

Supplementary Information

Synthesis and Evaluation of Peptidic Thrombin Inhibitors Bearing Acid-Stable Sulfotyrosine Analogues

Luke J. Dowman,^{a,b} Stijn M. Agten,^a Jorge Ripoll-Rozada,^{c,d} Bárbara M. Calisto,^e Pedro José Barbosa Pereira,^{c,d} and Richard J. Payne^{a,b*}

^aSchool of Chemistry, The University of Sydney, Sydney, NSW 2006, Australia

^bAustralian Research Council Centre of Excellence for Innovations in Peptide and Protein Science

^cIBMC – Instituto de Biologia Molecular e Celular, Universidade do Porto, 4200-135 Porto, Portugal

^dInstituto de Investigação e Inovação em Saúde, Universidade do Porto, 4200-135 Porto, Portugal

^eALBA Synchrotron, 08290 Cerdanyola del Vallès, Spain

Correspondence and requests for materials should be addressed to Richard J. Payne

(Email: richard.payne@sydney.edu.au)

TABLE OF CONTENTS

1	GENERAL MATERIALS	3
2	GENERAL PROCEDURES	4
2.1	RESIN LOADING.....	4
2.1.1	2-CHLOROTRITYL CHLORIDE (2-CTC) RESIN.....	4
2.1.2	WANG RESIN	4
2.2	ITERATIVE PEPTIDE ASSEMBLY	5
2.2.1	DEPROTECTION CYCLES	5
2.2.2	COUPLING CYCLES	5
2.2.3	CAPPING CYCLES.....	6
2.2.4	CLEAVAGE FROM RESIN	6
2.3	PREPARATIVE CHROMATOGRAPHY.....	6
2.3.1	REVERSED-PHASE HIGH PERFORMANCE LIQUID CHROMATOGRAPHY (RP-HPLC) 6	
2.4	ANALYTICAL CHROMATOGRAPHY-MASS SPECTROMETRY.....	7
2.4.1	ULTRA PERFORMANCE LIQUID CHROMATOGRAPHY-MASS SPECTROMETRY (UPLC-MS)	7
2.4.2	ANALYTICAL ULTRA PERFORMANCE LIQUID CHROMATOGRAPHY (UPLC)	7
2.5	NUCLEAR MAGNETIC RESONANCE (NMR) SPECTROSCOPY	7
2.6	MASS SPECTROMETRY (MS)	8
2.6.1	ELECTROSPRAY IONISATION (ESI) LOW RESOLUTION MS	8
2.6.2	ELECTROSPRAY IONISATION (ESI) HIGH RESOLUTION MS	8
2.7	INFRARED (IR) SPECTROSCOPY	8
2.8	POLARIMETRY	8
2.9	MELTING POINT MEASUREMENT	8
3	SYNTHESIS OF Fmoc-PROTECTED SULFONATED TYROSINE BUILDING BLOCKS	9
4	SYNTHESIS OF PEPTIDIC THROMBIN INHIBITORS	20
4.1	TTI.....	20
4.2	VARIEGIN	28
5	OPTIMIZATION OF NEOPENTYL SULFONATE ESTER DEPROTECTION.....	28
6	THROMBIN INHIBITION ASSAY.....	38
7	ACID STABILITY ASSAYS.....	40
8	PEPTIDE CRYSTALLIZATION TRIALS	41
9	X-RAY CRYSTALLOGRAPHY.....	41
10	NMR SPECTRA FOR 2, 3 AND SYNTEHTIC INTERMEDIATES	42
11	REFERENCES.....	81

1 GENERAL MATERIALS

Peptide grade *N,N*-dimethylformamide (DMF) and dichloromethane (CH₂Cl₂) for peptide synthesis were purchased from RCI Labscan and Merck, respectively. Gradient grade acetonitrile (MeCN) for chromatography was purchased from Sigma Aldrich and ultrapure water (Type 1) was obtained from a Merck Millipore Direct-Q 5 water purification System. All chromatography solvents were supplemented with either trifluoroacetic acid (TFA) or formic acid (FA) purchased from Sigma-Aldrich as indicated. Standard Fmoc-protected amino acids (Fmoc-Xaa-OH), coupling reagents and resins were purchased from Mimotopes and Novabiochem. Fmoc-SPPS was performed manually in polypropylene Teflon-fritted syringes purchased from Torviq or through automated synthesis on a Gyros Protein Technologies[®] Symphony automated peptide synthesiser or a CEM[®] Liberty Blue automated microwave peptide synthesiser at temperatures as specified. All other reagents were purchased from Sigma Aldrich, AK Scientific or Merck and used as received.

All reactions were carried out under an argon atmosphere and at room temperature (22 °C) unless the reaction was performed under aqueous conditions or unless otherwise specified. Reactions undertaken at -78 °C utilised a bath of dry ice and acetone. Reactions carried out at 0 °C employed a bath of water and ice. Anhydrous THF, CH₂Cl₂ and MeOH were obtained using a PureSolv solvent purification system with water detectable only in low ppm levels. Reactions were monitored by thin layer chromatography (TLC) on aluminium backed silica plates (Merck Silica Gel 60 F254). Visualisation of TLC plates was undertaken with an ultraviolet (UV) light at $\lambda = 254$ nm and staining with solutions of vanillin, ninhydrin, phosphomolybdic acid (PMA), potassium permanganate or sulfuric acid, followed by exposure of the stained plates to heat. Silica flash column chromatography (Merck Silica Gel 60 40 – 63 μ m) was undertaken to purify crude reaction mixtures using solvents as specified.

2 GENERAL PROCEDURES

2.1 RESIN LOADING

2.1.1 2-CHLOROTRITYL CHLORIDE (2-CTC) RESIN

2-CTC resin (1.14 mmol g⁻¹ loading unless otherwise specified, Novabiochem) was swollen in CH₂Cl₂ for 30 min and then washed with CH₂Cl₂ (4 x 2 mL). The resin was treated with a solution of thionyl chloride in CH₂Cl₂ (2 vol%) for 30 minutes and then thoroughly washed with CH₂Cl₂ (10 x 2 mL). The washed resin was then treated with a solution of Fmoc-protected amino acid (2 equiv.) and *i*Pr₂NEt (8 equiv.) in CH₂Cl₂ (*c* = 0.1 M) for 16 h at room temperature. The resin was then filtered and washed with CH₂Cl₂ (4 x 2 mL) before being treated with a solution of methanol and *i*Pr₂NEt in CH₂Cl₂ (17:2:1 v/v/v CH₂Cl₂:MeOH:*i*Pr₂NEt) for 30 min at room temperature. The resin was finally filtered and washed with CH₂Cl₂ (4 x 2 mL) and DMF (4 x 2 mL) prior to iterative peptide assembly.

2.1.2 WANG RESIN

Wang resin (0.92 mmol g⁻¹ loading unless otherwise specified, Bachem) was swollen in CH₂Cl₂ for 30 min and then washed with CH₂Cl₂ (4 x 2 mL). While the resin was swelling, the Fmoc-Xaa-OH (10 equiv.) to be loaded was dissolved in CH₂Cl₂ (*c* = 0.2 M) and cooled to 0 °C. *N,N'*-Diisopropylcarbodiimide (DIC) (5 equiv.) was then added to the amino acid solution, which was subsequently warmed to room temperature and stirred for 30 min until a white precipitate formed. The mixture was then concentrated under a stream of nitrogen gas to form a crude solid. The solid was then dissolved in 1:1 v/v CH₂Cl₂:DMF (*c* = 1 M), to which a small amount of 4-dimethylaminopyridine (DMAP) (cat.) was then added. The loading solution was then applied to the swollen resin which was shaken at room temperature for 16 h. The loading solution was then ejected, and the resin washed with CH₂Cl₂ (4 x 2 mL), DMF (4 x 2 mL) and CH₂Cl₂ (5 x 2 mL) before being treated with a capping solution of 10 vol% Ac₂O in CH₂Cl₂ (with cat. DMAP) for 45 min at room temperature. Finally, the capping solution was ejected, and the resin was washed with CH₂Cl₂ (4 x 2 mL) and DMF (4 x 2 mL) prior to iterative peptide assembly.

2.2 ITERATIVE PEPTIDE ASSEMBLY

2.2.1 DEPROTECTION CYCLES

Automated Deprotection (Symphony): The resin was treated with a solution of 20 vol% piperidine in DMF (2 x 2 mL x 3 min), filtered and then washed with DMF (4 x 2 mL).

Automated Deprotection (Liberty Blue): The resin was treated with a solution of 20 vol% piperidine in DMF (1 x 10 mL) at 90 °C for 50 s, then filtered and washed with DMF (4 x 4 mL).

Manual Deprotection: The resin was treated with a solution of 20 vol% piperidine in DMF (3 x 2 mL x 3 min), filtered and then washed with DMF (4 x 2 mL).

2.2.2 COUPLING CYCLES

Automated Coupling (Symphony): The resin was treated with a solution of Fmoc-Xaa-OH (4 equiv.), DIC (4 equiv.) and Oxyma (4 equiv.) in DMF ([Fmoc-Xaa-OH] = 0.3 M) for 40 min at room temperature. The resin was then filtered and washed with DMF (4 x 2 mL).

Automated Coupling (Liberty Blue): The resin was treated with a solution of Fmoc-Xaa-OH (5 mL, 0.2 M), DIC (2 mL, 0.5 M) and Oxyma (1 mL, 1 M) at 90 °C for 2 min,* then filtered and subjected immediately to the next deprotection cycle.

**All Fmoc-Arg(Pbf)-OH residues were coupled twice before subsequent deprotection.*

**All Fmoc-His(Trt)-OH residues were coupled at 50 °C for 10 min.*

Manual Coupling (Non-Standard): The resin was treated with a solution of Fmoc-Xaa-OH (1.5 equiv.), DIC (1.5 equiv.) and 1-hydroxy-7-azabenzotriazole (HOAt) (3 equiv.) in DMF ([Fmoc-Xaa-OH] = 0.1 M) for 16 h at room temperature. The resin was then filtered and washed with DMF (4 x 2 mL).

2.2.3 CAPPING CYCLES

Automated Capping (Symphony): The resin was treated with a solution of Ac₂O (2.5 vol%) and *i*Pr₂NEt (5 vol%) in DMF for 5 min at room temperature then washed with DMF (4 x 2 mL).

Manual Capping: The resin was treated with a solution of Ac₂O (10 vol%) in piperidine for 5 min at room temperature then washed with DMF (4 x 2 mL).

2.2.4 CLEAVAGE FROM RESIN

The resin was washed with CH₂Cl₂ (10 x 2 mL) then treated with an acidic cocktail of TFA:*i*Pr₃SiH:H₂O (90:5:5 v/v/v, 1-5 mL) for 2-3 h at room temperature with agitation. The cleavage cocktail was then ejected into a 50 mL centrifuge tube and concentrated under a gentle stream of N₂ gas. Once reduced to a small volume (~0.5 mL), pre-cooled Et₂O (~40 mL) was added to precipitate crude peptide. The resulting precipitate was pelleted by centrifugation (4000 x g, 5 min, 4 °C), the ether supernatant decanted and the remaining peptide pellet allowed to dry under a gentle stream of N₂ gas. This dry pellet was then stored at -20 °C until purification or further use.

2.3 PREPARATIVE CHROMATOGRAPHY

2.3.1 REVERSED-PHASE HIGH PERFORMANCE LIQUID CHROMATOGRAPHY (RP-HPLC)

Preparative and semi-preparative reversed-phase high performance liquid chromatography (HPLC) was performed using a Waters 600E multisolvent delivery system with a Rheodyne 7725i injection valve (5 mL loading loop) with a Waters 500 pump and a Waters 490E programmable wavelength detector operating at 214 nm and 254 nm. Preparative reversed-phase HPLC was performed using a Waters Sunfire C18 column (5 μm, 19 x 150 mm or 5 μm, 30 x 150 mm) at a flow rate of either 14 mL min⁻¹ or 38 mL min⁻¹. Semi-preparative reversed-phase HPLC was performed using a Waters Sunfire C18 column (5 μm, 10 x 250 mm) at a flow rate of 4 mL min⁻¹. All preparative and semi-preparative HPLC used a mobile phase of ultrapure (type 1) water (Solvent A) and MeCN (Solvent B) with 0.1 vol% trifluoroacetic acid (TFA) on linear gradients, unless otherwise specified.

2.4 ANALYTICAL CHROMATOGRAPHY-MASS SPECTROMETRY

2.4.1 ULTRA PERFORMANCE LIQUID CHROMATOGRAPHY-MASS SPECTROMETRY (UPLC-MS)

Ultra-performance liquid Chromatography-Mass Spectrometry (UPLC-MS) was performed on a Shimadzu 2020 UPLC-MS instrument with a Nexera X2 LC-30AD pump, Nexera X2 SPD-M30A UV/Vis diode array detector and a Shimadzu 2020 (ESI) mass spectrometer operating in positive mode. Separations were performed on a Waters Acquity BEH300 1.7 μm , 2.1 x 50 mm (C18) column at a flow rate of 0.6 mL min⁻¹ unless otherwise specified. All separations were performed using a mobile phase of 0.1 vol% FA in water (Solvent A) and 0.1 vol% FA in MeCN (Solvent B) using linear gradients as specified.

2.4.2 ANALYTICAL ULTRA PERFORMANCE LIQUID CHROMATOGRAPHY (UPLC)

Analytical UPLC was performed on a Waters Acquity UPLC system equipped with a PDA $e\lambda$ detector ($\lambda = 210 - 400$ nm), a sample manager FAN and Quaternary Solvent Manager (H-Class) modules. Separations were performed on a Waters Acquity BEH300 1.7 μm , 2.1 x 50 mm (C18) column at a flow rate of 0.6 mL min⁻¹. All separations were performed using a mobile phase of 0.1 vol% TFA in water (Solvent A) and 0.1 vol% TFA in MeCN (Solvent B) using linear gradients as specified.

2.5 NUCLEAR MAGNETIC RESONANCE (NMR) SPECTROSCOPY

¹H NMR spectra were obtained at 300 K using a Bruker Avance DRX 400 or DRX 500 at frequencies of 400 MHz or 500 MHz, respectively, in CDCl₃, MeOD or D₂O. Chemical shifts are reported in parts per million (ppm) and coupling constant(s) (*J*) in Hertz (Hz). The residual solvent peaks were used as internal standards (e.g. CDCl₃ δ : 7.26 ppm) without the use of tetramethylsilane (TMS). ¹H NMR data are reported as follows: chemical shift values (ppm), relative integral, multiplicity (s = singlet, d = doublet, t = triplet, q = quartet, m = multiplet), *J* in Hz, and assignments where possible. ¹³C {¹H} NMR spectra were obtained using a Bruker DRX 400 or DRX 500 at 100 MHz or 126 MHz in CDCl₃, D₂O or MeOD unless otherwise specified. ¹³C {¹H} NMR data are reported as chemical shift values (ppm) referenced to the solvent resonance (e.g. CDCl₃ δ : 77.2 ppm).

2.6 MASS SPECTROMETRY (MS)

2.6.1 ELECTROSPRAY IONISATION (ESI) LOW RESOLUTION MS

Low resolution mass spectra for novel compounds were recorded on a Bruker amaZon SL mass spectrometer (ESI) operating in positive mode or on a Shimadzu 2020 (ESI) mass spectrometer operating in positive mode for previously reported compounds.

2.6.2 ELECTROSPRAY IONISATION (ESI) HIGH RESOLUTION MS

High resolution mass spectra were recorded on a Bruker-Daltonics Apex Ultra 7.0 T Fourier transform (FTICR) mass spectrometer using a matrix of α -cyano-4-hydroxycinnamic acid in 1:1 v/v water:MeCN containing 0.1 vol% TFA.

2.7 INFRARED (IR) SPECTROSCOPY

Infrared (IR) spectra were obtained on a Bruker ALPHA spectrometer with Attenuated Total Reflection (ATR) capability and using OPUS 6.5 software.

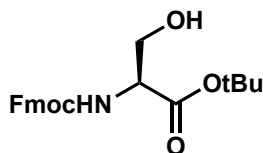
2.8 POLARIMETRY

Optical rotation measurements were obtained on a Perkin-Elmer 341 polarimeter at 589 nm (sodium D line) with a cell path length of 1 dm. Concentrations are reported in g/100 mL.

2.9 MELTING POINT MEASUREMENT

Melting point measurements were obtained on a Stanford Research Systems OptiMelt automated melting point system by visual inspection of the material.

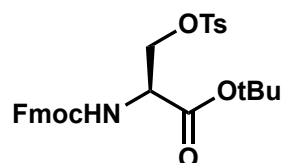
3 SYNTHESIS OF FMOC-PROTECTED SULFONATED TYROSINE BUILDING BLOCKS



tert-butyl (((9*H*-fluoren-9-yl)methoxy)carbonyl)-*L*-serinate

A solution of *tert*-butyl 2,2,2-trichloroacetimidate (21.8 mL, 122 mmol) in cyclohexane (125 mL) was added to a solution of Fmoc-*L*-serine (10.0 g, 30.6 mmol) in EtOAc (250 mL) and the resulting reaction mixture was stirred at room temperature for 16 h. The mixture was concentrated *in vacuo* and re-dissolved in 25 vol% EtOAc in hexane for purification by flash silica gel chromatography (20-40 vol% EtOAc in hexane) to afford the pure product as a white foam (6.82 g, 17.8 mmol, 58%).

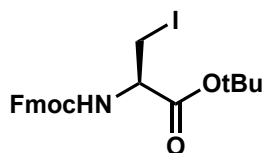
¹H NMR: (500 MHz, CDCl₃) δ 7.76 (d, *J* = 7.5 Hz, 2H), 7.60 (d, *J* = 7.5 Hz, 2H), 7.40 (td, *J* = 7.5, 1.0 Hz, 2H), 7.31 (tt, *J* = 7.4, 1.4 Hz, 2H), 5.79 (d, 1H), 4.41 (d, *J* = 7.2 Hz, 2H), 4.33 (d, *J* = 7.0 Hz, 1H), 4.22 (t, *J* = 7.0 Hz, 1H), 3.93 (s, 2H), 2.47 (s, 1H), 1.49 (s, 9H); **¹³C{¹H} NMR:** (126 MHz, CDCl₃) δ 169.59, 163.74, 156.37, 143.85, 143.73, 141.34, 141.31, 127.76, 127.12, 127.09, 125.12, 120.02, 120.00, 91.90, 82.95, 67.18, 63.68, 56.65, 47.17, 28.02; **LRMS:** (+ESI) *m/z* 406 [M+Na]⁺; **HRMS:** (+ESI) Calc. for C₂₂H₂₅NO₅Na: 406.16249 [M+Na]⁺, Found: 406.16182 [M+Na]⁺; **IR (ATR):** ν_{max} = 3430, 3343, 3066, 2978, 2945, 2889, 1702, 1606, 1516, 1477, 1450, 1369, 1341, 1229, 1153, 1058, 912, 826, 759, 739, 621, 536, 426 cm⁻¹; **[α]_D:** +0.023° (*c* 0.3, CH₂Cl₂). These data are in agreement with those published by Jobron and Hummel.¹



***tert*-butyl *N*-(((9*H*-fluoren-9-yl)methoxy)carbonyl)-*O*-tosyl-*L*-serinate**

Fmoc-*L*-Ser-OtBu (6.82 g, 17.8 mmol) was dissolved in anhydrous pyridine (70 mL) and cooled to -10 °C. TsCl (6.78 g, 35.6 mmol) was then added to the reaction mixture, which was stirred at -10 °C for 16 h. After 16 h, the reaction mixture was poured onto ice-cold water (100 mL) and the aqueous mixture was extracted with EtOAc (100 mL). The organic phase was washed with 1 M citric acid (3 x 100 mL), saturated aqueous NaHCO₃ (2 x 100 mL), brine (100 mL), 1 M aqueous HCl (2 x 100 mL), saturated aqueous sodium bicarbonate (2 x 100 mL) and brine (3 x 100 mL). The washed organic phase was then dried over MgSO₄, filtered and concentrated *in vacuo* to a yellow oil. The resulting crude material was purified by flash silica gel chromatography (15-30 vol% EtOAc in hexane) affording the pure product as a white foam (7.85 g, 14.6 mmol, 82%).

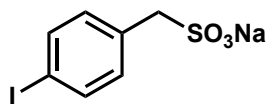
¹H NMR: (500 MHz, CDCl₃) δ 7.80 – 7.73 (m, 4H), 7.59 (dd, *J* = 10.3, 7.4 Hz, 2H), 7.41 (td, *J* = 7.4, 2.6 Hz, 2H), 7.36 – 7.29 (m, 2H), 7.26 (d, *J* = 8.2 Hz, 2H), 5.62 (d, *J* = 7.5 Hz, 1H), 4.49 – 4.41 (m, 2H), 4.37 – 4.22 (m, 3H), 4.18 (t, *J* = 7.3 Hz, 1H), 2.35 (s, 3H), 1.46 (s, 9H); **¹³C{¹H} NMR:** (126 MHz, CDCl₃) δ 167.08, 155.57, 145.15, 143.78, 143.65, 141.29, 132.39, 129.94, 128.00, 127.81, 127.14, 125.24, 125.16, 120.02, 83.79, 69.53, 67.42, 53.78, 47.01, 27.87, 21.56; **LRMS:** (+ESI) *m/z* 560.19 [M+Na]⁺; **IR (ATR):** ν_{max} = 3434, 3326, 3064, 2979, 2931, 2896, 1721, 1598, 1509, 1450, 1367, 1344, 1248, 1223, 1190, 1177, 1156, 1086, 1056, 995, 974, 908, 842, 816, 760, 740, 665, 554 cm⁻¹; **[α]_D:** +0.093° (*c* 0.3, CH₂Cl₂).



***tert*-butyl (*R*)-2-((((9*H*-fluoren-9-yl)methoxy)carbonyl)amino)-3-iodopropanoate (**6**)**

Fmoc-L-Ser(OTs)-OtBu (**6**) (1.91 g, 3.55 mmol) was dissolved in acetone (8 mL) and to this solution was added a solution of sodium iodide (1.07 g, 7.11 mmol) in acetone (4 mL). The reaction mixture was stirred under nitrogen for 24 h at room temperature then filtered. The filtrate was concentrated *in vacuo* and the resulting foam was redissolved in CHCl₃ (50 mL) and washed with H₂O (3 x 50 mL), saturated sodium thiosulfate (2 x 50 mL) and brine (50 mL). The washed organic layer was concentrated *in vacuo* to afford a white foam which was purified by flash chromatography (10-30 vol% EtOAc in hexane) to afford the pure product **6** as a white foam (1.31 g, 2.66 mmol, 75%).

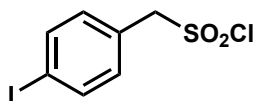
¹H NMR: (500 MHz, CDCl₃) δ 7.78 (d, *J* = 7.5 Hz, 2H), 7.63 (d, *J* = 7.5 Hz, 2H), 7.41 (t, *J* = 7.4 Hz, 2H), 7.34 (tdd, *J* = 7.5, 3.4, 1.2 Hz, 2H), 5.74 (d, *J* = 7.2 Hz, 1H), 4.44 (td, *J* = 7.4, 3.6 Hz, 2H), 4.37 (dd, *J* = 10.6, 7.2 Hz, 1H), 4.26 (t, *J* = 7.3 Hz, 1H), 3.67 – 3.57 (m, 2H), 1.54 (s, 9H); **¹³C{¹H} NMR:** (126 MHz, CDCl₃) δ 168.21, 155.43, 143.82, 143.74, 141.33, 127.79, 127.16, 127.13, 125.25, 125.18, 120.05, 83.63, 67.34, 54.13, 47.13, 28.04, 8.46; **LRMS:** (+ESI) *m/z* 516.07 [M+Na]⁺; **IR (ATR):** *v*_{max} = 3419, 3329, 3065, 3040, 2977, 2943, 2900, 1710, 1502, 1449, 1369, 1338, 1299, 1249, 1216, 1152, 1118, 1060, 987, 909, 843, 758, 736, 647, 621, 544, 473, 425 cm⁻¹; **[α]_D:** +0.15° (*c* 0.3, CH₂Cl₂). These data are in agreement with those published by Jobron and Hummel.¹



Sodium 4-iodobenzylsulfonate

4-iodobenzyl bromide (25.31 g, 85.24 mmol) was dissolved in acetone (185 mL) and to this solution was added a solution of sodium sulfite (10.74 g, 85.24 mmol) in water (185 mL). The reaction was refluxed at 110 °C for 24 h. After 24 h the reaction mixture was concentrated under a stream of nitrogen gas to approximately half its original volume, during which a white precipitate formed. The precipitated solution was filtered the resulting solid was washed with acetone (500 mL), yielding the pure product as a white crystalline solid (23.44 g, 73.23 mmol, 86%).

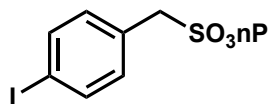
¹H NMR: (500 MHz, D₂O) δ 7.74 (d, *J* = 8.3 Hz, 2H), 7.14 (d, *J* = 8.4 Hz, 2H), 4.08 (s, 2H); **¹³C{¹H} NMR:** (126 MHz, D₂O) δ 137.65, 132.29, 131.54, 93.24, 56.39; **LRMS:** (-ESI) *m/z* 297 [M-H]⁻; **HRMS:** (-ESI) Calc. for C₇H₆IO₃S: 296.90878 [M]⁻; Found: 296.90845 [M]⁻; **IR (ATR):** *v*_{max} = 2942, 1480, 1414, 1215, 1189, 1142, 1042, 1003, 892, 819, 762, 704, 636, 580, 536, 523 cm⁻¹; **m.p.:** >400 °C (decomp.). These data are in agreement with those published by Liu *et al.*²



(4-iodophenyl)methanesulfonyl chloride

Sodium (4-iodophenyl)methanesulfonate (2.07 g, 6.47 mmol) was dissolved in a mixture of sulfolane and MeCN (1:1 v/v, 8.30 mL) and heated to 60 °C. Phosphorus oxychloride (3.62 mL, 38.8 mmol) was added to the mixture which was then stirred at 60 °C for 4 h. The mixture was cooled to room temperature and poured over ice-cold H₂O (50 mL) to form a white precipitate. The resulting suspension was filtered, and the solid product was re-dissolved in CH₂Cl₂ (100 mL). The CH₂Cl₂ solution was washed with H₂O (3 x 100 mL) and brine (2 x 100 mL), then dried over MgSO₄, filtered and concentrated *in vacuo* to afford the pure product as a white crystalline solid (1.82 g, 5.75 mmol, 89%).

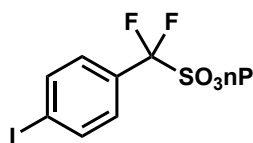
¹H NMR: (500 MHz, CDCl₃) δ 7.73 (d, *J* = 8.3 Hz, 2H), 7.14 (d, *J* = 8.4 Hz, 2H), 4.72 (s, 2H); **¹³C{¹H} NMR:** (126 MHz, CDCl₃) δ 138.51, 132.94, 125.76, 96.96, 70.25; **LRMS:** (-ESI) *m/z* 314 [M-H]⁻; **HRMS:** (-ESI) Calc. for C₁₂H₁₇IO₃SNa: 314.87489 [M-H]⁻, Found: 314.87515 [M-H]⁻; **IR (ATR):** ν_{\max} = 3344, 3001, 2946, 1634, 1482, 1405, 1354, 1153, 1101, 630, 562, 512 cm⁻¹; **m.p.:** 145-147 °C. These data are in agreement with those published by Liu *et al.*²



Neopentyl (4-iodophenyl)methanesulfonate (**4**)

(4-iodophenyl)methanesulfonyl chloride (3.64 g, 11.4 mmol) was dissolved in dry THF (40 mL) and cooled to 0 °C. Neopentyl alcohol (1.12 g, 12.6 mmol) was added to the solution followed by Et₃N (1.75 mL, 12.6 mmol). The reaction mixture was warmed to room temperature and stirred for 20 h before being concentrated under a stream of nitrogen gas to afford a crude solid. The solid was re-dissolved in CH₂Cl₂ (100 mL) and washed with H₂O (3 x 100 mL) and brine (2 x 100 mL) before being dried over MgSO₄, filtered and concentrated *in vacuo* to afford the pure product **4** as an off-white solid (3.58 g, 9.72 mmol, 85%).

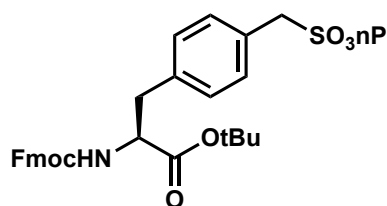
¹H NMR: (500 MHz, CDCl₃) δ 7.66 (d, *J* = 8.4 Hz, 2H), 7.08 (d, *J* = 8.3 Hz, 2H), 4.21 (s, 2H), 3.69 (s, 2H), 0.85 (s, 9H); **¹³C{¹H} NMR:** (126 MHz, CDCl₃) δ 138.07, 132.43, 127.67, 95.14, 79.57, 55.99, 31.84, 26.00; **LRMS:** (+ESI) *m/z* 391 [M+Na]⁺; **HRMS:** (+ESI) Calc. for C₁₂H₁₇IO₃SNa: 390.98353 [M+Na]⁺, Found: 390.98326 [M+Na]⁺; **IR (ATR):** ν_{max} = 2959, 2905, 2869, 1588, 1482, 1402, 1366, 1345, 1266, 1166, 954, 936, 832, 705, 632, 522, 475 cm⁻¹; **m.p.:** 112-114 °C. These data are in agreement with those published by Liu *et al.*²



Neopentyl difluoro(4-iodophenyl)methanesulfonate (**5**)

Neopentyl (4-iodophenyl)methanesulfonate (**4**) (2.70 g, 7.33 mmol) and *N*-fluorobenzensulfonimide (5.55 g, 17.6 mmol) were dissolved in dry THF (100 mL) and cooled to -78 °C. A 1 M solution of NaHMDS in THF (16.1 mL, 16.1 mmol) was added dropwise over 10 min and the reaction mixture was stirred at -78 °C for 2 h before being warmed to room temperature and stirred for an additional 2 h. The reaction was quenched with saturated aqueous NH₄Cl (100 mL) and extracted with Et₂O (3 x 100 mL). The ethereal extracts were washed with 5% w/v NaHCO₃ in H₂O (2 x 300 mL) and brine (300 mL), then dried over MgSO₄, filtered and concentrated *in vacuo* to afford a crude white oil which was purified by flash silica gel chromatography (0-20 vol% EtOAc in hexane) to afford the pure product **5** as a yellow oil (2.51 g, 6.21 mmol, 85%).

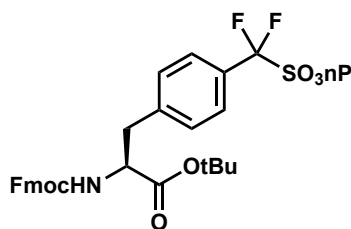
¹H NMR: (500 MHz, CDCl₃) δ 7.78 (d, *J* = 8.8 Hz, 2H), 7.32 (d, *J* = 8.5 Hz, 2H), 4.04 (s, 2H), 0.92 (s, 9H); **¹³C{¹H} NMR:** (126 MHz, CDCl₃) δ 137.02, 127.61, 127.56, 127.51, 126.72, 126.54, 126.36, 122.06, 119.81, 117.55, 98.81, 98.79, 98.77, 83.55, 31.08, 24.79; **¹⁹F{¹H} NMR:** (471 MHz, CDCl₃) δ -100.53; **LRMS:** (+ESI) *m/z* 427 [M+Na]⁺; **HRMS:** (+ESI) Calc. for C₁₂H₁₅F₂IO₃SNa: 426.96469 [M+Na]⁺, Found: 426.96451 [M+Na]⁺; **IR (ATR):** ν_{max} = 2962, 2872, 1590, 1486, 1384, 1368, 1275, 1195, 1139, 1085, 1010, 971, 950, 922, 628, 599, 534 cm⁻¹. These data are in agreement with those published by Liu *et al.*²



***tert*-butyl (*S*)-2-(((9*H*-fluoren-9-yl)methoxy)carbonyl)amino)-3-(4-
(((neopentyloxy)sulfonyl)methyl)phenyl)propanoate (**7**)**

Zinc dust (1.07 g, 16.4 mmol) and a magnetic stirrer were added to a 25 mL round bottom flask and dried *in vacuo* under heat. The flask was cooled to room temperature and iodine (416 mg, 1.64 μ mol) was added followed by a solution of Fmoc-iodoalanine-*Ot*Bu (**6**) (2.69 g, 5.46 mmol) in dry degassed DMF (5 mL) and another catalytic amount of iodine. The reaction was stirred at room temperature for 20 min at which point TLC analysis showed formation of the zincate. A solution of Pd₂(dba)₃ (125 mg, 137 μ mol) and SPhos (112 mg, 273 μ mol) in dry degassed DMF (2.5 mL) was added to the zincate mixture. The flask was washed with additional dry DMF (1 mL) and this wash was added to the reaction mixture. A solution of neopentyl (4-iodophenyl)methanesulfonate **4** (2.61 g, 7.10 mmol) in dry degassed DMF (2.5 mL) was then added to the reaction mixture. The reaction mixture was stirred at room temperature for 24 h then filtered through a celite plug, concentrated under nitrogen, re-dissolved in EtOAc (50 mL) and washed with H₂O (2 x 50 mL), saturated aqueous NH₄Cl (2 x 50 mL) and brine (50 mL). The washed organic phase was dried over MgSO₄, filtered and concentrated *in vacuo*, affording a crude solid purified by flash chromatography (5-30 vol% EtOAc in hexane) to afford the pure product **7** as a yellow foam (1.31 g, 2.16 mmol, 39%).

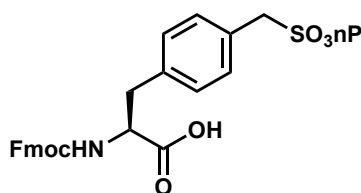
¹H NMR: (500 MHz, CDCl₃) δ 7.77 (d, *J* = 7.6 Hz, 2H), 7.58 (dd, *J* = 7.5, 4.7 Hz, 2H), 7.41 (t, *J* = 7.5 Hz, 2H), 7.36 – 7.29 (m, 4H), 7.19 (d, *J* = 7.7 Hz, 2H), 5.31 (d, *J* = 8.0 Hz, 1H), 4.58 – 4.51 (m, 1H), 4.35 (dd, *J* = 10.6, 6.9 Hz, 1H), 4.38 – 4.34 (m, 1H), 4.32 (s, 2H), 4.21 (t, *J* = 6.9 Hz, 1H), 3.73 (s, 2H), 3.17 – 3.05 (m, 2H), 1.42 (s, 9H), 0.91 (s, 9H); **¹³C{¹H} NMR:** (126 MHz, CDCl₃) δ 170.45, 155.63, 143.97, 143.90, 141.44, 137.37, 130.82, 130.17, 127.86, 127.82, 127.18, 126.76, 125.24, 125.16, 120.13, 120.11, 82.77, 79.64, 67.03, 56.32, 55.14, 47.31, 47.28, 38.26, 31.91, 28.14, 28.10, 26.10; **LRMS:** (+ESI) *m/z* 630 [M+Na]⁺; **IR (ATR):** ν_{\max} = 3351, 3067, 3041, 2972, 2940, 2871, 1719, 1513, 1478, 1450, 1354, 1251, 1223, 1168, 1154, 1107, 1053, 963, 937, 913, 889, 844, 760, 740, 590, 533 cm⁻¹; **[α]_D:** +0.035° (*c* 0.3, CH₂Cl₂).



***tert*-butyl (*S*)-2-(((9*H*-fluoren-9-yl)methoxy)carbonyl)amino)-3-(4-(difluoro((neopentyloxy)sulfonyl)methyl)phenyl)propanoate (**8**)**

Zinc dust (543 mg, 8.32 mmol) and a magnetic stirrer were added to a 10 mL round bottom flask and dried *in vacuo* under heat. The flask was cooled to room temperature, iodine (208 mg, 819 μ mol) was added and the flask again heated until a purple haze was visible. A solution of Fmoc-iodoalanine-*Ot*Bu (**6**) (1.37 g, 2.78 mmol) in DMF (2 mL) was added to the zinc mixture and stirred at room temperature for 2 h, with zincate formation proceeding exothermically. A solution of Pd₂(dba)₃ (63.9 mg, 79.9 μ mol) and SPhos (57.1 mg, 139 μ mol) in DMF (1 mL) was then added to the zincate mixture followed by a solution of neopentyl difluoro(4-iodophenyl)methanesulfonate (**5**) (1.46 g, 3.63 mmol) in DMF (2 mL). The reaction mixture was then stirred at room temperature for 16 h. The mixture was filtered through celite and concentrated under a stream of N₂ gas before being re-dissolved in EtOAc (10 mL), washed with H₂O (2 x 10 mL), saturated NH₄Cl (2 x 10 mL) and brine (10 mL). The organic layer was dried over MgSO₄, then filtered and concentrated *in vacuo* to give crude material which was purified by silica flash chromatography (5-30 vol% EtOAc in hexane) to afford the product **8** as a white foam (449 mg, 0.912 mmol, 33%).

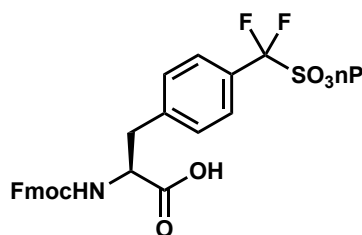
¹H NMR: (500 MHz, CDCl₃) δ 7.77 (d, 7.55 Hz, 2H), 7.62 (d, 7.84 Hz, 4H), 7.58 (d, 7.64 Hz, 2H), 7.41 (t, 7.55 Hz), 7.31 (m, 4H), 5.34 (d, 7.57 Hz, 1H), 4.56 (dd, 6.75 Hz, 6.44 Hz, 1 H), 4.47 (m, 1H), 4.37 (m, 1H), 4.22 (t, 6.80 Hz, 1H), 4.10 (s, 2H), 3.16 (m, 2H), 1.39 (s, 9H), 1.01 (s, 9H); **¹³C{¹H} NMR:** (126 MHz, CDCl₃) δ 169.9, 155.3, 143.5, 141.1, 129.7, 127.5, 127.0, 127.0, 126.9, 126.9, 124.9, 124.8, 119.8, 119.8, 84.2, 82.7, 66.7, 54.7, 47.0, 38.2, 31.9, 27.7, 25.6; **¹⁹F{¹H} NMR:** (471 MHz, CDCl₃) δ -99.81; **LRMS:** (+ESI) *m/z* 666 [M+Na]⁺; **HRMS:** (+ESI) Calc. for C₃₄H₃₉F₂NO₇SNa: 666.23075 [M+Na]⁺, Found: 666.22952 [M+Na]⁺; **IR (ATR):** ν_{max} = 3330, 3067, 3041, 2978, 2937, 2886, 1720, 1518, 1478, 1450, 1384, 1369, 1341, 1251, 1224, 1156, 1106, 1077, 974, 954, 927, 846, 759, 740, 605, 537, 427 cm⁻¹; **[α]_D:** +0.062° (*c* 0.3, CH₂Cl₂).



(S)-2-((((9H-fluoren-9-yl)methoxy)carbonyl)amino)-3-(4-(((neopentyloxy)sulfonyl)methyl)phenyl)propanoic acid (2)

Fmoc-L-Smp(nP)-OtBu (**7**) (1.26 g, 2.07 mmol) was dissolved in a 1:1 v/v mixture of TFA and CH₂Cl₂ (10 mL). The reaction mixture was stirred at room temperature for 2 h. The reaction mixture was concentrated under a stream of nitrogen and then azeotroped with CH₂Cl₂ (x 2), toluene (x 3) and CHCl₃ (x 2), affording the crude product which was purified by flash silica gel chromatography (0-10 vol% MeOH in CH₂Cl₂ with 1 vol% acetic acid), affording the pure product **2** as an orange foam (879 mg, 1.59 mmol, 77%).

¹H NMR: (500 MHz, MeOD) δ 7.81 (d, *J* = 7.6 Hz, 2H), 7.63 (t, *J* = 7.1 Hz, 2H), 7.44 – 7.36 (m, 4H), 7.36 – 7.28 (m, 3H), 7.29 (d, *J* = 6.0 Hz, 1H), 4.48 (s, 2H), 4.44 (dd, *J* = 9.2, 4.6 Hz, 1H), 4.34 – 4.23 (m, 2H), 4.17 (t, *J* = 6.9 Hz, 1H), 3.76 (s, 2H), 3.25 (dd, *J* = 13.9, 4.7 Hz, 1H), 2.99 (dd, *J* = 13.9, 9.3 Hz, 1H), 0.90 (s, 9H); **¹³C{¹H} NMR:** (126 MHz, MeOD) δ 173.72, 156.93, 143.83, 143.81, 141.15, 138.26, 130.61, 129.28, 127.38, 126.98, 126.78, 124.91, 124.86, 119.50, 79.57, 66.57, 55.36, 54.98, 36.86, 31.19, 24.91; **LRMS:** (+ESI) *m/z* 596 [M+2Na]²⁺; **HRMS:** (+ESI) Calc. for C₃₀H₃₃NO₇SNa: 574.18699 [M+Na]⁺, Found: 574.18633 [M+Na]⁺; **IR (ATR):** ν_{max} = 3060, 2962, 2872, 1712, 1515, 1451, 1427, 1349, 1169, 1106, 1051, 961, 937, 891, 842, 760, 741, 593, 538, 426 cm⁻¹; **[α]_D:** +0.191° (*c* 0.3, CH₂Cl₂).



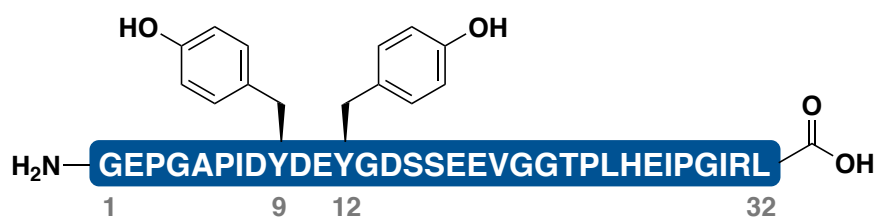
(S)-2-((((9H-fluoren-9-yl)methoxy)carbonyl)amino)-3-(4-(difluoro((neopentyloxy)sulfonyl)methyl)phenyl)propanoic acid (3)

Fmoc-L-F₂Smp(nP)-OtBu (**8**) (238 mg, 370 μmol) was dissolved in a 1:1 v/v mixture of TFA and CH₂Cl₂ (10 mL). The reaction mixture was stirred at room temperature for 2 h. The reaction mixture was concentrated under a stream of nitrogen and then azeotroped with CH₂Cl₂ (x 2), toluene (x 3) and CHCl₃ (x 2), affording the crude product which was purified by flash silica gel chromatography (0-10 vol% MeOH in CH₂Cl₂ with 1 vol% acetic acid), affording the pure product **3** as an orange foam (132 mg, 231 μmol, 62%).

¹H NMR: (500 MHz, MeOD) δ 7.75 (d, *J* = 7.6 Hz, 2H), 7.58 (t, *J* = 8.1 Hz, 4H), 7.44 – 7.32 (m, 4H), 7.31 – 7.24 (m, 2H), 4.43 (dd, *J* = 9.1, 4.9 Hz, 1H), 4.32 (dd, *J* = 10.6, 7.1 Hz, 1H), 4.22 (dd, *J* = 10.6, 6.9 Hz, 1H), 4.12 (t, *J* = 7.0 Hz, 1H), 4.03 (s, 2H), 3.34 – 3.27 (m, 1H), 3.05 (dd, *J* = 13.8, 9.0 Hz, 1H), 0.94 (s, 9H); **¹³C{¹H} NMR:** (126 MHz, MeOD) δ 174.92, 156.87, 143.84, 143.77, 143.11, 141.17, 129.61, 127.40, 126.83, 126.77, 124.85, 124.78, 123.24, 120.99, 119.55, 118.75, 84.14, 66.47, 55.66, 37.18, 31.50, 24.74; **¹⁹F{¹H} NMR:** (471 MHz, MeOD) δ -76.87 (TFA-CF₃), -100.75; **LRMS:** (+ESI) *m/z* 586 [M+H]⁺; **HRMS:** (+ESI) Calc. for C₃₀H₃₁F₂NO₇SNa: 610.16815 [M+Na]⁺, Found: 610.16708 [M+Na]⁺; **IR (ATR):** *v*_{max} = 3392, 3067, 2962, 2872, 2495, 2228, 2074, 1694, 1614, 1589, 1450, 1423, 1384, 1368, 1279, 1195, 1105, 1084, 973, 925, 806, 759, 740, 606, 536, 454, 424 cm⁻¹; **[α]_D:** +0.317° (*c* 0.3, CH₂Cl₂). These data are in agreement with those published by Liu *et al.*²

4 SYNTHESIS OF PEPTIDIC THROMBIN INHIBITORS

4.1 TTI



TTI (Y9, Y12) (9)

Wang resin (0.28 mmol g⁻¹ loading) was loaded with Fmoc-Leu-OH according to the general procedures. Synthesis of the G13-R31 fragment was then performed using automated coupling protocols (*see General Procedures – Automated Coupling (Liberty Blue)*) on a CEM Liberty Blue[®] peptide synthesiser with a double coupling of R31. Fragment G1-Y12 was then synthesised manually (*see General Procedures – Manual Coupling (Standard)*) with double couplings for E2, I7, D8 and E11. After completion of the synthesis, the peptide was cleaved from the resin and deprotected by treatment with an acidic cleavage cocktail (90:5:5 v/v/v TFA:*i*Pr₃SiH:H₂O) at room temperature for 2 h. The deprotection solution was concentrated under a stream of nitrogen until a small volume remained (<0.5 mL). Cold Et₂O (40 mL) was then added to the remaining deprotection solution to precipitate peptidic material. The resulting suspension was then centrifuged at 4 °C (2000 x g, 5 min) and the ether supernatant was decanted, leaving the crude peptide material to dry under a gentle stream of nitrogen. The crude peptide was dissolved in 5 vol% MeCN in H₂O (0.1 vol% FA) (5 mL) and purified by preparative reversed-phase chromatography (Waters Sunfire C18, 30 x 150 mm, 38 mL min⁻¹) on a 0-50%B gradient over 45 min (*see general procedures*). Subsequent lyophilisation afforded the purified TTI (Y9, Y12) (9) (16.2 mg, 4.61 μmol, 23% from resin loading [64 steps]).

See analytical data on next page.

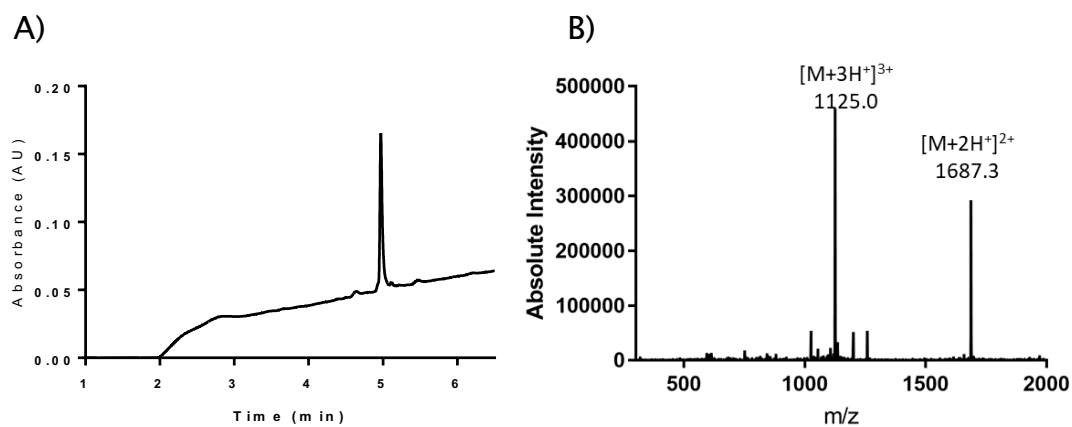
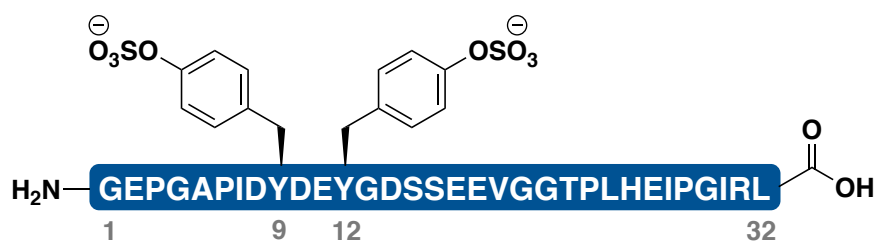


Figure S1. **A)** Analytical reversed-phase HPLC analysis of purified TTI (Y9, Y12) (**9**) (0-50%B over 5 min, $\lambda = 214$ nm) collected on a Waters Acquity UPLC system, as per general procedures. **B)** Mass spectrum (ESI+) of purified TTI (Y9, Y12) (**9**) collected on a Shimadzu 2020 (ESI) mass spectrometer, as per general procedures.



TTI (sY9, sY12) (10)

Wang resin (0.28 mmol g⁻¹ loading) was loaded with Fmoc-Leu-OH according to the general procedures. Synthesis of the G13-R31 fragment was then performed using automated coupling protocols (*see General Procedures – Automated Coupling (Liberty Blue)*) on a Liberty Blue[®] peptide synthesiser with double coupling of R31. Coupling of Fmoc-Tyr(SO₃nP)-OH was then performed manually according to *General Procedures (Manual Coupling (Non-Standard))*. Fragment D10-E11 was then synthesised manually (*see General Procedures – Manual Coupling (Standard)*) with double coupling of E11, before a second manual coupling of Fmoc-Tyr(SO₃nP)-OH according to *General Procedures (Manual Coupling (Non-Standard))*. The resin-bound peptide was then transferred to a Liberty Blue[®] peptide synthesiser for completion of the G1-D8 fragment with 50 °C single couplings of all residues and a final Fmoc-deprotection. After completion of the synthesis, the peptide was cleaved from the resin and deprotected by treatment with an acidic cleavage cocktail (90:5:5 v/v/v TFA:*i*Pr₃SiH:H₂O) at room temperature for 2 h. The deprotection solution was concentrated under a stream of nitrogen until a small volume remained (<0.5 mL). Cold Et₂O (40 mL) was then added to the remaining deprotection solution to precipitate peptidic material. The resulting suspension was then centrifuged at 4 °C (2000 x g, 5 min) and the ether supernatant was decanted, leaving the crude peptide material to dry under a gentle stream of nitrogen. The precipitated material was dissolved in 1.5 mL of NH₄OAc buffer (1 M NH₄OAc, 6 M Gn.HCl, 0.1 M Na₂HPO₄) at pH 7 and incubated at 37 °C for 3 h to facilitate the removal of the sulfonyl neopentyl protecting group. After complete neopentyl removal, as judged by UPLC-MS analysis, the reaction mixture was diluted to 5 mL total volume with H₂O (0.1 vol% FA) and purified by preparative reversed-phase chromatography (Waters Sunfire C18, 30 x 150 mm, 38 mL min⁻¹) on a 0-50%B gradient over 45 min (*see general procedures*). Subsequent lyophilisation afforded the purified TTI (sY9, sY12) (10) (5.2 mg, 1.4 μmol, 7% from resin loading [65 steps]).

See analytical data on next page.

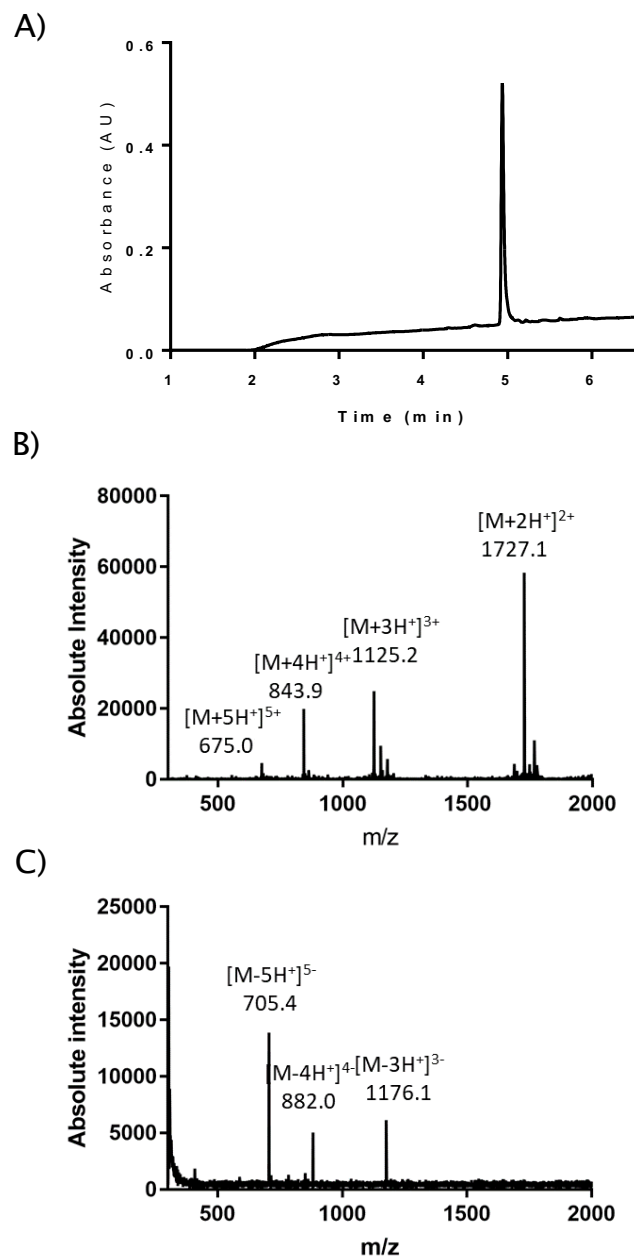
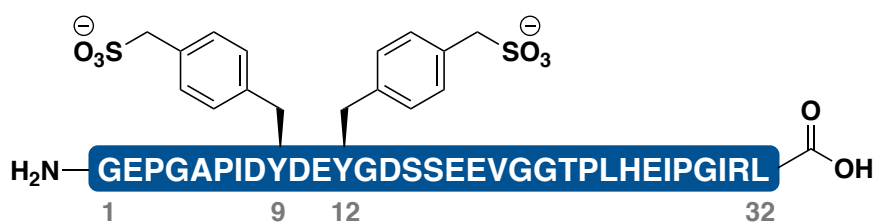


Figure S2. **A)** Analytical reversed-phase HPLC analysis of purified TTI (sY9, sY12) (**10**) (0-50%B over 5 min, $\lambda = 214$ nm) collected on a Waters Acquity UPLC system, as per general procedures. **B)** Mass spectrum (ESI+) of purified TTI (sY9, sY12) (**10**) collected on a Shimadzu 2020 (ESI) mass spectrometer, as per general procedures. **C)** Mass spectrum (ESI-) of purified TTI (sY9, sY12) (**10**) collected on a Shimadzu 2020 (ESI) mass spectrometer, as per general procedures.



TTI (Smp9, Smp12) (11)

Wang resin (0.28 mmol g⁻¹ loading) was loaded with Fmoc-Leu-OH according to the general procedures. Synthesis of the G13-R31 fragment was then performed using automated coupling protocols (*see General Procedures – Automated Coupling (Liberty Blue)*) on a Liberty Blue[®] peptide synthesiser with double coupling of R31. Coupling of Fmoc-Smp(nP)-OH (**2**) was then performed manually according to the *General Procedures (Manual Coupling (Non-Standard))*. Fragment D10-E11 was then synthesised manually (*see General Procedures – Manual Coupling (Standard)*) with double coupling of E11, before a second manual coupling of Fmoc-Smp(nP)-OH (**2**) according to *General Procedures (Manual Coupling (Non-Standard))*. The resin-bound peptide was then transferred to a Liberty Blue[®] peptide synthesiser for completion of the G1-D8 fragment with 50 °C single couplings of all residues and a final Fmoc-deprotection. After completion of the synthesis, the peptide was cleaved from the resin and deprotected by treatment with an acidic cleavage cocktail (90:5:5 v/v/v TFA:*i*Pr₃SiH:H₂O) at room temperature for 2 h. The deprotection solution was concentrated under a stream of nitrogen until a small volume remained (<0.5 mL). Cold Et₂O (40 mL) was then added to the remaining deprotection solution to precipitate peptidic material. The resulting suspension was then centrifuged at 4 °C (2000 x g, 5 min) and the ether supernatant was decanted, leaving the crude peptide material to dry under a gentle stream of nitrogen. The precipitated material was dissolved in 1.5 mL of NH₄OAc buffer (1 M NH₄OAc, 6 M Gn.HCl, 0.1 M Na₂HPO₄) at pH 7 and incubated at 70 °C for 15 h to facilitate the removal of the sulfonyl neopentyl protecting group. After complete neopentyl removal, as judged by UPLC-MS analysis, the reaction mixture was diluted to 5 mL total volume with H₂O (0.1 vol% FA) and purified by preparative reversed-phase chromatography (Waters Sunfire C18, 30 x 150 mm, 38 mL min⁻¹) on a 0-50%B gradient over 45 min (*see general procedures*). Subsequent lyophilisation afforded the purified TTI (Smp9, Smp12) (**11**) (8.6 mg, 2.3 µmol, 23% from resin loading [65 steps]).

See analytical data on next page.

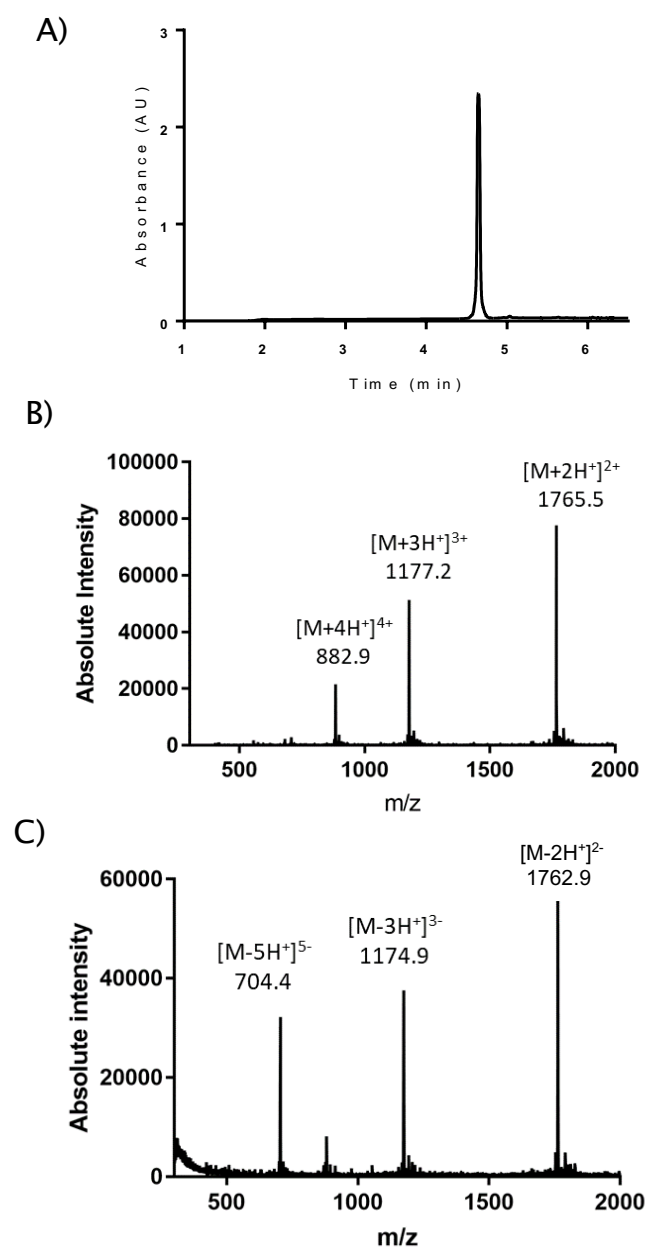
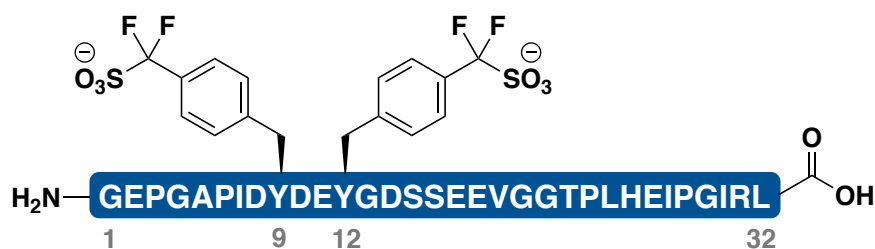


Figure S3. **A)** Analytical UPLC analysis of purified TTI (Smp9, Smp12) (**11**) (0-50%B over 5 min, $\lambda = 214$ nm) collected on a Waters Acquity UPLC system, as per general procedures. **B)** Mass spectrum (ESI+) of purified TTI (Smp9, Smp12) (**11**) collected on a Shimadzu 2020 (ESI) mass spectrometer, as per general procedures. **C)** Mass spectrum (ESI-) of purified TTI (Smp9, Smp12) (**11**) collected on a Shimadzu 2020 (ESI) mass spectrometer, as per general procedures.



TTI (F₂Smp₉, F₂Smp₁₂) (12)

Wang resin (0.28 mmol g⁻¹ loading) was loaded with Fmoc-Leu-OH according to the general procedures. Synthesis of the G13-R31 fragment was then performed using automated coupling protocols (*see General Procedures – Automated Coupling (Liberty Blue)*) on a Liberty Blue[®] peptide synthesiser with a double coupling of R31. Coupling of Fmoc-F₂Smp(nP)-OH (**3**) was then performed manually according to the General Procedures (*Manual Coupling (Non-Standard)*). Fragment D10-E11 was then synthesised manually (*see General Procedures – Manual Coupling (Standard)*) with double coupling of E11, before a second manual coupling of Fmoc-F₂Smp(nP)-OH (**3**) according to *General Procedures (Manual Coupling (Non-Standard))*. The resin-bound peptide was then transferred to a Liberty Blue[®] peptide synthesiser for completion of the G1-D8 fragment with 50 °C single couplings of all residues and a final Fmoc-deprotection. After completion of the synthesis, the peptide was cleaved from the resin and deprotected by treatment with an acidic cleavage cocktail (90:5:5 v/v/v TFA:*t*-Pr₃SiH:H₂O) at room temperature for 3 h. The deprotection solution was concentrated under a stream of nitrogen until a small volume remained (<0.5 mL). Cold Et₂O (40 mL) was then added to the remaining deprotection solution to precipitate peptidic material. The resulting suspension was then centrifuged at 4 °C (2000 x g, 5 min) and the ether supernatant was decanted, leaving the crude peptide material to dry under a gentle stream of nitrogen. The precipitated material was dissolved in 1.5 mL of NH₄OAc buffer (1 M NH₄OAc, 6 M Gn.HCl, 0.1 M Na₂HPO₄) at pH 7 and incubated at 37 °C for 3 h to facilitate the removal of the sulfonyl neopentyl protecting group. After complete neopentyl removal, as judged by UPLC-MS analysis, the reaction mixture was diluted to 5 mL total volume with H₂O (0.1 vol% FA) and purified by preparative RP-HPLC (Waters Sunfire C18, 19 x 150 mm, 14 mL min⁻¹) on a 0-50%B gradient over 45 min (*see general procedures*). Subsequent lyophilisation afforded the purified TTI (F₂Smp₉, F₂Smp₁₂) (**12**) (4.8 mg, 1.3 μmol, 13% from resin loading [65 steps]).

See analytical data on next page.

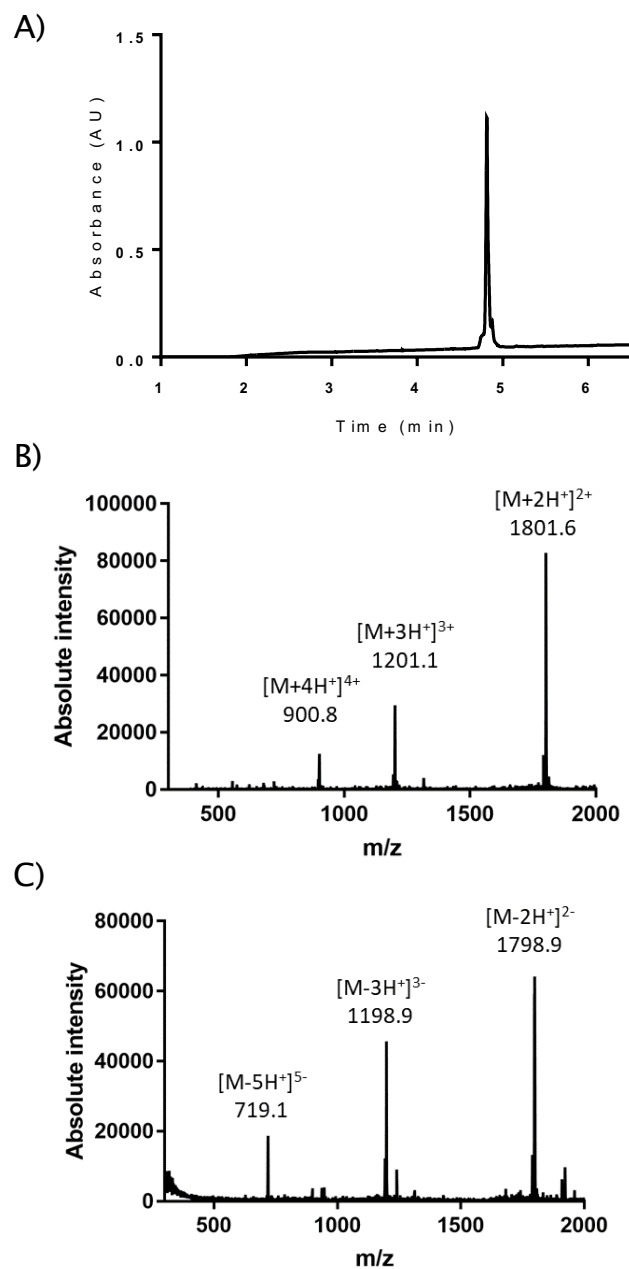
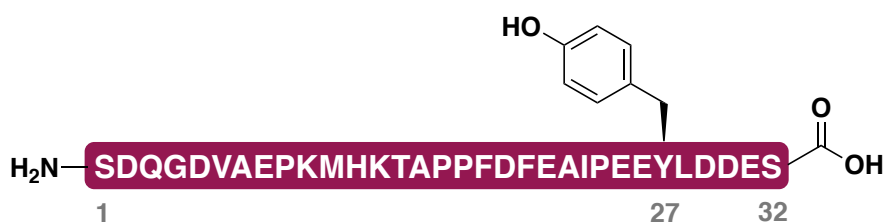


Figure S4. **A)** Analytical UPLC analysis of purified TTI (F₂Smp9, F₂Smp12) (**12**) (0-50%B over 5 min, $\lambda = 214$ nm) collected on a Waters Acquity UPLC system, as per general procedures. **B)** Mass spectrum (ESI+) of purified TTI (F₂Smp9, F₂Smp12) (**12**) collected on a Shimadzu 2020 (ESI) mass spectrometer, as per general procedures. **C)** Mass spectrum (ESI-) of purified TTI (F₂Smp9, F₂Smp12) (**12**) collected on a Shimadzu 2020 (ESI) mass spectrometer, as per general procedures.

4.2 VARIEGIN



Variegin (Y27) (13)

2-CTC resin (0.51 mmol g⁻¹ loading) was loaded with Fmoc-Ser(*t*Bu)-OH according to the general procedures. Synthesis of the S1-E31 fragment was then performed using automated coupling protocols (*see General Procedures – Automated Coupling (Symphony)*) on a Gyros Protein Technologies Symphony[®] peptide synthesiser, with double couplings at Q3, D5, V6, E8, H12, K13, A15, P16, A22, I23 and E26. After completion of the synthesis, the peptide was cleaved from the resin and deprotected by treatment with an acidic cleavage cocktail (90:5:5 v/v/v TFA:*i*Pr₃SiH:H₂O) at room temperature for 3 h. The deprotection solution was concentrated under a stream of nitrogen until a small volume remained (<0.5 mL). Cold Et₂O (40 mL) was then added to the remaining deprotection solution to precipitate peptidic material. The resulting suspension was then centrifuged at 4 °C (2000 x g, 5 min) and the ether supernatant was decanted, leaving the crude peptide material to dry under a gentle stream of nitrogen. The crude peptide was dissolved in 5 vol% MeCN in H₂O (0.1 vol% FA) (5 mL) and purified by preparative reversed-phase chromatography (Waters Sunfire C18, 30 x 150 mm, 38 mL min⁻¹) on a 0-50%B gradient over 45 min (*see general procedures*). Subsequent lyophilisation afforded the purified Variegin (Y27) (13) (5.7 mg, 1.5 μmol, 6% from resin loading [64 steps]).

See analytical data on next page.

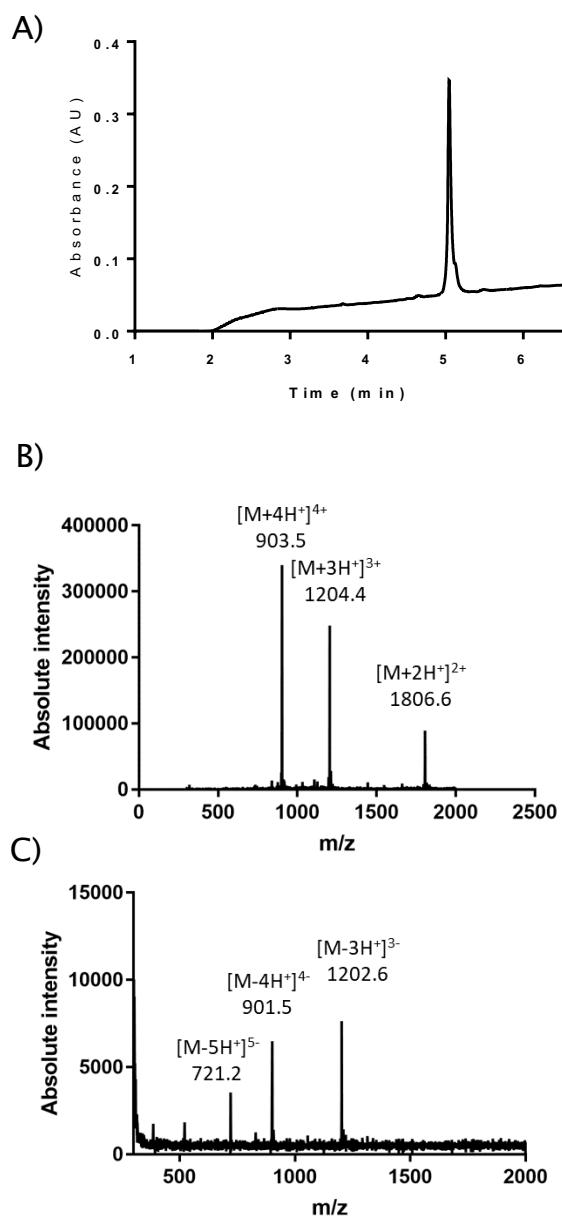
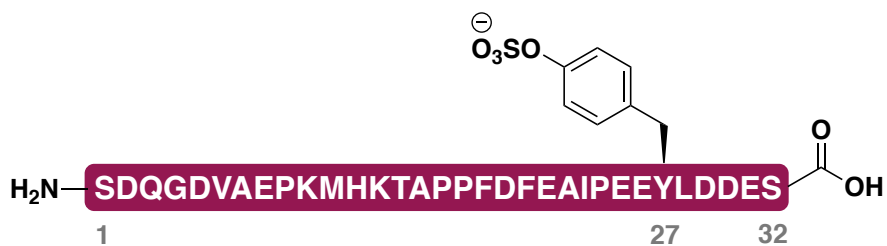


Figure S5. **A)** Analytical reversed-phase HPLC analysis of purified Variegin (Y27) (**13**) (0-50%B over 5 min, $\lambda = 214$ nm) collected on a Waters Acquity UPLC system, as per general procedures. **B)** Mass spectrum (ESI+) of purified Variegin (Y27) (**13**) collected on a Shimadzu 2020 (ESI) mass spectrometer, as per general procedures. **C)** Mass spectrum (ESI-) of purified Variegin (Y27) (**13**) collected on a Shimadzu 2020 (ESI) mass spectrometer, as per general procedures.



Variegin (sY27) (14)

2-CTC resin (0.28 mmol g⁻¹ loading) was loaded with Fmoc-Ser(*t*Bu)-OH according to the general procedures. Synthesis of the L28-E31 fragment was then performed using automated coupling protocols (*see General Procedures – Automated Coupling (Symphony)*) on a Gyros Protein Technologies Symphony[®] peptide synthesiser. Coupling of Fmoc-Tyr(SO₃nP)-OH was then performed manually according to the *General Procedures (Manual Coupling (Non-Standard))*. Fragment S1-E26 was then completed using automated coupling protocols (*see General Procedures – Automated Coupling (Symphony)*) with double couplings at Q3, D5, V6, E8, H12, K13, A15, P16, A22, I23 and E26. After completion of the synthesis, the peptide was cleaved from the resin and deprotected by treatment with an acidic cleavage cocktail (90:5:5 v/v/v TFA:*i*Pr₃SiH:H₂O) at room temperature for 3 h. The deprotection solution was concentrated under a stream of nitrogen until a small volume remained (<0.5 mL). Cold Et₂O (40 mL) was then added to the remaining deprotection solution to precipitate peptidic material. The resulting suspension was then centrifuged at 4 °C (2000 x g, 5 min) and the ether supernatant was decanted, leaving the crude peptide material to dry under a gentle stream of nitrogen. The precipitated material was dissolved in 2 mL of NH₄OAc buffer (1 M NH₄OAc, 6 M Gn.HCl, 0.1 M Na₂HPO₄) at pH 7 and incubated at 37 °C for 3 h to facilitate the removal of the sulfate neopentyl protecting group. After complete neopentyl removal, as judged by UPLC-MS analysis, the reaction mixture was diluted to 5 mL total volume with H₂O (0.1 vol% FA) and purified by preparative reversed-phase chromatography (Waters Sunfire C18, 30 x 150 mm, 38 mL min⁻¹) on a 0-50%B gradient over 45 min (*see general procedures*). Subsequent lyophilisation afforded the purified Variegin (sY27) (14) (18.2 mg, 4.6 μmol, 15% from resin loading [65 steps]).

See analytical data on next page.

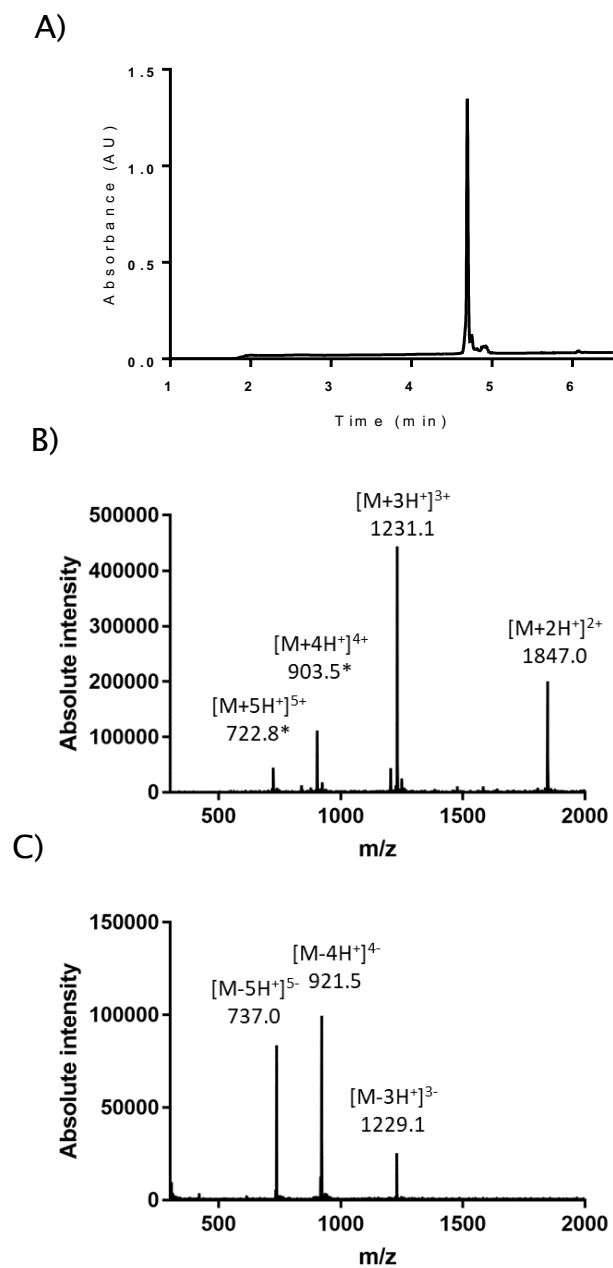
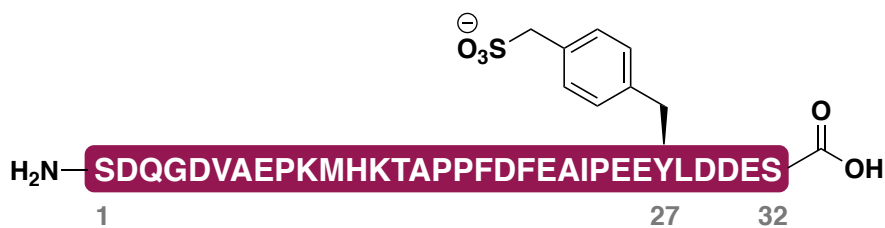


Figure S6. **A)** Analytical reversed-phase HPLC analysis of purified Variegin (sY27) (**14**) (0-50%B over 5 min, $\lambda = 214$ nm) collected on a Waters Acquity UPLC system, as per general procedures. **B)** Mass spectrum (ESI+) of purified Variegin (sY27) (**14**) collected on a Shimadzu 2020 (ESI) mass spectrometer, as per general procedures. **C)** Mass spectrum (ESI-) of purified Variegin (sY27) (**14**) collected on a Shimadzu 2020 (ESI) mass spectrometer, as per general procedures.



Variegin (Smp27) (15)

2-CTC resin (0.28 mmol g⁻¹ loading) was loaded with Fmoc-Ser(*t*Bu)-OH according to the general procedures. Synthesis of the L28-E31 fragment was then performed using automated coupling protocols (*see General Procedures – Automated Coupling (Symphony)*) on a Gyros Protein Technologies Symphony[®] peptide synthesiser. Coupling of Fmoc-Smp(nP)-OH (**2**) was then performed manually according to the *General Procedures (Manual Coupling (Non-Standard))*. Fragment S1-E26 was then completed using automated coupling protocols (*see General Procedures – Automated Coupling (Symphony)*) with double couplings at Q3, D5, V6, E8, H12, K13, A15, P16, A22, I23 and E26. After completion of the synthesis, the peptide was cleaved from the resin and deprotected by treatment with an acidic cleavage cocktail (90:5:5 v/v/v TFA:*i*Pr₃SiH:H₂O) at room temperature for 3 h. The deprotection solution was concentrated under a stream of nitrogen until a small volume remained (<0.5 mL). Cold Et₂O (40 mL) was then added to the remaining deprotection solution to precipitate peptidic material. The resulting suspension was then centrifuged at 4 °C (2000 x g, 5 min) and the ether supernatant was decanted, leaving the crude peptide material to dry under a gentle stream of nitrogen. The precipitated material was dissolved in 2 mL of NH₄OAc buffer (1 M NH₄OAc, 6 M Gn.HCl, 0.1 M Na₂HPO₄) at pH 7 and incubated at 70 °C for 16 h to facilitate the removal of the sulfonyl neopentyl protecting group. After complete neopentyl removal, as judged by UPLC-MS analysis, the reaction mixture was diluted to 5 mL total volume with H₂O (0.1 vol% FA) and purified by preparative reversed-phase chromatography (Waters Sunfire C18, 19 x 150 mm, 14 mL min⁻¹) on a 0-50%B gradient over 45 min (*see general procedures*). Subsequent lyophilisation afforded the purified Variegin (Smp27) (**15**) (1.9 mg, 0.48 μmol, 4% from resin loading [65 steps]).

See analytical data on next page.

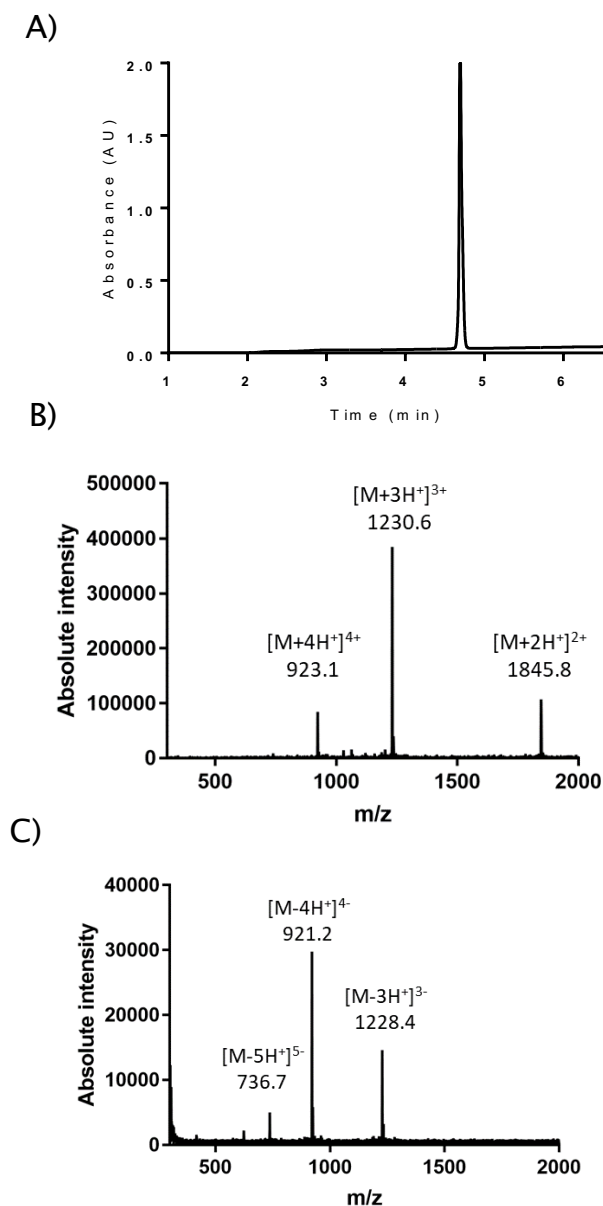
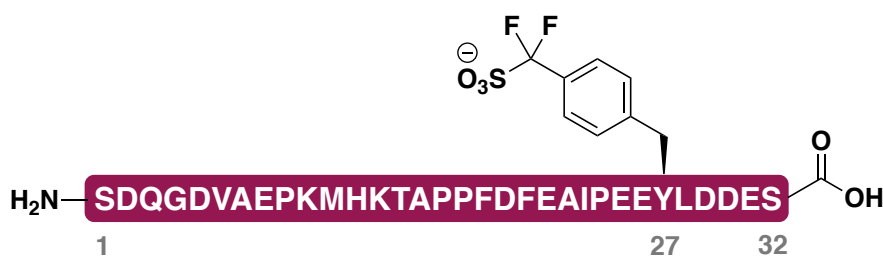


Figure S7. **A)** Analytical reversed-phase HPLC analysis of purified Variegin (Smp27) (**15**) (0-50%B over 5 min, $\lambda = 214$ nm) collected on a Waters Acquity UPLC system, as per general procedures. **B)** Mass spectrum (ESI+) of purified Variegin (Smp27) (**15**) collected on a Shimadzu 2020 (ESI) mass spectrometer, as per general procedures. **C)** Mass spectrum (ESI-) of purified Variegin (Smp27) (**15**) collected on a Shimadzu 2020 (ESI) mass spectrometer, as per general procedures.



Variegin (F₂Smp27) (16)

2-CTC resin (0.28 mmol g⁻¹ loading) was loaded with Fmoc-Ser(*t*Bu)-OH according to the general procedures. Synthesis of the L28-E31 fragment was then performed using automated coupling protocols (*see General Procedures – Automated Coupling (Symphony)*) on a Gyros Protein Technologies Symphony[®] peptide synthesiser. Coupling of Fmoc-F₂Smp(nP)-OH (**3**) was then performed manually according to the *General Procedures (Manual Coupling (Non-Standard))*. Fragment S1-E26 was then completed using automated coupling protocols (*see General Procedures – Automated Coupling (Symphony)*) with double couplings at Q3, D5, V6, E8, H12, K13, A15, P16, A22, I23 and E26. After completion of the synthesis, the peptide was cleaved from the resin and deprotected by treatment with an acidic cleavage cocktail (90:5:5 v/v/v TFA:*i*Pr₃SiH:H₂O) at room temperature for 3 h. The deprotection solution was concentrated under a stream of nitrogen until a small volume remained (<0.5 mL). Cold Et₂O (40 mL) was then added to the remaining deprotection solution to precipitate peptidic material. The resulting suspension was then centrifuged at 4 °C (2000 x g, 5 min) and the ether supernatant was decanted, leaving the crude peptide material to dry under a gentle stream of nitrogen. The precipitated material was dissolved in 2 mL of NH₄OAc buffer (1 M NH₄OAc, 6 M Gn.HCl, 0.1 M Na₂HPO₄) at pH 7 and incubated at 37 °C for 3 h to facilitate the removal of the sulfonyl neopentyl protecting group. After complete neopentyl removal, as judged by UPLC-MS analysis, the reaction mixture was diluted to 5 mL total volume with H₂O (0.1 vol% FA) and purified by preparative reversed-phase chromatography (Waters Sunfire C18, 19 x 150 mm, 14 mL min⁻¹) on a 0-50%B gradient over 45 min (*see general procedures*). Subsequent lyophilisation afforded the purified Variegin (F₂Smp27) (**16**) (1.7 mg, 0.42 μmol, 4% from resin loading [65 steps]).

See analytical data on next page.

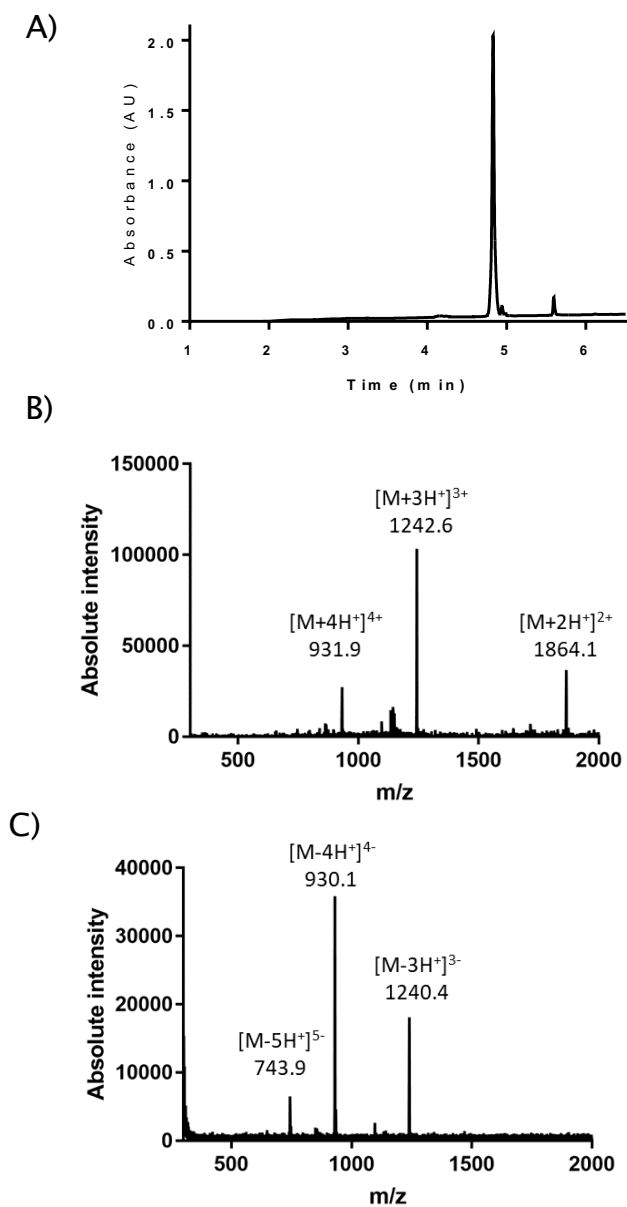


Figure S8. **A)** Analytical reversed-phase HPLC analysis of purified Variegin (F₂Smp27) (**16**) (0-50%B over 5 min, $\lambda = 214$ nm) collected on a Waters Acquity UPLC system, as per general procedures. **B)** Mass spectrum (ESI+) of purified Variegin (F₂Smp27) (**16**) collected on a Shimadzu 2020 (ESI) mass spectrometer, as per general procedures. **C)** Mass spectrum (ESI-) of purified Variegin (F₂Smp27) (**16**) collected on a Shimadzu 2020 (ESI) mass spectrometer, as per general procedures.

5 OPTIMISATION OF NEOPENTYL SULFONATE ESTER DEPROTECTION

Samples of neopentyl-protected TTI (sY9, sY12) (10 mg, 3 μ mol) were dissolved in different mildly nucleophilic deprotection mixtures to a concentration of 10 mM:

- 1) NaN_3 (7.2 mg, 40 eq.) in DMSO (50 $^\circ\text{C}$, 3 h)
- 2) NaN_3 (7.2 mg, 40 eq.) in DMF (50 $^\circ\text{C}$, 3 h)
- 3) 1 M NH_4OAc , 6 M Gn.HCl , 0.1 M Na_2HPO_4 , pH 7 (37 $^\circ\text{C}$, 3 h)
- 4) 10 M NH_4OAc , 6 M Gn.HCl , 0.1 M Na_2HPO_4 , pH 7 (37 $^\circ\text{C}$, 3 h)

The different NaN_3 and NH_4OAc deprotection conditions were incubated for 3 h at 50 $^\circ\text{C}$ and 37 $^\circ\text{C}$, respectively. *Condition 1* (40 eq. NaN_3 in DMSO) (*figure S9A*) led to successful nP deprotection over the 3 h, with some degree of peptide degradation. *Condition 2* (40 eq. NaN_3 in DMF) (*figure S9B*) led exclusively to degradation of the peptide over the 3 h. *Conditions 3 and 4* (1 M and 10 M NH_4OAc in aqueous buffer) (*figure S9C*) led to successful nP deprotection over the 3 h, with some degree of peptide degradation, with condition 3 (1 M NH_4OAc in aqueous buffer) leading to more consistent and complete deprotection (overlaid conditions: *figure S9D*). As such, *condition 3* (1 M NH_4OAc , 6 M Gn.HCl , 0.1 M Na_2HPO_4 , pH 7) was chosen for subsequent nP deprotections.

The deprotection of nP-protected sulfonates (i.e. TTI (Smp9, Smp12) (**11**) and Variegin (Smp27) (**15**)) using the optimised conditions (1 M NH_4OAc , 6 M Gn.HCl , 0.1 M Na_2HPO_4 , pH 7) were found to require elevated temperatures of 70 $^\circ\text{C}$ and extended reaction times of up to 16 h to reach completion. nP-protected difluorosulfonates (i.e. TTI (F₂Smp9, F₂Smp12) (**12**) and Variegin (F₂Smp27) (**16**)) were successfully deprotected under identical conditions to neopentyl-protected sulfates, as optimised above (1 M NH_4OAc , 6 M Gn.HCl , 0.1 M Na_2HPO_4 , pH 7, 37 $^\circ\text{C}$ for 3 h).

See analytical data on next page.

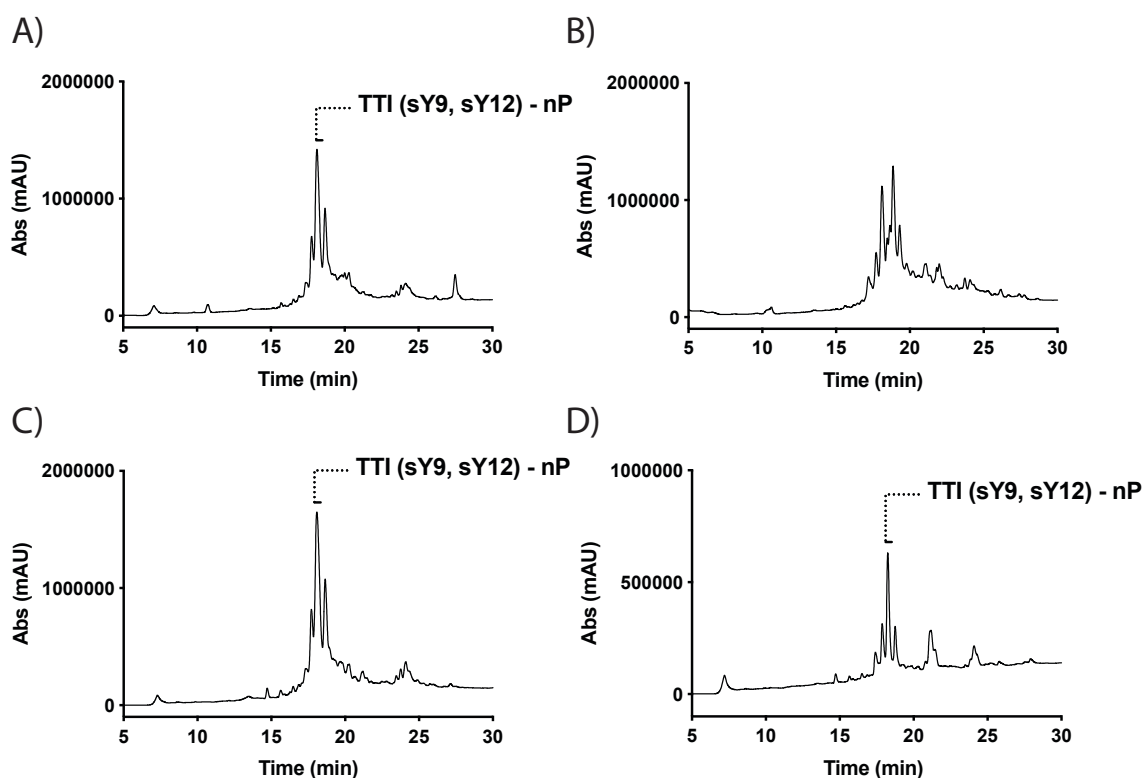


Figure S9. UPLC analysis (0-80%B over 30 min) of the trial deprotections of nP-protected TTI (sY9, sY12) ($c = 10$ mM) at $t = 3$ h under the following reaction conditions: **A)** NaN_3 (40 eq.) in DMSO at 50°C , **B)** NaN_3 (40 eq.) in DMF at 50°C , **C)** 1 M NH_4OAc in aqueous 6 M Gn.HCl (0.1 M Na_2HPO_4 , pH 7) at 37°C , and **D)** 10 M NH_4OAc in aqueous 6 M Gn.HCl (0.1 M Na_2HPO_4 , pH 7) at 37°C .

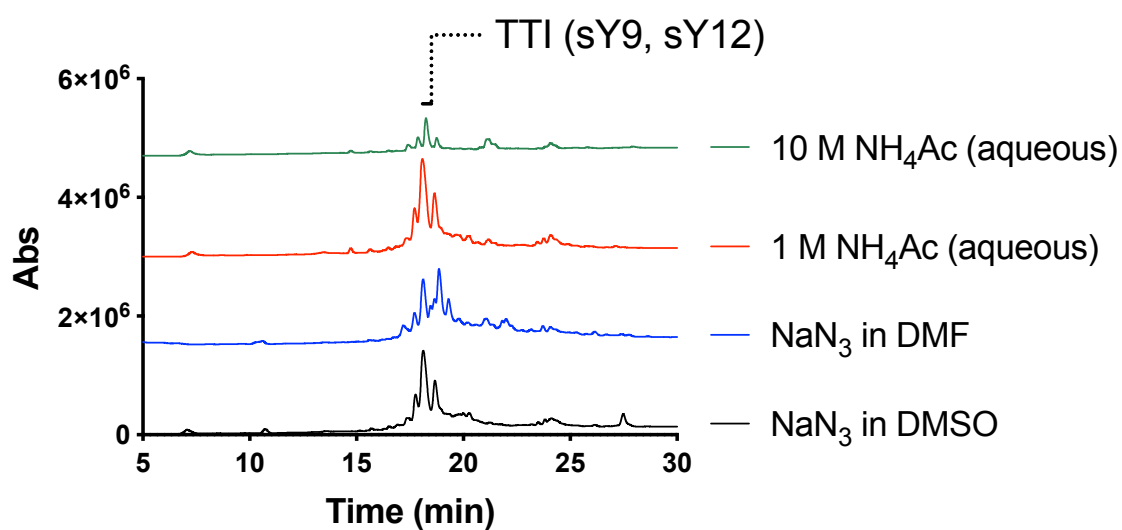


Figure S10. Overlaid conditions for the neopentyl deprotection of nP-protected TTI (sY9, sY12).

6 THROMBIN INHIBITION ASSAY

The inhibition of the amidolytic activity of human α - or γ -thrombin (Haematologic Technologies) was followed spectrophotometrically using Tos-Gly-Pro-Arg-*p*-nitroanilide (Chromozym TH, Roche) as chromogenic substrate. Inhibition assays were performed in 50 mM Tris.HCl pH 8.0, 50 mM NaCl and 1 mg mL⁻¹ bovine serum albumin (BSA) with 0.2 nM enzyme, 100 μ M substrate and varying concentrations of TTI and Variegin inhibitor variants **10-16** from 0-80 nM, except in the case of **9**, where concentration was varied from 0-1.25 μ M. The inhibitory potency of Variegin variants **13-16** against human γ -thrombin was assessed varying concentrations of inhibitor from 0-83 nM. The concentration of each variant was determined by measuring the amide bonds using a Direct Detect Infrared Spectrometer (Millipore). All reactions were initiated by the addition of thrombin and carried out at 37 °C in 96-well microtiter plates. Reaction progress was monitored at 405 nm for 60 mins on a Synergy2 multi-mode microplate reader (Biotek). All measurements were made in duplicate. Inhibition constants (K_i) were determined according to a tight-binding inhibitor model, using the Morrison equation with Prism (GraphPad Software).

Table S1. Determined K_i values for the synthetic inhibitors **9-16** against human α - and γ -thrombin.

TTI variant	α -Thrombin (pM)	R ²	γ -Thrombin (pM)	R ²
Y9, Y12 (9)	826.9 \pm 70.85	0.992	1042 \pm 26.85	0.999
sY9, sY12 (10)	0.59 \pm 0.05	0.999	1.00 \pm 0.52	0.999
Smp9, Smp12 (11)	3.82 \pm 0.34	0.999	2.85 \pm 0.37	0.999
F ₂ Smp9, F ₂ Smp12 (12)	0.27 \pm 0.02	0.999	0.61 \pm 0.08	0.999
Variegin variant	α -Thrombin (pM)	R ²	γ -Thrombin (nM)	R ²
Y27 (13)	65.4 \pm 6.5	0.992	854.1 \pm 88.92	0.984
sY27 (14)	3.81 \pm 0.60	0.996	1017 \pm 31.02	0.998
Smp27 (15)	5.59 \pm 1.81	0.981	1806 \pm 146.1	0.985
F ₂ Smp27 (16)	6.27 \pm 0.80	0.997	2626 \pm 171.7	0.989

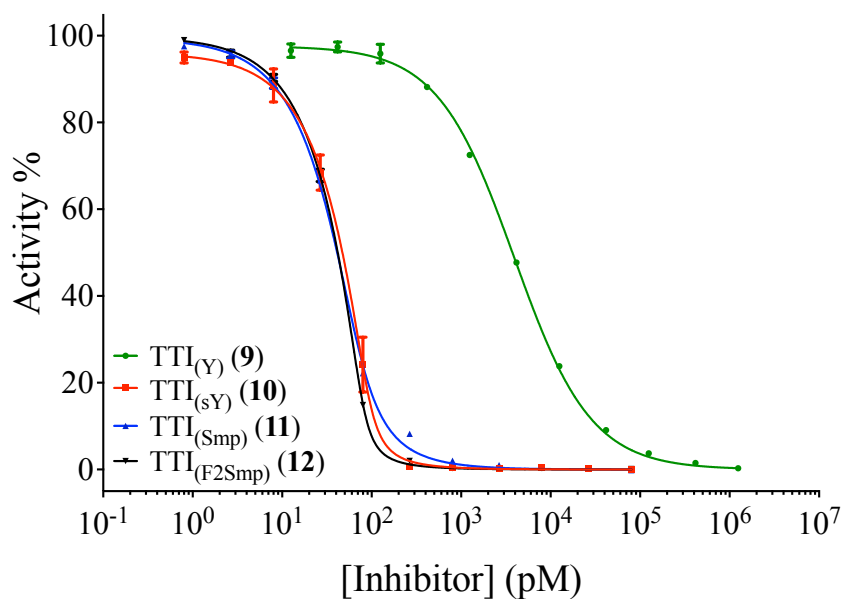


Figure S11. Effect of TTI tyrosine modification on human γ -thrombin amidolytic activity. Activity assays were performed as described (see above – Thrombin Inhibition Assay). Amidolytic activity of human γ -thrombin in the presence of TTI variants was measured at increasing concentrations of unsulfated **9** (green), disulfated **10** (red), Smp-containing **11** (blue) and F₂Smp-containing **12** (black). Activities are represented as a percentage assuming maximum activity (100%) in the absence of inhibitor. Error bars represent the standard deviation of two independent experiments. Data were fitted to the Morrison inhibition function using GraphPad Prism 6 (GraphPad Software).

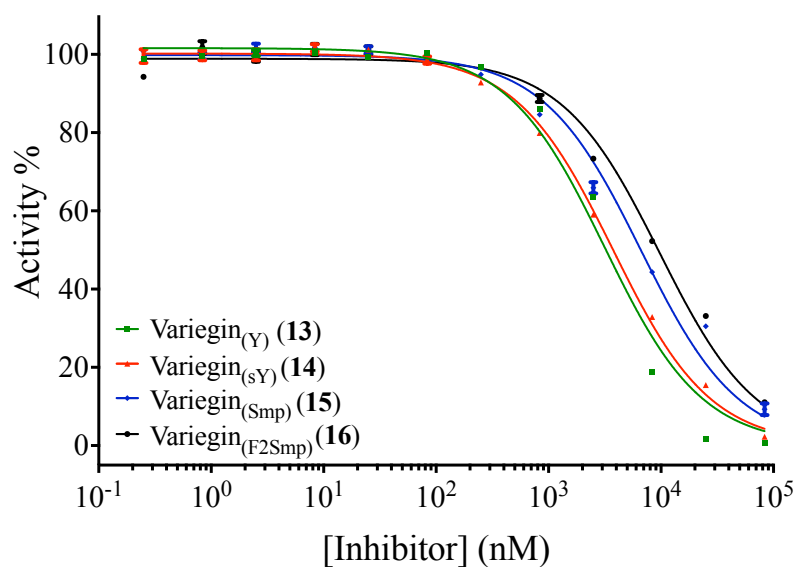


Figure S12. Effect of Variegin tyrosine modification on human γ -thrombin amidolytic activity. Activity assays were performed as described (see above – Thrombin Inhibition Assay). Amidolytic activity of human γ -thrombin in the presence of Variegin was measured at increasing concentrations of unsulfated **13** (green), sulfated **14** (red), Smp-containing **15** (blue) and F₂Smp-containing **16** (black) variants. Activities are represented as a percentage assuming maximum activity (100%) in the absence of inhibitor. Error bars represent the standard deviation of two independent experiments. Data were fitted to the Morrison inhibition function using GraphPad Prism 6 (GraphPad Software).

7 ACID STABILITY ASSAYS

To test the acid stability of the sulfonate moiety of TTI (Smp9, Smp12) (**11**) and TTI (F₂Smp9, F₂Smp12) (**12**), these thrombin inhibitors were dissolved in ultrapure H₂O (type 1) with 0.1 vol% TFA (pH 2) to a concentration of 100 mM and subsequently incubated at room temperature for 10 h. Aliquots were taken at 1 h intervals and analyzed by UPLC and UPLC-MS.

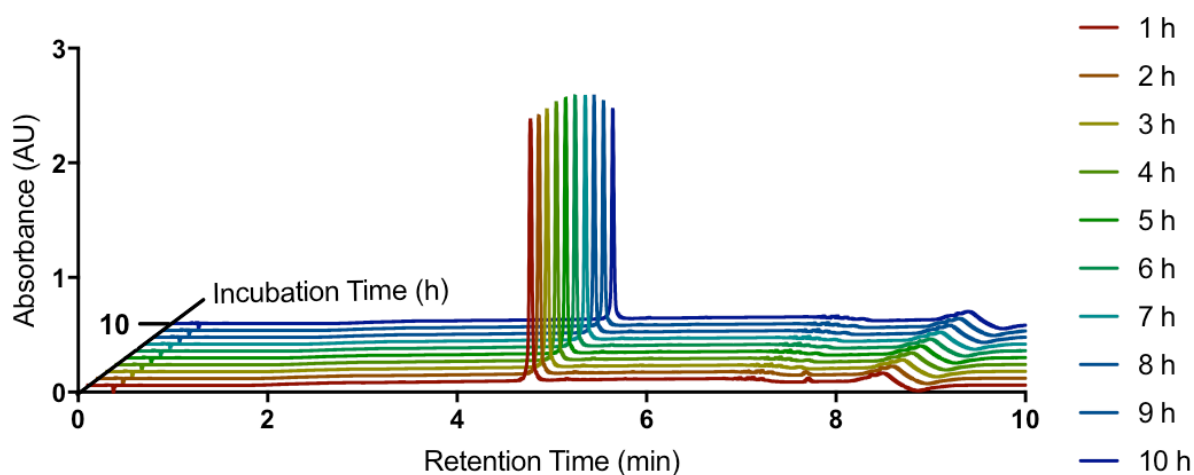


Figure S13. UPLC analysis of TTI (Smp9, Smp12) (**11**) at 1 h time intervals during incubation in H₂O with 0.1 vol% TFA (pH 2) to a concentration of 100 mM.

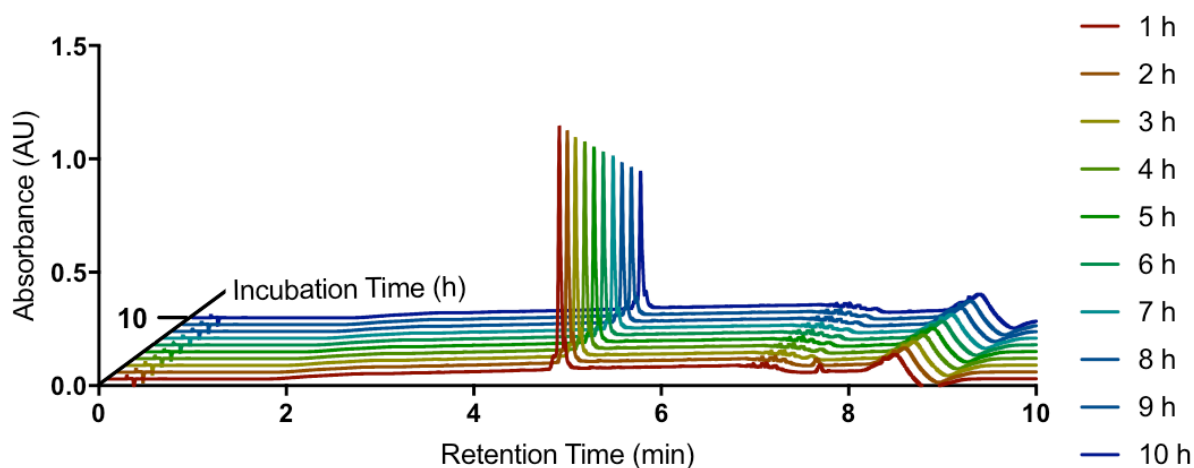


Figure S14. UPLC analysis of TTI (F₂Smp9, F₂Smp12) (**12**) at 1 h time intervals during incubation in H₂O with 0.1 vol% TFA (pH 2) to a concentration of 100 mM.

8 COMPLEX CRYSTALLISATION TRIALS

Human α -thrombin (Haematologic Technologies) was mixed in a 1:3 molar ratio with TTI (Smp9, Smp12) (**11**) in 0.02 M HEPES pH 7.5, 0.125 M NaCl. The solution was incubated on ice for 30 min and then concentrated to 14 mg/mL using a 2 kDa cut-off centrifugal ultrafiltration device (Sartorius). Crystallization conditions were screened at 20 °C in sitting drop geometry using 96-well plates. Drops were prepared with a dispensing robot (Mosquito, TTP LabTech Ltd) by mixing equal volumes (150 nL) of the complex and reservoir solutions and equilibrated against 80 μ L of the latter. A crystallization condition yielding orthorhombic crystals (space group $P2_12_12_1$) was identified (0.1 M HEPES pH 7.5, 0.2 M ammonium acetate, 25% (w/v) PEG 3350). Crystals were recovered from the drops, cryopreserved in 0.1 M HEPES pH 7.5, 0.2 M ammonium acetate, 30% (w/v) PEG 3350, 15% (v/v) glycerol, and flash-cooled in liquid nitrogen.

9 X-RAY CRYSTALLOGRAPHY

X-ray diffraction data collection on crystals of human α -thrombin in complex with TTI (Smp9, Smp12) (**11**) was performed at 100K on the BL13-XALOC beamline³ of the ALBA Synchrotron (Cerdanyola del Vallès, Spain) using a PILATUS 6M detector (Dectris) (900 images, 0.1° rotation, 0.097 s exposure).

Data was indexed and integrated with XDS⁴ and reduced with utilities from the CCP4 suite.⁵ The raw diffraction images were deposited with the Structural Biology Data Grid (doi: 10.15785/SBGRID/846).⁶ The structure was solved by molecular replacement with PHASER⁷ using the coordinates from human α -thrombin (PDB: 6TKG) as a search model.⁸ Refinement and model building were conducted iteratively using COOT⁹ and PHENIX, respectively.¹⁰ The final refined three-dimensional coordinates and structure factors were deposited at the Protein Data Bank (PDB: 7PHX, doi: 10.2210/pdb7PHX/pdb). All structural representations were produced using PyMOL (Schrödinger).

Table S2. Data collection and refinement statistics*.

Dataset	TB: TTI-Smp9,Smp12
Data collection	
Beamline	ALBA BL13-XALOC
Wavelength (Å)	0.97926
Resolution range (Å)	42.95 -1.80 (1.84 - 1.80)
Space group	P2 ₁ 2 ₁ 2 ₁
Unit cell dimensions (Å)	a=43.7, b=80.8, c=85.9
Number of reflections (observed / unique)	92,228 / 27,532 (5,220 / 1,617)
Multiplicity	3.3 (3.2)
Completeness (%)	96.0 (97.0)
Mean I/σ(I)	14.8 (1.9)
R _{merge} (%)	3.9 (53.6)
CC ^{1/2}	0.999 (0.834)
Complexes per a.u.	1
Matthews coefficient (Å ³ Da ⁻¹)	2.06
Solvent content (%)	40.2
Refinement	
R _{work}	0.183
R _{free}	0.221
Protein residues	300
Water molecules	133
r.m.s.d. bond lengths (Å)	0.008
r.m.s.d. bond angles (°)	1.005
Ramachandran favored (%)	97.6
Ramachandran outliers (%)	0.0
PDB code	7PHX

* Values in parenthesis correspond to the highest resolution shell.

10 NMR SPECTRA FOR 2, 3 AND SYNTHETIC INTERMEDIATES

Continued on next page.

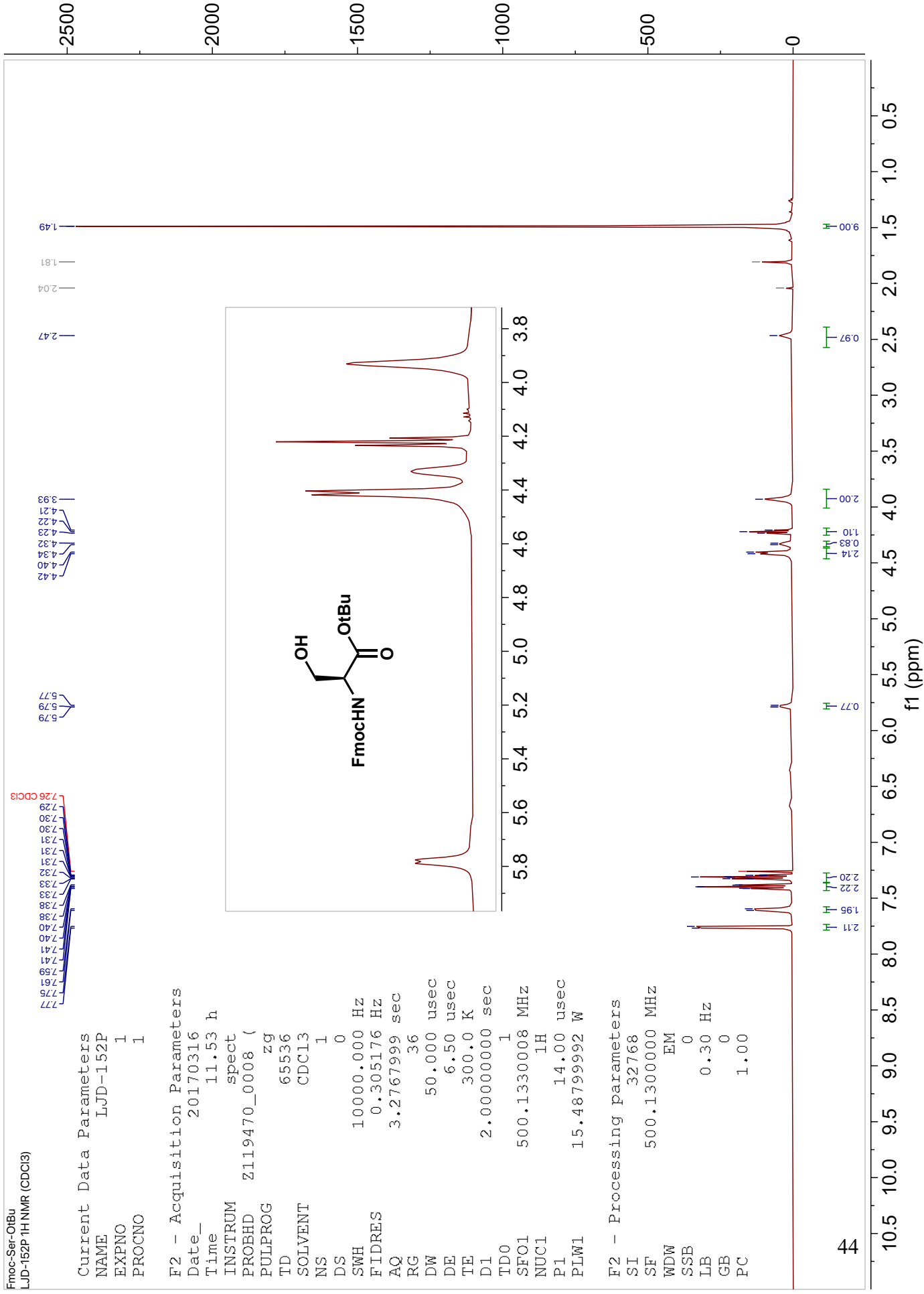
Current Data Parameters
 NAME LJD-152P
 EXPNO 1
 PROCNO 1

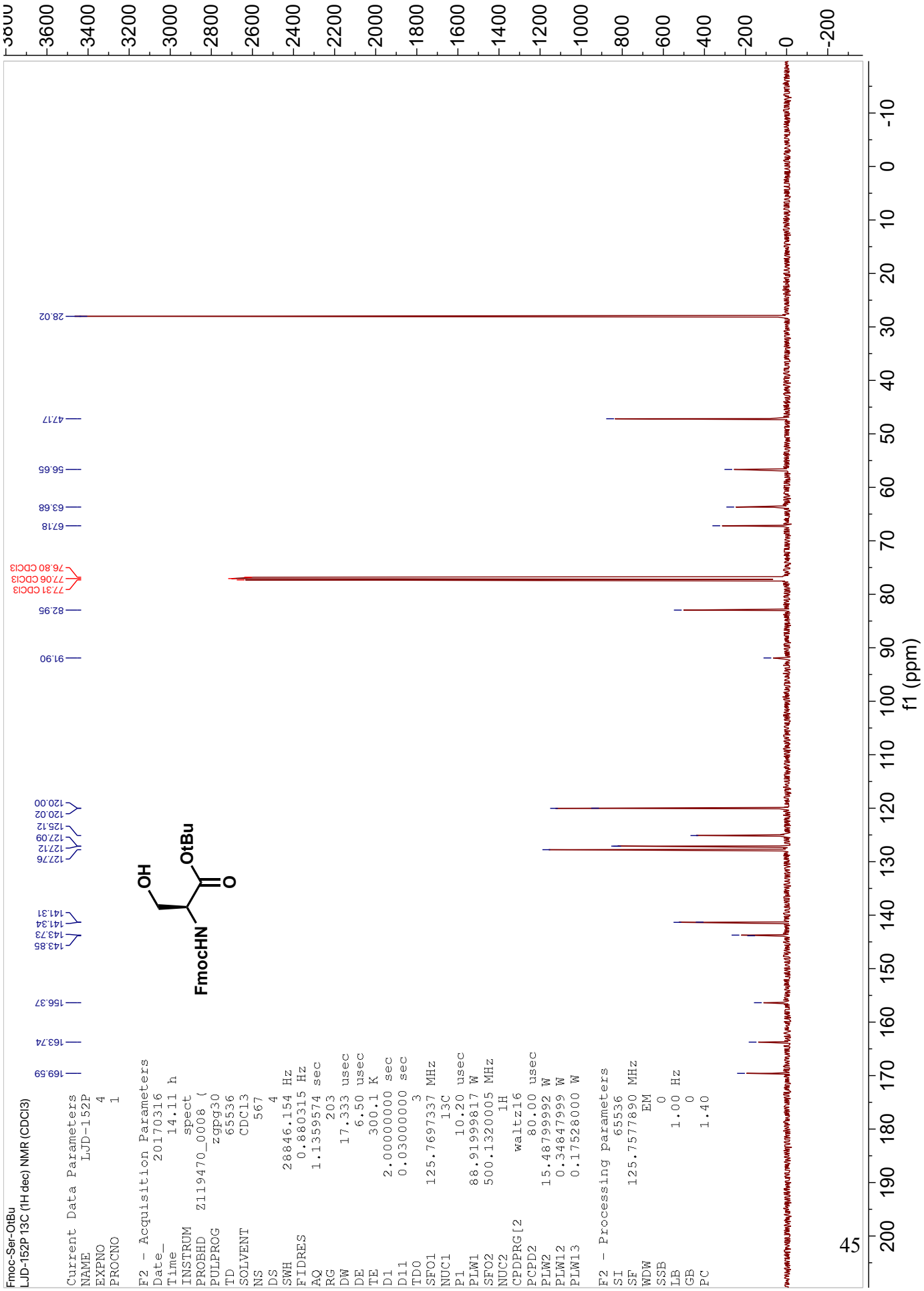
F2 - Acquisition Parameters

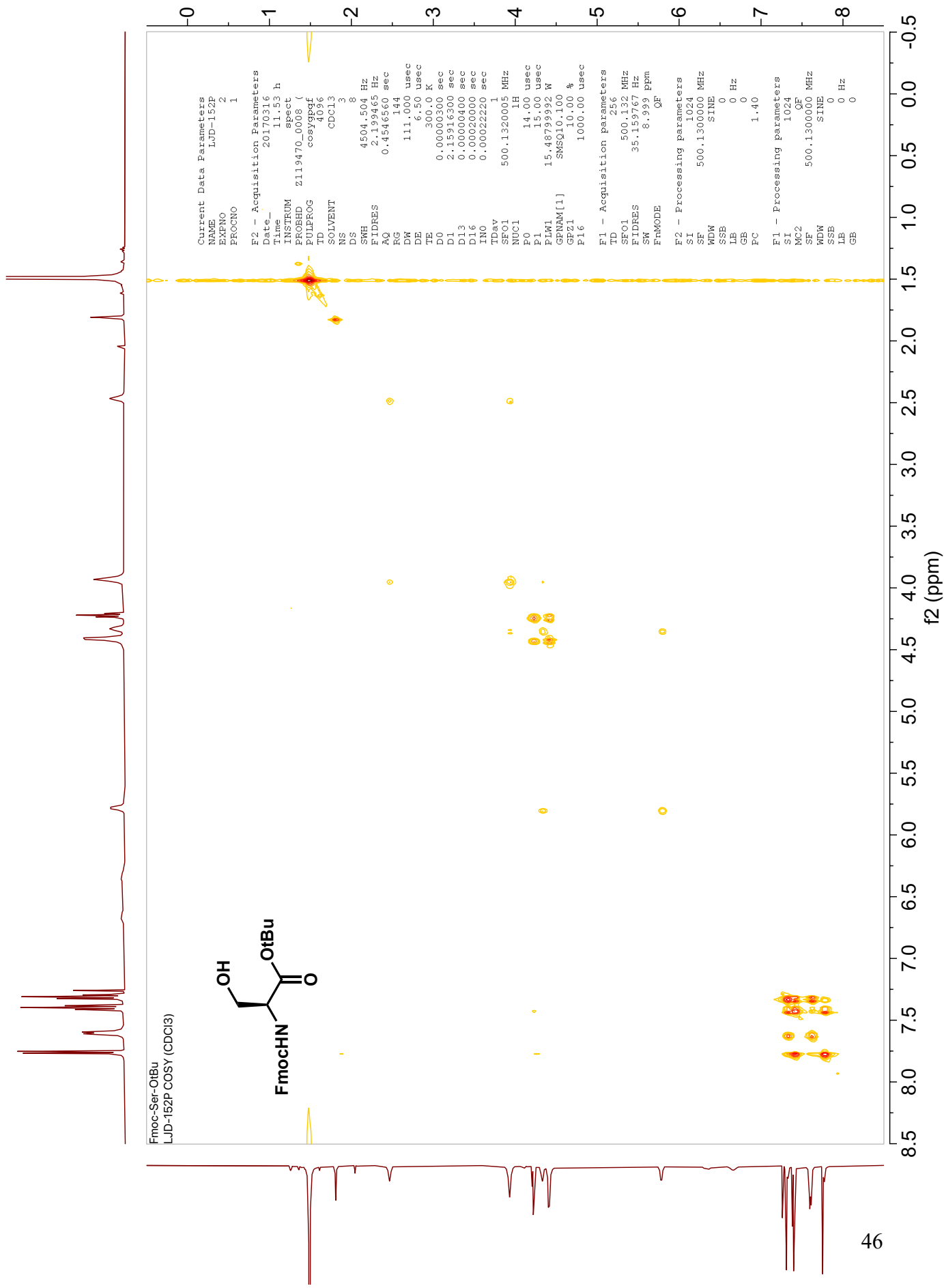
Date_ 20170316
 Time 11.53 h
 INSTRUM spect
 PROBHD Z119470_0008 (zg)
 PULPROG CDCL3
 TD 65536
 SOLVENT CDCL3
 NS 1
 DS 0
 SWH 10000.000 Hz
 FIDRES 0.305176 Hz
 AQ 3.2767999 sec
 RG 36
 DW 50.000 usec
 DE 6.50 usec
 TE 300.0 K
 D1 2.00000000 sec
 TD0 1
 SFO1 500.1330008 MHz
 NUC1 1H
 P1 14.00 usec
 PLW1 15.48799992 W

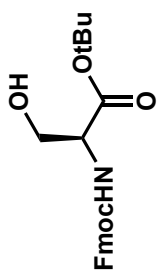
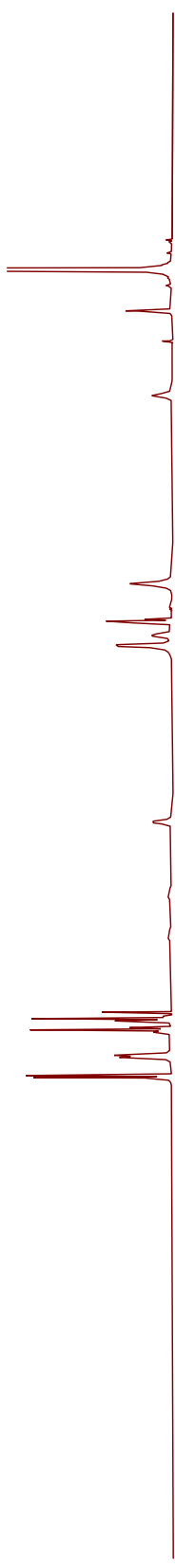
F2 - Processing parameters

SI 32768
 SF 500.1300000 MHz
 WDW EM
 SSB 0
 LB 0.30 Hz
 GB 0
 PC 1.00









Fmoc-Ser-OtBu

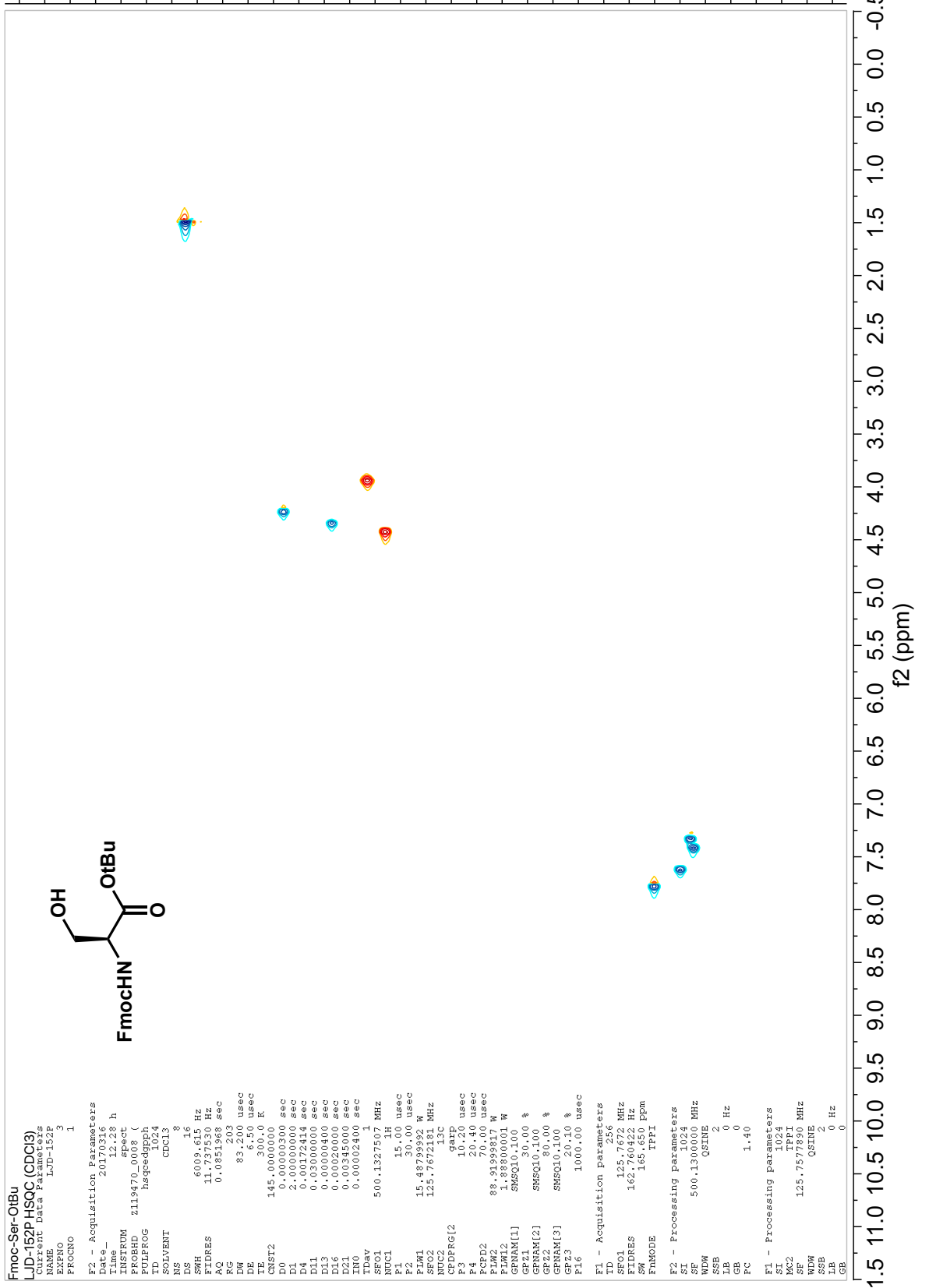
LJID-15ZPHSQC (CDCI3)

Name
 EXPNO 1
 PROCNO 1
 F2 - Acquisition Parameters
 Date_ 20170316
 Time 12:28 h
 INSTRUM spect
 PROBHD z119470.0008 (1
 PULPROG zgpg30
 ID 1024
 SOLVENT CDCl3
 NS 8
 DS 1
 SWH 6009.615 Hz
 FIDRES 11.737530 Hz
 AQ 0.0851968 sec
 RG 203
 DM 83.200 usec
 DE 6.50 usec
 TE 300.2 K
 C12ST2 145.0000000
 D0 0.00000300 sec
 D1 2.00000000 sec
 D4 0.00172414 sec
 D11 0.03000000 sec
 D13 0.00000400 sec
 D16 0.00000000 sec
 D21 0.00350000 sec
 INO 0.00002400 sec
 TDav 1
 SFO1 500.1327507 MHz
 NUC1 1H
 P1 15.00 usec
 PL1 0.00 dB
 PLW1 15.48799992 W
 SFO2 125.7672181 MHz
 NUC2 13C
 P2 13C
 PL2 0.00 dB
 PLW2 88.91999817 W
 P1M12 1.88800001 W
 GPNAM(1) SMSQ10.100
 GPZ1 30.00 %
 GPNAM(2) SMSQ10.100
 GPZ2 60.00 %
 GPNAM(3) SMSQ10.100
 GPZ3 20.10 %
 P16 1000.00 usec

F1 - Acquisition Parameters
 ID 125.7236
 SFO1 125.76022 MHz
 FIDRES 162.76022
 SW 165.650 Ppm
 ENMODE TPPI

F2 - Processing Parameters
 SI 1024
 SF 500.1300000 MHz
 DS 2
 SSB 0 Hz
 GB 0
 PC 1.40

F1 - Processing Parameters
 SI 1024
 SF 125.76022 MHz
 WDW Hanning
 SSB 0 Hz
 GB 0
 PC 1.40



Fmoc-Ser(OTs)-OtBu
LJD-044 1H NMR (CDCl3)

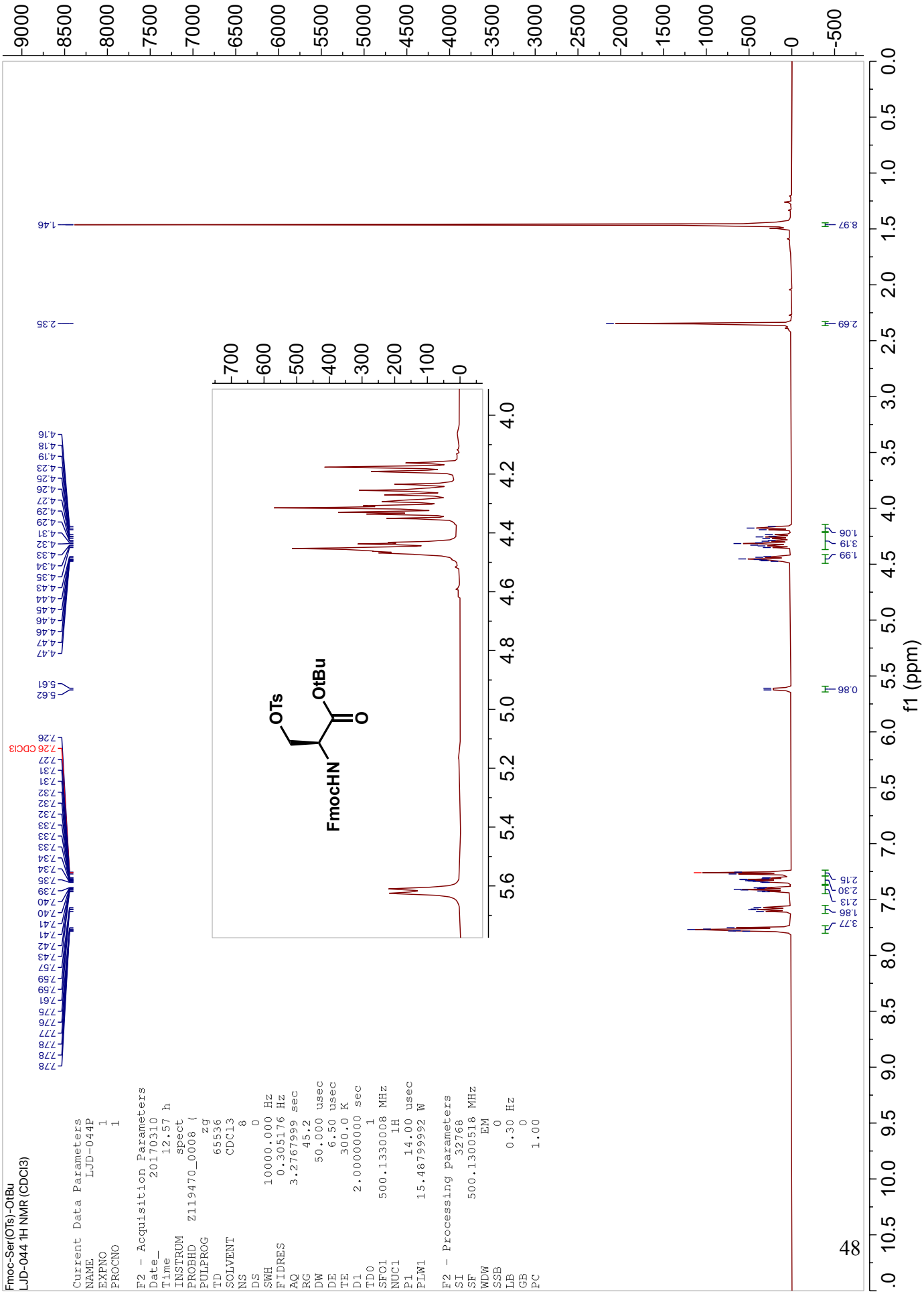
Current Data Parameters
NAME LJD-044P
EXPNO 1
PROCNO 1

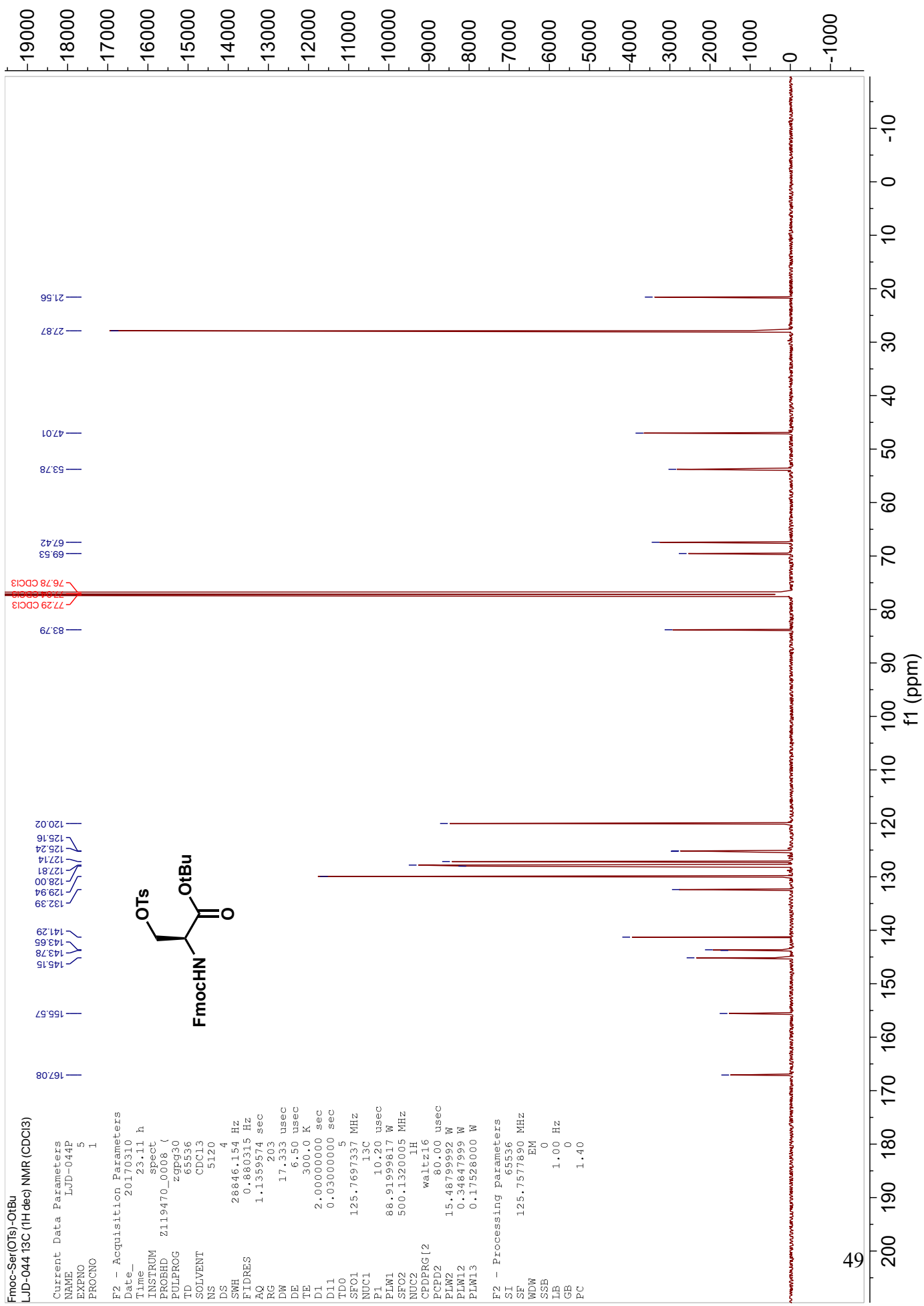
F2 - Acquisition Parameters

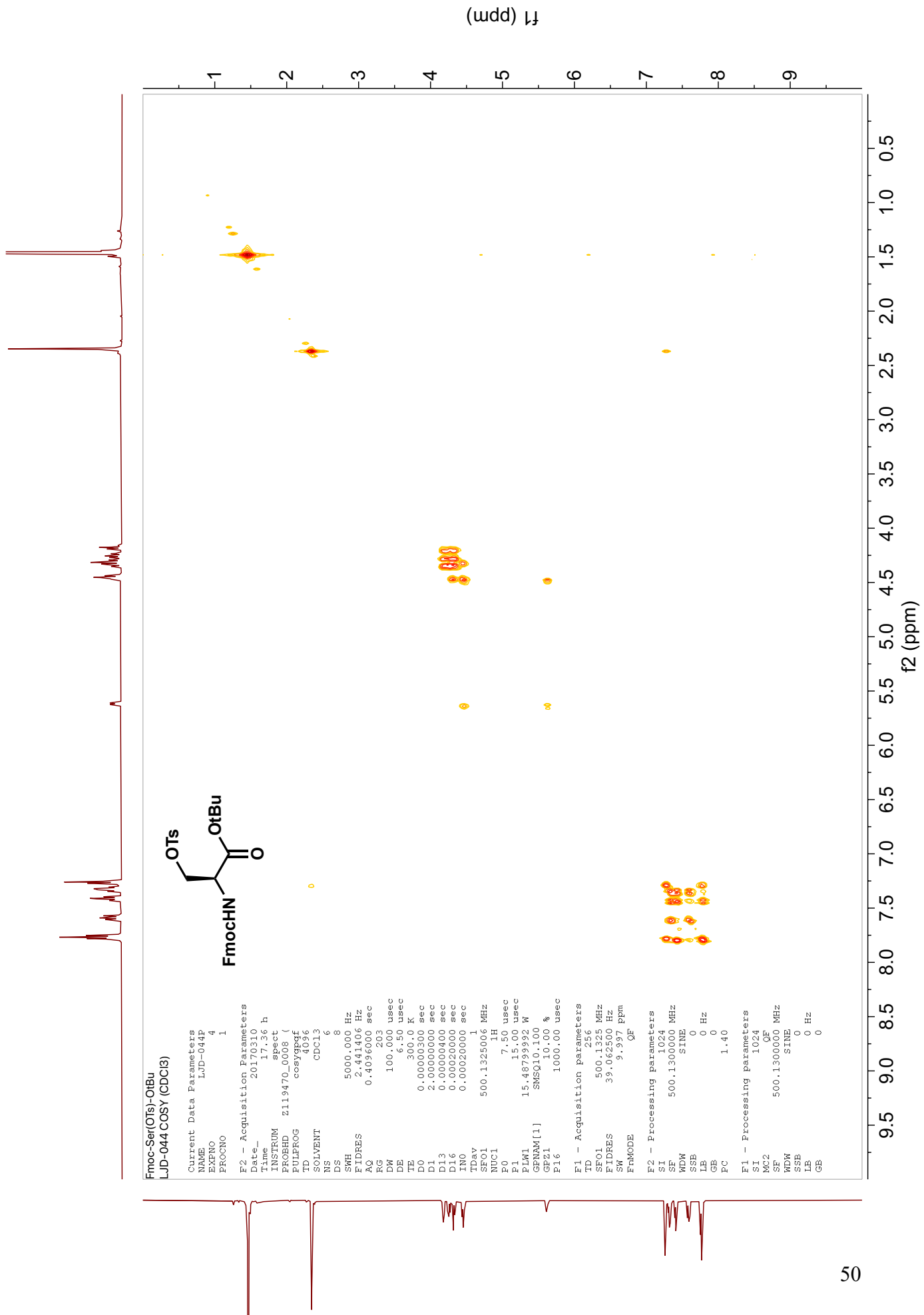
Date_ 20170310
Time 12.57 h
INSTRUM spect
PROBHD zg
PULPROG zg
TD 65536
SOLVENT CDCl3
NS 8
DS 0
SWH 10000.000 Hz
FIDRES 0.305176 Hz
AQ 3.2767999 sec
RG 45.2
DW 50.000 usec
DE 6.50 usec
TE 300.0 K
D1 2.00000000 sec
TD0 1
SFO1 500.1330008 MHz
NUC1 1H
P1 14.00 usec
PLW1 15.48789992 W

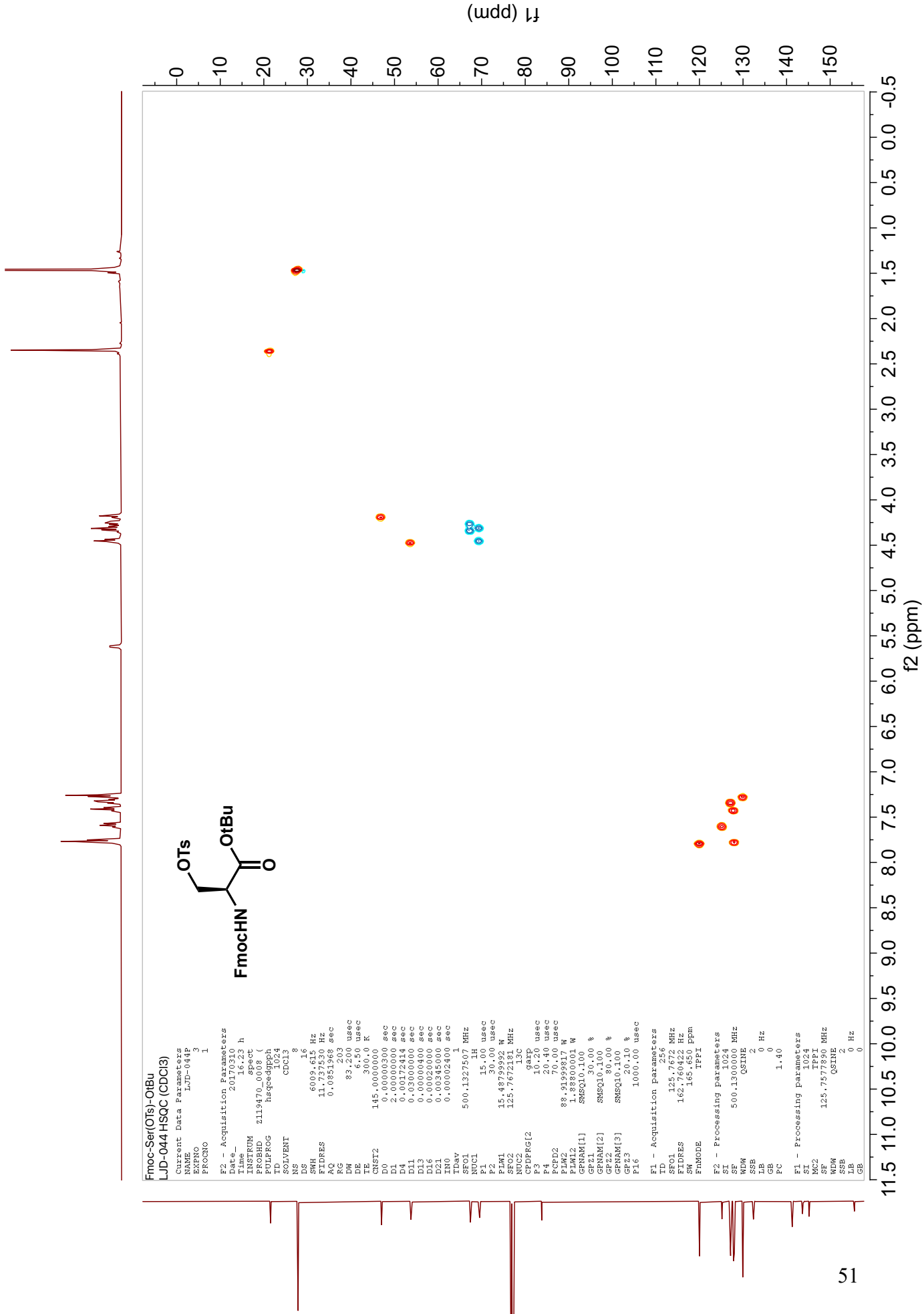
F2 - Processing parameters

SI 32768
SF 500.1300518 MHz
WDW EM
SSB 0
LB 0.30 Hz
GB 0
PC 1.00









Fmoc-iodoalanine-OtBu
LJD-032 1H NMR (CDCl3)

Current Data Parameters
NAME LJD-032P
EXPNO 1
PROCNO 1

F2 - Acquisition Parameters
Date_ 20170310
Time_ 13.02 h

INSTRUM spect
PROBHD z119470_0008 (zg)
PULPROG zg

TD 65536
SOLVENT CDCl3
NS 8
DS 0

SWH 10000.000 Hz
FIDRES 0.305176 Hz
AQ 3.2767999 sec

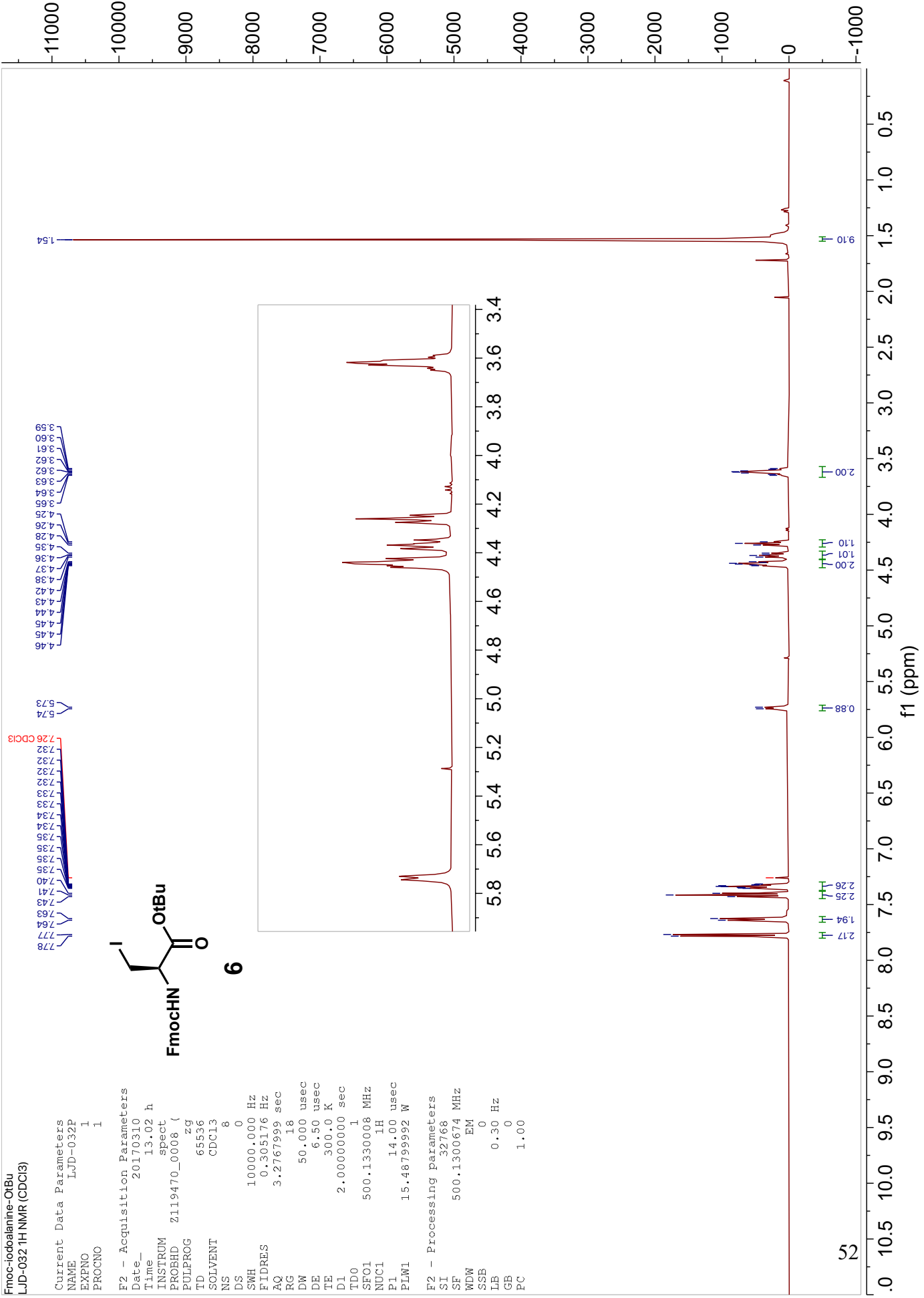
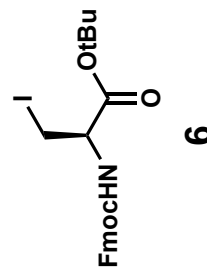
RG 18
DW 50.000 usec
DE 6.50 usec
TE 300.0 K

D1 2.00000000 sec
TD0 1
SF01 500.1330008 MHz
NUC1 1H

P1 14.00 usec
PLW1 15.48799992 W

F2 - Processing parameters
SI 32768
SF 500.1300674 MHz
WDW EM

SSB 0
LB 0.30 Hz
GB 0
PC 1.00



Fmoc-iodoalanine-OtBu
 LJD-032.13C (1H dec) NMR (CDCl3)

Current Data Parameters
 Name LJD-032F
 EXPNO 5
 PROCNO 1

F2 - Acquisition Parameters
 Date_ 20170311
 Time 5.45 h

INSTRUM spect
 PROBDH z119470_0008 ()
 PULPROG zgpg30
 TD 65536

SOLVENT CDCl3
 NS 5120
 DS 4

SWH 28846.154 Hz
 FIDRES 0.880315 Hz
 AQ 1.1359574 sec

RG 203
 DW 17.333 usec
 DE 6.50 usec
 TE 300.0 K

D1 2.00000000 sec
 D11 0.03000000 sec
 TD0 5

SFO1 125.7697337 MHz
 NUC1 13C

F1 10.20 usec
 PLW1 88.91999817 W
 SFO2 500.1320005 MHz

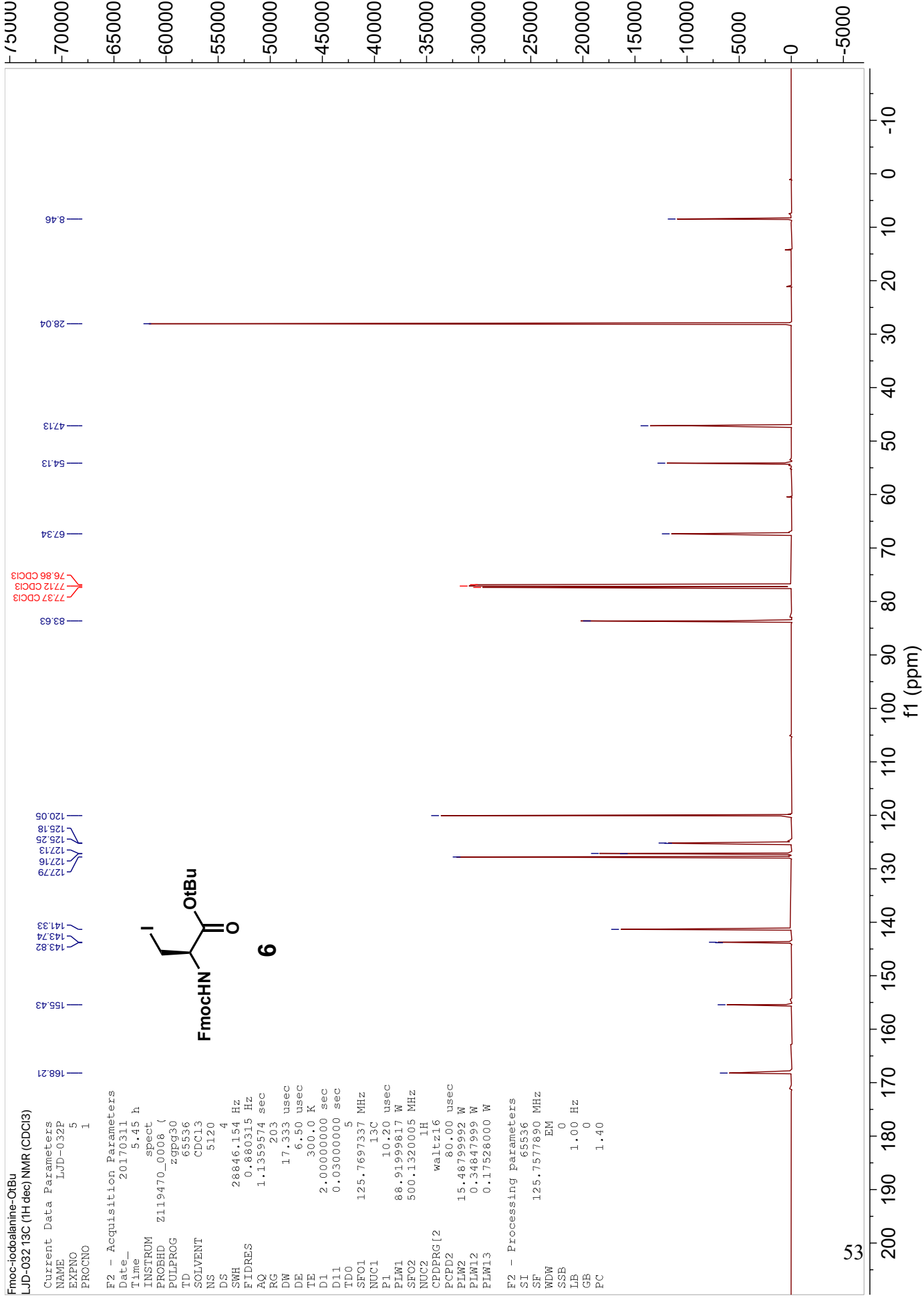
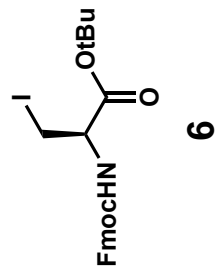
NUC2 1H
 CPDPRG[2] waltz16
 PCPD2 80.00 usec

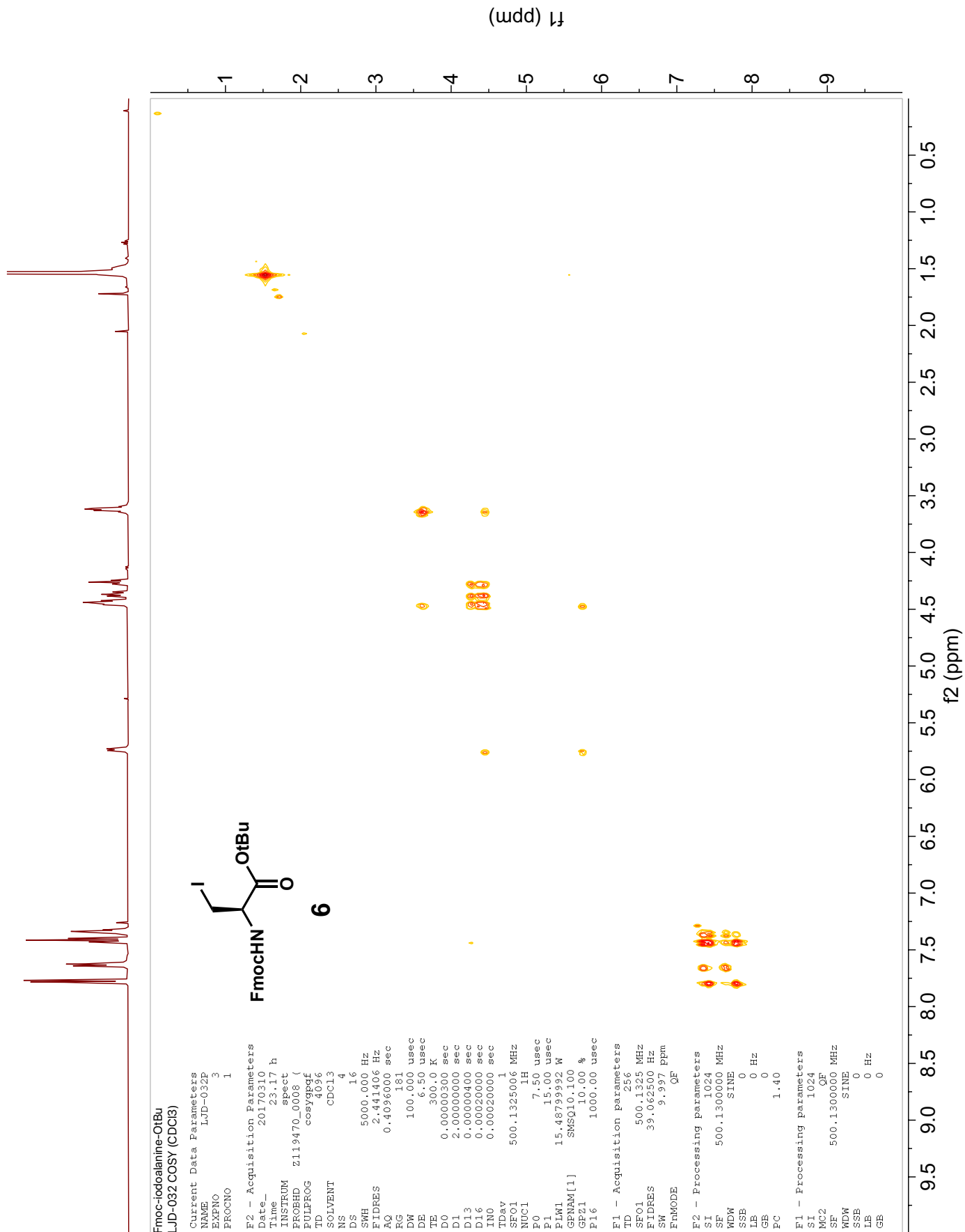
PLW2 15.48799992 W
 PLW12 0.34847999 W
 PLW13 0.17528000 W

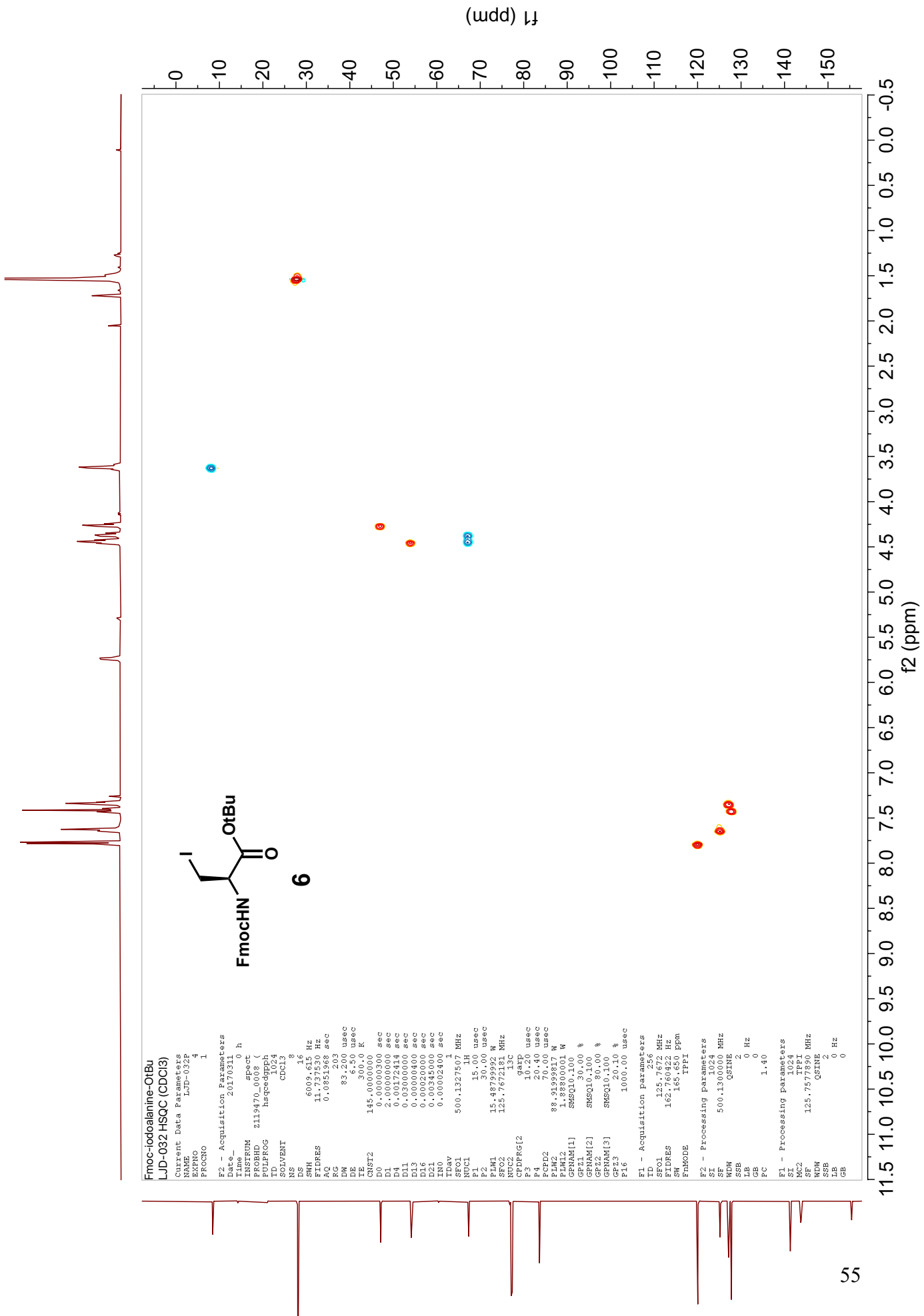
F2 - Processing parameters
 SI 65536
 SF 125.7577890 MHz

WDW EM
 SSB 0
 LB 1.00 Hz

GB 0
 PC 1.40







Sodium 4-iodobenzenesulfonate

LJD-138C 1H NMR (D2O)

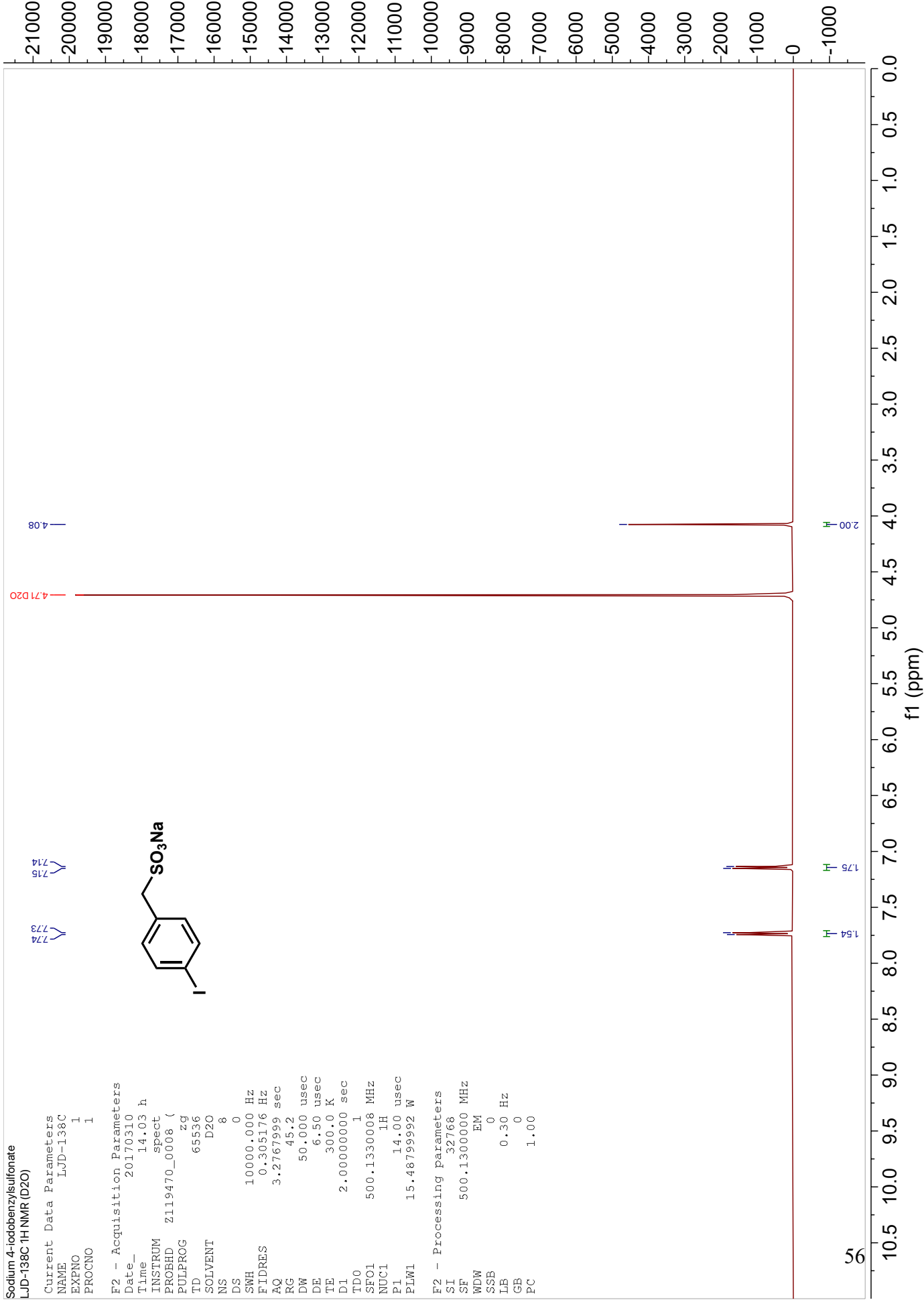
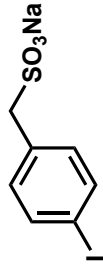
Current Data Parameters
NAME LJD-138C
EXPNO 1
PROCNO 1

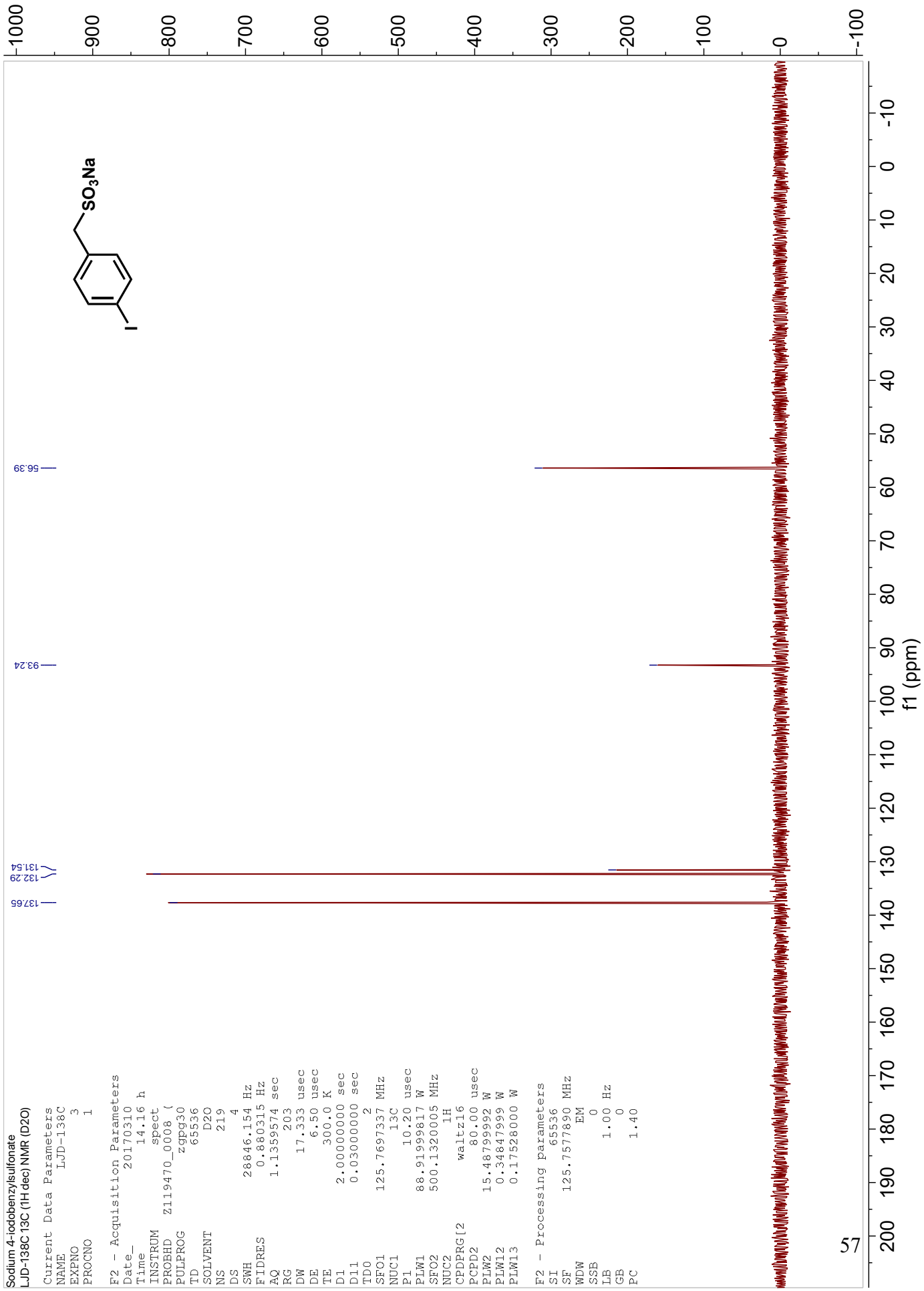
F2 - Acquisition Parameters

Date_ 20170310
Time_ 14.03 h
INSTRUM spect
PROBHD Z119470_0008 (zq)
PULPROG zg
TD 65536
SOLVENT D2O
NS 8
DS 0
SWH 10000.000 Hz
FIDRES 0.305176 Hz
AQ 3.2767999 sec
RG 45.2
DW 50.000 usec
DE 6.50 usec
TE 300.0 K
D1 2.00000000 sec
TD0 1
SF01 500.1330008 MHz
NUC1 1H
P1 14.00 usec
PLW1 15.4879992 W

F2 - Processing parameters

SI 32768
SF 500.1300000 MHz
WDW EM
SSB 0
LB 0.30 Hz
GB 0
PC 1.00





4-iodobenzylsulfonfyl chloride

LJD-096C 1H NMR (CDCl3)

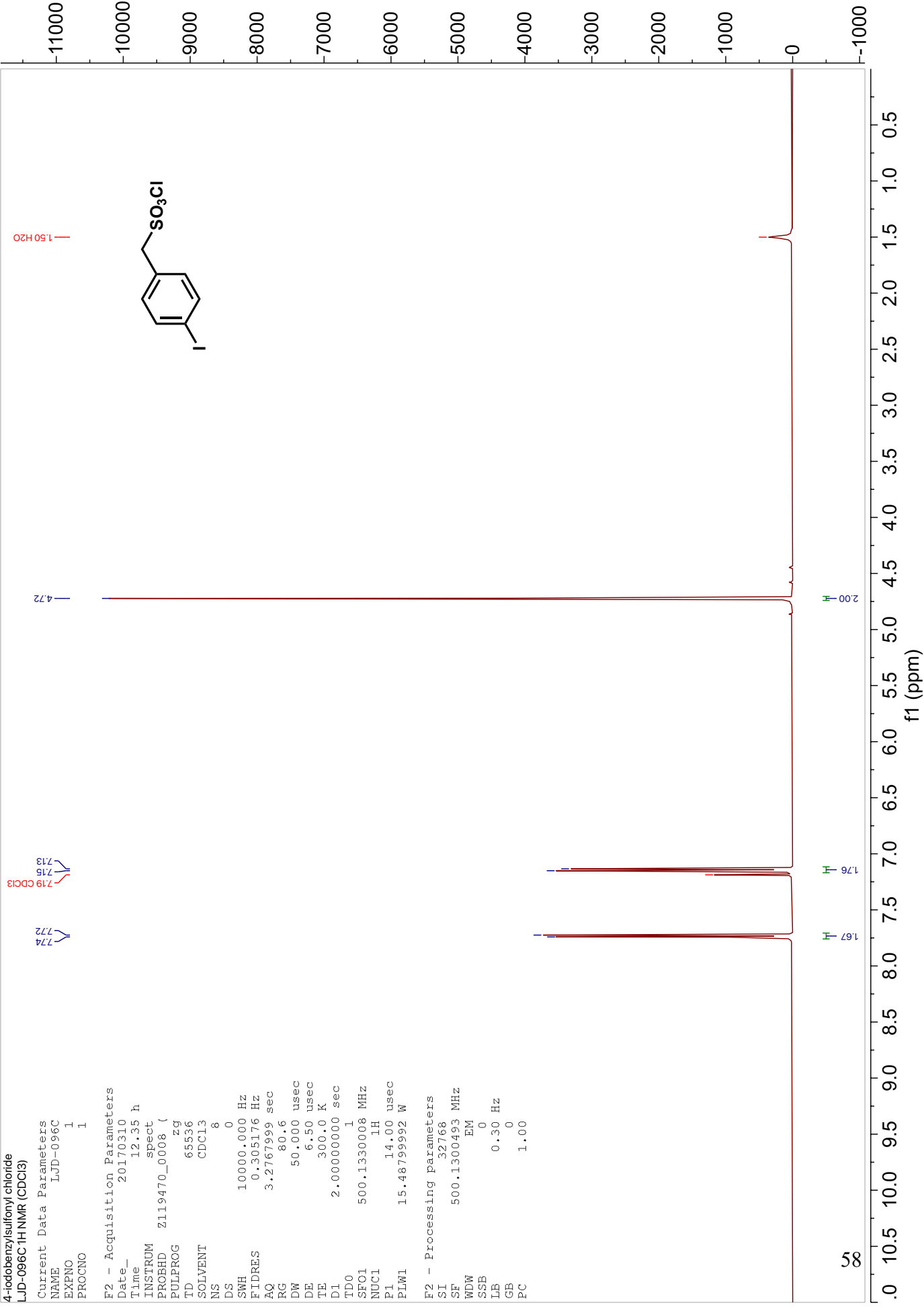
Current Data Parameters
NAME LJD-096C
EXPNO 1
PROCNO 1

F2 - Acquisition Parameters

Date_ 20170310
Time 12.35 h
INSTRUM spect
PROBHD Z119470_0008 (PULPROG zg)
TD 65536
SOLVENT CDCl3
NS 8
DS 0
SMH 10000.000 Hz
FIDRES 0.305176 Hz
AQ 3.2767999 sec
RG 80.6
DM 50.000 usec
DE 6.50 usec
TE 300.0 K
D1 2.00000000 sec
TD0 1
SFO1 500.1330008 MHz
NUC1 1H
P1 14.00 usec
PLW1 15.48799992 W

F2 - Processing parameters

SI 32768
SF 500.1300493 MHz
WDW EM
SSB 0
LB 0.30 Hz
GB 0
PC 1.00



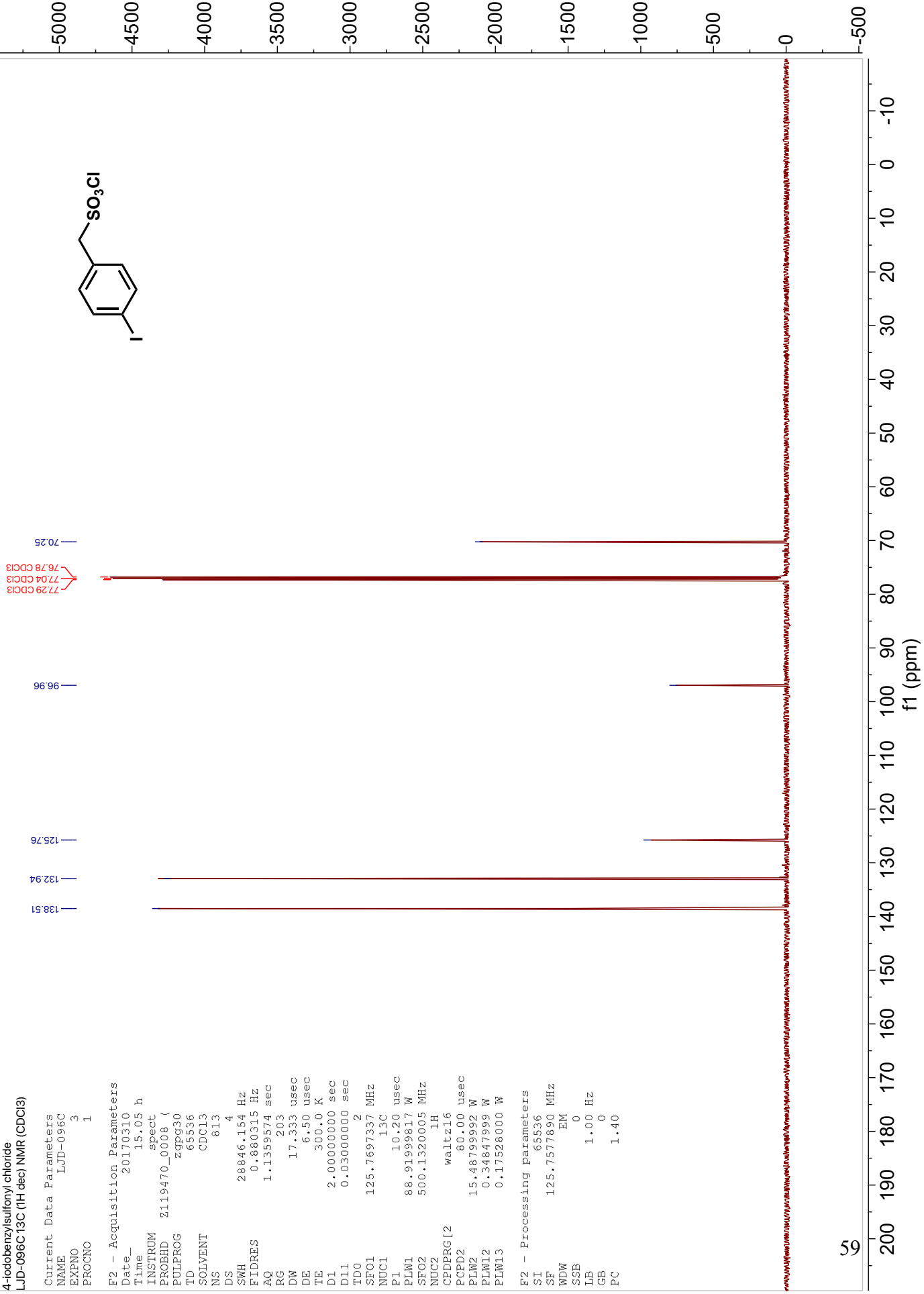
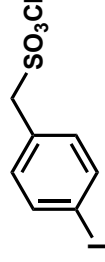
4-iodobenzylsulfonfyl chloride

LJD-096C 13C (1H dec) NMR (CDCl3)

Current Data Parameters
 NAME LJD-096C
 EXPNO 3
 PROCNO 1

F2 - Acquisition Parameters
 Date_ 20170310
 Time 15.05 h
 INSTRUM spect
 PROBHD Z119470_0008 (zgpqd30
 PULPROG zgpg30
 TD 65536
 SOLVENT CDCl3
 NS 813
 DS 4
 SWH 28846.154 Hz
 FIDRES 0.880315 Hz
 AQ 1.1359574 sec
 RG 203
 DW 17.333 usec
 DE 6.50 usec
 TE 300.0 K
 D1 2.00000000 sec
 D11 0.03000000 sec
 TD0 2
 SF01 125.7697337 MHz
 NUC1 13C
 P1 10.20 usec
 PLW1 88.9199817 W
 SF02 500.1320005 MHz
 NUC2 1H
 CPDPRG2 waltz16
 PCPD2 80.00 usec
 PLW2 15.48799992 W
 PLW12 0.34847999 W
 PLW13 0.17528000 W

F2 - Processing parameters
 SI 65536
 SF 125.7577890 MHz
 WDW EM
 SSB 0
 LB 1.00 Hz
 GB 0
 PC 1.40



Neopentyl 4-iodobenzylsulfonate

LJD-073-1 1H NMR (CDCl3)

Current Data Parameters
NAME LJD-073-1
EXPNO 1
PROCNO 1

F2 - Acquisition Parameters

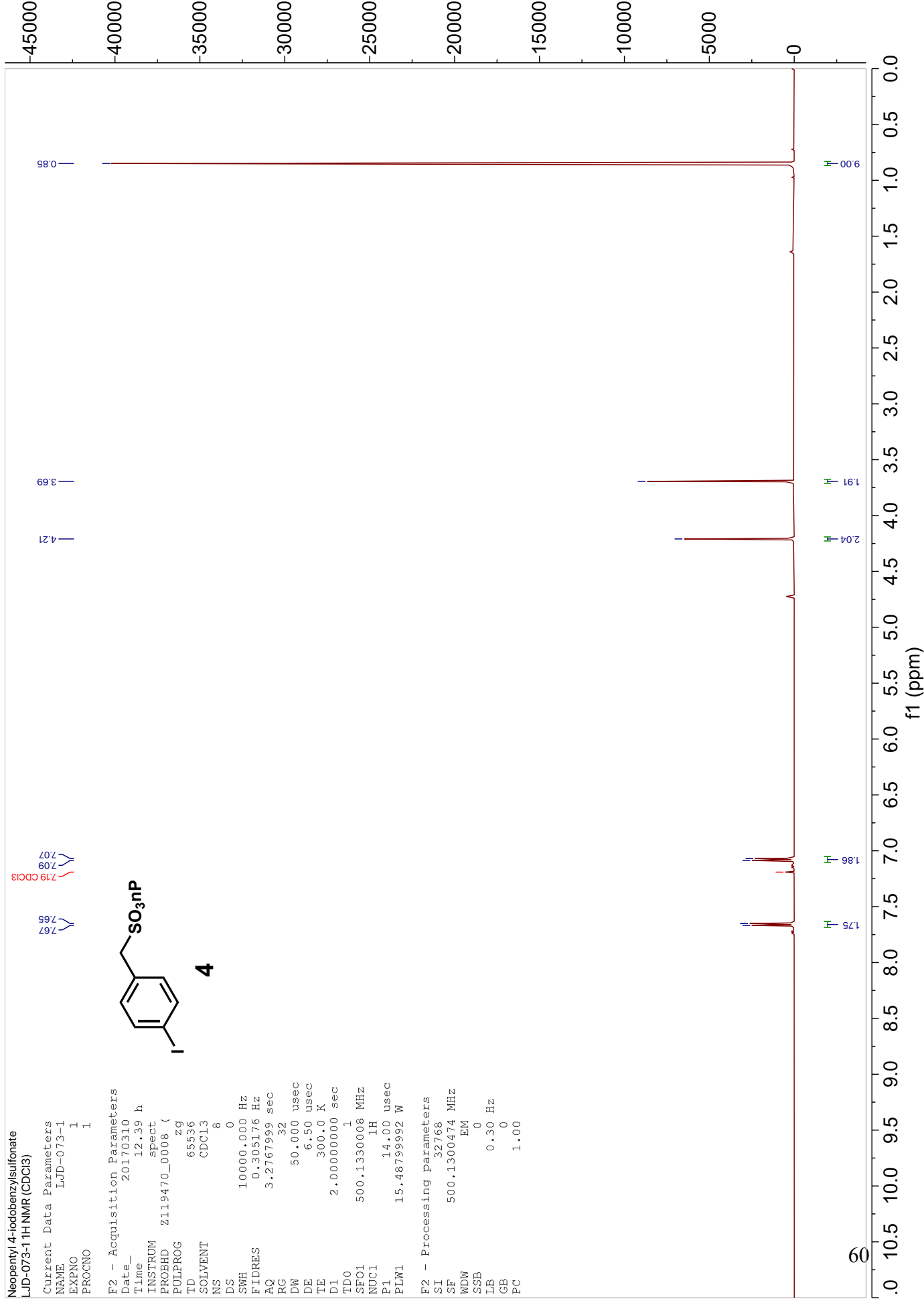
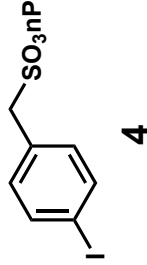
Date_ 201107310
Time 12.39 h
INSTRUM spect
PROBHD z119470_0008 (zq)
PULPROG zg
TD 65536
SOLVENT CDCl3
NS 8
DS 0
SWH 10000.000 Hz
FIDRES 0.305176 Hz
AQ 3.2767999 sec
RG 32
DM 50.000 usec
DE 6.50 usec
TE 300.0 K
D1 2.00000000 sec
TD0 1
SFO1 500.1330008 MHz
NUC1 1H
P1 14.00 usec
PLW1 15.48799992 W

F2 - Processing Parameters

SI 32768
SF 500.1300474 MHz
WDW EM
SSB 0
LB 0.30 Hz
GB 0
PC 1.00

7.19 CDCl3

7.66
7.09
7.07



Neopentyl 4-iodobenzylsulfonate
LJD-073-113C (1H dec) NMR (CDCl3)

Current Data Parameters
NAME LJD-073-1
EXPNO 3
PROCNO 1

F2 - Acquisition Parameters
Date_ 20170310
Time 15.15 h
INSTRUM spect
PROBHD z119470_0008 (

PULPROG zgpg30
TD 65536
SOLVENT CDCl3

NS 83
DS 4

SWH 28846.154 Hz
FIDRES 0.880315 Hz

AQ 1.1359574 sec
RG 203
DE 17.333 usec
TE 300.0 K

D1 2.0000000 sec
D11 0.0300000 sec
TD0 1

SF01 125.7697337 MHz
NUC1 13C

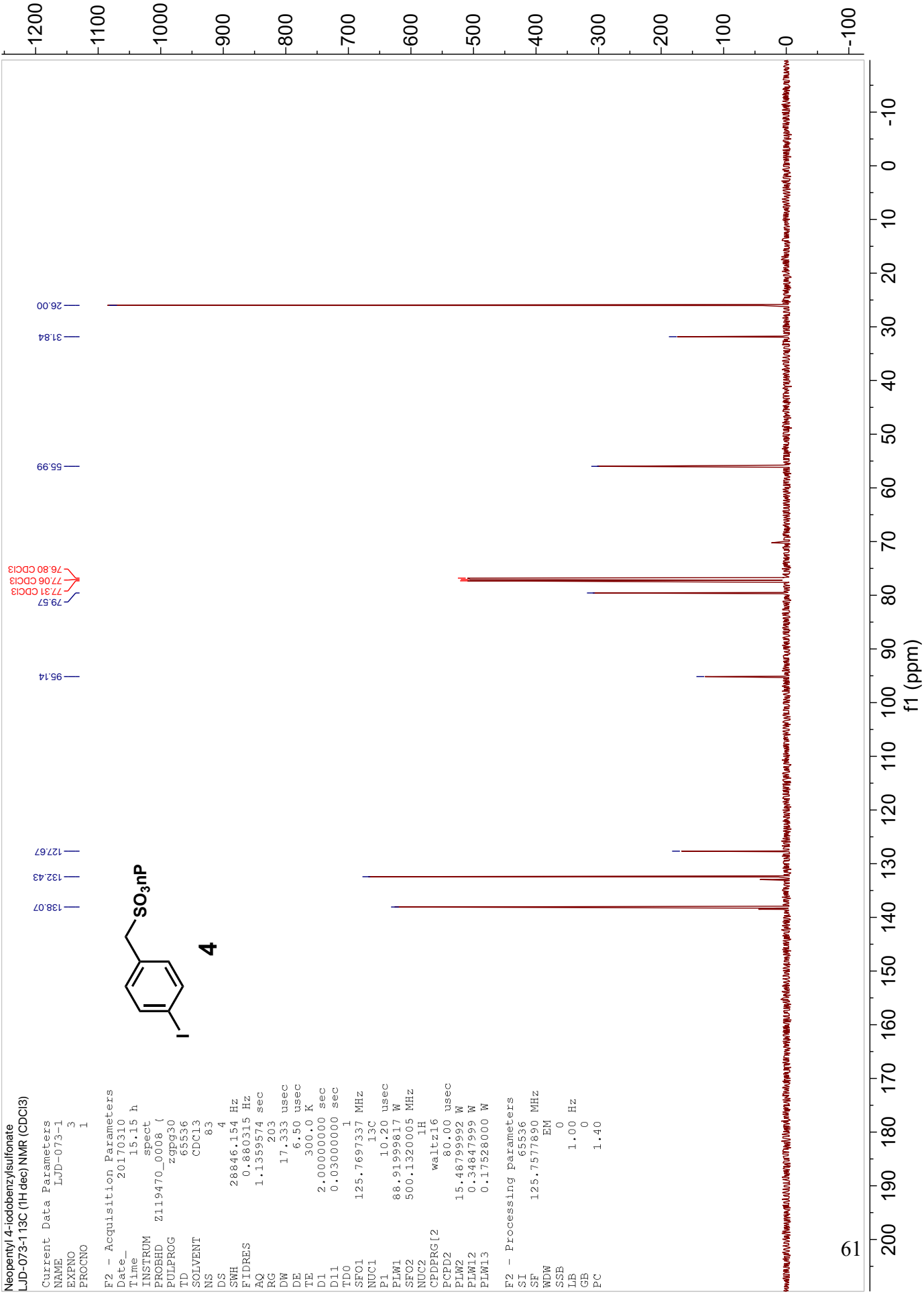
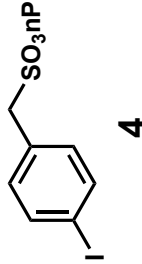
P1 10.20 usec
PLW1 88.9199817 W
SF02 500.1320005 MHz

NUC2 1H
CPDPRG2 waltz16
PCPD2 80.00 usec

PLW2 15.4879992 W
PLWI2 0.34847999 W
PLWI3 0.17528000 W

F2 - Processing parameters
SI 65536
SF 125.7577890 MHz

WDW EM
SSB 0
LB 1.00 Hz
GB 0
PC 1.40



Neopentyl difluoro(4-iodobenzyl)sulfonate

LJD-010 1H NMR (CDCl3)

Current Data Parameters
NAME LJD-010P
EXPNO 1
PROCNO 1

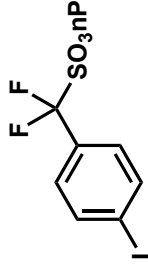
F2 - Acquisition Parameters

Date_ 20170310
Time 12.48 h
INSTRUM spect
PROBHD Z119470_0008 (PULPROG zg)
TD 65536
SOLVENT CDCl3
NS 8
DS 0
SWH 10000.000 Hz
FIDRES 0.305176 Hz
AQ 3.2767959 sec
RG 14.2
DW 50.000 usec
DE 6.50 usec
TE 300.0 K
D1 2.00000000 sec
TDO 1
SFO1 500.1330008 MHz
NUC1 1H
P1 14.00 usec
PLW1 15.48799992 W

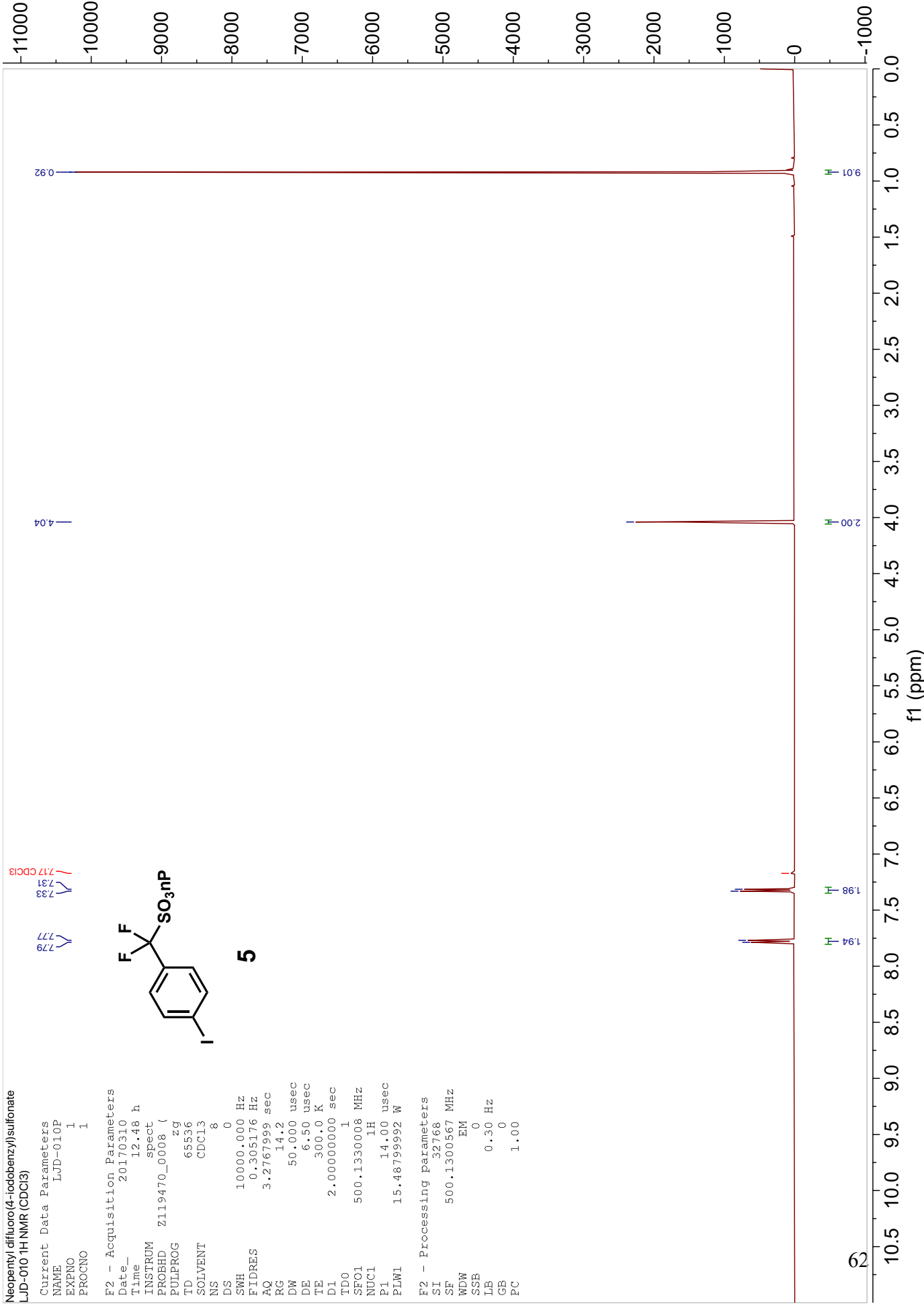
F2 - Processing parameters

SF 32768
SF 500.1300567 MHz
WDW EM
SSB 0
LB 0.30 Hz
GB 0
PC 1.00

779
777
731
733
717 CDCl3



5



Neopentyl difluoro(4-iodobenzyl)sulfonate
LJD-010 13C (1H dec) NMR (CDCl3)

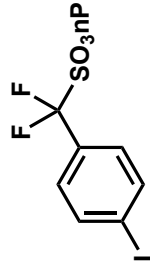
Current Data Parameters
NAME LJD-010P
EXPNO 4
PROCNO 1

F2 - Acquisition Parameters

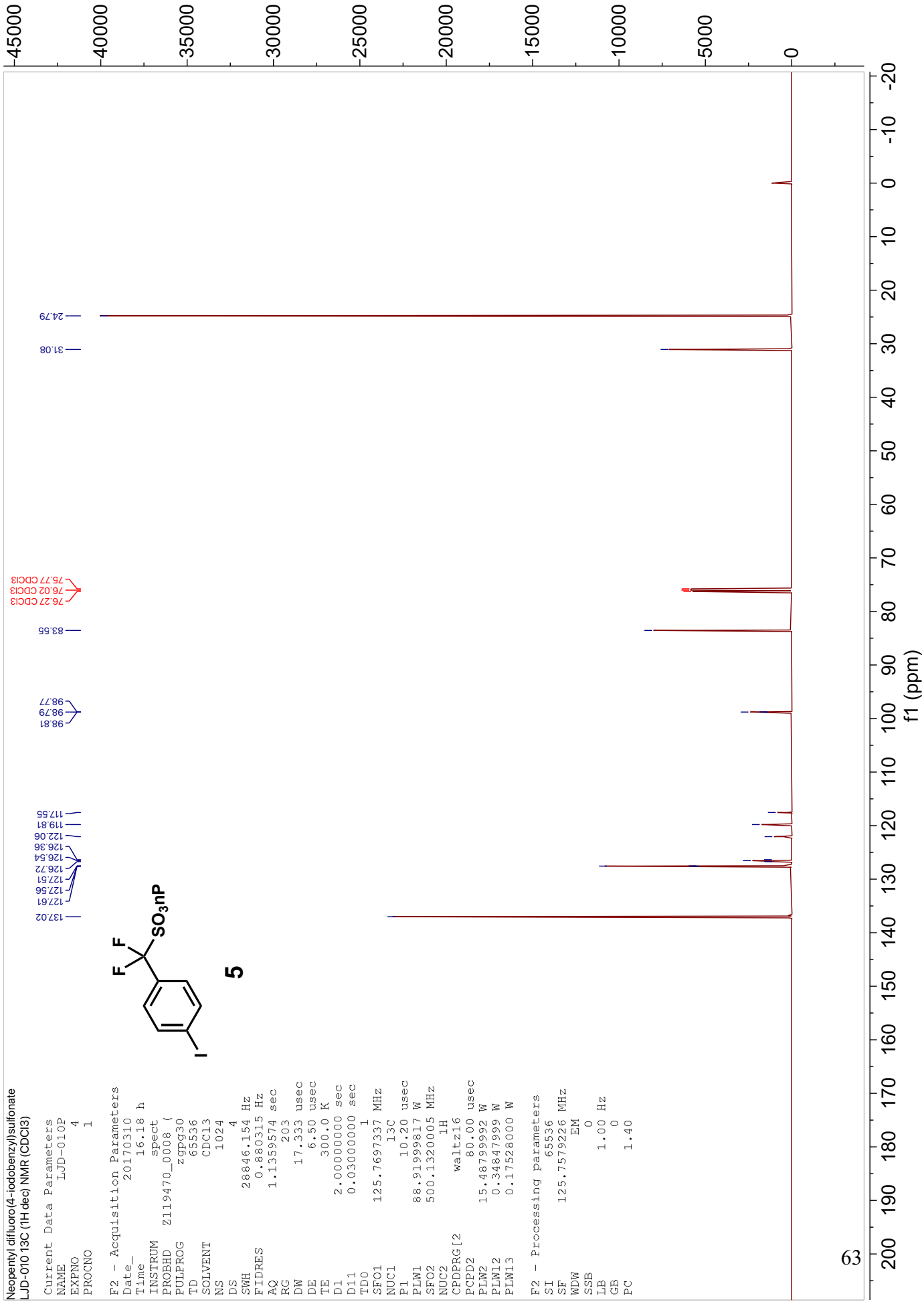
Date_ 20170310
Time_ 16.18 h
INSTRUM spect
PROBHD Z119470_0008 (zjgpg30)
PULPROG zgpg30
TD 65536
SOLVENT CDCl3
NS 1024
DS 4
SMH 28846.154 Hz
FIDRES 0.860315 Hz
AQ 1.1359574 sec
RG 203
DW 17.333 usec
DE 6.50 usec
TE 300.0 K
D1 2.00000000 sec
D11 0.03000000 sec
TDO 1
SFO1 125.7697337 MHz
NUC1 13C
P1 10.20 usec
PLW1 88.91999817 W
SFO2 500.1320005 MHz
NUC2 1H
CPDPRG2 waltz16
PCPD2 80.00 usec
PLW2 15.48799992 W
PLWL2 0.34847999 W
PLWL3 0.17528000 W

F2 - Processing parameters

SI 65536
SF 125.7579226 MHz
WDW EM
SSB 0
LB 1.00 Hz
GB 0
PC 1.40



5



Neopentyl difluoro(4-iodobenzyl)sulfonate
LJD-010 19F (1H dec) NMR (CDCl3)

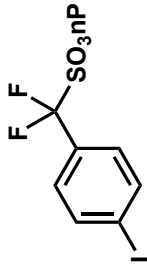
Current Data Parameters
NAME LJD-010P
EXPNO 3
PROCNO 1

F2 - Acquisition Parameters

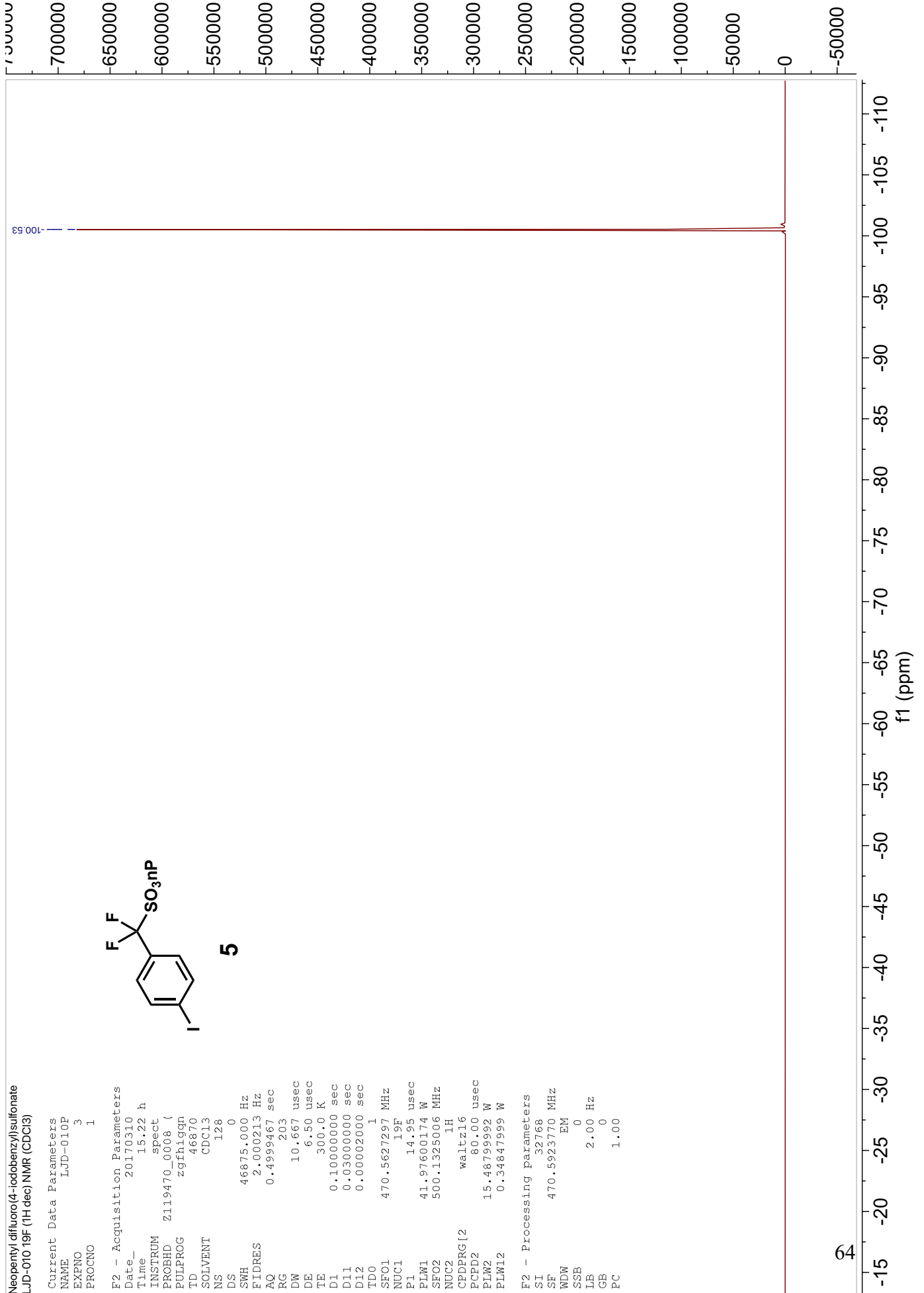
Date_ 20170310
Time_ 15.22 h
INSTRUM spect
PROBHD Z119470_0008 (zgpg30)
PULPROG zgpg30
TD 46870
SOLVENT CDCl3
NS 128
DS 0
SWH 46875.000 Hz
FIDRES 2.000213 Hz
AQ 0.4999467 sec
RG 203
DW 10.667 usec
DE 6.50 usec
TE 300.0 K
D1 0.10000000 sec
D11 0.03000000 sec
D12 0.00002000 sec
TD0 1
SFO1 470.5627297 MHz
NUC1 19F
P1 14.95 usec
PLW1 41.97600174 W
SFO2 500.1325006 MHz
NUC2 1H
CPDPRG2 waltzi6
PCPD2 80.00 usec
PLW2 15.48799992 W
PLW12 0.34847999 W

F2 - Processing parameters

SI 32768
SF 470.5923770 MHz
WDW EM
SSB 0
LB 2.00 Hz
GB 0
PC 1.00



5



Fmoc-Smp(nP)-OtBu
LJ-D-074 1H NMR (CDCl3)

Current Data Parameters
NAME LJ-D-074P
EXPNO 1
PROCNO 1

F2 - Acquisition Parameters

Date 20170310
Time 13.11 h

INSTRUM spect

PROBHD Z119470_0008 (

PULPROG zg

TD 65536

SOLVENT CDCl3

NS 8

DS 0

SWH 10000.000 Hz

FIDRES 0.305176 Hz

AQ 3.2767999 sec

RG 28.5

DW 50.000 usec

DE 6.50 usec

TE 300.0 K

D1 2.00000000 sec

TD0 1

SFO1 500.1330008 MHz

NUC1 1H

PL 14.00 usec

PLW1 15.48799992 W

F2 - Processing parameters

SI 32768

SF 500.1300000 MHz

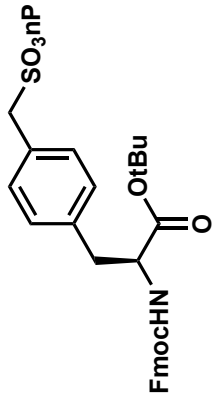
WDW EM

SSB 0

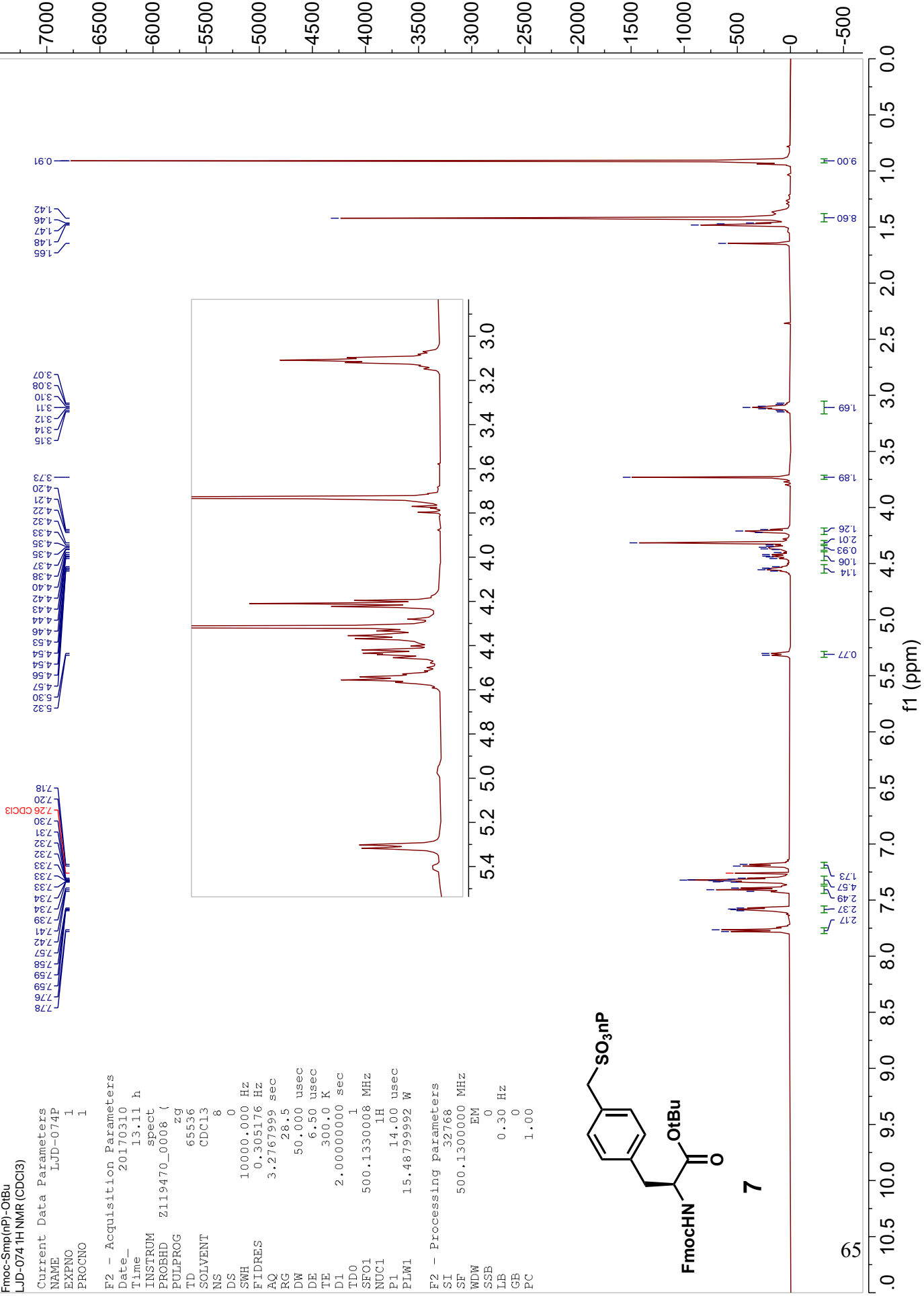
LB 0.30 Hz

GB 0

PC 1.00



7



Fmoc-Smp(nP)-OtBu
 LJD-074 13C (1H dec) NMR (CDCl3)

Current Data Parameters

NAME LJD-074P

EXPNO 6

PROCNO 1

F2 - Acquisition Parameters

Date_ 20170311

Time 15.12 h

INSTRUM spect

PROBHD Z119470_0008 (

PULPROG zgpg30

TD 65536

SOLVENT CDCl3

NS 5120

DS 4

SWH 28846.154 Hz

FIDRES 0.880315 Hz

AQ 1.1359574 sec

RG 203

DW 17.333 usec

DE 6.50 usec

TE 300.0 K

D1 2.0000000 sec

D11 0.0300000 sec

TDO 5

SFO1 125.769737 MHz

NUC1 13C

P1 10.20 usec

PLW1 88.91999817 W

SFO2 500.1320005 MHz

NUC2 1H

CPDPRG [2 waltz16

PCPD2 80.00 usec

PLW2 15.48799992 W

PLW12 0.34847999 W

PLW13 0.17528000 W

F2 - Processing parameters

SI 65536

SF 125.7577890 MHz

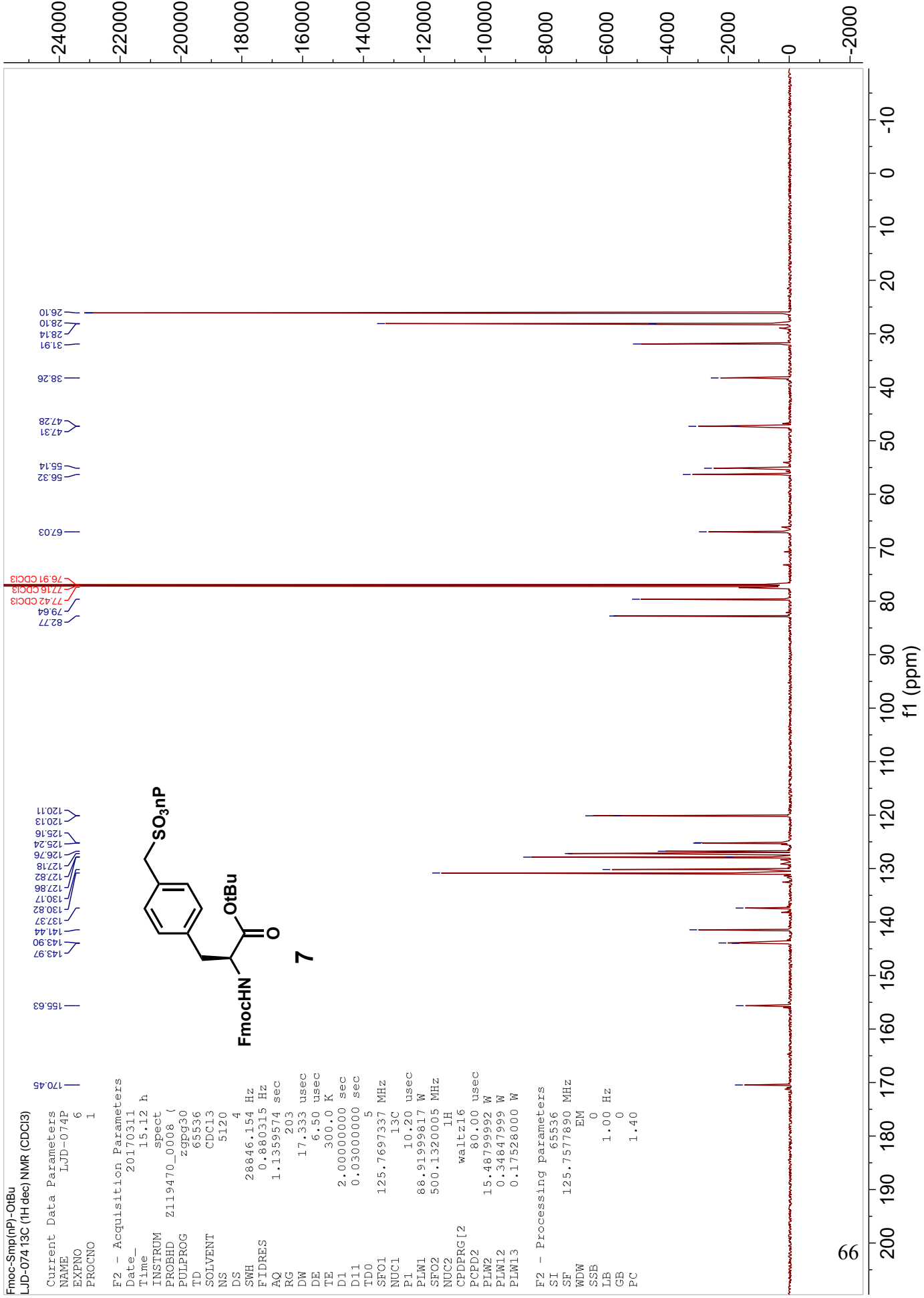
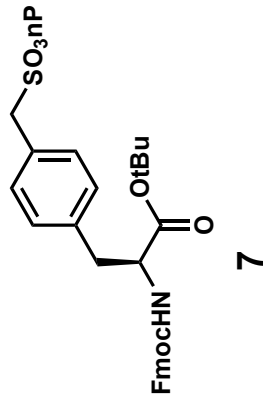
WDW EM

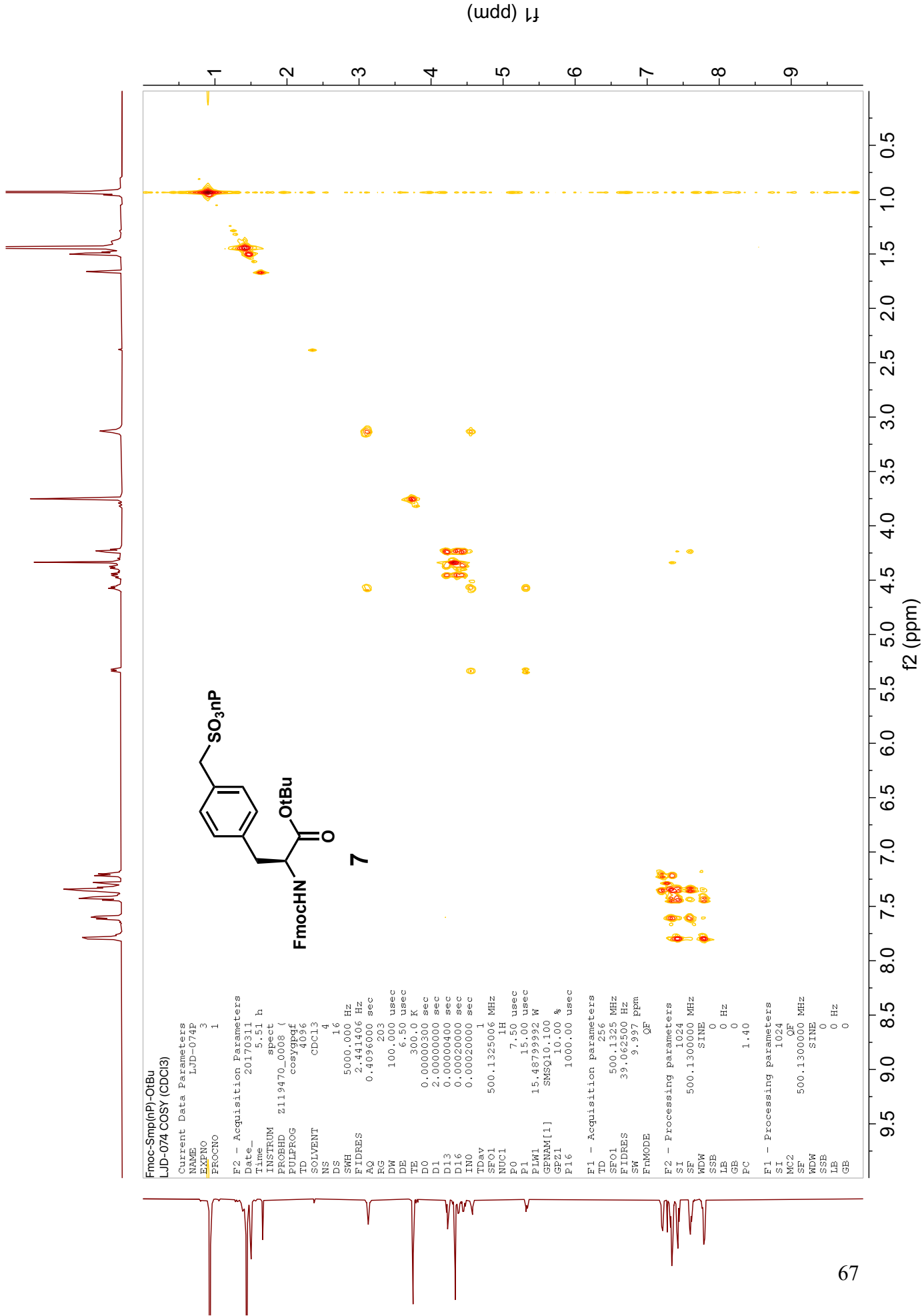
SSB 0

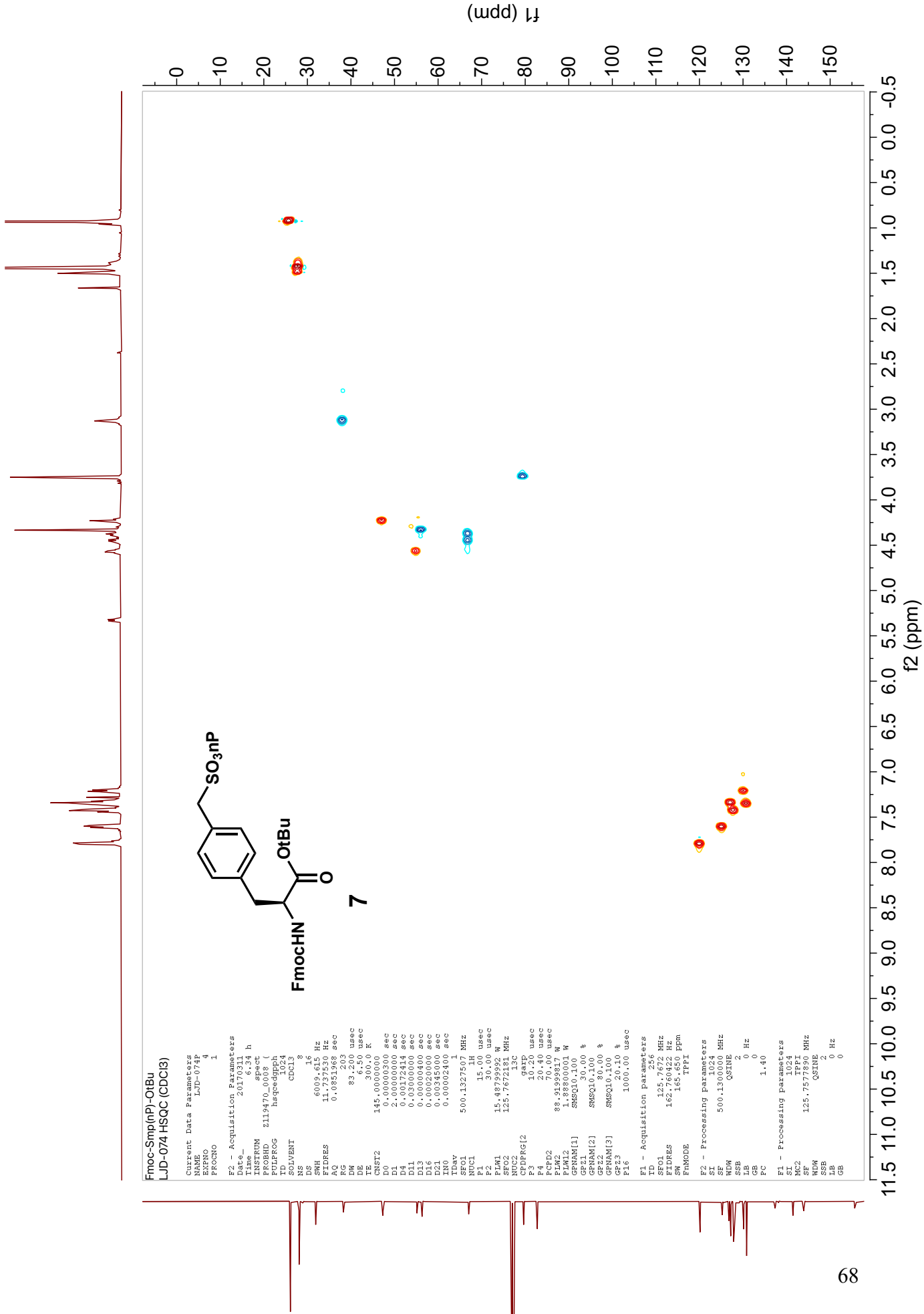
LB 1.00 Hz

GB 0

PC 1.40







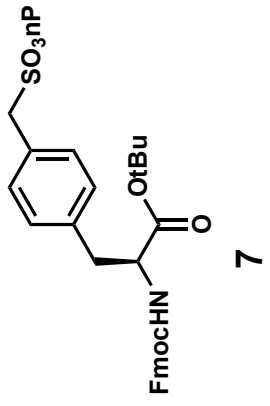
Fmoc-Smp(nP)-OtBu
LJD-074 HSQC (CDCl3)

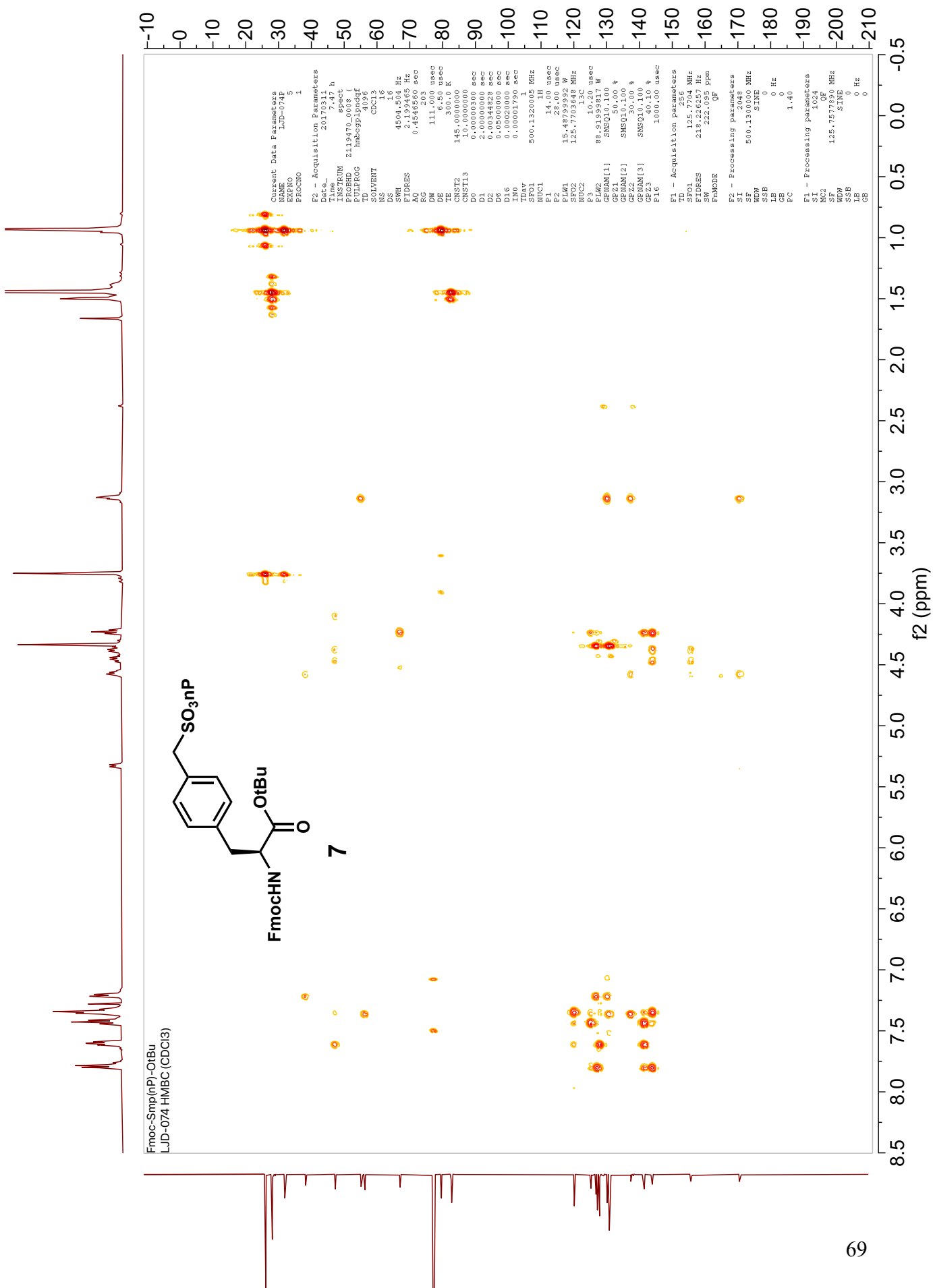
Current Data Parameters
 NAME LJD-074p
 EXPNO 4
 PROCNO 1
 F2 - Acquisition Parameters
 Date_ 20170311
 Time 6.24 h
 INSTRUM spect
 PULPROG zgpg30
 FIDRES 0.165000
 ID 1024
 SOLVENT cdcl3
 NS 18
 SH 1
 SBH 6009.615 Hz
 FIDRES 11.737530 Hz
 AQ 0.0851988 sec
 RG 203
 DE 83.650 usec
 TE 300.0 K
 CNST2 145.0000000
 D0 0.0000300 sec
 D1 0.0000300 sec
 D4 0.0017244 sec
 D11 0.0300000 sec
 DL3 0.00000400 sec
 DL6 0.0002000 sec
 DL7 0.0004500 sec
 DL8 0.0002410 sec
 TDAV 1
 SF01 500.1327507 MHz
 NUC1 1H
 P1 15.00 usec
 PL1 3.00 dB
 PLW1 15.4879892 W
 SF02 125.7672181 MHz
 NUC2 13C
 CPDPRG2 zgpg30
 P4 15.00 usec
 P4 20.40 usec
 PCPD2 70.00 usec
 PLW2 88.3199817 W
 SF03 125.7672181 MHz
 PL1 3.00 dB
 GENAM[1] SMSQ10.100 %
 GENAM[2] SMSQ10.100 %
 GENAM[3] SMSQ10.100 %
 P4 20.10 %
 P4 1000.00 usec

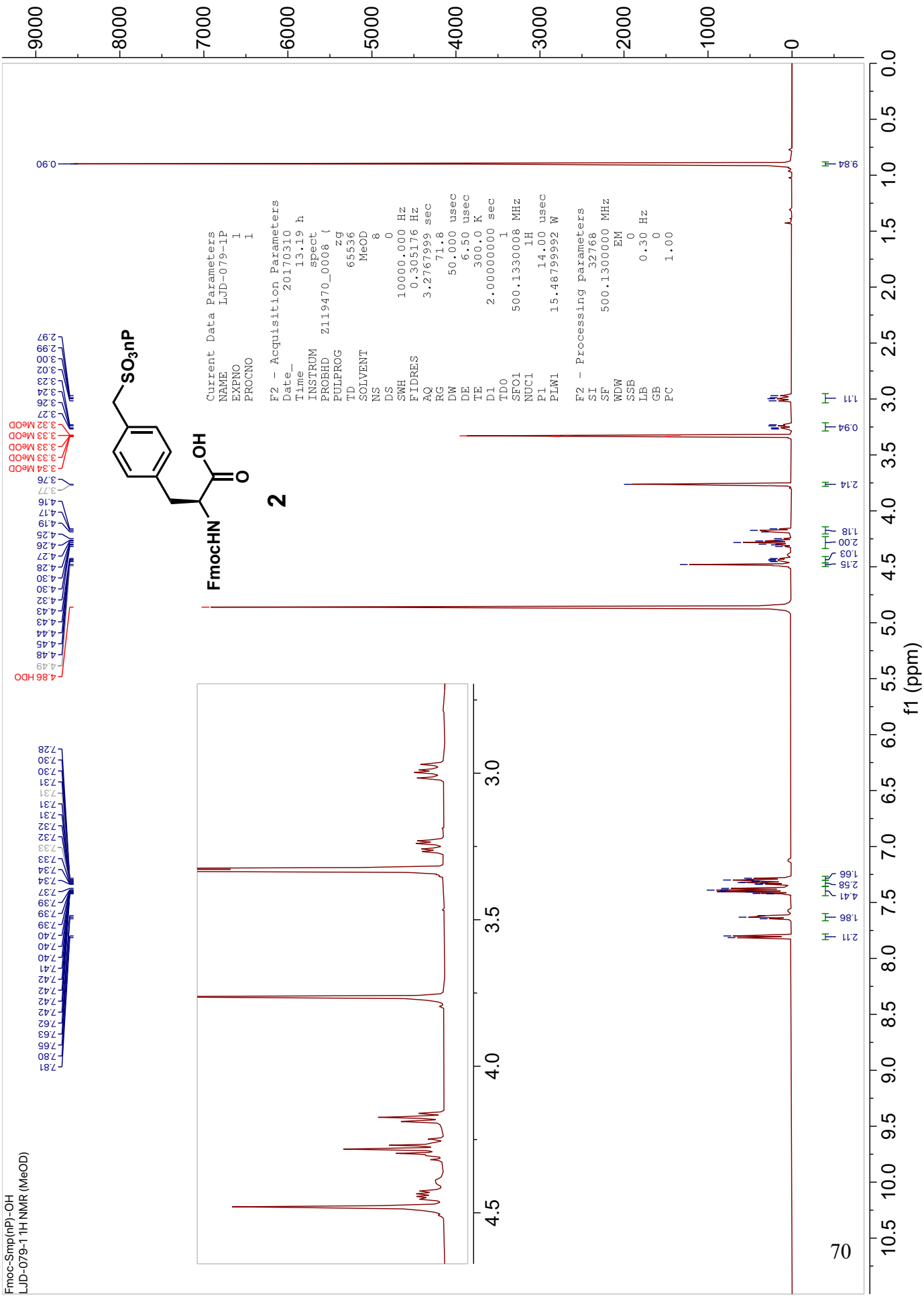
F1 - Acquisition Parameters
 ID 256
 SF01 125.7672 MHz
 SF 162.56077 MHz
 SN 165.650 PPM
 FMODE 1PFI

F2 - Processing Parameters
 SF 500.130000 MHz
 WDM 2
 LB 0 Hz
 GB 0
 PC 1.40

F1 - Processing Parameters
 SI 1024
 SF 125.7577850 MHz
 WDM 2
 LB 0 Hz
 GB 0







Fmoc-Smp(nP)-OH

LJD-079-1 13C (1H dec) NMR (MeOD)

Current Data Parameters
 NAME LJD-079-1P
 EXPNO 6
 PROCNO 1

F2 - Acquisition Parameters
 Date_ 20170312
 Time 11.53 h
 INSTRUM spect
 PROBHD zll19470_0008 (

PULPROG zgpg30
 TD 65536
 SOLVENT MeOD
 NS 12288
 DS 4

SWH 28846.154 Hz
 FIDRES 0.880315 Hz
 AQ 1.1359574 sec
 RG 203

DW 17.333 usec
 DE 6.50 usec
 TE 300.0 K
 D1 2.00000000 sec
 D11 0.03000000 sec

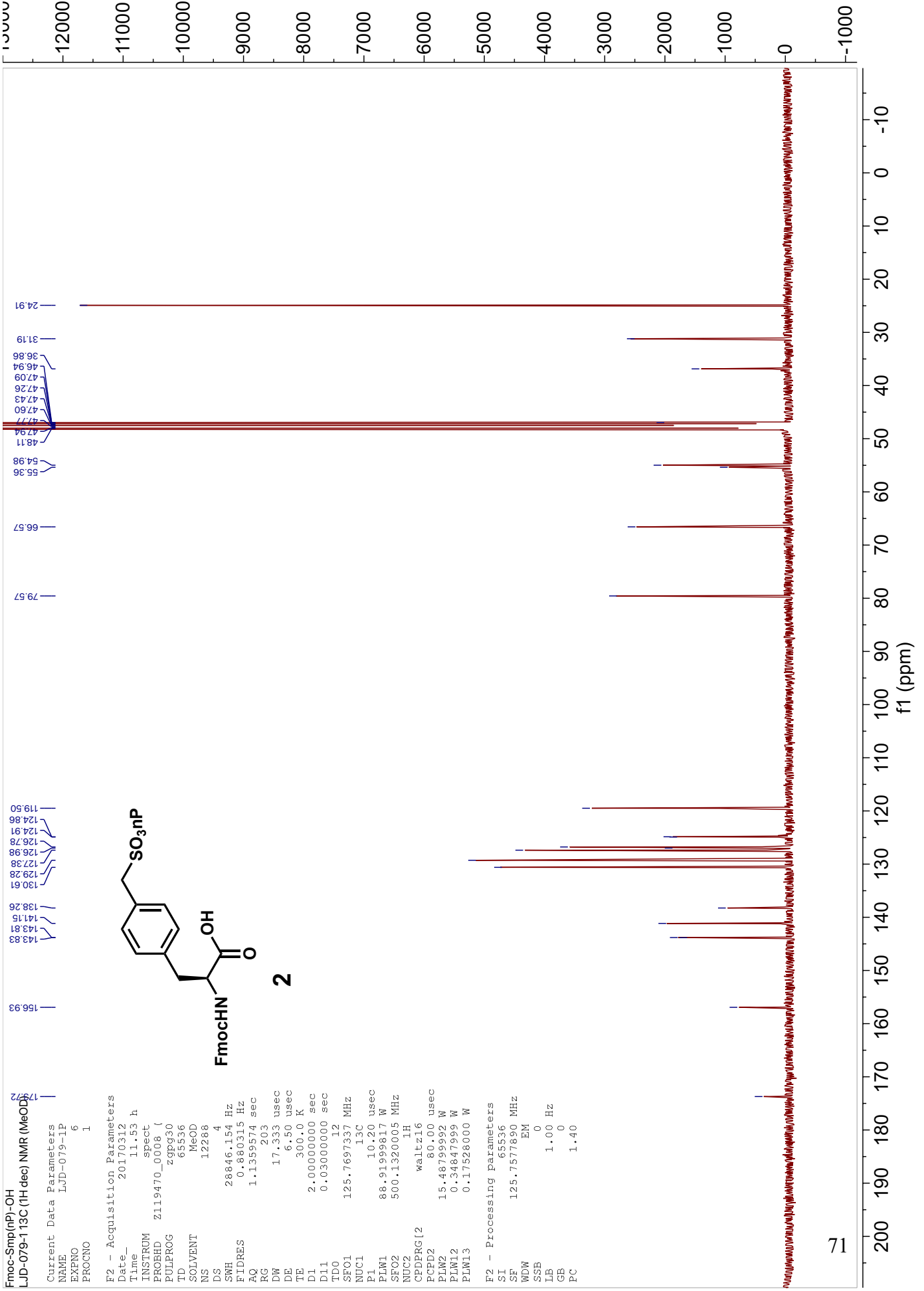
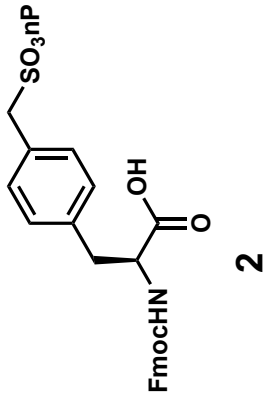
TDO 12
 SFO1 125.7697337 MHz
 NUC1 13C

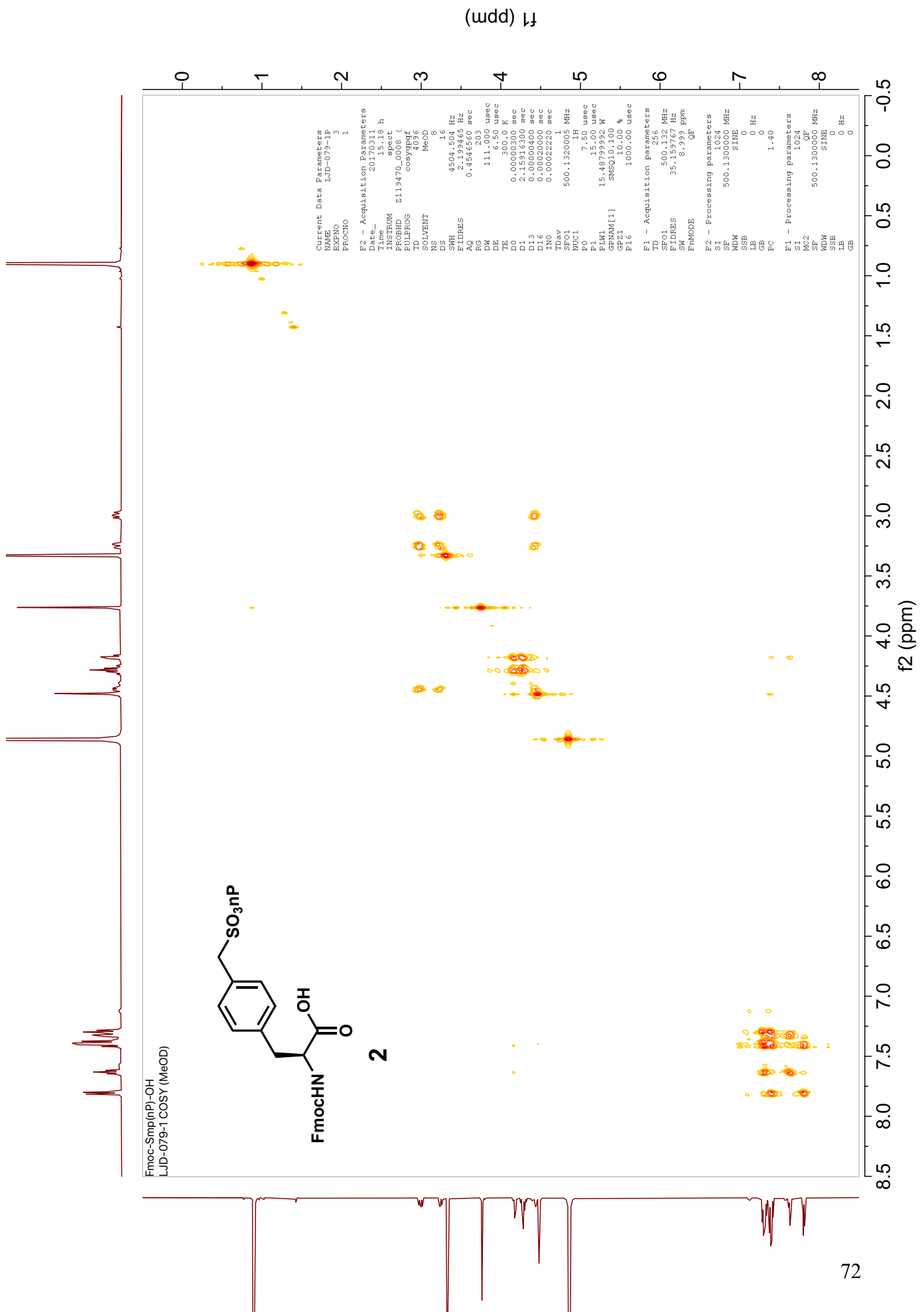
P1 10.20 usec
 PLW1 88.91999817 W
 SFO2 500.1320005 MHz
 NUC2 1H

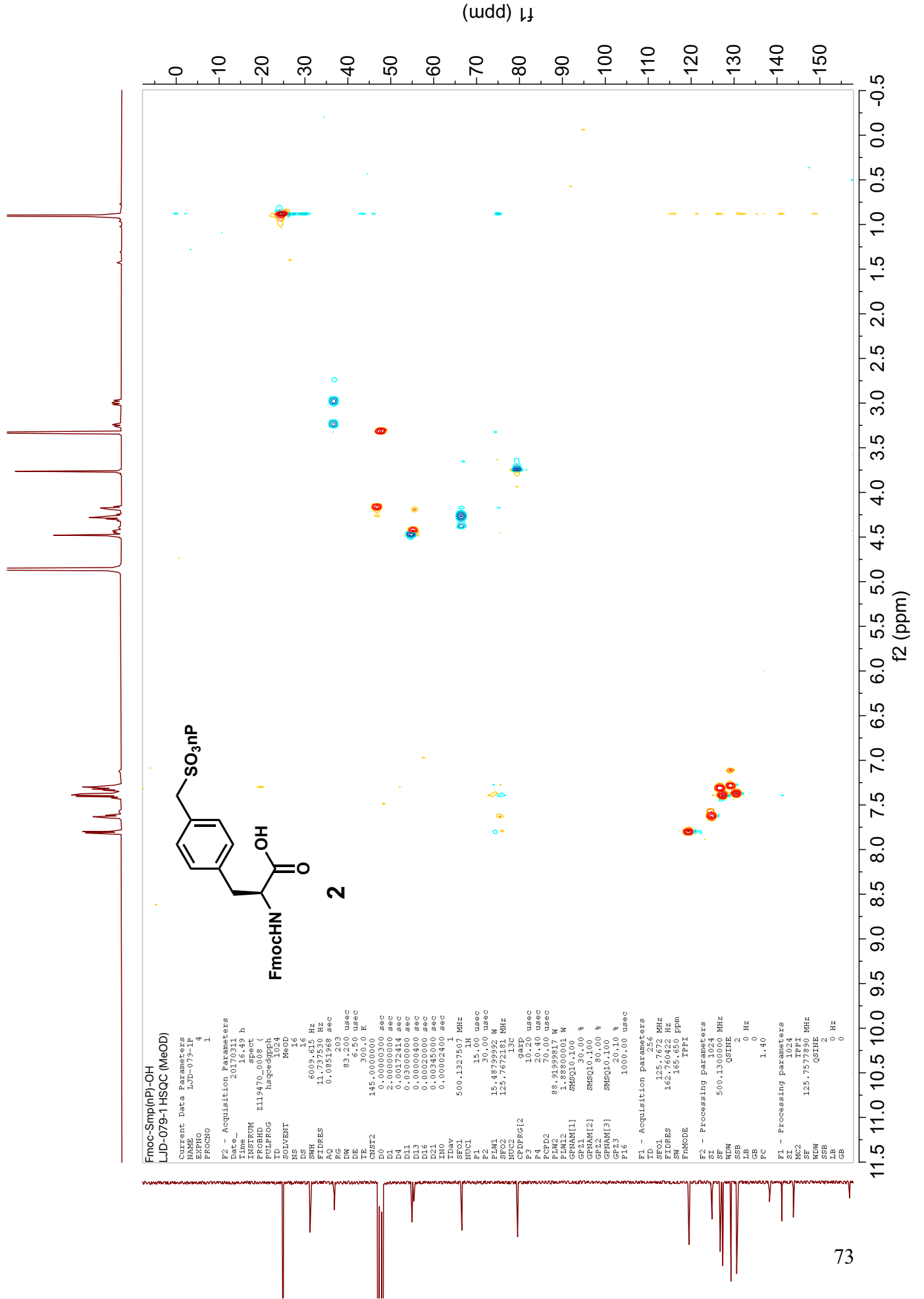
CPDPRG12 waltz16
 PCPD2 80.00 usec
 PLW2 15.48799992 W

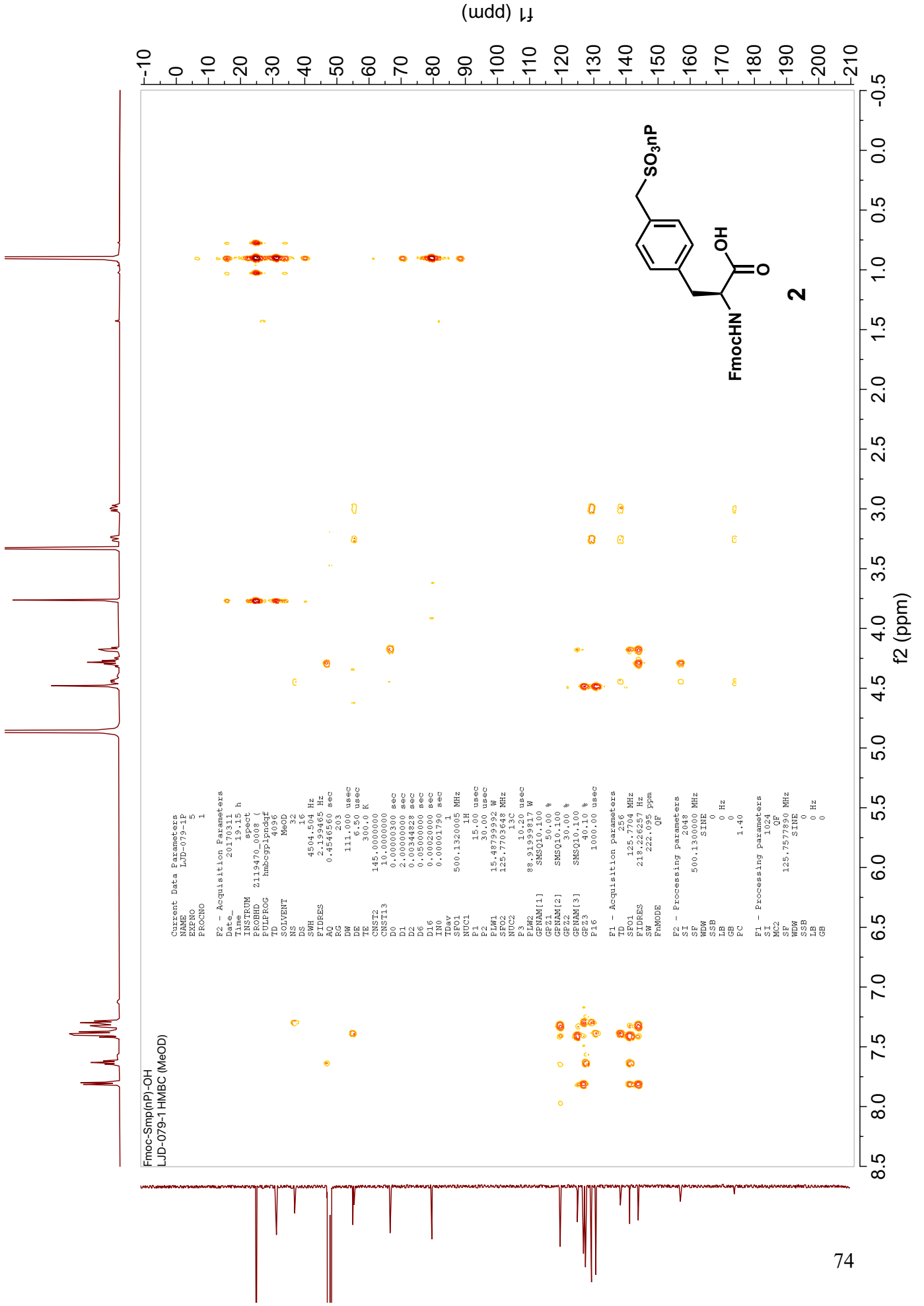
PLW12 0.34847999 W
 PLW13 0.17528000 W

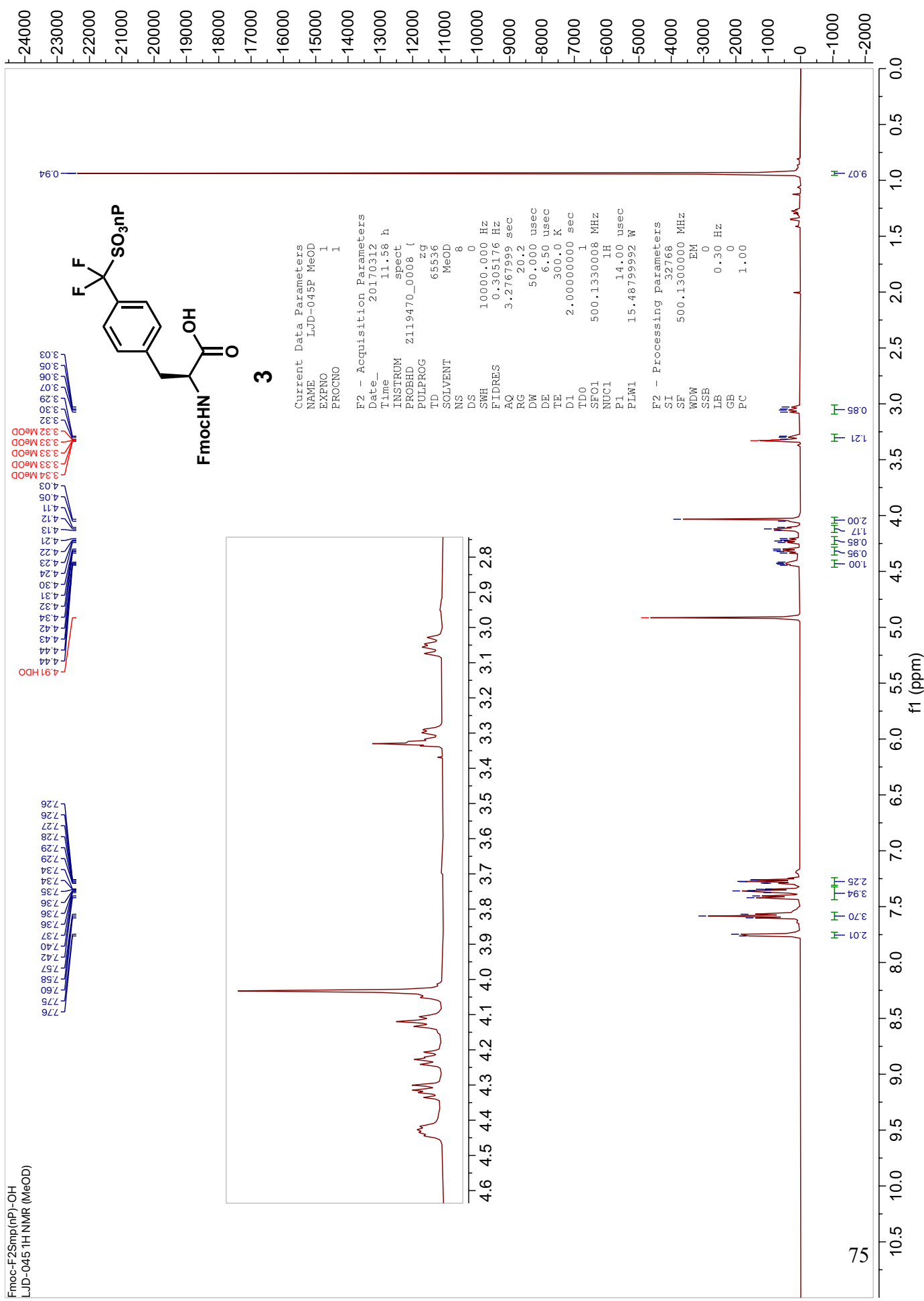
F2 - Processing parameters
 SI 65536
 SF 125.7577690 MHz
 WDW EM
 SSB 0
 LB 1.00 Hz
 GB 0
 PC 1.40











Current Data Parameters
NAME LJD-045P MeOD
EXPNO 1
PROCNO 1

F2 - Acquisition Parameters
Date_ 20170312
Time 11.58 h
INSTRUM spect
PROBHD Z119470_0008 ()
PULPROG zg
TD 65536
SOLVENT MeOD
NS 8
DS 0
SWH 10000.000 Hz
FIDRES 0.305176 Hz
AQ 3.276799 sec
RG 20.2
DW 50.000 usec
DE 6.50 usec
TE 300.0 K
D1 2.00000000 sec
TD0 1
SFO1 500.1330008 MHz
NUC1 1H
P1 14.00 usec
PLW1 15.4879992 W

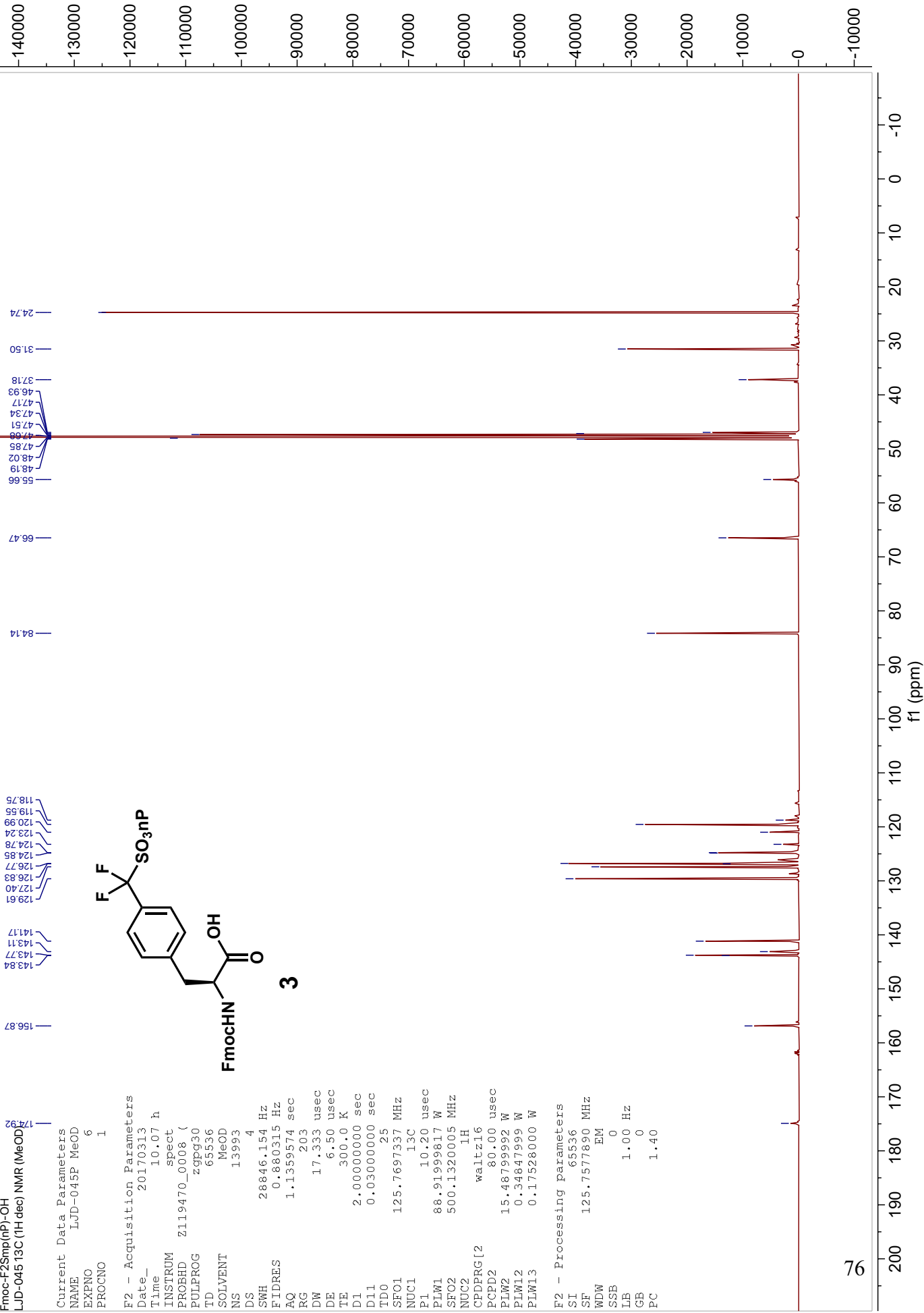
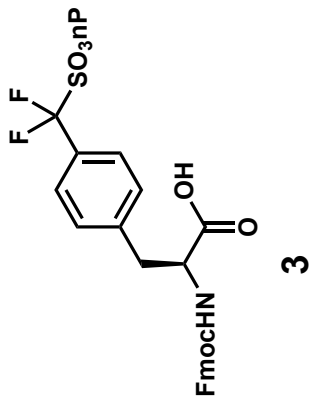
F2 - Processing Parameters
SI 32768
SF 500.1300000 MHz
EM
WDW EM
SSB 0
LB 0.30 Hz
GB 0
PC 1.00

Fmoc-F25mp(nP)-OH
 LJD-045.13C (1H dec) NMR (MeOD)

Current Data Parameters
 NAME LJD-045P MeOD
 EXPNO 6
 PROCNO 1

F2 - Acquisition Parameters
 Date_ 20170313
 Time 10.07 h
 INSTRUM spect
 PROBH0 Z119470_0008 (zgp930
 PULPROG 65536
 TD 13993
 NS 4
 DS 28846.154 Hz
 SWH 0.880315 Hz
 FIDRES 1.1339574 sec
 AQ 203
 RG 17.333 usec
 DW 6.50 usec
 TE 300.0 K
 D1 2.0000000 sec
 D11 0.0300000 sec
 TD0 25
 SFO1 125.7697337 MHz
 NUC1 13C
 P1 10.20 usec
 PLW1 88.91999817 W
 SFO2 500.1320005 MHz
 NUC2 1H
 CPDPRG2 waltz16
 PCPD2 80.00 usec
 PLW2 15.48799992 W
 PLWI2 0.34847999 W
 PLWI3 0.17828000 W

F2 - Processing parameters
 SI 65536
 SF 125.7577890 MHz
 WDW EM
 SSB 0
 LB 1.00 Hz
 GB 0
 PC 1.40



Fmoc-FZSmp(nP)-OH
LJD-045 19F (1H dec) NMR (MeOD)

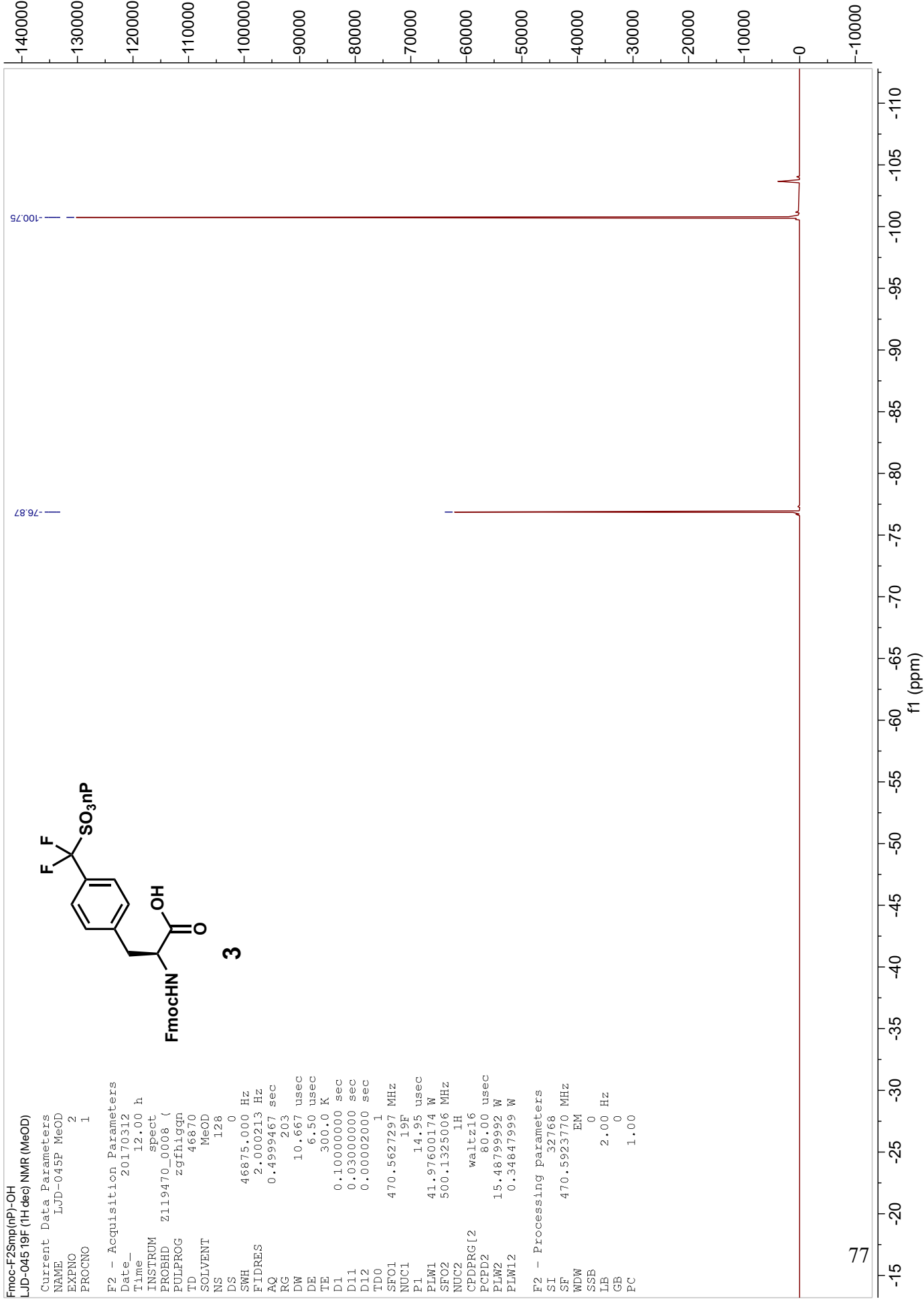
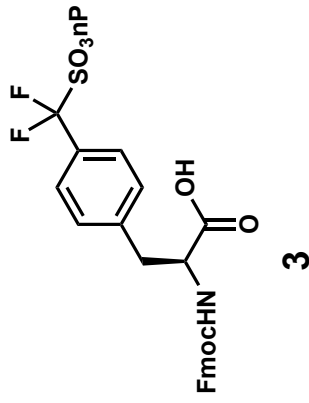
Current Data Parameters
NAME LJD-045P MeOD
EXPNO 2
PROCNO 1

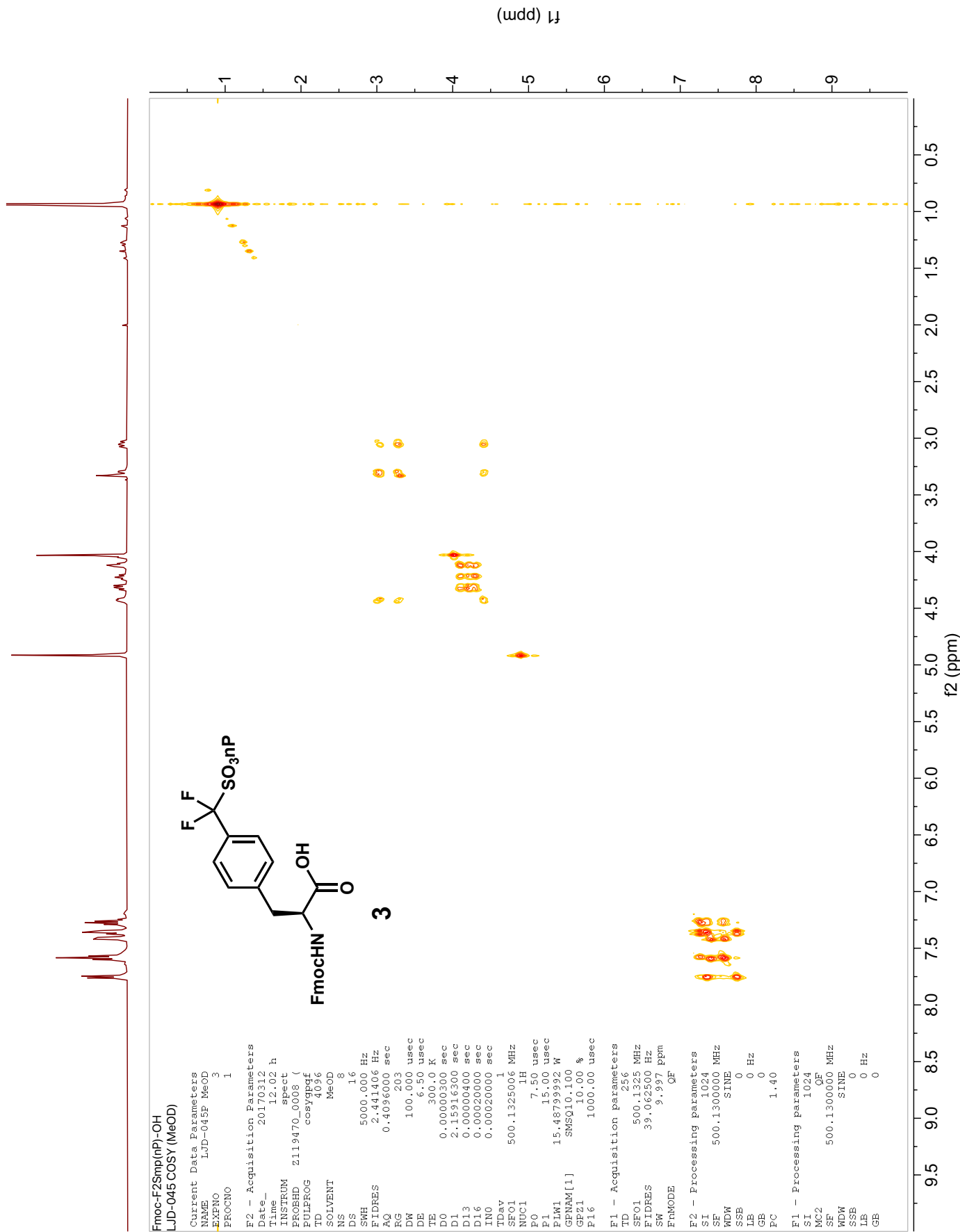
F2 - Acquisition Parameters

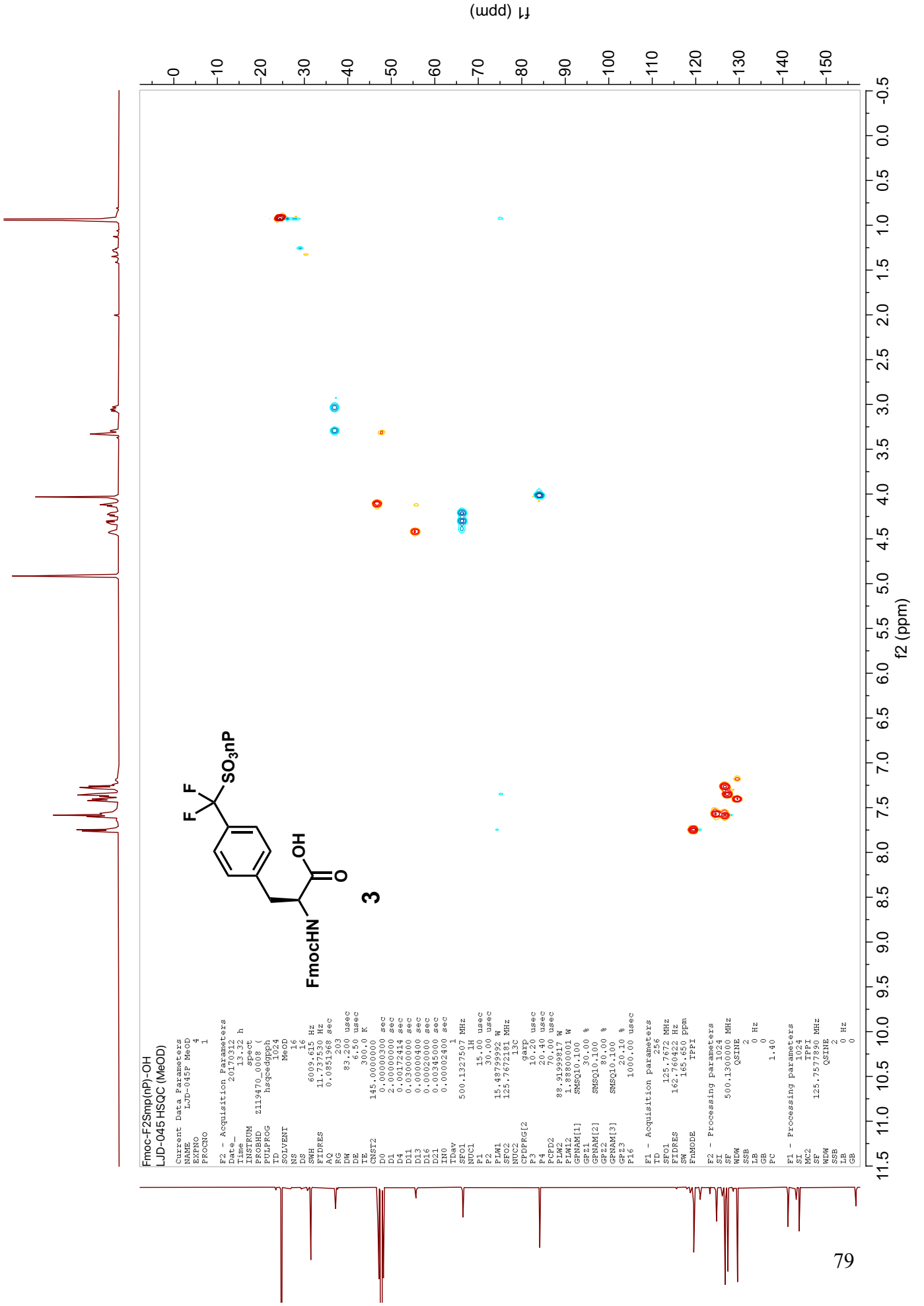
Date_ 20170312
Time 12.00 h
INSTRUM spect
PROBHD Zll19470_0008 (zgfhlgn)
PULPROG zgpg30
TD 46870
SOLVENT MeOD
NS 128
DS 0
SWH 46875.000 Hz
FIDRES 2.000213 Hz
AQ 0.4999467 sec
RG 203
DW 10.667 usec
DE 6.50 usec
TE 300.0 K
D1 0.10000000 sec
D11 0.03000000 sec
D12 0.00002000 sec
TD0 1
SFO1 470.5627297 MHz
NUC1 19F
P1 14.95 usec
PLW1 41.97600174 W
SFO2 500.1325006 MHz
NUC2 1H
CPDPRG[2] waltz16
PCPD2 80.00 usec
PLW2 15.48799992 W
PLWI2 0.34847999 W

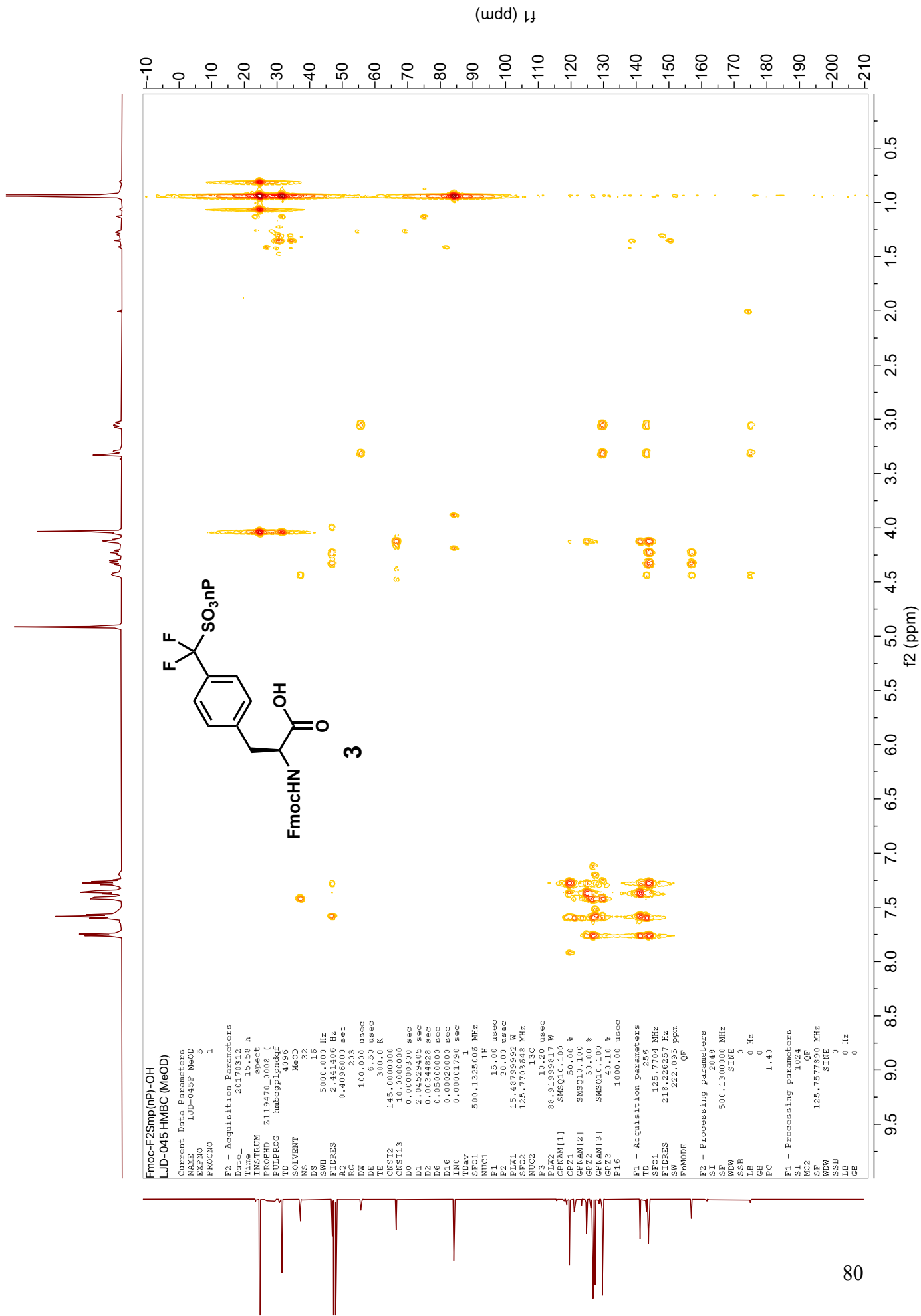
F2 - Processing parameters

SI 32768
SF 470.5923770 MHz
WDW EM
SSB 0
LB 2.00 Hz
GB 0
PC 1.00









11 References

1. L. Jobron and G. Hummel, *Org. Lett.*, 2000, **2**, 2265-2267.
2. S. Liu, C. Dockendorff and S. D. Taylor, *Org. Lett.*, 2001, **3**, 1571-1574.
3. J. Juanhuix, F. Gil-Ortiz, G. Cuní, C. Colldelram, J. Nicolás, J. Lidón, E. Boter, C. Ruget, S. Ferrer and J. Benach, *J. Synchrotron Radiat.*, 2014, **21**, 679-689.
4. W. Kabsch, *Acta Crystallogr. D Biol. Crystallogr.*, 2010, **66**, 133-144.
5. M. D. Winn, C. C. Ballard, K. D. Cowtan, E. J. Dodson, P. Emsley, P. R. Evans, R. M. Keegan, E. B. Krissinel, A. G. Leslie, A. McCoy, S. J. McNicholas, G. N. Murshudov, N. S. Pannu, E. A. Potterton, H. R. Powell, R. J. Read, A. Vagin and K. S. Wilson, *Acta Crystallogr. D Biol. Crystallogr.*, 2011, **67**, 235-242.
6. P. A. Meyer, S. Socias, J. Key, E. Ransey, E. C. Tjon, A. Buschiazzo, M. Lei, C. Botka, J. Withrow, D. Neau, K. Rajashankar, K. S. Anderson, R. H. Baxter, S. C. Blacklow, T. J. Boggon, A. M. J. J. Bonvin, D. Borek, T. J. Brett, A. Caflisch, C.-I. Chang, W. J. Chazin, K. D. Corbett, M. S. Cosgrove, S. Crosson, S. Dhe-Paganon, E. Di Cera, C. L. Drennan, M. J. Eck, B. F. Eichman, Q. R. Fan, A. R. Ferré-D'Amaré, J. Christopher Fromme, K. C. Garcia, R. Gaudet, P. Gong, S. C. Harrison, E. E. Heldwein, Z. Jia, R. J. Keenan, A. C. Kruse, M. Kvansakul, J. S. McLellan, Y. Modis, Y. Nam, Z. Otwinowski, E. F. Pai, P. J. B. Pereira, C. Petosa, C. S. Raman, T. A. Rapoport, A. Roll-Mecak, M. K. Rosen, G. Rudenko, J. Schlessinger, T. U. Schwartz, Y. Shamoo, H. Sondermann, Y. J. Tao, N. H. Tolia, O. V. Tsodikov, K. D. Westover, H. Wu, I. Foster, J. S. Fraser, F. R. N. C. Maia, T. Gonen, T. Kirchhausen, K. Diederichs, M. Crosas and P. Sliz, *Nat. Commun.*, 2016, **7**, 10882.
7. A. J. McCoy, R. W. Grosse-Kunstleve, P. D. Adams, M. D. Winn, L. C. Storoni and R. J. Read, *J. App. Crystallogr.*, 2007, **40**, 658-674.
8. A. C. Figueiredo, D. de Sanctis and P. J. B. Pereira, *PLoS One*, 2013, **8**, e71866.
9. P. Emsley, B. Lohkamp, W. G. Scott and K. Cowtan, *Acta Crystallogr. D Biol. Crystallogr.*, 2010, **66**, 486-501.
10. P. D. Adams, P. V. Afonine, G. Bunkoczi, V. B. Chen, I. W. Davis, N. Echols, J. J. Headd, L. W. Hung, G. J. Kapral, R. W. Grosse-Kunstleve, A. J. McCoy, N. W. Moriarty, R. Oeffner, R. J. Read, D. C. Richardson, J. S. Richardson, T. C. Terwilliger and P. H. Zwart, *Acta Crystallogr. D Biol. Crystallogr.*, 2010, **66**, 213-221.