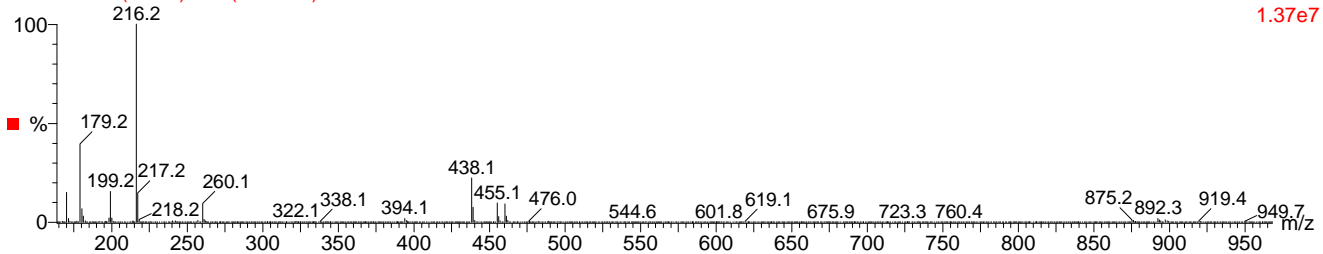
T15-A3 Sm (Mn, 1x1)



T15-A3 242 (6.480) Cm (241:244)

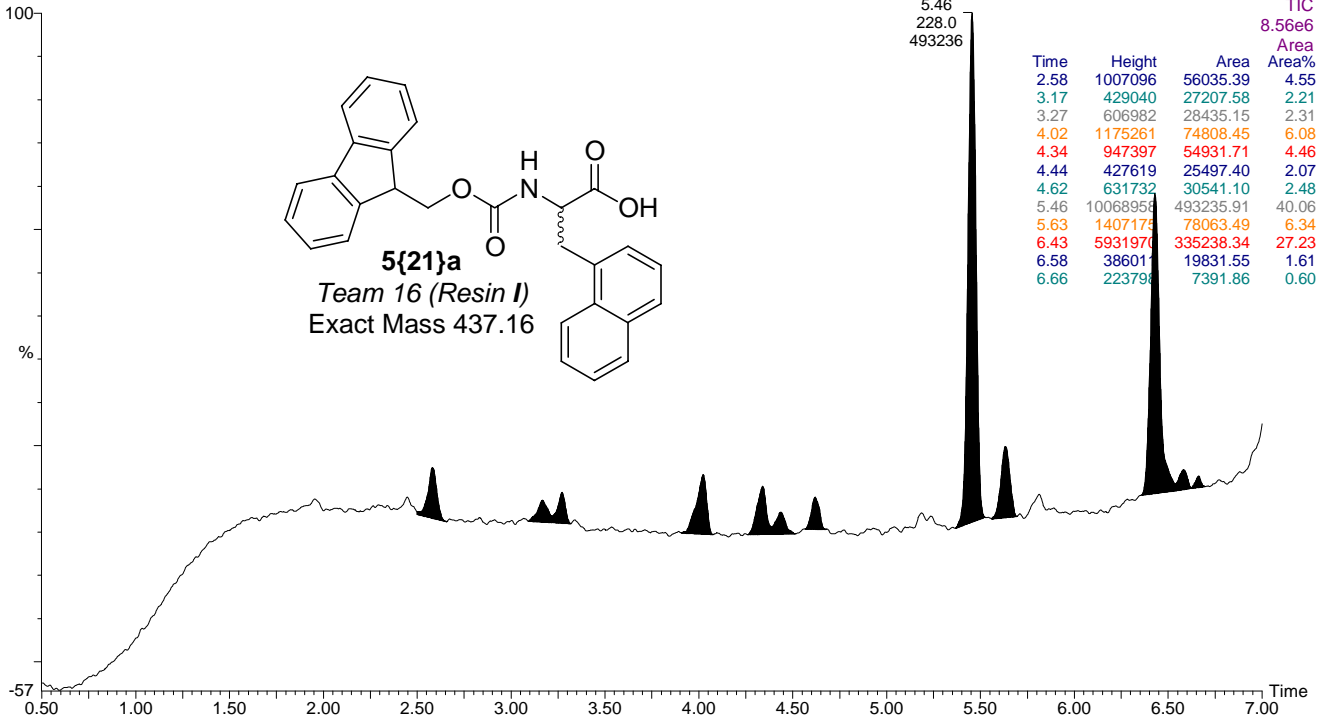


T15-A3 206 (5.514) Cm (205:207)

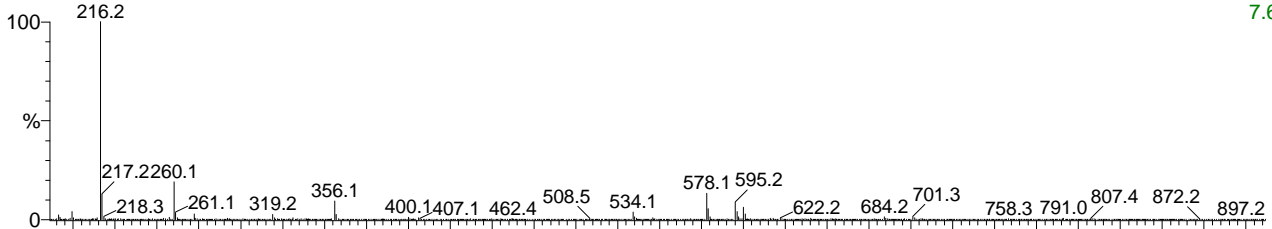


5{21}a

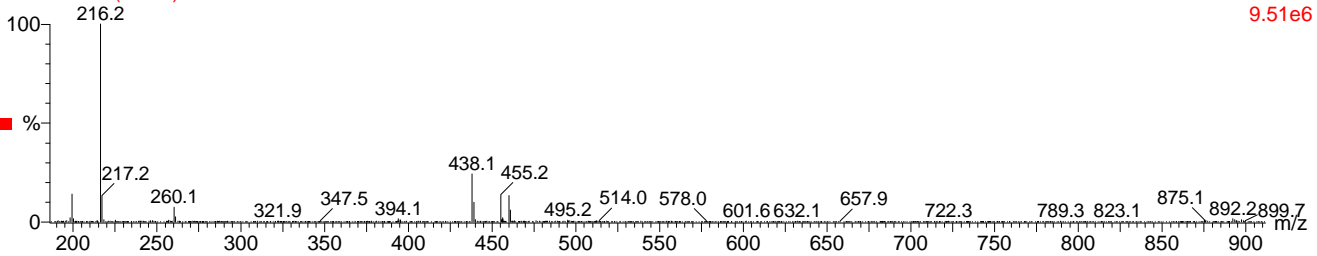
T16-A2 Sm (Mn, 1x1)



T16-A2 242 (6.480) Cm (241:243)



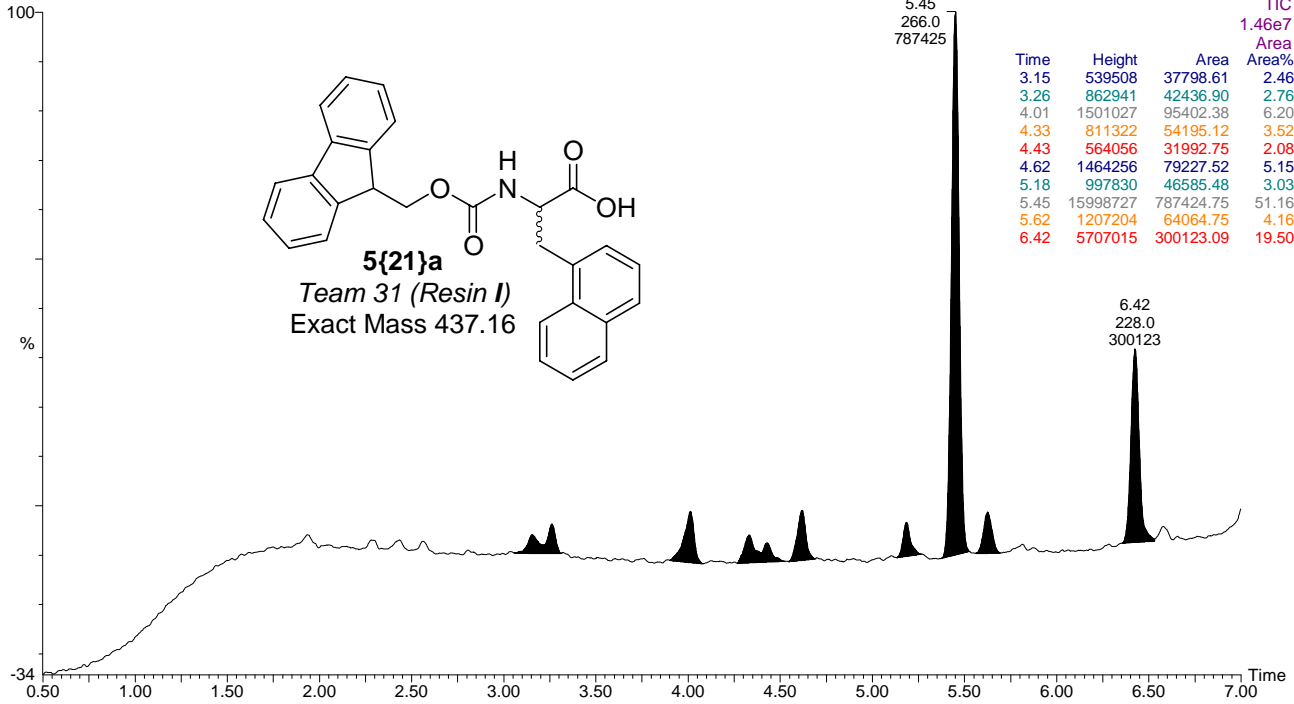
T16-A2 205 (5.487)



5{21}a

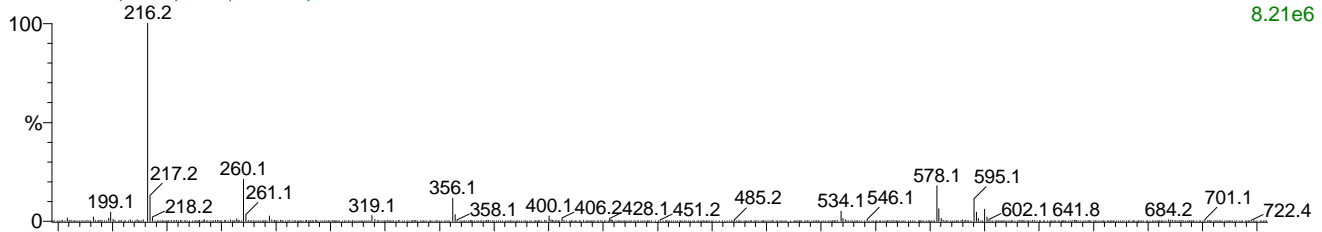
T31-A3 Sm (Mn, 1x1)

3: Diode Array
TIC
1.46e7



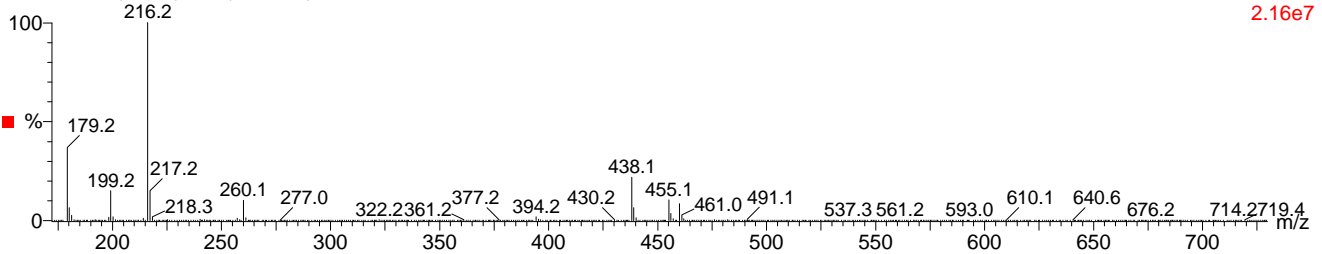
T31-A3 242 (6.480) Cm (241:243)

1: Scan ES+
8.21e6



T31-A3 206 (5.514) Cm (205:207)

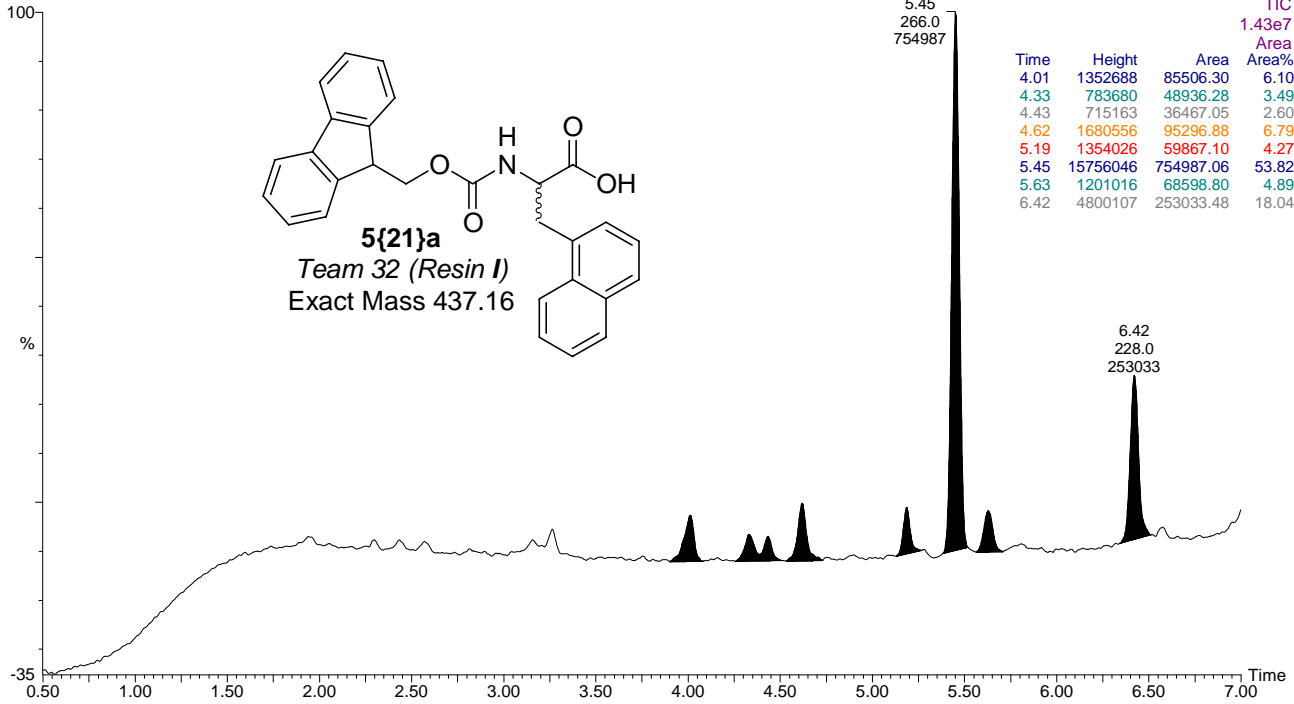
1: Scan ES+
2.16e7



5{21}a

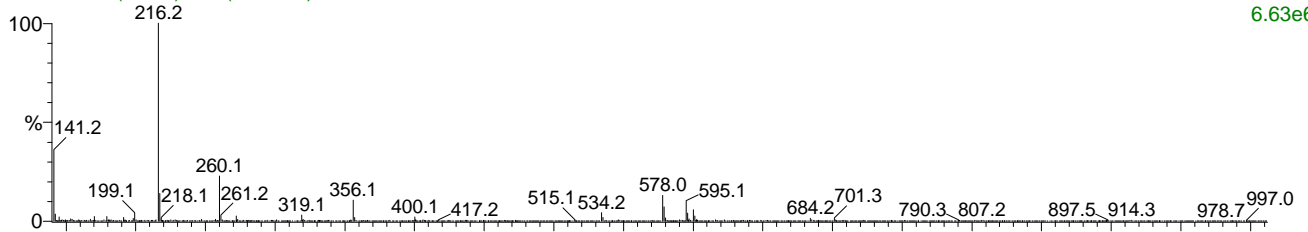
T32-A2 Sm (Mn, 1x1)

3: Diode Array
TIC
1.43e7



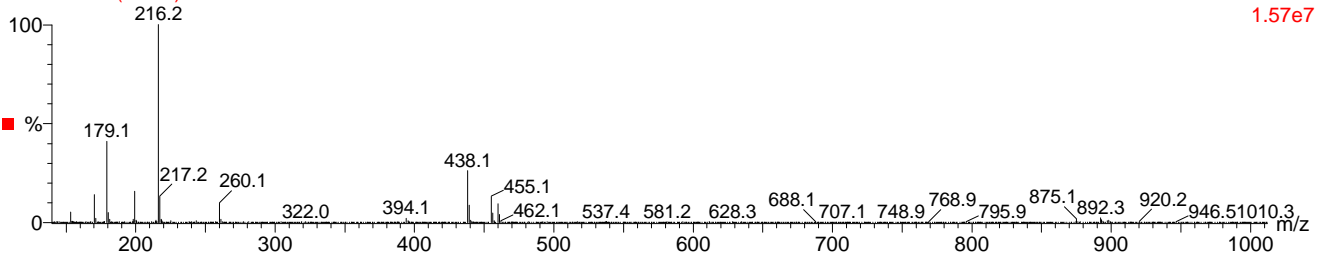
T32-A2 242 (6.480) Cm (241:244)

1: Scan ES+
6.63e6



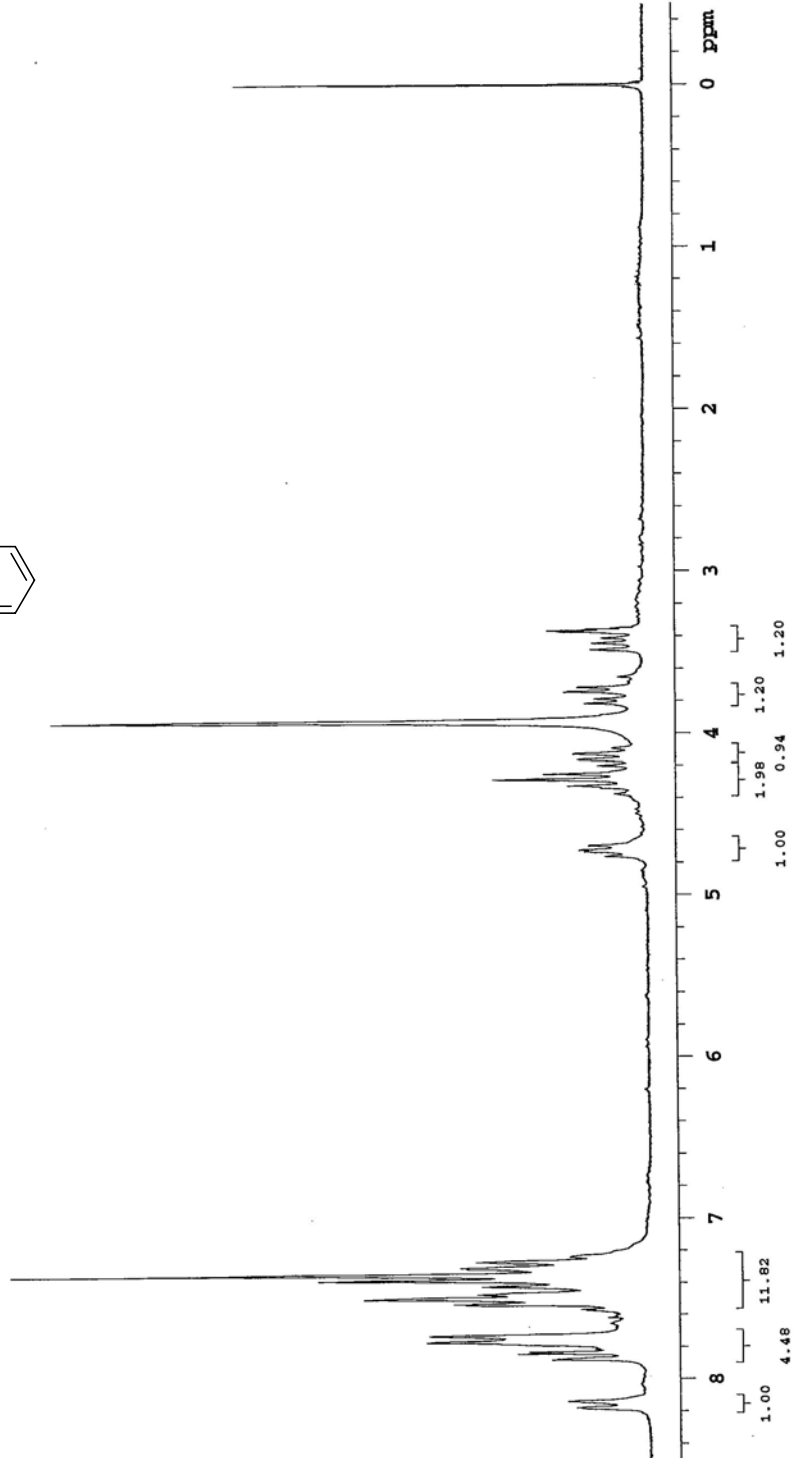
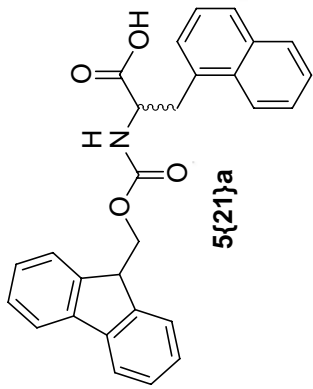
T32-A2 205 (5.487)

1: Scan ES+
1.57e7



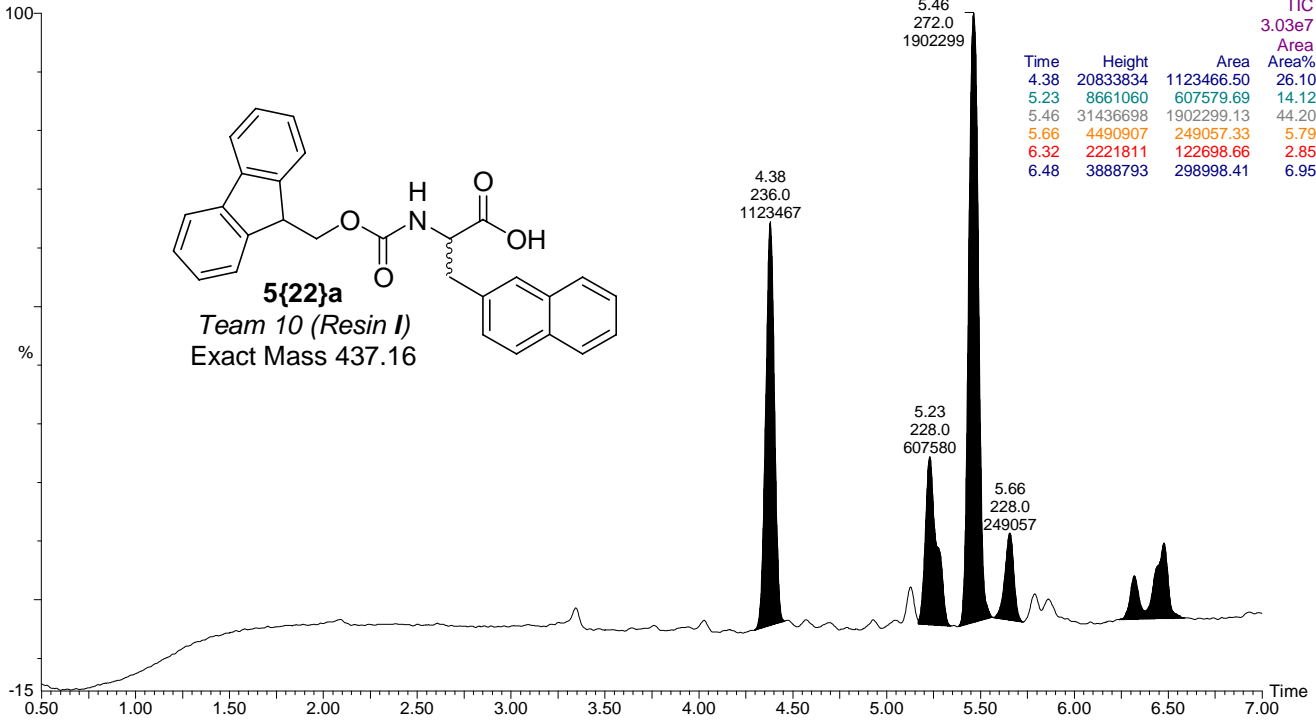
1H_ER#41_A1_CD3ODinCDCl3_03_07

Pulse Sequence: s2pul



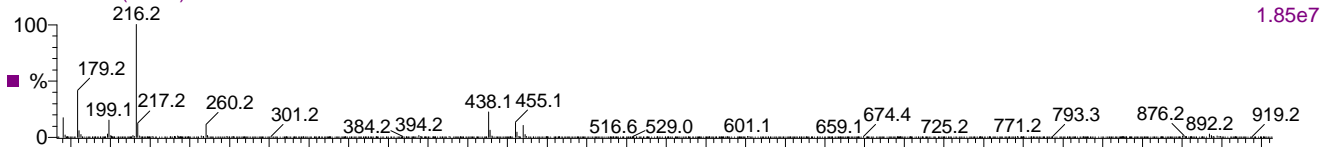
5{22}a

T10-A2 Sm (Mn, 1x1)

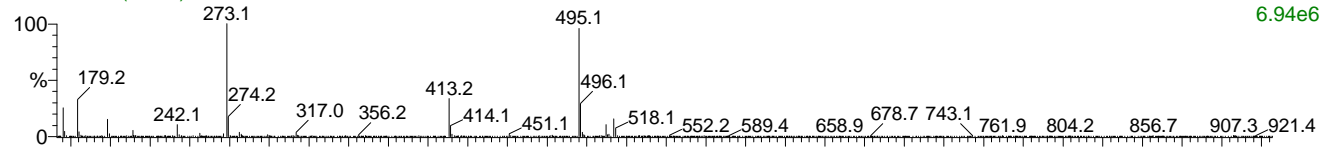


3: Diode Array
TIC
3.03e7

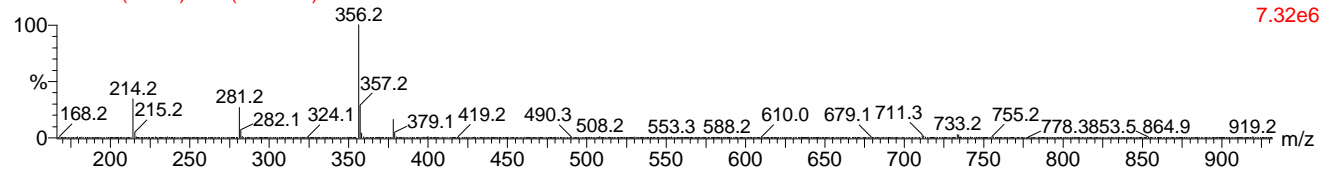
T10-A2 205 (5.487)



T10-A2 198 (5.299)



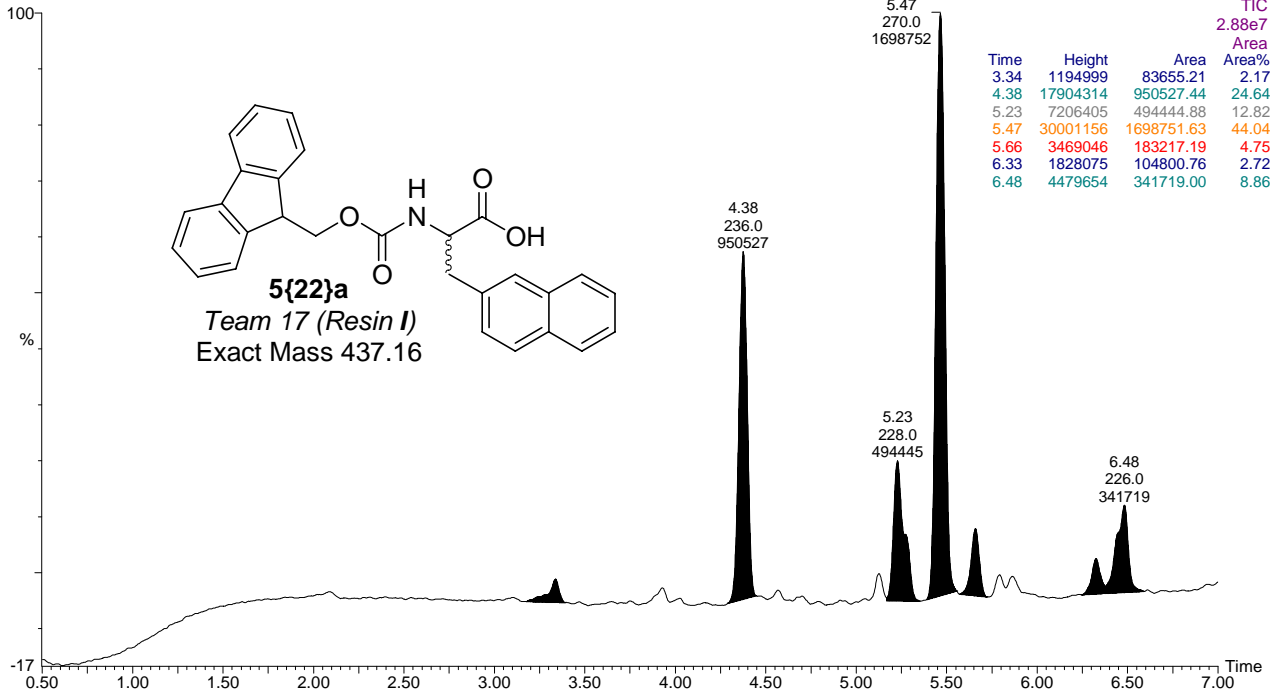
T10-A2 166 (4.441) Cm (165:170)



5{22}a

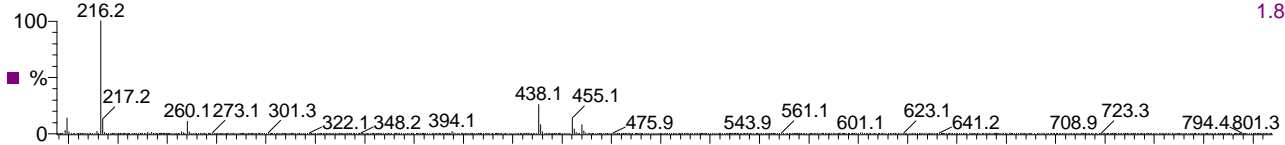
T17-A3 Sm (Mn, 1x1)

3: Diode Array



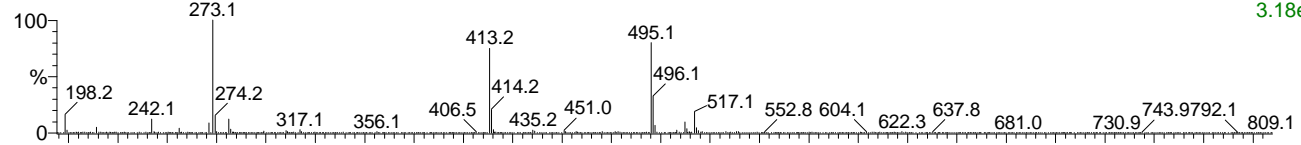
T17-A3 206 (5.514) Cm (205:208)

1: Scan ES+
1.85e7



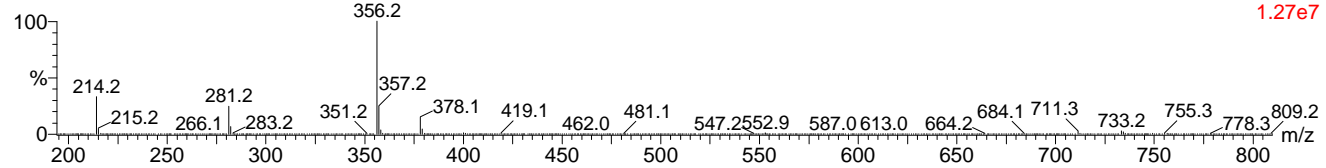
T17-A3 198 (5.299) Cm (198:200)

1: Scan ES+
3.18e6



T17-A3 166 (4.441) Cm (165:167)

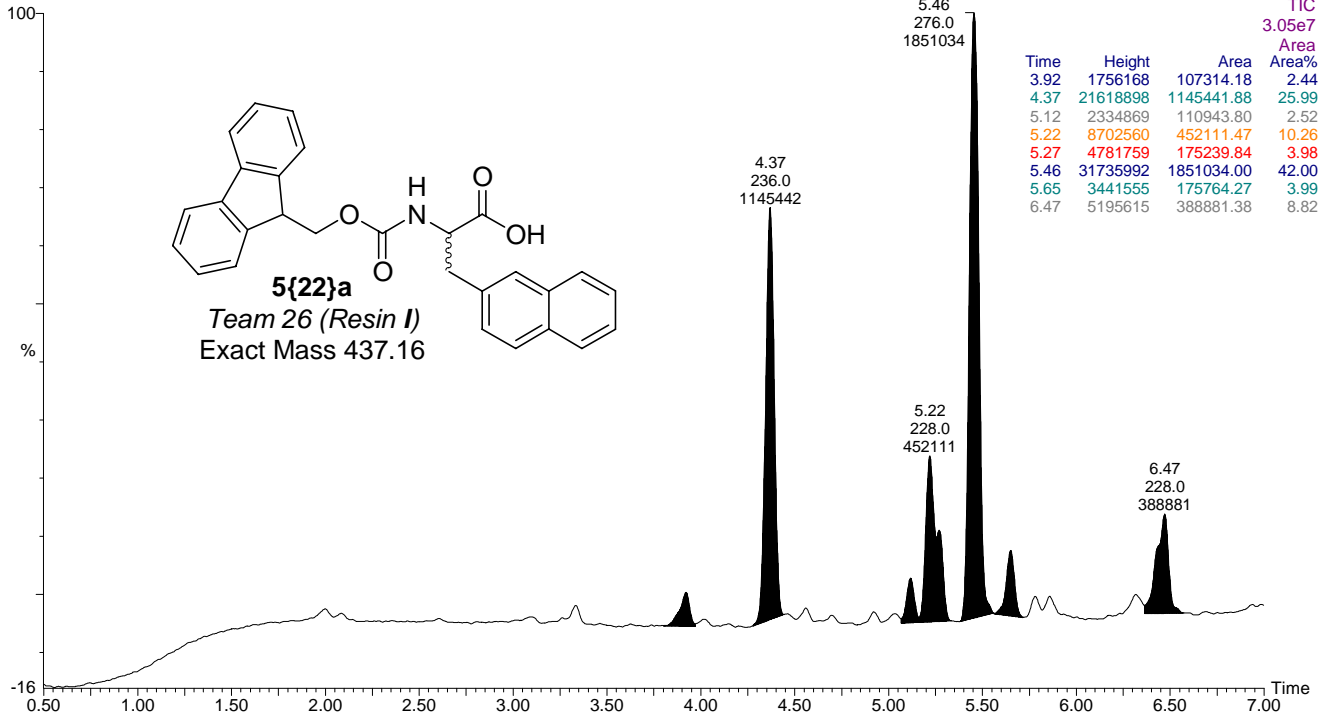
1: Scan ES+
1.27e7



5{22}a

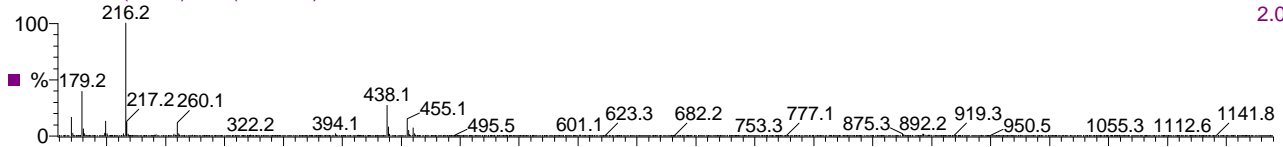
T26-A2 Sm (Mn, 1x1)

3: Diode Array
TIC



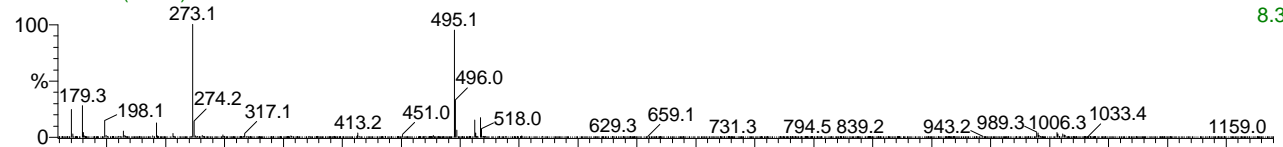
T26-A2 206 (5.514) Cm (205:208)

1: Scan ES+
2.03e7



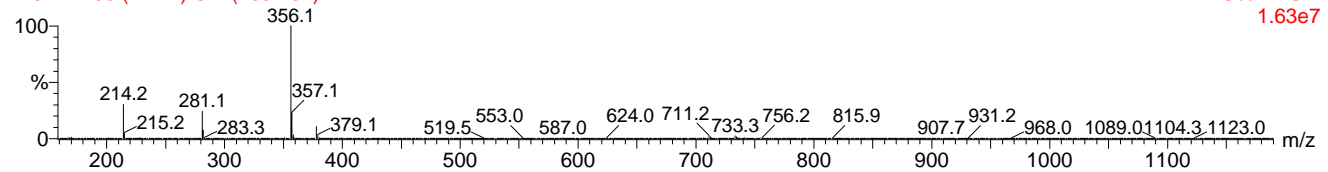
T26-A2 197 (5.273)

1: Scan ES+
8.32e6



T26-A2 166 (4.441) Cm (165:167)

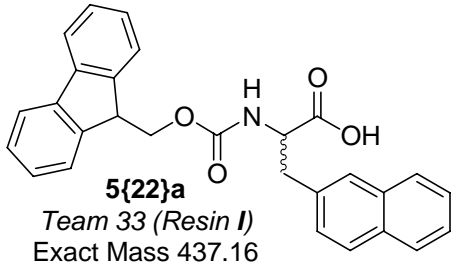
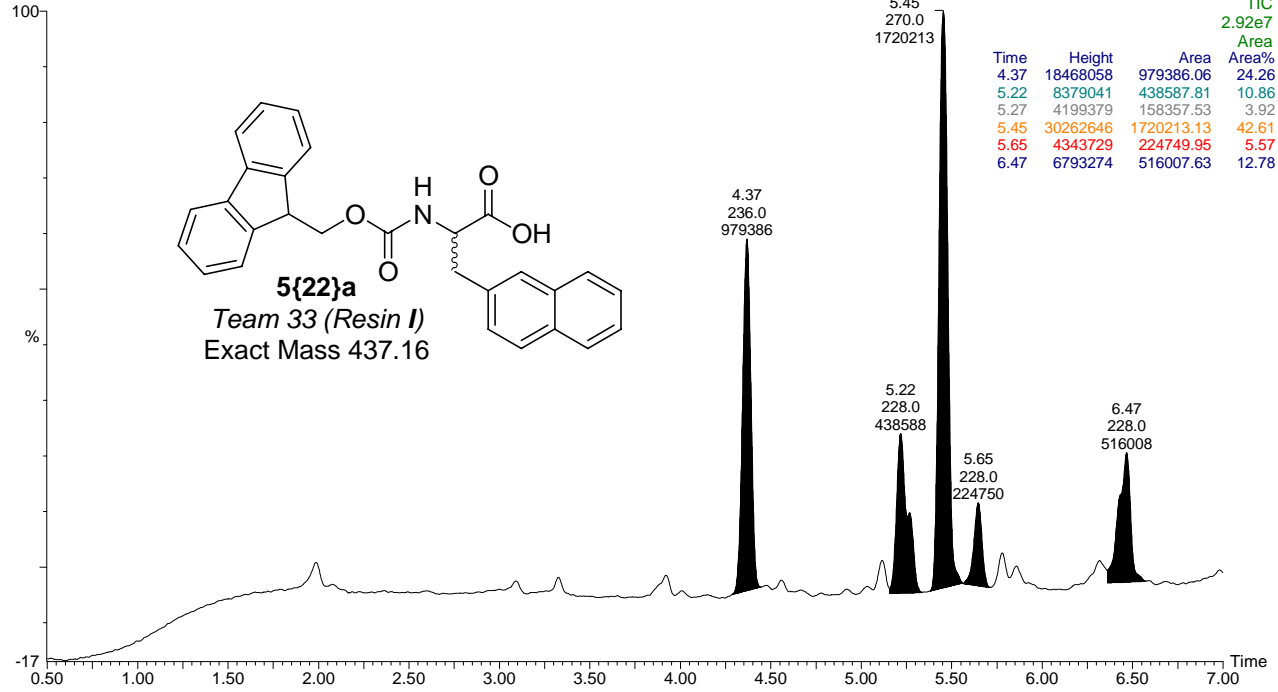
1: Scan ES+
1.63e7



5{22}a

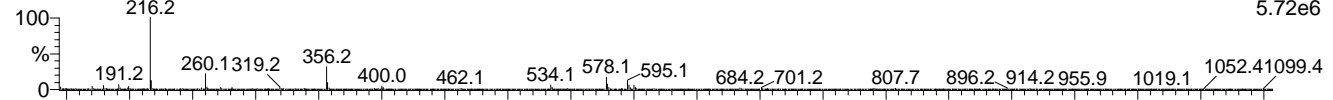
T33-A3 Sm (Mn, 1x1)

3: Diode Array



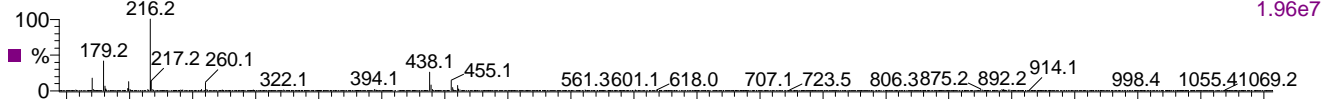
T33-A3 244 (6.534) Cm (242:246)

1: Scan ES+
5.72e6



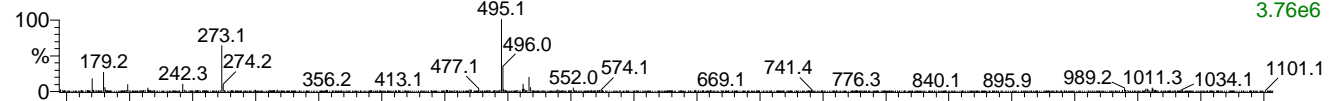
T33-A3 206 (5.514) Cm (205:208)

1: Scan ES+
1.96e7



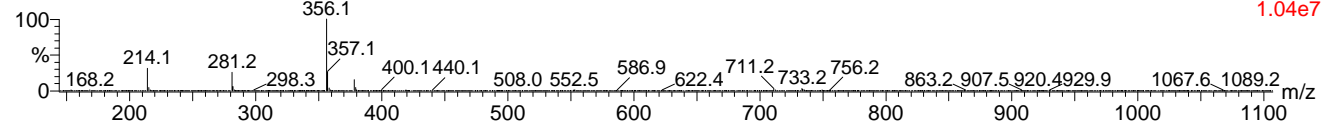
T33-A3 196 (5.246)

1: Scan ES+
3.76e6



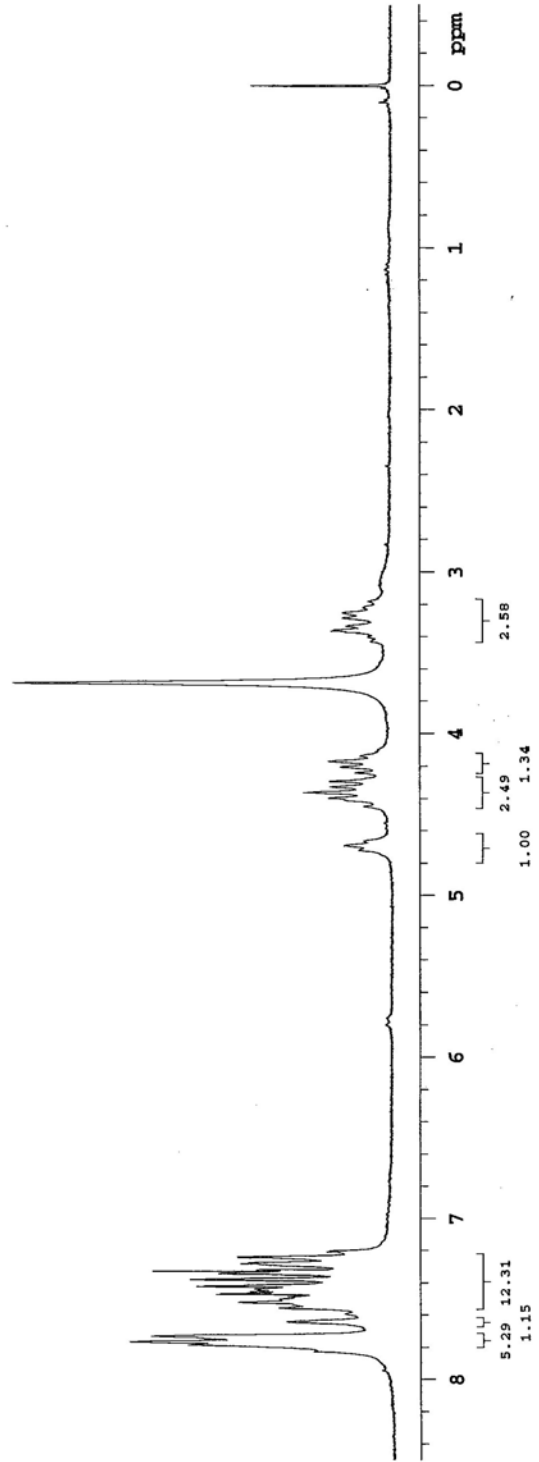
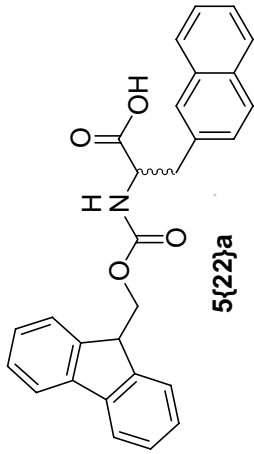
T33-A3 166 (4.441) Cm (164:167)

1: Scan ES+
1.04e7



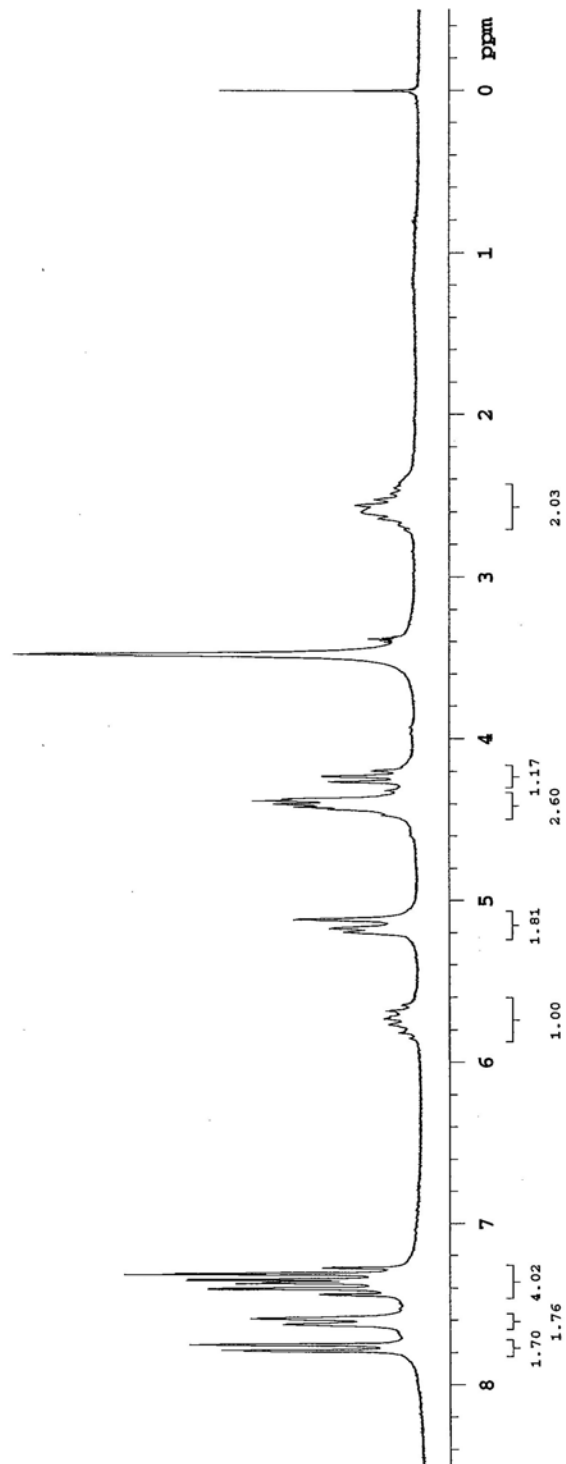
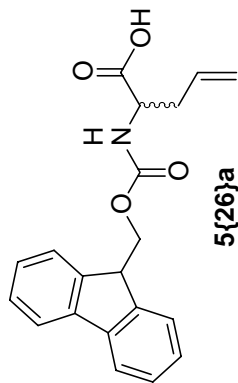
1H_BB#27_B2_CD3ODinCDCl3_02_07

Pulse Sequence: s2pul



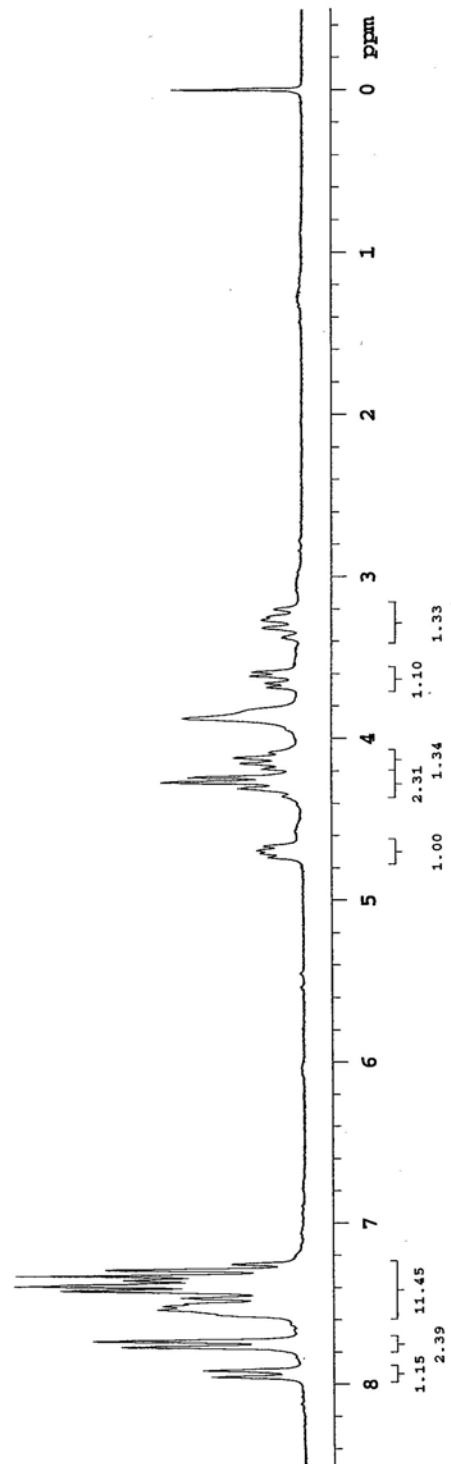
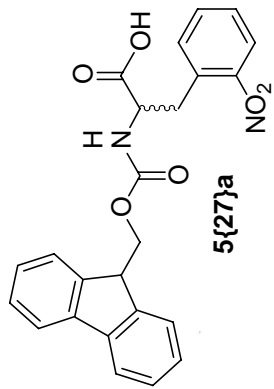
1H_BB#41_A2_CD3ODinCDCl3_03_07

Pulse Sequence: s2pul



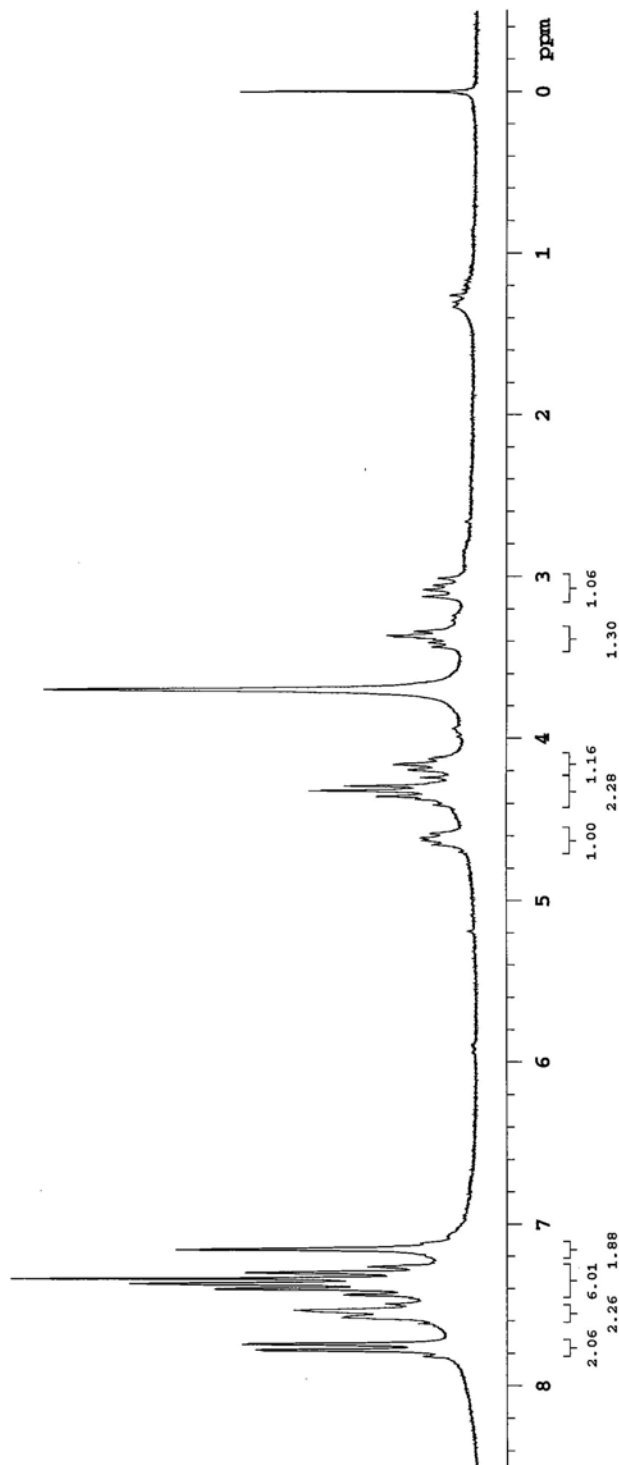
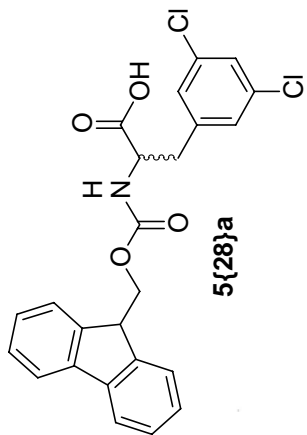
1H_RR#40_B2_CDCl3withCD3OD_03_09_07

Pulse Sequence: s2pul



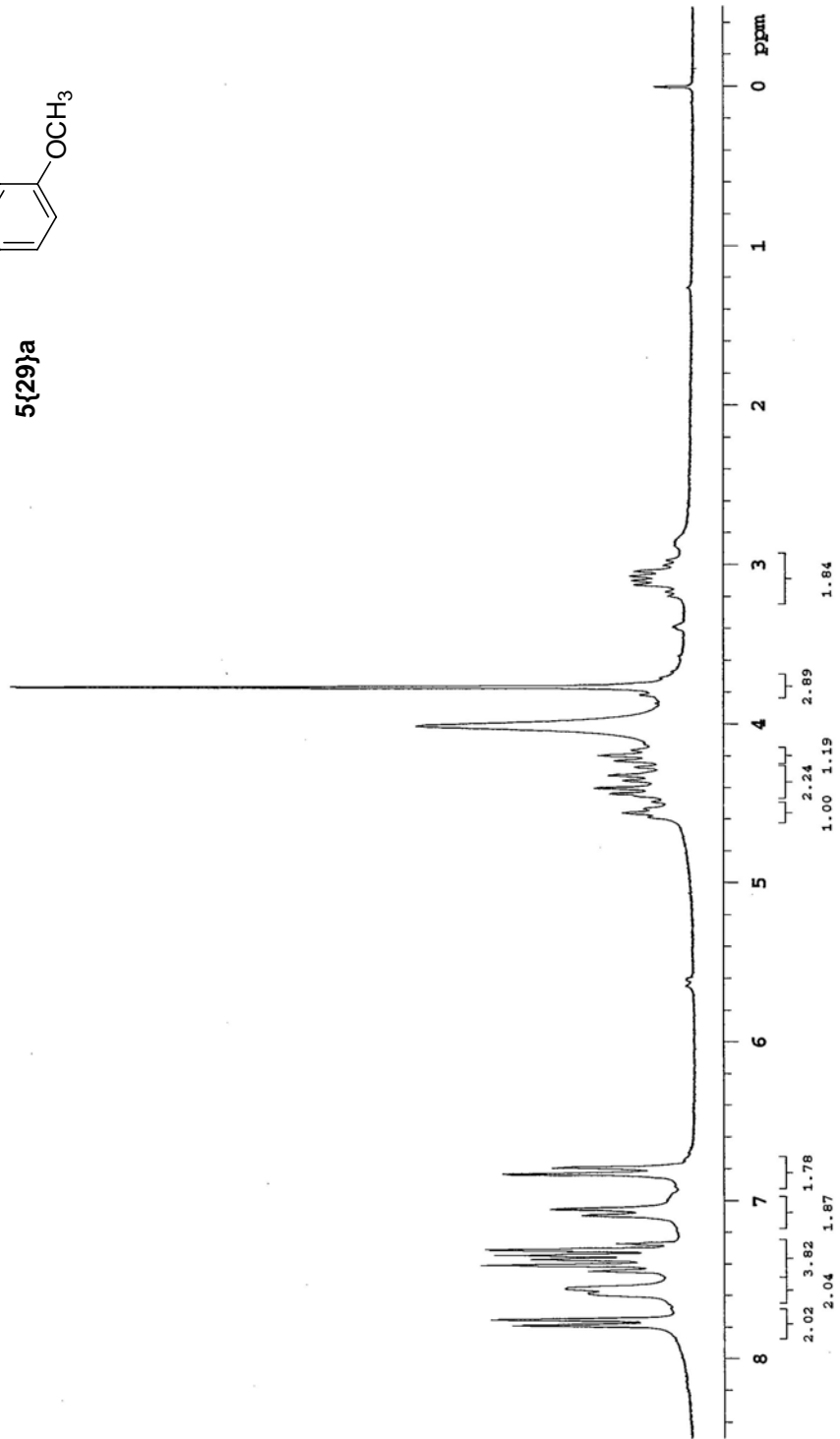
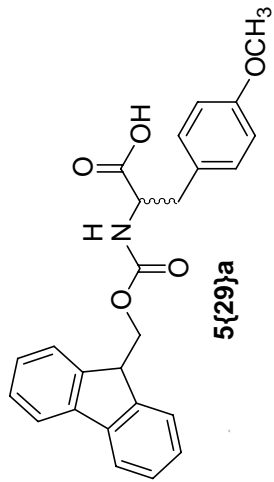
1H_BB#40_B3_CD3ODincDCI3_02_07

Pulse Sequence: s2pul



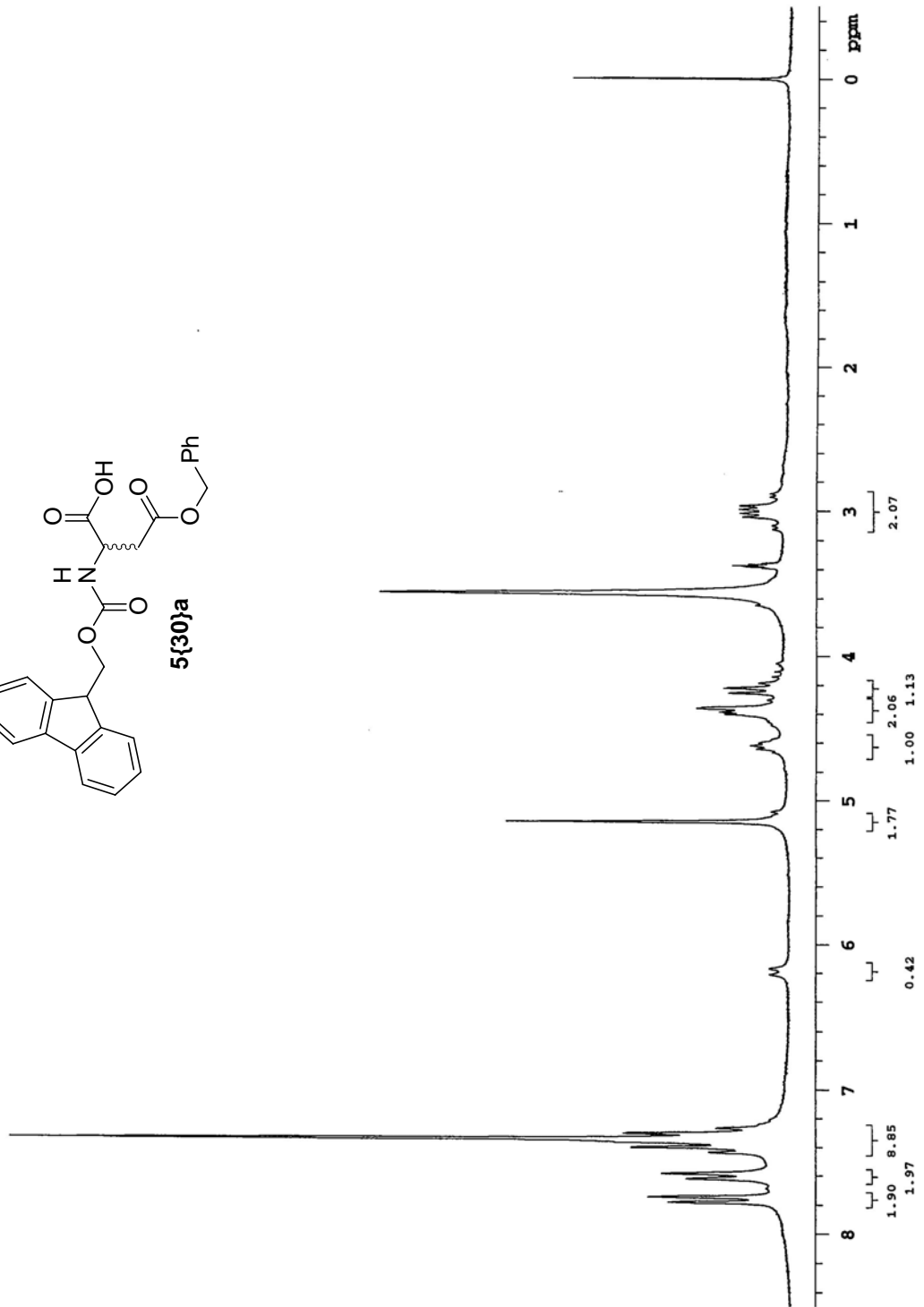
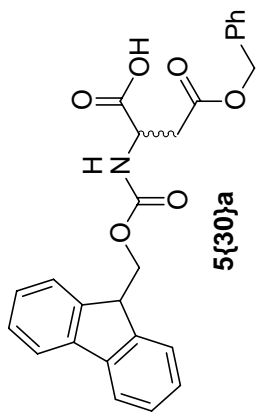
1H_BB#41_A3_CD3ODincDC13_02_07

Pulse Sequence: s2pul



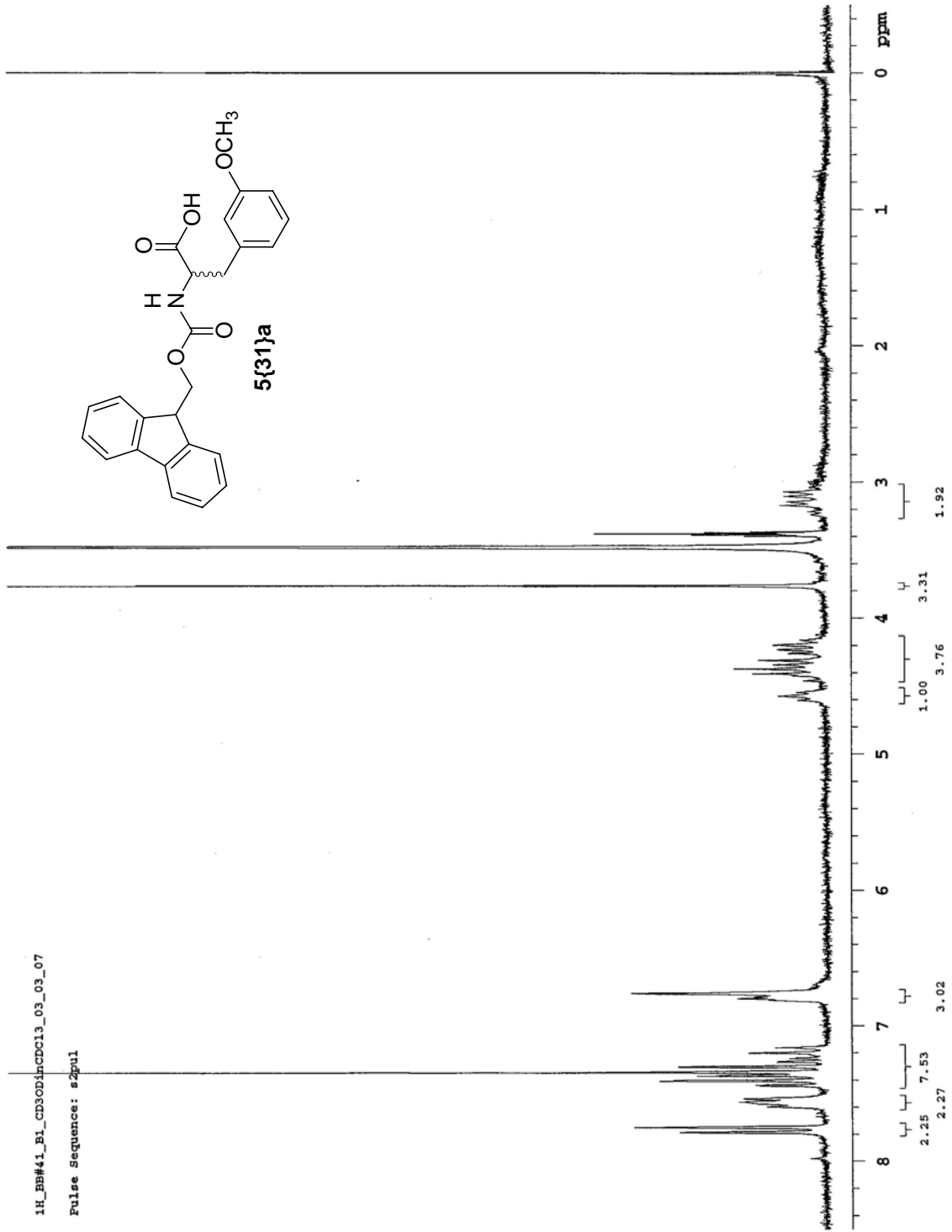
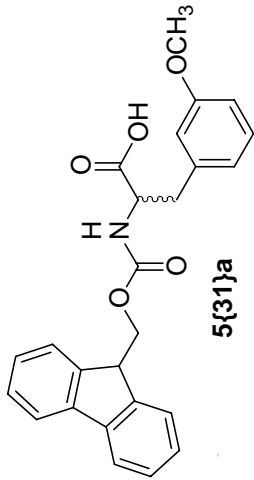
1H_BB#41_B2_CD3ODinCDC13_03_07

Pulse Sequence: s2pul



1H_BB#41_B1_CD3ODinCDCl3_03_03_07

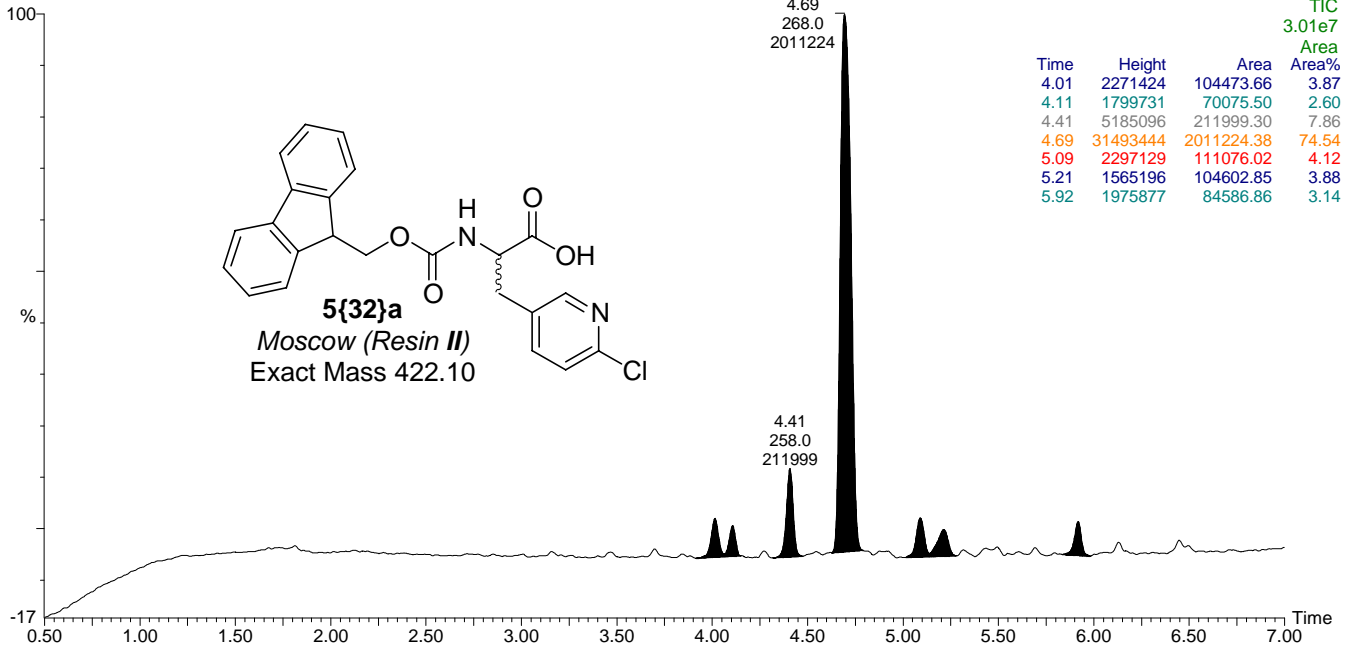
Pulse Sequence: s2pul



5{32}a

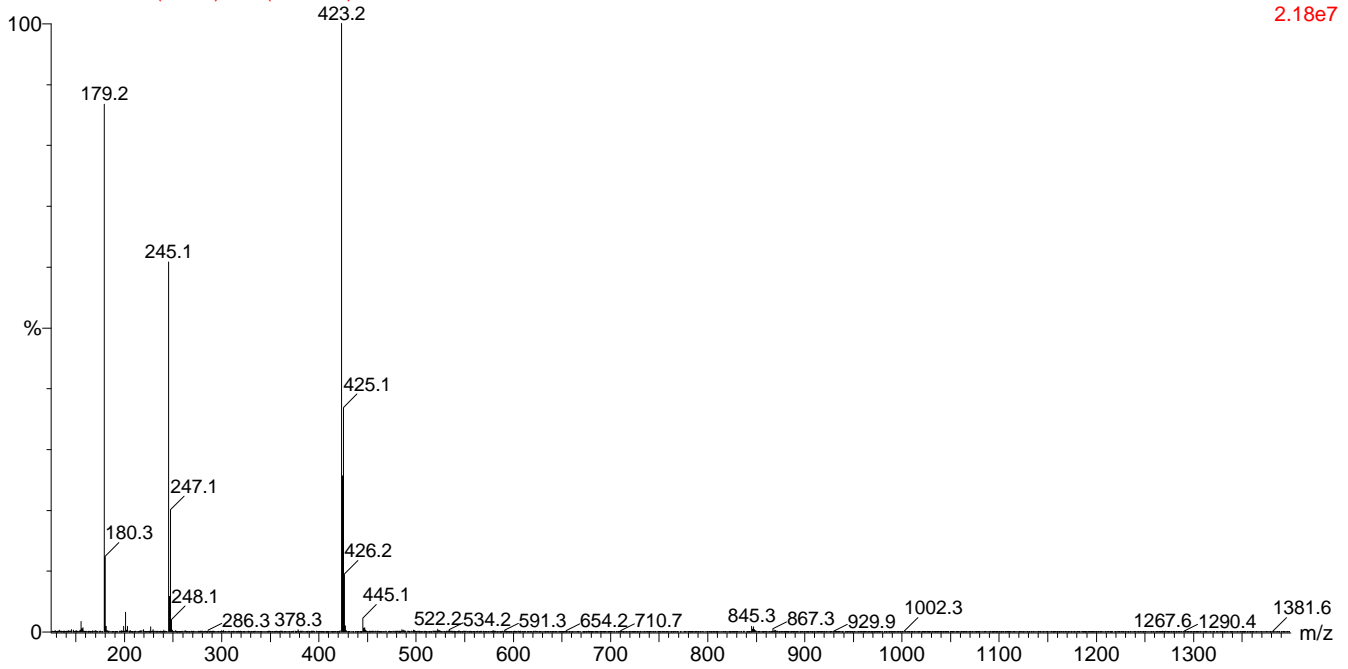
Moscow-A3 Sm (Mn, 1x1)

3: Diode Array



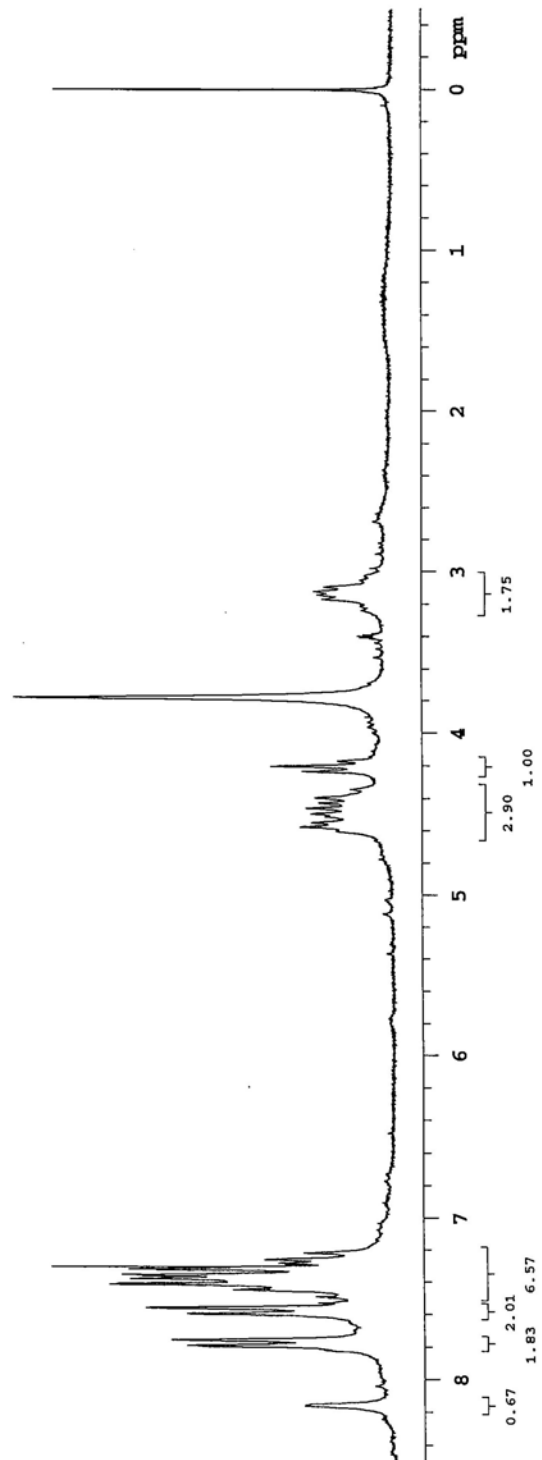
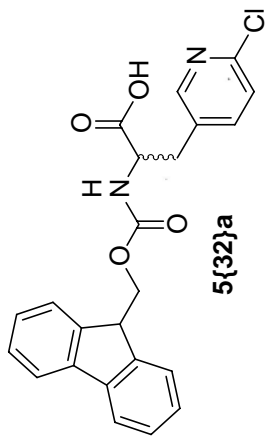
Moscow-A3 177 (4.736) Cm (175:181)

1: Scan ES+
2.18e7



1H_ZZN#47_B_CD3ODinDC13_04_24_07

Pulse Sequence: s2pul

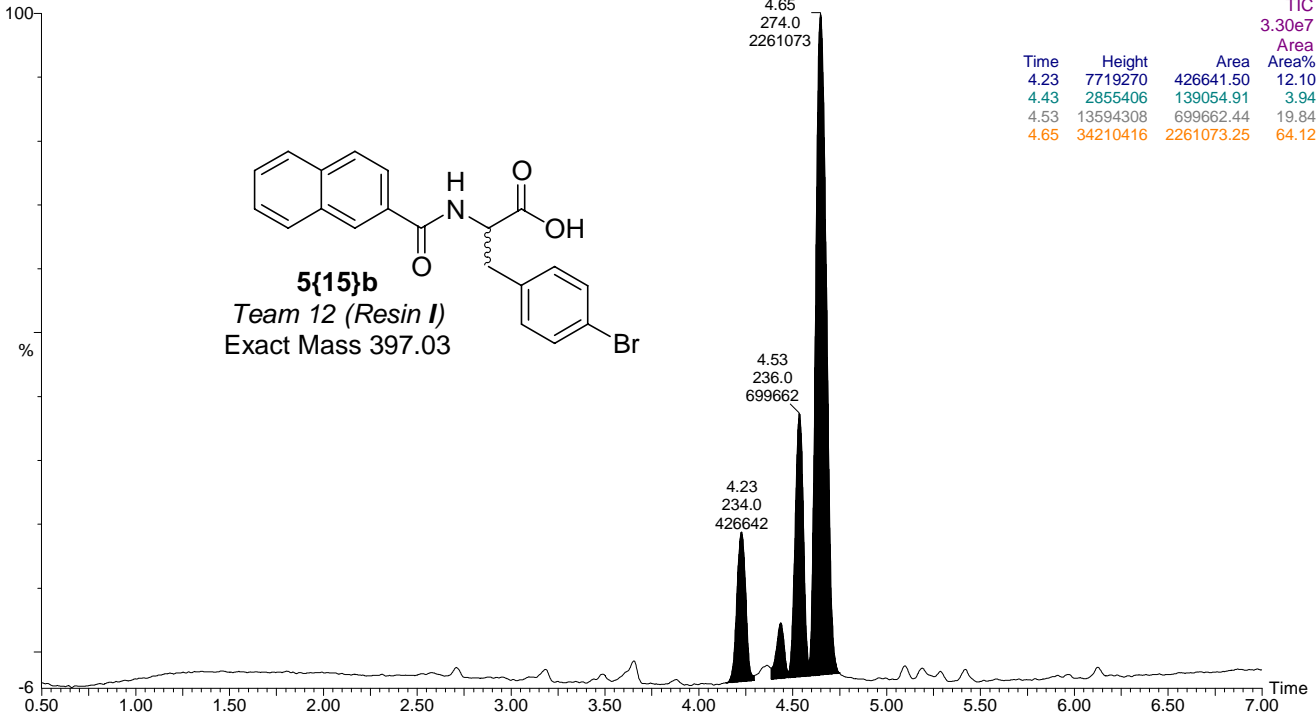


5{15}b

T12-B3 Sm (Mn, 1x1)

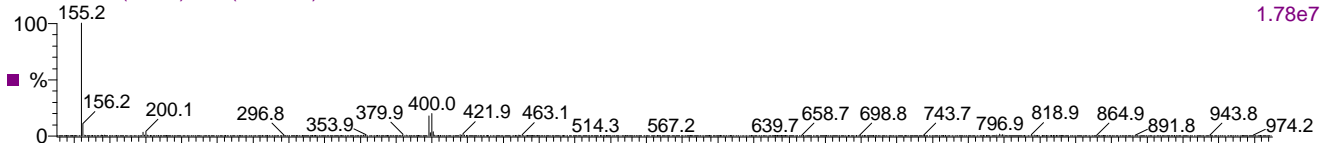
3: Diode Array
TIC
3.30e7

Time	Height	Area	Area%
4.23	7719270	426641.50	12.10
4.43	2855406	139054.91	3.94
4.53	13594308	699662.44	19.84
4.65	34210416	2261073.25	64.12



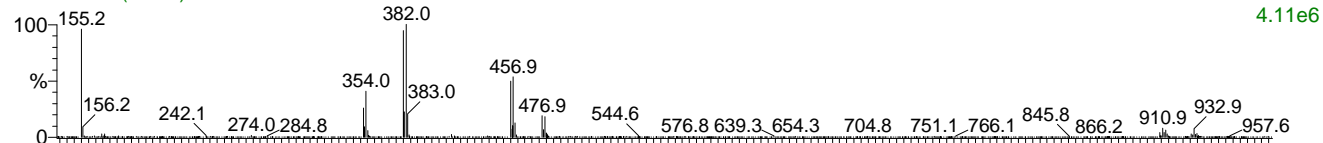
T12-B3 176 (4.709) Cm (176:179)

1: Scan ES+
1.78e7



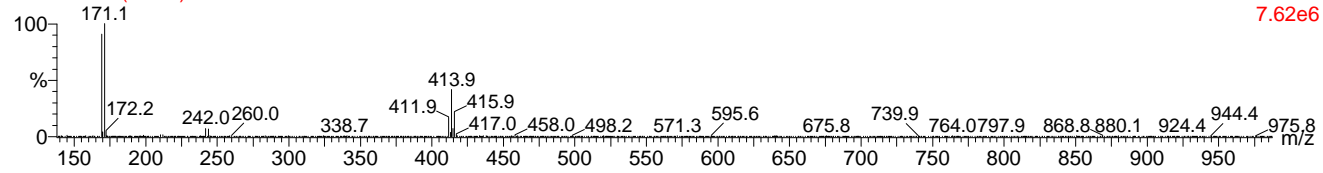
T12-B3 172 (4.602)

1: Scan ES+
4.11e6



T12-B3 159 (4.253)

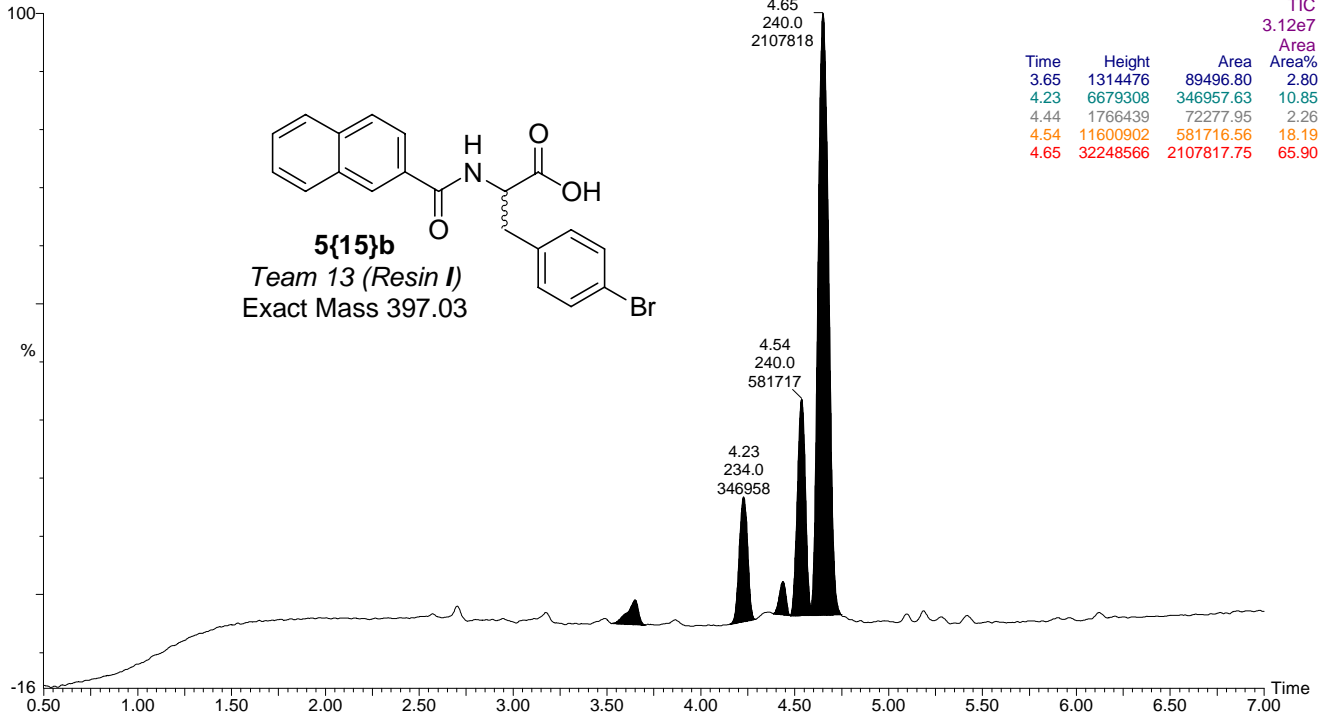
1: Scan ES+
7.62e6



5{15}b

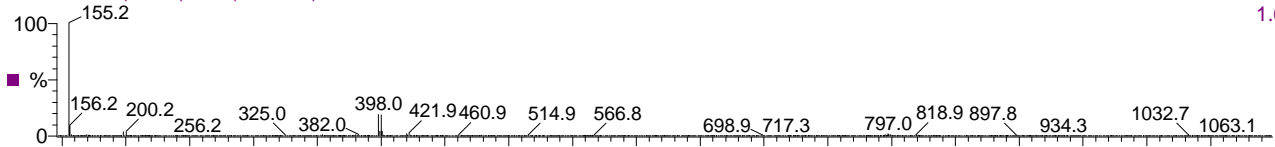
T13-B2 Sm (Mn, 1x1)

3: Diode Array



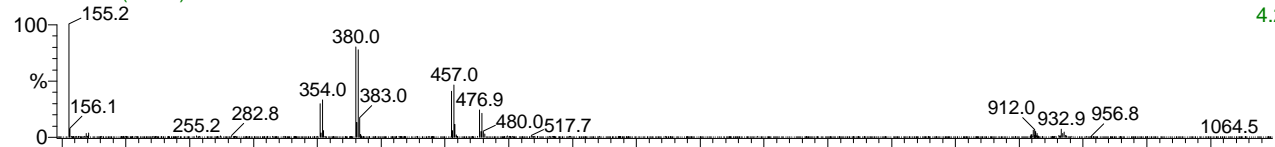
T13-B2 176 (4.709) Cm (174:178)

1: Scan ES+
1.65e7



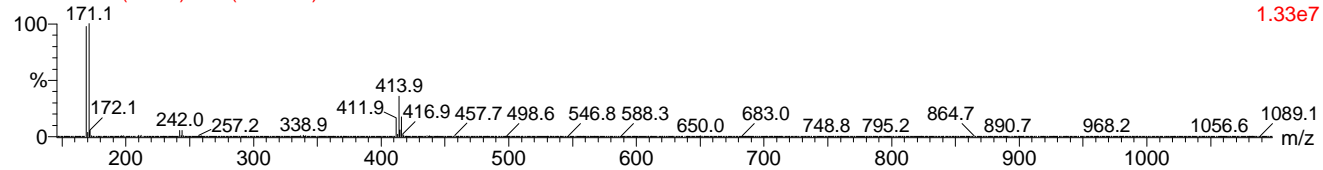
T13-B2 172 (4.602)

1: Scan ES+
4.25e6



T13-B2 160 (4.280) Cm (159:162)

1: Scan ES+
1.33e7

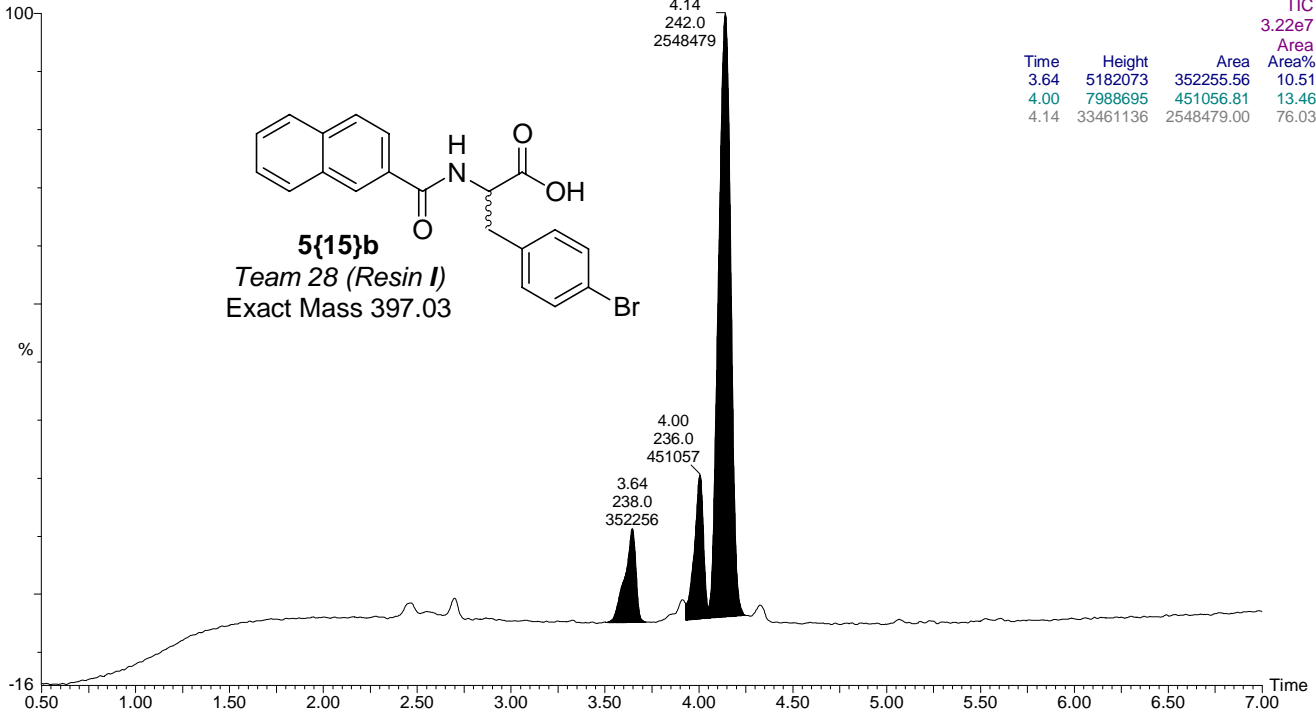


5{15}b

T28-B3 Sm (Mn, 1x1)

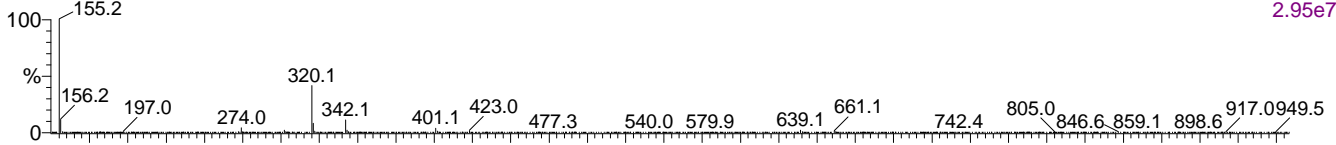
3: Diode Array
TIC
3.22e7

Time	Height	Area	Area%
3.64	5182073	352255.56	10.51
4.00	7988695	451056.81	13.46
4.14	33461136	2548479.00	76.03



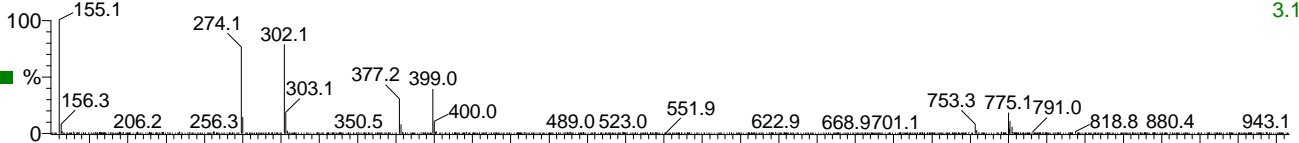
T28-B3 156 (4.172)

1: Scan ES+
2.95e7



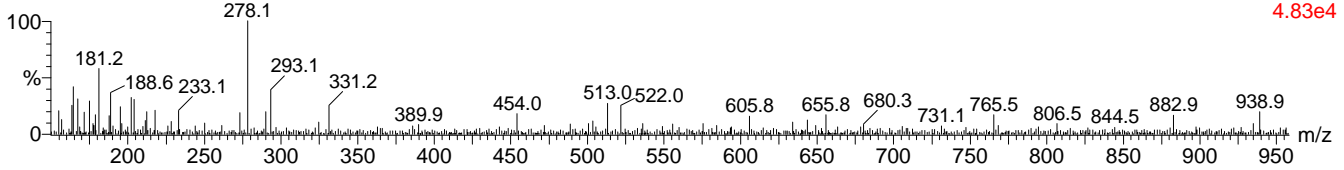
T28-B3 152 (4.065)

1: Scan ES+
3.11e6



T28-B3 137 (3.663) Cm (137)

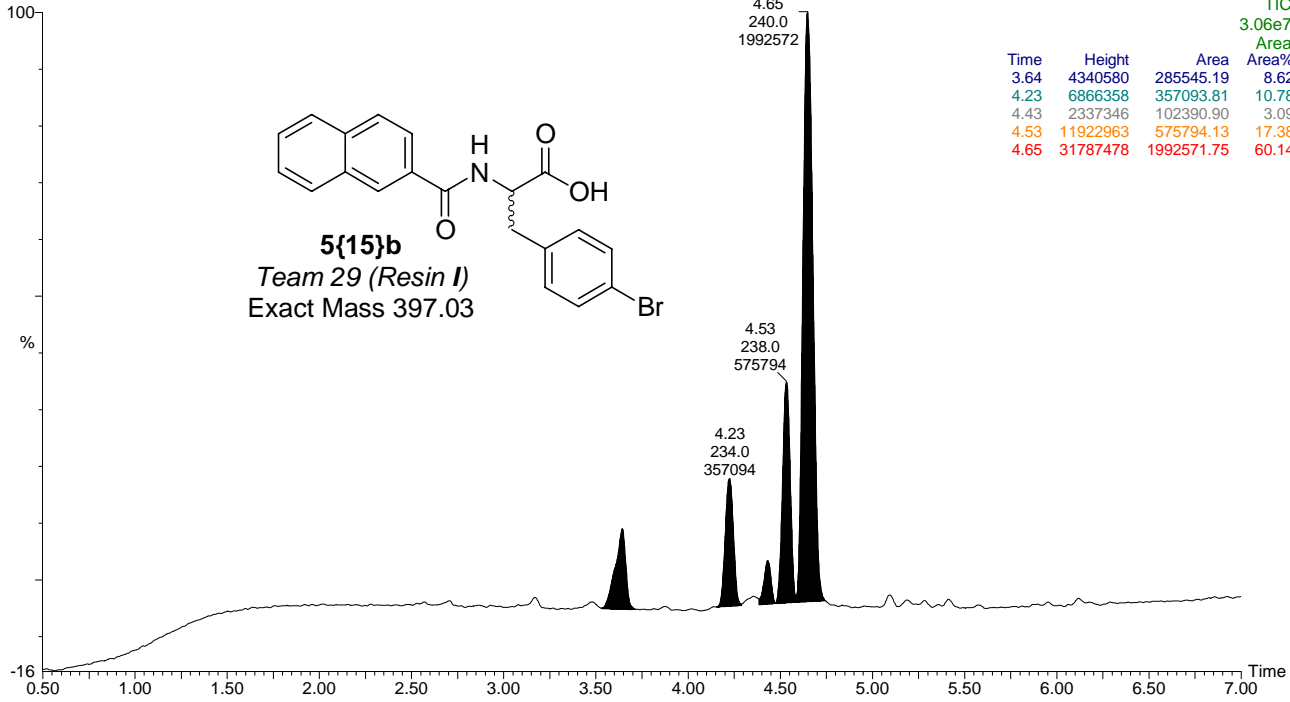
1: Scan ES+
4.83e4



5{15}b

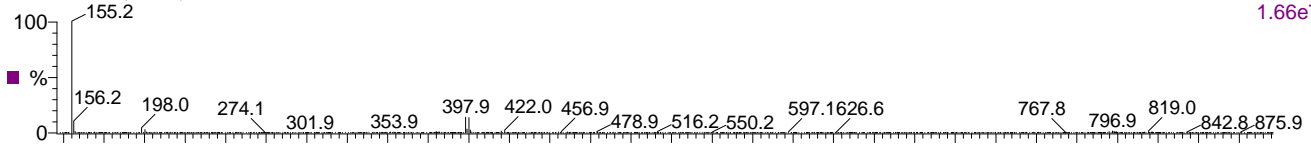
T29-B2 Sm (Mn, 1x1)

3: Diode Array
TIC
3.06e7



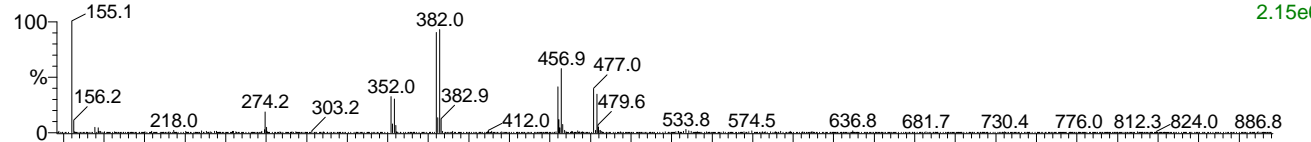
T29-B2 175 (4.682)

1: Scan ES+
1.66e7



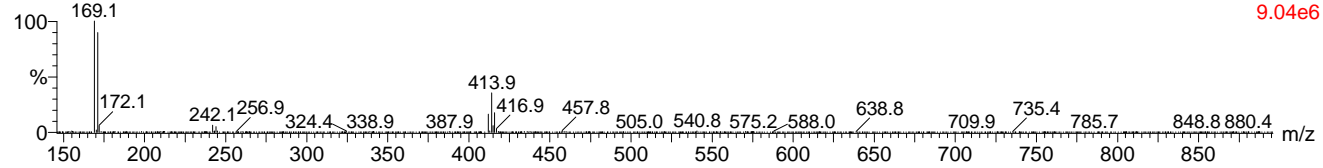
T29-B2 171 (4.575)

1: Scan ES+
2.15e6



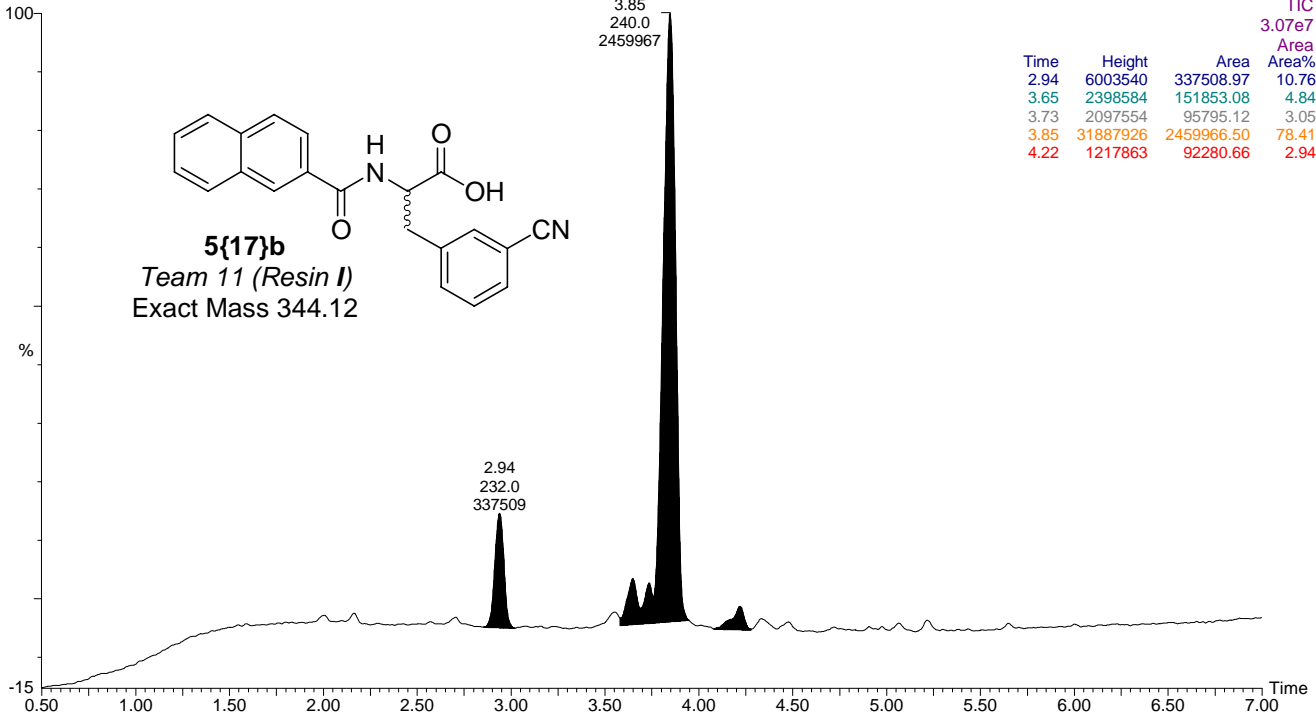
T29-B2 159 (4.253)

1: Scan ES+
9.04e6

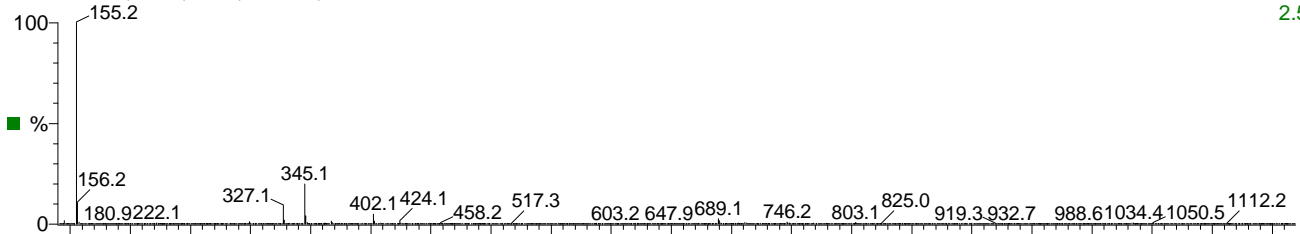


5{17}b

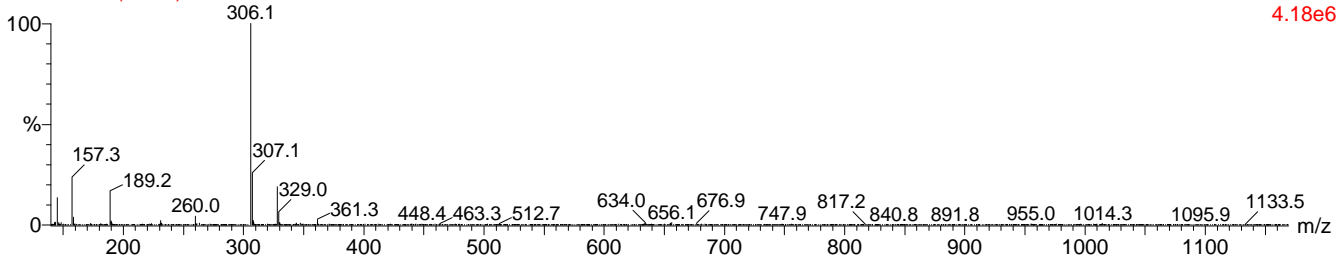
T11-B3 Sm (Mn, 1x1)



T11-B3 146 (3.904) Cm (145:147)



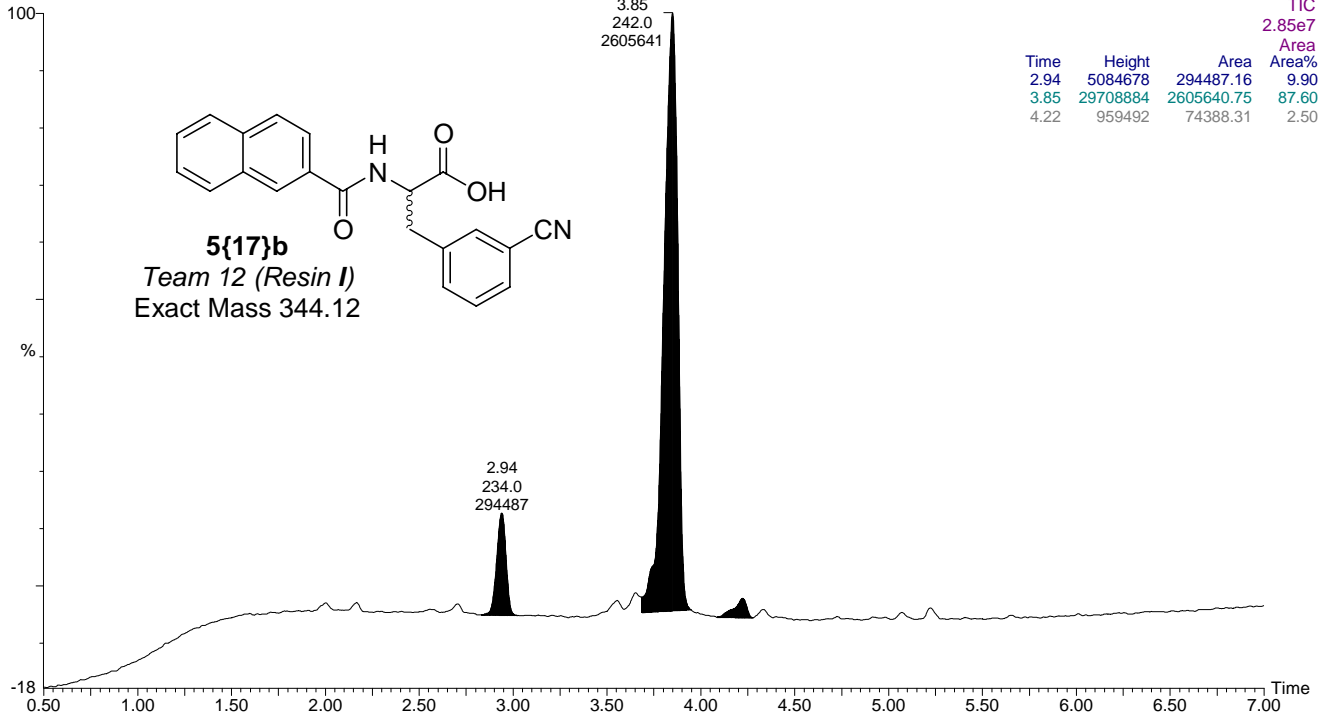
T11-B3 111 (2.965)



5{17}b

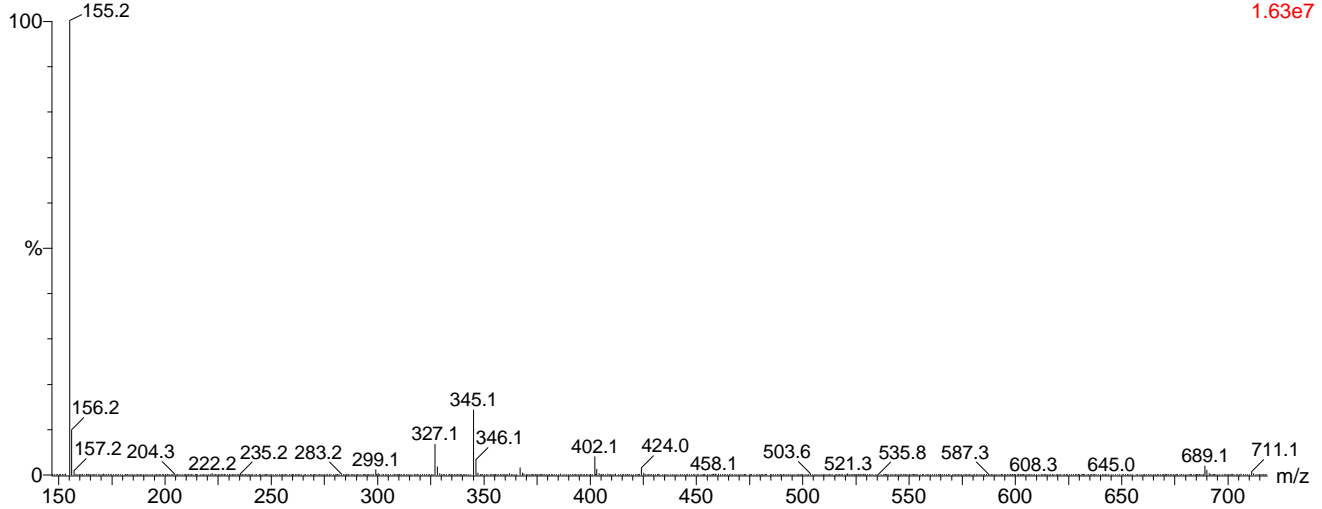
T12-B2 Sm (Mn, 1x1)

3: Diode Array



T12-B2 146 (3.904) Cm (144:149)

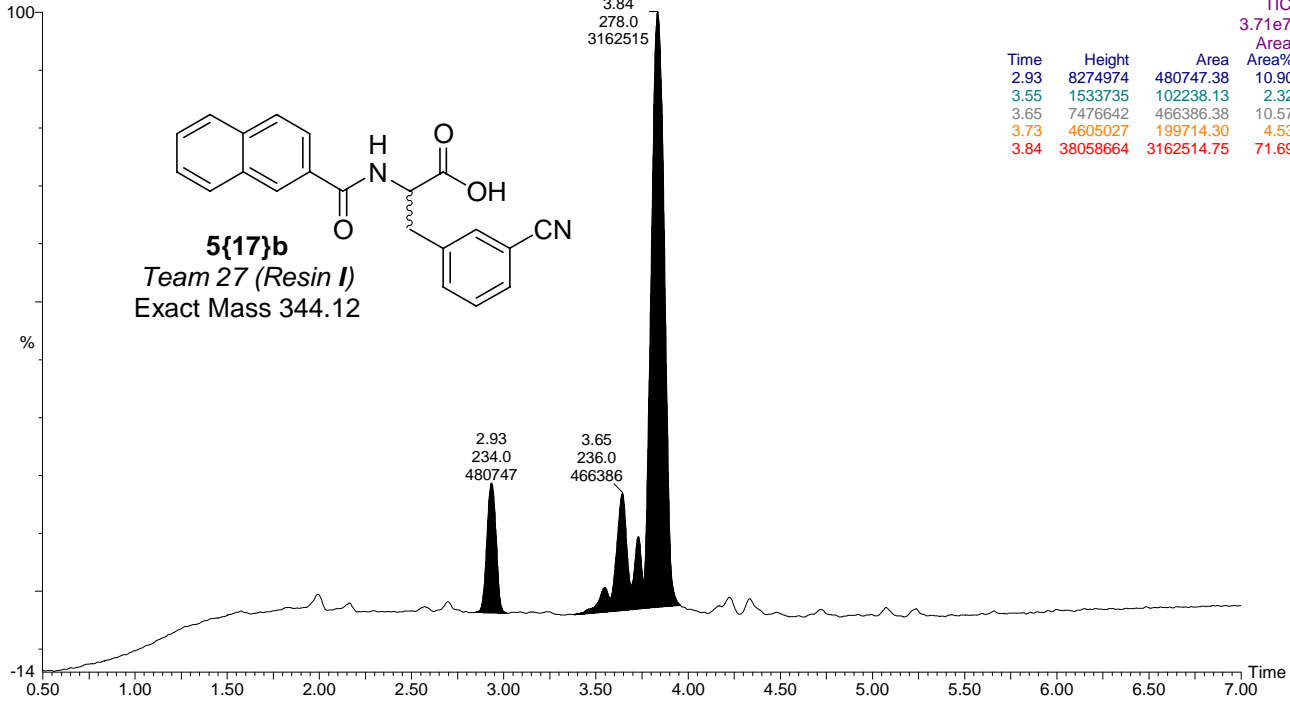
1: Scan ES+
1.63e7



5{17}b

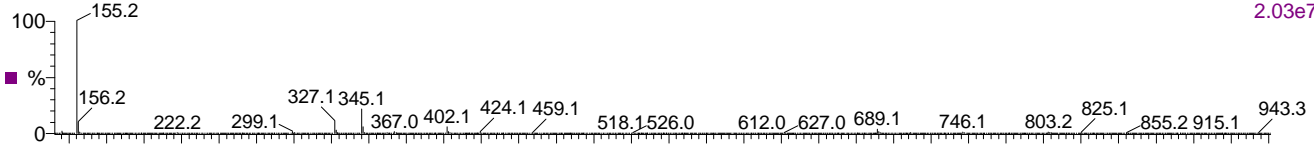
T27-B3 Sm (Mn, 1x1)

3: Diode Array
TIC



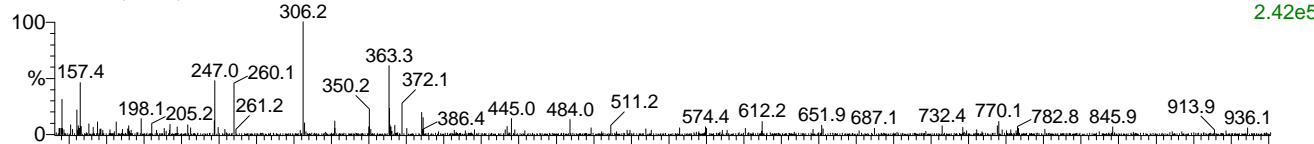
T27-B3 146 (3.904) Cm (144:148)

1: Scan ES+
2.03e7



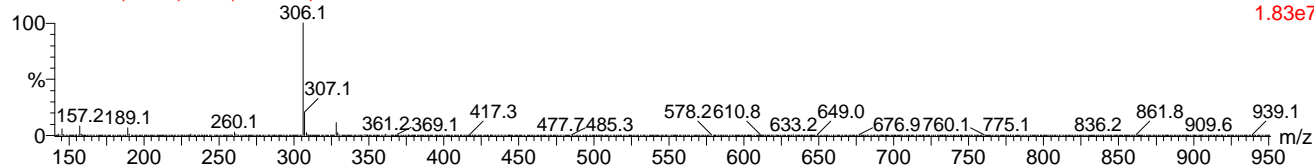
T27-B3 137 (3.663)

1: Scan ES+
2.42e5



T27-B3 112 (2.992) Cm (111:113)

1: Scan ES+
1.83e7

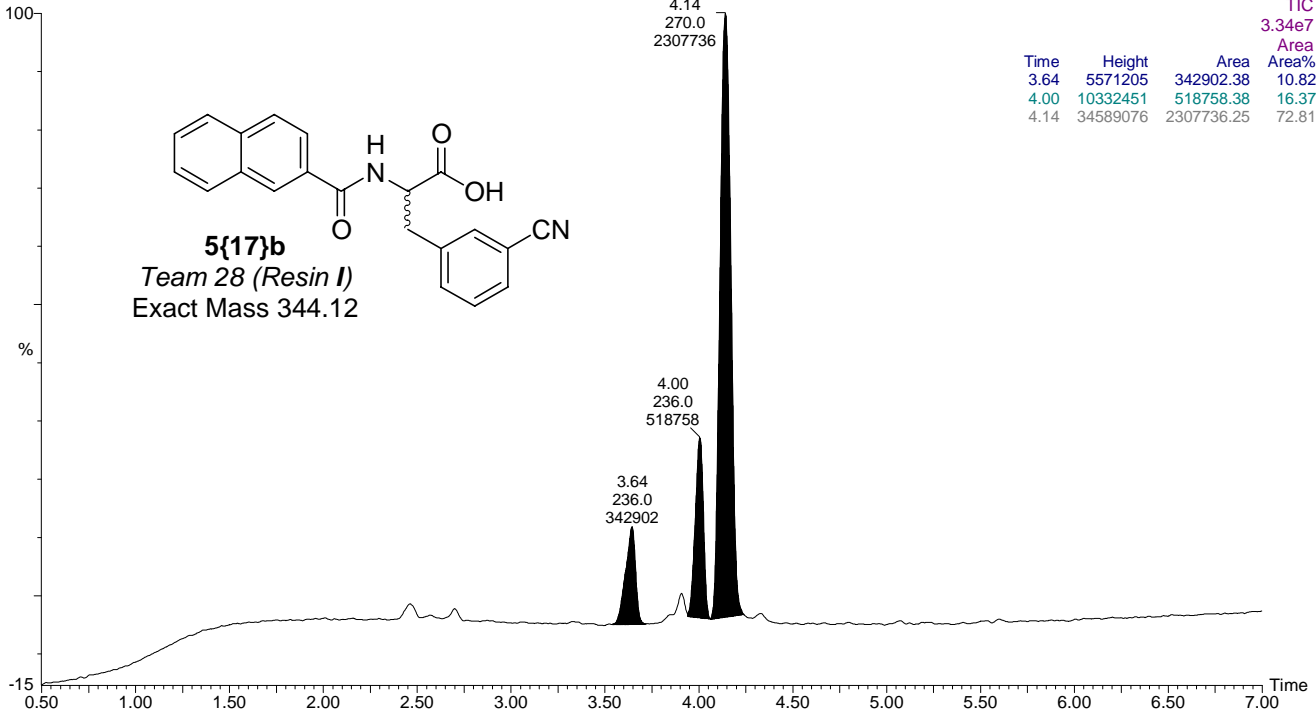


5{17}b

T28-B2 Sm (Mn, 1x1)

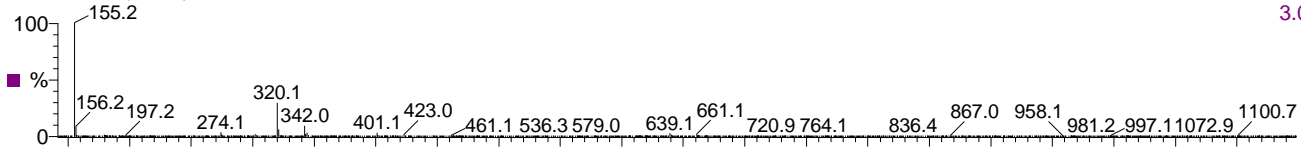
3: Diode Array
TIC
3.34e7

Time	Height	Area	Area%
3.64	5571205	342902.38	10.82
4.00	10332451	518758.38	16.37
4.14	34589076	2307736.25	72.81



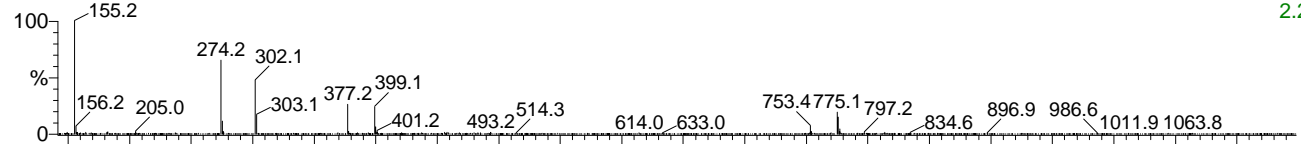
T28-B2 156 (4.172)

1: Scan ES+
3.09e7



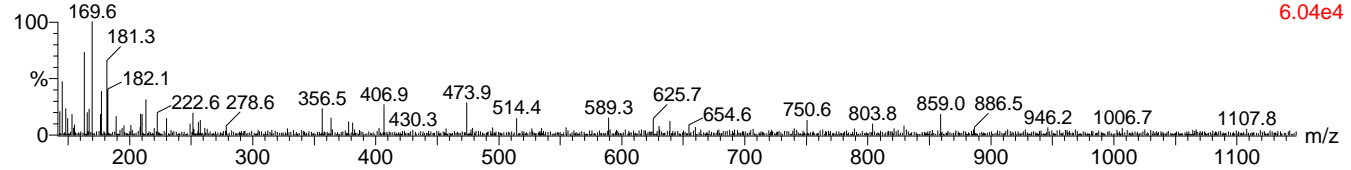
T28-B2 151 (4.038)

1: Scan ES+
2.22e6



T28-B2 137 (3.663) Cm (137)

1: Scan ES+
6.04e4



References

Numbers in this Supporting Information refer to compounds in the article text; letters refer to compounds not in the article text.

1. (a) Atherton, E.; Gait, M. J.; Sheppard, R. C.; Williams, B. J. *Bioorg. Chem.* **1979**, *8*, 351-370. (b) Grandas, A.; Jorba, X.; Giralt, E.; Pedroso, E. *Int. J. Pept. Protein Res.* **1989**, *33*, 386-390.
2. Stanger, K. J.; Krchnak, V. *J. Comb. Chem.* **2006**, *8*, 652-654.

(Ref for Wang Linker adduct) Stanger, K. J.; Krchnak, V. *J. Comb. Chem.* **2006**, *8*, 652-654.