

Supplementary Material

Anticancer Potential of Some Imidazole and Fused Imidazole Derivatives: Exploring mechanism via Epidermal Growth Factor Receptor (EGFR) Inhibition

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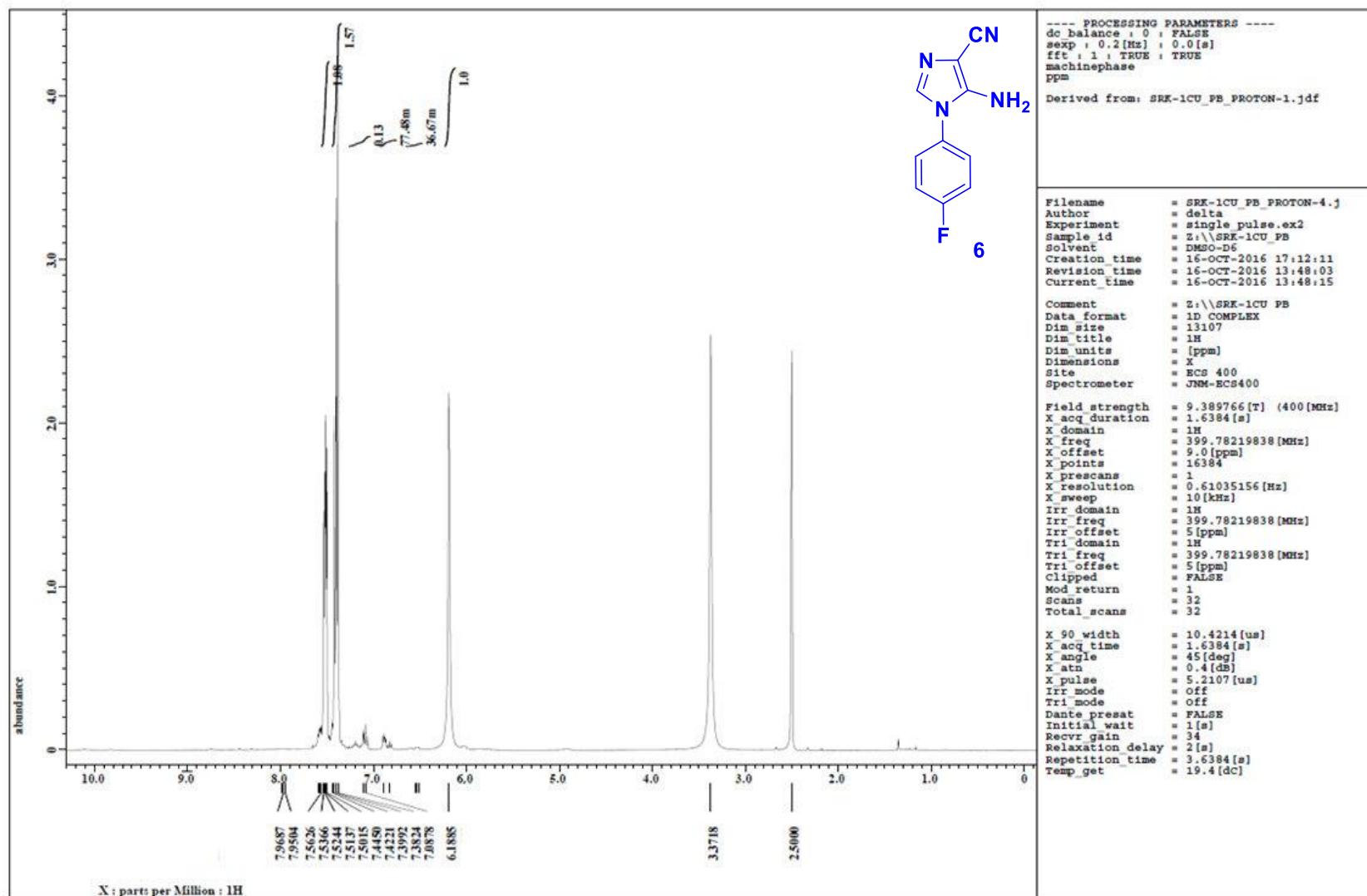
^cDesh Bhagat Dental College and Hospital, Mandi Gobindgarh, India

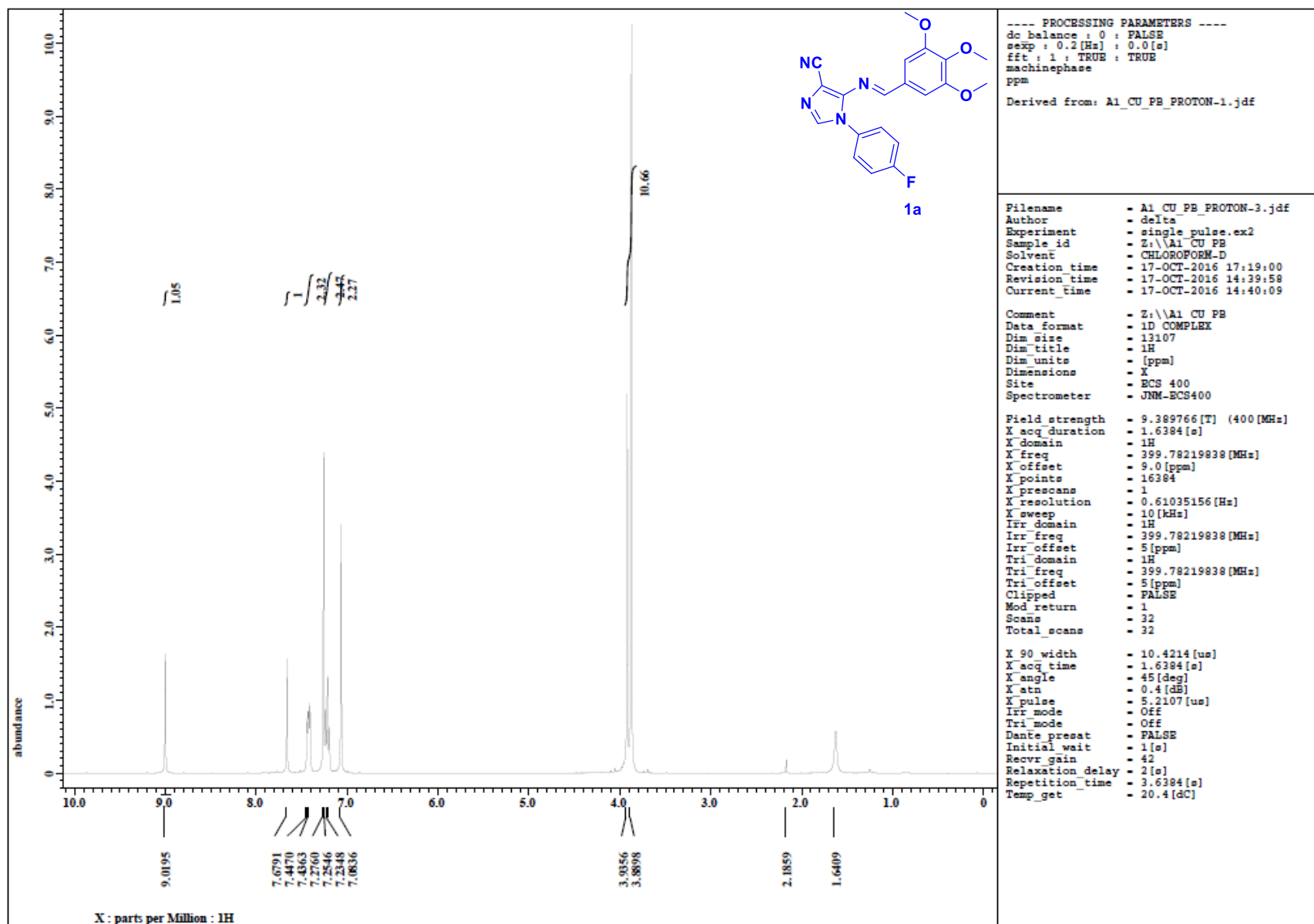
**E-mail: raj.khunger@gmail.com; rajcps@cup.ac.in

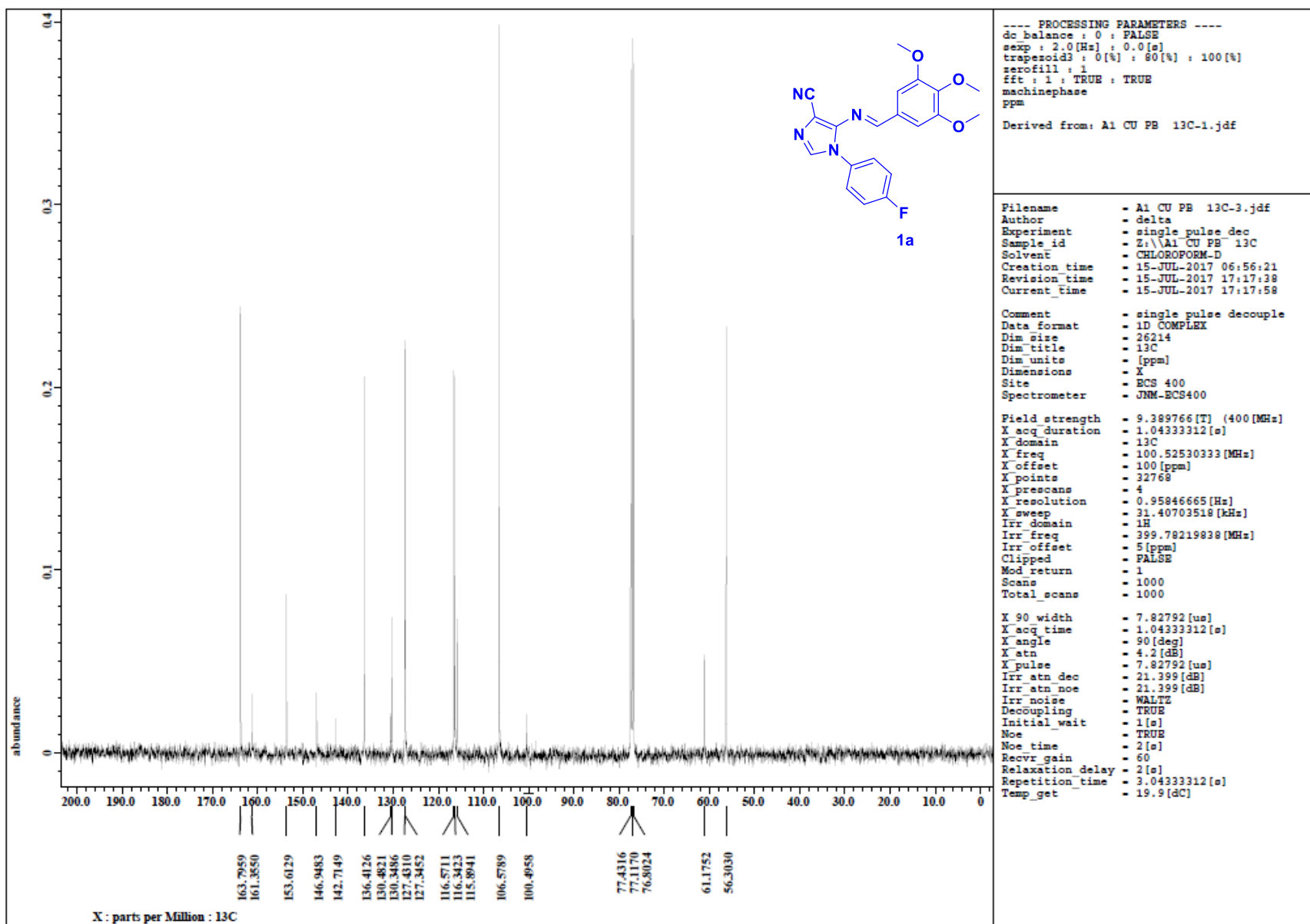
Co-corresponding authors*E-mail: anjanadurani@yahoo.co.in; sandeepsingh82@gmail.com

Spectra for representative compounds

Data ¹H, ¹³C NMR, and HRMS







Elemental Composition Report

Page 1

Single Mass Analysis

Tolerance = 3.0 PPM / DBE: min = -1.5, max = 50.0

Element prediction: Off

Number of isotope peaks used for i-FIT = 5

Monoisotopic Mass, Even Electron Ions

40 formula(e) evaluated with 1 results within limits (up to 50 best isotopic matches for each mass)

Elements Used:

C: 9-25 H: 11-30 N: 0-4 O: 0-3 F: 0-1

Sample Name : A-1

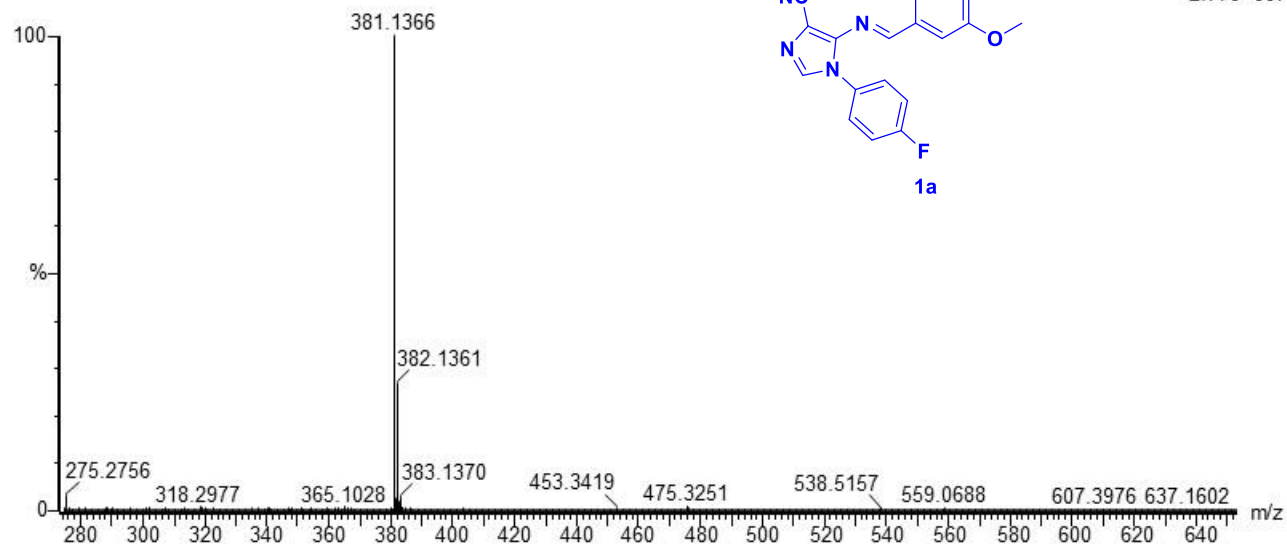
Test Name : HRMS-1

160120-A-1 17 (0.174)

IITRPR

XEVO G2-XS QTOF

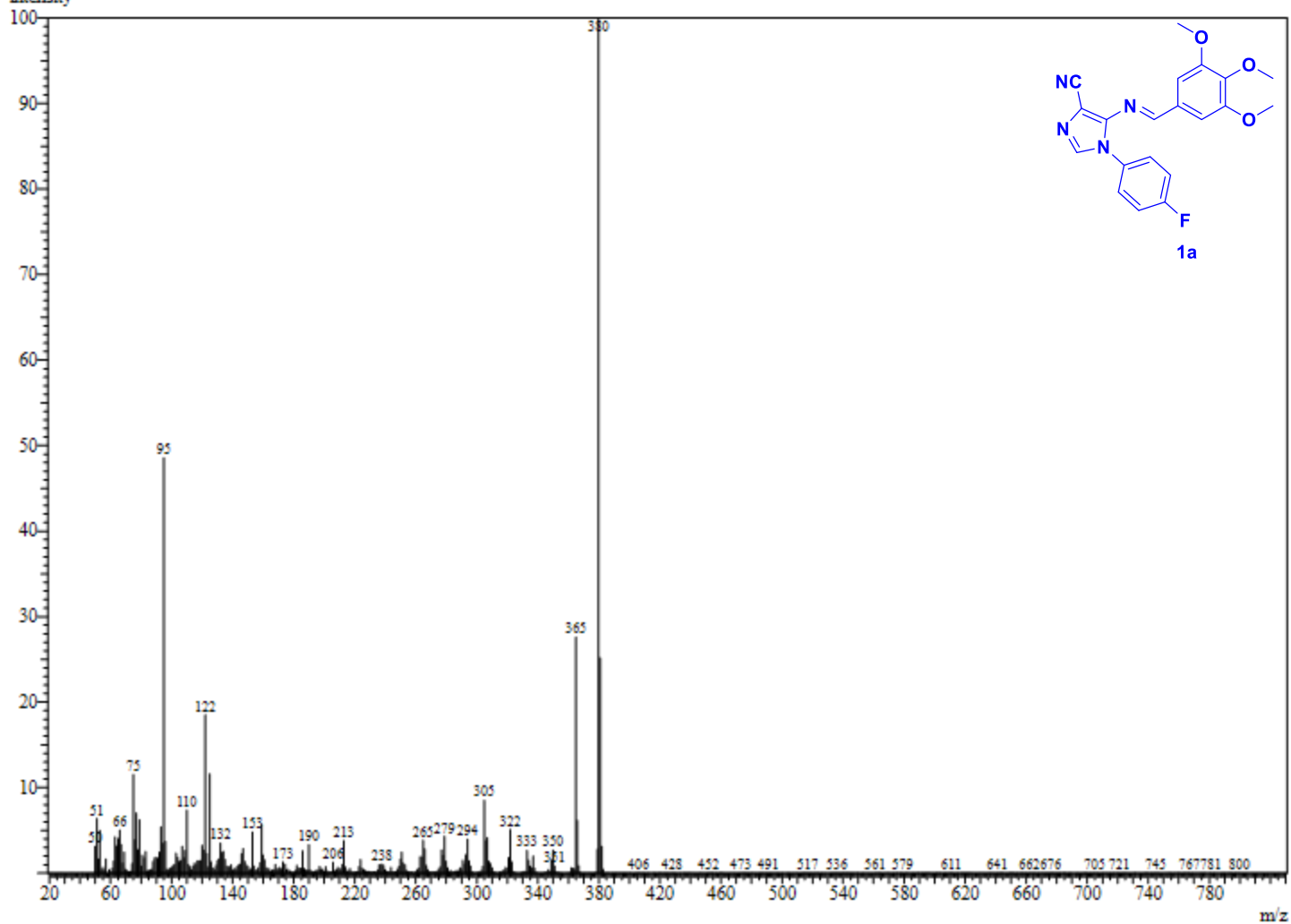
1: TOF MS ES+
2.77e+007

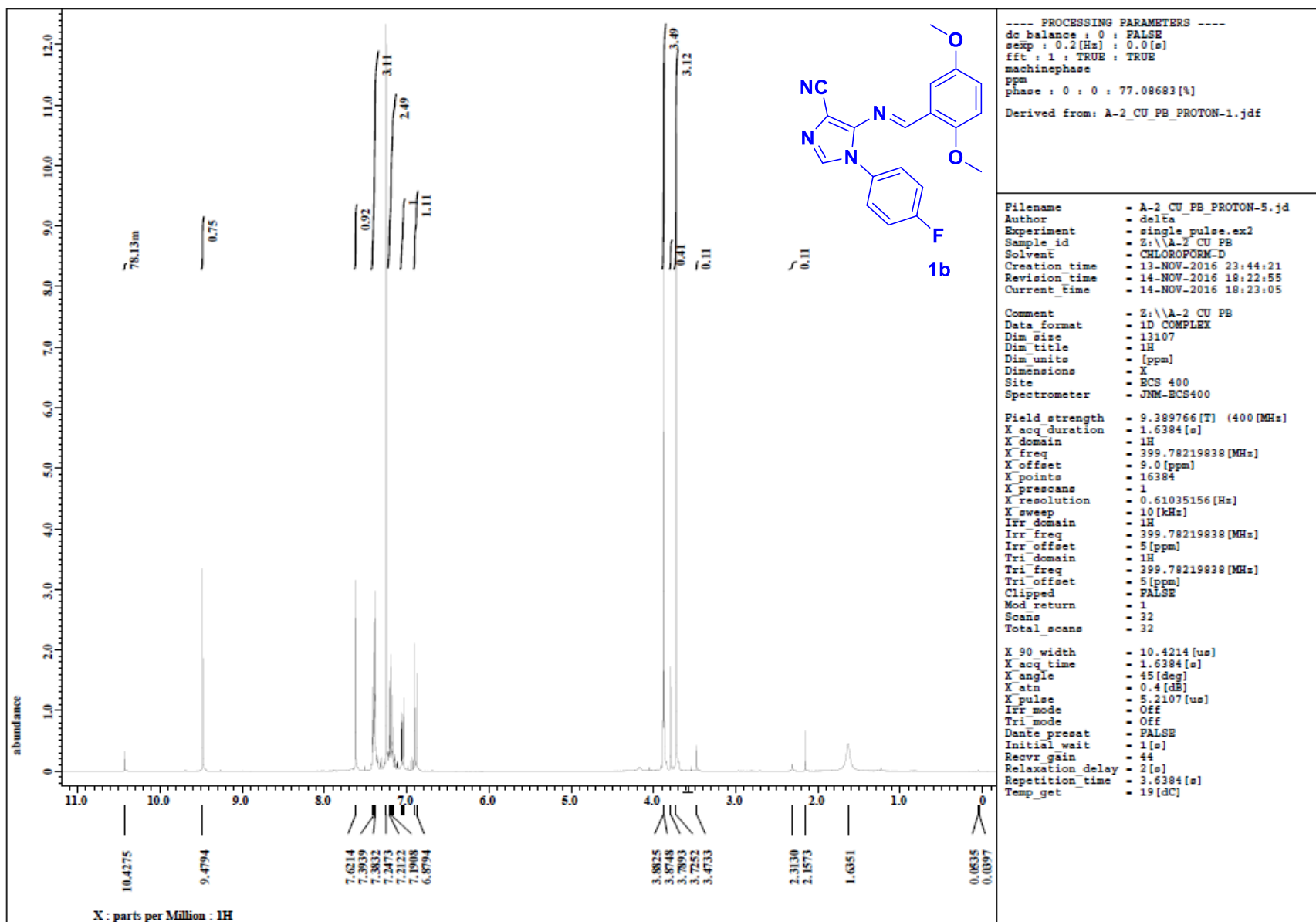


Minimum: -1.5
Maximum: 5.0 3.0 50.0

Mass	Calc. Mass	mDa	PPM	DBE	i-FIT	Norm	Conf(%)	Formula
381.1366	381.1363	0.3	0.8	13.5	1449.5	n/a	n/a	C ₂₀ H ₁₈ N ₄ O ₃ F

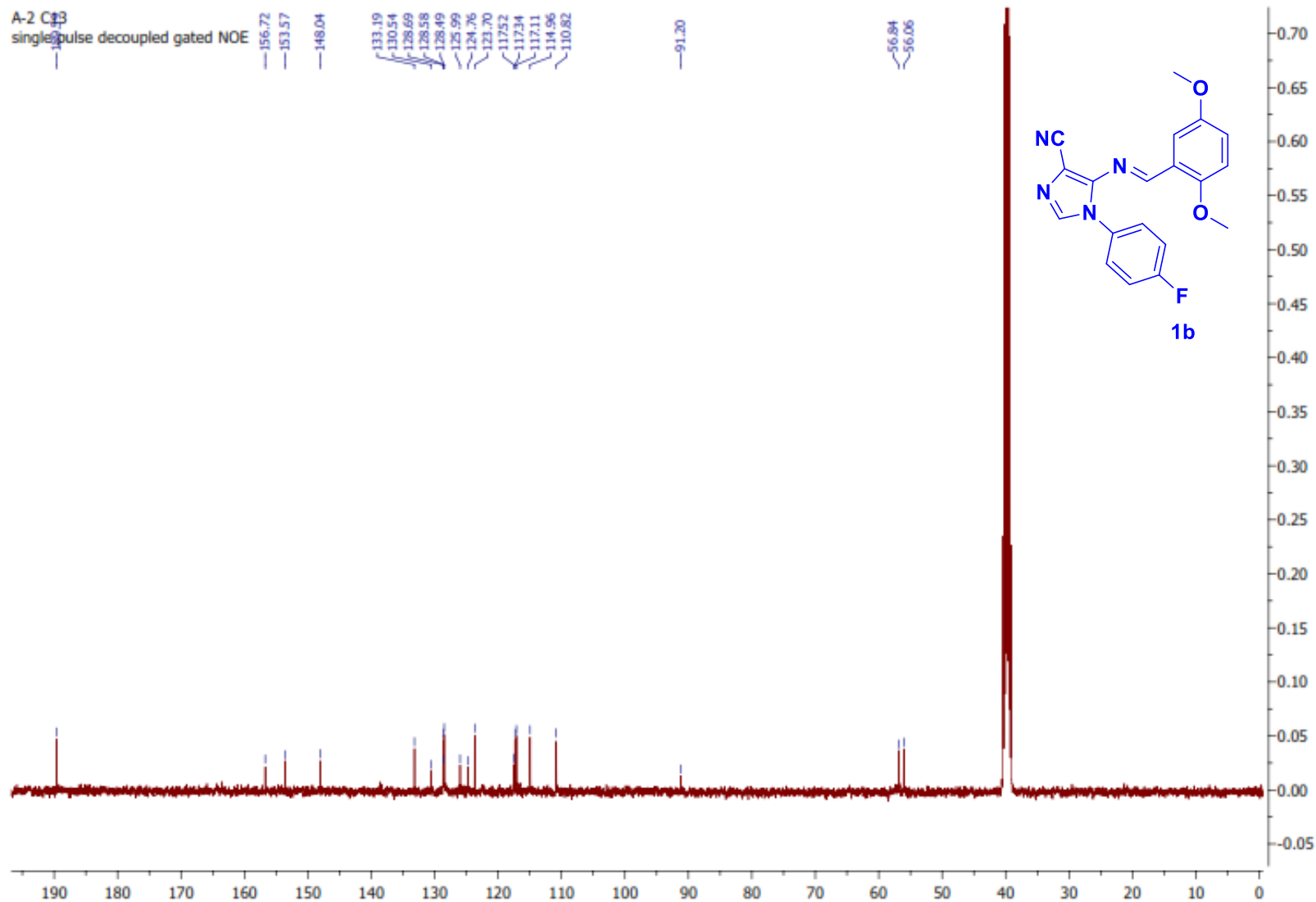
Line#:1 R.Time:4.860(Scan#:673)
MassPeaks:541
RawMode:Averaged 4.855-4.865(672-674) BasePeak:380(492565)
BG Mode:Calc. from Peak Group 1 - Event 1
intensity





A-2 C13

single pulse decoupled gated NOE



Elemental Composition Report

Page 1

Single Mass Analysis

Tolerance = 5.0 PPM / DBE: min = -1.5, max = 50.0

Element prediction: Off

Number of isotope peaks used for i-FIT = 5

Monoisotopic Mass, Even Electron Ions

39 formula(e) evaluated with 1 results within limits (up to 50 best isotopic matches for each mass)

Elements Used:

C: 9-21 H: 8-25 N: 0-5 O: 0-3 F: 0-1

Sample Name : A-2

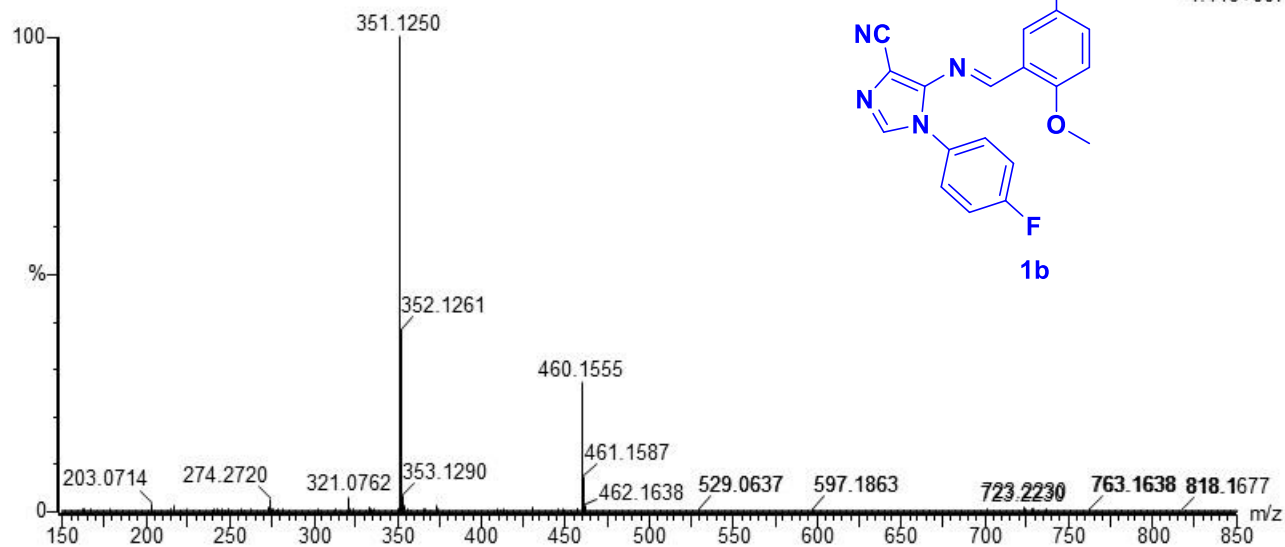
IITRPR

XEVO G2-XS QTOF

Test Name : HRMS-1

160120-A-2- 16 (0.165)

1: TOF MS ES+
4.44e+007



Minimum: -1.5
Maximum: 5.0 5.0 50.0

Mass	Calc. Mass	mDa	PPM	DBE	i-FIT	Norm	Conf(%)	Formula
351.1250	351.1257	-0.7	-2.0	13.5	1726.8	n/a	n/a	C ₁₉ H ₁₆ N ₄ O ₂ F

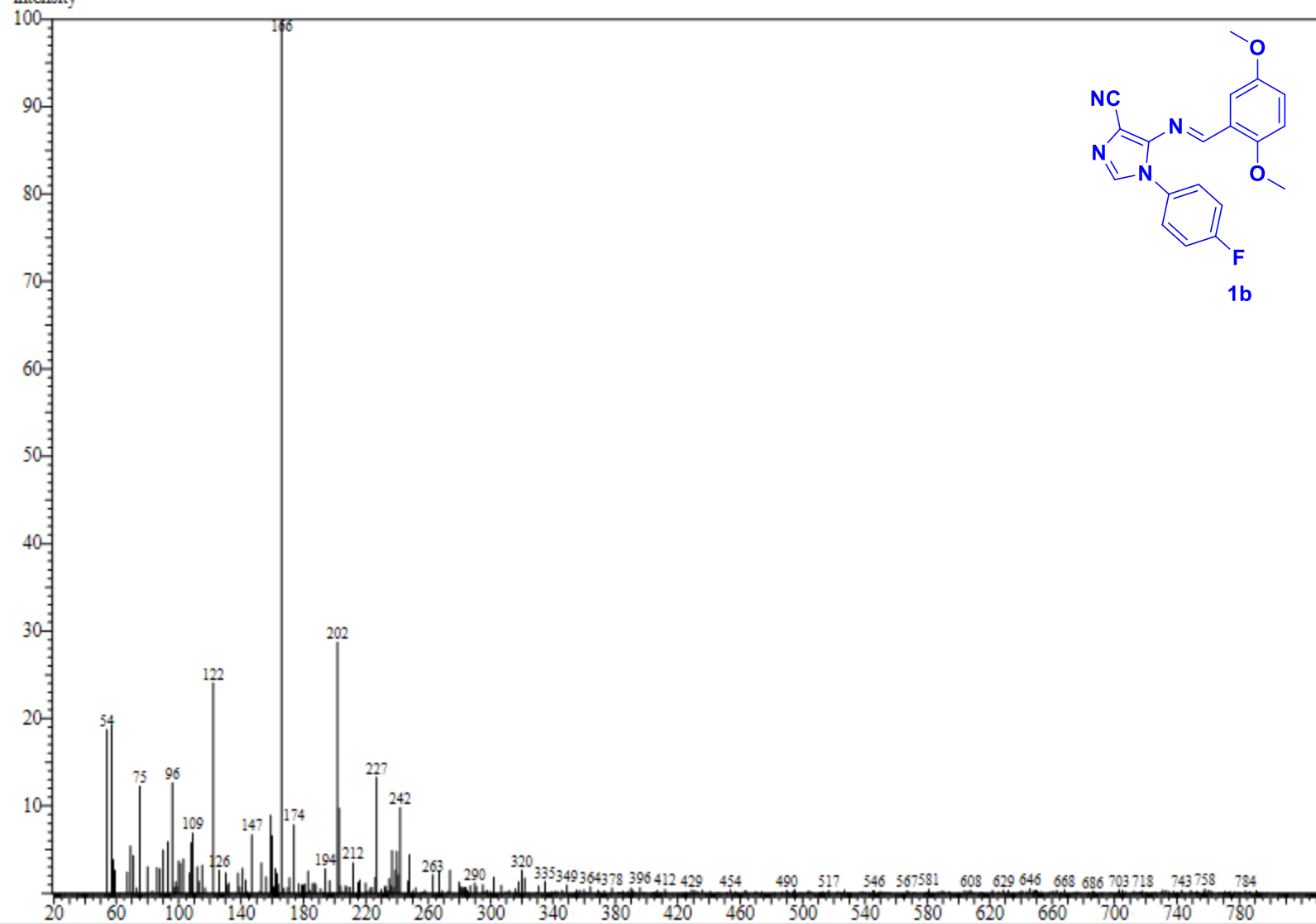
Line#1 R.Time:4.000(Scan#:501)

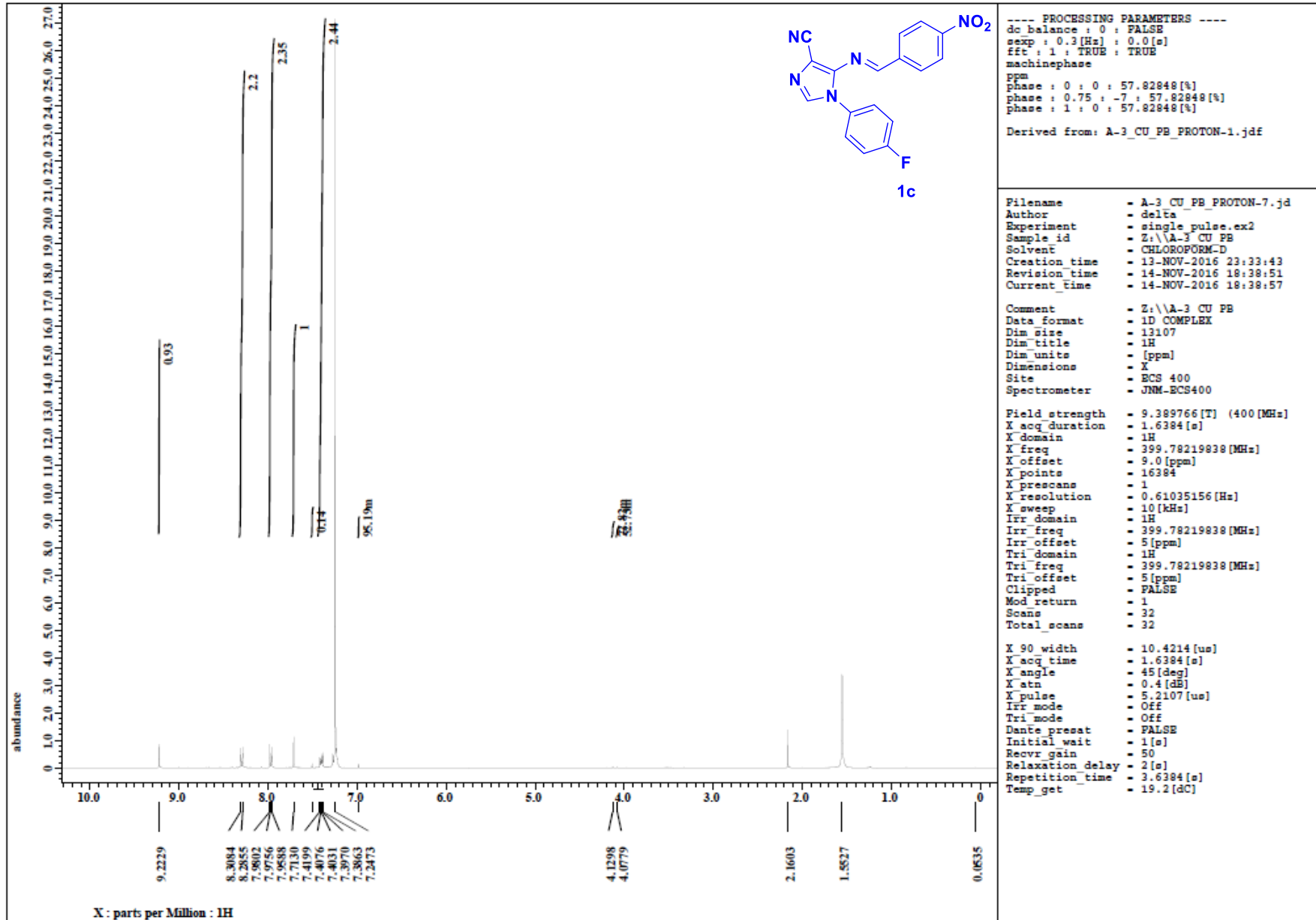
MassPeaks:336

RawMode:Averaged 4.000-4.005(501-502) BasePeak:166(3373)

BG Mode:Calc. from Peak Group 1 - Event 1

intensity





Elemental Composition Report

Page 1

Single Mass Analysis

Tolerance = 5.0 PPM / DBE: min = -1.5, max = 50.0

Element prediction: Off

Number of isotope peaks used for i-FIT = 5

Monoisotopic Mass, Even Electron Ions

52 formula(e) evaluated with 1 results within limits (up to 50 best isotopic matches for each mass)

Elements Used:

C: 9-21 H: 11-30 N: 0-5 O: 0-3 F: 0-1

Sample Name : A-3

IITRPR

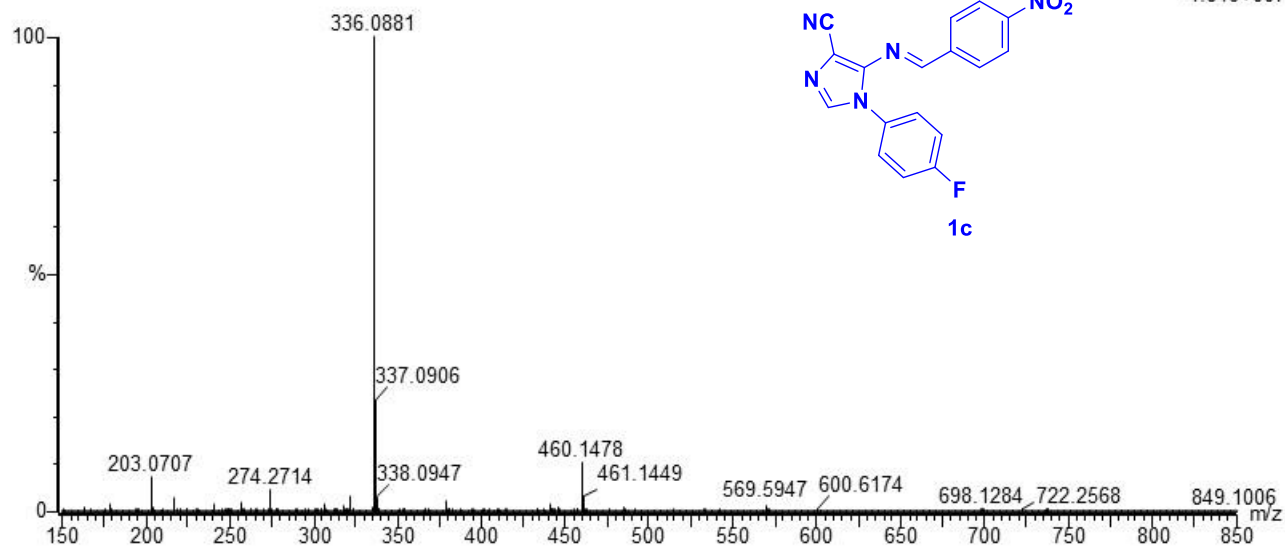
XEVO G2-XS QTOF

Test Name : HRMS-1

160120-A-3 14 (0.148)

1: TOF MS ES+

4.81e+007



Minimum: -1.5
Maximum: 5.0 5.0 50.0

Mass	Calc. Mass	mDa	PPM	DBE	i-FIT	Norm	Conf(%)	Formula
336.0881	336.0897	-1.6	-4.8	14.5	1585.4	n/a	n/a	C17 H11 N5 O2 F

x

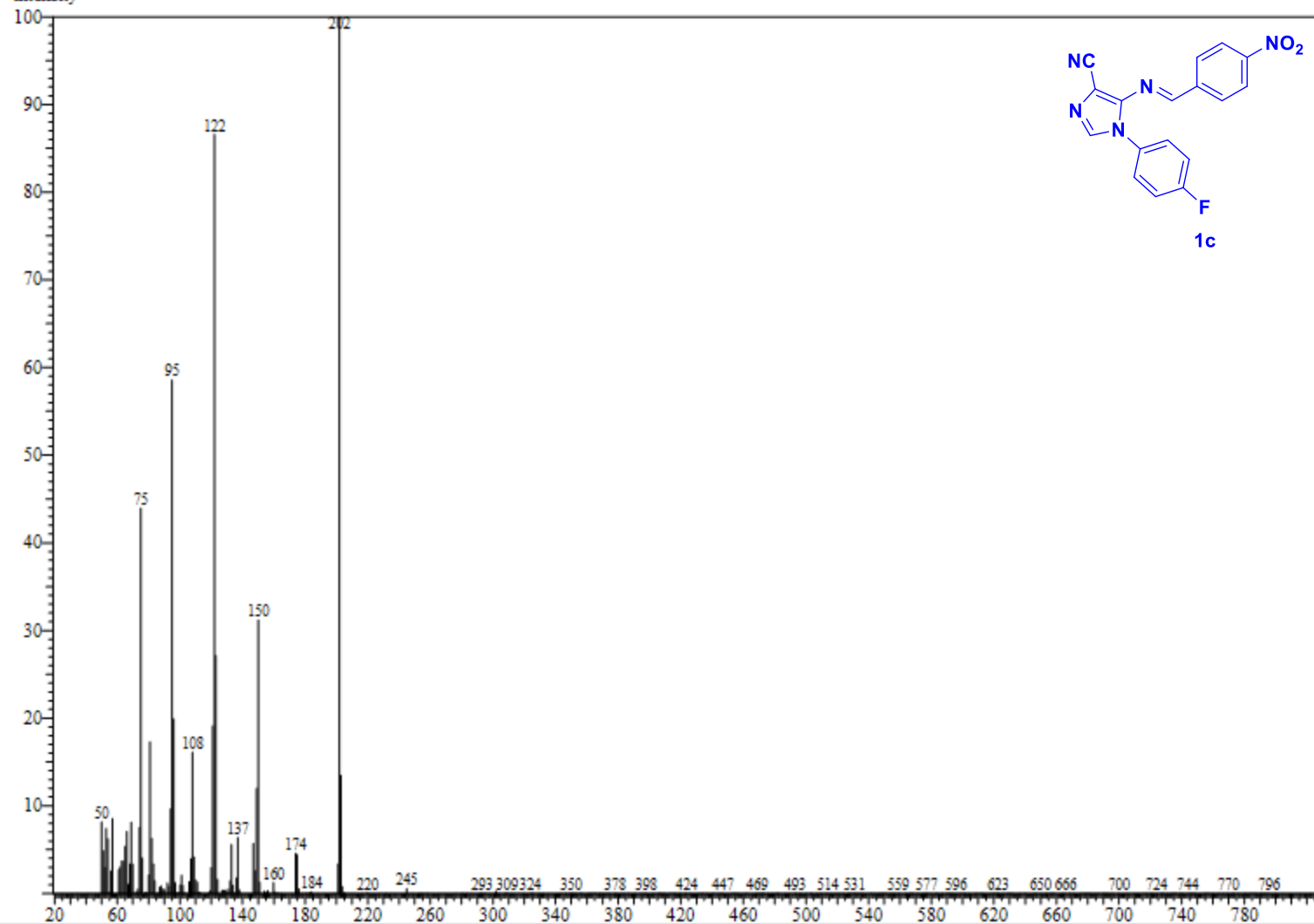
Line#:1 R.Time:3.420(Scan#:385)

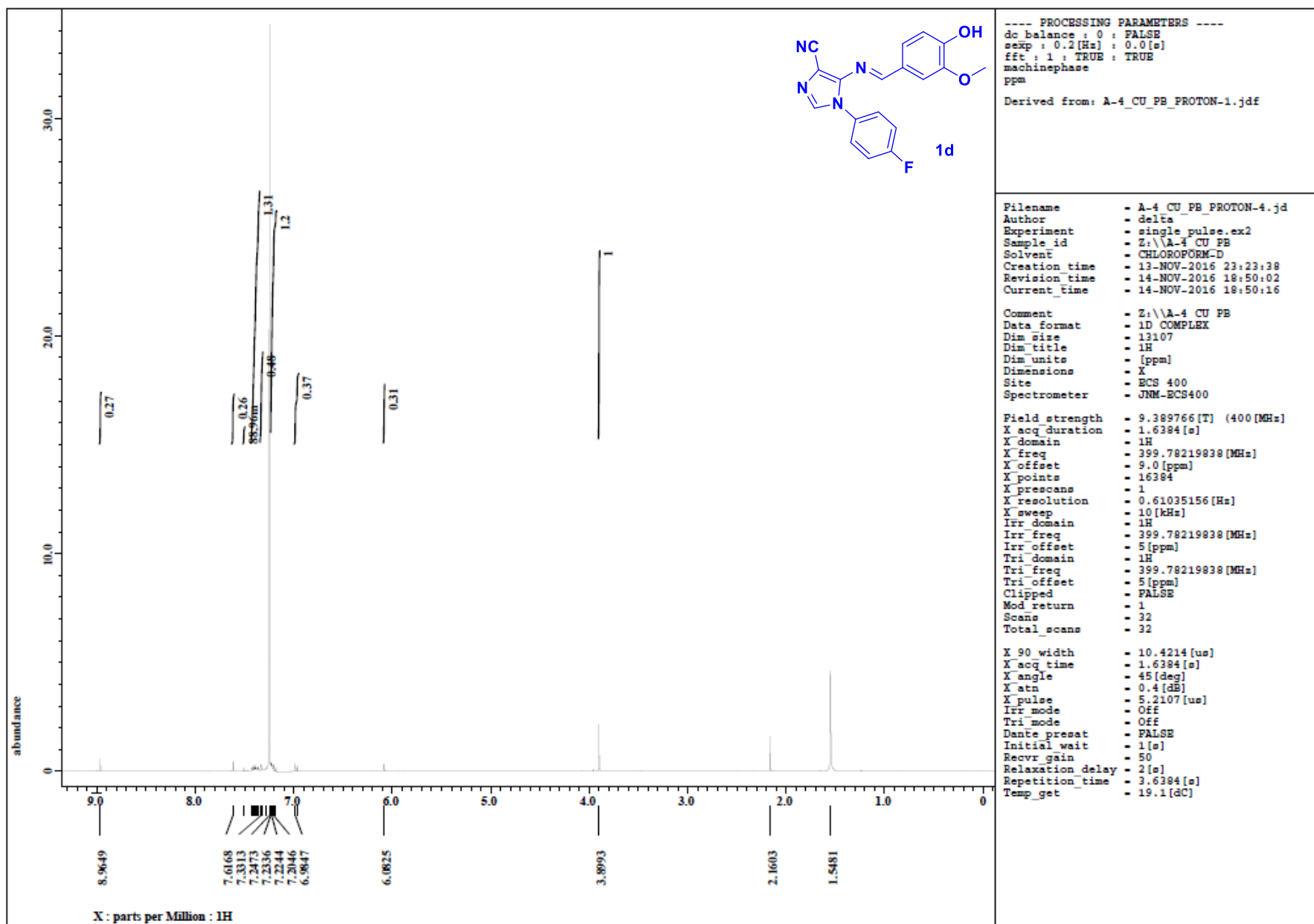
MassPeaks:365

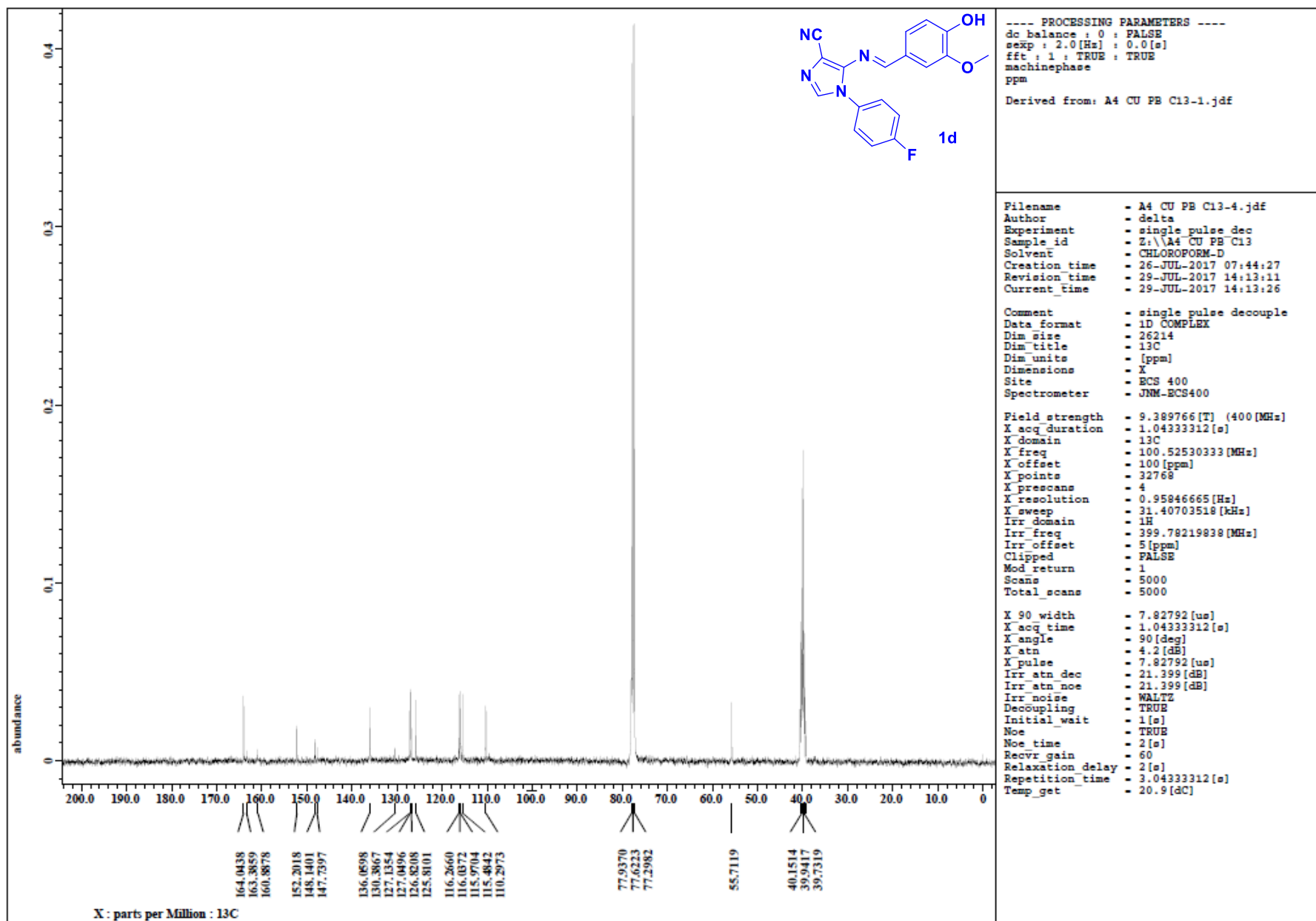
RawMode:Averaged 3.415-3.425(384-386) BasePeak:202(290256)

BG Mode:Calc. from Peak Group 1 - Event 1

intensity







Elemental Composition Report

Page 1

Single Mass Analysis

Tolerance = 6.0 PPM / DBE: min = -1.5, max = 50.0

Element prediction: Off

Number of isotope peaks used for i-FIT = 5

Monoisotopic Mass, Odd and Even Electron Ions

46 formula(e) evaluated with 1 results within limits (up to 50 best isotopic matches for each mass)

Elements Used:

C: 9-20 H: 11-30 N: 0-5 O: 0-3 F: 0-1

Sample Name : A-4

IITRPR

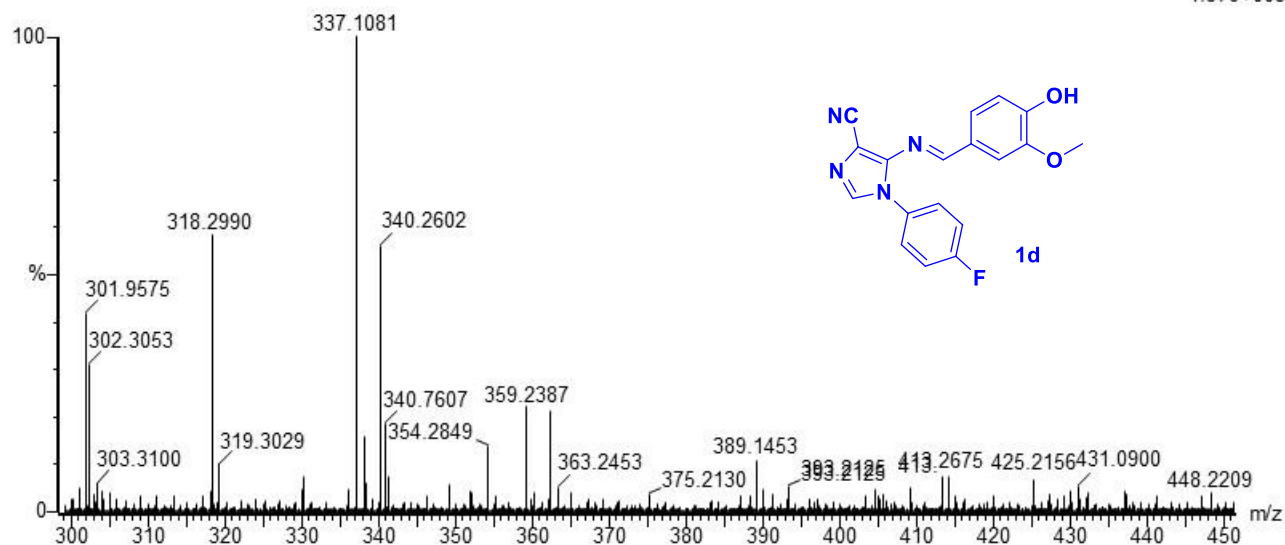
XEVO G2-XS QTOF

Test Name : HRMS-1

160120-A-4 16 (0.165)

1: TOF MS ES+

1.57e+005



Minimum: -1.5
Maximum: 5.0 6.0 50.0

Mass	Calc. Mass	mDa	PPM	DBE	i-FIT	Norm	Conf(%)	Formula
337.1081	337.1101	-2.0	-5.9	13.5	1087.3	n/a	n/a	C18 H14 N4 O2 F

Spectrum

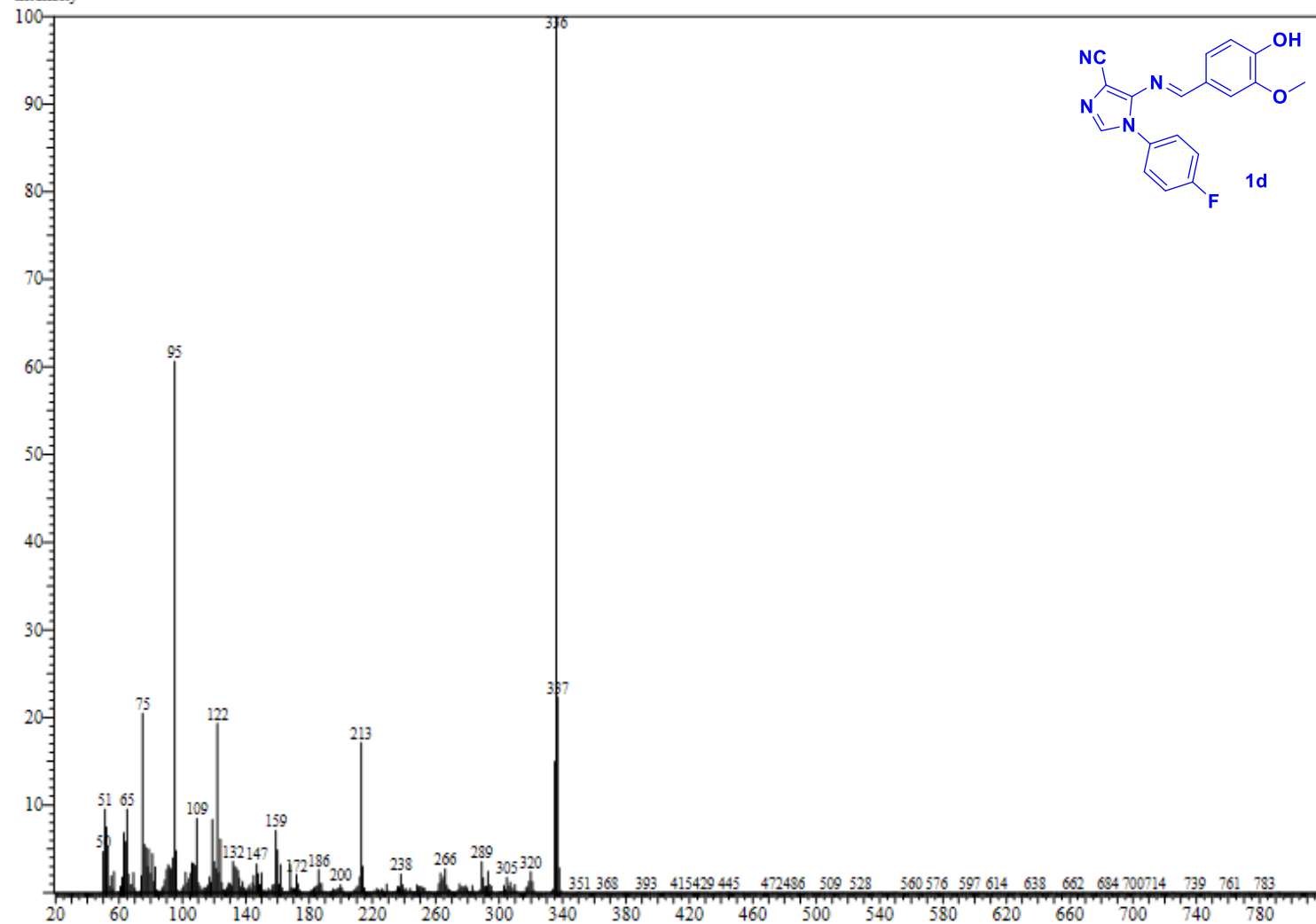
Line#:1 R.Time:6.470(Scan#:995)

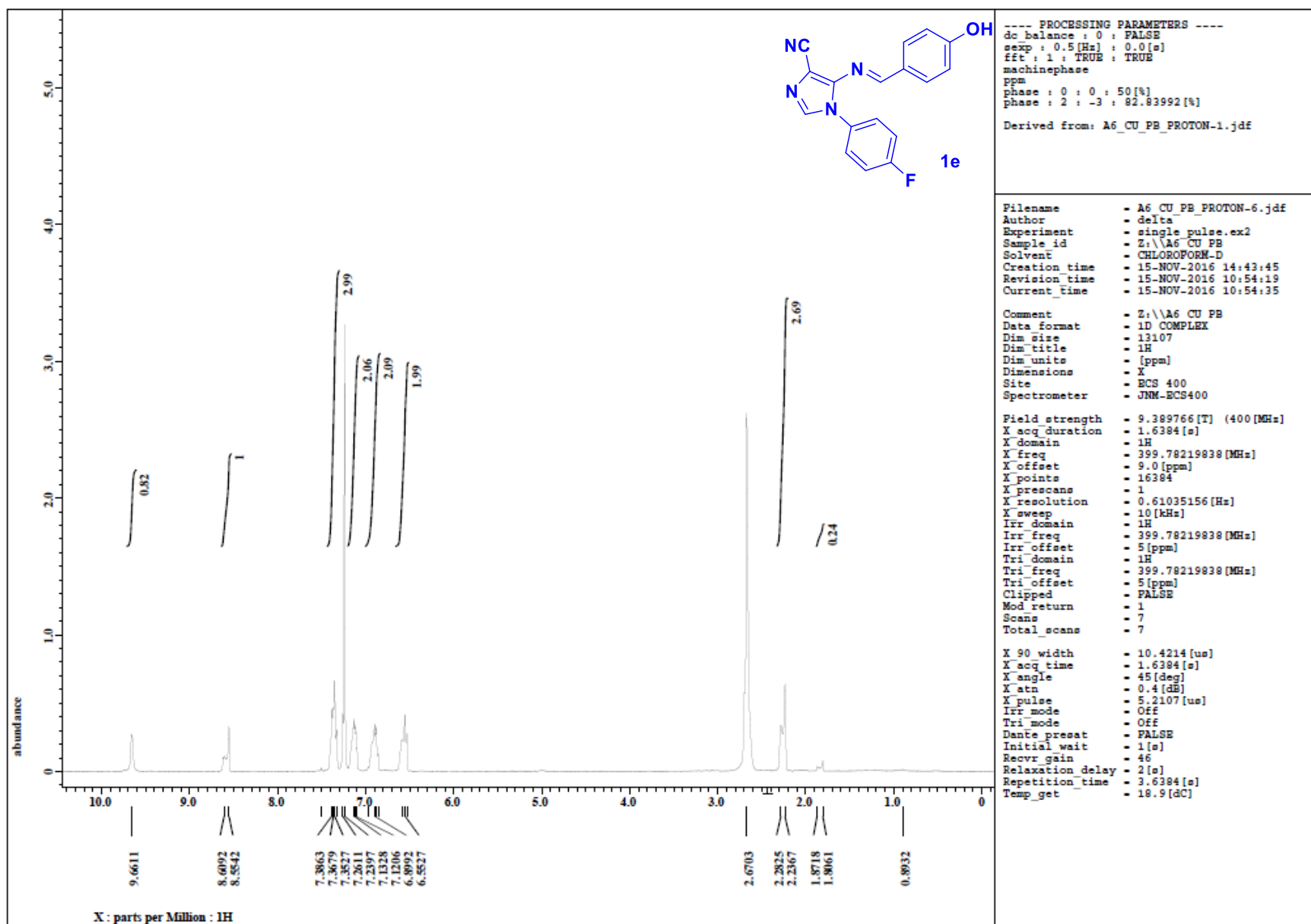
MassPeaks:582

RawMode:Averaged 6.465-6.475(994-996) BasePeak:336(1955400)

BG Mode:Calc. from Peak Group 1 - Event 1

intensity





Elemental Composition Report

Page 1

Single Mass Analysis

Tolerance = 6.0 PPM / DBE: min = -1.5, max = 50.0

Element prediction: Off

Number of isotope peaks used for i-FIT = 5

Monoisotopic Mass, Even Electron Ions

59 formula(e) evaluated with 1 results within limits (up to 50 best isotopic matches for each mass)

Elements Used:

C: 9-19 H: 11-30 N: 0-5 O: 0-3 F: 0-1

Sample Name : A-6

IITRPR

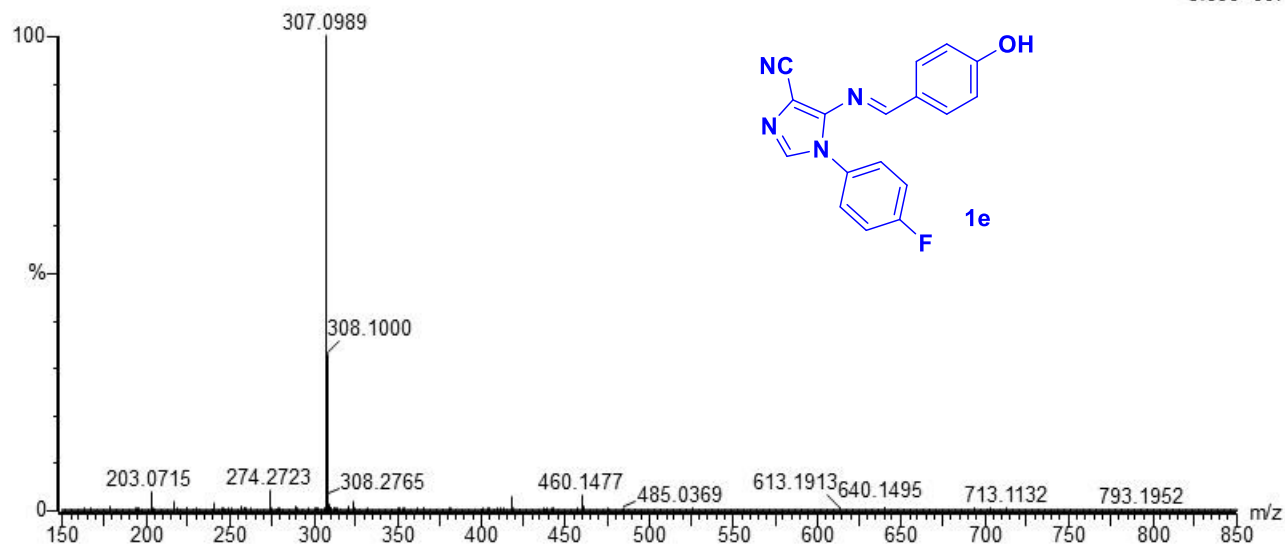
XEVO G2-XS QTOF

Test Name : HRMS-1

160120-A-6 15 (0.157)

1: TOF MS ES+

5.89e+007



Minimum:

-1.5

Maximum:

5.0 6.0 50.0

Mass	Calc. Mass	mDa	PPM	DBE	i-FIT	Norm	Conf(%)	Formula
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307.0989	307.0995	-0.6	-2.0	13.5	1777.2	n/a	n/a	C17 H12 N4 O F
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Spectrum

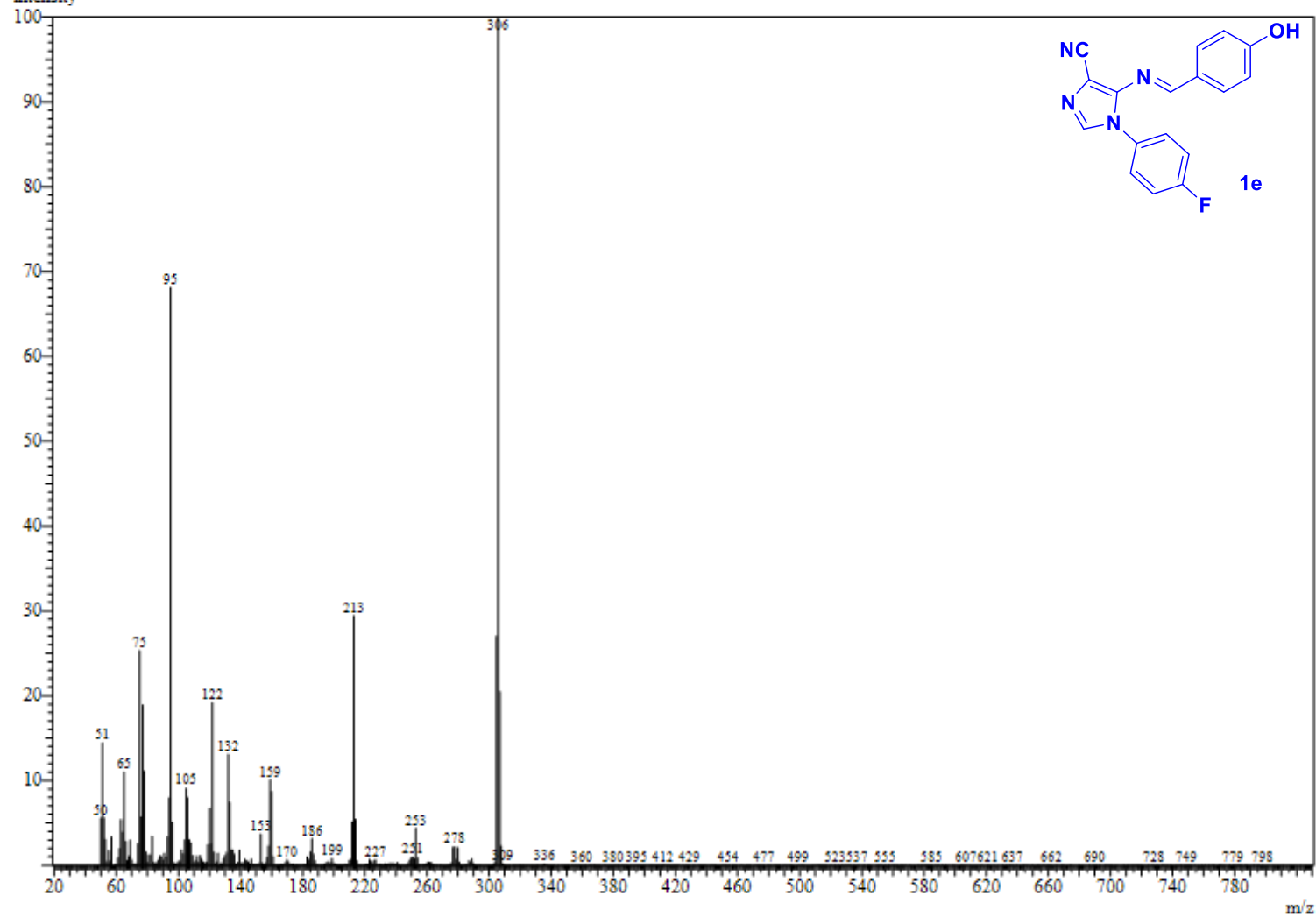
Line#:1 R.Time:6.270(Scan#:955)

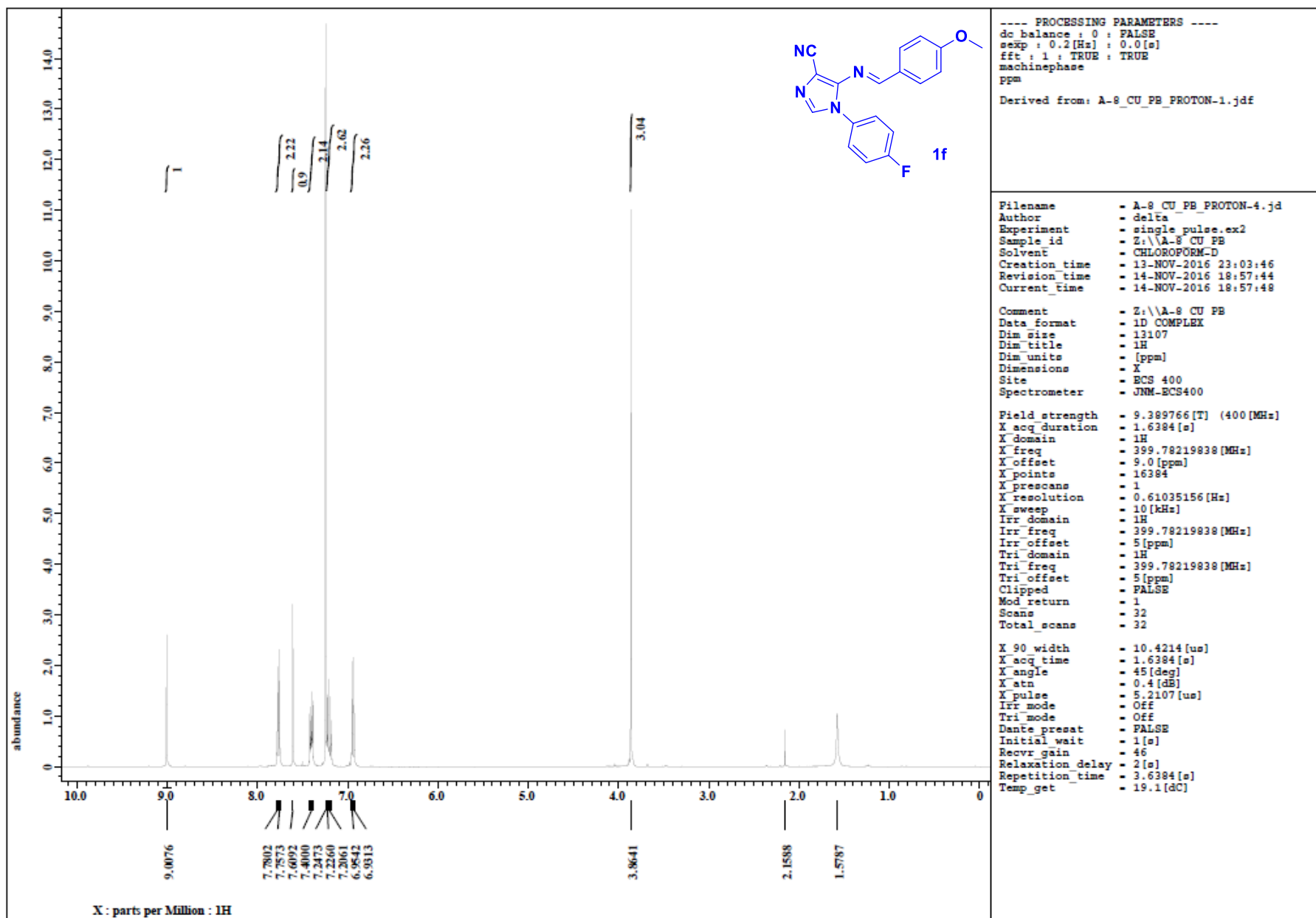
MassPeaks:557

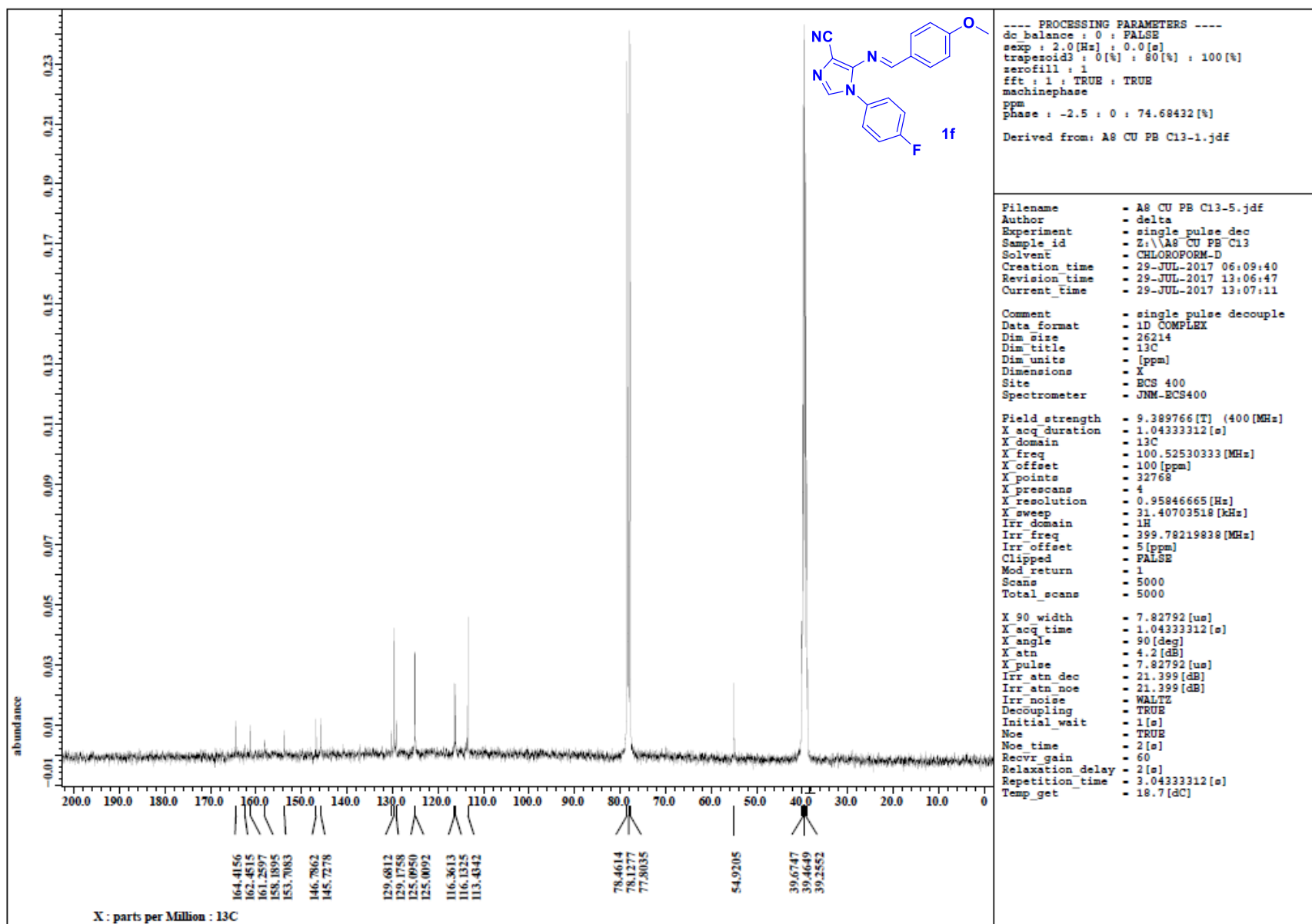
RawMode:Averaged 6.265-6.275(954-956) BasePeak:306(2138462)

BG Mode:Calc. from Peak Group 1 - Event 1

intensity







Spectrum

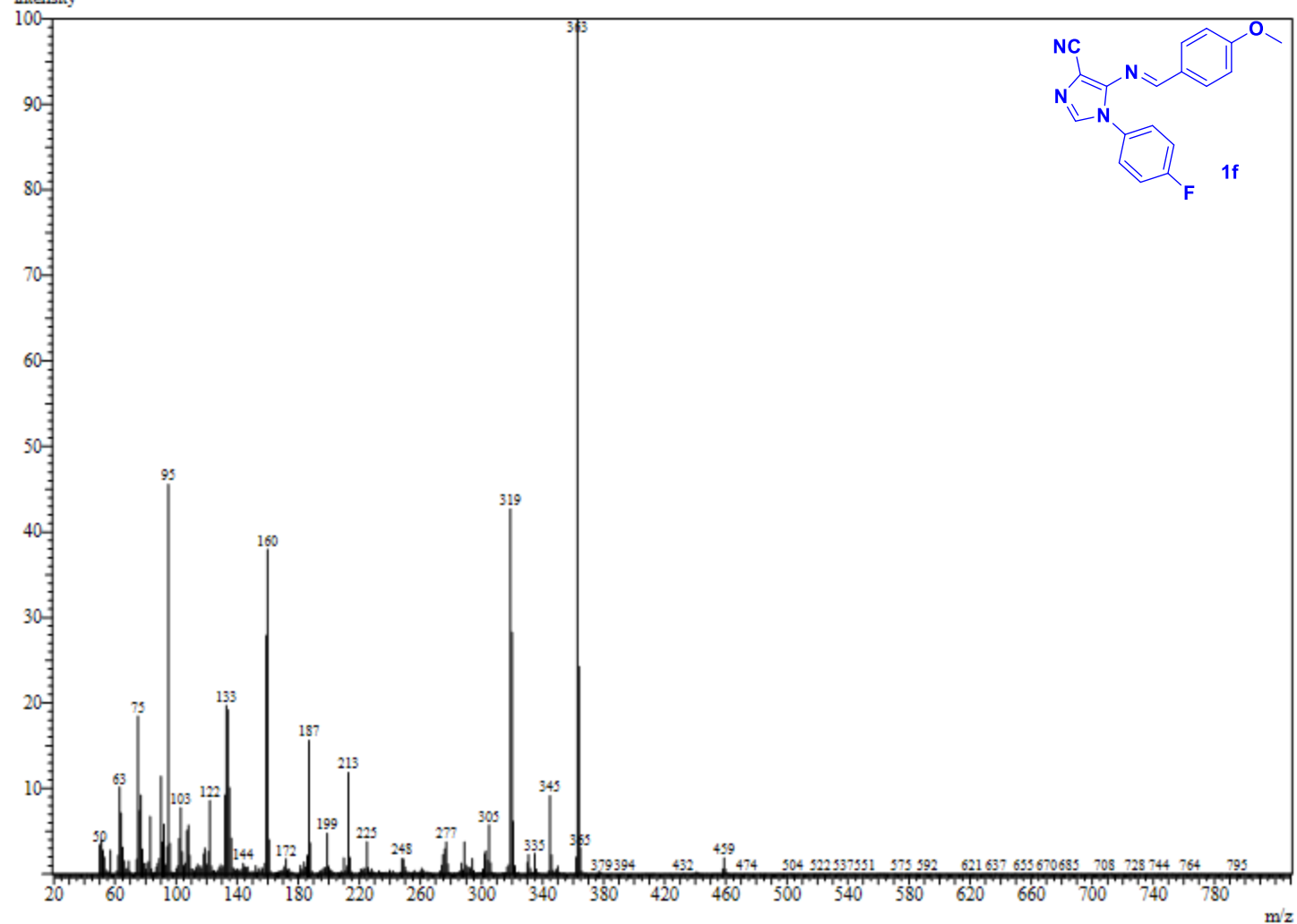
Line#:1 R.Time:7.815(Scan#:1264)

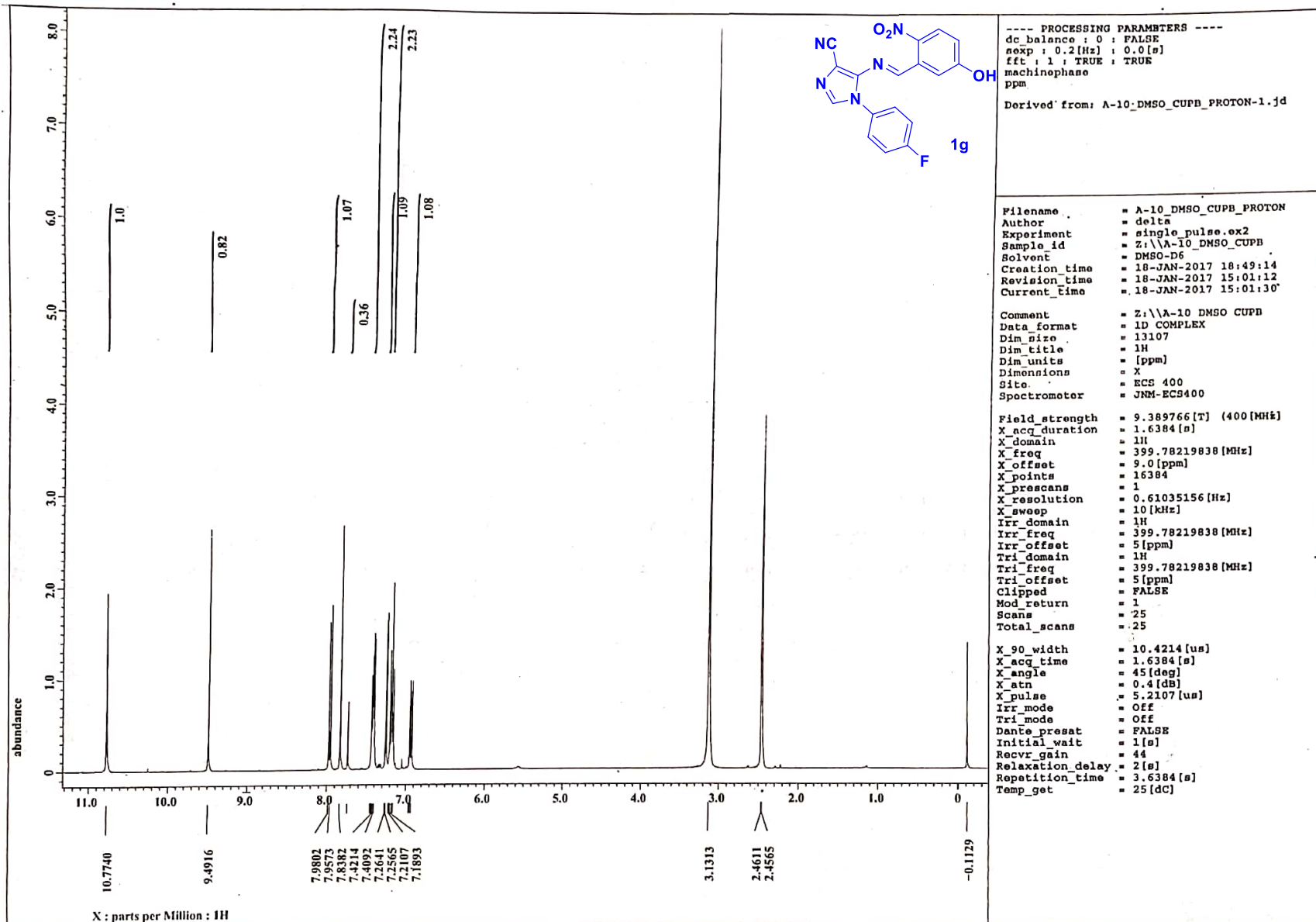
MassPeaks:479

RawMode:Averaged 7.810-7.820(1263-1265) BasePeak:363(347447)

BG Mode:Calc. from Peak Group 1 - Event 1

intensity





Elemental Composition Report

Page 1

Single Mass Analysis

Tolerance = 6.0 PPM / DBE: min = -1.5, max = 50.0

Element prediction: Off

Number of isotope peaks used for i-FIT = 5

Monoisotopic Mass, Even Electron Ions

40 formula(e) evaluated with 1 results within limits (up to 50 best isotopic matches for each mass)

Elements Used:

C: 9-19 H: 11-30 N: 0-5 O: 0-3 F: 0-1

Sample Name : A-10

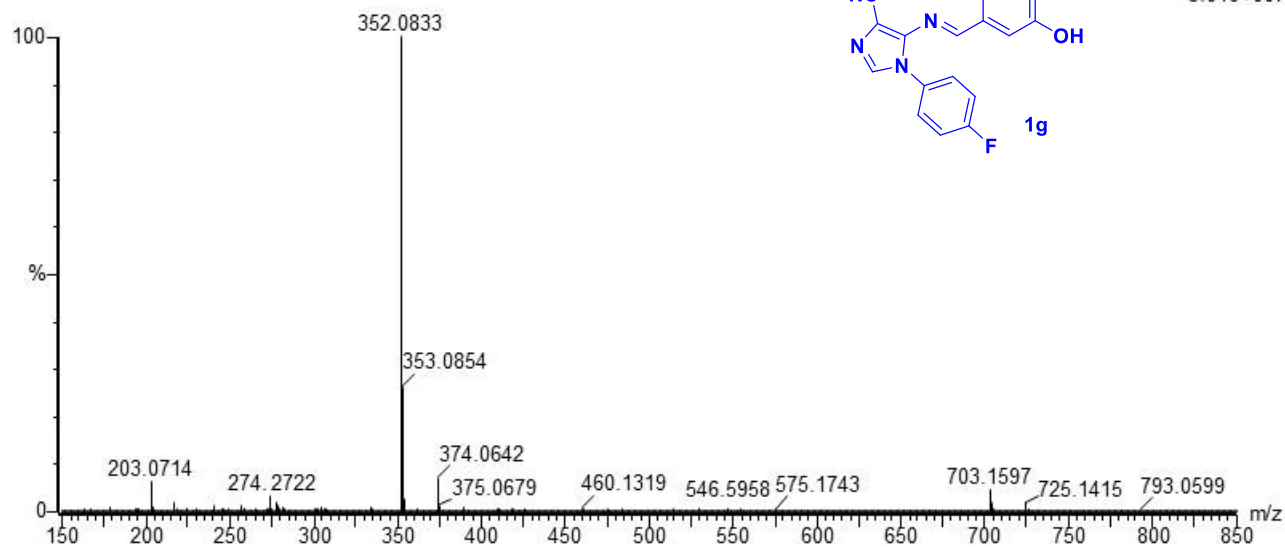
IITRPR

XEVO G2-XS QTOF

Test Name : HRMS-1

160120-A-10 17 (0.174)

1: TOF MS ES+
3.04e+007



Minimum: -1.5
Maximum: 5.0 6.0 50.0

Mass	Calc. Mass	mDa	PPM	DBE	i-FIT	Norm	Conf(%)	Formula
352.0833	352.0846	-1.3	-3.7	14.5	1530.9	n/a	n/a	C17 H11 N5 O3 F

Spectrum

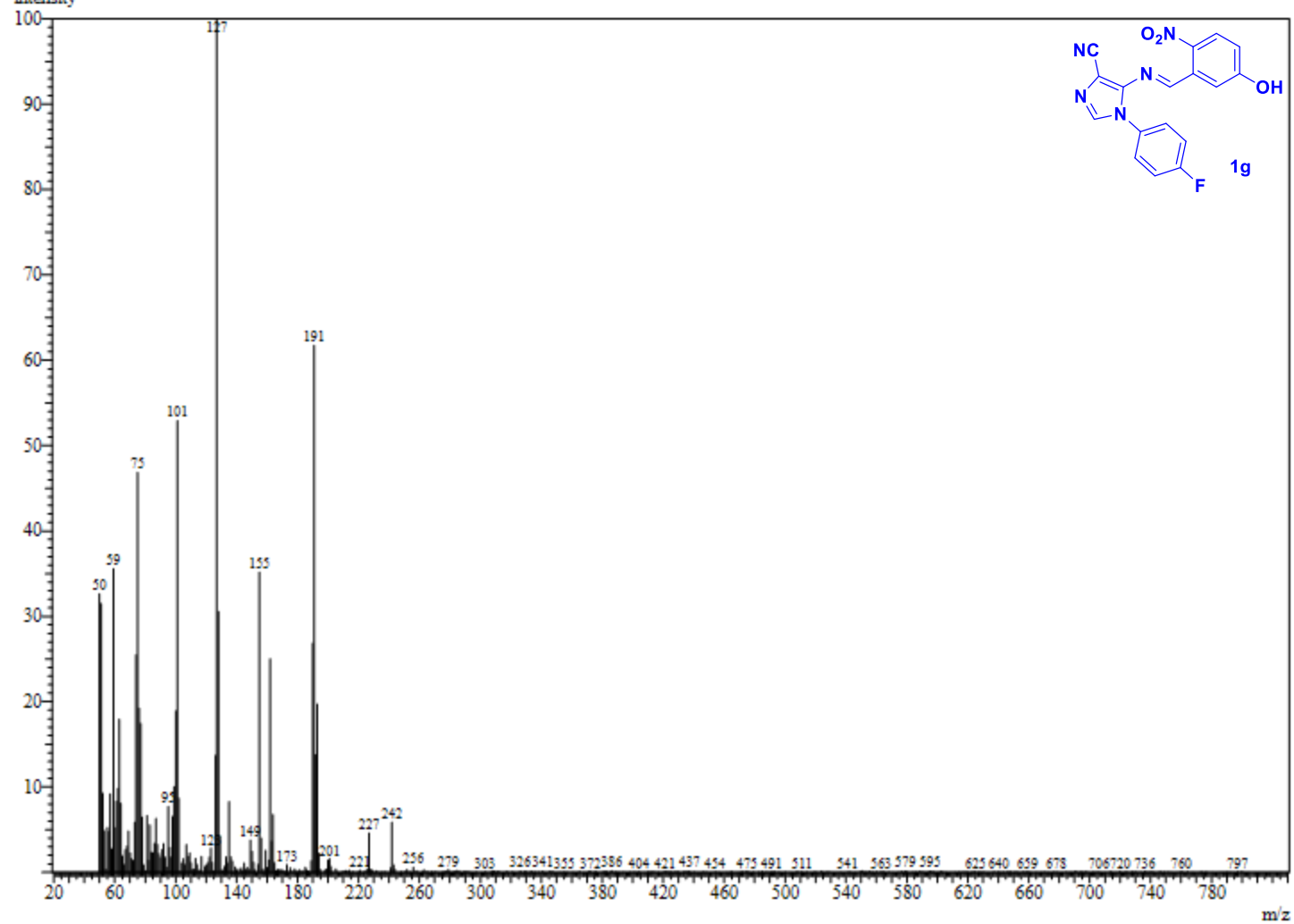
Line#:1 R.Time:2.155(Scan#:132)

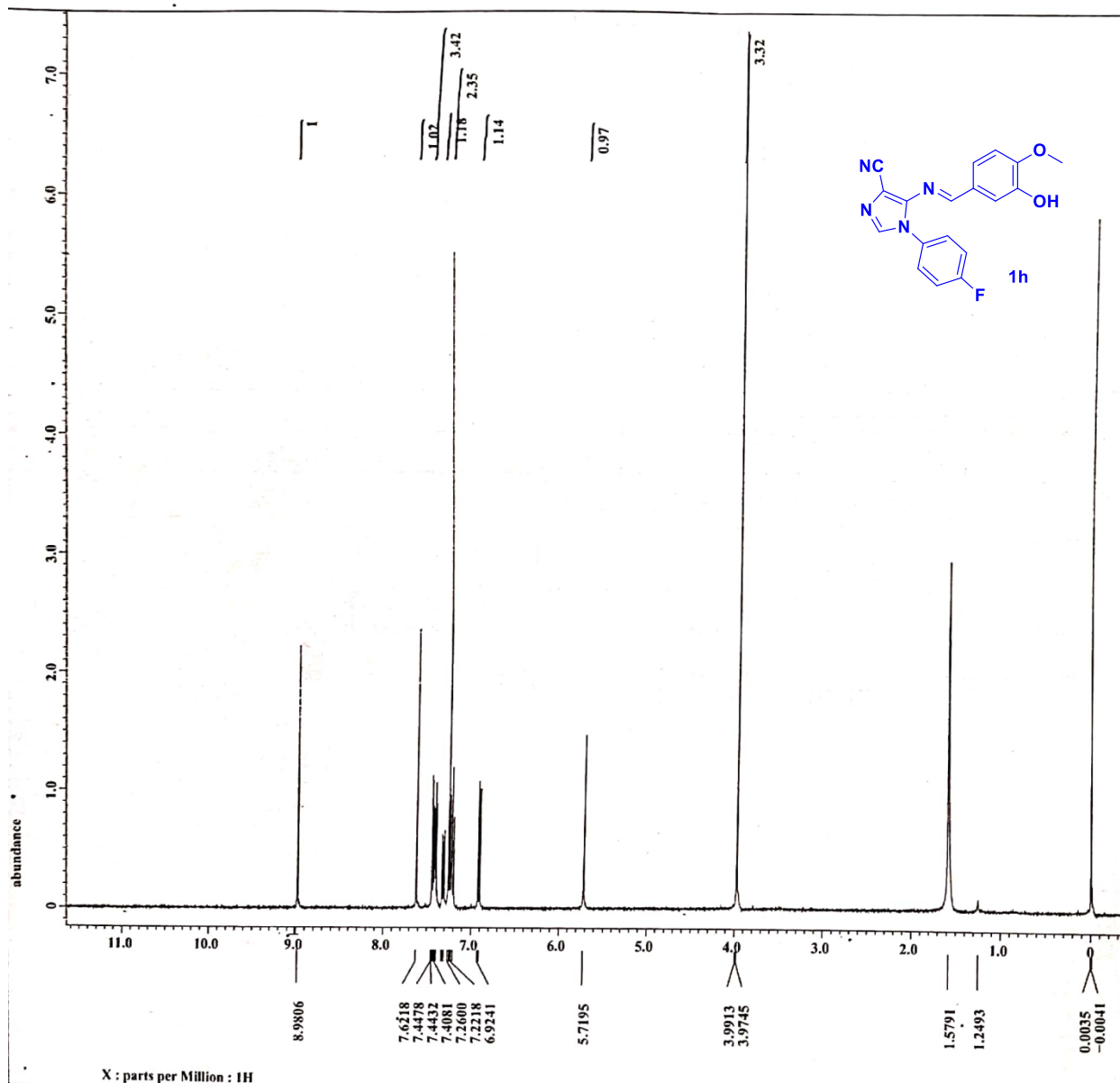
MassPeaks:430

RawMode:Averaged 2.150-2.160(131-133) BasePeak:127(43367)

BGMode:Calc. from Peak Group 1 - Event 1

intensity





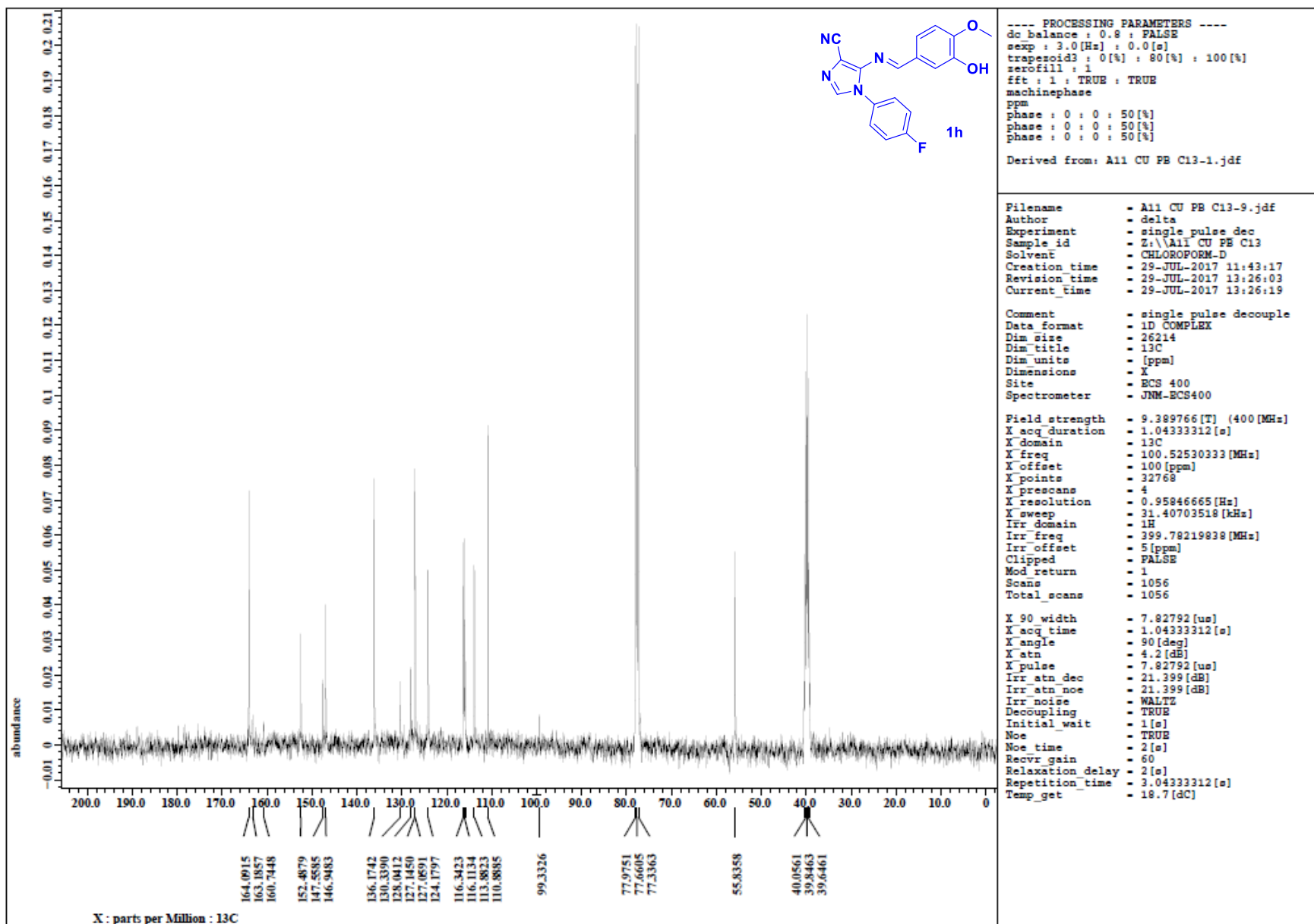
----- PROCESSING PARAMETERS -----
 dc_balance : 0 : FALSE
 sexp : 0.2 [Hz] : 0.0 [s]
 fft : 1 : TRUE : TRUE
 machinephase
 ppm
 Derived from: A-11_CUPB_PROTON-1.jdf

Filename = A-11_CUPB_PROTON-4.jd
 Author = delta
 Experiment = single_pulse.ex2
 Sample_id = Z:\\A-11_CUPB
 Solvent = CHLOROFORM-D
 Creation_time = 18-JAN-2017 17:19:05
 Revision_time = 18-JAN-2017 14:09:44
 Current_time = 18-JAN-2017 14:09:52

Comment = Z:\\A-11_CUPB
 Data_format = 1D_COMPLEX
 Dim_size = 13107
 Dim_title = 1H
 Dim_units = [ppm]
 Dimensions = X
 Site = ECS 400
 Spectrometer = JNM-ECS400

Field_strength = 9.389766 [T] (400 [MHz])
 X_acq_duration = 1.6384 [s]
 X_domain = 1H
 X_freq = 399.78219838 [MHz]
 X_offset = 9.0 [ppm]
 X_points = 16384
 X_prescans = 1
 X_resolution = 0.61035156 [Hz]
 X_sweep = 10 [kHz]
 Irr_domain = 1H
 Irr_freq = 399.78219838 [MHz]
 Irr_offset = 5 [ppm]
 Tri_domain = 1H
 Tri_freq = 399.78219838 [MHz]
 Tri_offset = 5 [ppm]
 Clipped = FALSE
 Mod_return = 1
 Scans = 3
 Total_scans = 3

X_90_width = 10.4214 [us]
 X_acq_time = 1.6384 [s]
 X_angle = 45 [deg]
 X_atn = 0.4 [dB]
 X_pulse = 5.2107 [us]
 Irr_mode = Off
 Tri_mode = Off
 Dante_preset = FALSE
 Initial_wait = 1 [s]
 Recvr_gain = 50
 Relaxation_delay = 2 [s]
 Repetition_time = 3.6384 [s]
 Temp_get = 18.1 [dC]



Elemental Composition Report

Page 1

Single Mass Analysis

Tolerance = 6.0 PPM / DBE: min = -1.5, max = 50.0

Element prediction: Off

Number of isotope peaks used for i-FIT = 5

Monoisotopic Mass, Even Electron Ions

43 formula(e) evaluated with 1 results within limits (up to 50 best isotopic matches for each mass)

Elements Used:

C: 9-19 H: 11-30 N: 0-5 O: 0-3 F: 0-1

Sample Name : A-11

IITRPR

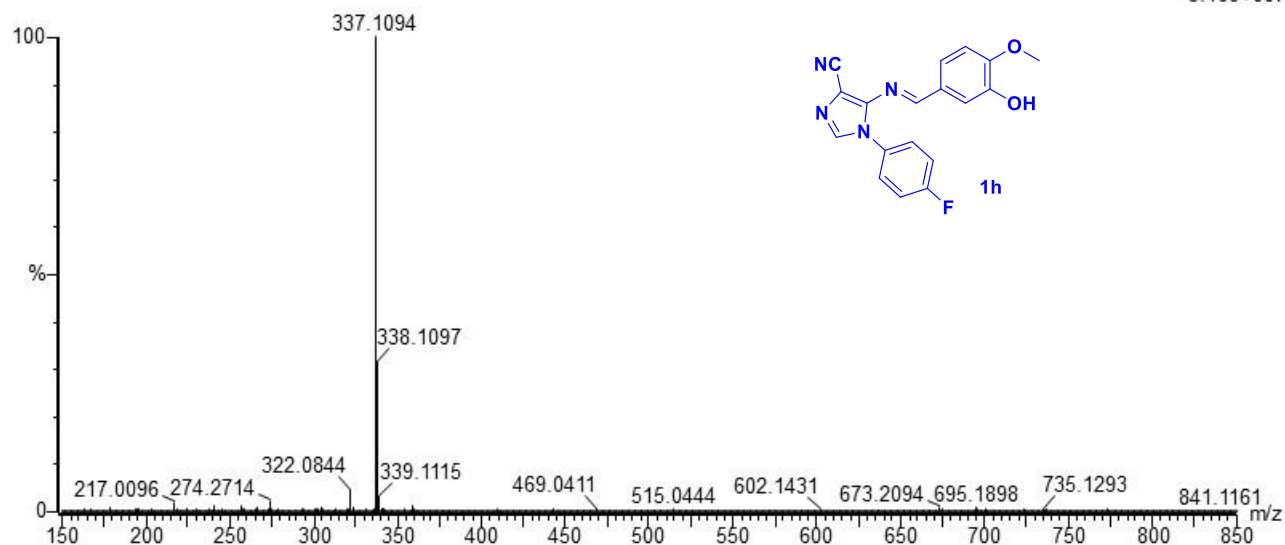
XEVO G2-XS QTOF

Test Name : HRMS-1

160120-A-11 17 (0.174)

1: TOF MS ES+

3.46e+007



Minimum:

-1.5

Maximum:

5.0 6.0 50.0

Mass	Calc. Mass	mDa	PPM	DBE	i-FIT	Norm	Conf(%)	Formula
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337.1094	337.1101	-0.7	-2.1	13.5	2165.1	n/a	n/a	C18 H14 N4 O2 F
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Spectrum

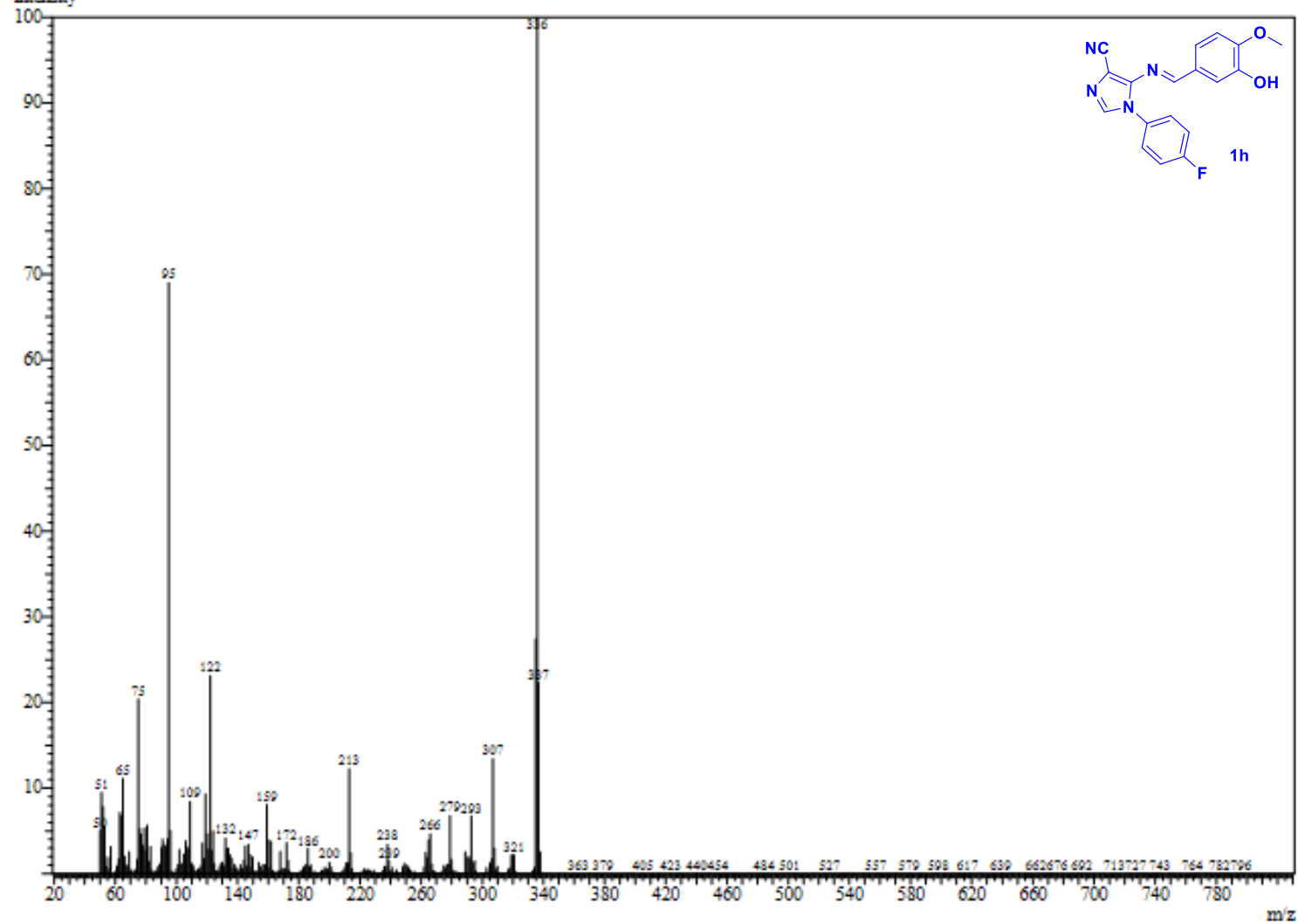
Line#:1 R.Time:6.180(Scan#:937)

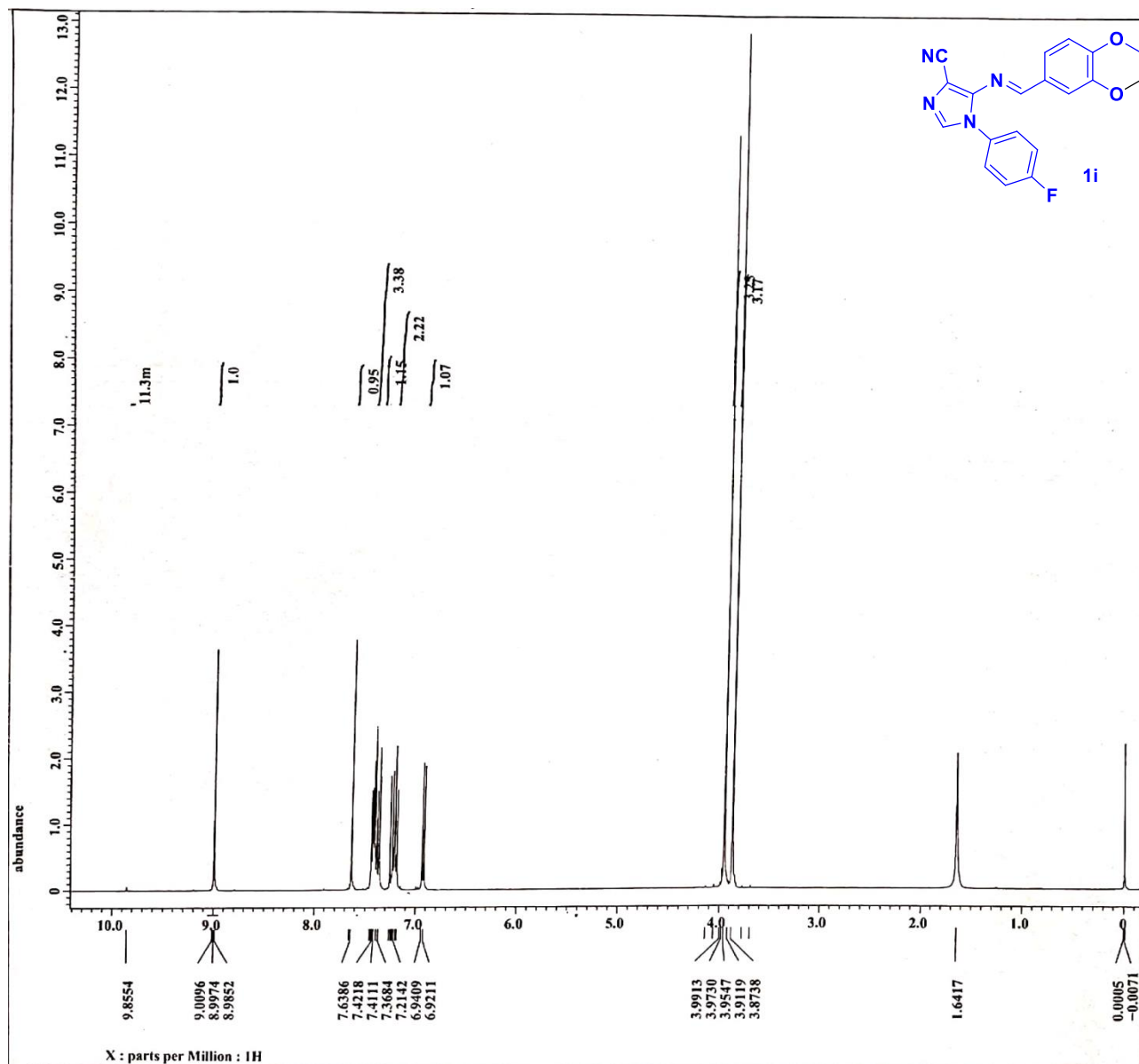
MassPeaks:522

RawMode:Averaged 6.175-6.185(936-938) BasePeak:336(307885)

BG Mode:Calc. from Peak Group 1 - Event 1

intensity





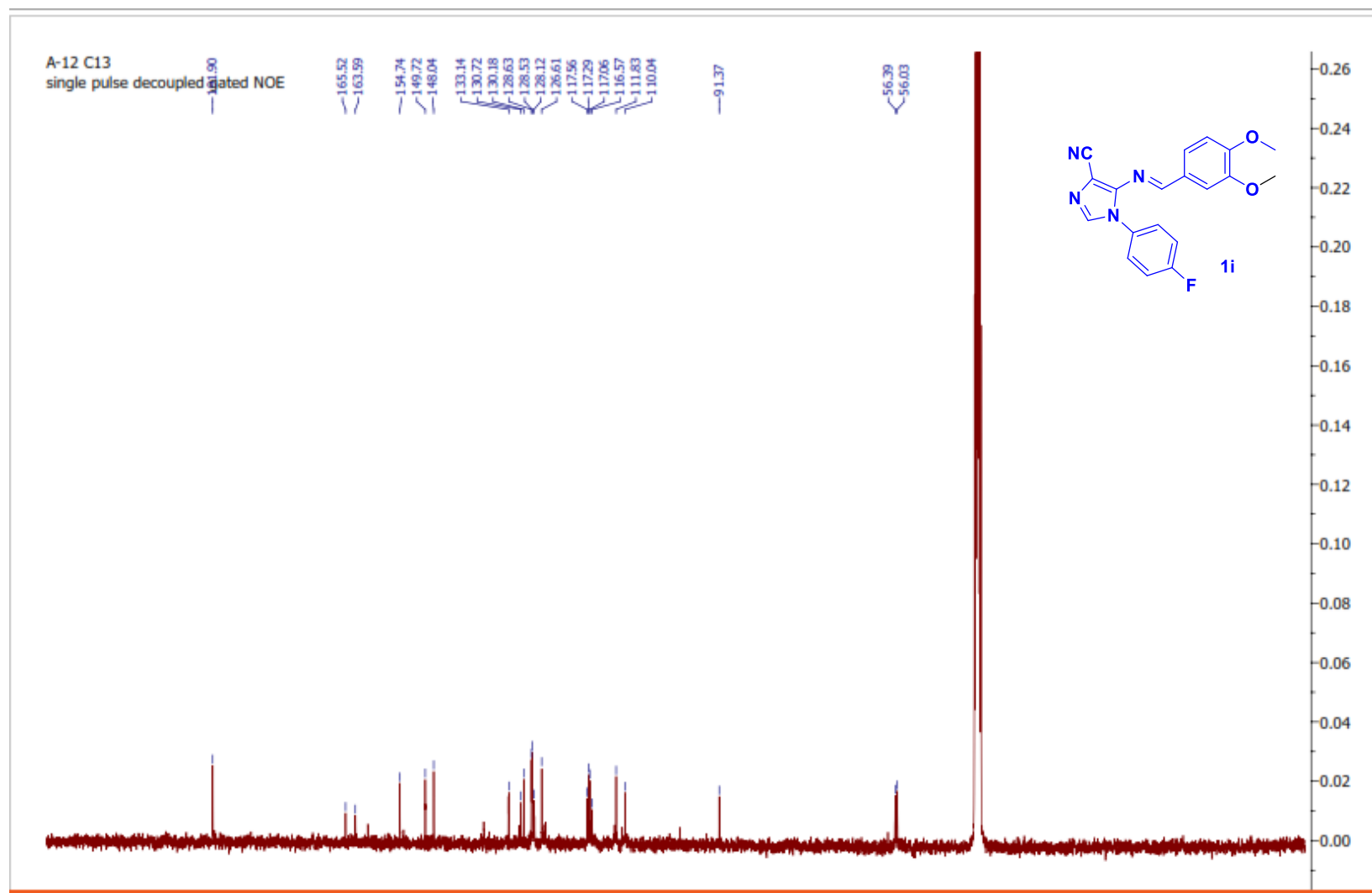
----- PROCESSING PARAMETERS -----
 dc_balance : 0 : FALSE
 secp : 0.2[Hz] : 0.0[s]
 fft : 1 : TRUE : TRUE
 machinephase
 ppm
 Derived from: A-12_CU_PB_PROTON-1.jdf

Filename = A-12_CU_PB_PROTON-4.j
 Author = delta
 Experiment = single_pulse.ex2
 Sample_id = Z:\A-12_CU_PB
 Solvent = CHLOROFORM-D
 Creation_time = 17-JAN-2017 21:30:56
 Revision_time = 17-JAN-2017 19:00:11
 Current_time = 17-JAN-2017 19:00:21

Comment = Z:\A-12_CU_PB
 Data_format = 1D_COMPLEX
 Dim_size = 13107
 Dim_title = 1H
 Dim_units = [ppm]
 Dimensions = X
 Site = ECS 400
 Spectrometer = JNM-ECS400

Field_strength = 9.389766[T] (400[MHz])
 X_acq_duration = 1.6384[s]
 X_domain = 1H
 X_freq = 399.78219838[MHz]
 X_offset = 9.0[ppm]
 X_points = 16384
 X_prescans = 1
 X_resolution = 0.61035156[Hz]
 X_sweep = 10[kHz]
 X_domain = 1H
 Irr_freq = 399.78219838[MHz]
 Irr_offset = 5[ppm]
 Tri_domain = 1H
 Tri_freq = 399.78219838[MHz]
 Tri_offset = 5[ppm]
 Clipped = FALSE
 Mod_return = 1
 Scans = 32
 Total_scans = 32

X_90_width = 10.4214[us]
 X_acq_time = 1.6384[s]
 X_angle = 45[deg]
 X_atn = 0.4[dB]
 X_pulse = 5.2107[us]
 Irr_mode = Off
 Tri_mode = Off
 Dante_presat = FALSE
 Initial_wait = 1[s]
 Recvr_gain = 44
 Relaxation_delay = 2[s]
 Repetition_time = 3.6384[s]
 Temp_get = 18.5[dc]



Elemental Composition Report

Page 1

Single Mass Analysis

Tolerance = 6.0 PPM / DBE: min = -1.5, max = 50.0

Element prediction: Off

Number of isotope peaks used for i-FIT = 5

Monoisotopic Mass, Even Electron Ions

40 formula(e) evaluated with 1 results within limits (up to 50 best isotopic matches for each mass)

Elements Used:

C: 9-19 H: 11-30 N: 0-5 O: 0-3 F: 0-1

Sample Name : A-12

IITRPR

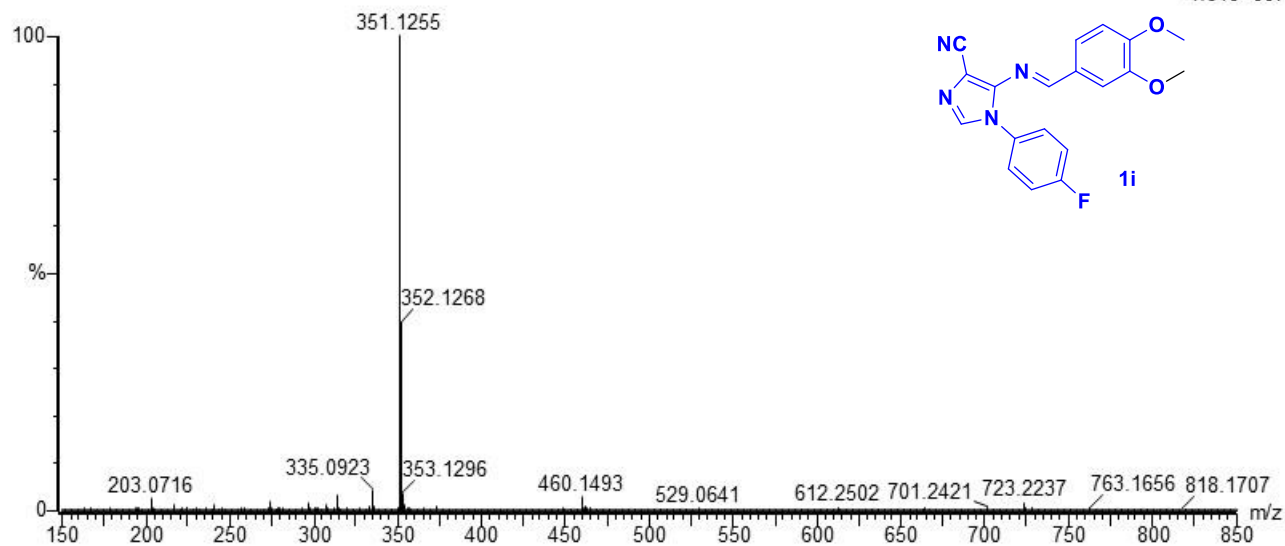
XEVO G2-XS QTOF

Test Name : HRMS-1

160120-A-12 17 (0.174)

1: TOF MS ES+

4.64e+007



Minimum: -1.5
Maximum: 5.0 6.0 50.0

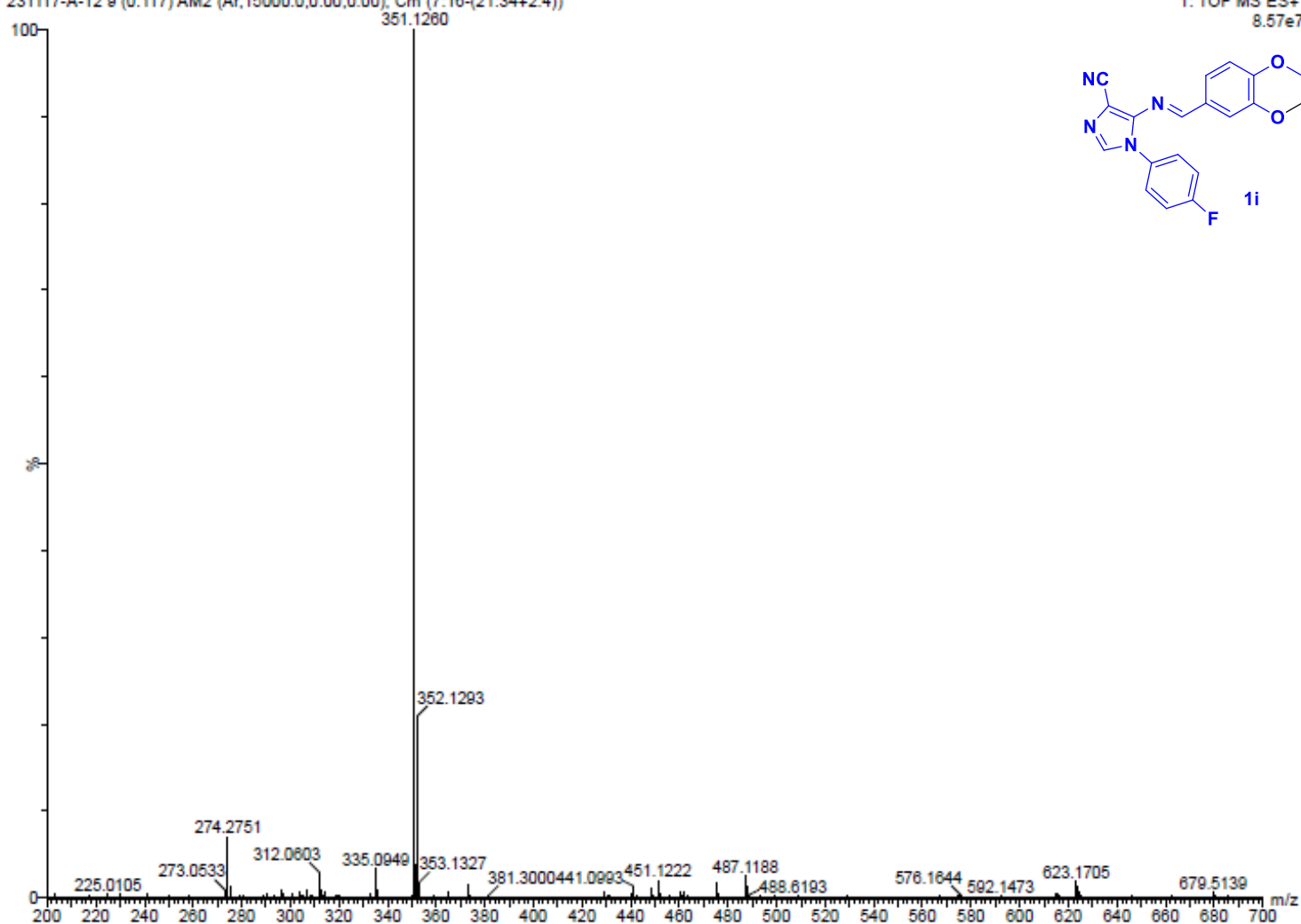
Mass	Calc. Mass	mDa	PPM	DBE	i-FIT	Norm	Conf(%)	Formula
351.1255	351.1257	-0.2	-0.6	13.5	1738.3	n/a	n/a	C ₁₉ H ₁₆ N ₄ O ₂ F

Sample Name : A-12
Test Name : HRMS-1

INDIAN INSTITUTE OF TECHNOLOGY
ROPAR

XEVO G2-XS QTOF

1: TOF MS ES+
8.57e7



Spectrum

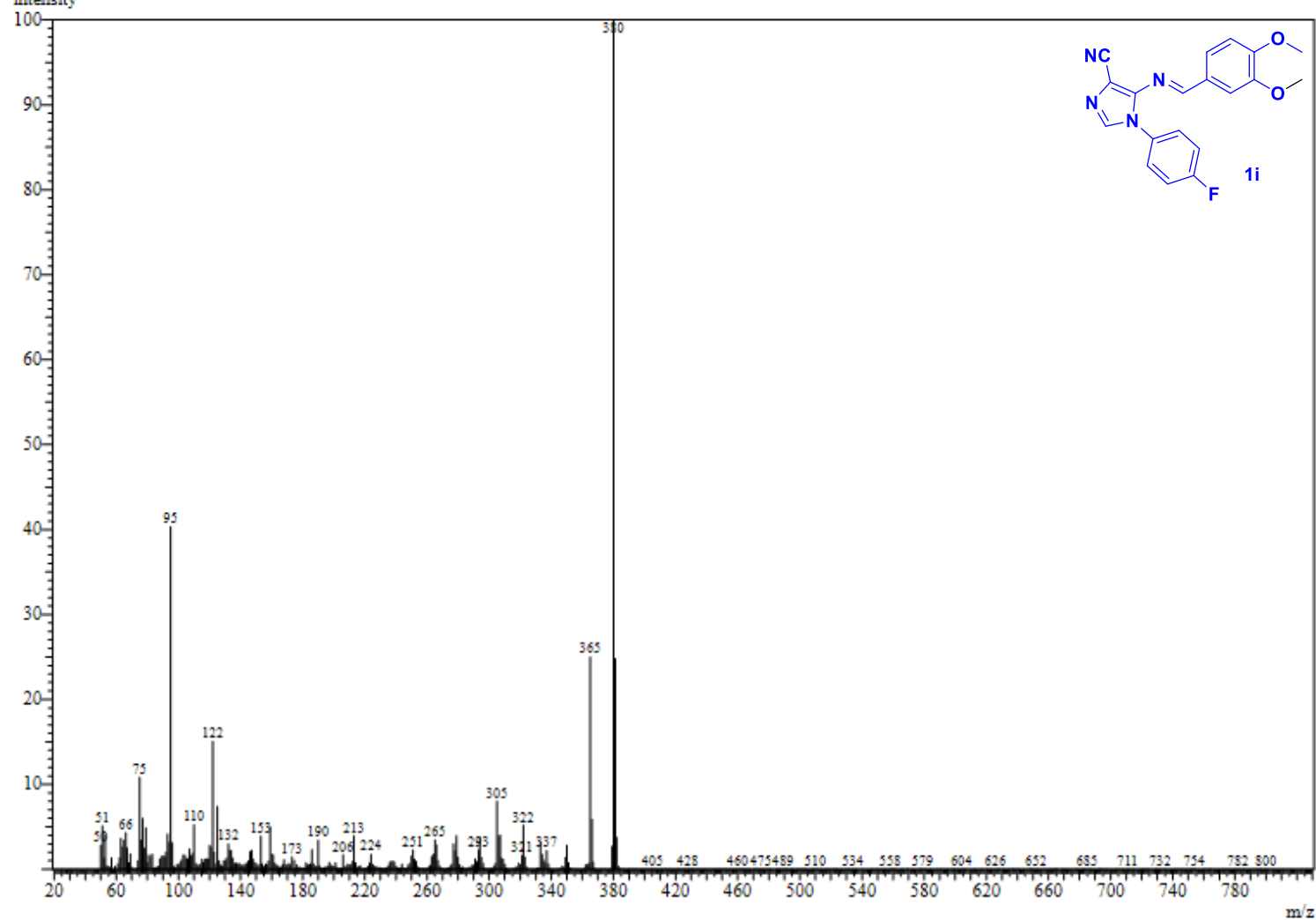
Line#:1 R.Time:7.425(Scan#:1186)

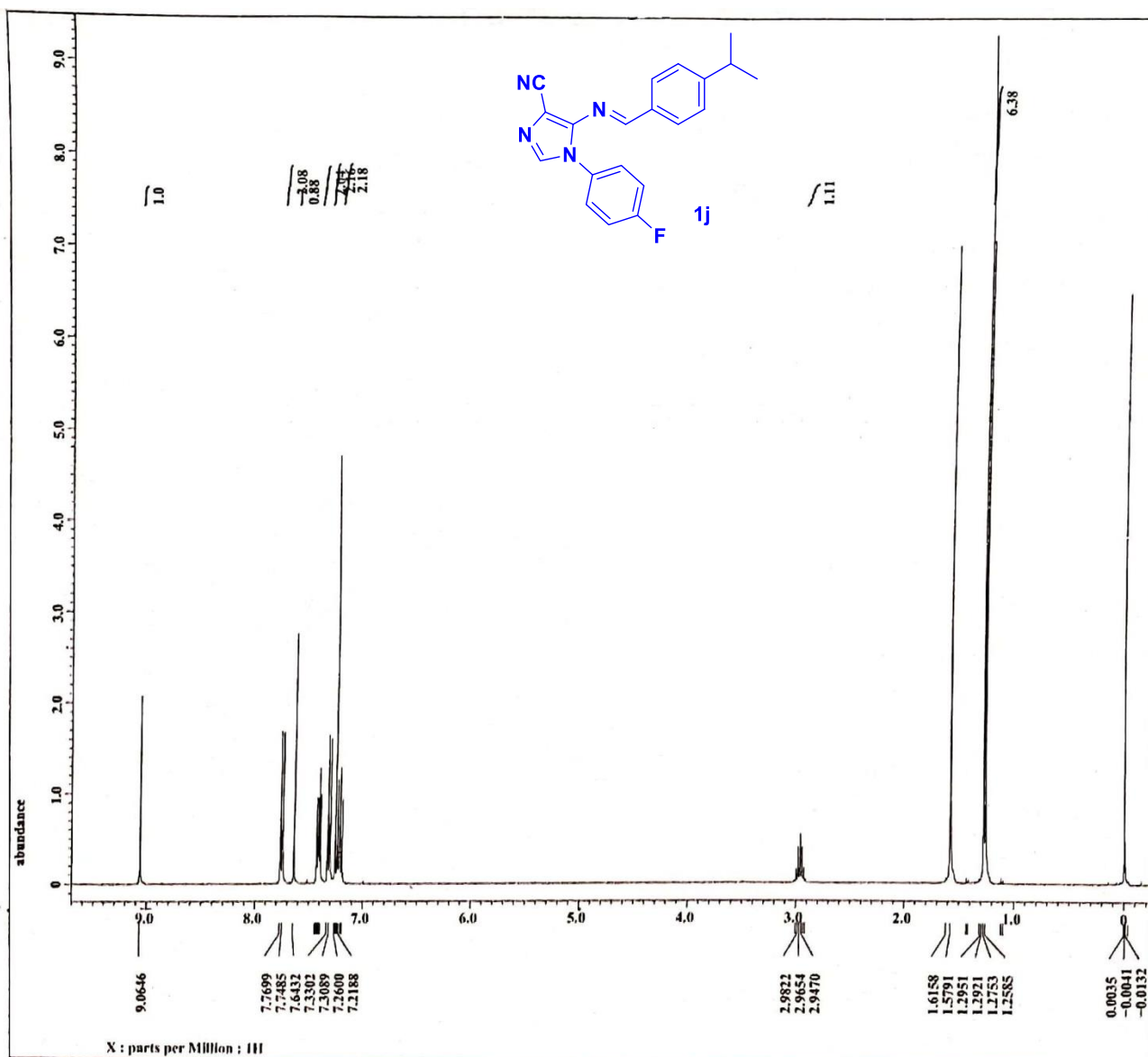
MassPeaks:583

RawMode:Averaged 7.420-7.430(1185-1187) BasePeak:380(6661844)

BG Mode:Calc. from Peak Group 1 - Event 1

intensity





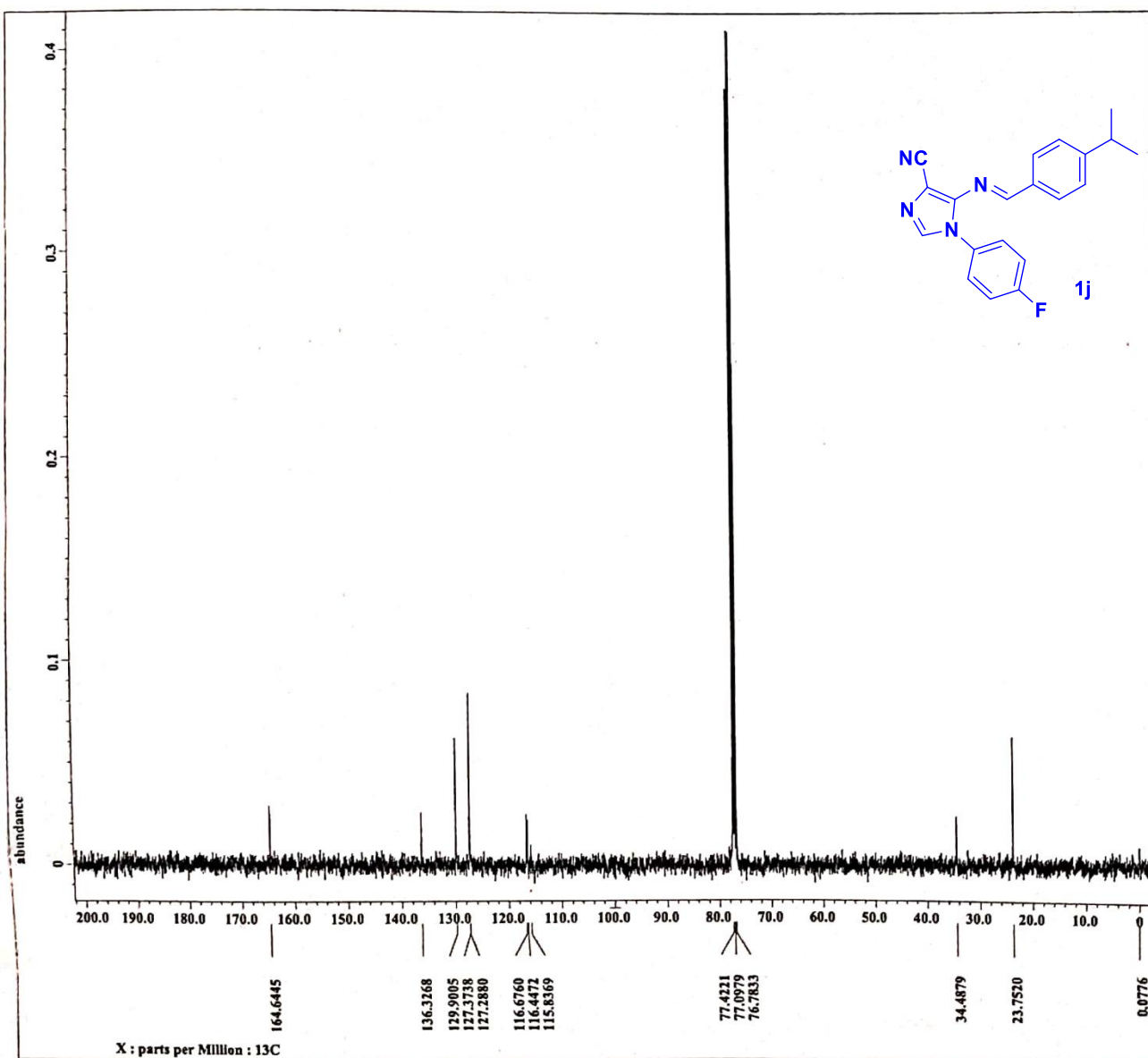
----- PROCESSING PARAMETERS -----
 dc balance : 0 : FALSE
 sexp : 0.2[Hz] : 0.0[s]
 fft : 1 : TRUE : TRUE
 machinephase
 ppm
 Derived from: A-14_CU_PB_PROTON-1.jdf

Filename = A-14_CU_PB_PROTON-4.j
 Author = delta
 Experiment = single_pulse.ex2
 Sample_id = Z:\A-14_CU_PB
 Solvent = CHLOROFORM-D
 Creation_time = 17-JAN-2017 21:41:16
 Revision_time = 17-JAN-2017 19:02:15
 Current_time = 17-JAN-2017 19:02:24

Comment = Z:\A-14_CU_PB
 Data format = 1D COMPLEX
 Dim_size = 13107
 Dim_title = 1H
 Dim_units = [ppm]
 Dimensions = X
 Site = ECS 400
 Spectrometer = JNM-ECS400

Field_strength = 9.389766[T] (400[MHz])
 X_acq_duration = 1.6384[s]
 X_domain = 1H
 X_freq = 399.78219838[MHz]
 X_offset = 9.0[ppm]
 X_points = 16384
 X_prescans = 1
 X_resolution = 0.61035156[Hz]
 X_sweep = 10[kHz]
 Irr_domain = 1H
 Irr_freq = 399.78219838[MHz]
 Irr_offset = 5[ppm]
 Tri_domain = 1H
 Tri_freq = 399.78219838[MHz]
 Tri_offset = 5[ppm]
 Clipped = FALSE
 Mod_return = 1
 Scans = 32
 Total_scans = 32

X_90_width = 10.4214[us]
 X_acq_time = 1.6384[s]
 X_angle = 45[deg]
 X_atn = 0.4[db]
 X_pulse = 5.2107[us]
 Irr_mode = Off
 Tri_mode = Off
 Dante_preset = FALSE
 Initial_wait = 1[s]
 Recvr_gain = 50
 Relaxation_delay = 2[s]
 Repetition_time = 3.6384[s]
 Temp_get = 18[dc]



----- PROCESSING PARAMETERS -----
 dc_balance : 0 : FALSE
 sexp : 2.0[Hz] : 0.0[s]
 trapexoid3 : 0[%] : 80[%] : 100[%]
 zerofill : 1
 fft : 1 : TRUE : TRUE
 machinephase
 ppm
 Derived from: A-14 CU PB 13C-1.jdf

Filename = A-14 CU PB 13C-4.jdf
 Author = delta
 Experiment = single_pulse_dec
 Sample_id = Z:\A-14 CU PB 13C
 Solvent = CHLOROFORM-D
 Creation_time = 15-JUL-2017 05:56:56
 Revision_time = 15-JUL-2017 17:16:33
 Current_time = 15-JUL-2017 17:16:45

Comment = single pulse decouple
 Data format = 1D COMPLEX
 Dim_size = 26214
 Dim_title = 13C
 Dim_units = [ppm]
 Dimensions = X
 Site = ECS 400
 Spectrometer = JNM-ECS400

Field_strength = 9.389766[T] (400[MHz])
 X_acq_duration = 1.04333312[s]
 X_domain = 13C
 X_freq = 100.52530333[MHz]
 X_offset = 100[ppm]
 X_points = 32768
 X_prescans = 4
 X_resolution = 0.95846665[Hz]
 X_sweep = 31.40703518[kHz]
 Irr_domain = 1H
 Irr_freq = 399.78219838[MHz]
 Irr_offset = 5[ppm]
 Clipped = FALSE
 Mod_return = 1
 Scans = 1000
 Total_scans = 1000

X_90_width = 7.82792[us]
 X_acq_time = 1.04333312[s]
 X_angle = 90[deg]
 X_atn = 4.2[dB]
 X_pulse = 7.82792[us]
 Irr_atn_dec = 21.399[dB]
 Irr_atn_noe = 21.399[dB]
 Irr_noise = WALTZ
 Decoupling = TRUE
 Initial_wait = 1[s]
 Noe = TRUE
 Noe_time = 2[s]
 Recvr_gain = 60
 Relaxation_delay = 2[s]
 Repetition_time = 3.04333312[s]
 Temp_get = 19.9[dC]

Spectrum

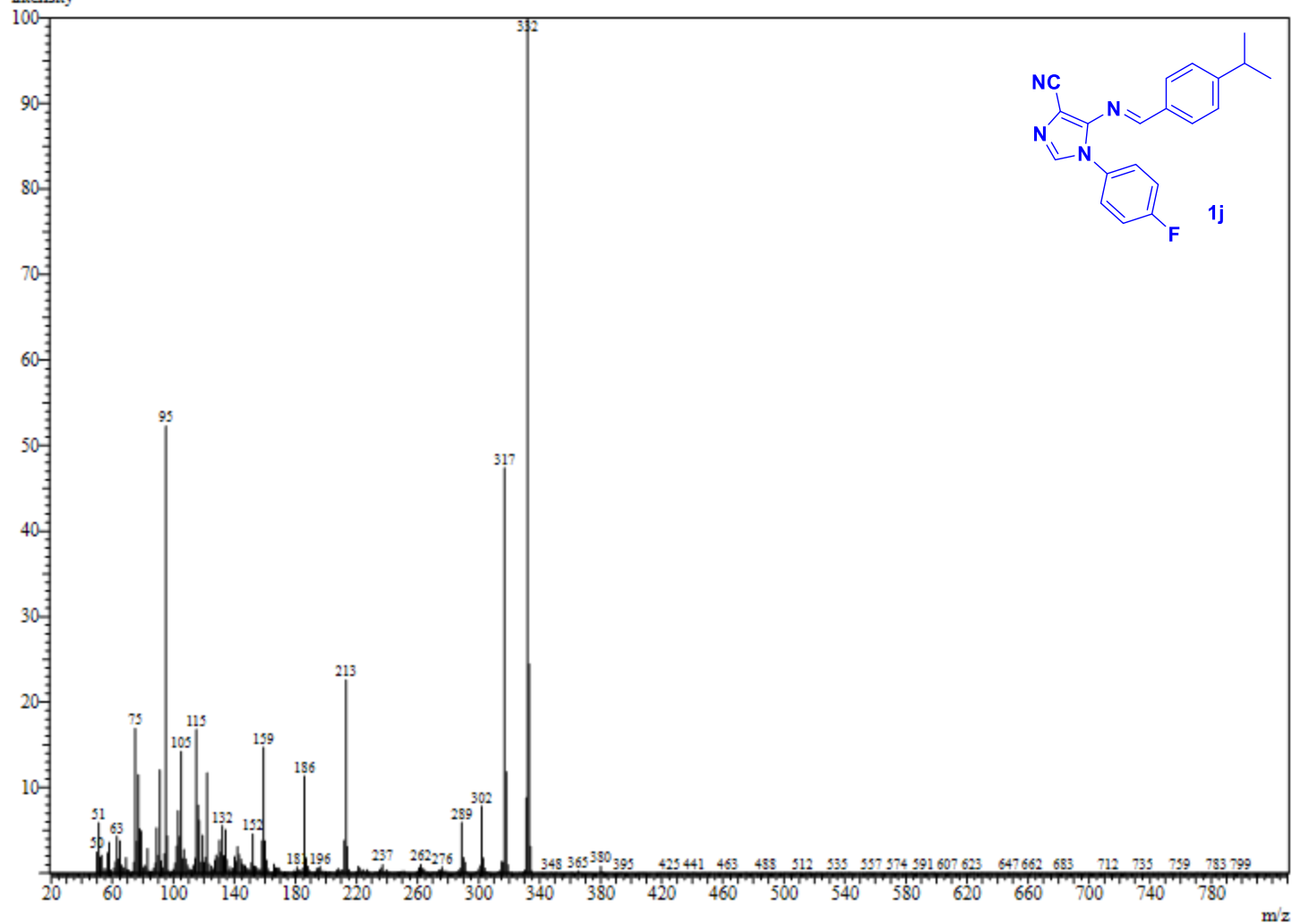
Line#:1 R.Time:4.880(Scan#:677)

MassPeaks:519

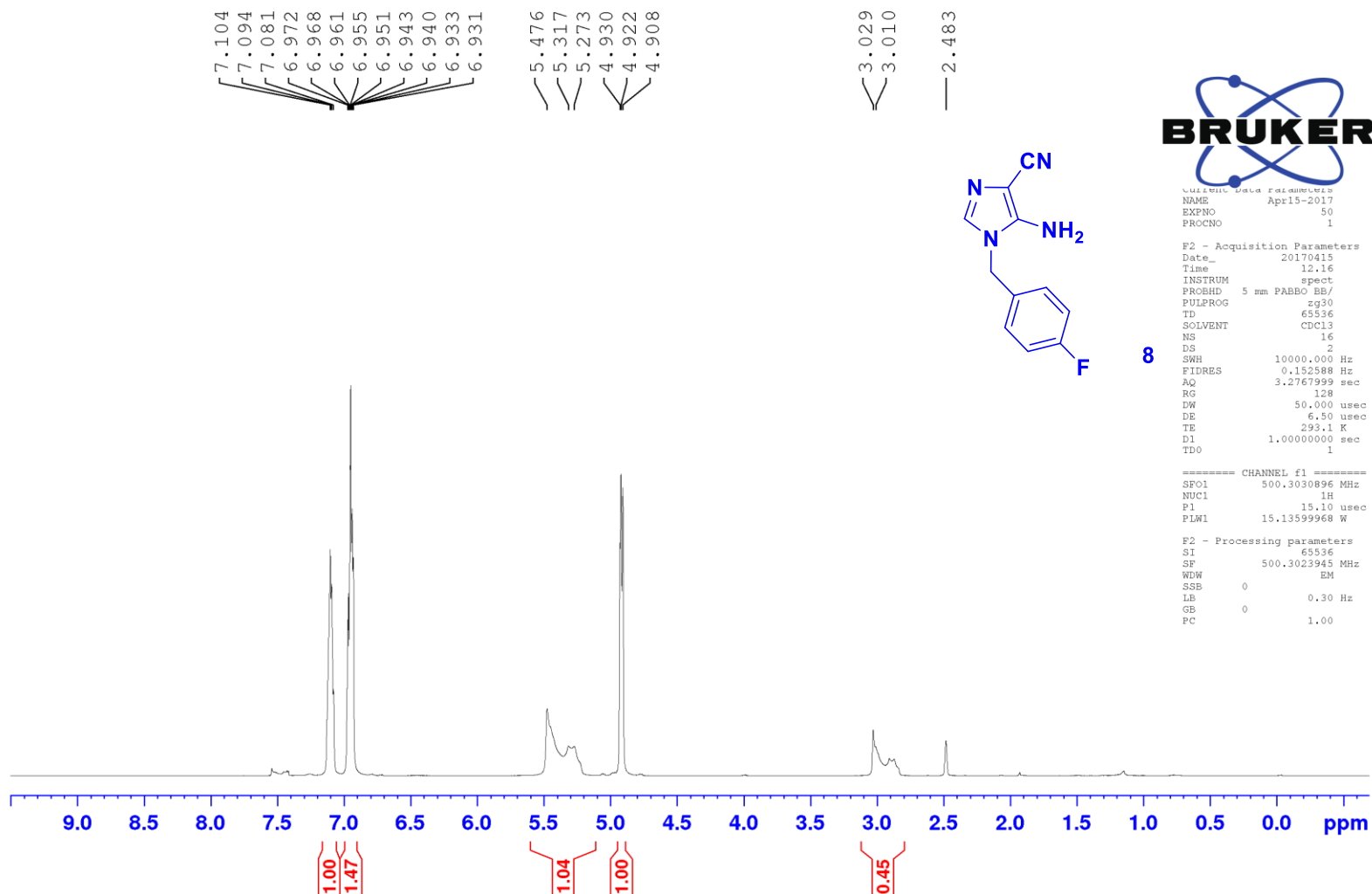
RawMode:Averaged 4.875-4.885(676-678) BasePeak:332(535382)

BG Mode:Calc. from Peak Group 1 - Event 1

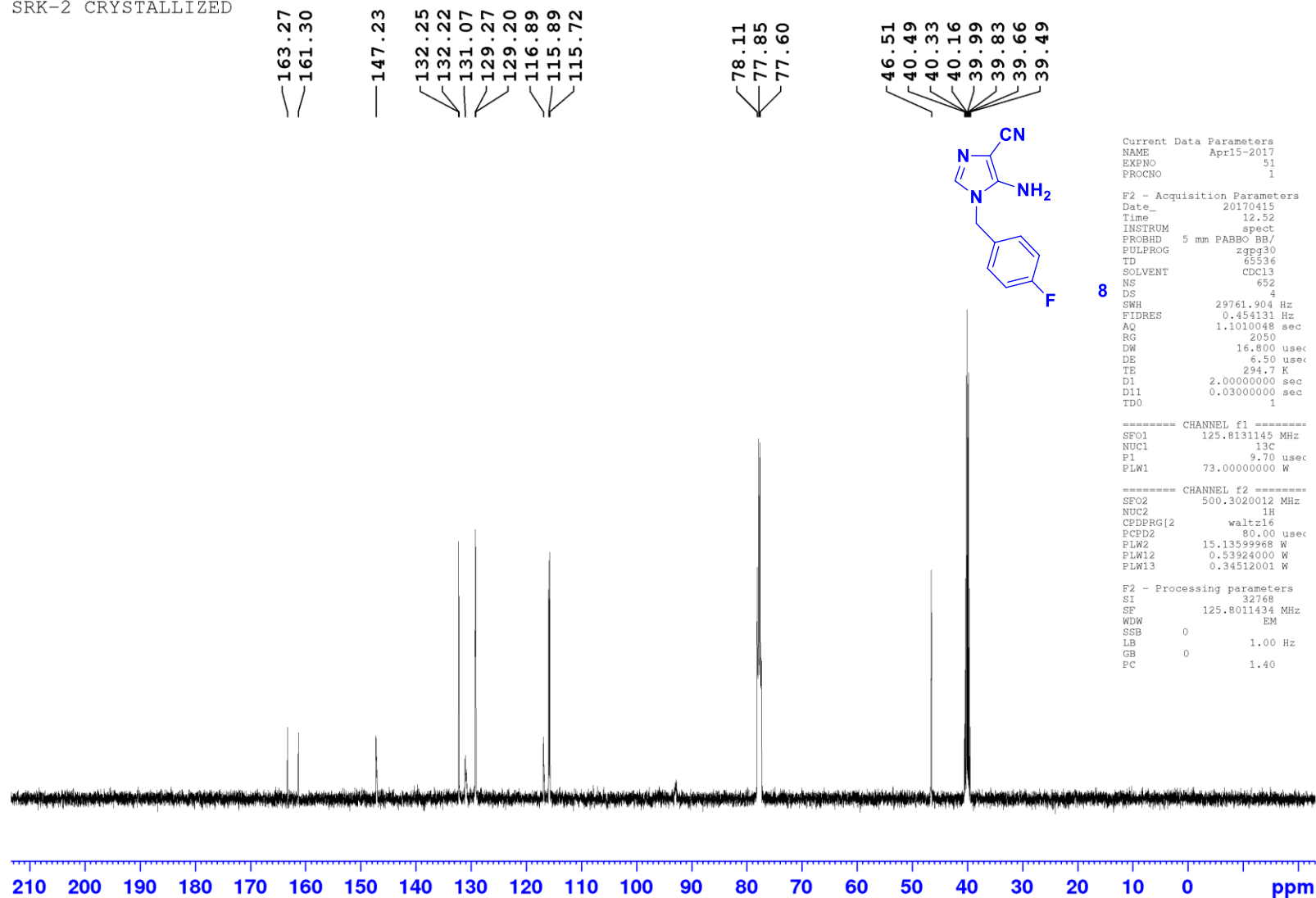
intensity



SRK-2 CRYSTALLIZED



SRK-2 CRYSTALLIZED



Spectrum

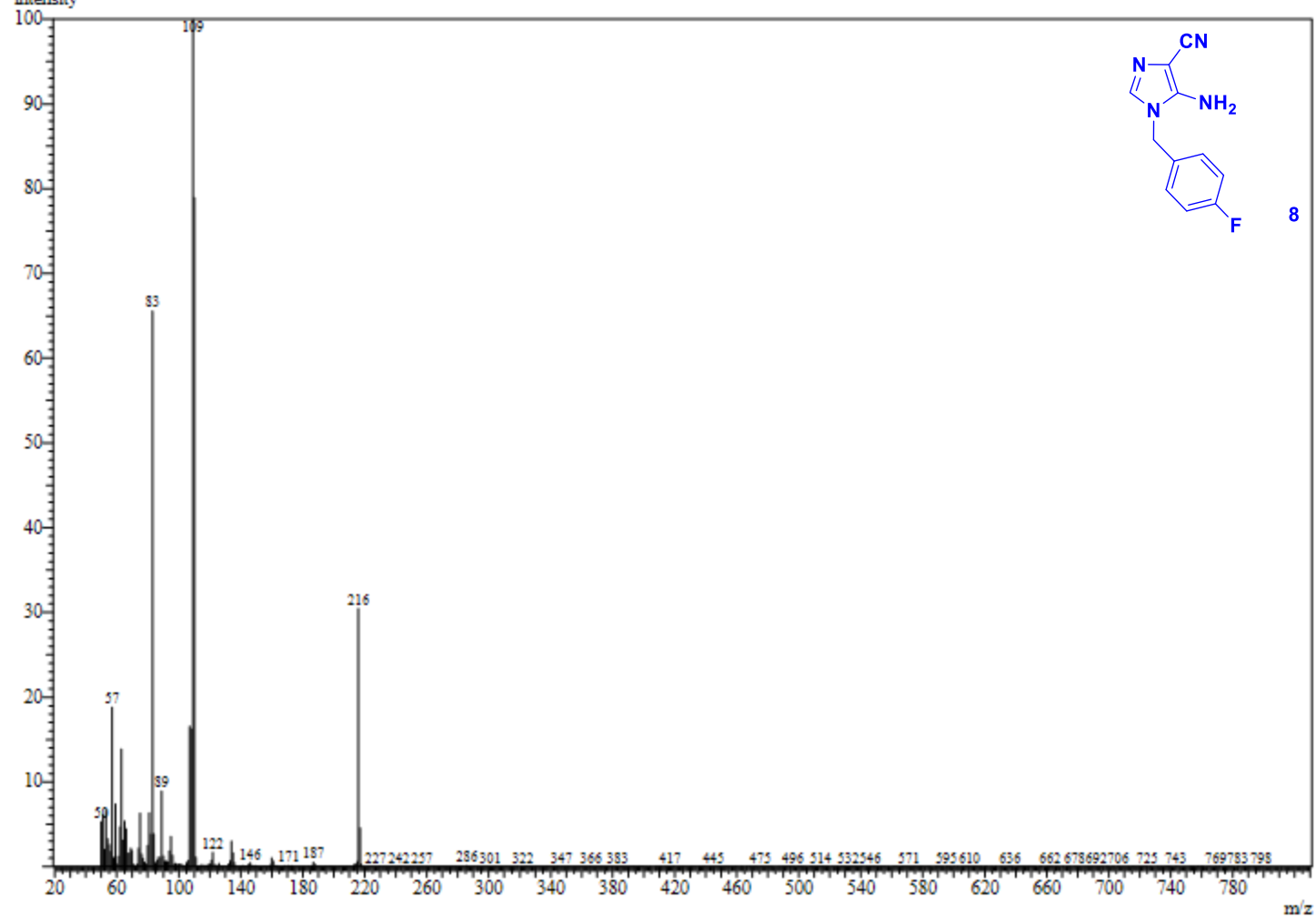
Line#:1 R.Time:6.290(Scan#:959)

MassPeaks:642

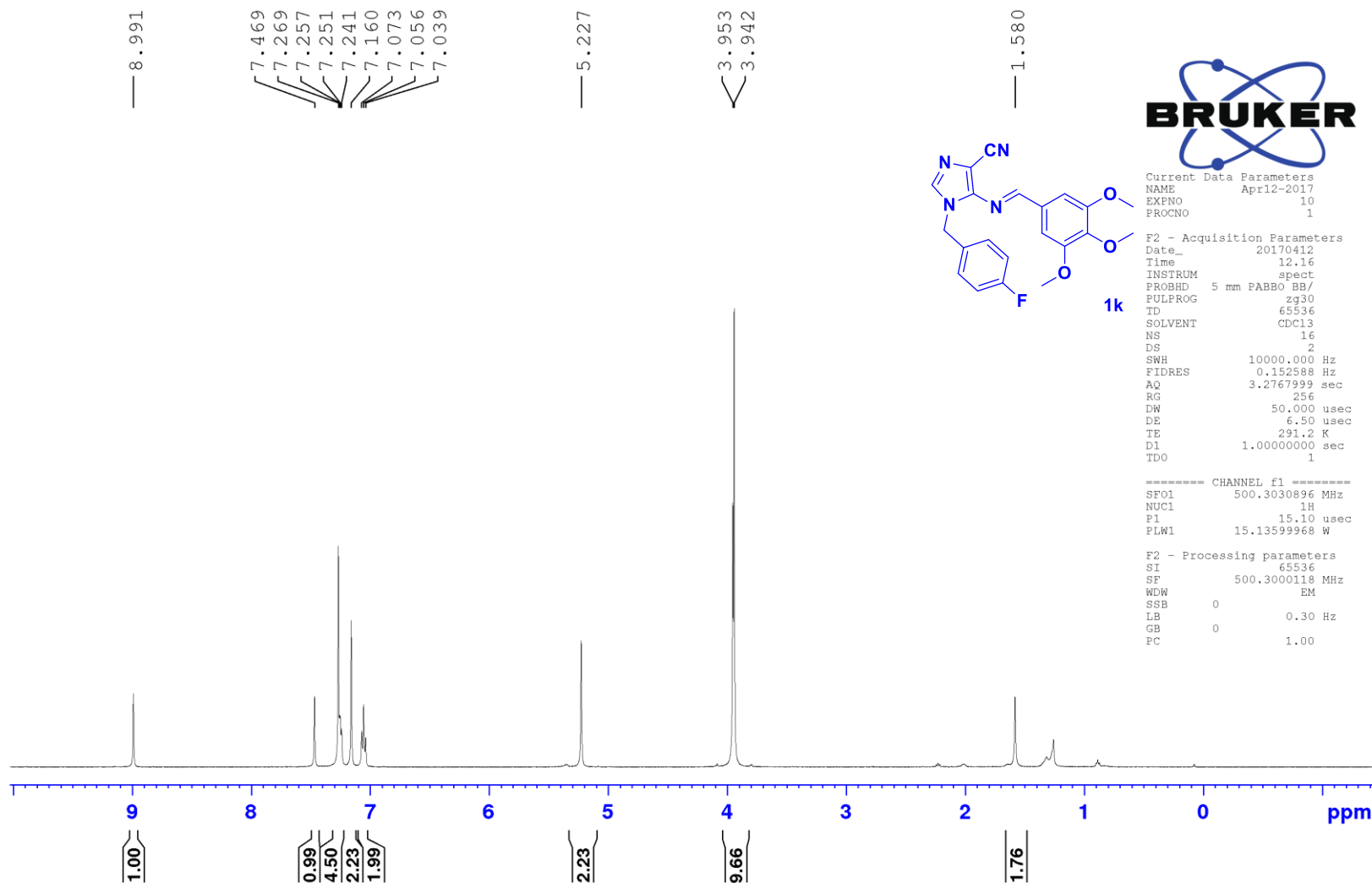
RawMode:Averaged 6.285-6.295(958-960) BasePeak:109(7591332)

BG Mode:Calc. from Peak Group 1 - Event 1

intensity



SA-1



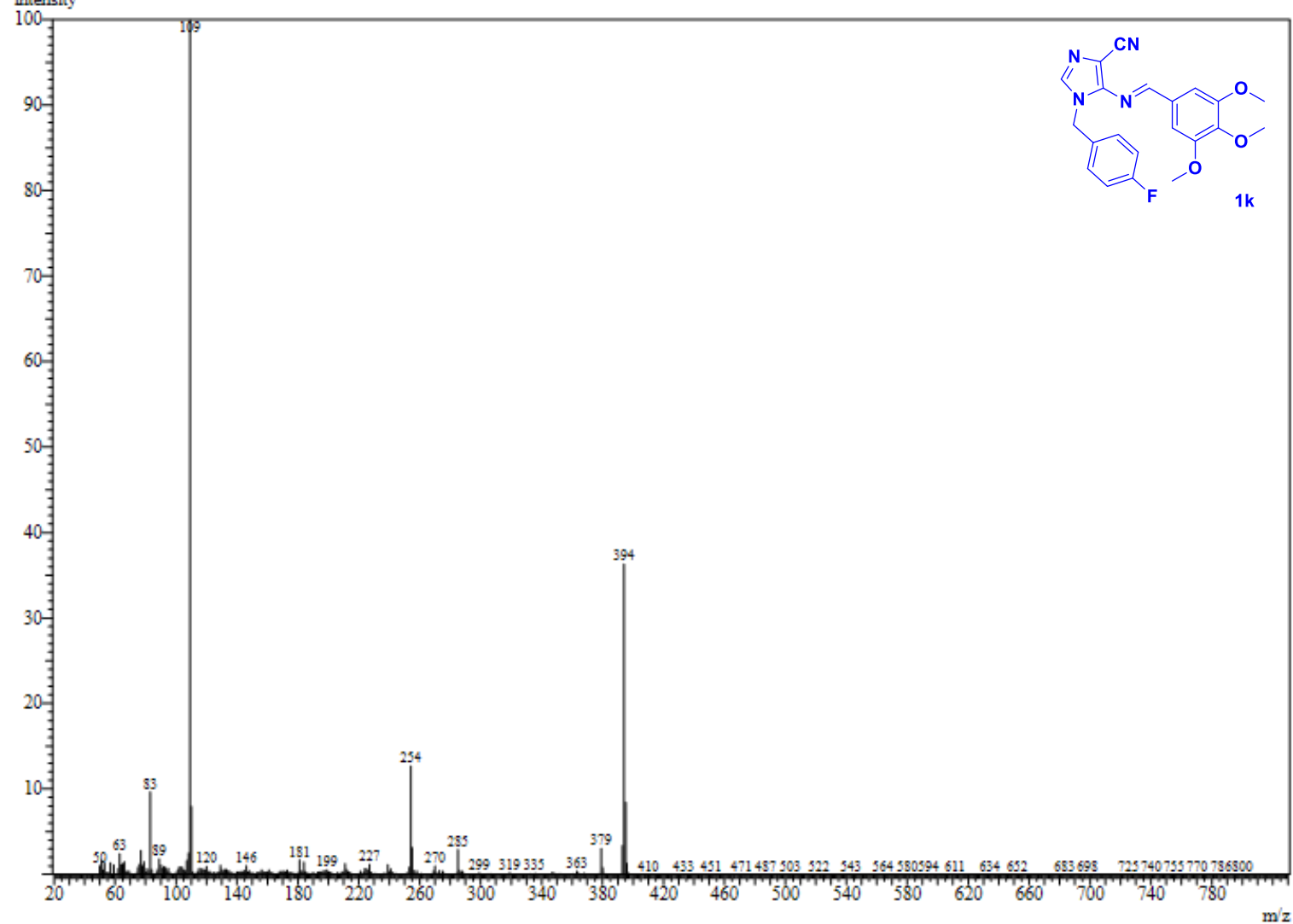
Line#:2 R.Time:6.590(Scan#:1019)

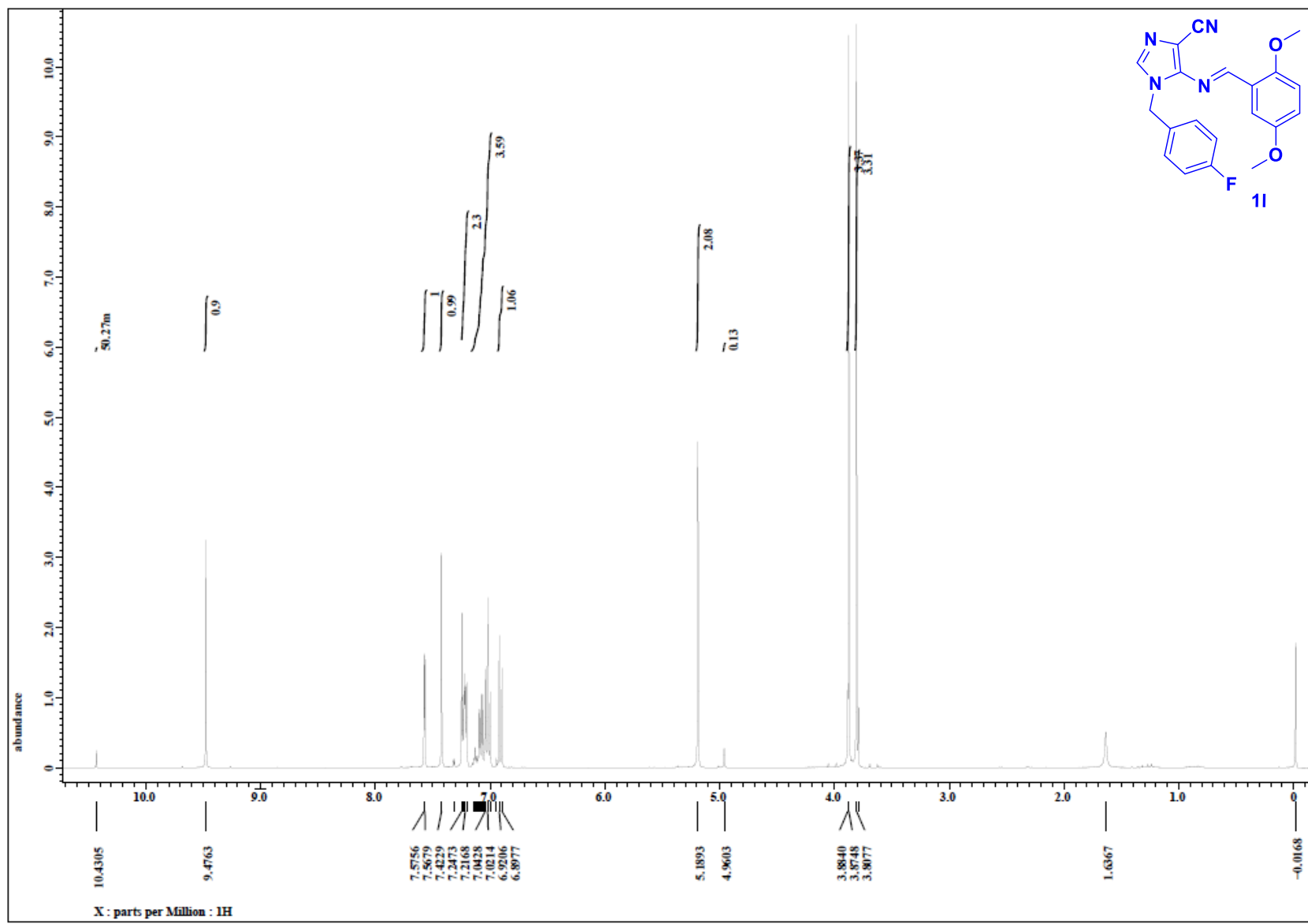
MassPeaks:567

RawMode:Averaged 6.585-6.595(1018-1020) BasePeak:109(2294380)

BG Mode:Calc. from Peak Group 1 - Event 1

intensity





Elemental Composition Report

Page 1

Single Mass Analysis

Tolerance = 10.0 PPM / DBE: min = -1.5, max = 50.0

Element prediction: Off

Number of isotope peaks used for i-FIT = 5

Monoisotopic Mass, Even Electron Ions

43 formula(e) evaluated with 1 results within limits (up to 50 best isotopic matches for each mass)

Elements Used:

C: 9-22 H: 11-30 N: 0-5 O: 0-3 F: 0-1

Sample Name : SA-2

IITRPR

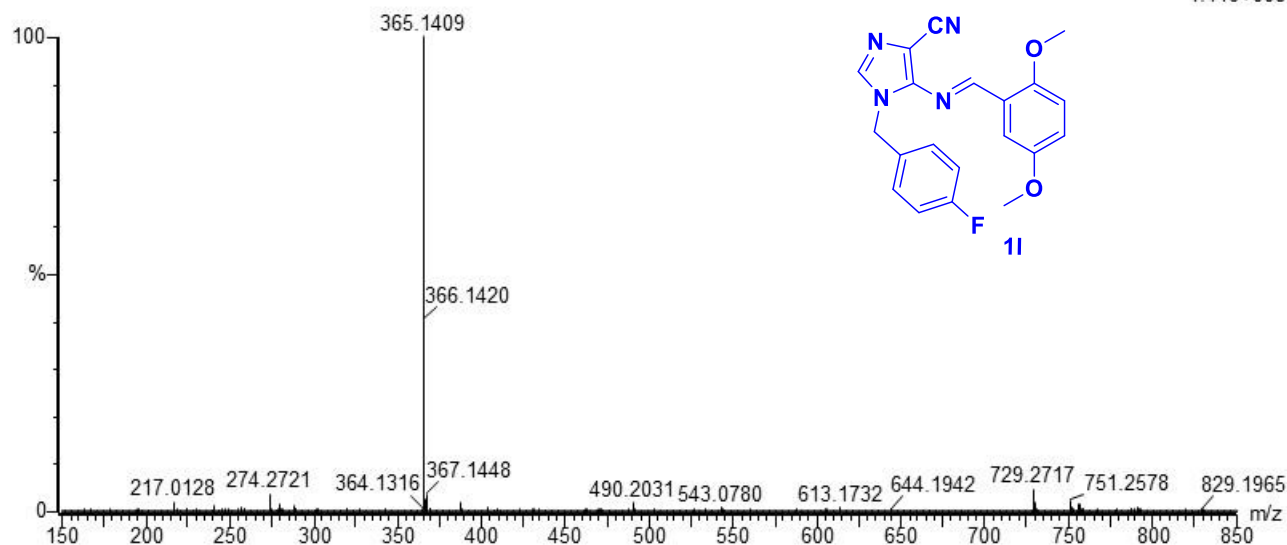
XEVO G2-XS QTOF

Test Name : HRMS-1

160120-SA-2 12 (0.131)

1: TOF MS ES+

1.44e+008



Minimum: -1.5
Maximum: 5.0 10.0 50.0

Mass	Calc. Mass	mDa	PPM	DBE	i-FIT	Norm	Conf(%)	Formula
365.1409	365.1414	-0.5	-1.4	13.5	1846.9	n/a	n/a	C20 H18 N4 O2 F

Spectrum

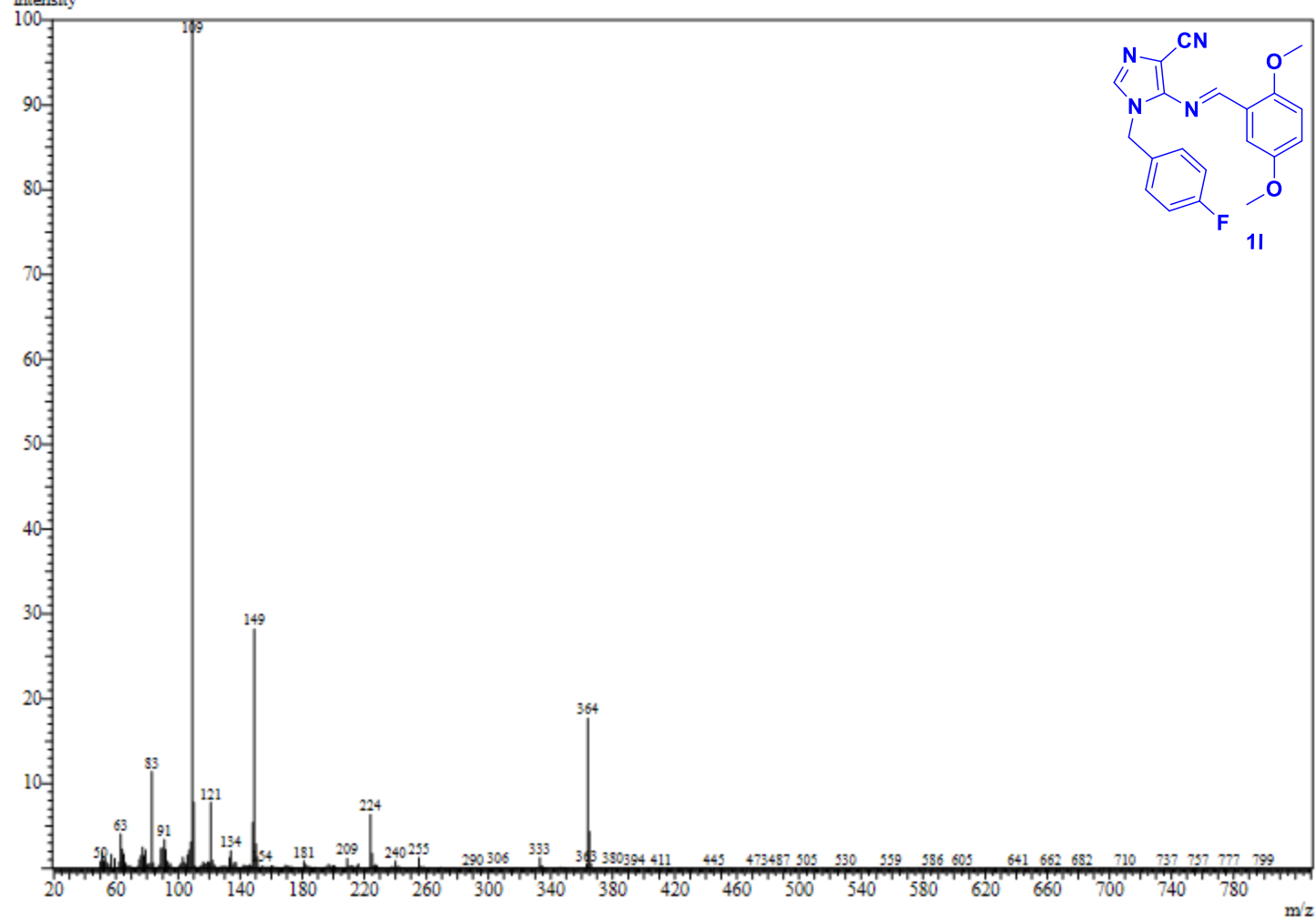
Line#:1 R.Time:5.230(Scan#:747)

MassPeaks:585

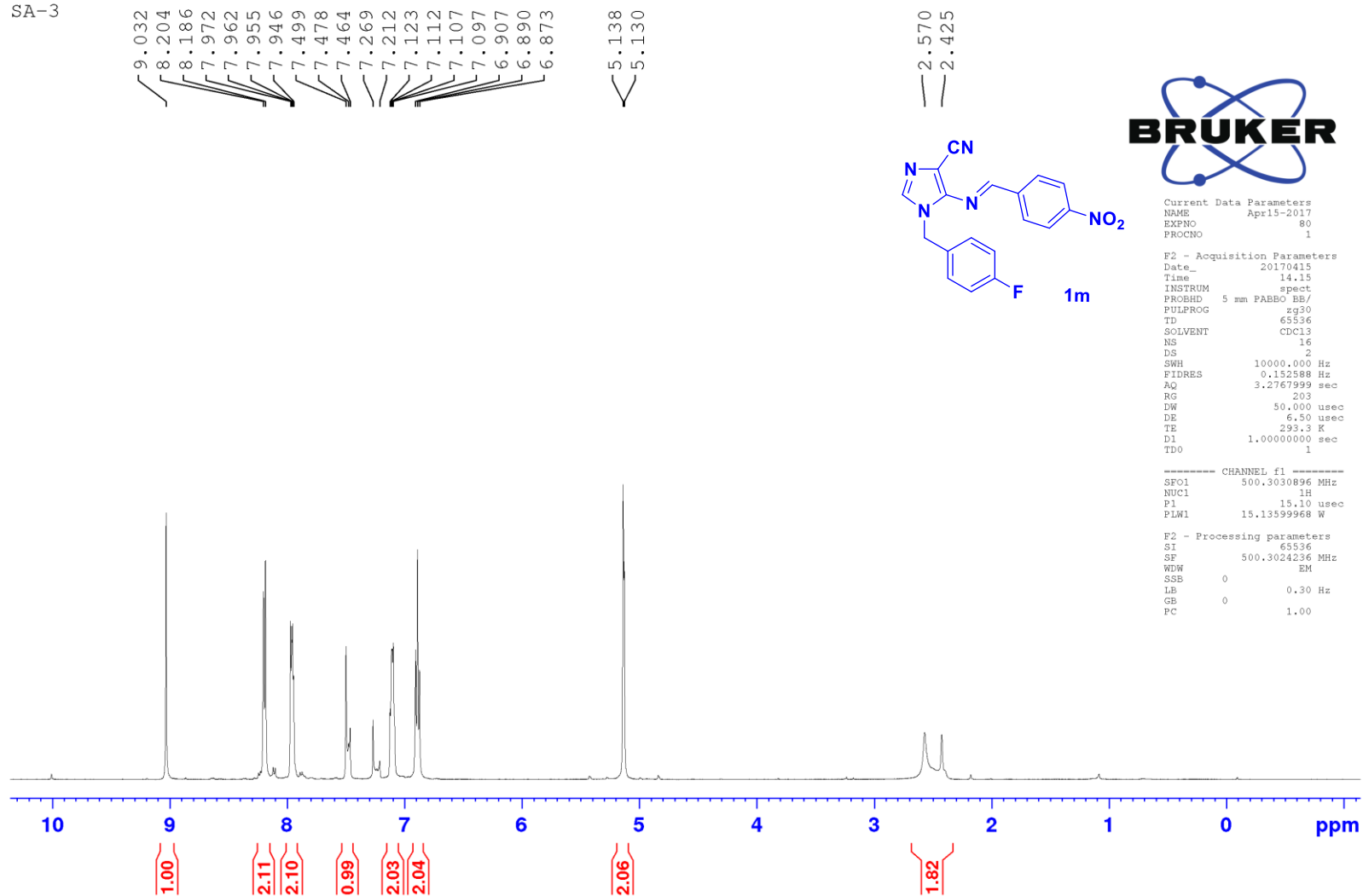
RawMode:Averaged 5.225-5.235(746-748) BasePeak:109(5182759)

BGMode:Calc. from Peak Group 1 - Event 1

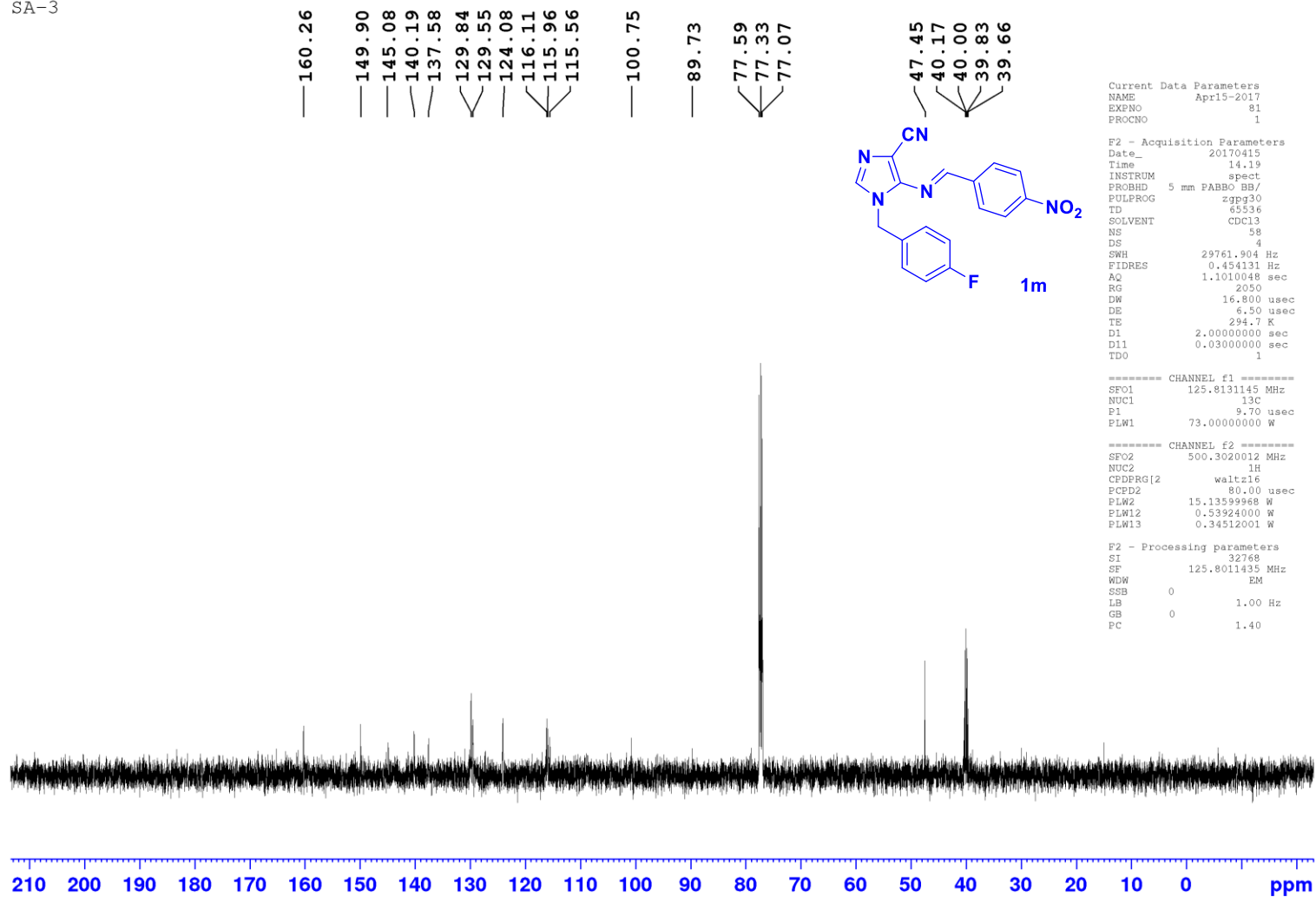
intensity



SA-3



SA-3



Spectrum

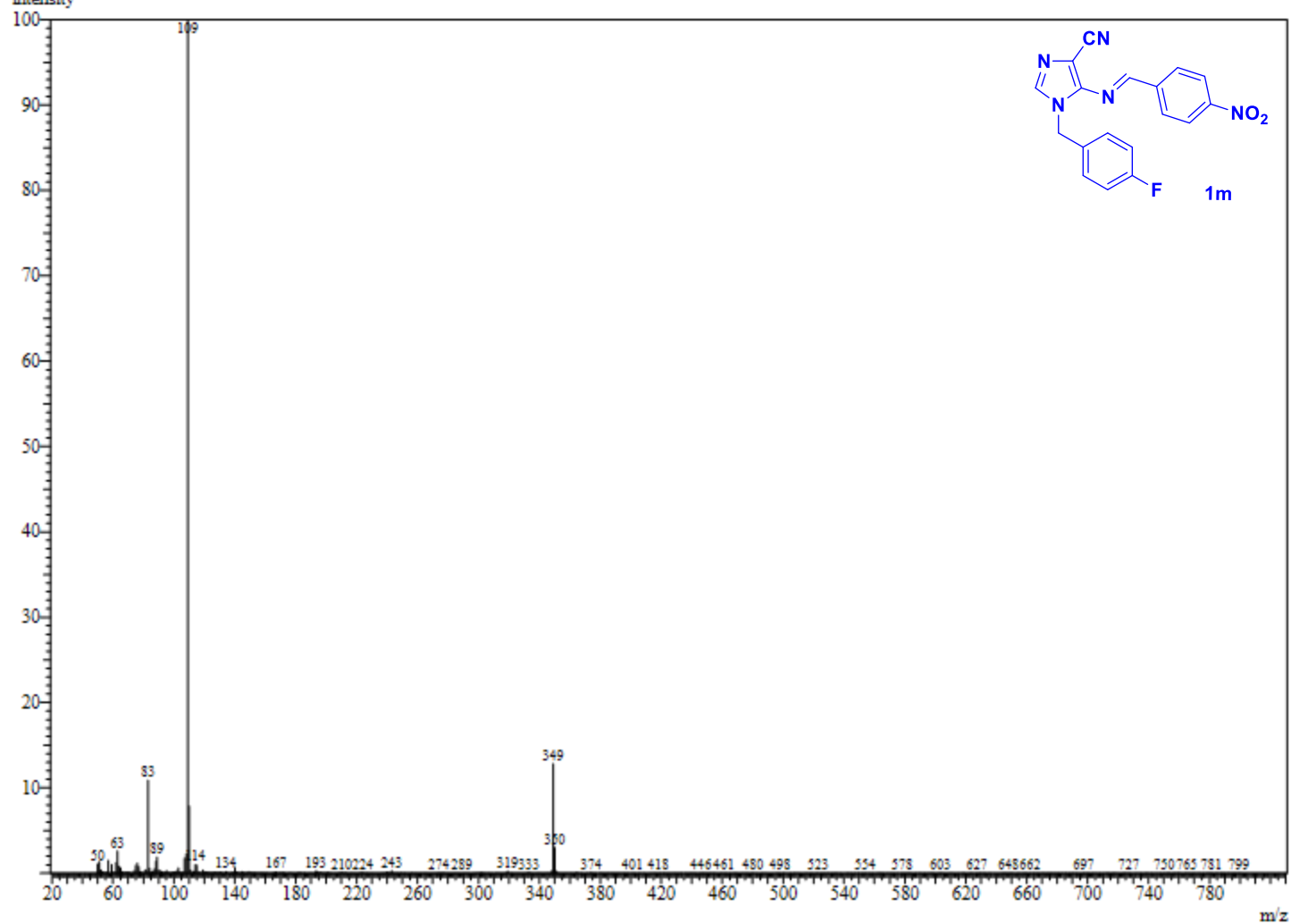
Line#:1 R.Time:5.910(Scan#:883)

MassPeaks:561

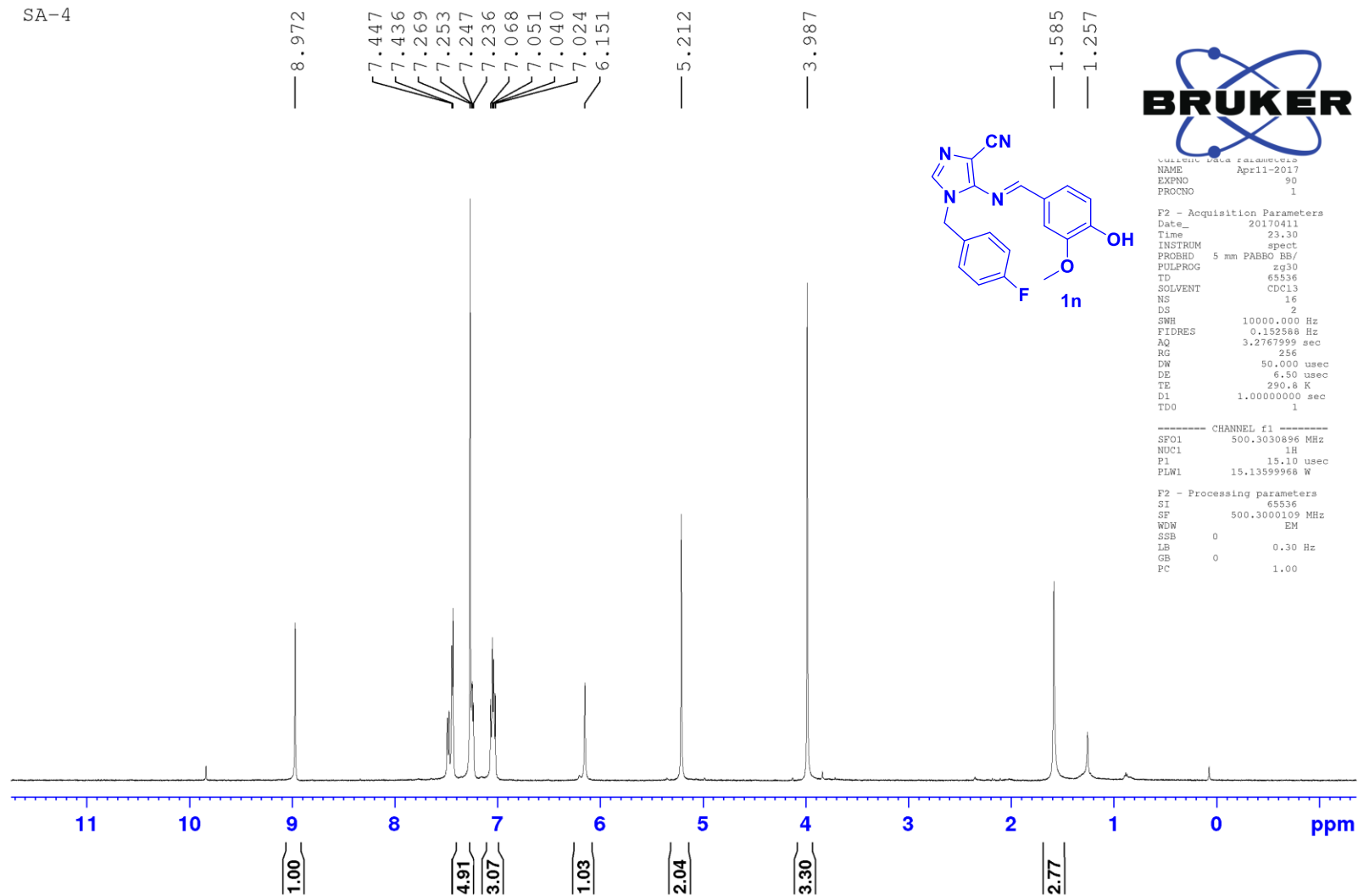
RawMode:Averaged 5.905-5.915(882-884) BasePeak:109(2769141)

BGMode:Calc. from Peak Group 1 - Event 1

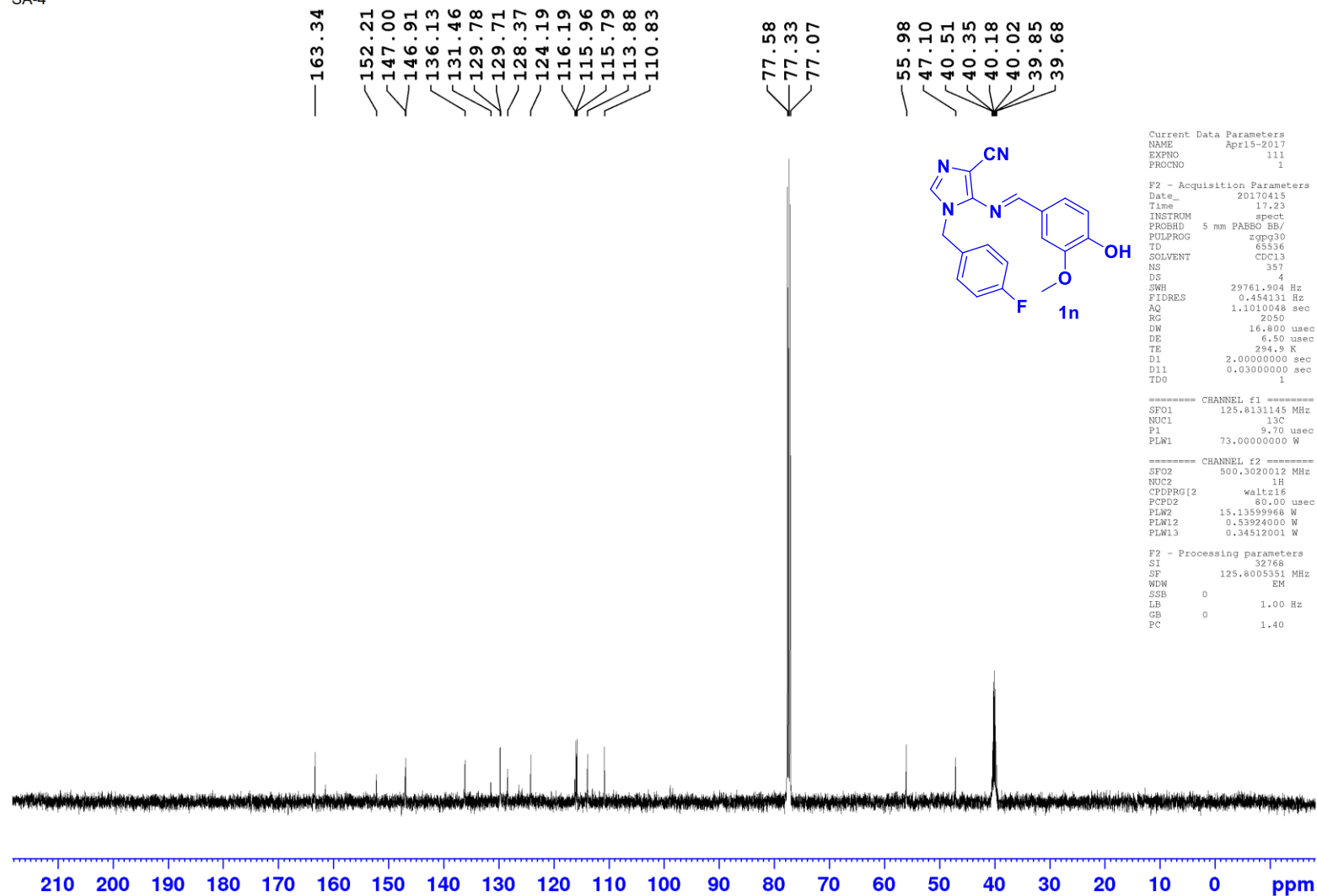
intensity



SA-4



SA-4



Spectrum

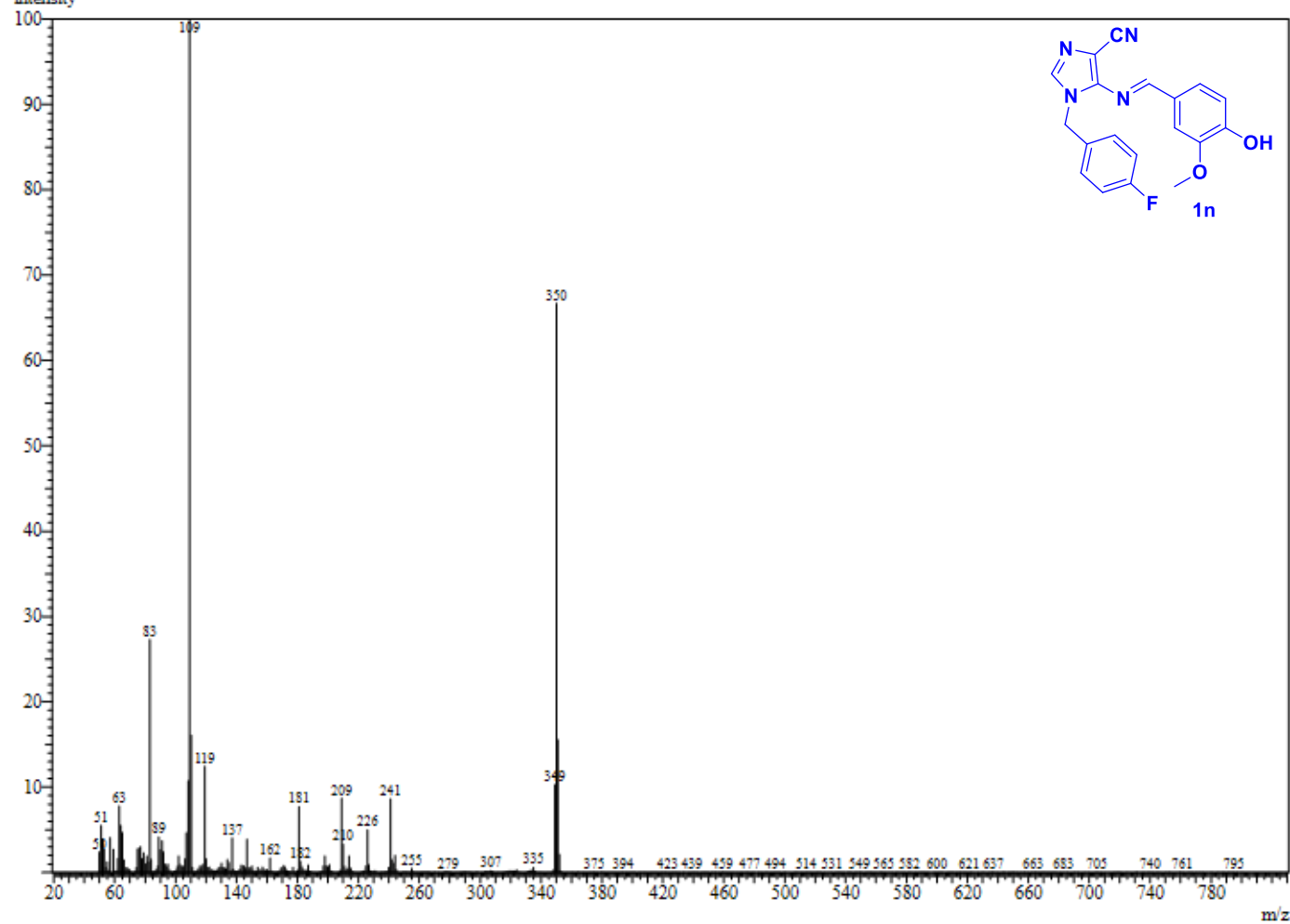
Line#:1 R.Time:6.445(Scan#:990)

MassPeaks:621

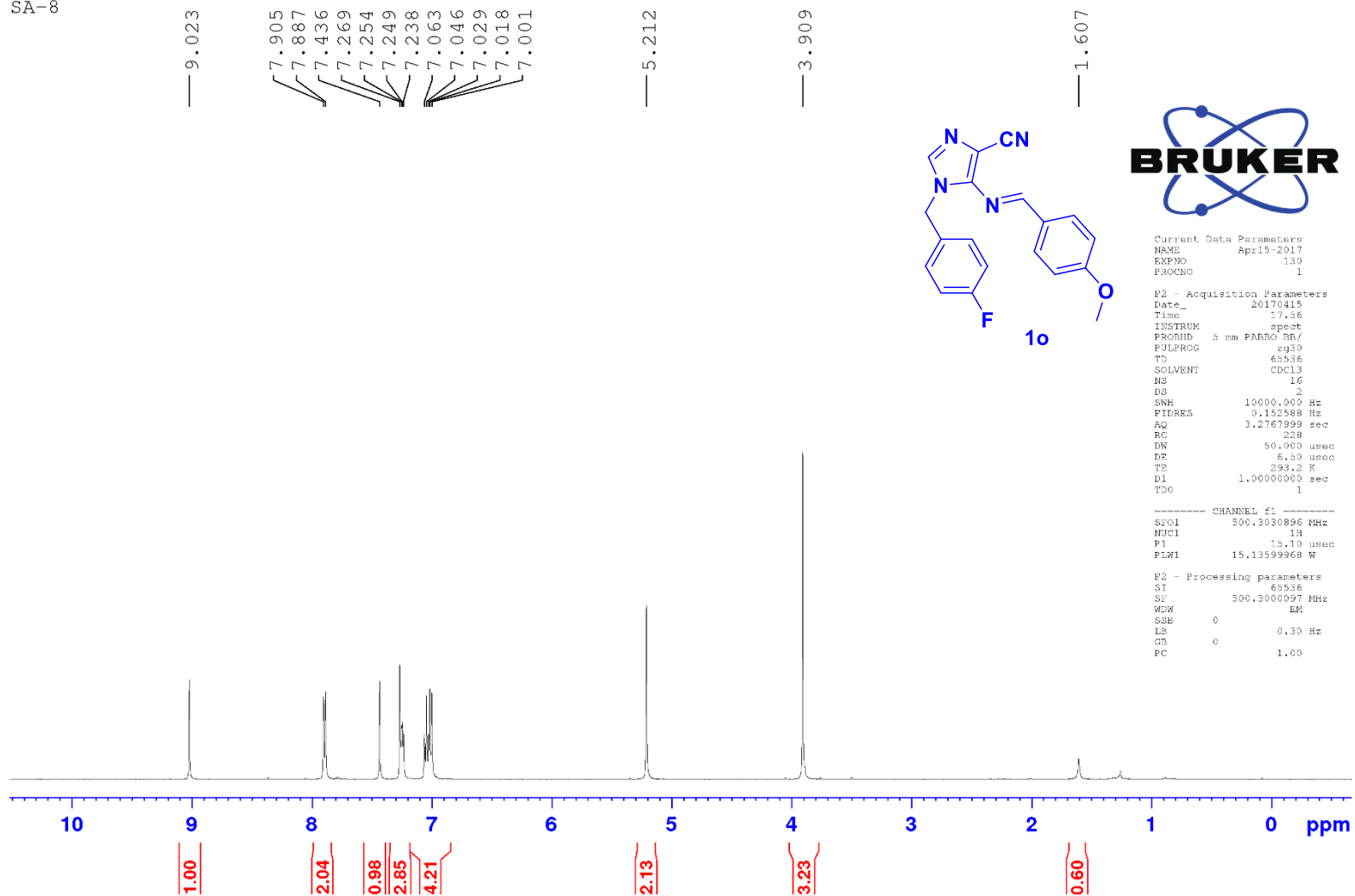
RawMode:Averaged 6.440-6.450(989-991) BasePeak:109(7420310)

BG Mode:Calc. from Peak Group 1 - Event 1

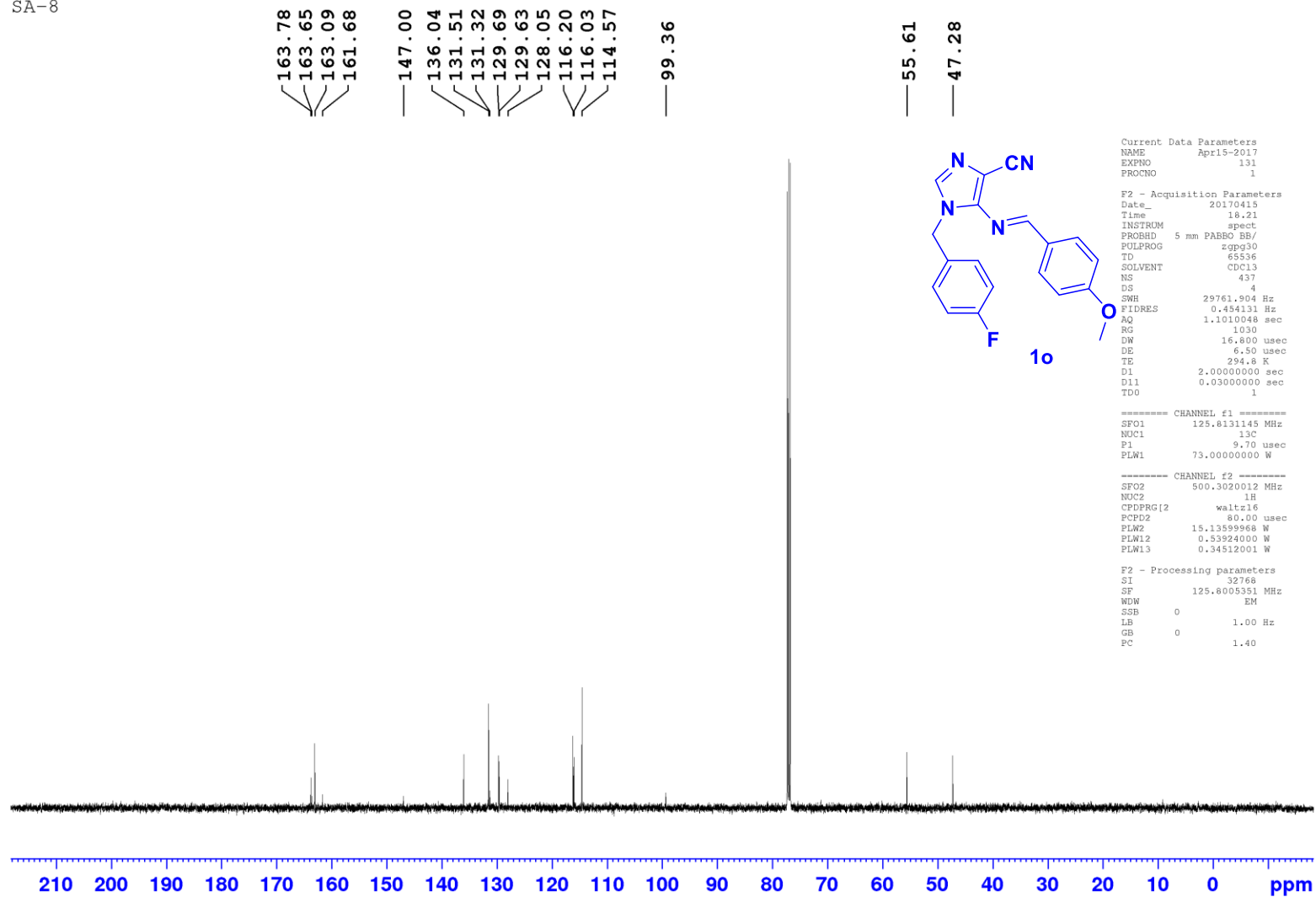
intensity



SA-8



SA-8

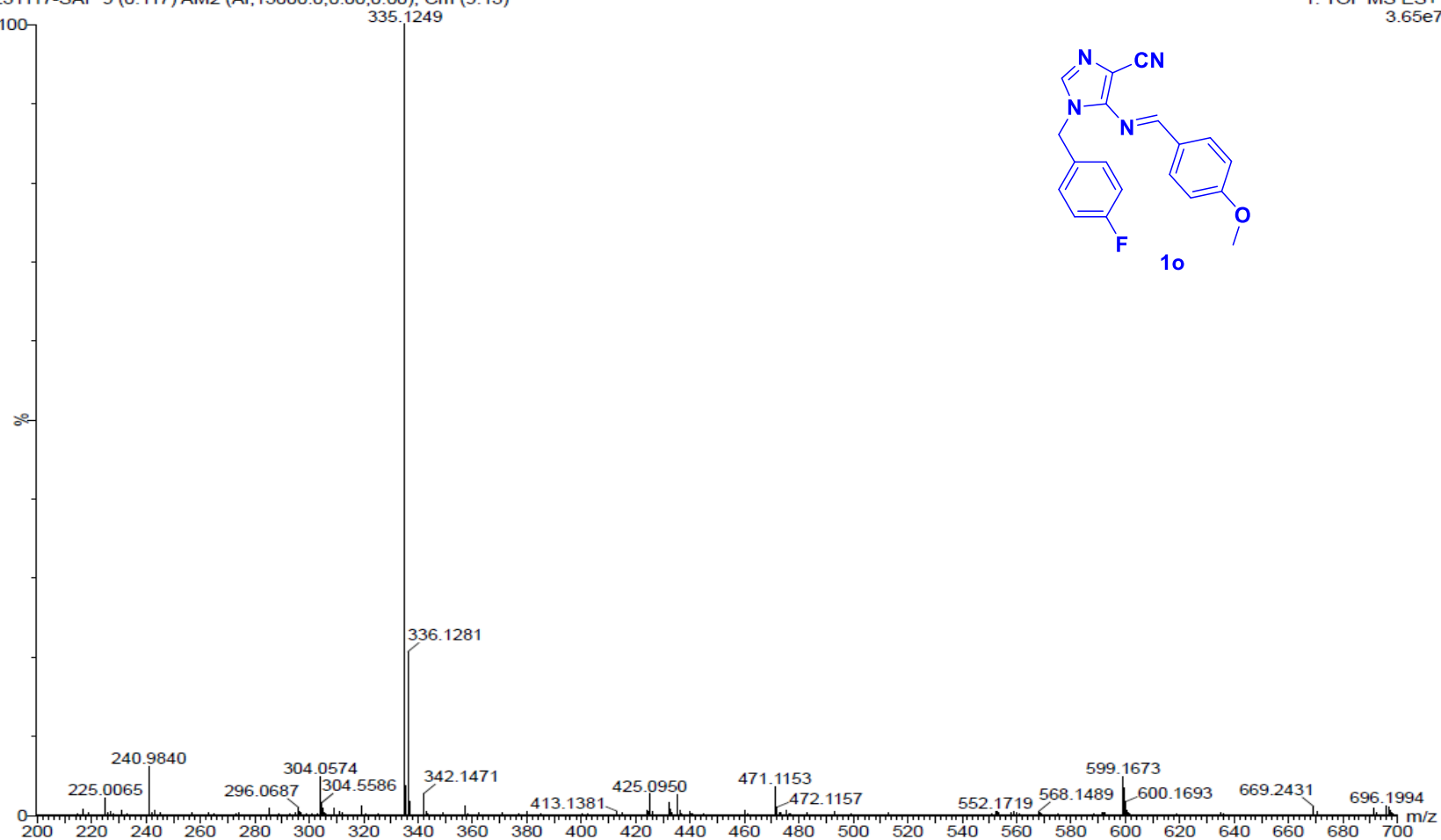


Sample Name : SAP
Test Name : HRMS-1
231117-SAP 9 (0.117) AM2 (Ar,15000.0,0.00,0.00); Cm (9:13)

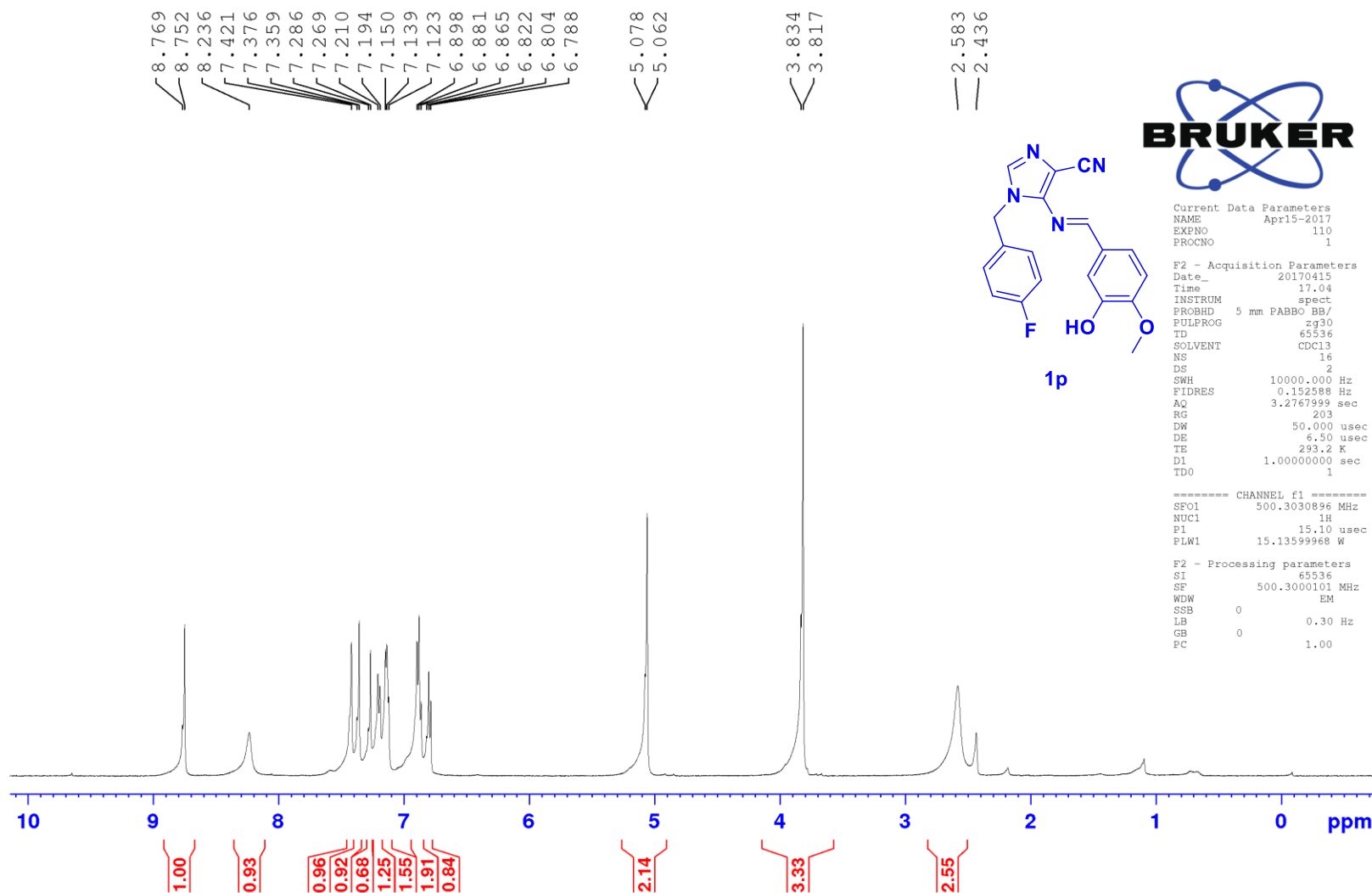
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XEVO G2-XS QTOF

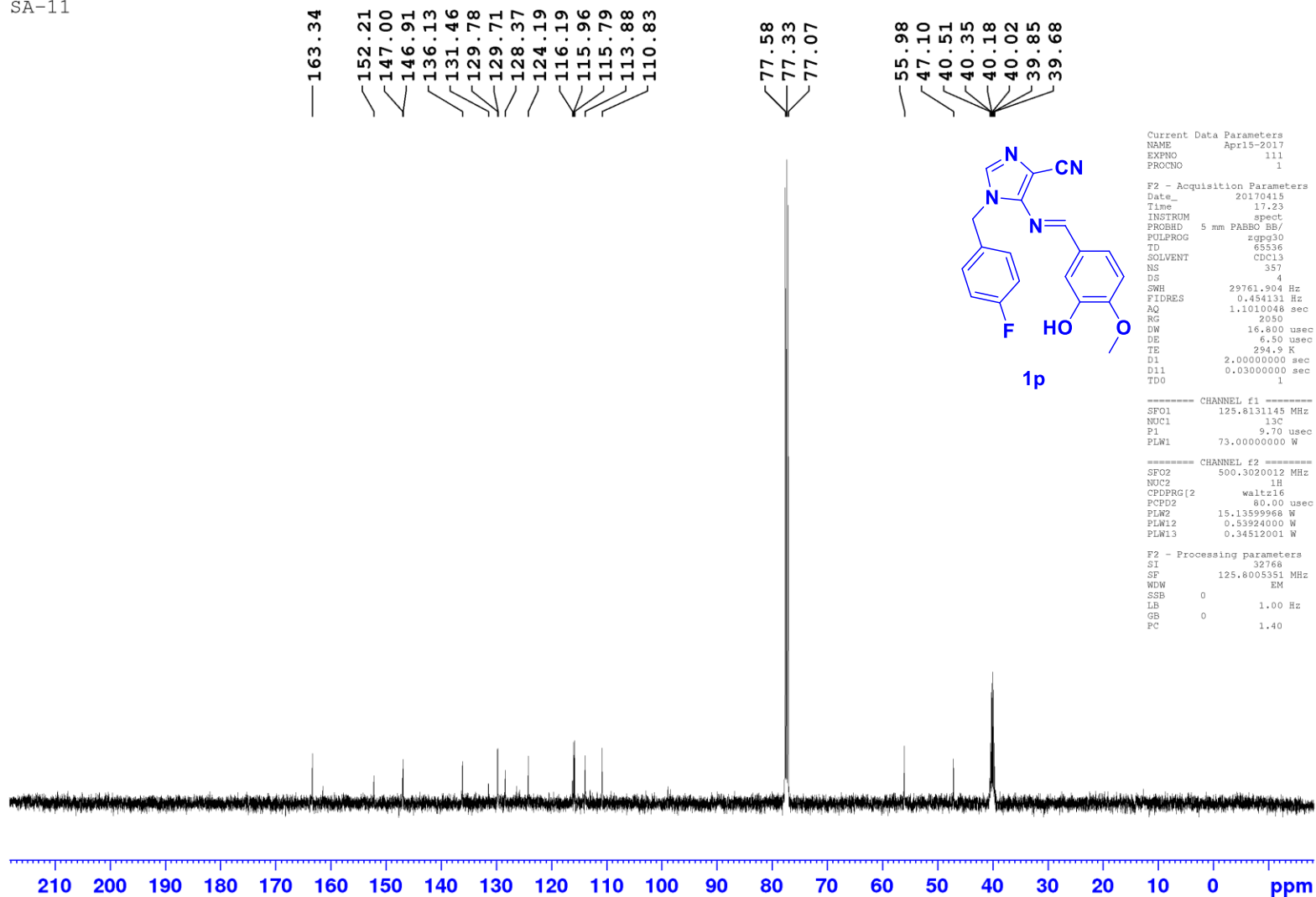
1: TOF MS ES+
3.65e7



SA-11



SA-11



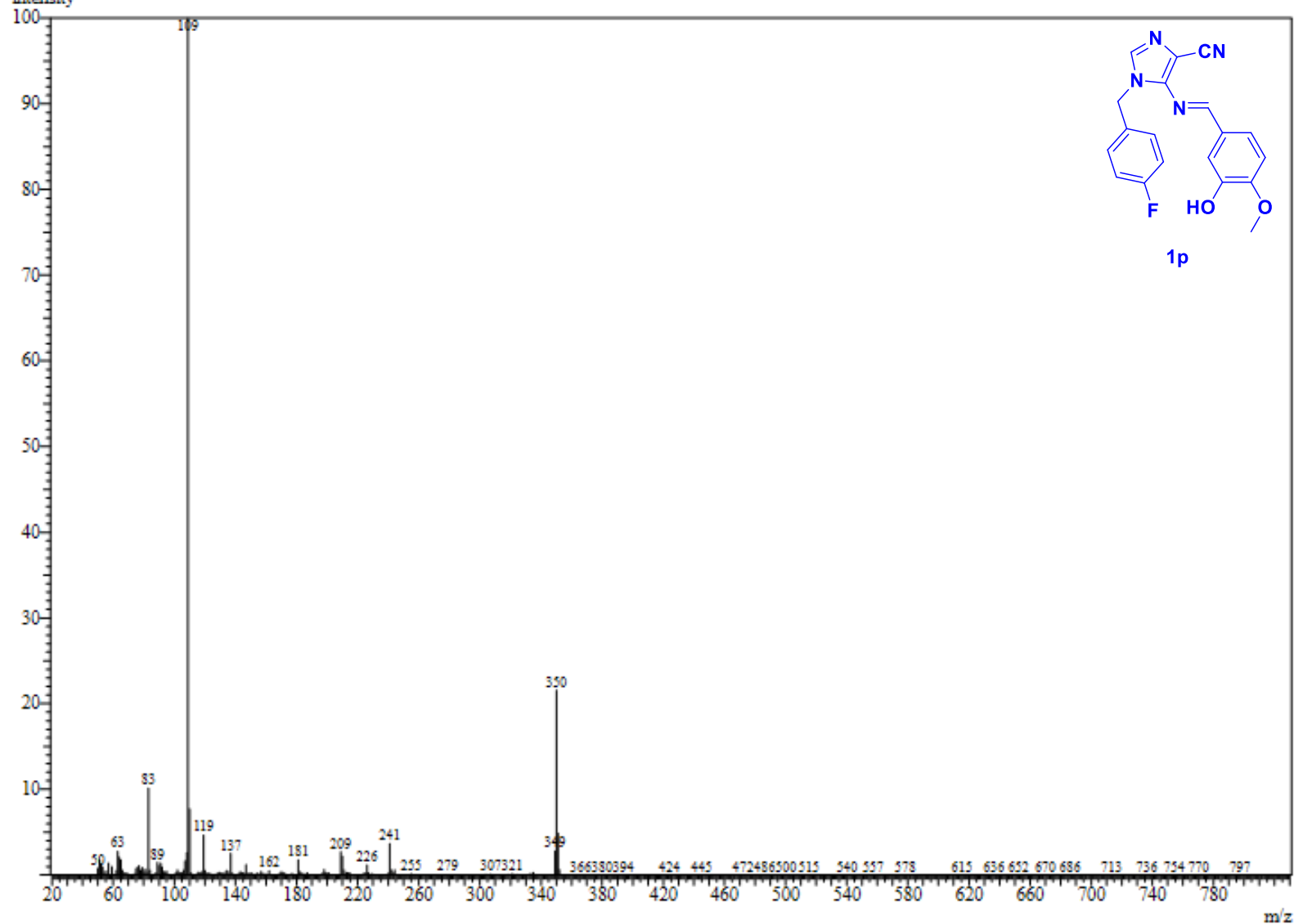
Line#:2 R.Time:5.600(Scan#:821)

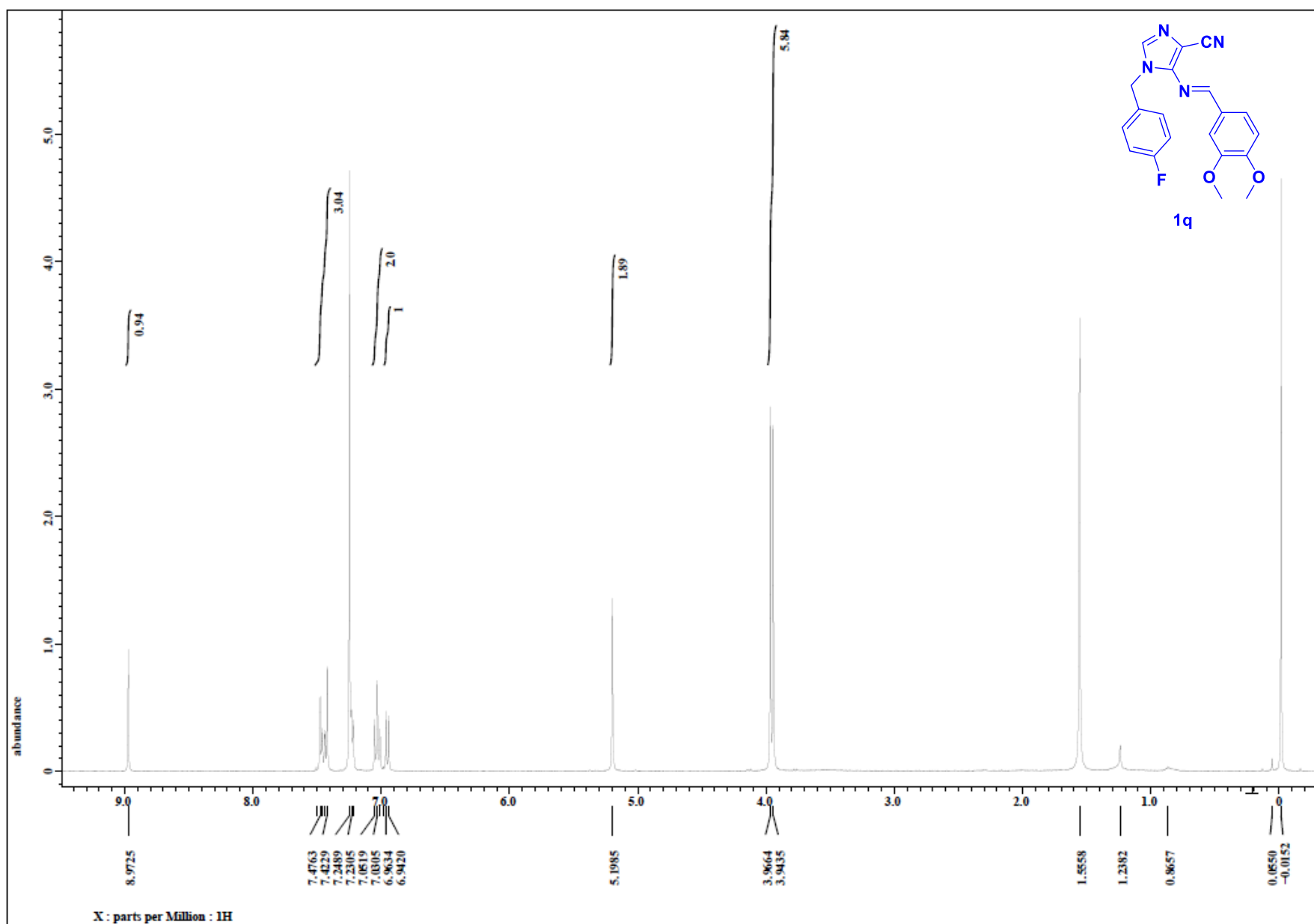
MassPeaks:564

RawMode:Averaged 5.595-5.605(820-822) BasePeak:109(3565792)

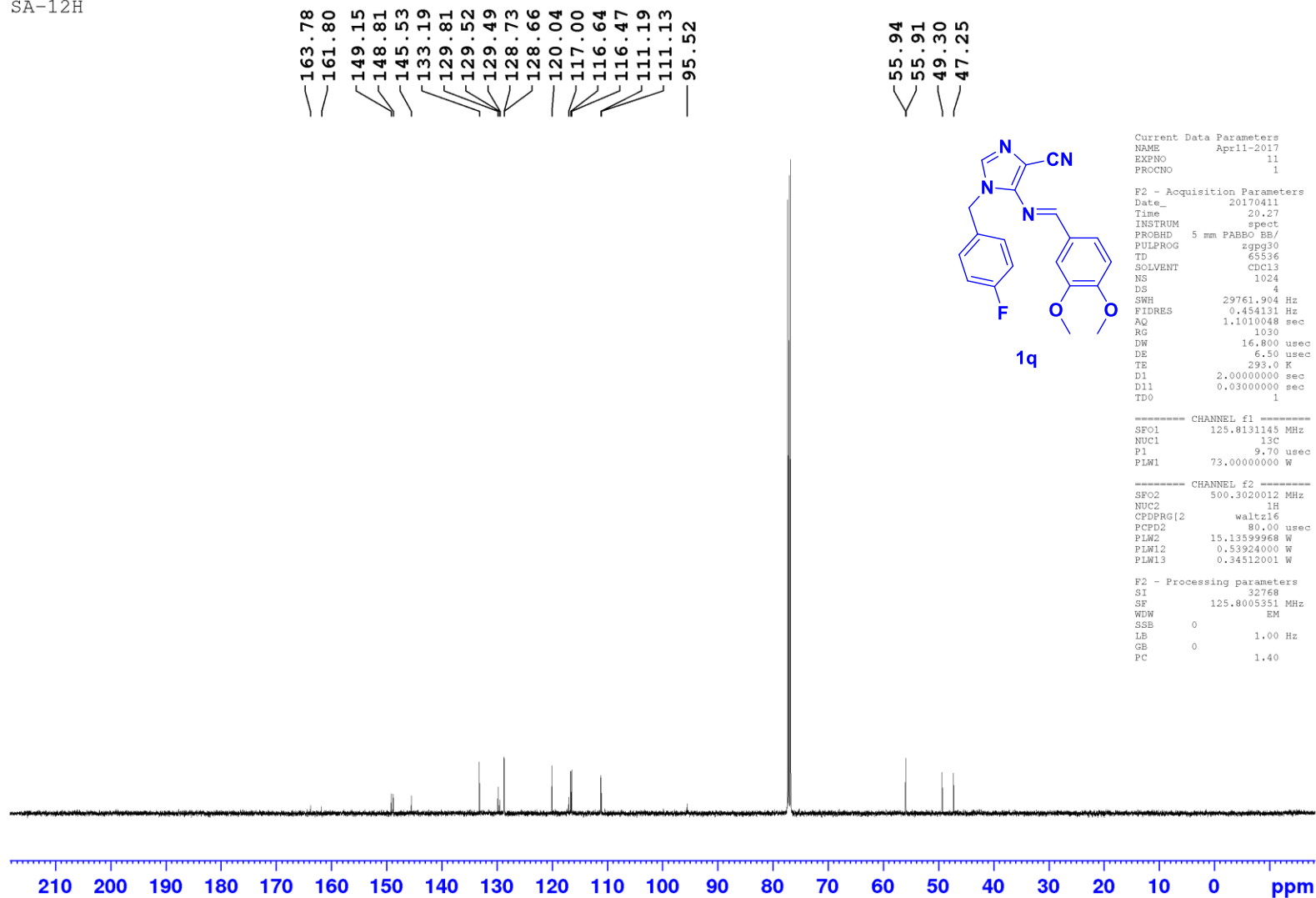
BG Mode:Calc. from Peak Group 1 - Event 1

intensity





SA-12H



Elemental Composition Report

Page 1

Single Mass Analysis

Tolerance = 10.0 PPM / DBE: min = -1.5, max = 50.0

Element prediction: Off

Number of isotope peaks used for i-FIT = 5

Monoisotopic Mass, Even Electron Ions

43 formula(e) evaluated with 1 results within limits (up to 50 best isotopic matches for each mass)

Elements Used:

C: 9-22 H: 11-30 N: 0-5 O: 0-3 F: 0-1

Sample Name : SA-12

IITRPR

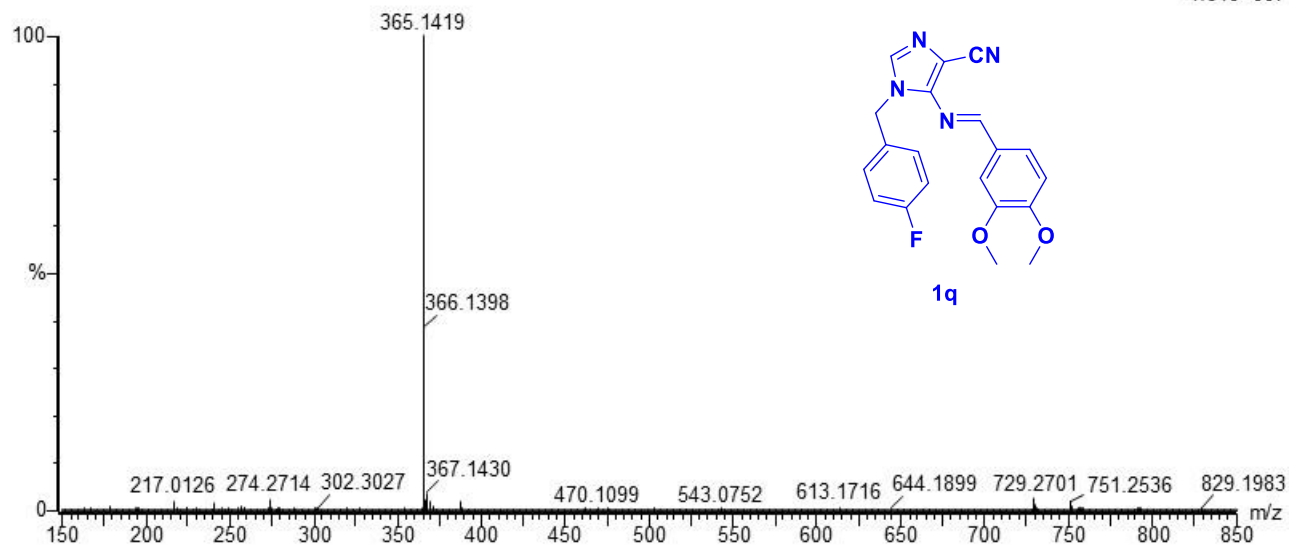
XEVO G2-XS QTOF

Test Name : HRMS-1

160120-SA-12 17 (0.174)

1: TOF MS ES+

4.61e+007



Minimum: -1.5

Maximum: 5.0 10.0 50.0

Mass	Calc. Mass	mDa	PPM	DBE	i-FIT	Norm	Conf(%)	Formula
365.1419	365.1414	0.5	1.4	13.5	2169.2	n/a	n/a	C ₂₀ H ₁₈ N ₄ O ₂ F

Spectrum

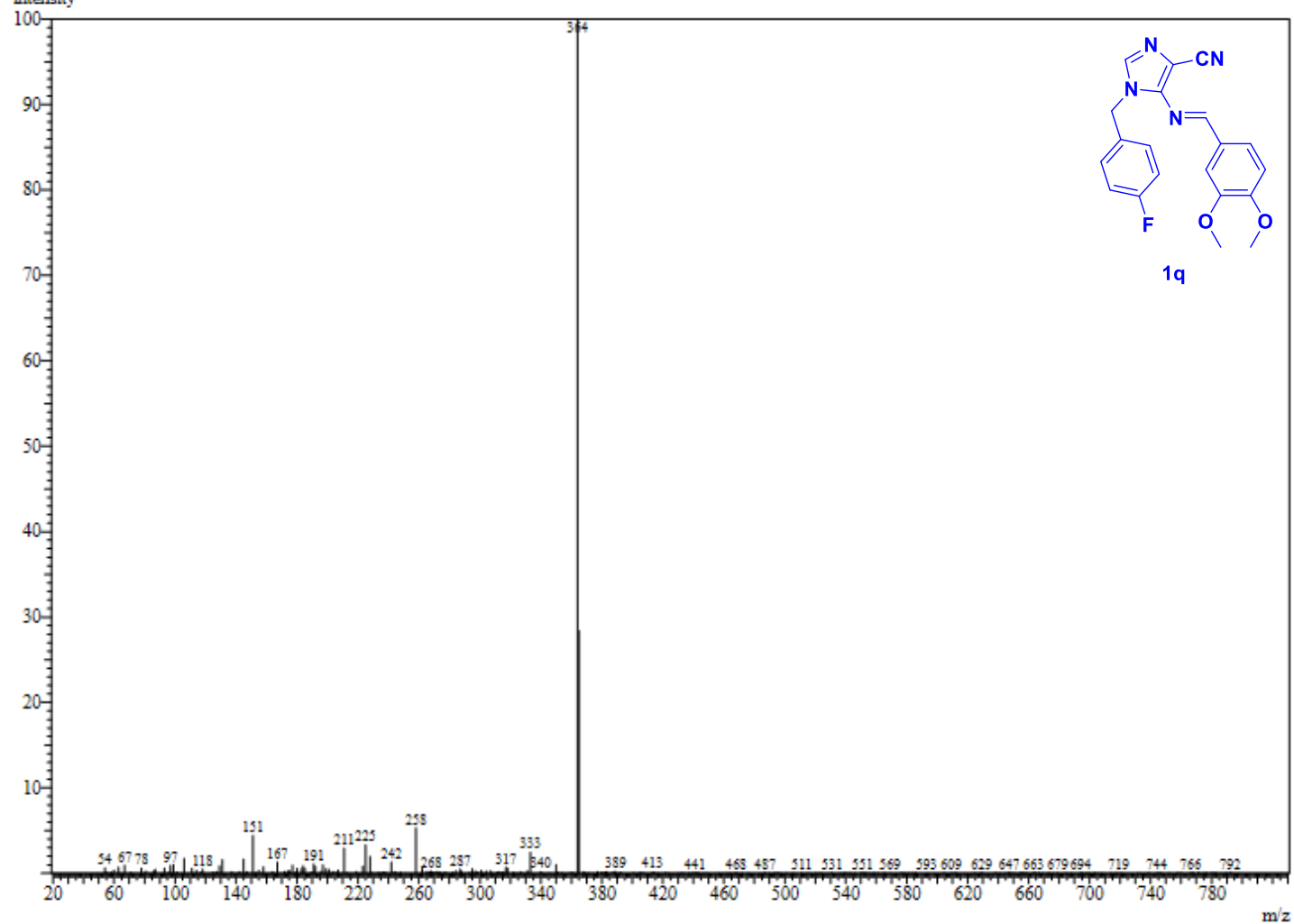
Line#:1 R.Time:6.395(Scan#:980)

MassPeaks:305

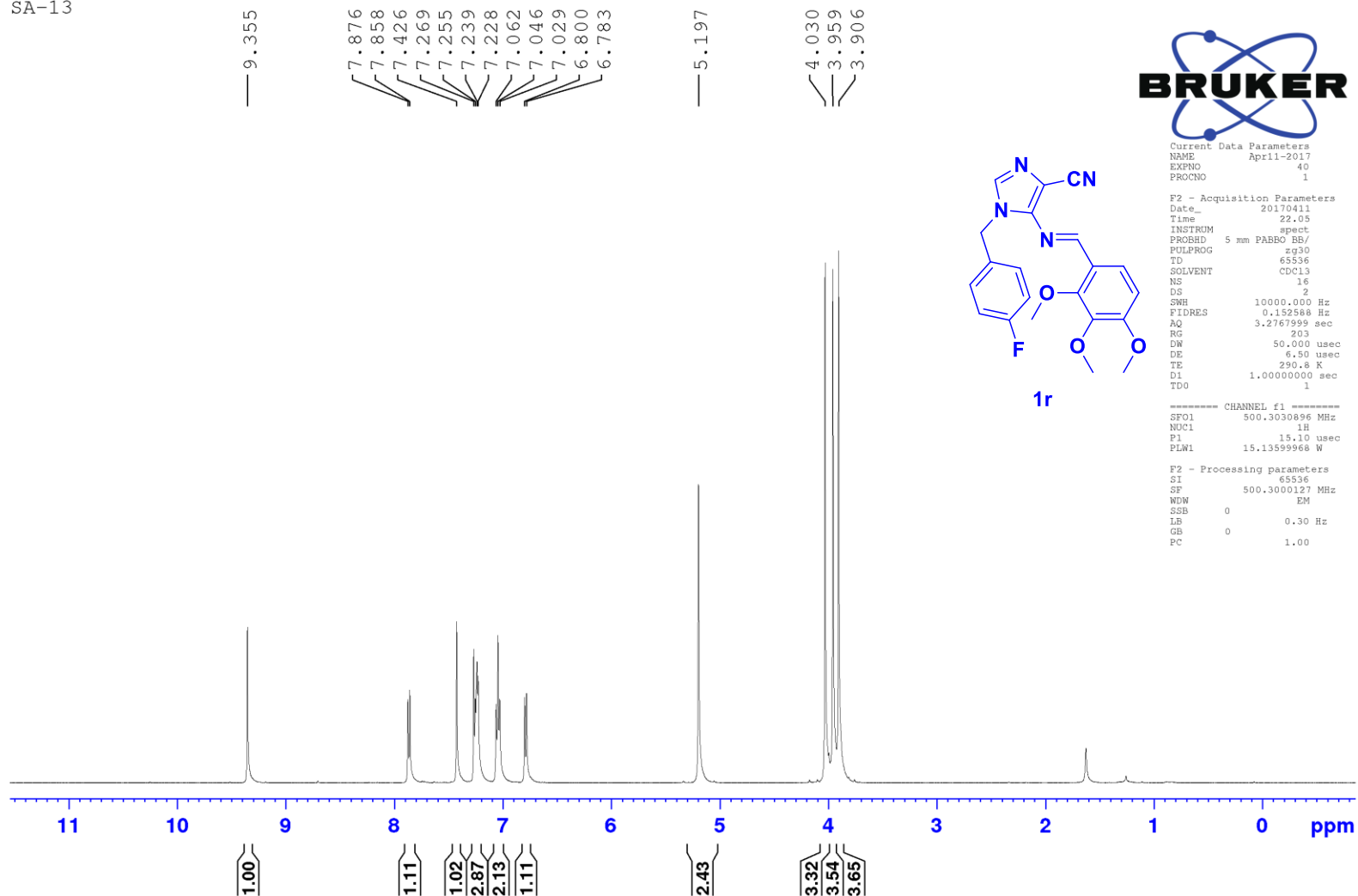
RawMode:Averaged 6.395-6.400(980-981) BasePeak:364(14417)

BG Mode:Calc. from Peak Group 1 - Event 1

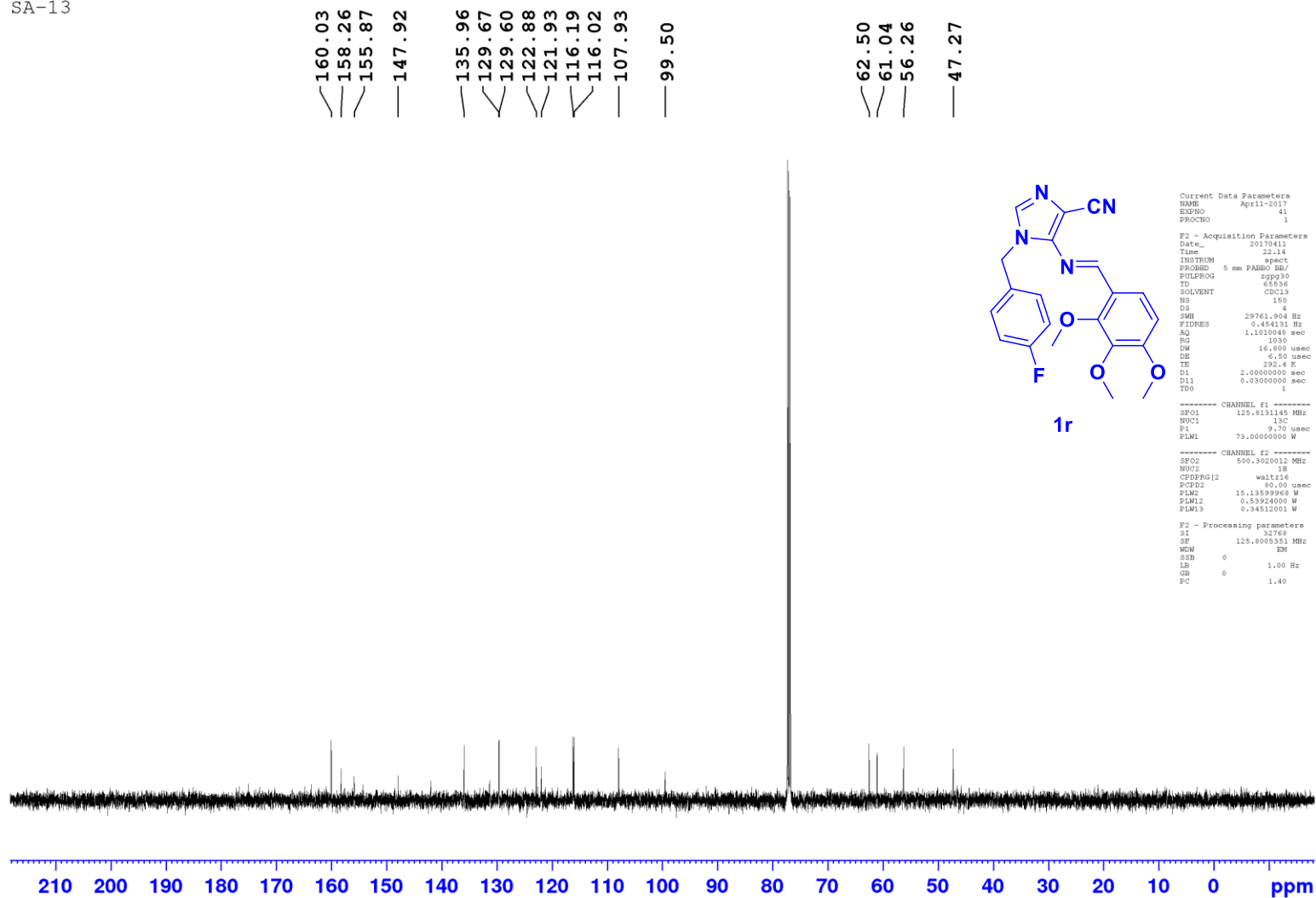
intensity



SA-13



SA-13



Spectrum

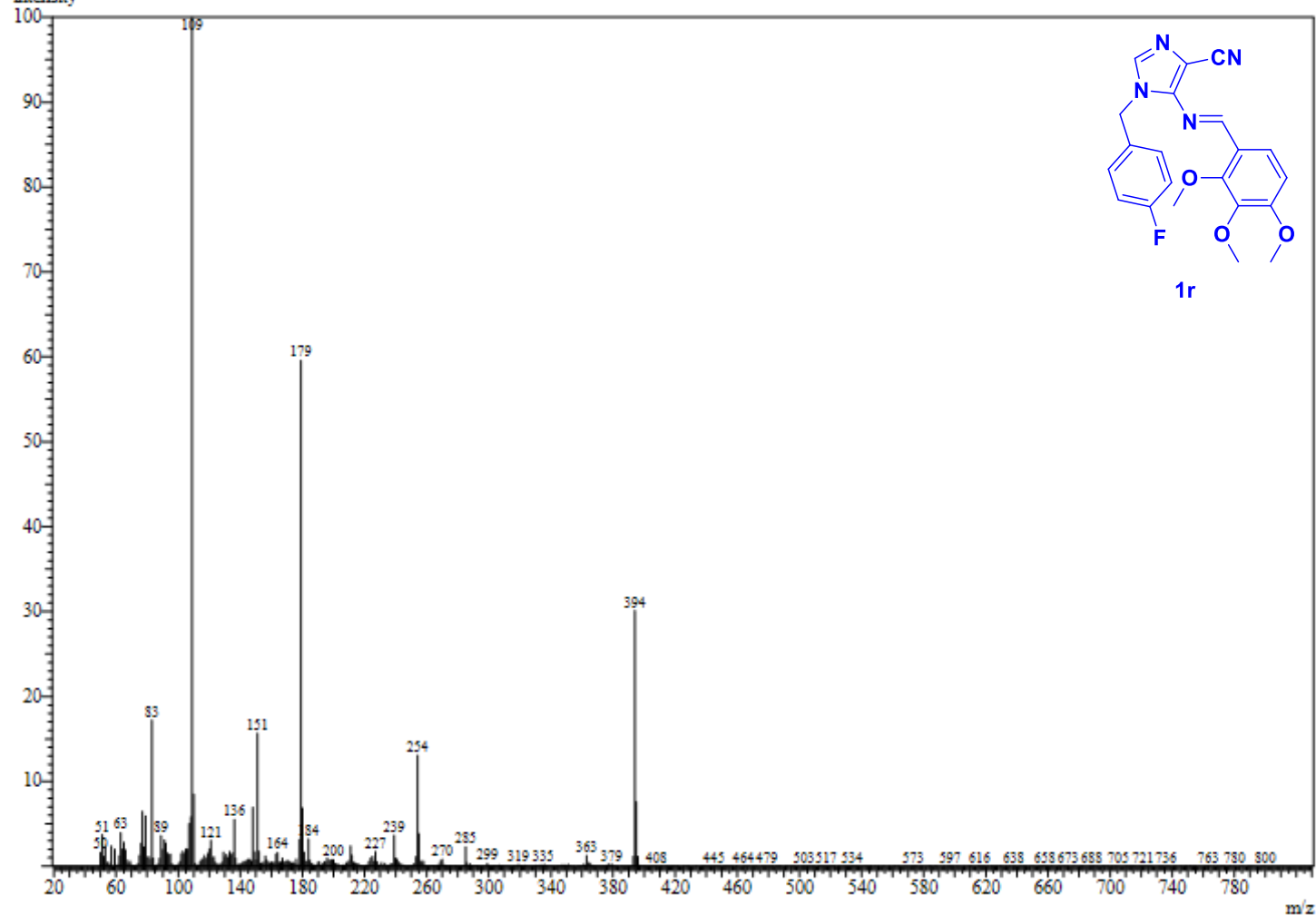
Line#:1 R.Time:6.410(Scan#:983)

MassPeaks:589

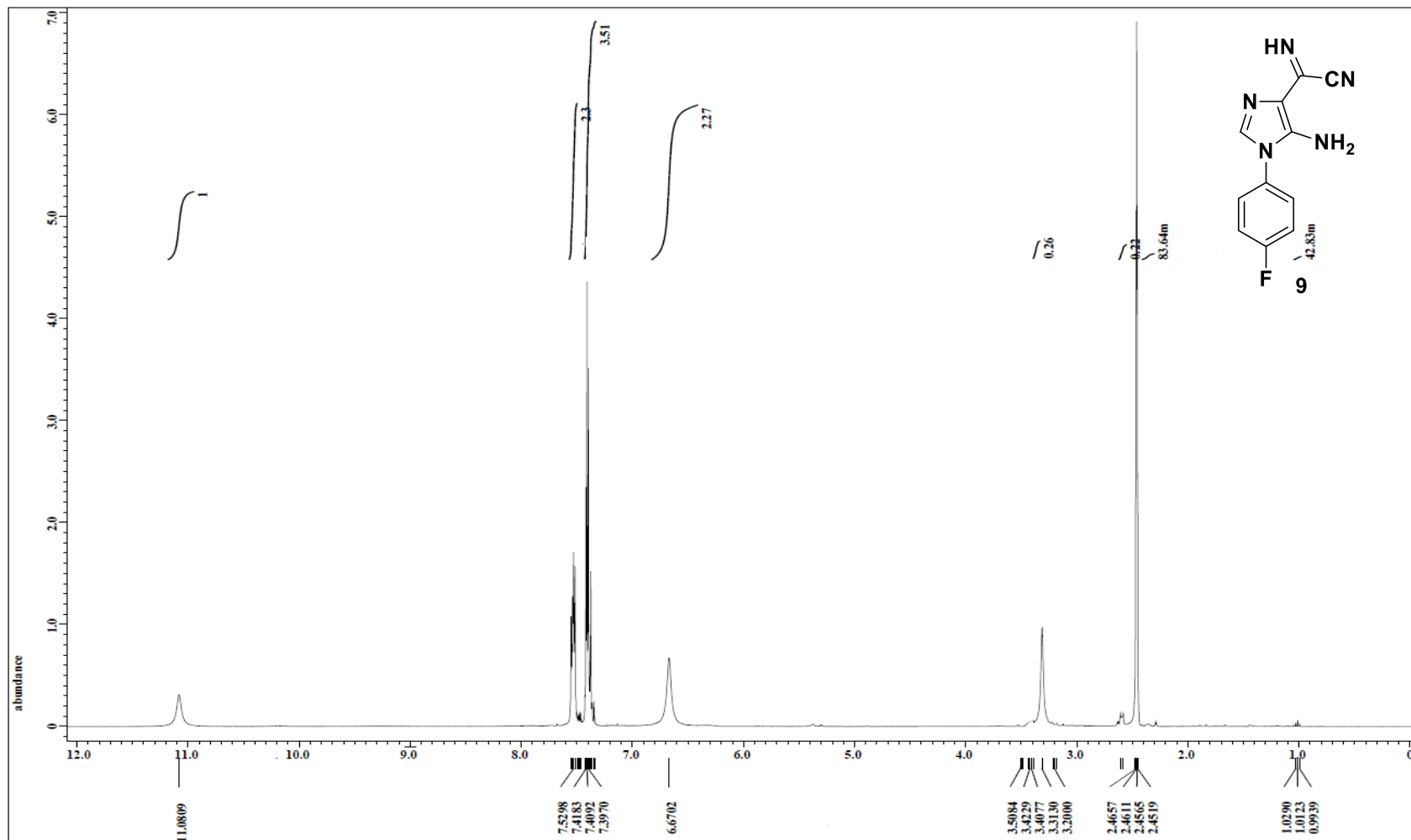
RawMode:Averaged 6.405-6.415(982-984) BasePeak:109(6930995)

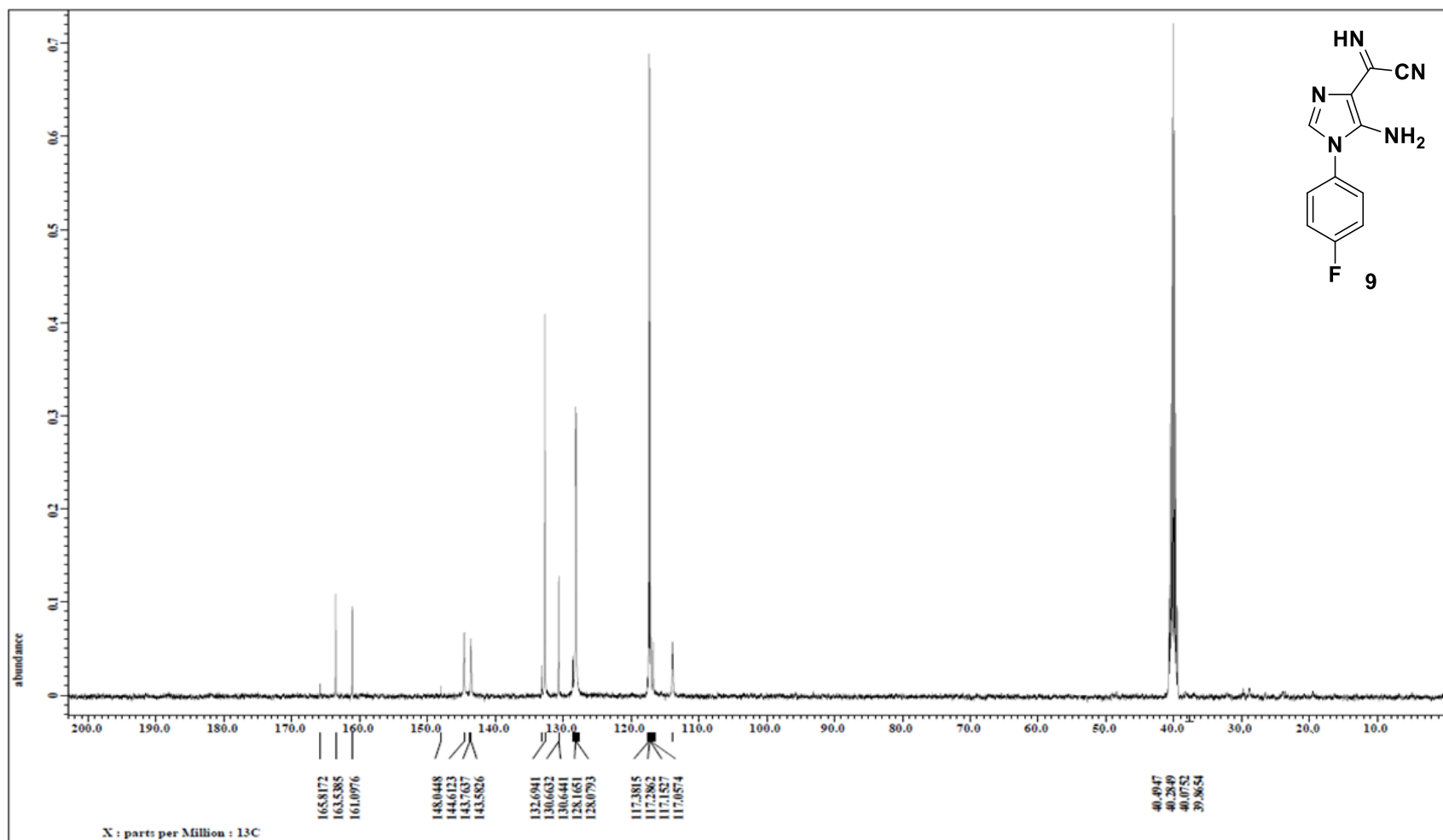
BG Mode:Calc. from Peak Group 1 - Event 1

intensity



Series 2





Elemental Composition Report

Page 1

Single Mass Analysis

Tolerance = 5.0 PPM / DBE: min = -1.5, max = 50.0

Element prediction: Off

Number of isotope peaks used for i-FIT = 5

Monoisotopic Mass, Even Electron Ions

65 formula(e) evaluated with 1 results within limits (up to 50 best isotopic matches for each mass)

Elements Used:

C: 9-22 H: 8-25 N: 0-5 O: 0-3 F: 0-1

Sample Name : Int-2

IITRPR

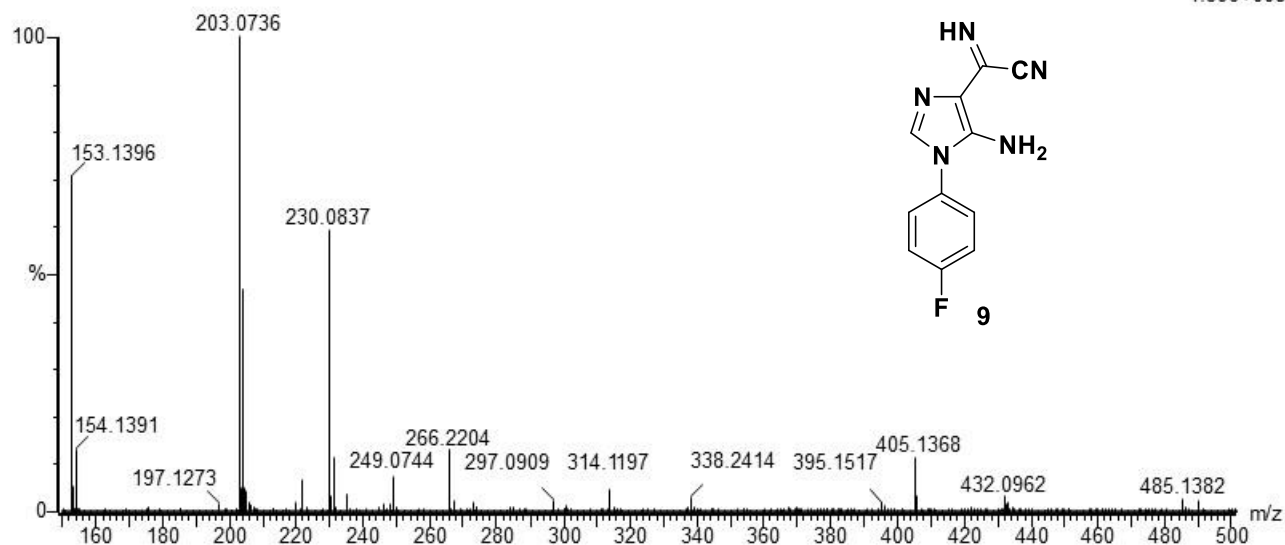
XEVO G2-XS QTOF

Test Name : HRMS-1

160120-Int-2 12 (0.131)

1: TOF MS ES+

1.59e+008



Minimum: -1.5

Maximum: 5.0 5.0 50.0

Mass	Calc. Mass	mDa	PPM	DBE	i-FIT	Norm	Conf(%)	Formula
230.0837	230.0842	-0.5	-2.2	9.5	2053.6	n/a	n/a	C11 H9 N5 F

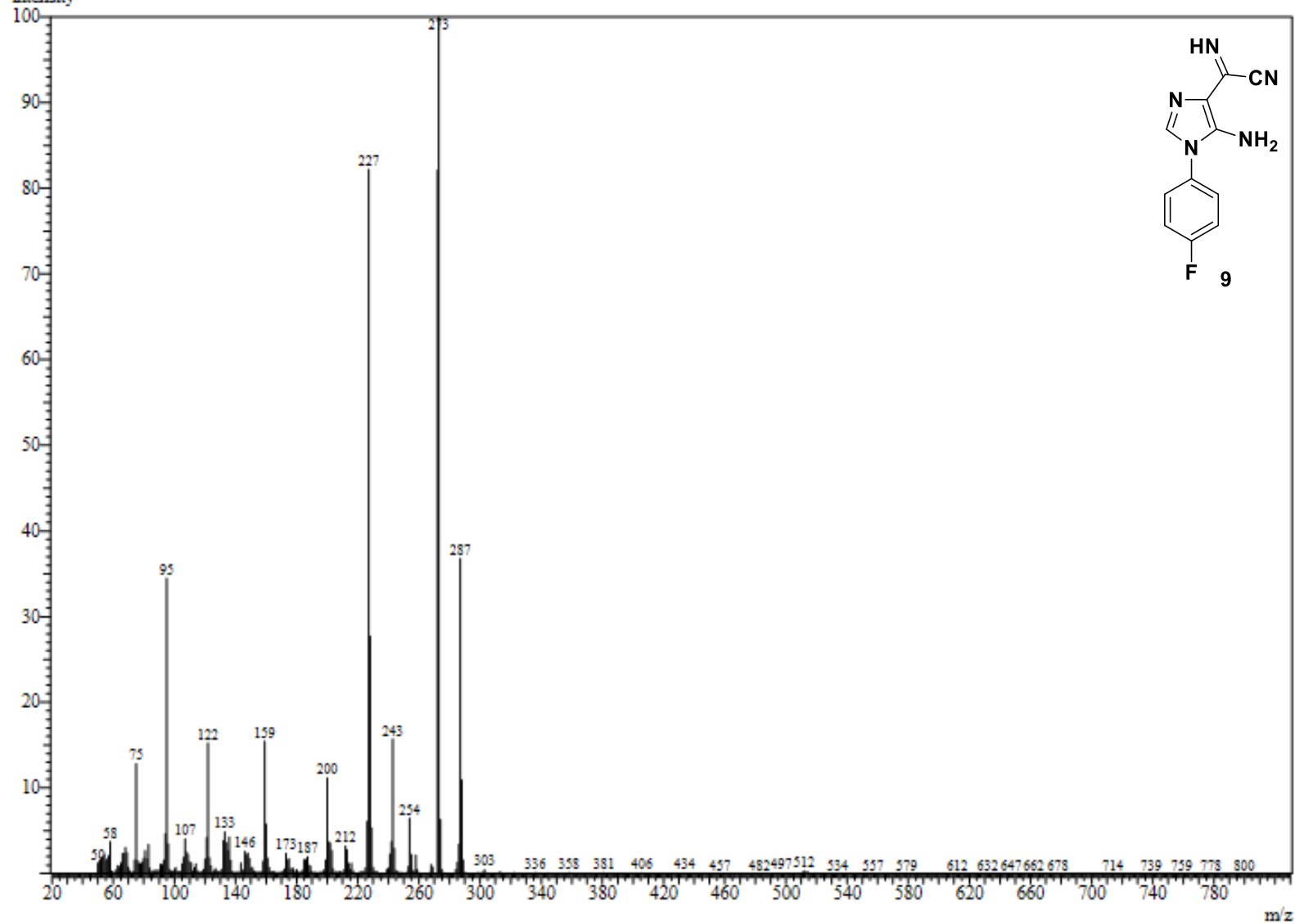
Line#:2 R.Time:5.775(Scan#:856)

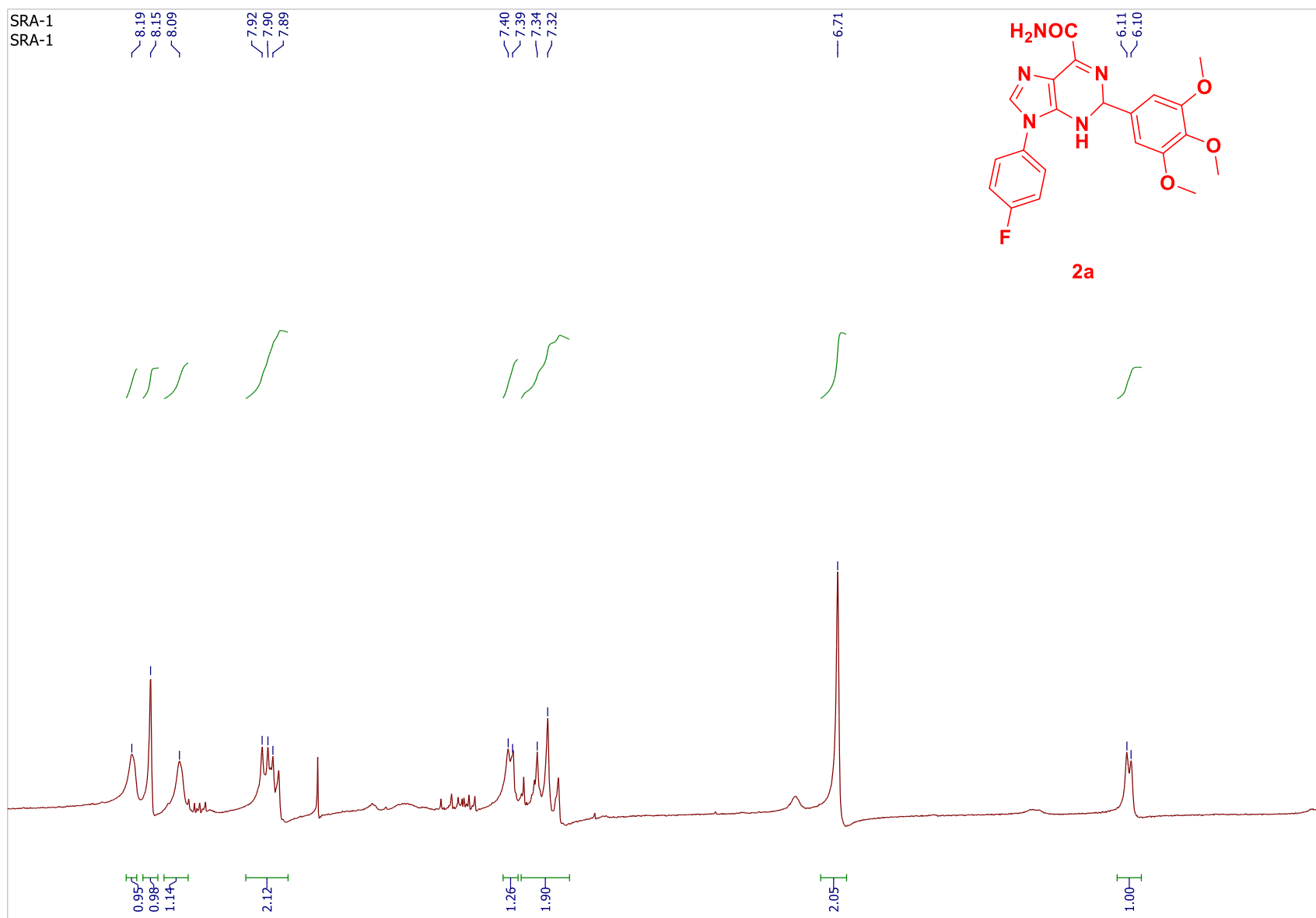
MassPeaks:687

RawMode:Averaged 5.770-5.780(855-857) BasePeak:273(1487875)

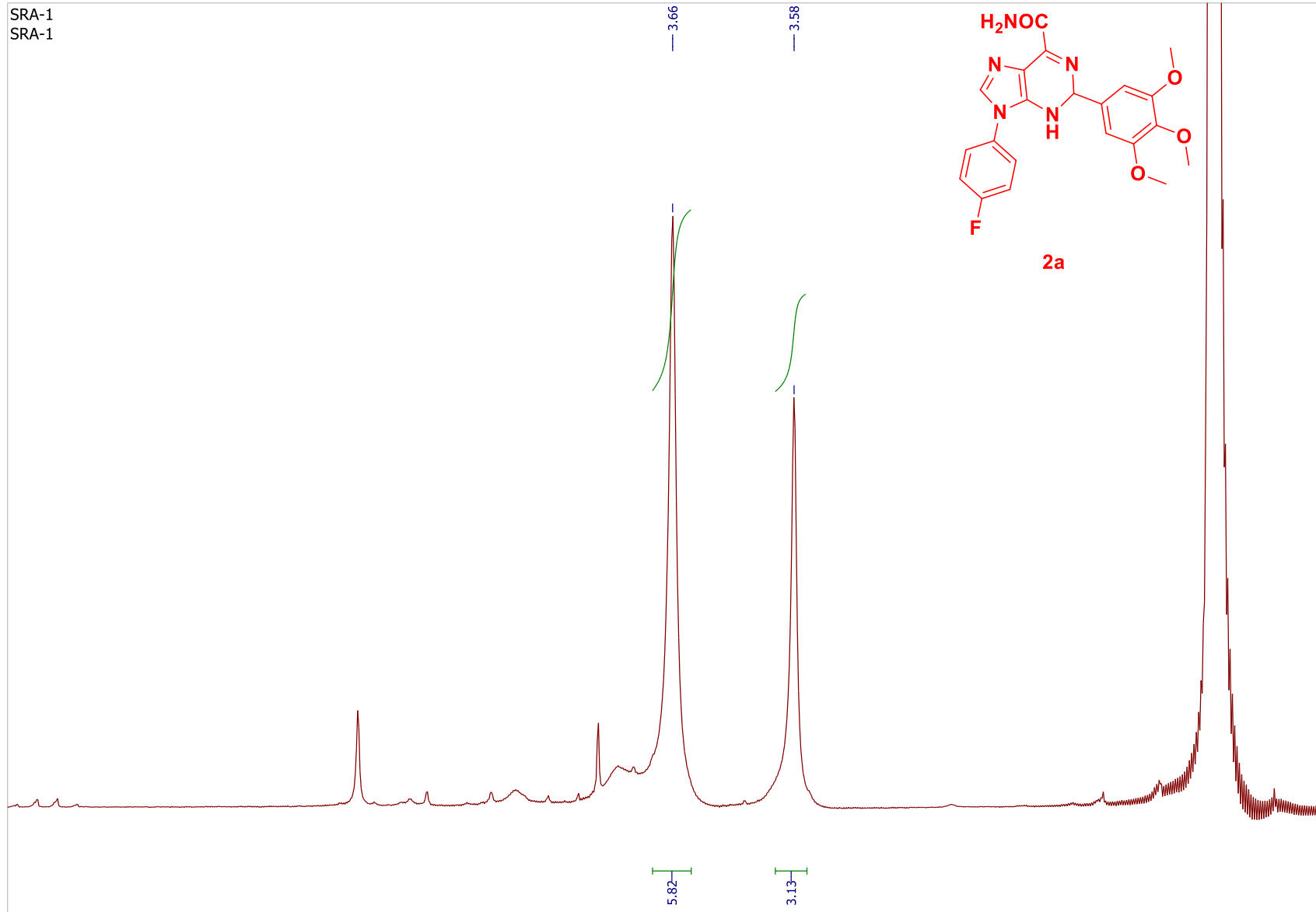
BG Mode:Calc. from Peak Group 1 - Event 1

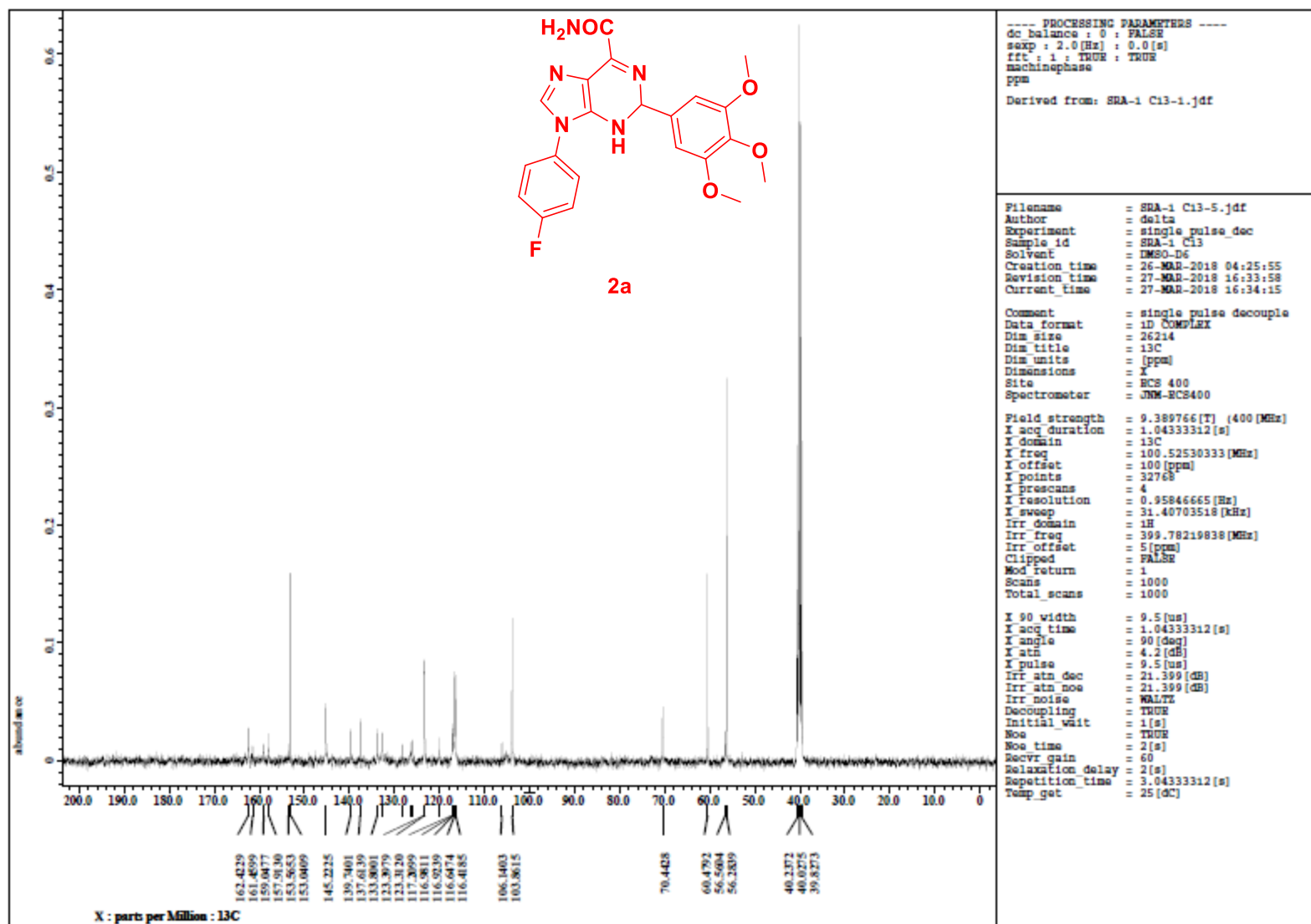
intensity





SRA-1
SRA-1



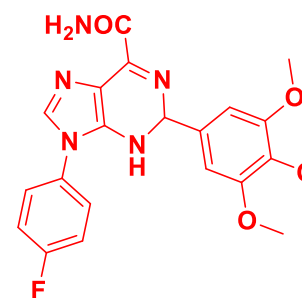
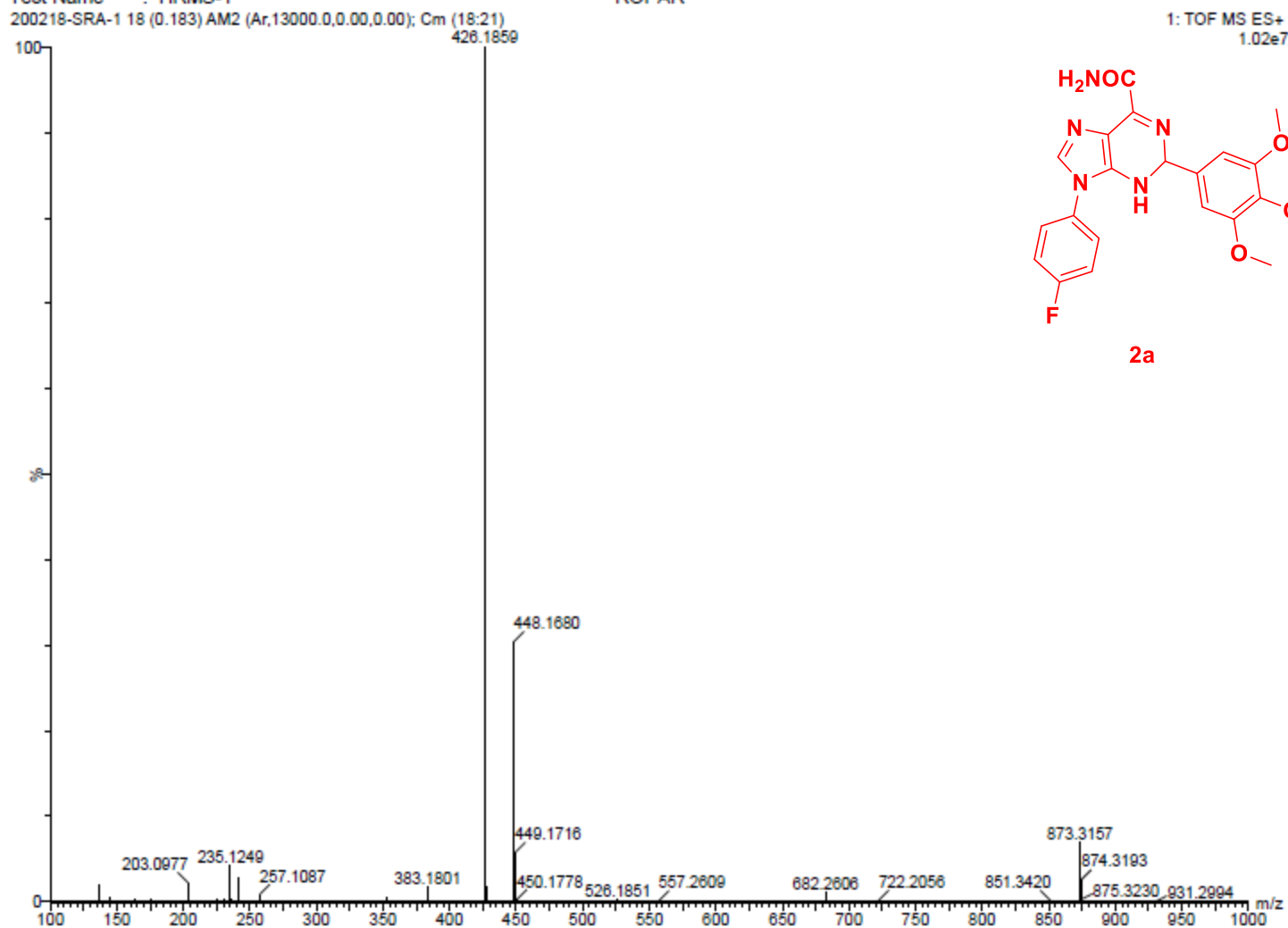


Sample Name : SRA-1
Test Name : HRMS-1

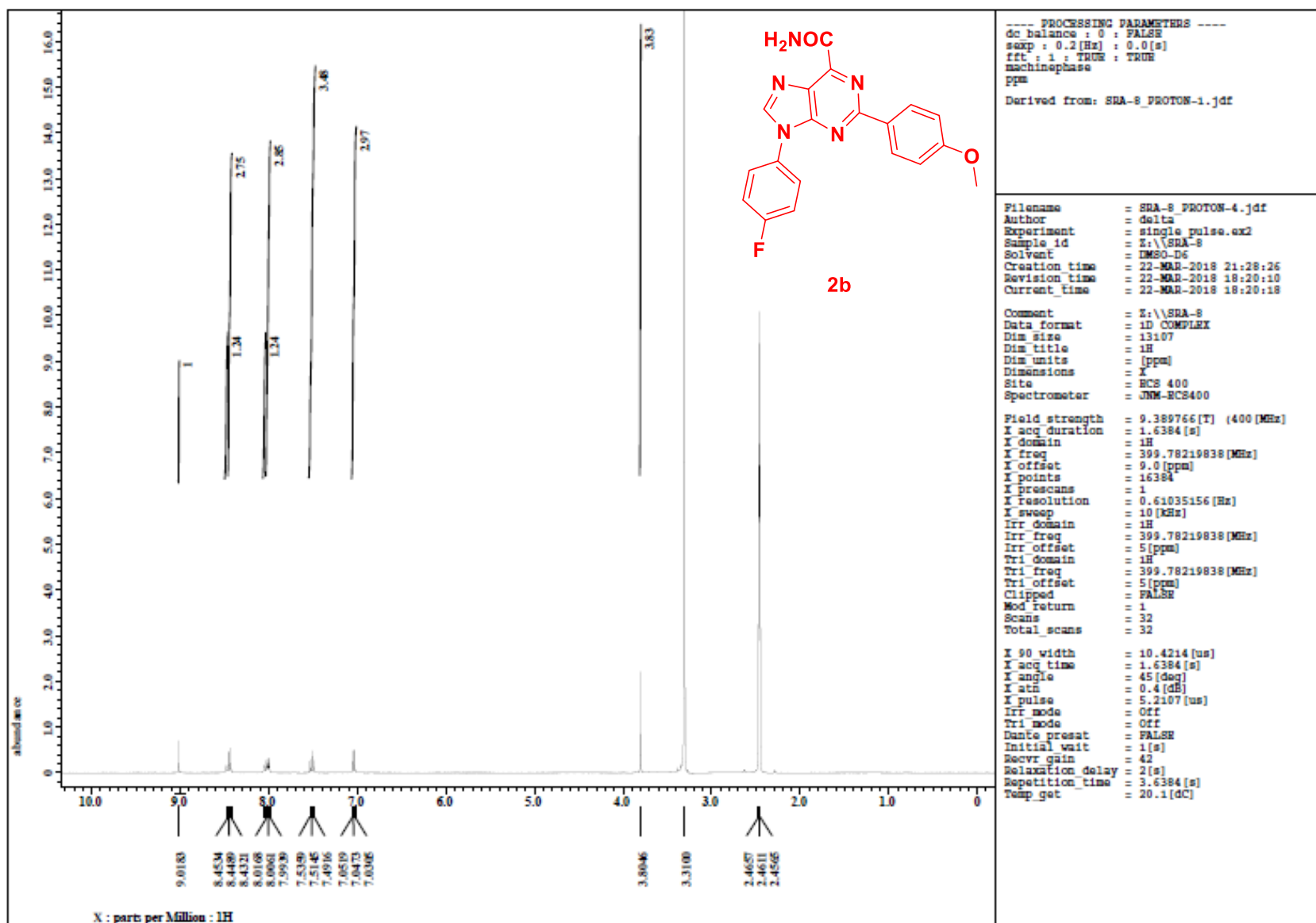
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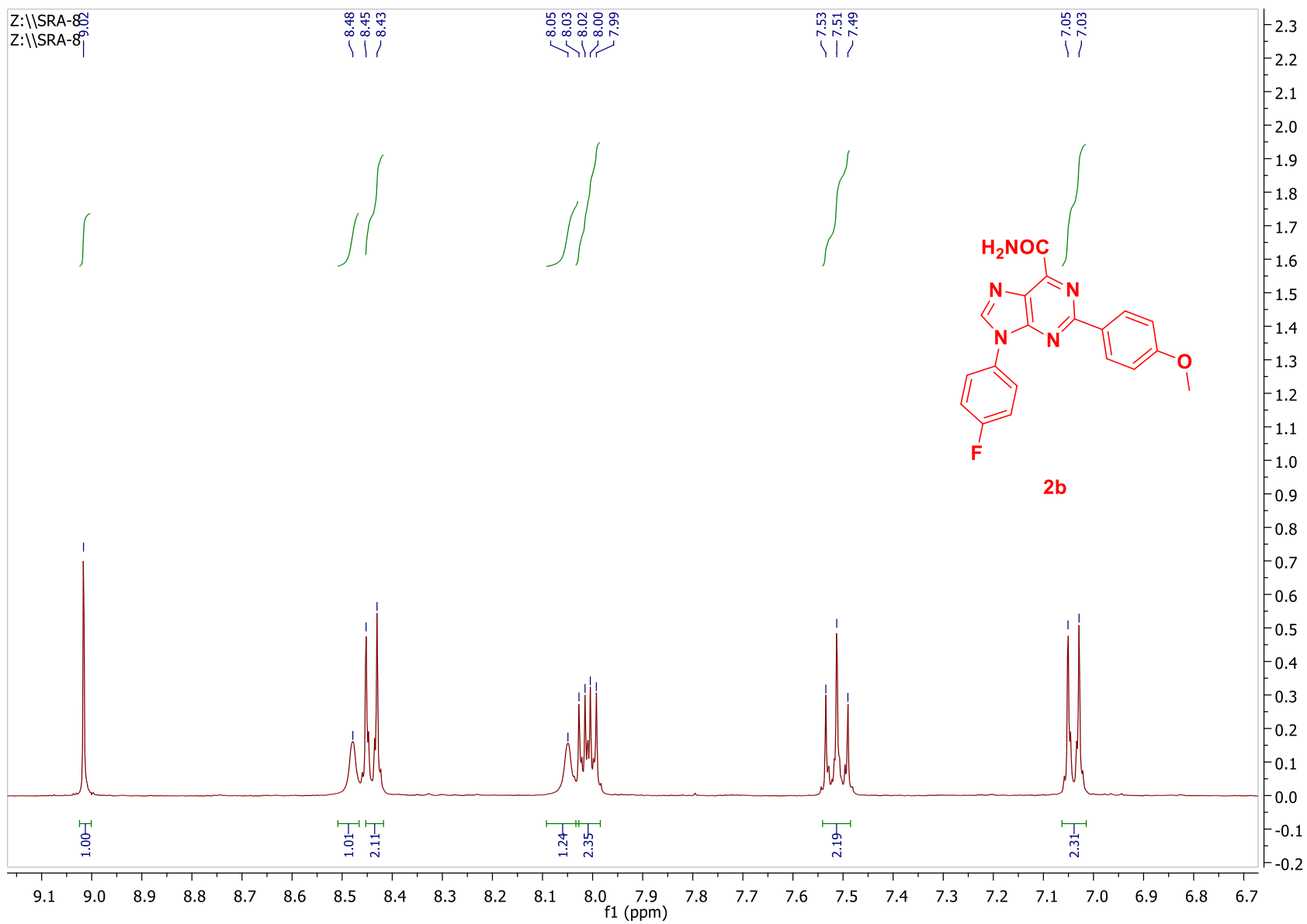
XEVO G2-XS QTOF

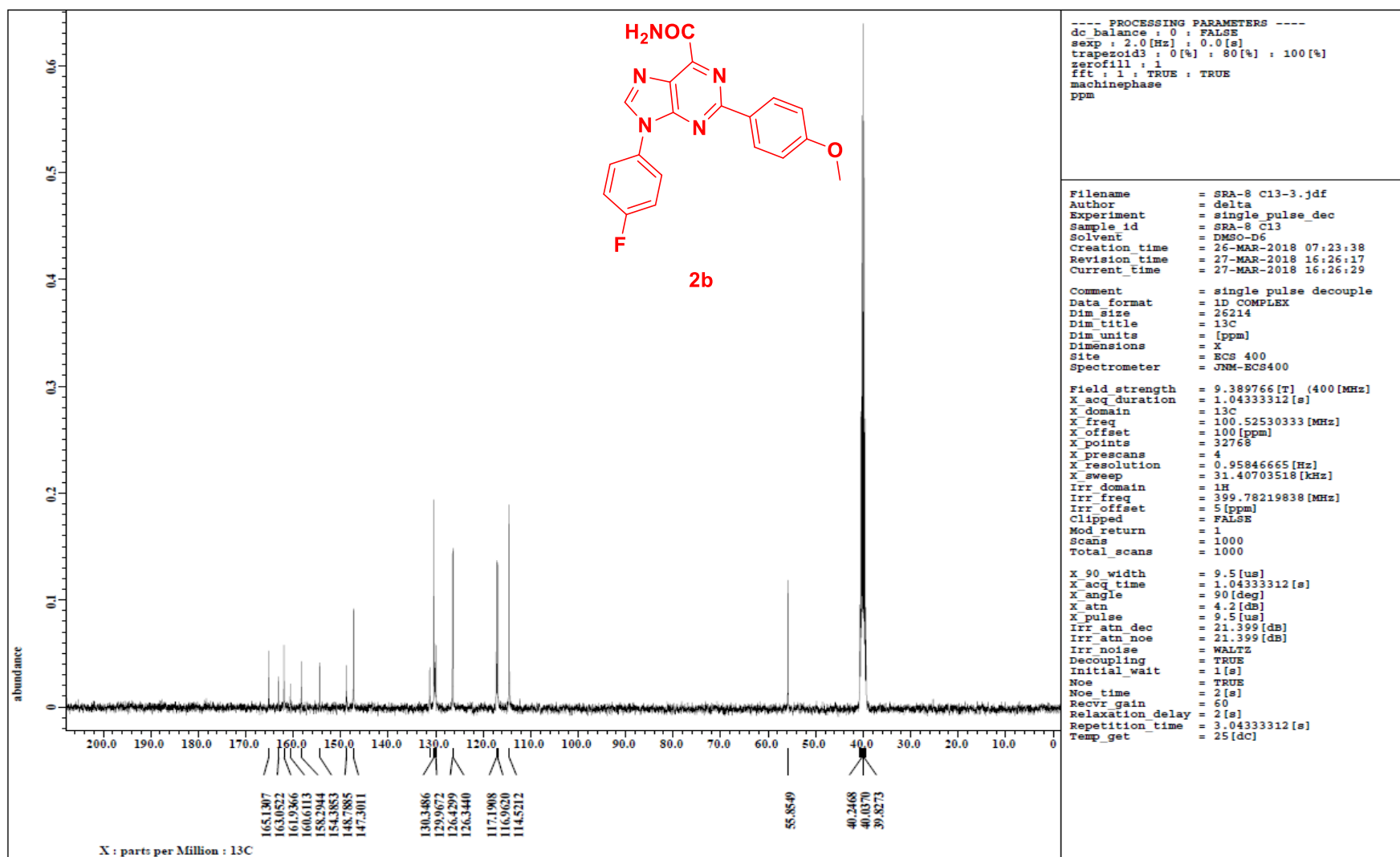
1: TOF MS ES+
1.02e7



2a





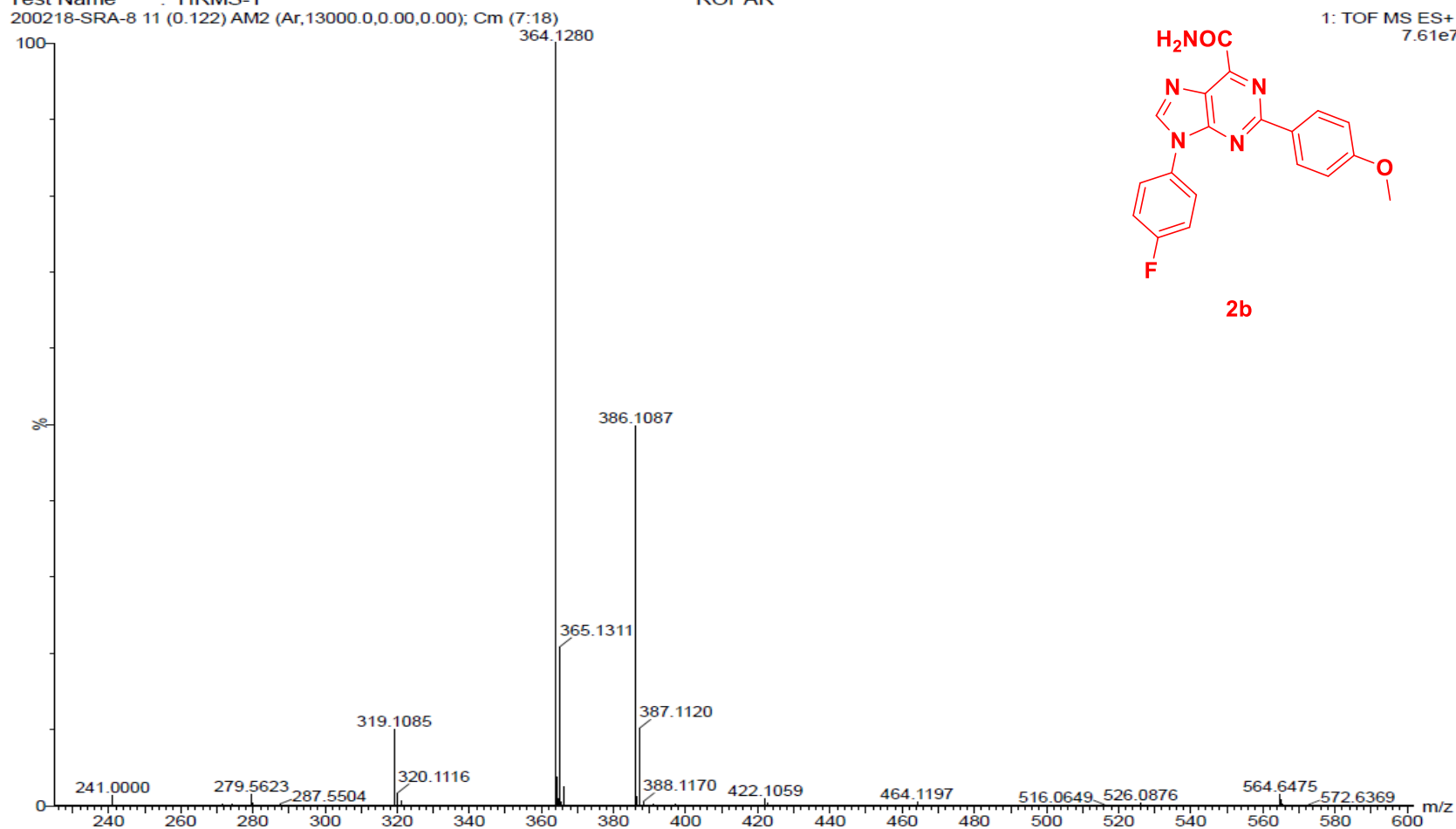


Sample Name : SRA-8
Test Name : HRMS-1

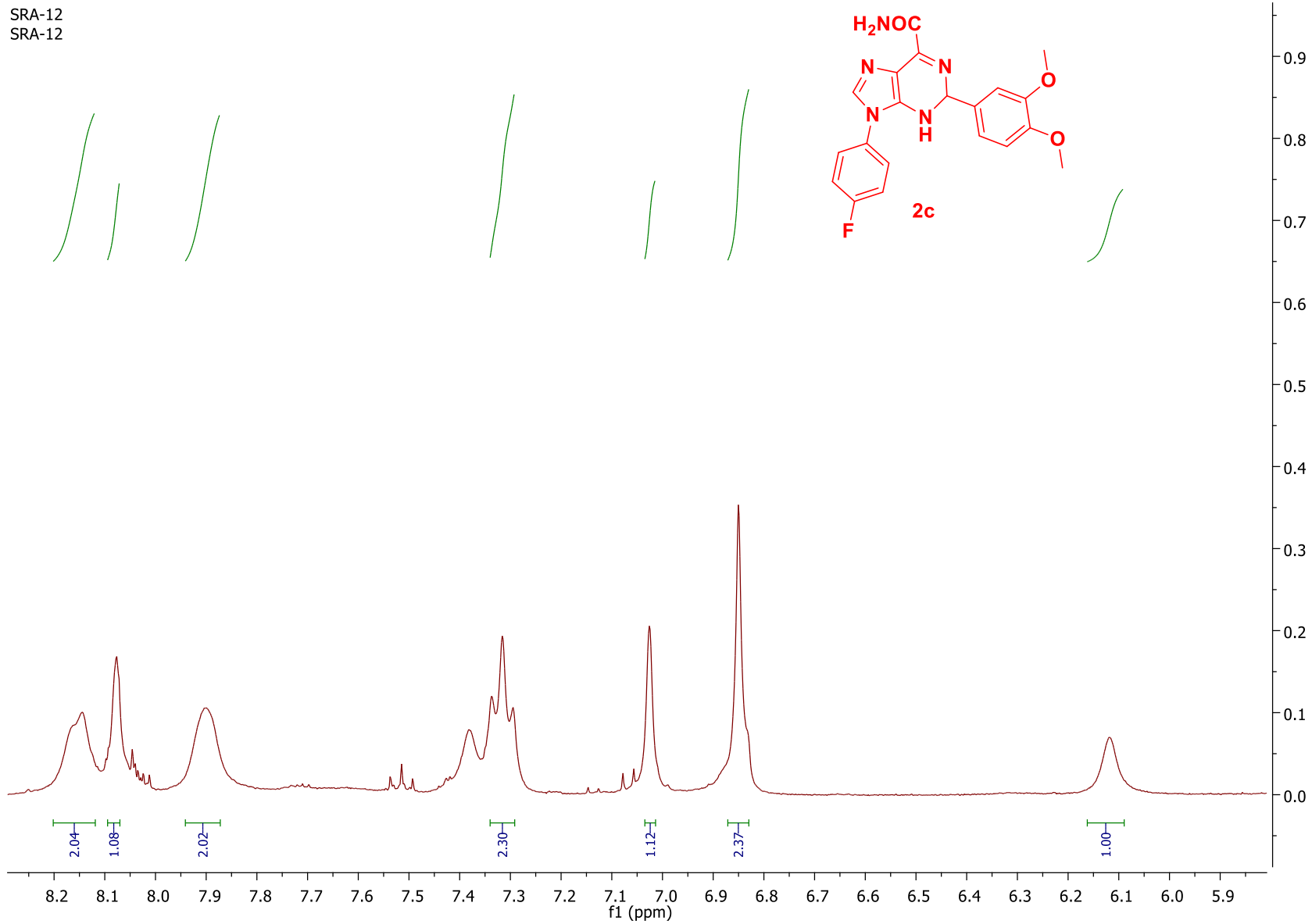
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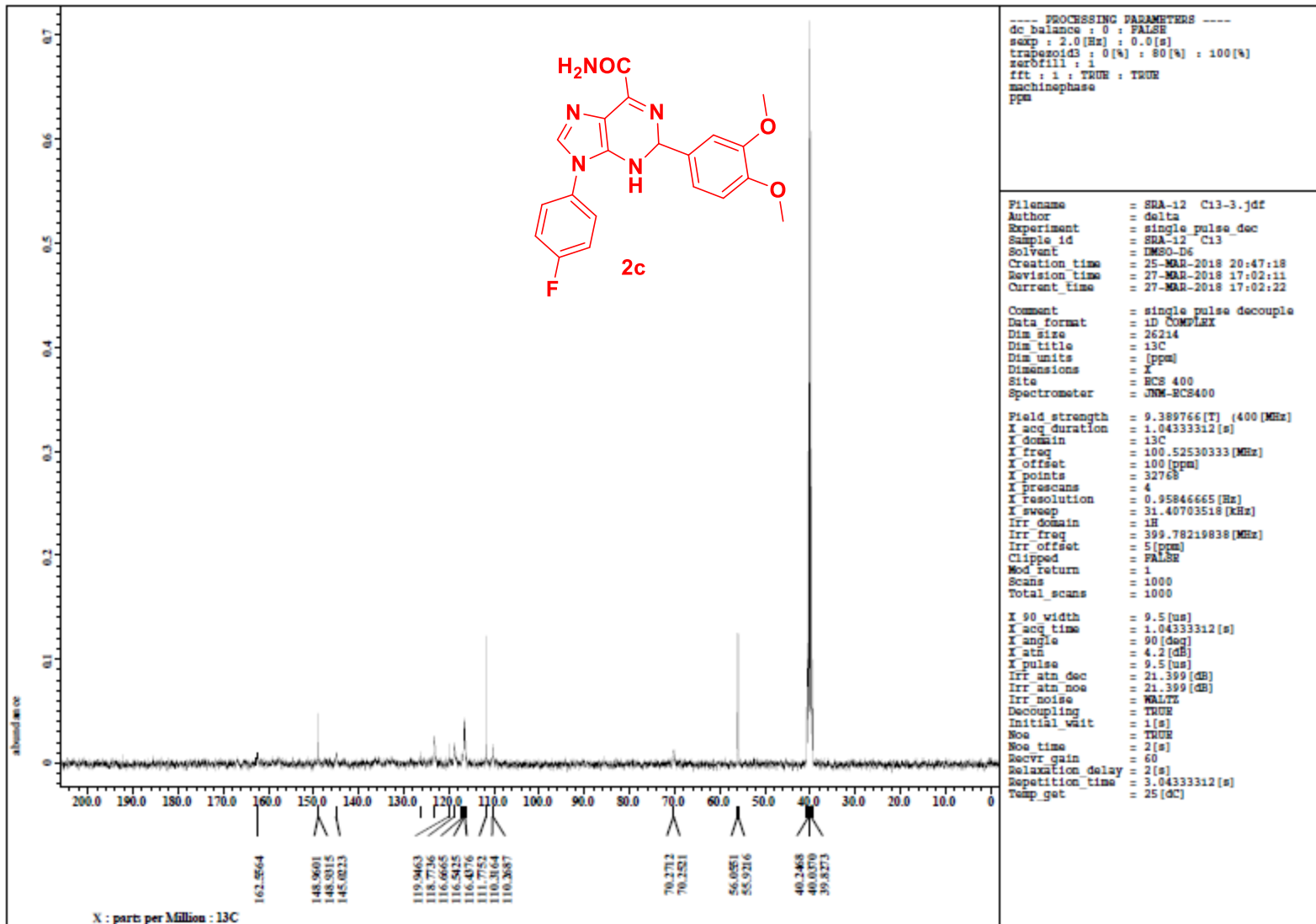
XEVO G2-XS QTOF

1: TOF MS ES+
7.61e7



SRA-12
SRA-12





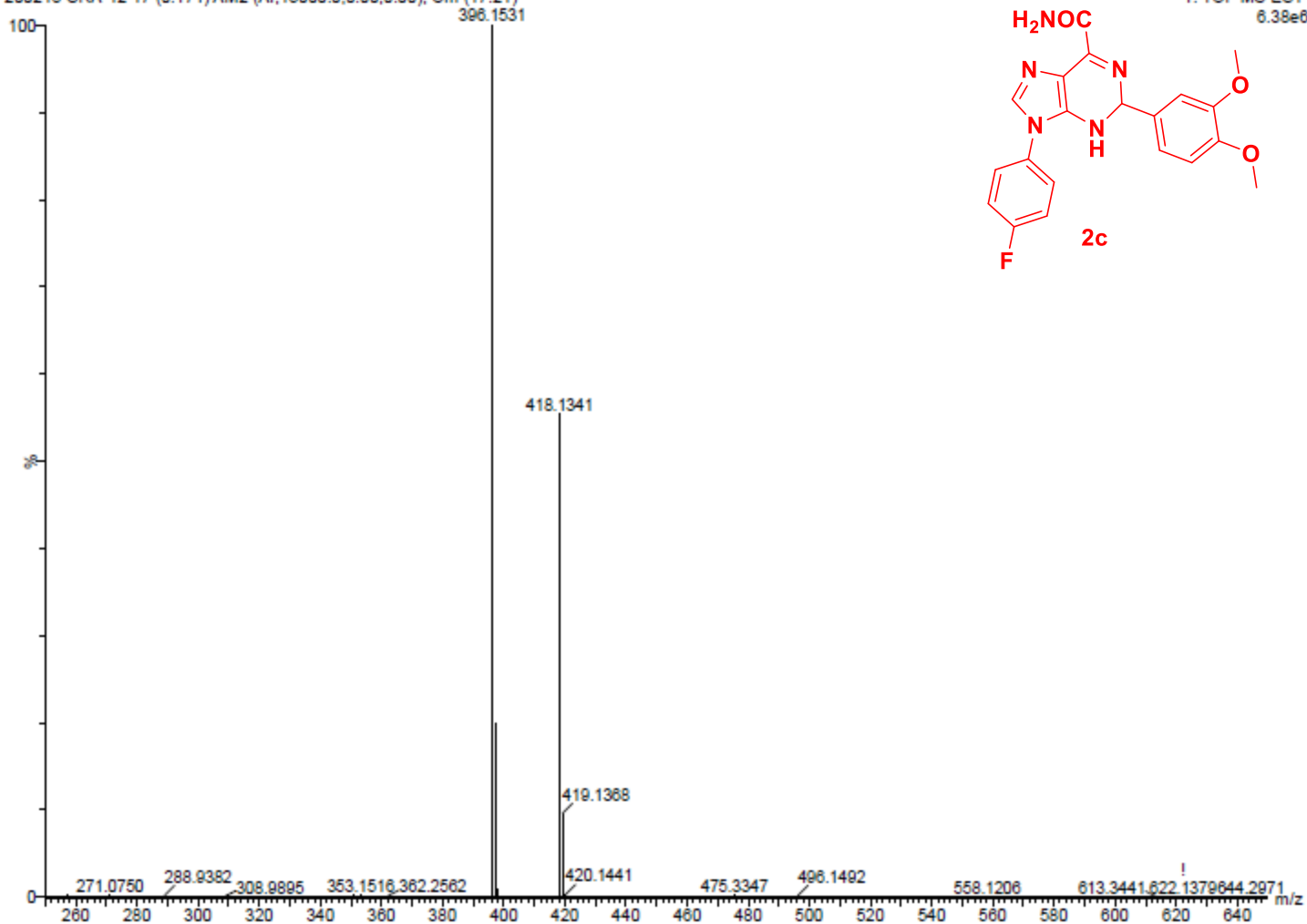
Sample Name : SRA-12
Test Name : HRMS-1

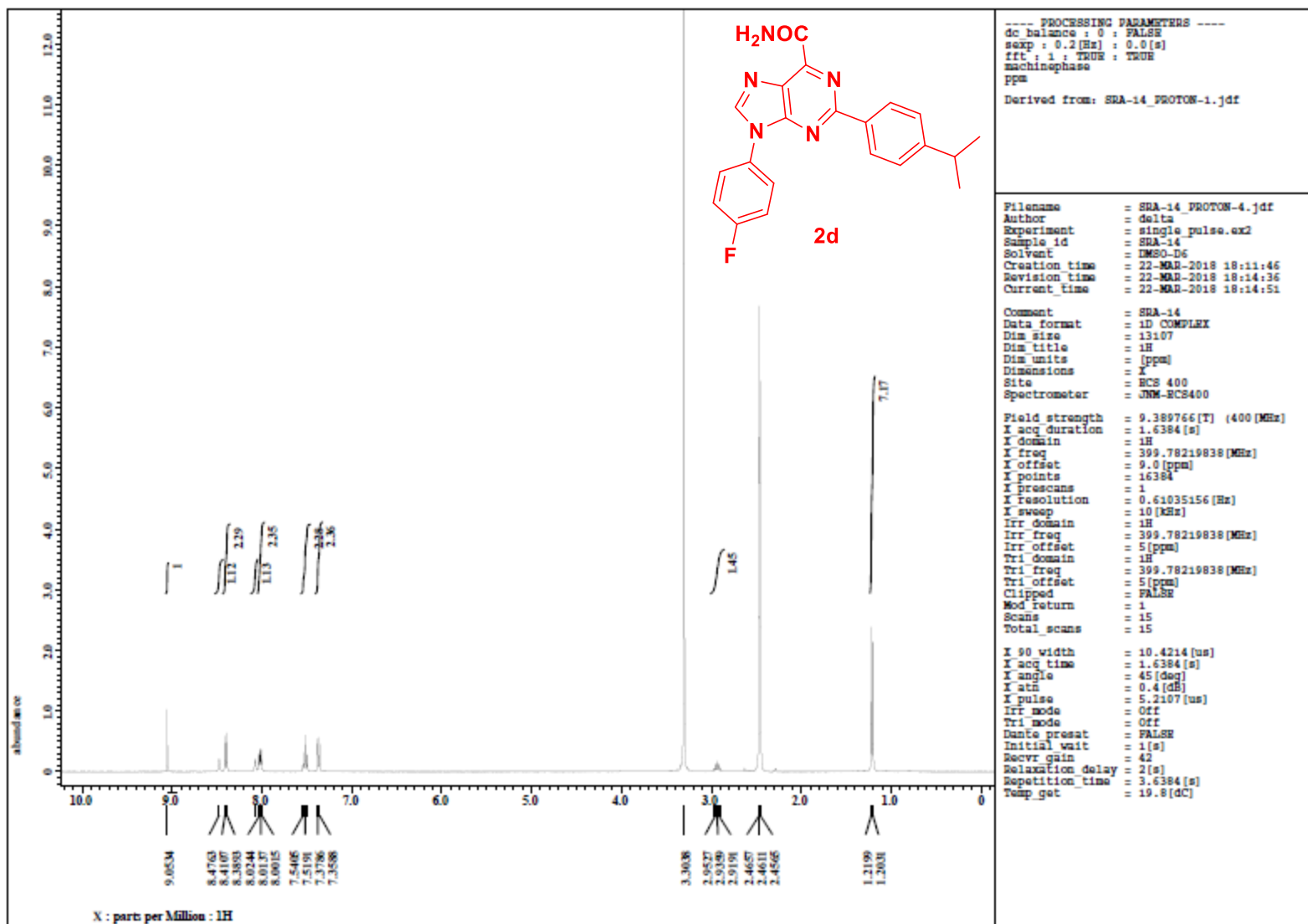
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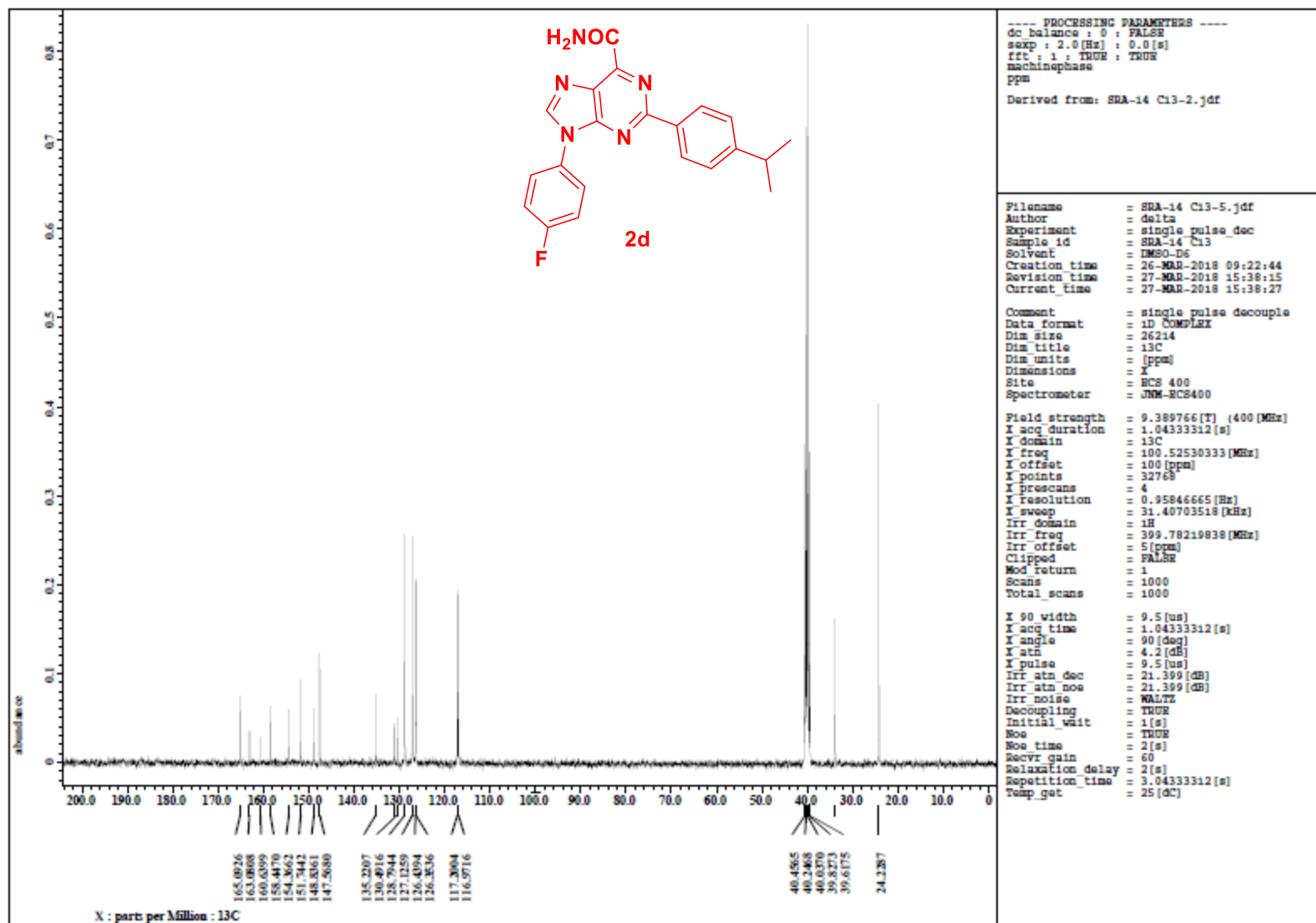
XEVO G2-XS QTOF

200218-SRA-12 17 (0.174) AM2 (Ar,13000.0,0.00,0.00); Cm (17:21)

1: TOF MS ES+
6.38e6







Elemental Composition Report

Page 1

Single Mass Analysis

Tolerance = 5.0 PPM / DBE: min = -1.5, max = 50.0

Element prediction: Off

Number of isotope peaks used for i-FIT = 5

Monoisotopic Mass, Even Electron Ions

37 formula(e) evaluated with 1 results within limits (up to 50 best isotopic matches for each mass)

Elements Used:

C: 9-22 H: 6-25 N: 0-5 O: 0-3 F: 0-1

Sample Name : SRA-14

IITRPR

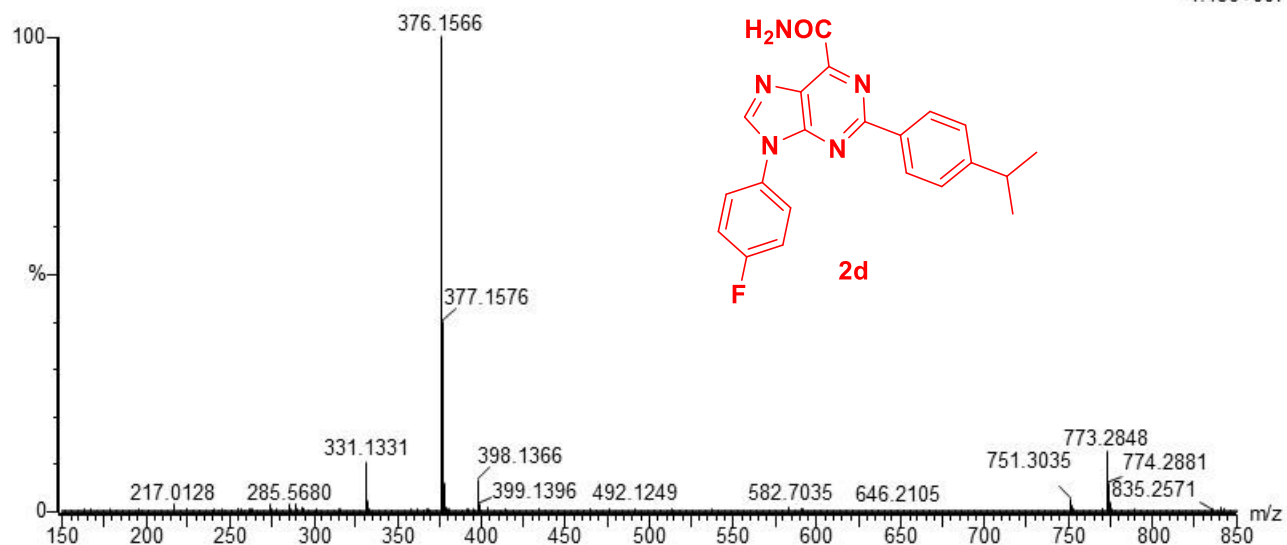
XEVO G2-XS QTOF

Test Name : HRMS-1

160120-SRA-14 16 (0.165)

1: TOF MS ES+

4.43e+007



Minimum: -1.5
Maximum: 5.0 5.0 50.0

Mass	Calc. Mass	mDa	PPM	DBE	i-FIT	Norm	Conf(%)	Formula
376.1566	376.1574	-0.8	-2.1	14.5	1626.0	n/a	n/a	C ₂₁ H ₁₉ N ₅ O F

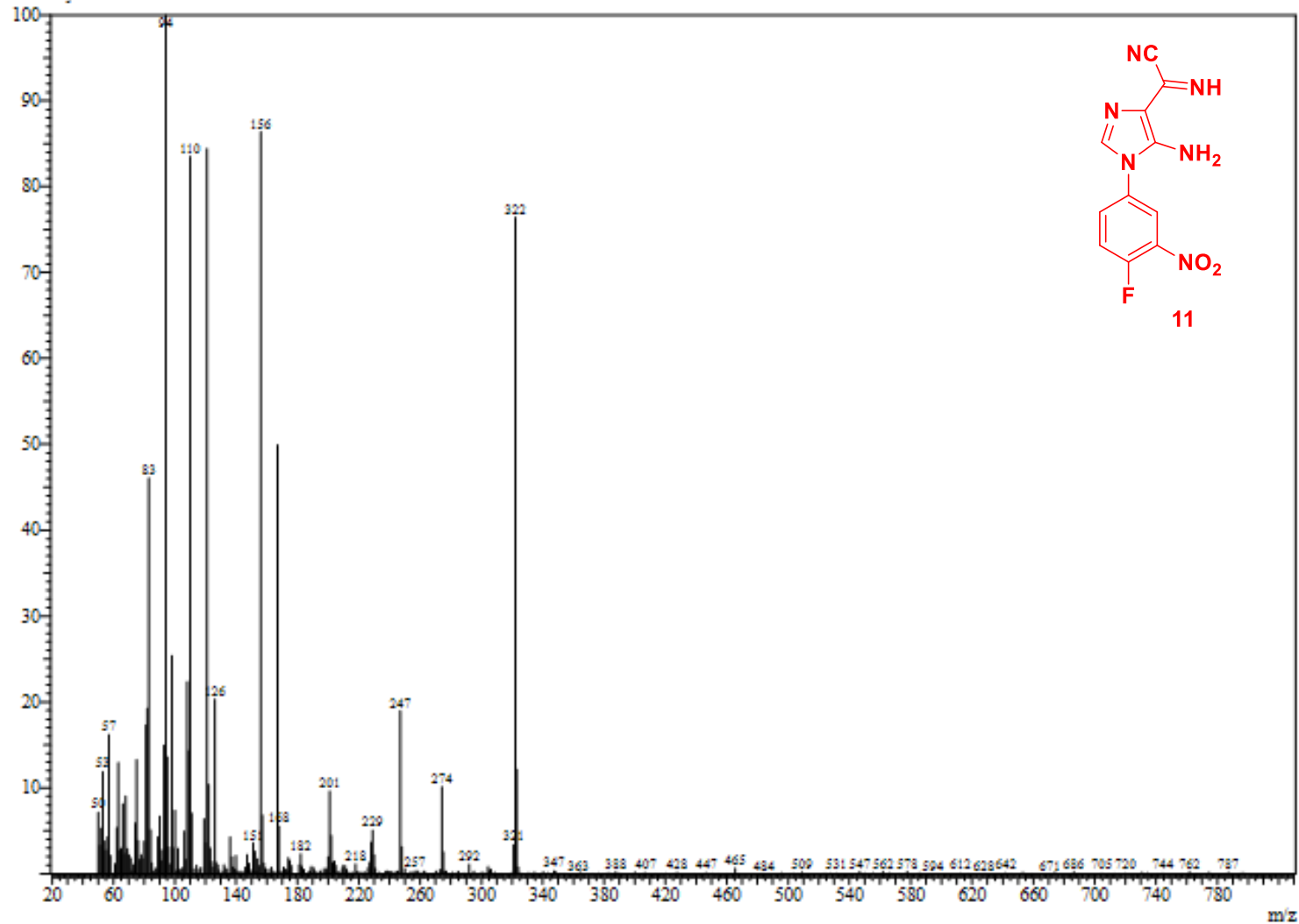
Line#2 R.Time:7.485(Scan#:1198)

MassPeaks:487

RawMode:Averaged 7.480-7.490(1197-1199) BasePeak:94(1695199)

BG Mode:Calc. from Peak Group 1 - Event 1

intensity



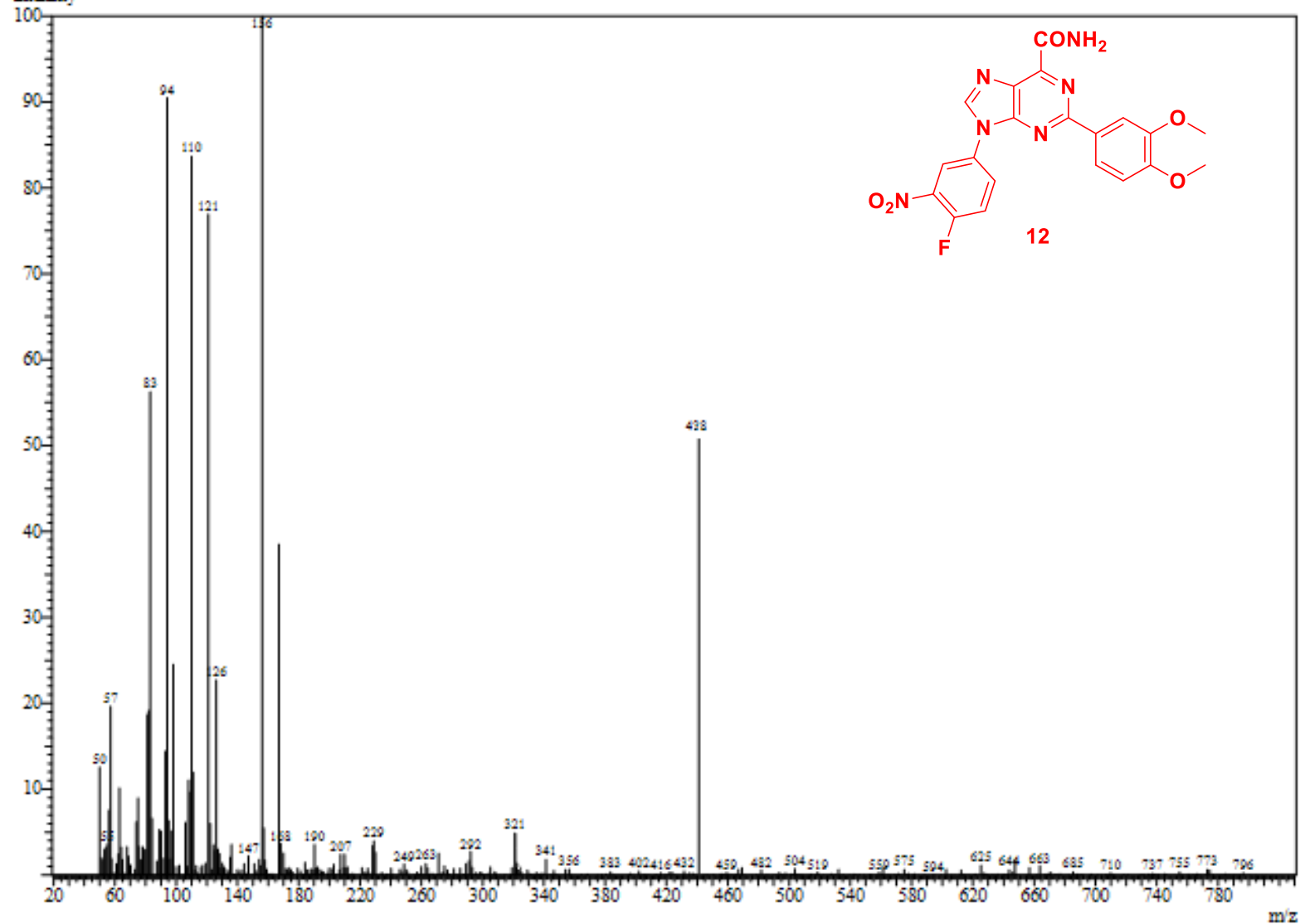
Line#1 R.Time:6.935(Scan#:1088)

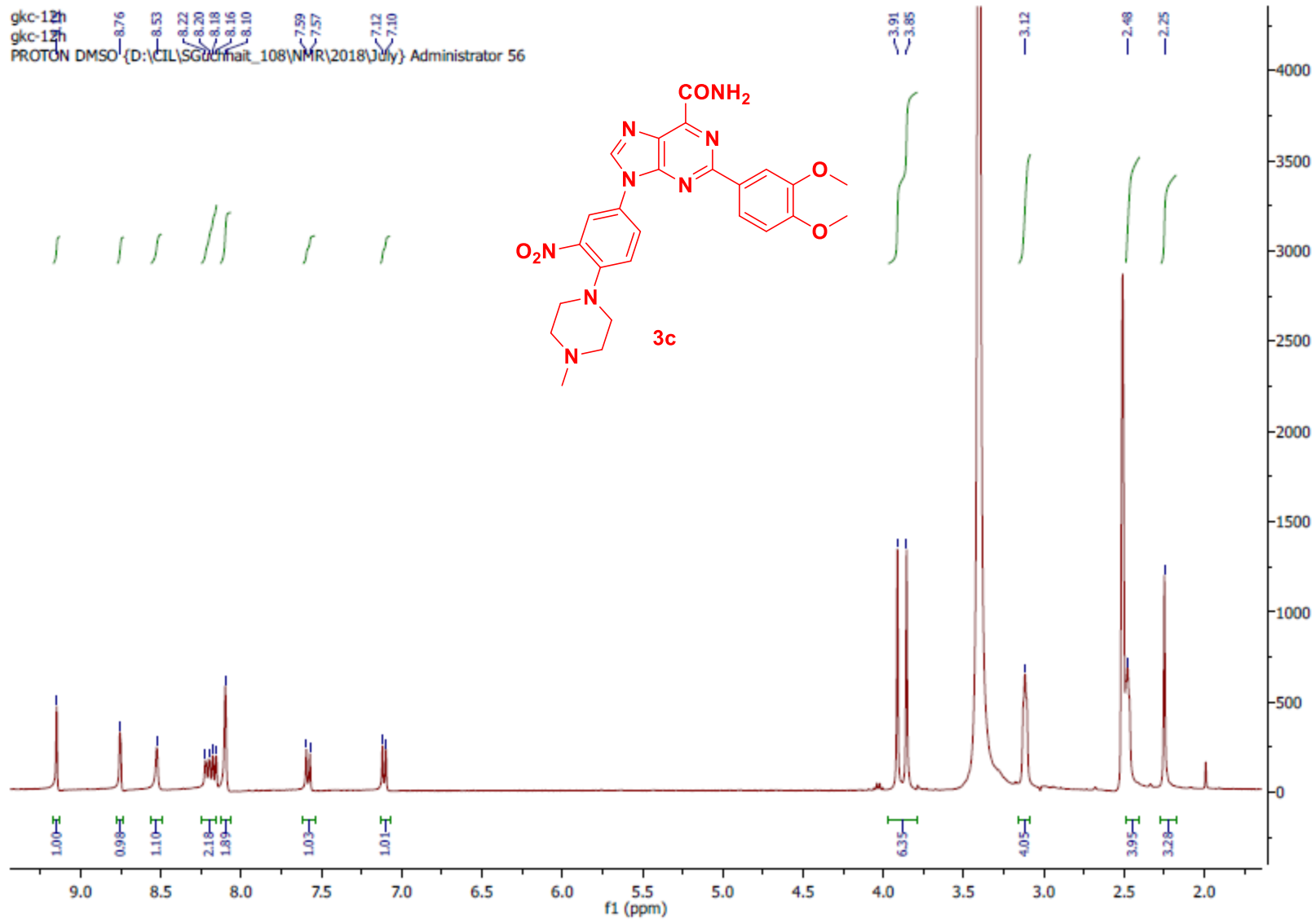
MassPeaks:431

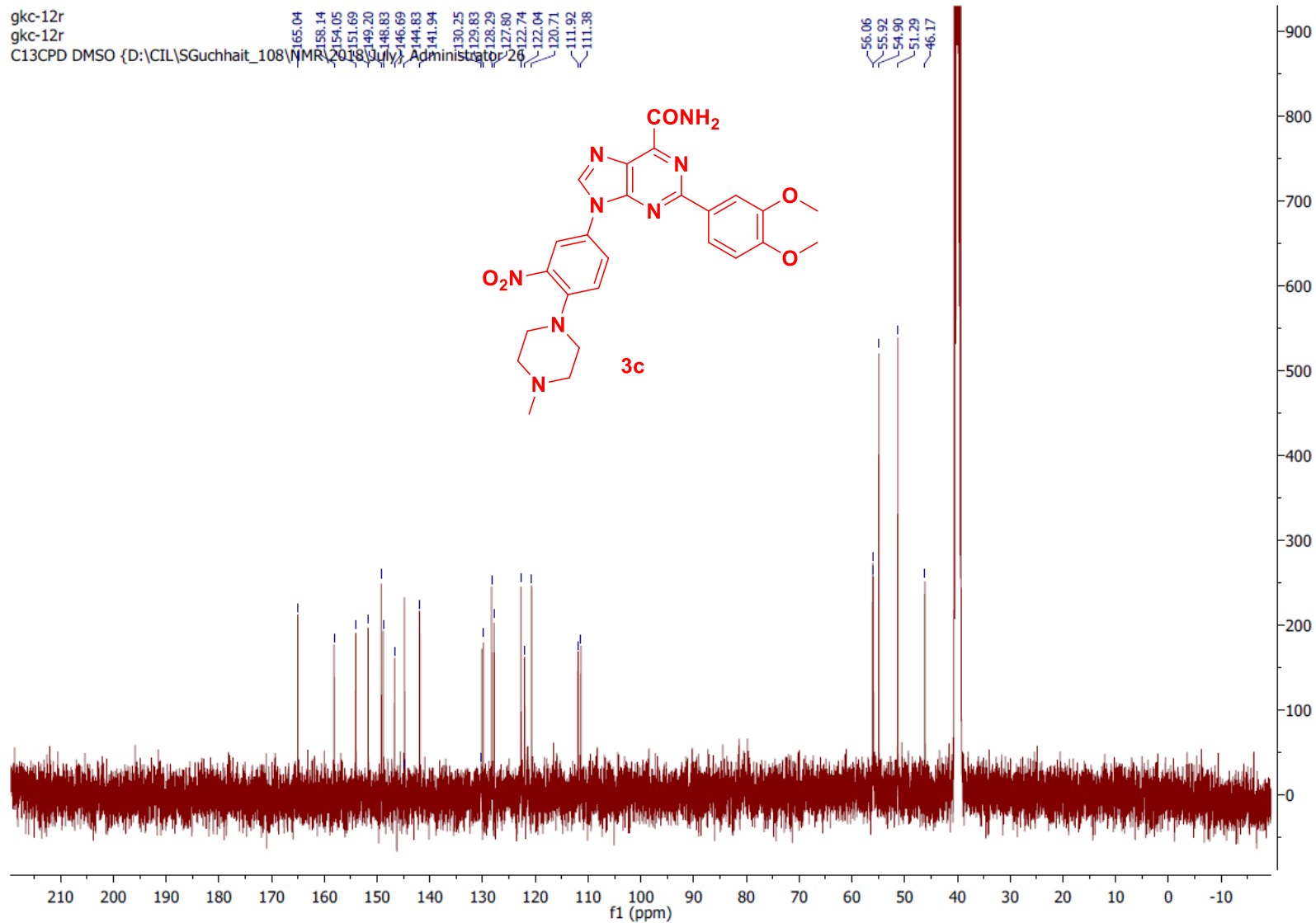
RawMode:Averaged 6.930-6.940(1087-1089) BasePeak:156(346019)

BGMode:Calc. from Peak Group 1 - Event 1

intensity







Sample Name : ANP12

Test Name : HRMS-1

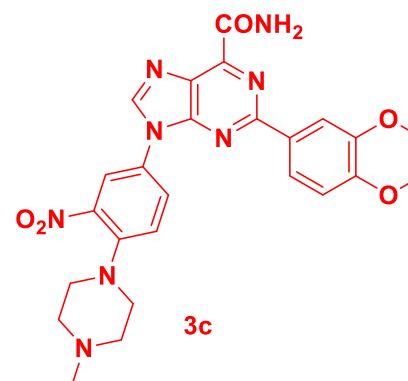
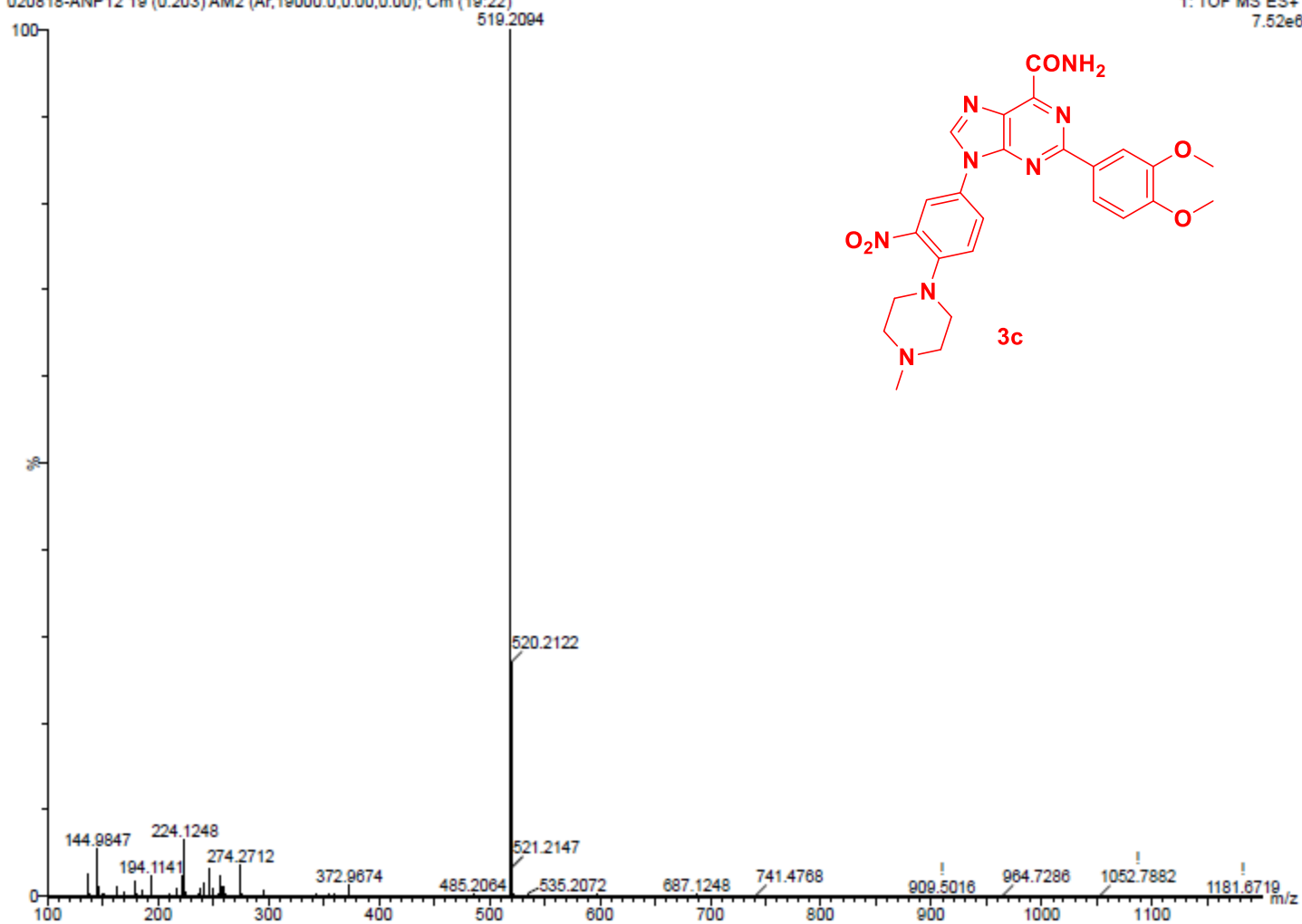
020818-ANP12 19 (0.203) AM2 (Ar, 19000.0,0.00,0.00); Cm (19:22)

I.I.T.ROPAR

XEVO G2-XS QTOF

1: TOF MS ES+

7.52e6



Molecular docking of 3c in HER-2 and other proteins

We performed molecular docking of most potent compound 3c into the HER-2 kinase and other related proteins such as CDK-2, 4, 6, ER α and PR and results were compared with their positive controls (Table S1). The Figure S1 represents the 3D binding pose of the lapatinib (positive control) and the compound 3c in the active site of the HER-2 (PDB: 3RCD). The lapatinib occupied more surface area of 521.59 Å² of binding cavity of HER-2 protein than compound 3c (471.50 Å²). This could be due to the presence of an extra fluorenyl ring in lapatinib structure which increases the surface area of lapatinib by 50 Å² and supports the crucial π - π interaction with PHE891 (Figure S1). Moreover, it was observed that lapatinib binding to active site was favoured by the hydrophobic interaction (LEU796, MET 801 and PHE891) and salt bridge interaction (ASP808) whereas compound 3c showed only one hydrophobic interaction (MET801), one polar interaction (GLN799) and one salt bridge interaction with LYS753 and hence lapatinib showed better dock score (-12.39) than our compound 3c (-6.08).

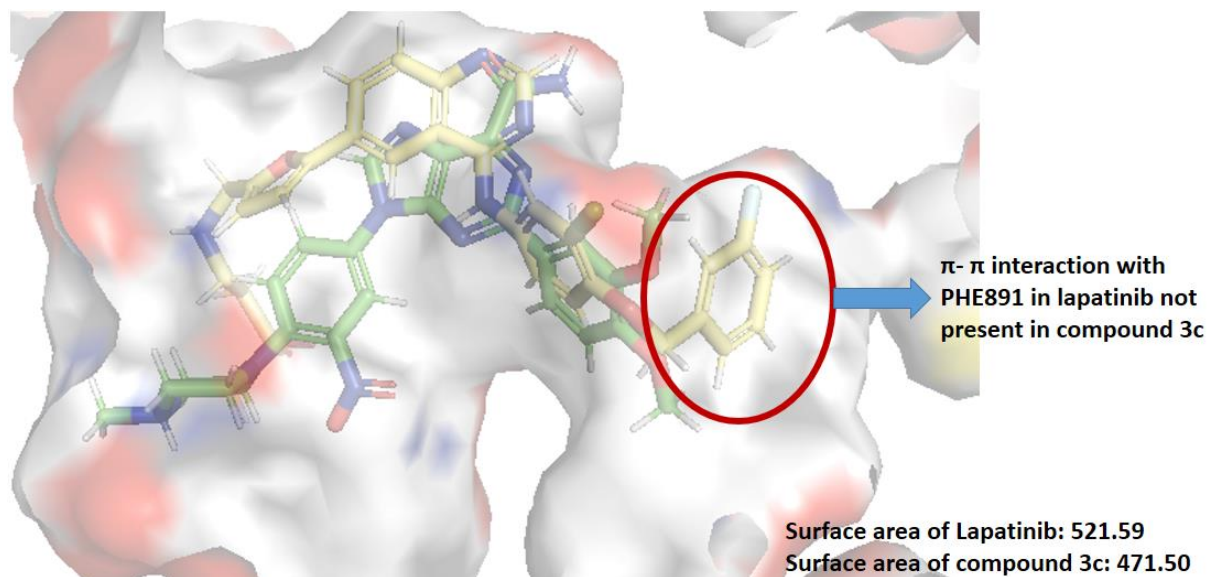
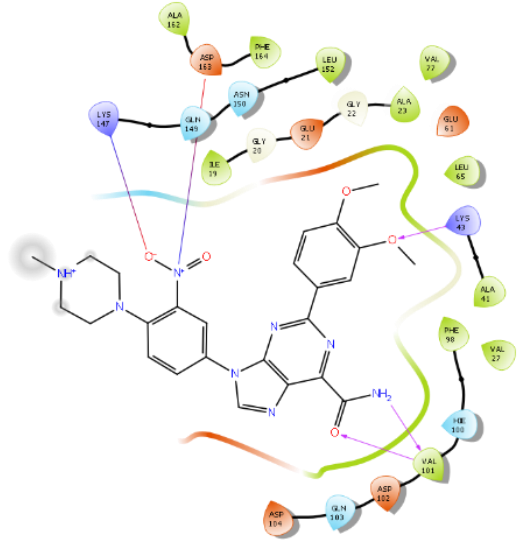


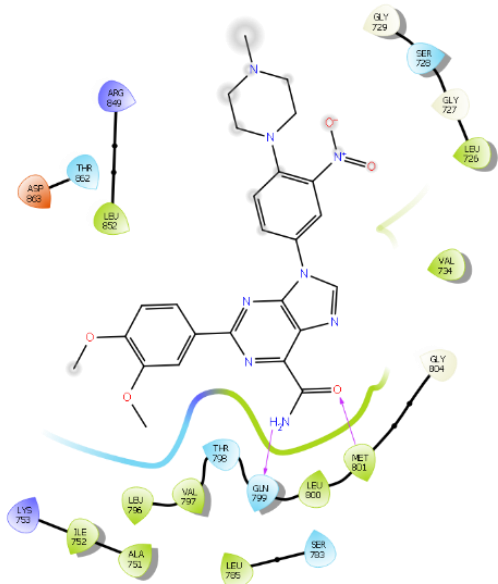
Figure S1: Represents the structure of lapatinib (yellow) and compound 3c (green) in HER-2 protein (PDB: 3RCD) with important fluorenyl ring in lapatinib that increases surface area of lapatinib by 50 Å² and supports π - π interaction with PHE891.

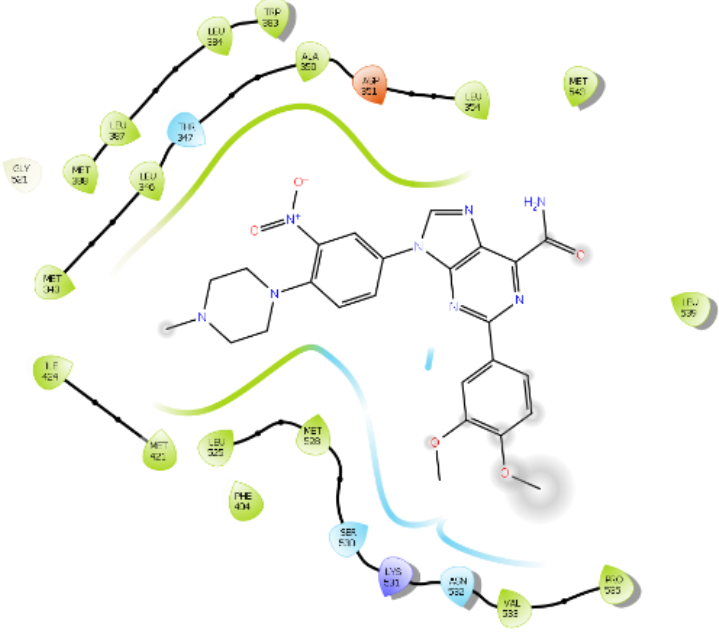
Similarly, docking results of compound **3c** were not favourable with other proteins as well (CDK-2, 4, 6, ER α and PR). We already mentioned in the manuscript that **3c** did not inhibit Cyclin dependant kinases (CDKs) under in vitro condition which could be due to poor binding and docking scores (Table S1). Compound **3c** could not even enter binding cavity of some PR. Therefore, EGDR inhibition could seem to be one of the major anticancer mechanisms.

Table S1: Docking of compound 3c into other proteins

Protein	ID	Positive Control (Dock Score)	Dock Score (Compound 3c)	2D interaction with 3c
CDK2	5L2W	Dinaciclib (-13.46)	-5.47	
CDK4	2W9Z	Pablociclib	No co-crystallized ligand	-----

		(NA)		
CDK6	2EUF	<p>Pablociclib</p> <p>(-10.46)</p>	-6.82	

HER2	3RCD	Lapatinib (-12.39)	-6.03	
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ER α	5W9C	Tamoxifen (-12.75)	-2.78	
PR	2W8Y	Mifepristone (NA)	Not entered in cavity	-----