Supporting information

Synthesis and Characterization of Biodegradable Peptide-Based Polymers Prepared by Microwave-Assisted Click Chemistry

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DSC data

GPC data

LC/MS/MS

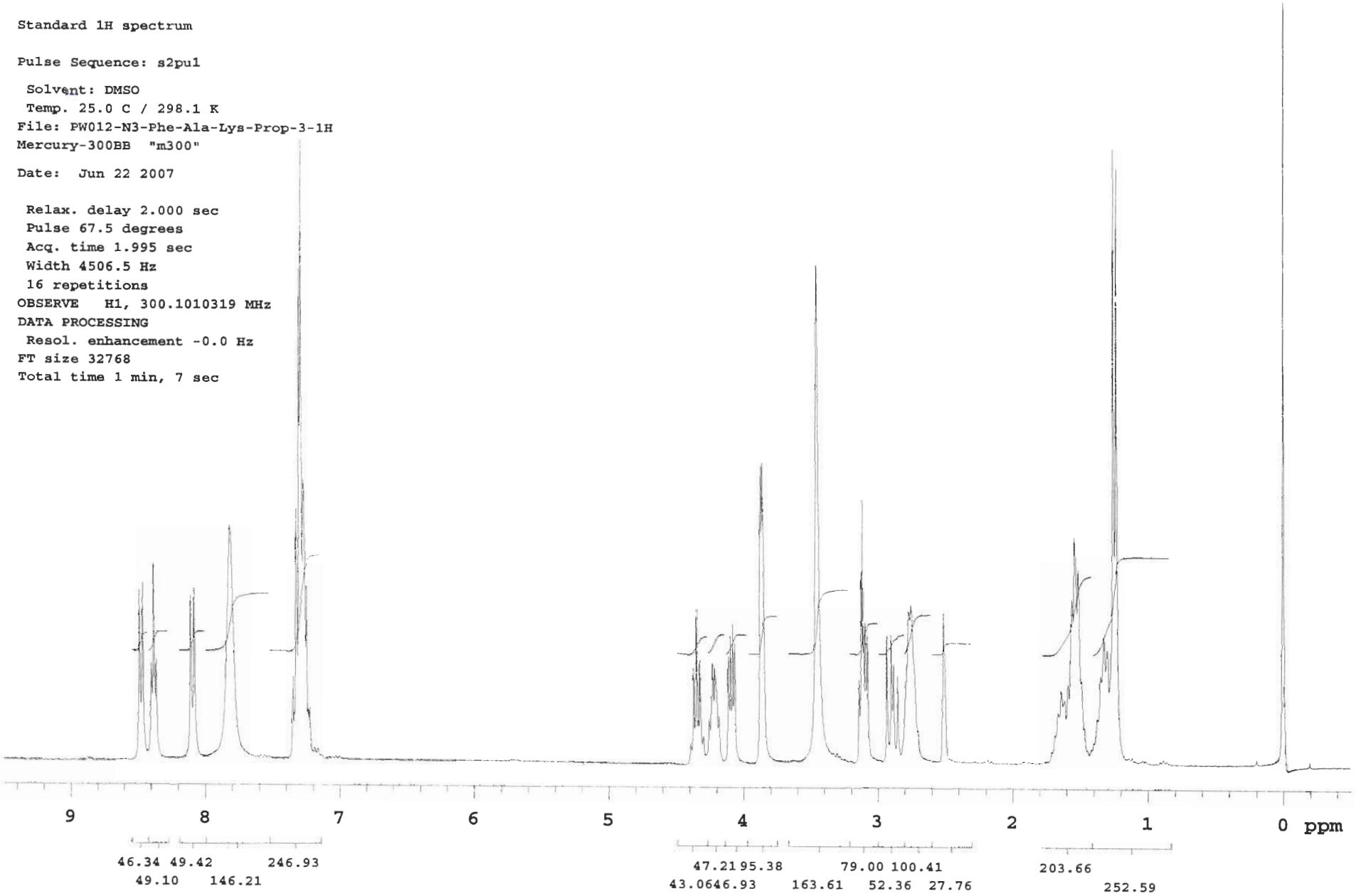
Standard 1H spectrum

Pulse Sequence: s2pu1

Solvent: DMSO
Temp. 25.0 C / 298.1 K
File: PW012-N3-Phe-Ala-Lys-Prop-3-1H
Mercury-300BB "m300"

Date: Jun 22 2007

Relax. delay 2.000 sec
Pulse 67.5 degrees
Acq. time 1.995 sec
Width 4506.5 Hz
16 repetitions
OBSERVE H1, 300.1010319 MHz
DATA PROCESSING
Resol. enhancement -0.0 Hz
FT size 32768
Total time 1 min, 7 sec



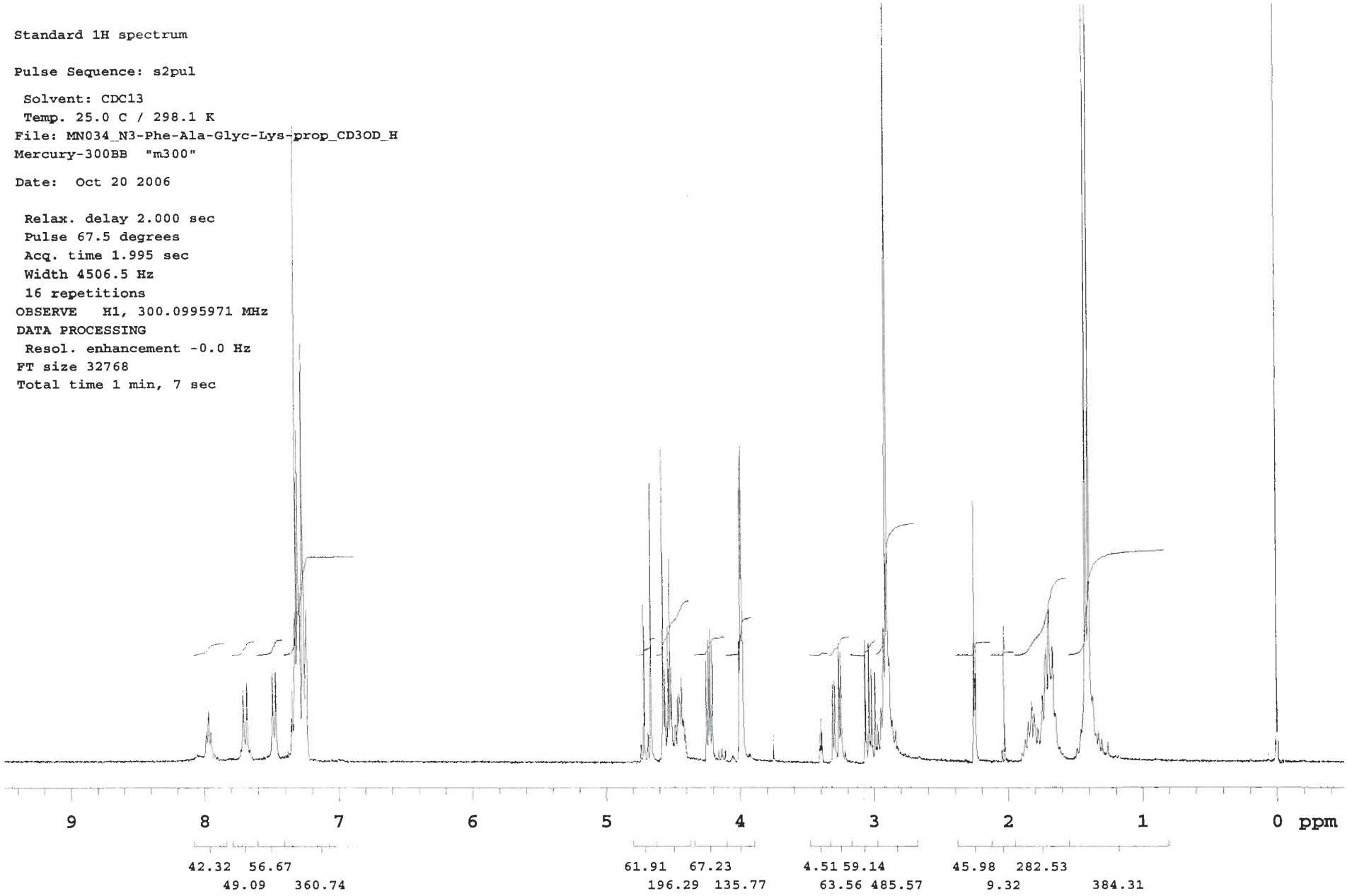
Standard 1H spectrum

Pulse Sequence: s2pul

Solvent: CDC13
Temp. 25.0 C / 298.1 K
File: MN034_N3-Phe-Ala-Glyc-Lys-prop_CD3OD_H
Mercury-300BB "m300"

Date: Oct 20 2006

Relax. delay 2.000 sec
Pulse 67.5 degrees
Acq. time 1.995 sec
Width 4506.5 Hz
16 repetitions
OBSERVE H1, 300.0995971 MHz
DATA PROCESSING
Resol. enhancement -0.0 Hz
FT size 32768
Total time 1 min, 7 sec



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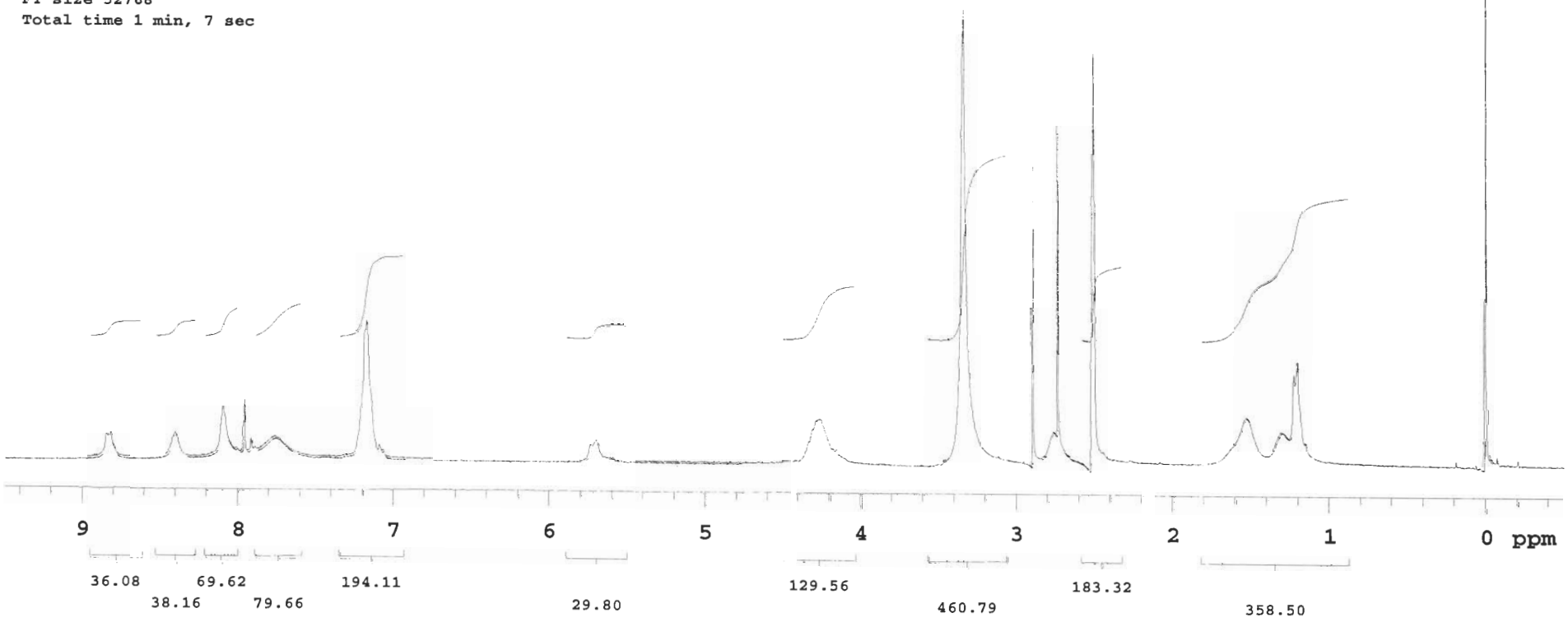
Standard 1H spectrum

Pulse Sequence: s2pul

Solvent: DMSO
Temp. 25.0 C / 298.1 K
File: PW0135-N3-Phe-Ala-Lys-Proppoly-1-1H
Mercury-300BB "m300"

Date: Jun 27 2007

Relax. delay 2.000 sec
Pulse 67.5 degrees
Acq. time 1.995 sec
Width 4506.5 Hz
16 repetitions
OBSERVE H1, 300.1010328 MHz
DATA PROCESSING
Resol. enhancement -0.0 Hz
FT size 32768
Total time 1 min, 7 sec



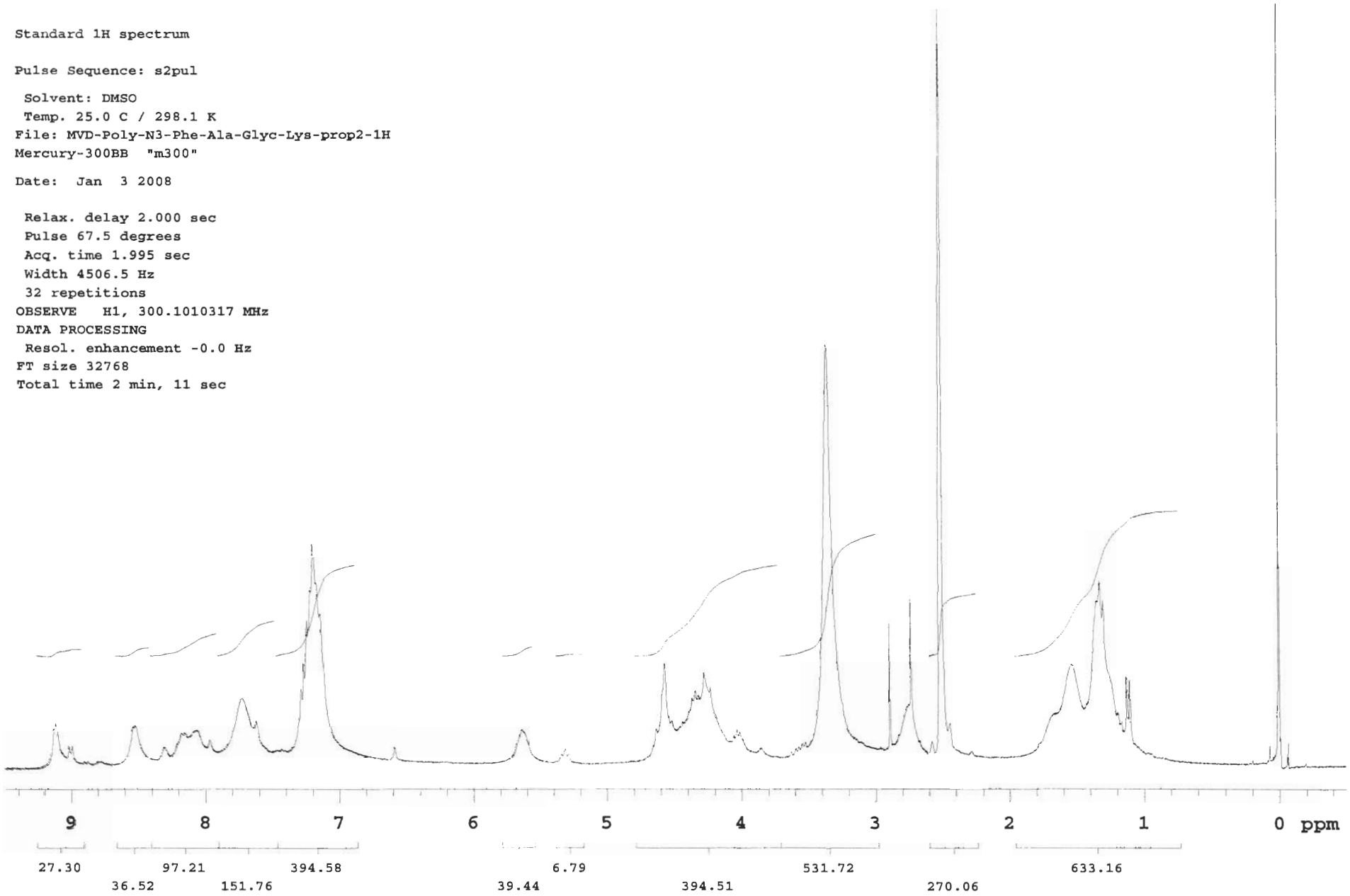
Standard 1H spectrum

Pulse Sequence: s2pul

Solvent: DMSO
Temp. 25.0 C / 298.1 K
File: MVD-Poly-N3-Phe-Ala-Glyc-Lys-prop2-1H
Mercury-300BB "m300"

Date: Jan 3 2008

Relax. delay 2.000 sec
Pulse 67.5 degrees
Acq. time 1.995 sec
Width 4506.5 Hz
32 repetitions
OBSERVE H1, 300.1010317 MHz
DATA PROCESSING
Resol. enhancement -0.0 Hz
FT size 32768
Total time 2 min, 11 sec



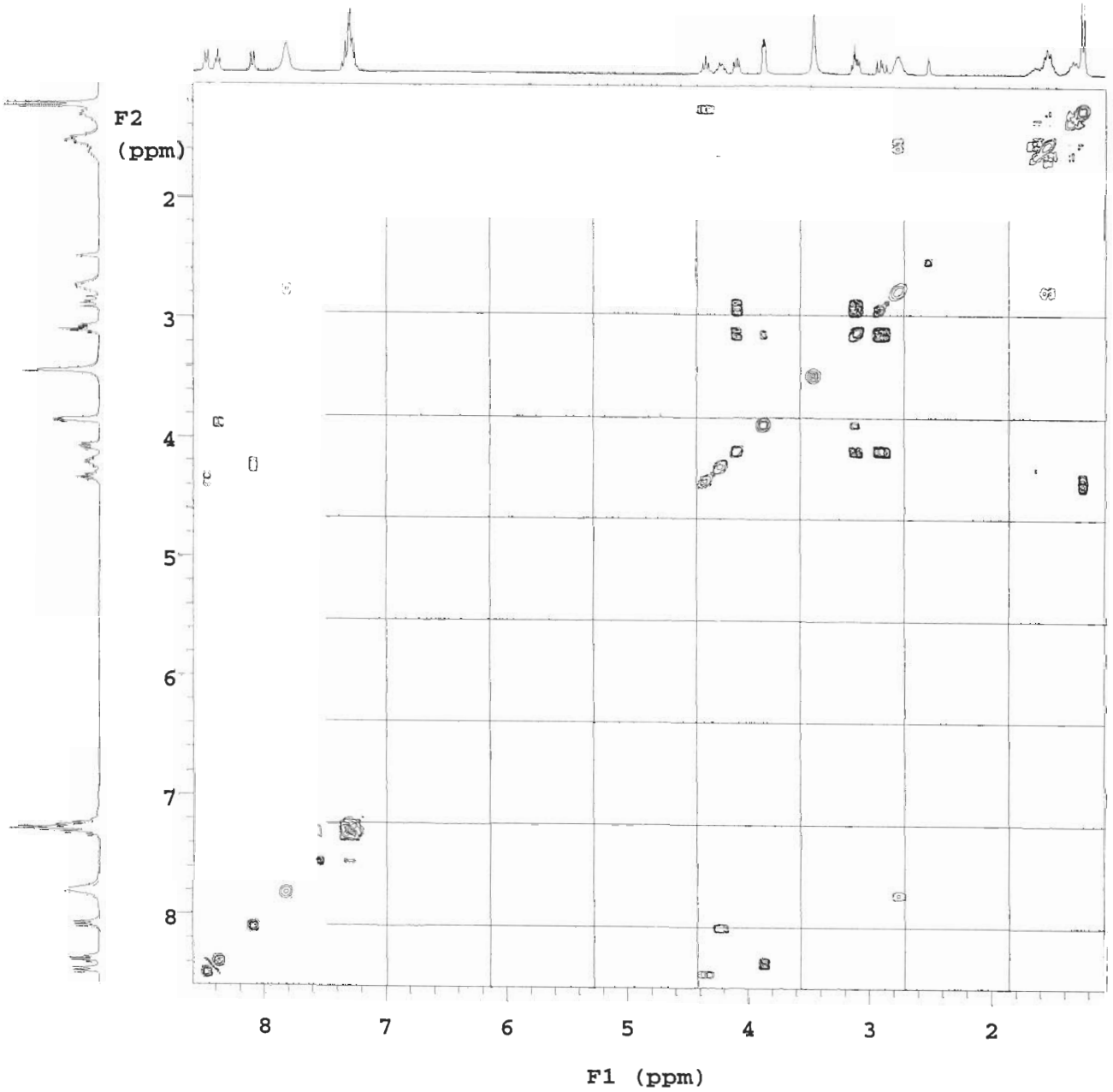
Standard 1H spectrum

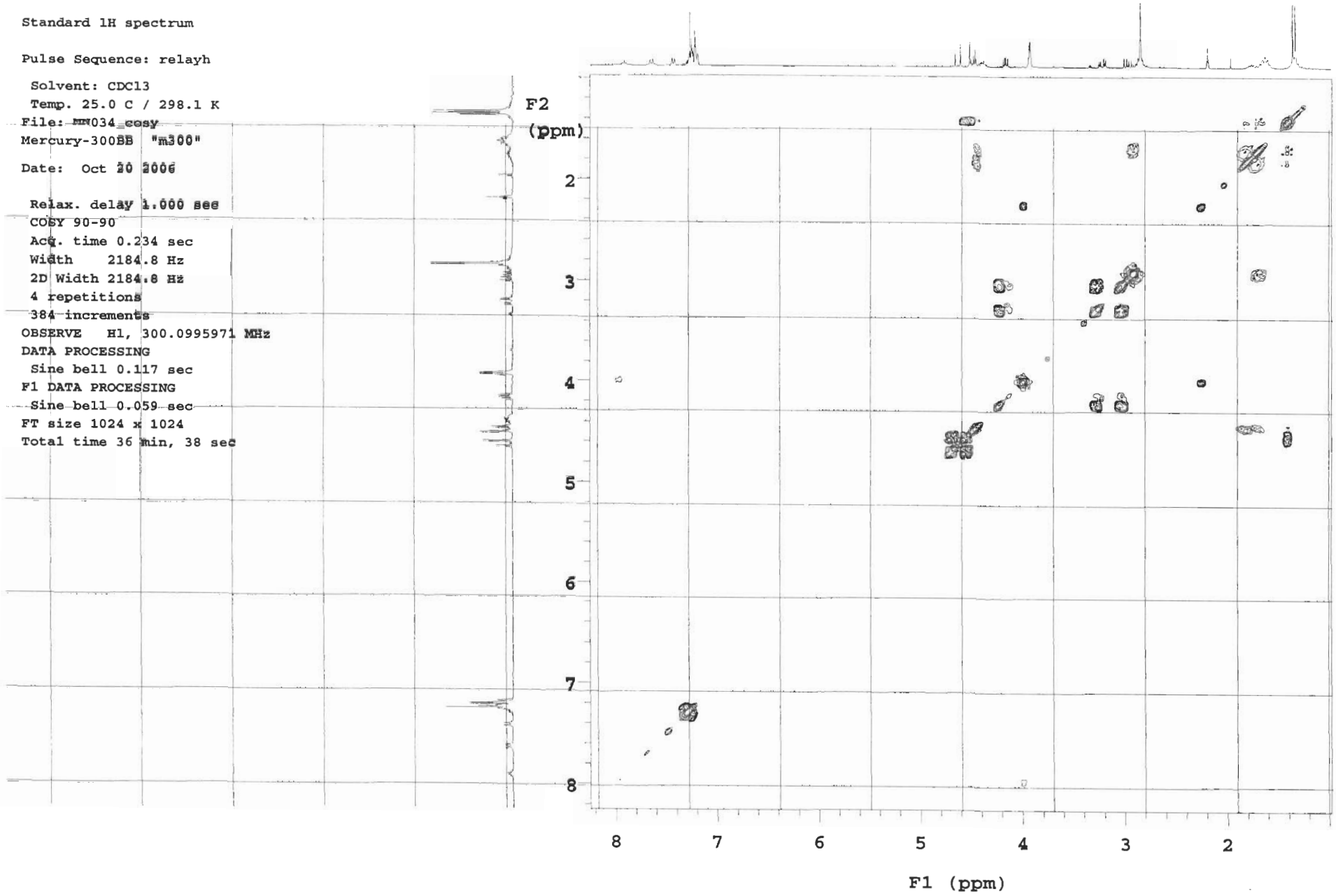
Pulse Sequence: relayh

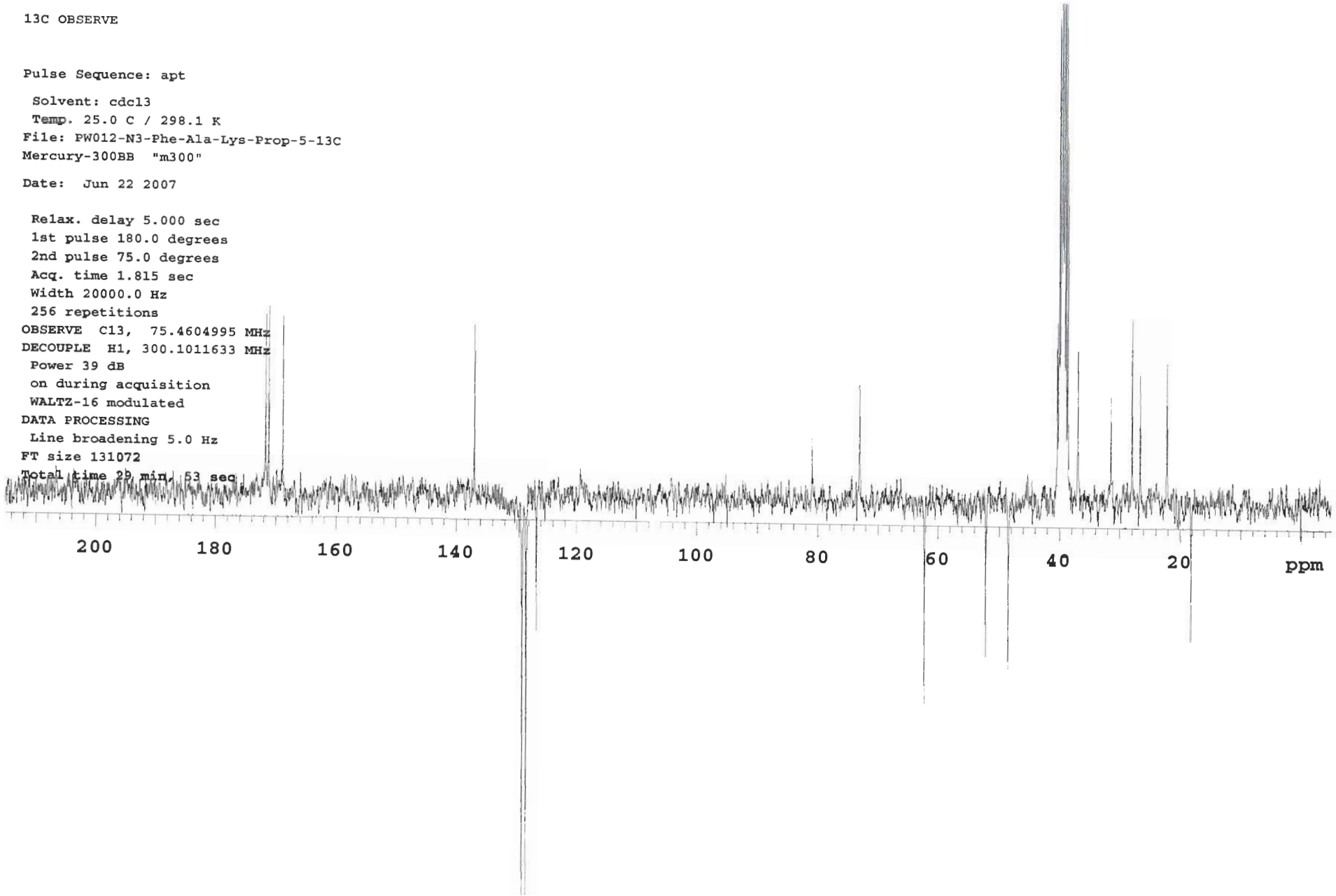
Solvent: DMSO
Temp. 25.0 C / 298.1 K
File: PW012-N3-Phe-Ala-Lys-Prop-4-Cosy
Mercury-300BB "m300"

Date: Jun 22 2007

Relax. delay 1.000 sec
COSY 90-90
Acq. time 0.226 sec
Width 2264.0 Hz
2D Width 2264.0 Hz
4 repetitions
128 increments
OBSERVE H1, 300.1010319 MHz
DATA PROCESSING
Sine bell 0.113 sec
F1 DATA PROCESSING
Sine bell 0.057 sec
FT size 1024 x 1024
Total time 11 min, 40 sec




Standard 1H spectrum
Pulse Sequence: relayh
Solvent: CDCl3
Temp. 25.0 C / 298.1 K
File: mm034_cosy
Mercury-300BB "m300"
Date: Oct 20 2006
Relax. delay 1.000 sec
COSY 90-90
Acq. time 0.234 sec
Width 2184.8 Hz
2D Width 2184.8 Hz
4 repetitions
384 increments
OBSERVE H1, 300.0995971 MHz
DATA PROCESSING
Sine bell 0.117 sec
F1 DATA PROCESSING
Sine bell 0.059 sec
FT size 1024 x 1024
Total time 36 min, 38 sec
F2 (ppm)
F1 (ppm)


13C OBSERVE
Pulse Sequence: apt
Solvent: cdcl3
Temp. 25.0 C / 298.1 K
File: PW012-N3-Phe-Ala-Lys-Prop-5-13C
Mercury-300BB "m300"
Date: Jun 22 2007
Relax. delay 5.000 sec
1st pulse 180.0 degrees
2nd pulse 75.0 degrees
Acq. time 1.815 sec
Width 20000.0 Hz
256 repetitions
OBSERVE C13, 75.4604995 MHz
DECOUPLE H1, 300.1011633 MHz
Power 39 dB
on during acquisition
WALTZ-16 modulated
DATA PROCESSING
Line broadening 5.0 Hz
FT size 131072
Total time 29 min, 53 sec
200
180
160
140
120
100
80
60
40
20
ppm

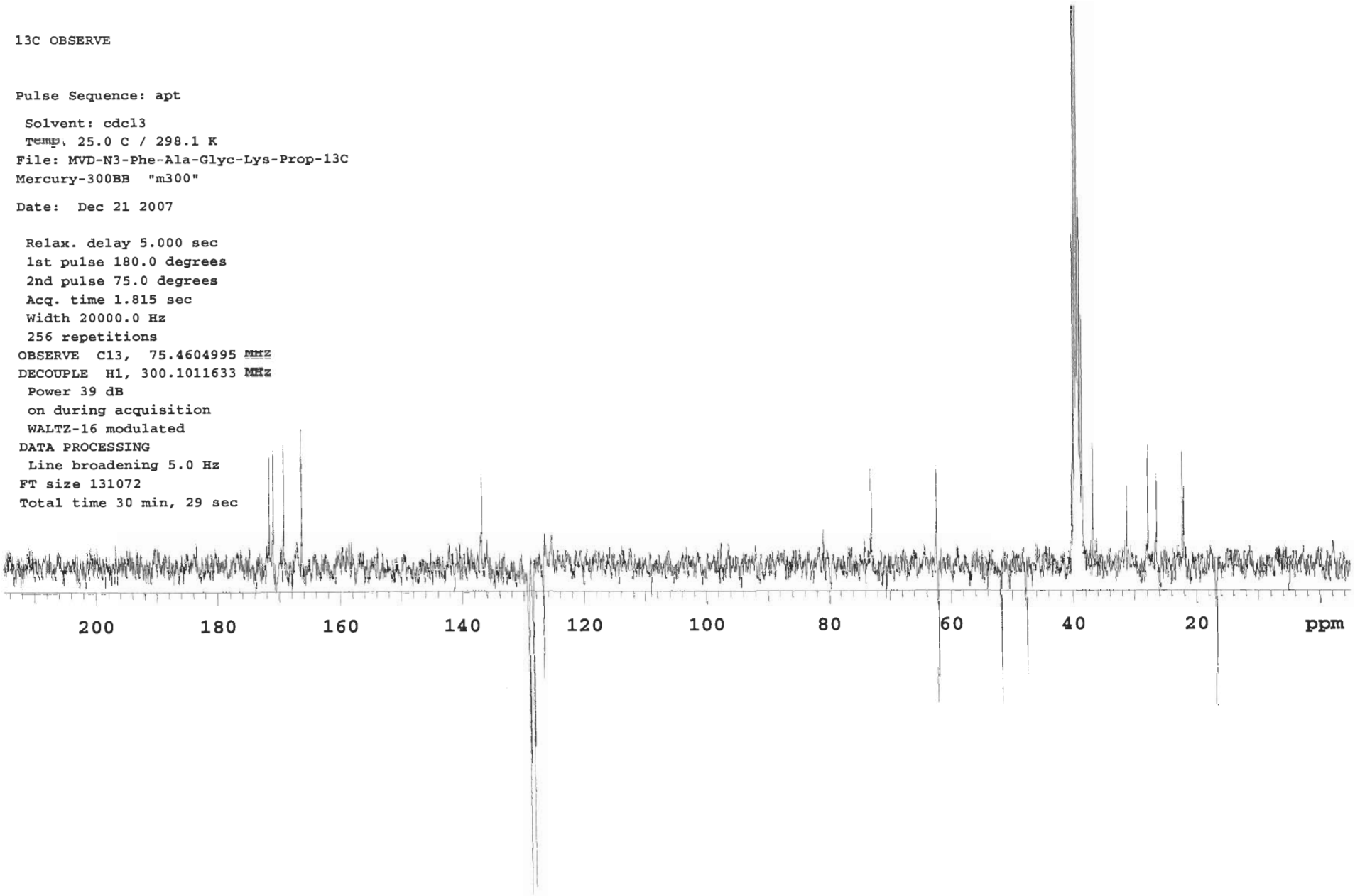
13C OBSERVE

Pulse Sequence: apt

Solvent: cdcl3
Temp. 25.0 C / 298.1 K
File: MVD-N3-Phe-Ala-Glyc-Lys-Prop-13C
Mercury-300BB "m300"

Date: Dec 21 2007

Relax. delay 5.000 sec
1st pulse 180.0 degrees
2nd pulse 75.0 degrees
Acq. time 1.815 sec
Width 20000.0 Hz
256 repetitions
OBSERVE C13, 75.4604995 MHz
DECOUPLE H1, 300.1011633 MHz
Power 39 dB
on during acquisition
WALTZ-16 modulated
DATA PROCESSING
Line broadening 5.0 Hz
FT size 131072
Total time 30 min, 29 sec



01

standard report Medicinal Chemistry

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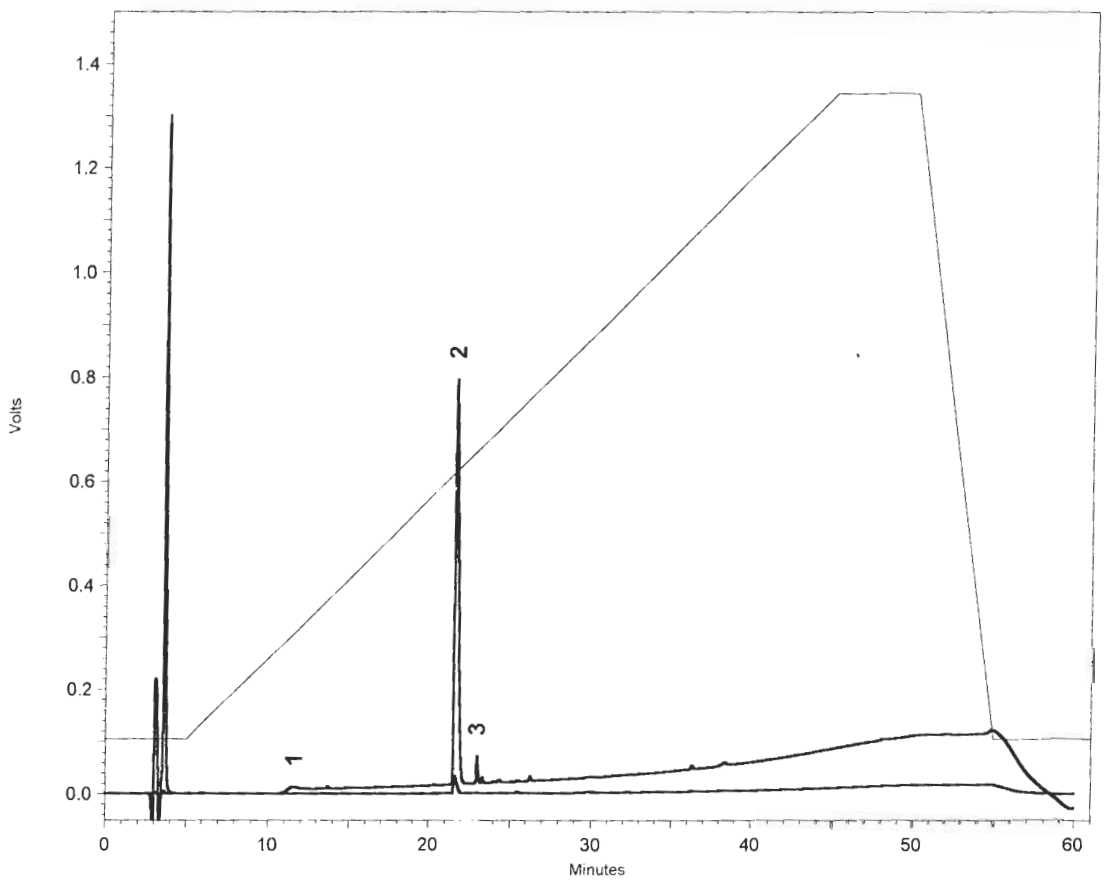
print time: 22-Apr-08 4:55:38 PM
sample description **{Sample Description}**



Detector A - 1
(220nm)

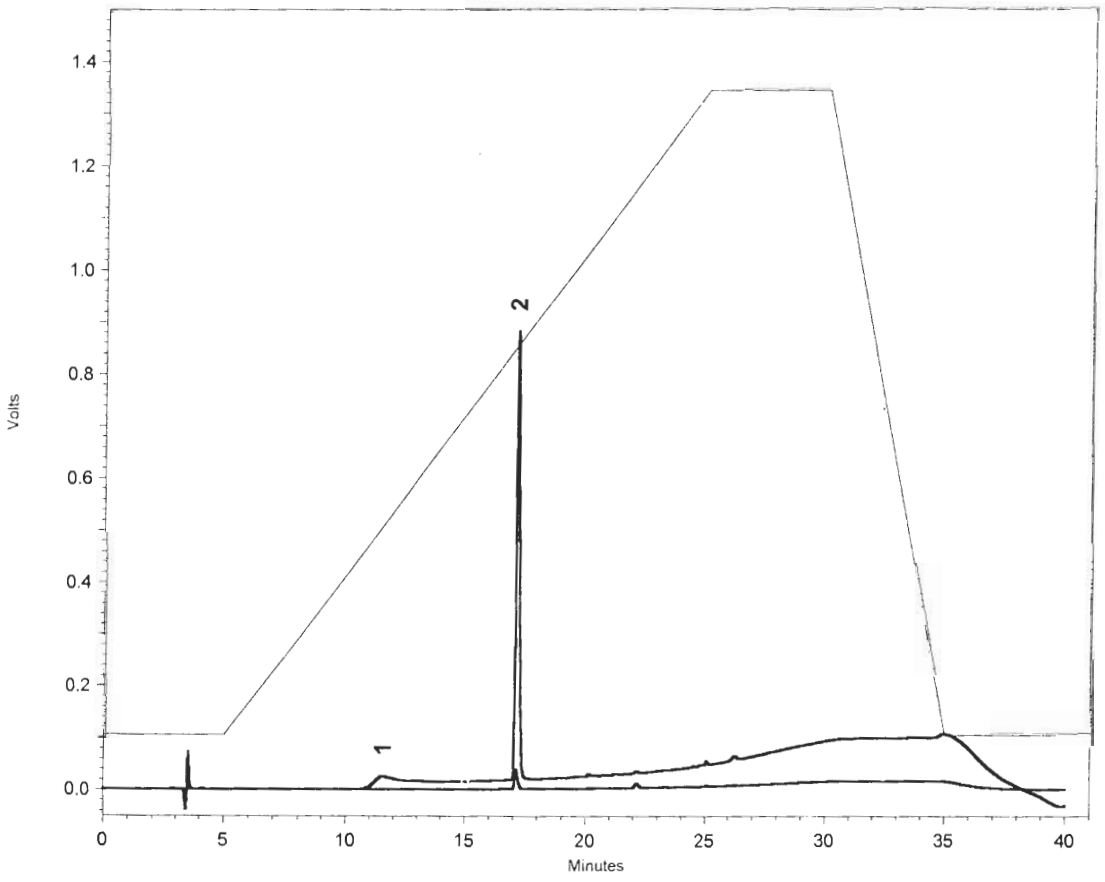
Pk #	Name	Retention Time	Area	Area Percent
1		11.617	576445	4.45
2		21.617	11982274	92.52
3		23.000	392599	3.03

Totals			12951318	100.00

einde

standard report Medicinal Chemistry

sample ID: MVD223S9
filename: C:\Users\Maarten\Mvd223s9
print time: 22-Apr-08 4:51:42 PM
sample description **{Sample Description}**



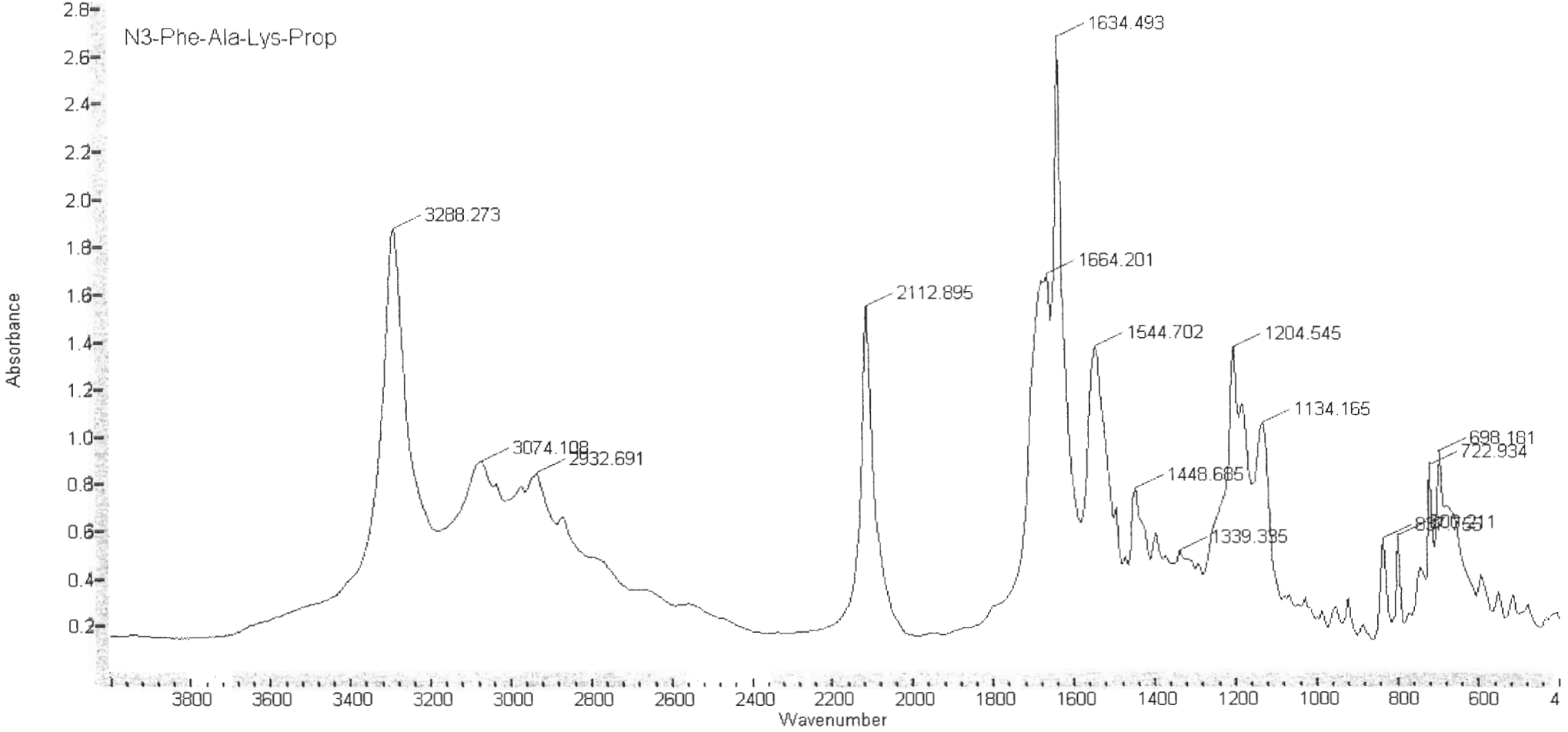
Detector A - 1
(220nm)

Pk #	Name	Retention Time	Area	Area Percent
1		11.567	876780	9.07
2		17.133	8791030	90.93

Totals			9667810	100.00

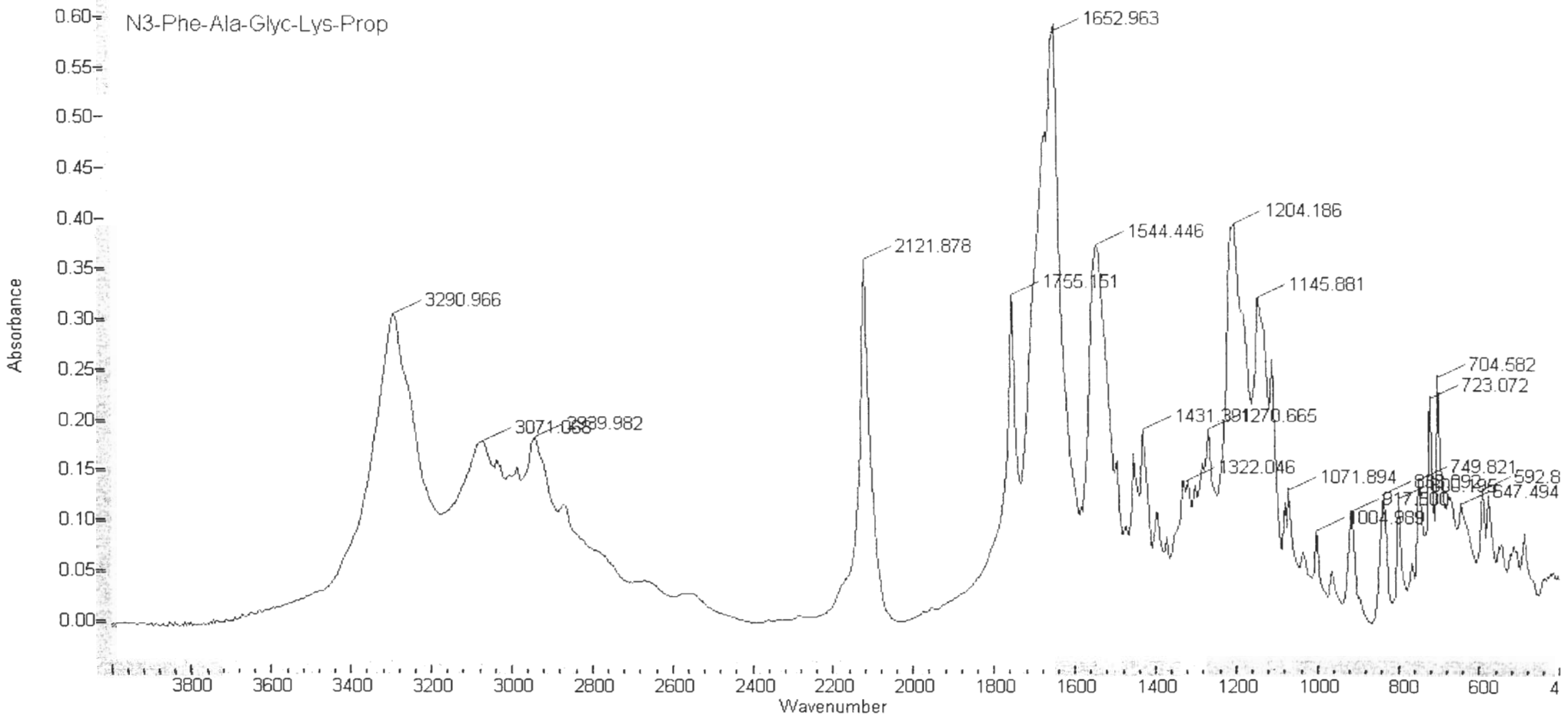
einde

Varian Resolutions Pro



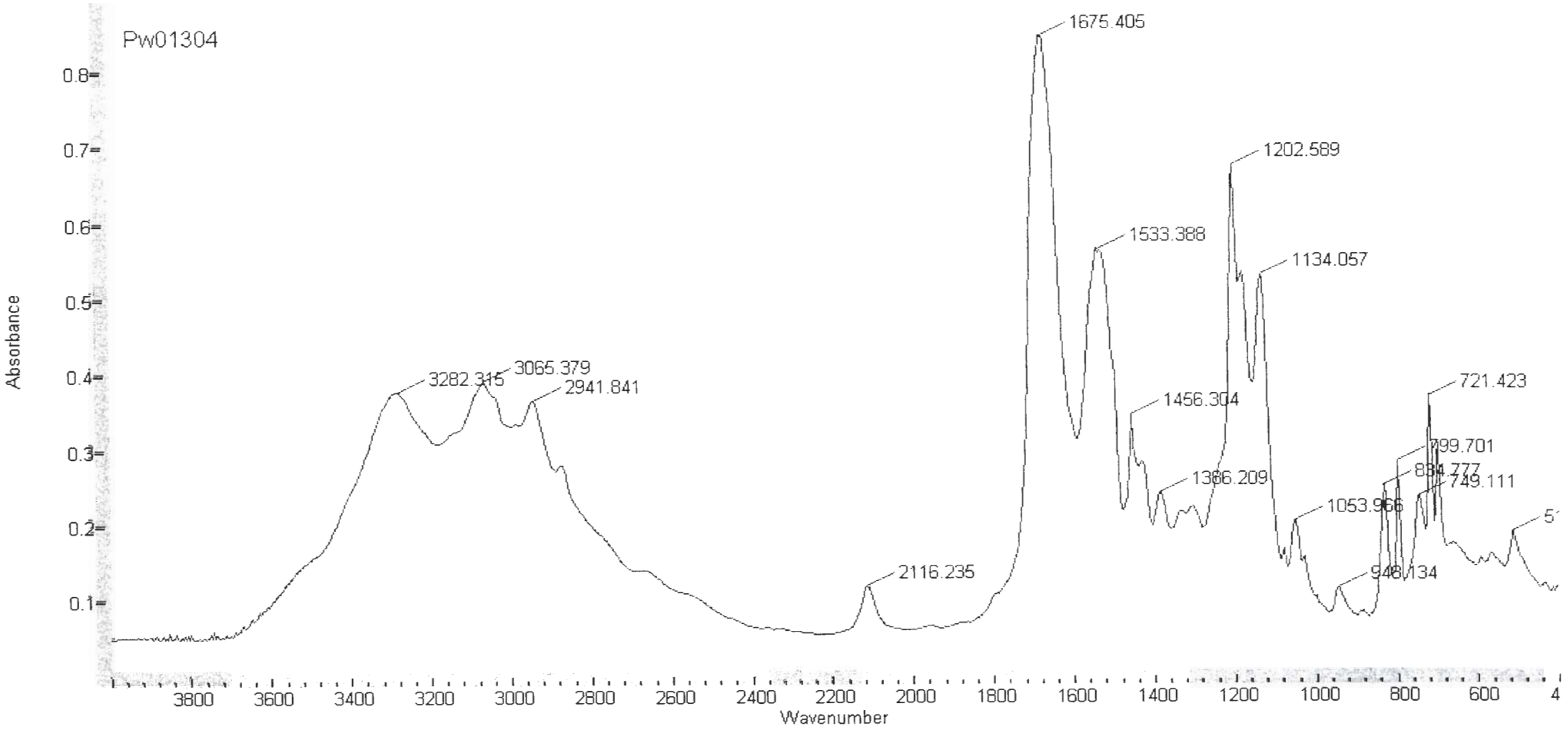
	Name	Spectrum	Peak1Area
Spectrum7	Pw01303		
Spectrum8	Pw01302		
Spectrum9	Pw01302metc02		
Spectrum10	Pw01301		
Spectrum11	N3-Phe-Ala-Lys-Prop		0.000
Spectrum12	background		

Varian Resolutions Pro



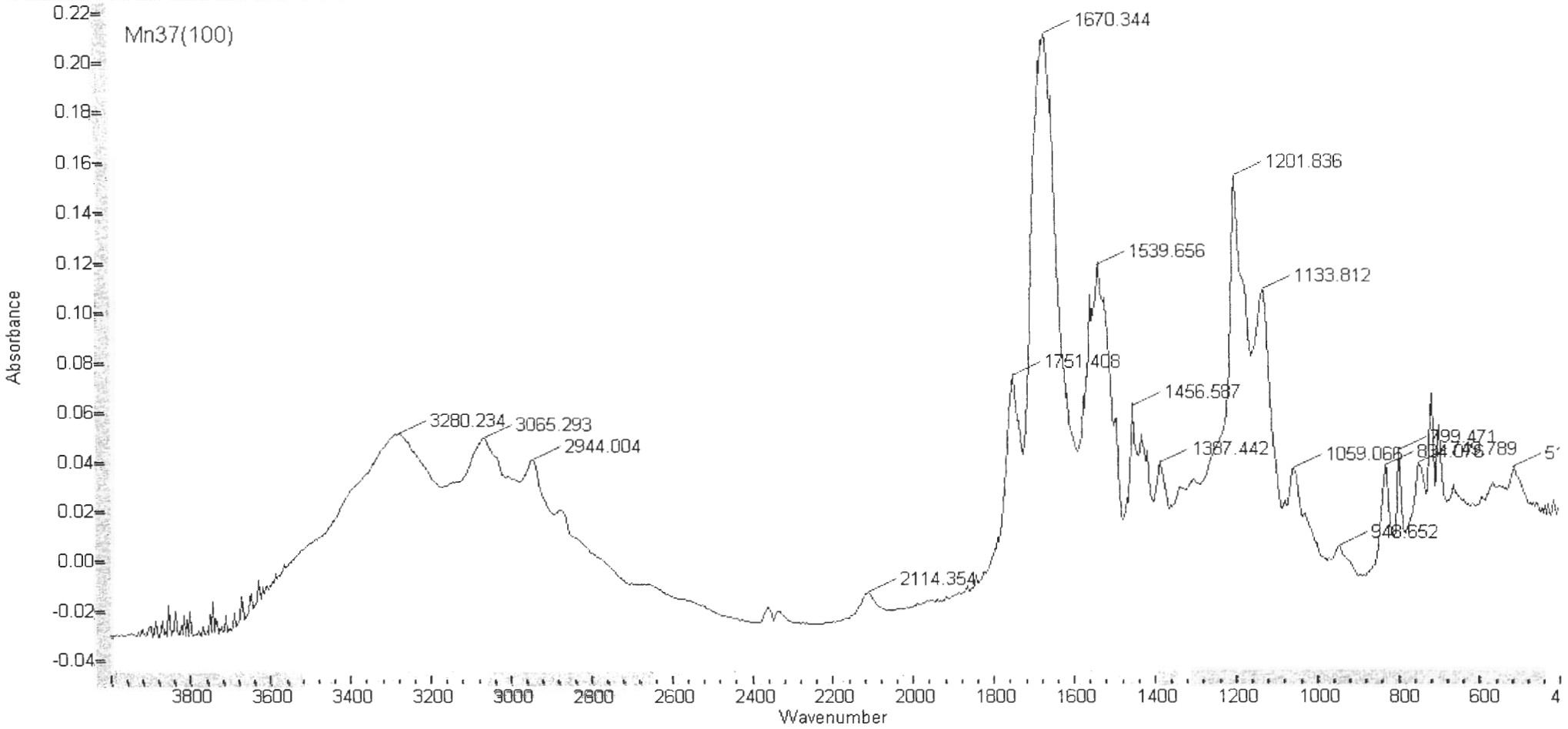
	Name	Spectrum	Peak1Area
Spectrum3	MVD137monomeer		
Spectrum4	Mn37(100)		
Spectrum5	Mn37(50)		
Spectrum6	Mn37(25)		
Spectrum7	N3-Phe-Ala-Glyc-Lys-Prop		0.000
Spectrum8	Background		

Varian Resolutions Pro



	Name	Spectrum	Peak1Area
Spectrum4	MVD193CuI		
Spectrum5	Pw01305		
Spectrum6	**Pw01304**		0.000
Spectrum7	Pw01303		
Spectrum8	Pw01302		
Spectrum9	Pw01302metc02		

Varian Resolutions Pro



	Name	Spectrum	Peak1Area
Spectrum1	MVD140(100)		
Spectrum2	MVD140(50)		
Spectrum3	MVD137monomeer		
Spectrum4	Mn37(100)		0.000
Spectrum5	Mn37(50)		
Spectrum6	Mn37(25)		

Sample: Pw15800
Size: 5.3600 mg
Method: Heat/Cool/Heat

DSC

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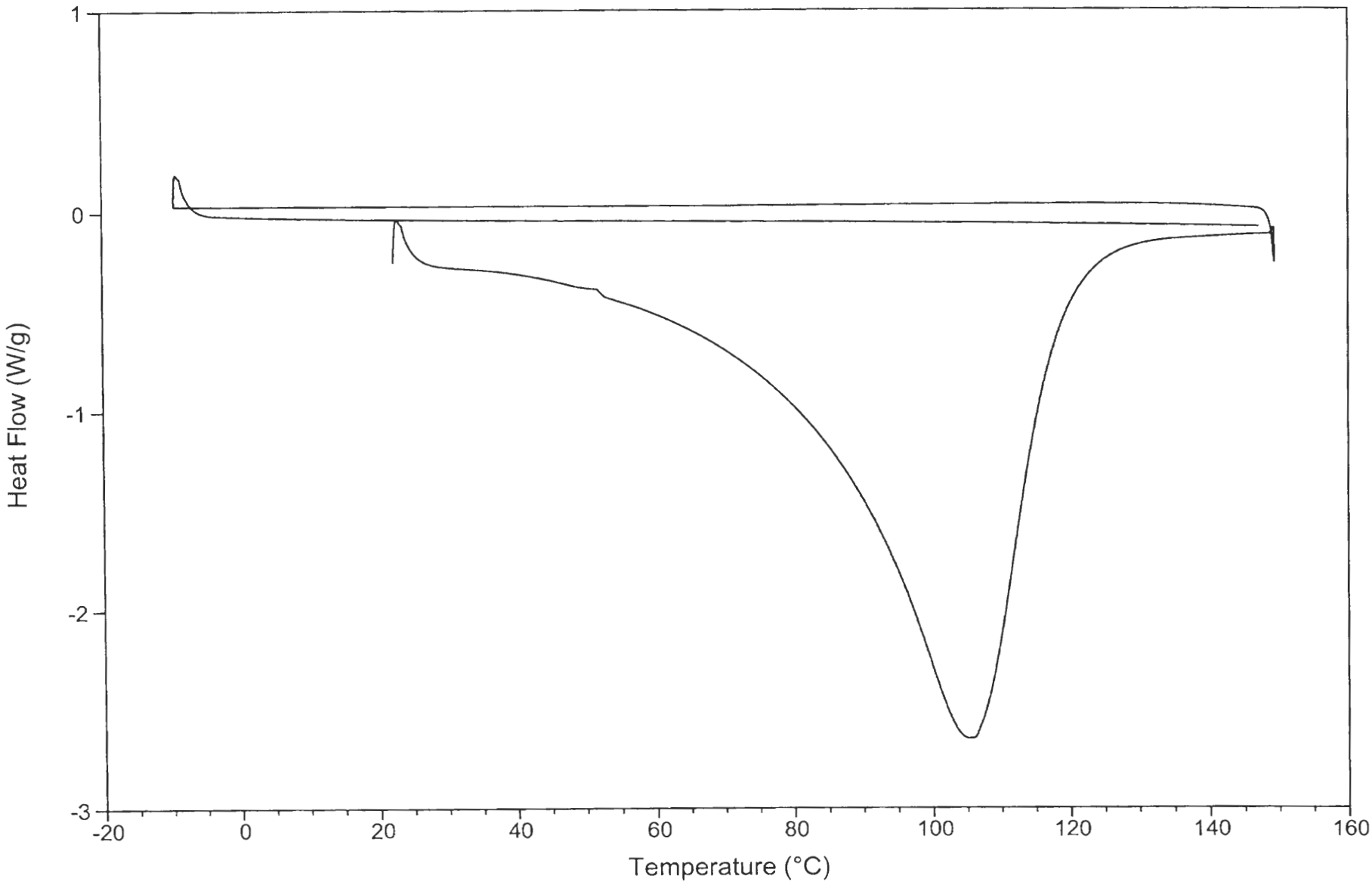
Operator: Maarten
Run Date: 2007-11-07 19:13
Instrument: DSC Q1000 V9.8 Build 296

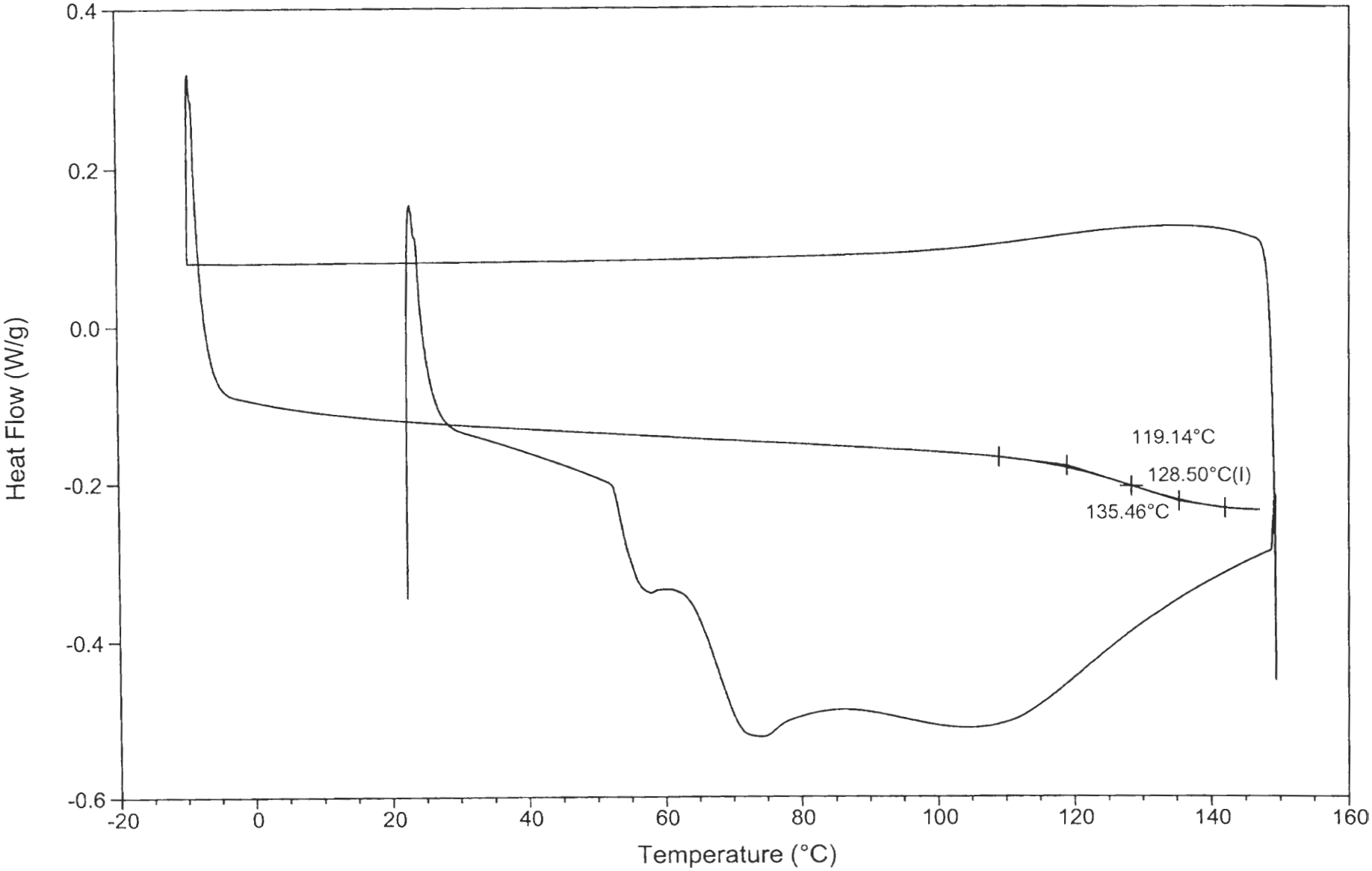


17

Sample: Mn38500
Size: 3.4400 mg
Method: Heat/Cool/Heat

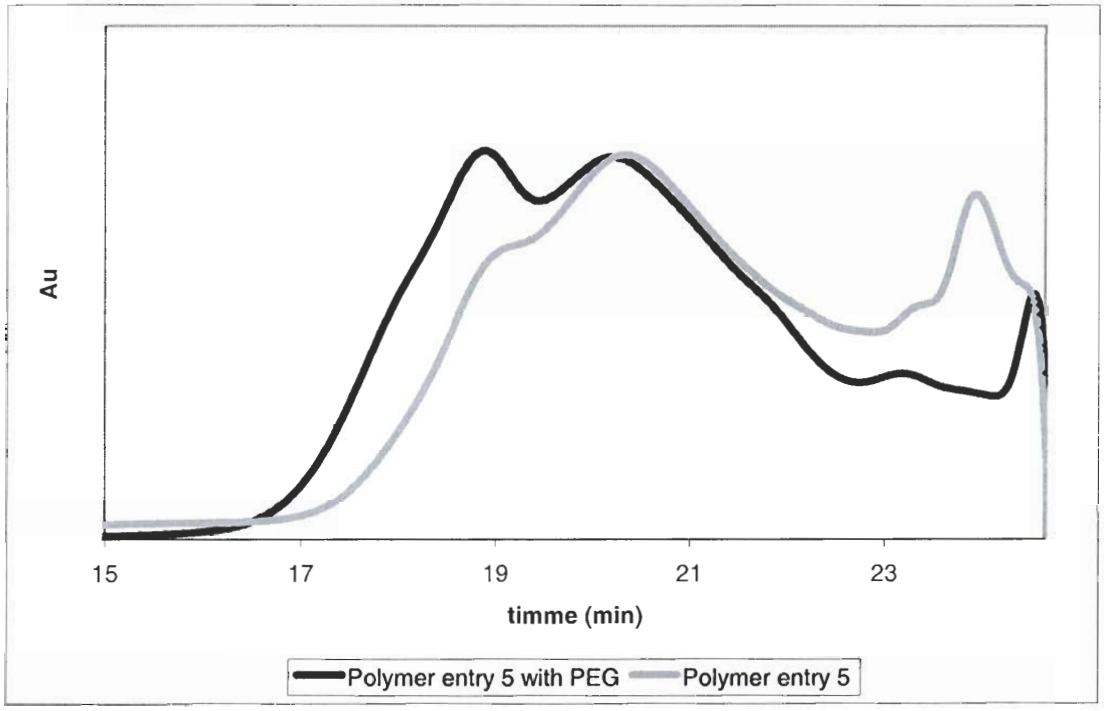
DSC

File: D:\MaartenvDijk\Data\mn38500.001
Operator: Maarten
Run Date: 2007-11-07 15:56
Instrument: DSC Q1000 V9.8 Build 296



8 1

GPC data


Au
15
17
19
21
23
timme (min)
Polymer entry 5 with PEG
Polymer entry 5

C:\Xcalibur\...\MVD228_A2_msms446_5 10/26/2007 9:37:10 AM

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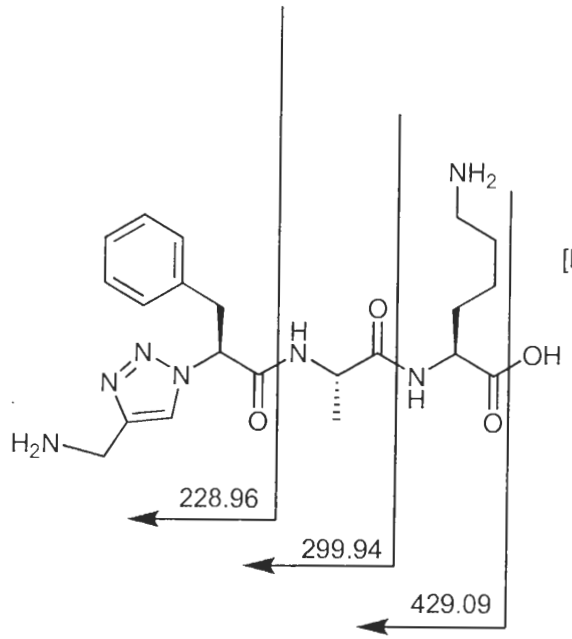
T: + c ESI Full ms2 446.50@35.00 [120.00-1000.00]



Relative Abundance

m/z

401.20
228.96
429.09
330.10
382.84
312.28
243.02
199.37
187.05
226.40
299.94
356.43
428.07
446.38
244.17

20

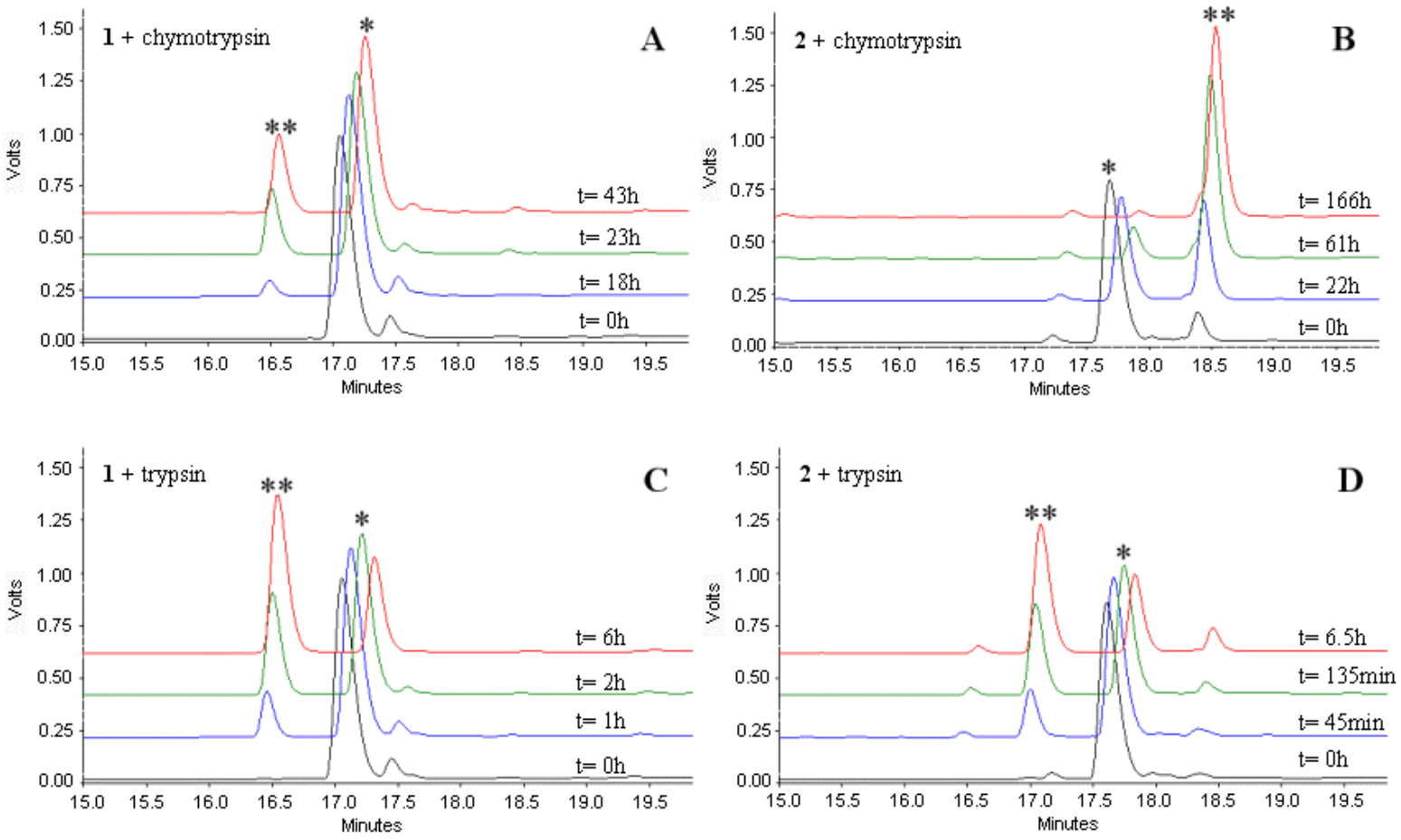


Figure SI-21. RP-HPLC chromatograms of monomer **1** (N_3-Phe-Ala-Lys-propargyl amide) incubated with chymotrypsin (A) * = N_3-Phe-Ala-Lys-propargyl amide, ** = N_3-Phe-OH, and trypsin (C) * = N_3-Phe-Ala-Lys-propargyl amide, ** = N_3-Phe-Ala-Lys-OH; and monomer **2** (N_3-Phe-Ala-Glyc-Lys-propargyl amide) incubated with chymotrypsin (B) * = N_3-Phe-Ala-Glyc-Lys-propargyl amide, ** = N_3-Phe-OH and trypsin (D) * = N_3-Phe-Ala-Glyc-Lys-propargyl amide, ** = N_3-Phe-Ala-Glyc-Lys-OH.