

Supplementary data

A highly selective turn-off fluorescent probe for Cu(II) based on dansyl derivative and its application in living cell imaging

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1. Optimization of condition for probe 1 measurement

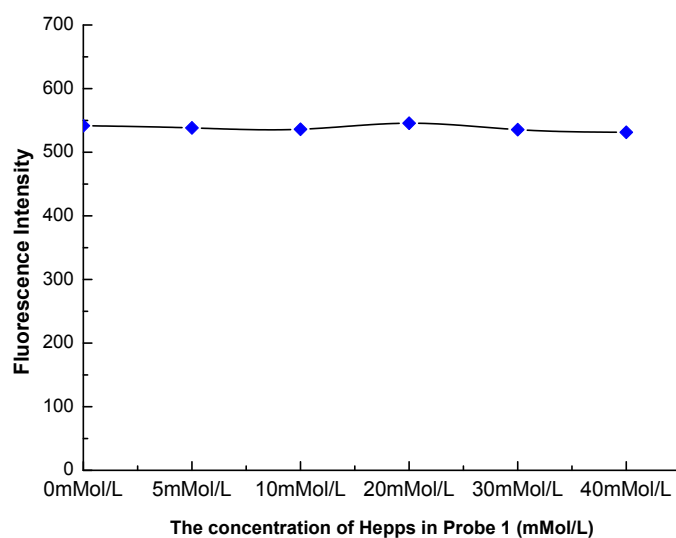


Fig. S1. Influence of the HEPES buffer solution concentration on the fluorescence intensity of 20 μM probe 1. (pH =7.0, $\lambda_{\text{ex}}/\lambda_{\text{em}} = 348 \text{ nm}/515 \text{ nm}$).

2. The UV response of 1 to various metal ions

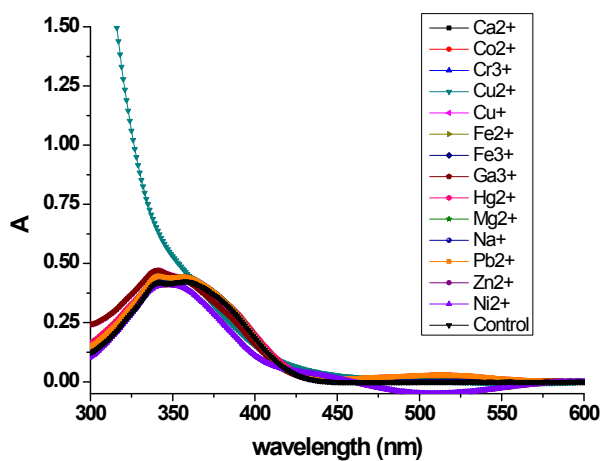
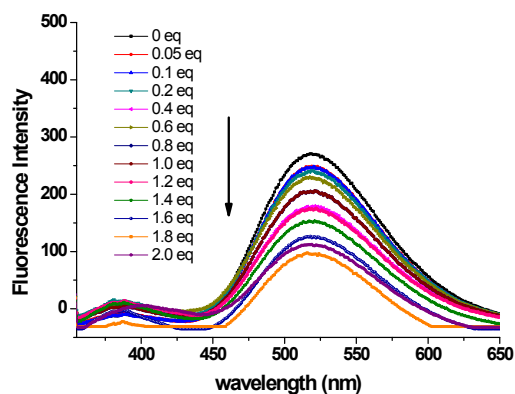


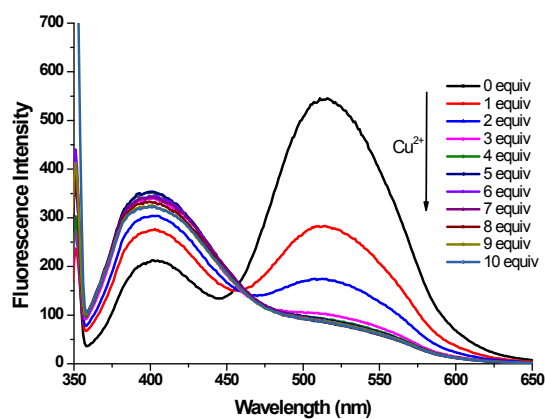
Fig. S2. UV-vis absorption spectra of probe 1 (16 μM) towards various metal ions (800 μM) in $\text{CH}_3\text{CN}/\text{HEPES}$ buffer (8/2, v/v, pH =7.0).

3. The titration experiments of probe 1

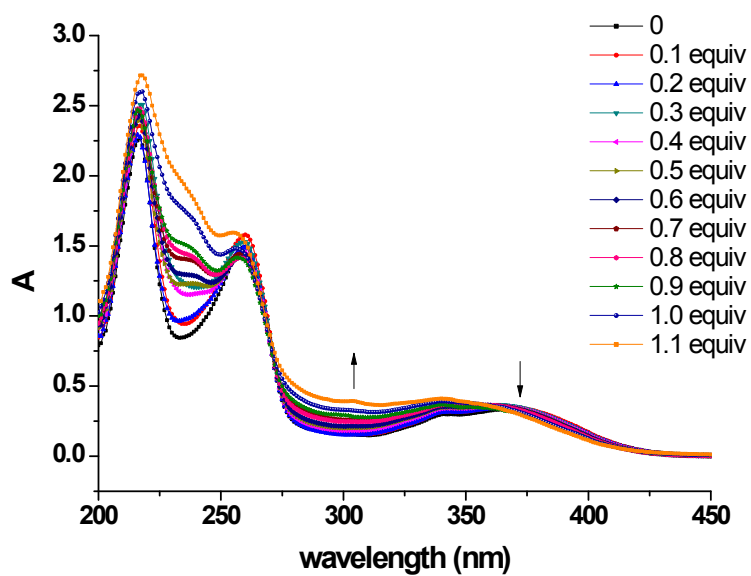
(a)



(b)



(c)



(d)

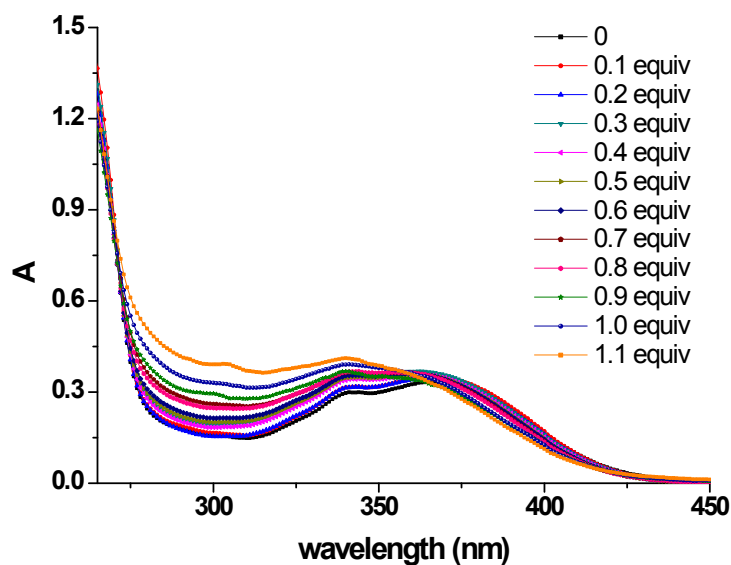


Fig. S3. (a) Fluorescence spectra of 8 μM probe 1 with Cu^{2+} between 0 and 2 equiv ($\text{CH}_3\text{CN}/\text{HEPES}$ buffer = 8/2, v/v, pH=7.0, $\lambda_{\text{ex}}/\lambda_{\text{em}}$ = 348 nm /515 nm); (b) Fluorescence spectra of 20 μM probe 1 with Cu^{2+} between 0 and 10 equiv (only HEPES buffer, pH=7.0, $\lambda_{\text{ex}} = 348$ nm); (c) UV-vis absorption spectra of probe 1 (16 μM) with Cu^{2+} between 0 and 1.1 equiv ($\text{CH}_3\text{CN}/\text{HEPES}$ buffer = 8/2, v/v, pH=7.0); (d) spectra of (c) from 260 nm to 450 nm.

4. The fluorescent intensity change of 1 to various anions

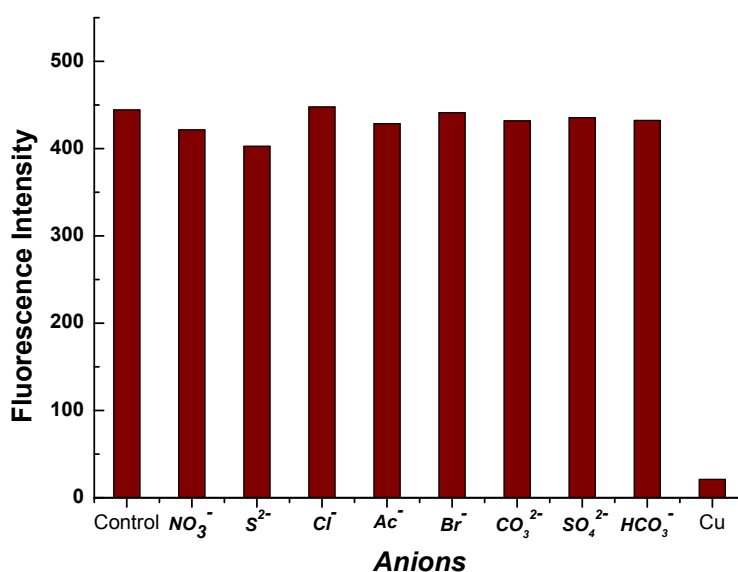


Fig. S4. The fluorescence variation of probe 1 (16 μM) to various anions at 800 μM concentration in $\text{CH}_3\text{CN}/\text{HEPES}$ buffer (8/2, v/v, pH=7.0, $\lambda_{\text{ex}}/\lambda_{\text{em}}$ = 348 nm /515 nm).

5. Binding Constant¹

The binding constant was calculated from the emission intensity - titration curves.

According to the equation:

$$(F-F_0)/F_0 = f/[1+(1/K_s [Cu^{2+}])],$$

where F_0 is the emission intensity of probe **1** at 515 nm, F is the emission intensity of **1** at 515 nm upon the addition of different concentration of Cu (II), f is the fraction of the initial fluorescence which is accessible to the sensor, $[Cu^{2+}]$ is the concentration of Cu^{2+} .

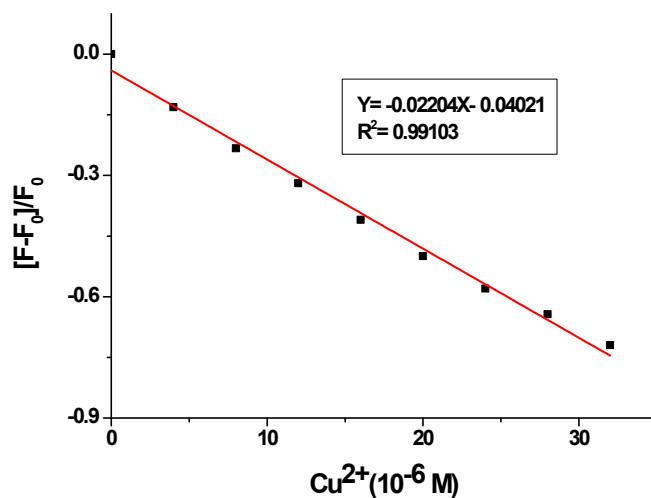


Fig. S5. Fitting of Fluorescence titration curve of **1** in $CH_3CN/HEPES$ (8: 2, v/v, pH =7.0). The binding constant is $K_s = 5.08 \times 10^4 M^{-1}$.

6. Job plot of the complexation between the probe **1** and Cu^{2+}

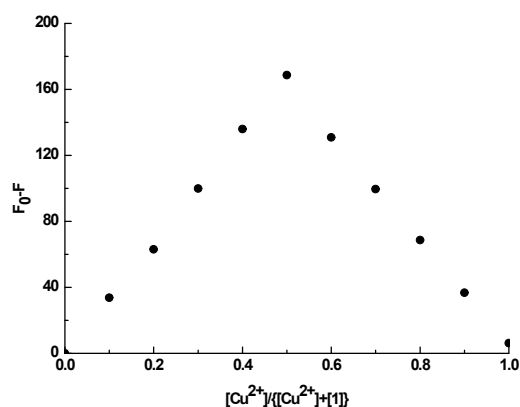


Fig. S6. Job plot of the complexation between the probe **1** and Cu^{2+} ($CH_3CN/HEPES$ buffer = 8/2, v/v, pH=7.0, $\lambda_{ex}/\lambda_{em} = 348 \text{ nm} / 515 \text{ nm}$). The total molar concentration of **1** and Cu^{2+} is $10 \mu M$;

7. The effect of pH

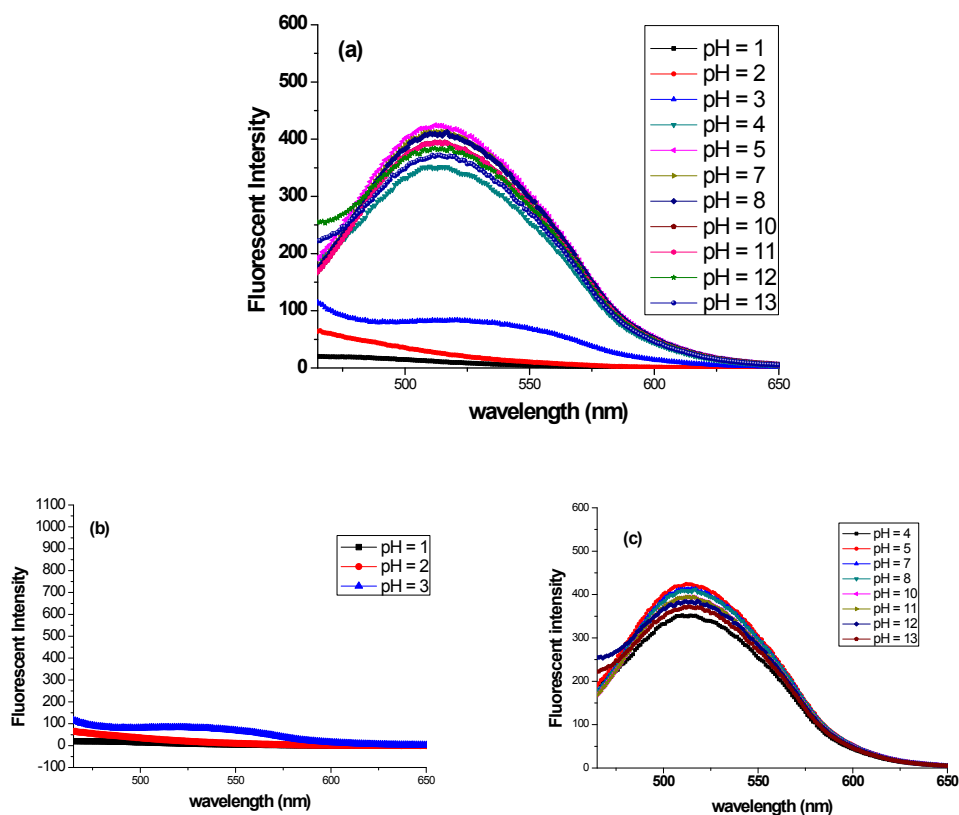


Fig. S7. (a) Influence of pH on fluorescence spectra of free **1** (16 μ M) in $\text{CH}_3\text{CN}/\text{H}_2\text{O}$ solution (8/2, v/v); (b) Influence of pH from 1.0 to 3.0; (c) Influence of pH 4.0 to 13.0.

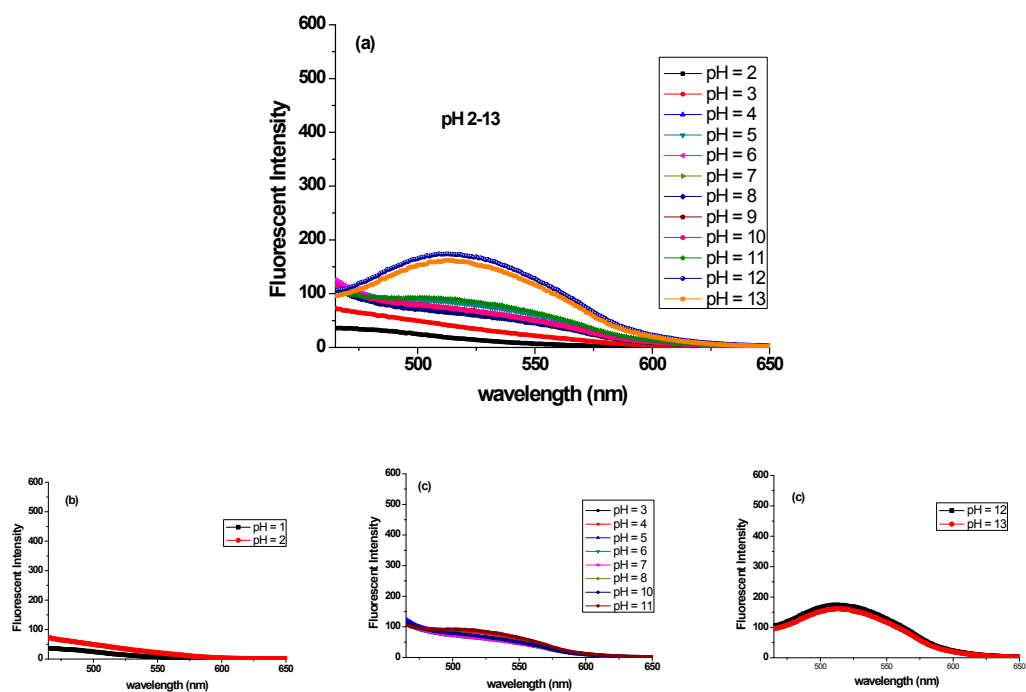


Fig. S8. (a) Influence of pH on fluorescence spectra of **1**/Cu²⁺ adduct (16 μM **1** and 80 μM Cu²⁺) in CH₃CN/H₂O solution (8/2, v/v); (b) Influence of pH from 1.0 to 2.0; (c) Influence of pH from 3.0 to 11.0; (d) Influence of pH from 12.0 to 13.0.

8. Fluorescence quantum yield

Table S1. Photophysical Data^a

Sample	F ₅₁₅	Φ _f (%)
1	178.03	8.2
1 + Cu ²⁺	9.23	0.42

^aF₅₁₅: Fluorescence intensity at 515nm. Φ_f: Fluorescence quantum yield.

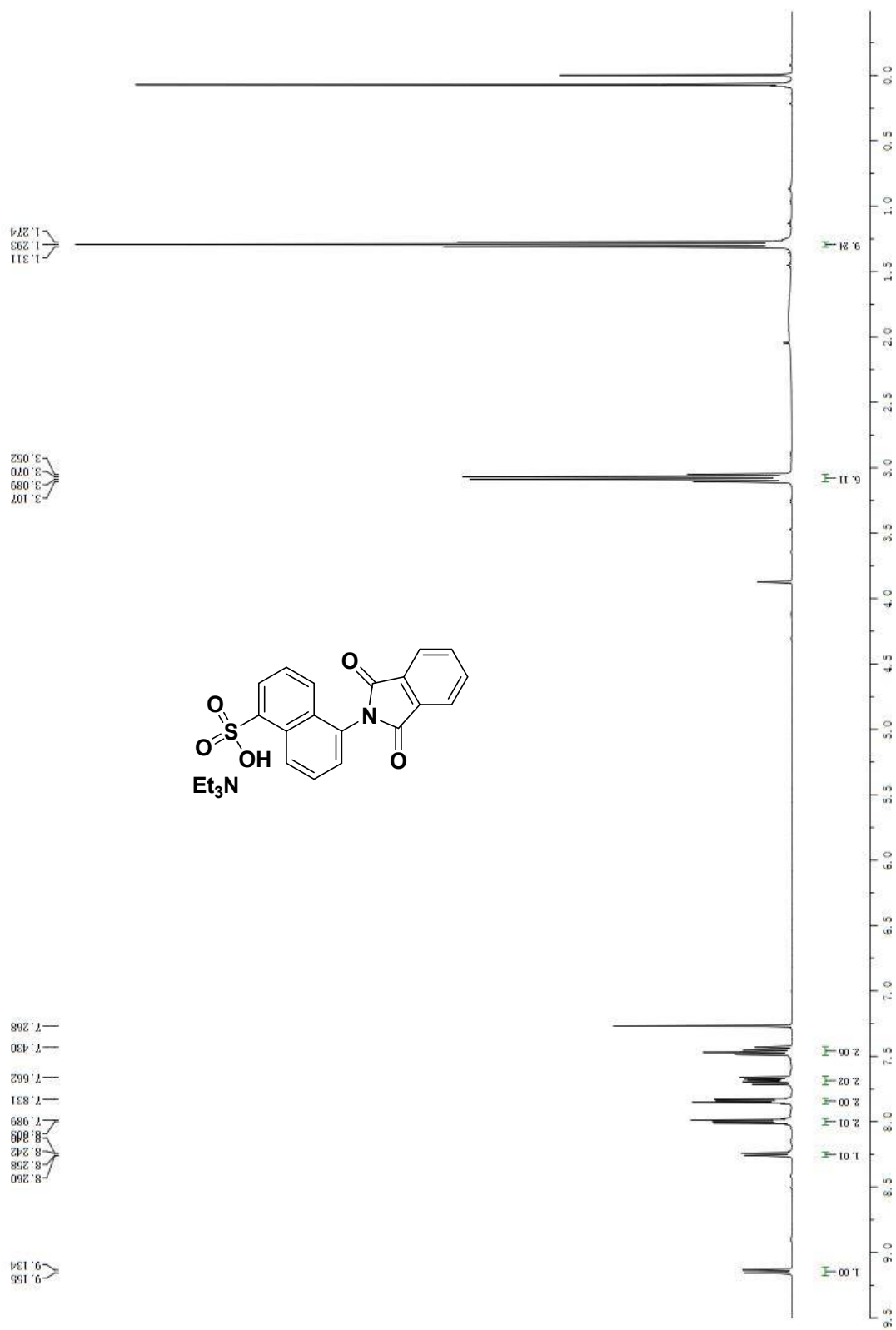
9. Reference

- Hou, F.P.; Huang, L.; Xi, P.X.; Cheng, J.; Zhao, X. F.; Xie, G.Q.; Shi, Y.J.; Cheng, F.J.; Yao, X.J.; Bai, D.C.; Zeng, Z. Z. *Inorg. Chem.* 2012, **51**, 2454.
- Melhuish, W. H. *J. Phys. Chem.* 1961, **65**, 229.

10. ^1H NMR, ^{13}C NMR, ESI-MS or HRMS spectra

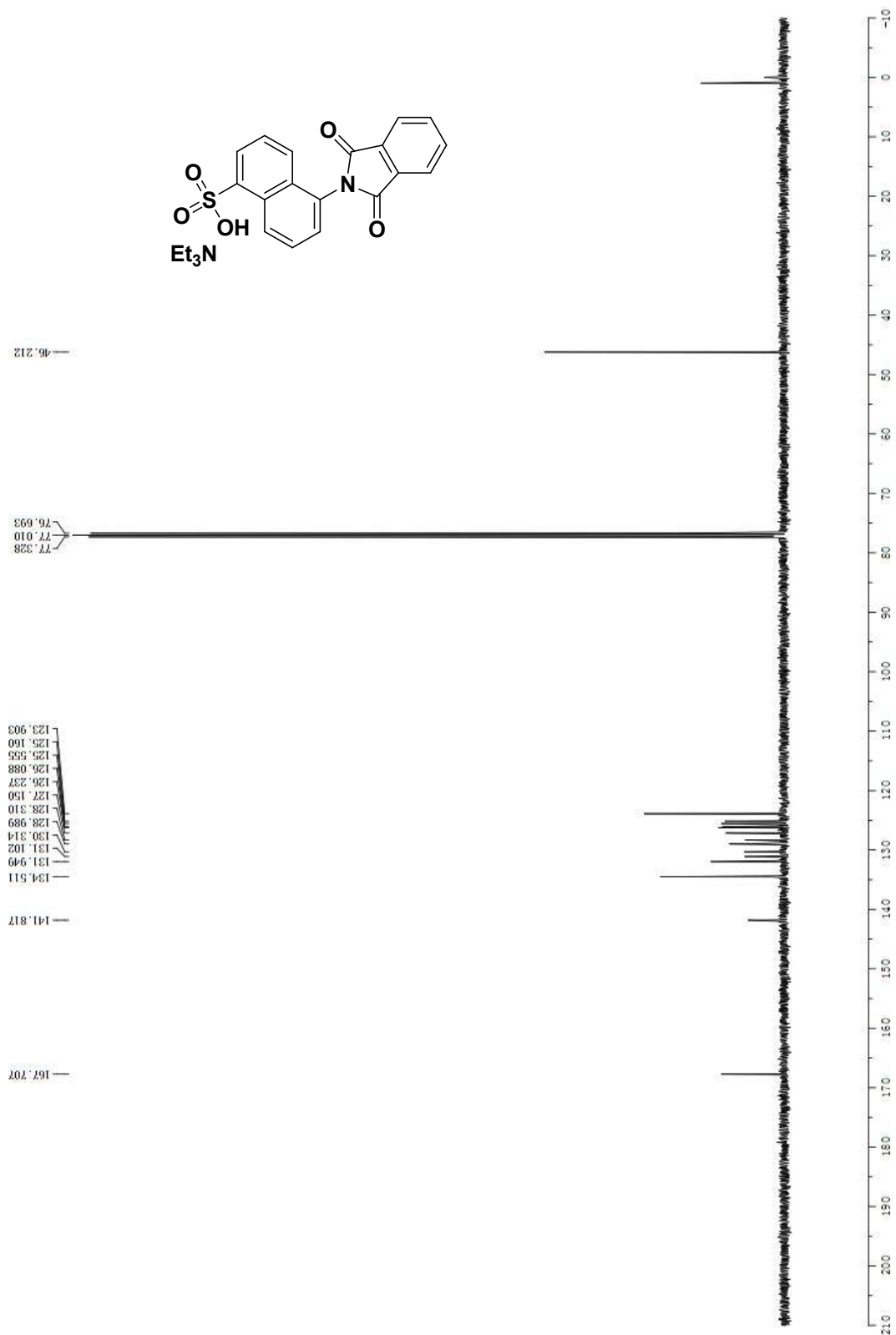
5-(1, 3-dioxoisindolin-2-yl)naphthalene-1-sulfonic acid (3)

^1H NMR (400 MHz, CDCl_3)



5-(1,3-dioxoisindolin-2-yl)naphthalene-1-sulfonic acid (3)

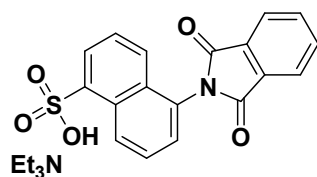
^{13}C NMR (400 MHz, CDCl_3)



5-(1,3-dioxisoindolin-2-yl)naphthalene-1-sulfonic acid (3)

HRMS

Page 1



1: TOF MS ES+
1.01e+000

Elemental Composition Report

Single Mass Analysis

Tolerance = 100.0 PPM / DBE: min = -1.8, max = 50.0

Element prediction: Off

Number of isotope peaks used for i-FIT = 3

Monoisotopic Mass, Even Electron Ions

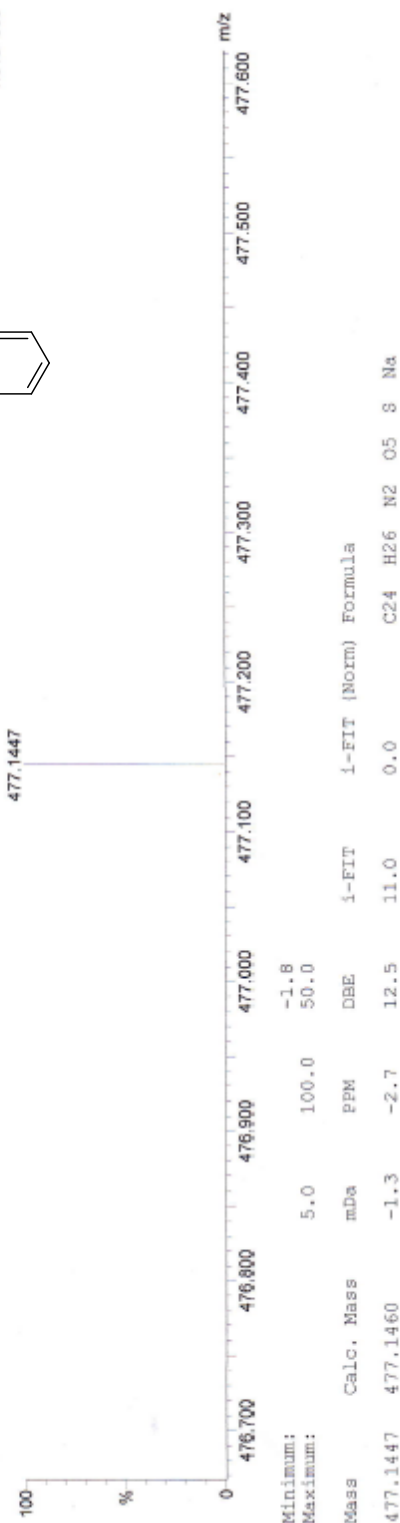
12 formula(e) evaluated with 1 results within limits (all results (up to 1000) for each mass)

Elements Used:

C: 24-24 H: 26-26 N: 0-3 O: 4-5 S: 0-2 Na: 0-1

454.1562

XFX-2.2 (0.054)



Minimum: -1.8

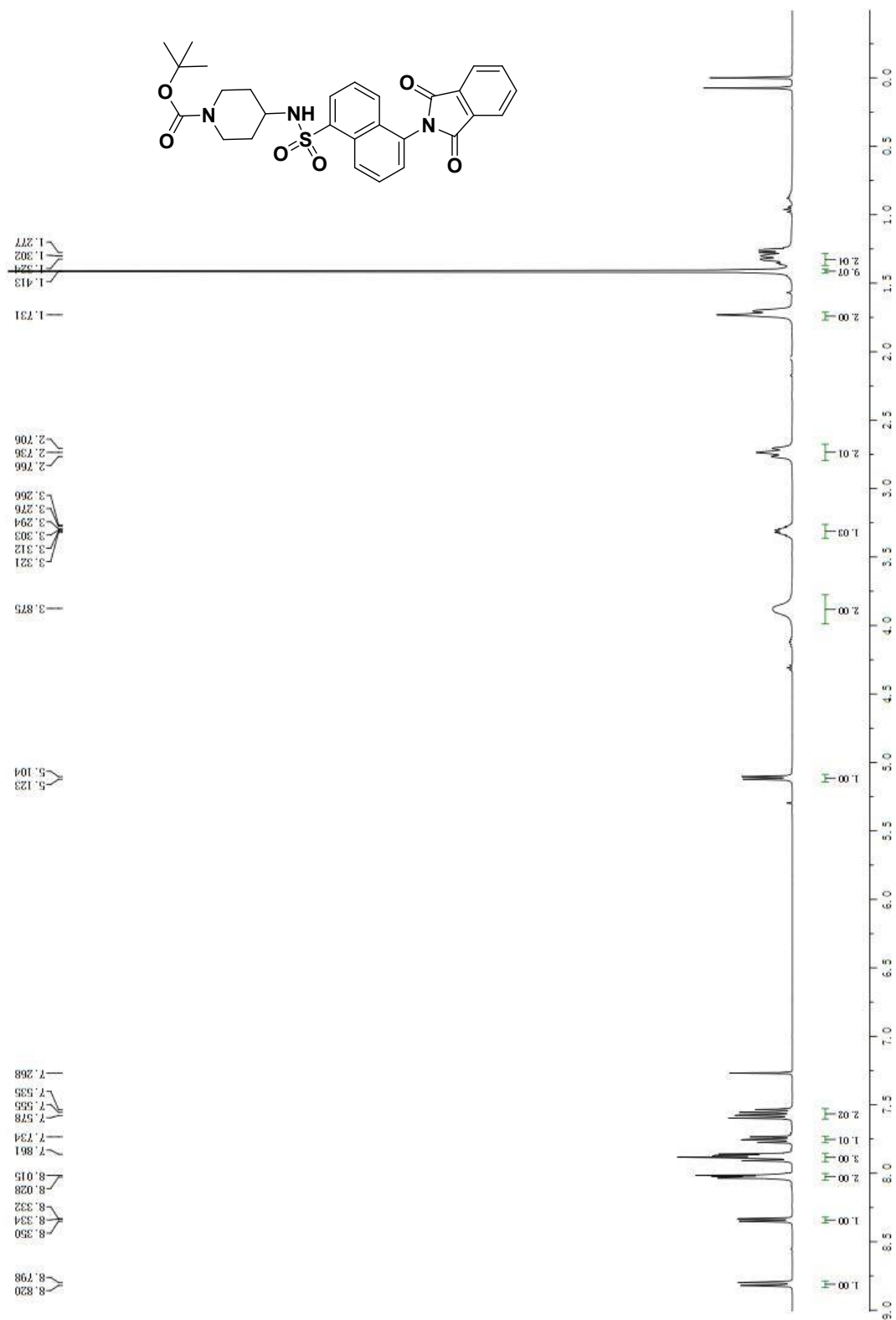
Maximum: 50.0

Mass Calc. Mass PPM DBE i-FIT i-FIT (Norm) Formula

477.1447 477.1460 -1.3 -2.7 12.5 11.0 0.0 C24 H26 N2 O5 S Na

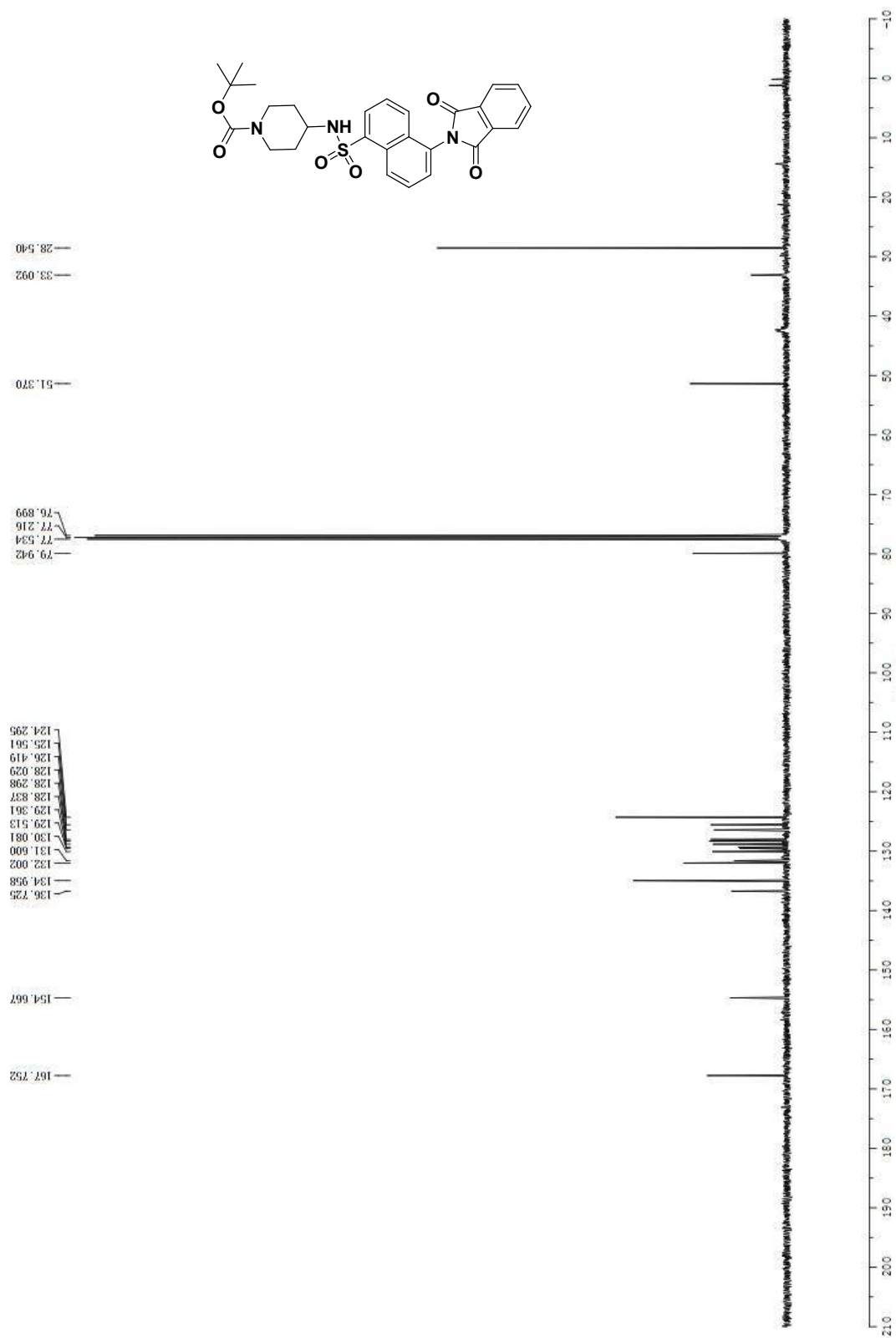
Tert-butyl 4-(5-(1,3-dioxoisindolin-2-yl)naphthalene-1-sulfonamido)piperidine-1-carboxylate (5)

¹H NMR (400 MHz, CDCl₃)



Tert-butyl 4-(5-(1,3-dioxisoindolin-2-yl)naphthalene-1-sulfonamido) piperidine -1-carboxylate (5)

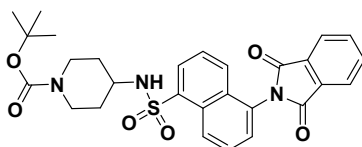
^{13}C NMR (400 MHz, CDCl_3)



Tert-butyl(4-(5-(1,3-dioxoisindolin-2-yl)naphthalene-1-sulfonamido) piperidine -1-carboxylate (5)

HRMS

Page 1



1: TOF MS ES+
4.56e+001

Elemental Composition Report

Single Mass Analysis

Tolerance = 10.0 PPM / DBE: min = -1.8, max = 50.0

Element prediction: Off

Number of isotope peaks used for i-FIT = 3

Monoisotopic Mass, Even Electron Ions

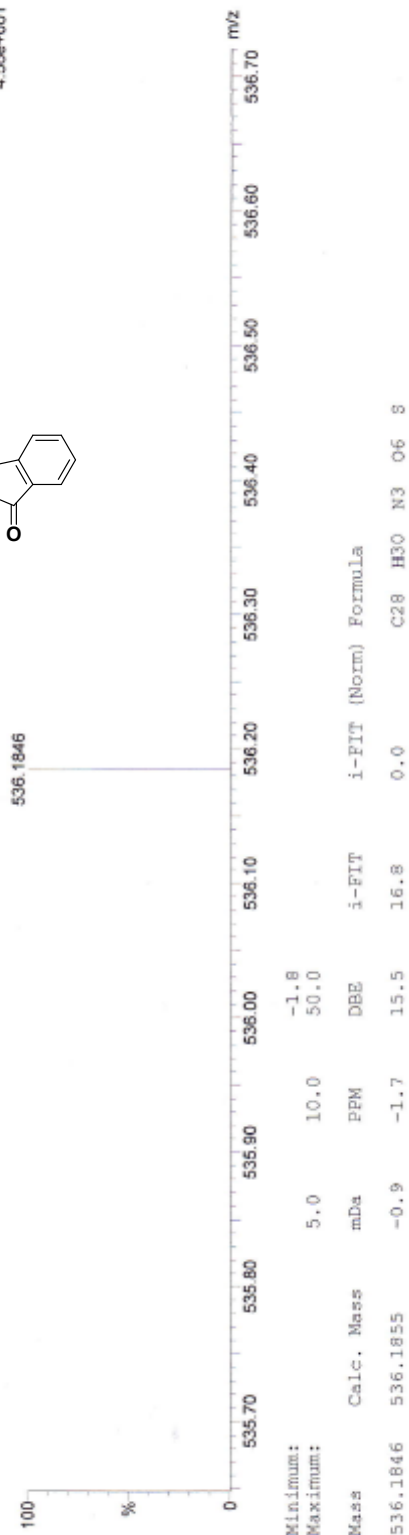
92 formulae) evaluated with 1 results within limits (all results (up to 1000) for each mass)

Elements Used:

C: 28-28 H: 29-329 N: 0-6 O: 0-6 S: 0-1

535.1777

FX-001 3 (0.083) Cm (2.34)



Minimum:

Maximum: 5.0 10.0 -1.8

Mass

536.1846

536.1855

-0.9

-1.7

15.5

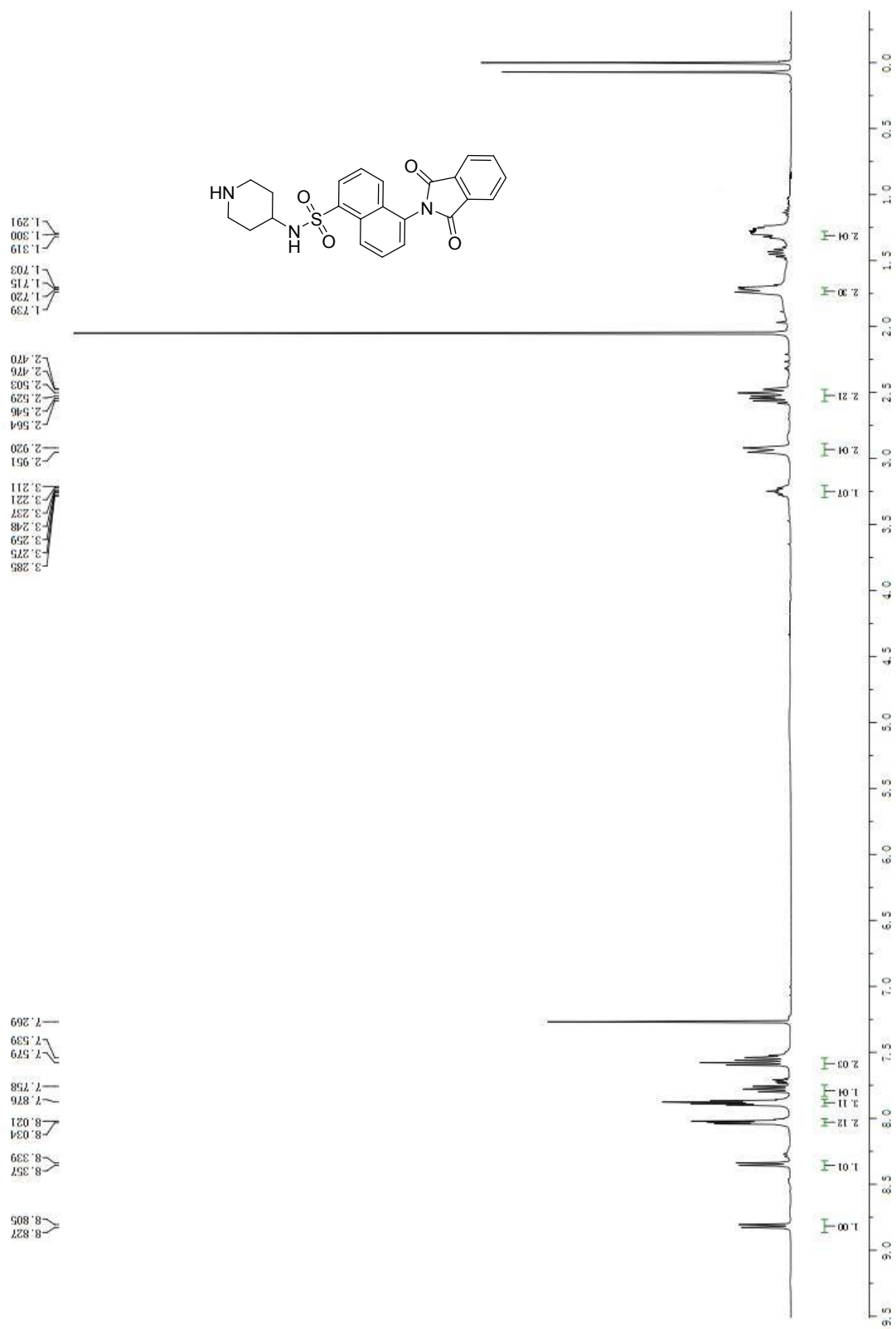
16.8

0.0

C28 H30 N3 O6 S

5-(1,3-dioxisoindolin-2-yl)-N-(piperidin-4-yl)naphthalene-1-sulfonamide (6)

¹H NMR (400 MHz, CDCl₃)



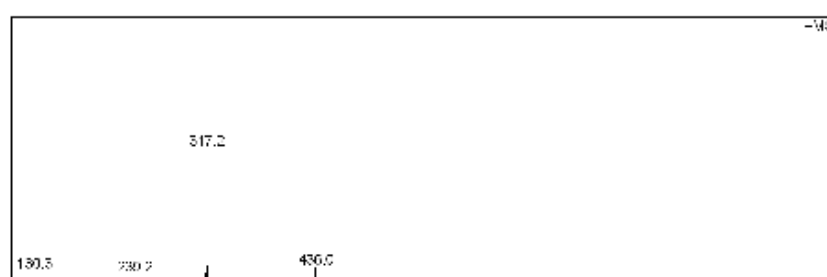
5-(1,3-dioxisoindolin-2-yl)-N-(piperidin-4-yl)naphthalene-1-sulfonamide (6)

ESI-MS

Mass Spectrum Deconvolution Report

Analysis Info		Acquisition Date 3/29/2012 6:38:57 PM	
Analysis Name	D:\Data\20120329-Jack-09.d	Operator	YLJ
Method	20111121-TEA.m	Instrument	esquire6000
Sample Name	20120329-Jack-09		
Comment	20120329-Jack-09		

Acquisition Parameter					
Ion Source Type	ESI	Ion Polarity	Positive	Alternating Ion Polarity	off
Mass Range Mode	Std/Normal	Scan Begin	105 m/z	Scan End	1000 m/z
Capillary Exit	113.5 Volt	Skimmer	40.0 Volt	Trap Drive	29.9
Accumulation Time	1162 μ s	Averages	2 Spectra	Auto MS/MS	off

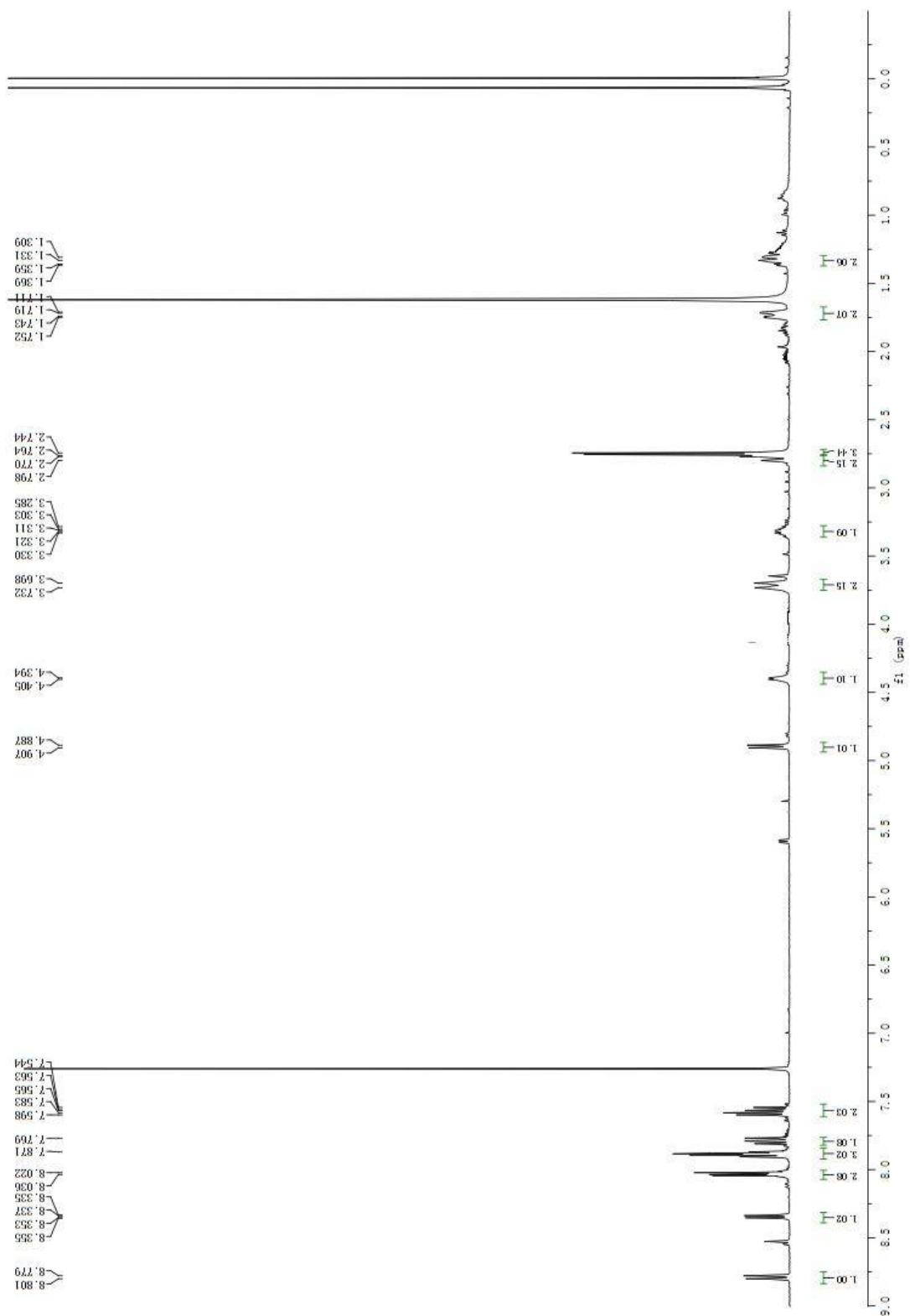


#	m/z	I
1	116.3	11708
2	130.3	19035
3	239.2	13555
4	241.2	3001
5	288.4	4146
6	317.2	240331
7	318.0	32527
8	319.2	3411
9	436.0	26177
10	437.0	7170

4-(5-(1,3-dioxisoindolin-2-yl)naphthalene-1-sulfonamido)-N-methylpiperidine-

1-carboxamide (7)

¹H NMR (400 MHz, CDCl₃)



4-(5-(1,3-dioxisoindolin-2-yl)naphthalene-1-sulfonamido)-N-methylpiperidine-

1-carboxamide (7)

HRMS

Page 1

Elemental Composition Report

Single Mass Analysis

Tolerance = 10.0 PPM / DBE: min = -1.8, max = 50.0

Element prediction: Off

Number of isotope peaks used for i-FIT = 3

Monoisotopic Mass, Even Electron Ions

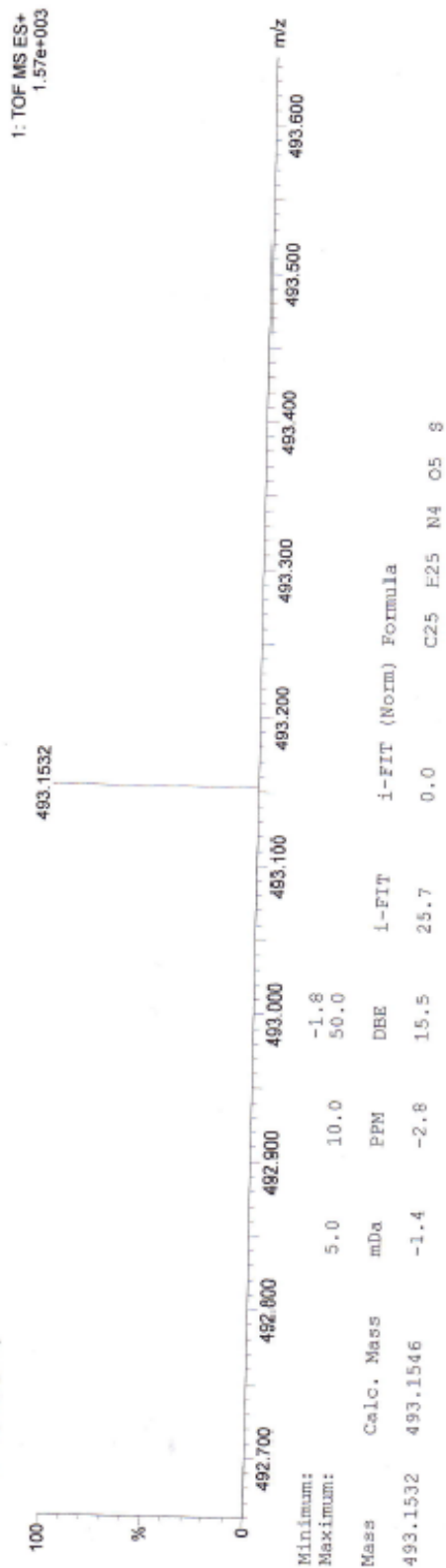
26 formula(e) evaluated with 1 results within limits (all results (up to 1000) for each mass)

Elements Used:

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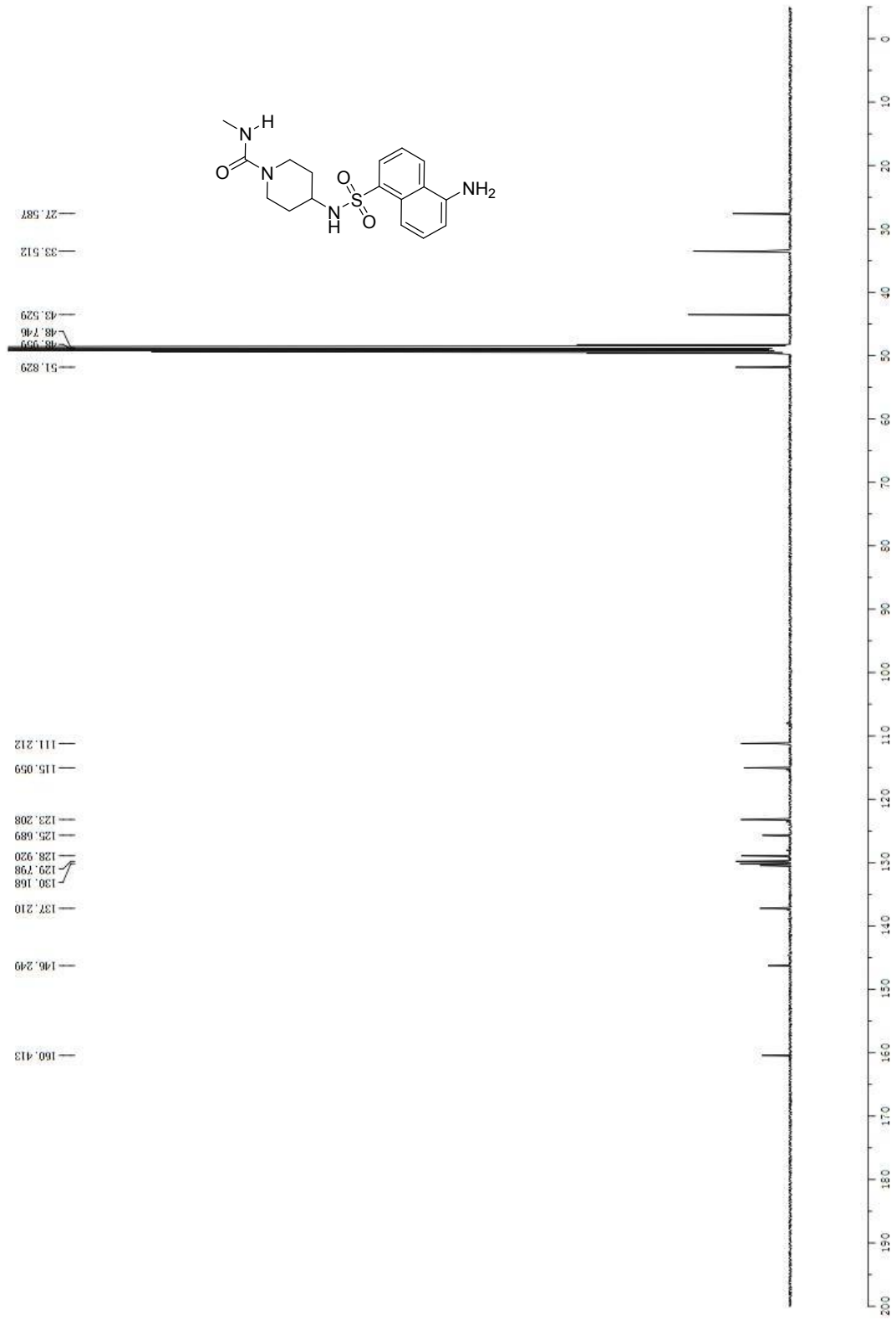
492.1467

FX-003 3 (0.082) Cm (3.48)



4-(5-aminonaphthalene-1-sulfonamido)-N-methylpiperidine-1-carboxamide (8)

¹³C NMR (400 MHz, CD₃OD)



4-(5-aminonaphthalene-1-sulfonamido)-N-methylpiperidine-1-carboxamide (8)

Elemental Composition Report

Single Mass Analysis

Tolerance = 10.0 PPM / DBE: min = -1.8, max = 50.0

Element prediction: Off

Number of isotope peaks used for i-FIT = 3

Monoisotopic Mass, Even Electron Ions

54 formulae) evaluated with 1 results within limits (all results (up to 1000) for each mass)

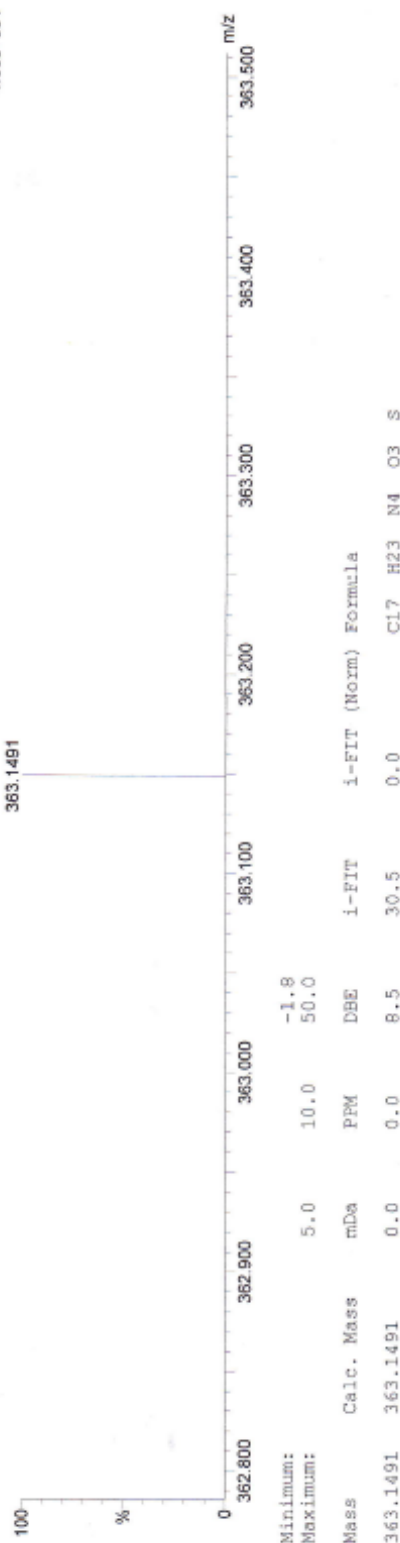
Elements Used:

C: 17-17 H: 22-23 N: 0-6 O: 0-6 S: 0-1

362.1413

FX-004 3 (0.082) Cm (2:39)

1: TOF MS ES+
1.50e+004



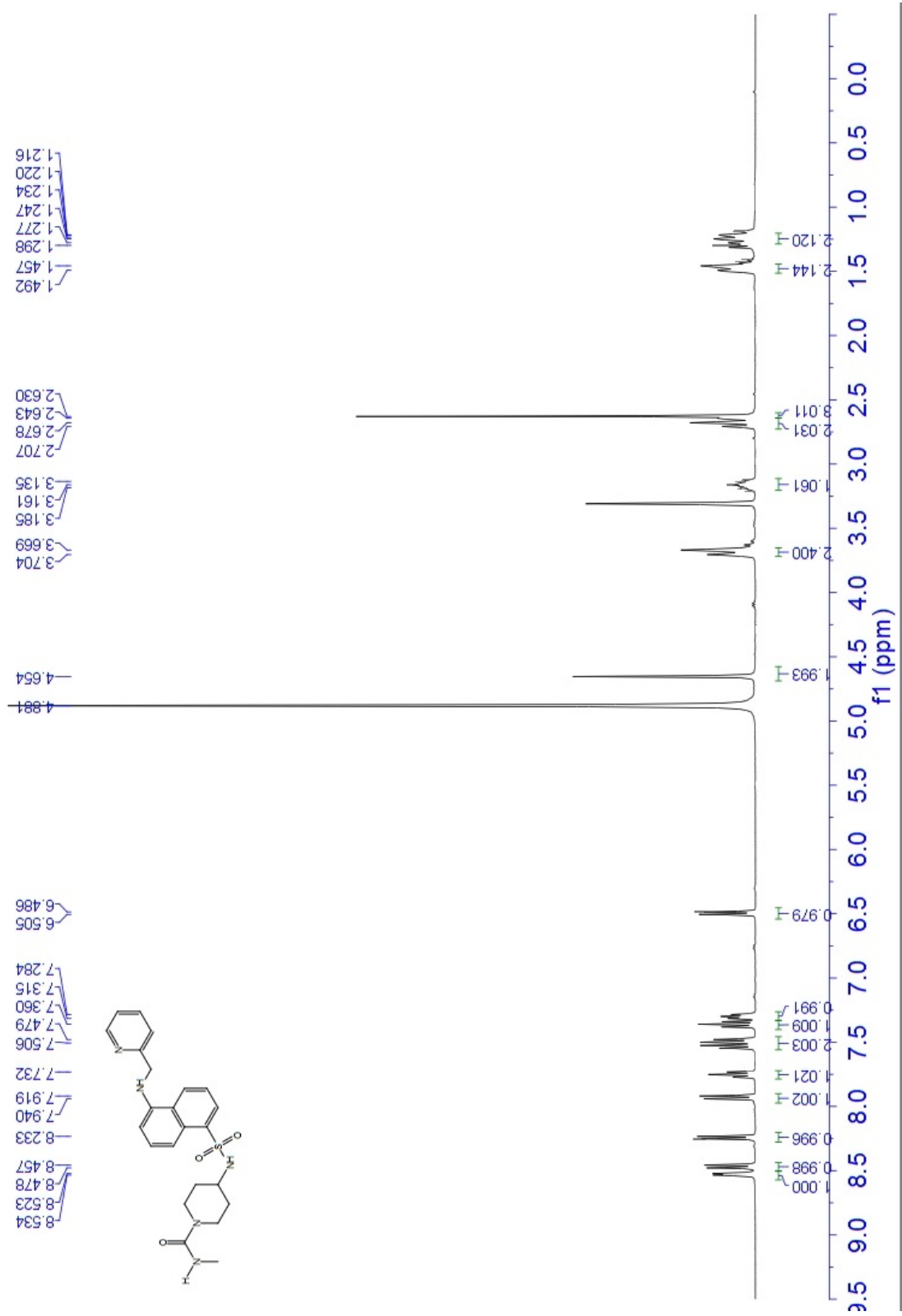
Minimum: -1.8
Maximum: 50.0

Mass	Calc. Mass	mDa	PPM	DBE	i-FIT	i-FIT (Norm)	Formula
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N-methyl-4-(5-(pyridin-2-ylmethylamino)naphthalene-1-sulfonamido)piperidine-

1-carboxamide (1)

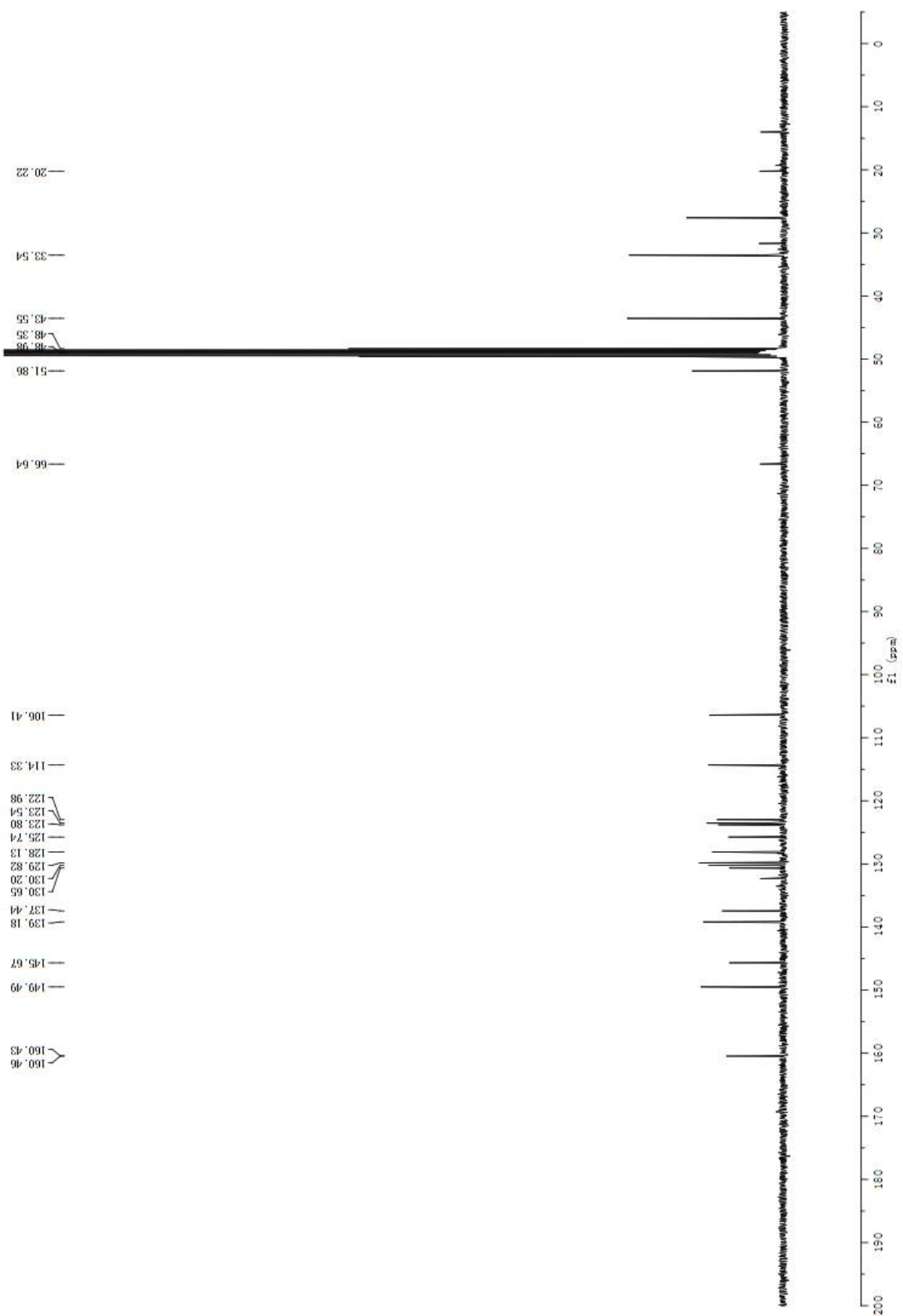
¹H NMR (400 MHz, CD₃OD)



N-methyl-4-(5-(pyridin-2-ylmethylamino)naphthalene-1-sulfonamido)piperidine-

1-carboxamide (1)

¹³C NMR (400 MHz, CD₃OD)



N-methyl-4-(5-(pyridin-2-ylmethylamino)naphthalene-1-sulfonamido)piperidine-

1-carboxamide (1)

HRMS

Page 1

Elemental Composition Report

Single Mass Analysis

Tolerance = 10.0 PPM / DBE: min = -1.8, max = 50.0

Element prediction: Off

Number of isotope peaks used for i-FIT = 3

Monoisotopic Mass, Even Electron Ions

53 formula(e) evaluated with 1 results within limits (all results (up to 1000) for each mass)

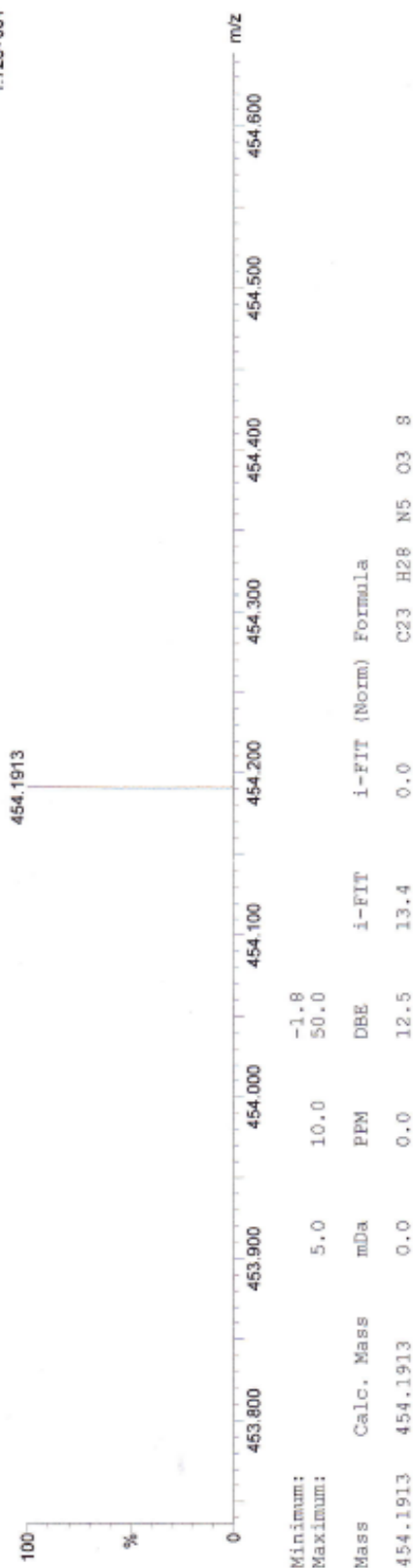
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453.1835

FX-008 9 (0.220)

1: TOF MS ES+
1.72e+001



Minimum: -1.8

Maximum: 50.0

Mass	Calc. Mass	mDa	PPM	DBE	i-FIT	i-FIT (Norm)	Formula
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454.1913	454.1913	0.0	0.0	12.5	13.4	0.0	C23 H28 N5 O3 8
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