

Synthesis, Molecular Modelling, and Evaluation of New Mono- and Bis-isoxazoline as Antibacterial Agents: *In vitro* and *In silico* Analysis

Ali Altharawi¹, Bharath Kumar Chagaleti^{2,*}, Mubarak A. Alamri¹, Yassine Riadi¹, Taibah Aldakhil¹, Ait Itto Moulay Youssef³, Ali Oubella⁴, Reda A. Haggam^{5*}

¹ Department of Pharmaceutical Chemistry, College of Pharmacy, Prince Sattam Bin Abdulaziz University, Al-Kharj 11942, Saudi Arabia

² Department of Pharmaceutical Chemistry, SRM College of Pharmacy, Faculty of Medicine and Health Sciences, SRM Institute of Science and Technology, Kattankulathur, Chengalpattu, Chennai 603203, India

³ Laboratory of Organic Synthesis and Physico-Molecular Chemistry, Department of Chemistry, Faculty of Sciences Semlalia, Université Cadi Ayyad, BP PO Box 2390, Marrakech 40001, Morocco

⁴ Laboratory of Organic & Physical Chemistry, Applied Bioorganic Chemistry Team, Faculty of Sciences, Ibn Zohr University. Agadir, Morocco

⁵ Department of Chemistry, Faculty of Science, Islamic University of Madinah, 42351 Madinah, Saudi Arabia

* *Corresponding authors.*

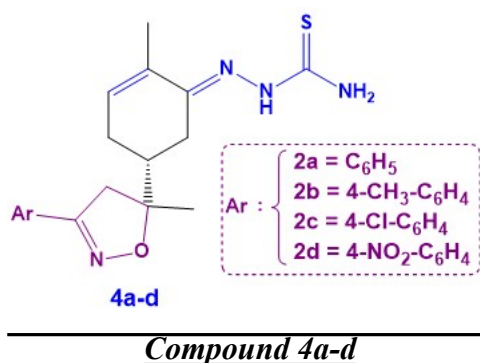
E-mail addresses : chagalek@srmist.edu.in (Bharath Kumar Chagaleti); relhaggan@iu.edu.sa (Reda A. Haggam)

Abstract

This study aimed to design, synthesize, and evaluate a novel series of isoxazoline-thiosemicarbazone derivatives as potential antibacterial agents, supported by computational investigations. Compounds were synthesized and characterized using ¹H and ¹³C NMR and HRMS. Compounds **4a-d** and **6** were evaluated for their *in vitro* antibacterial activity against Gram-positive and Gram-negative bacterial strains by determining their minimum inhibitory concentrations (MICs). Molecular docking studies were conducted to assess binding interactions with the PTGS2 protein, followed by molecular dynamics simulations to evaluate the stability of the ligand-protein complexes. MM-GBSA calculations were performed to estimate binding free energies, and *in silico* ADMET predictions were carried out to assess drug-likeness. Compounds **4a-d** and **6** exhibited potent antibacterial activity, with MIC values ranging from 0.31 to 0.5 µg/mL. Molecular docking results revealed strong binding affinities of compound **4a** toward the active site of PTGS2. Molecular dynamics confirmed the structural stability of the PTGS2-4a complex. MM-GBSA analysis demonstrated that PTGS2-4a displayed the most favorable binding free energy, showing superior or comparable performance to the reference inhibitor Resatorvid. *In silico* ADME-T analysis indicated acceptable pharmacokinetic properties. These results highlight compounds **4a-d** as promising

antibacterial candidates, providing a strong rationale for the development of novel isoxazoline-thiosemicarbazone-based antibacterial agents.

Keywords: Synthesis, Thiosemicarbazone, Isoxazoline, Antibacterial activity, Docking, ADME-T



Compound 4a

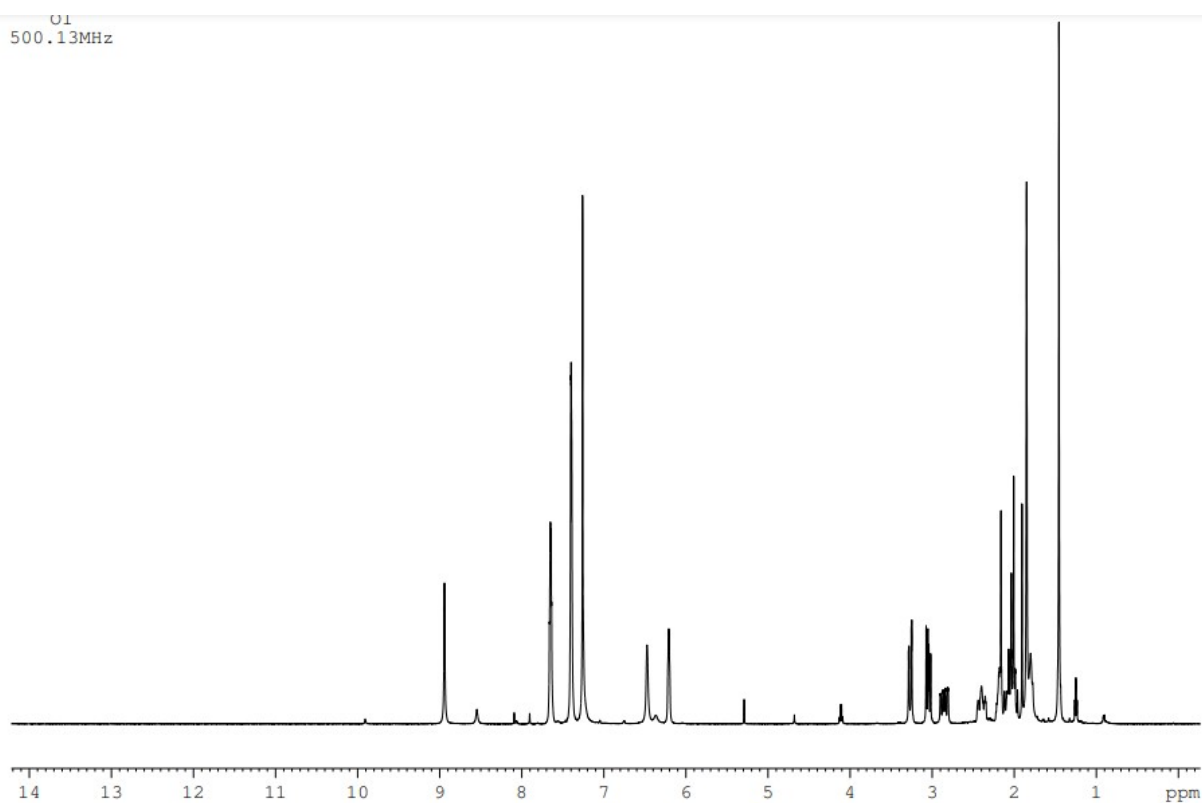


Fig. 1S. $^1\text{H-NMR}$ spectrum of compound **4a** (500 MHz, CDCl_3)

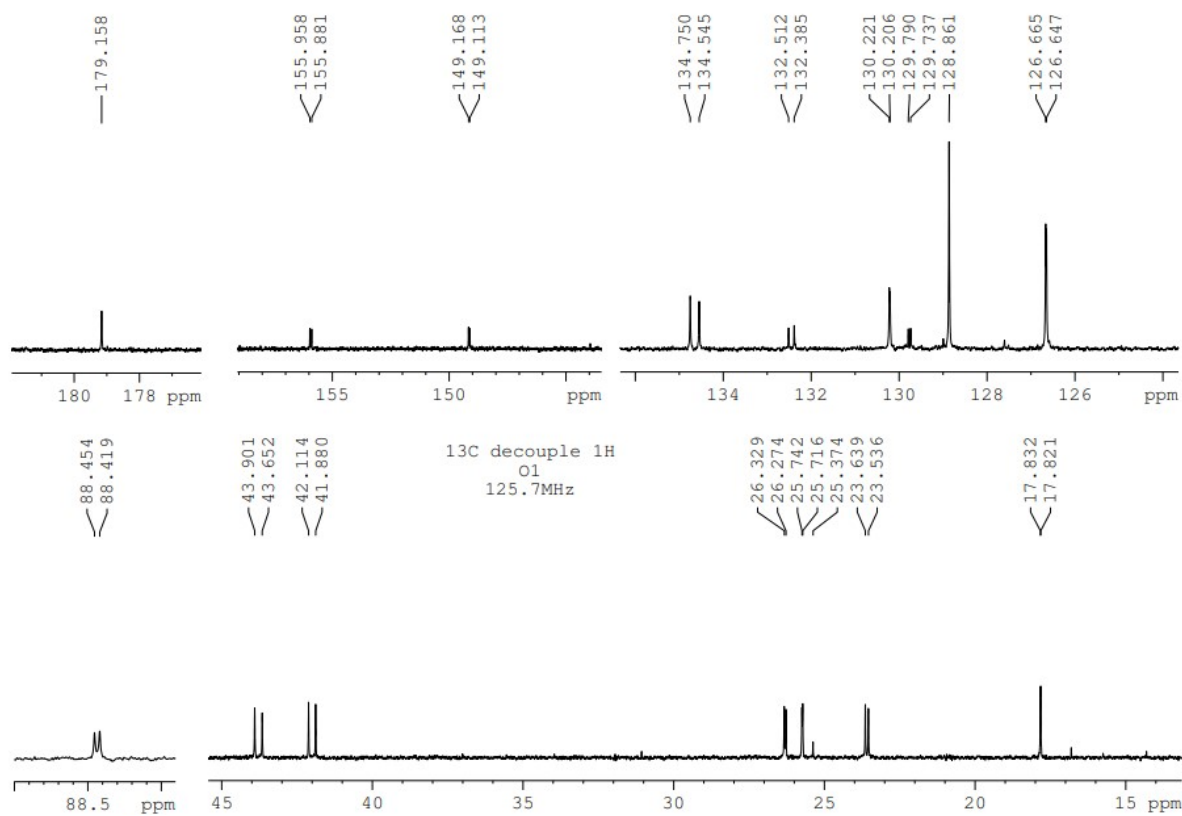


Fig. 2S. ^1H -NMR spectrum of compound 4a (500 MHz, CDCl_3 , "Zoom")

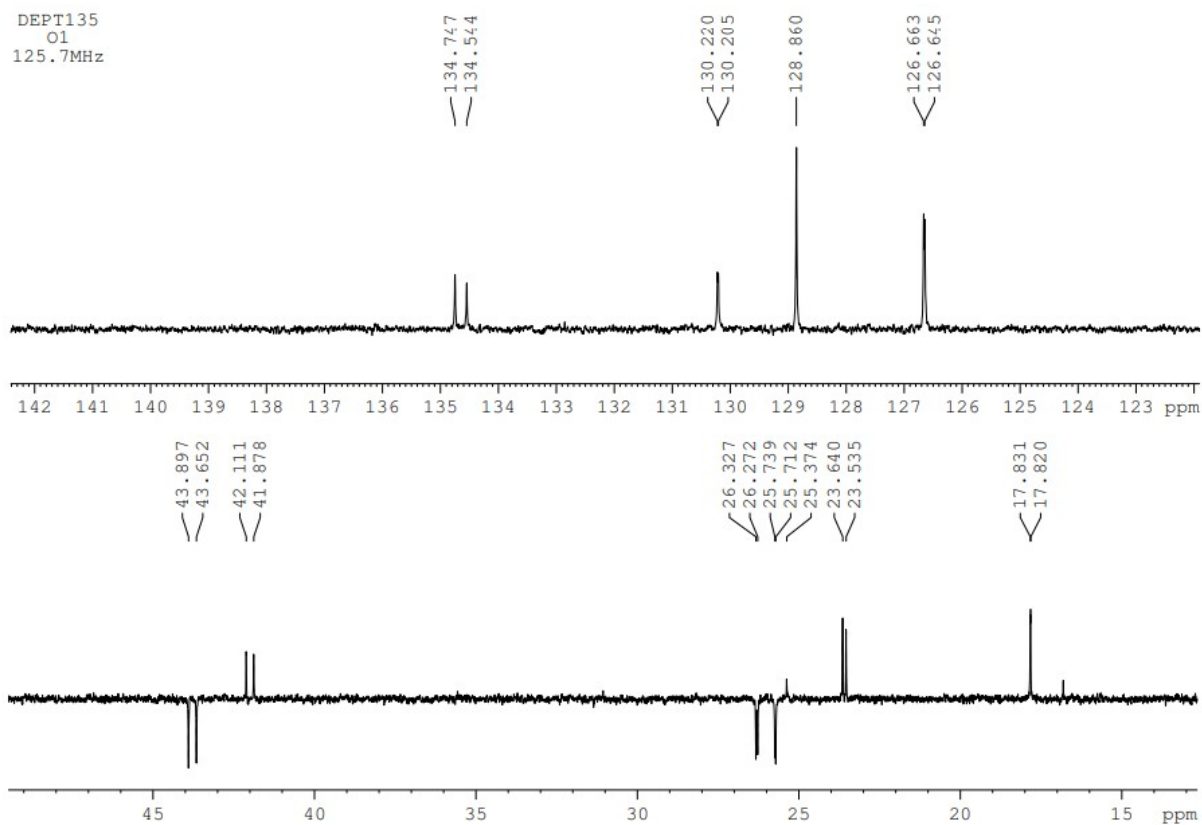


Fig. 3S. ^{13}C Decoupled ^1H -NMR spectrum DEPT 135 Mode (500 MHz, CDCl_3 , "Zoom")

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 = 3

Monoisotopic Mass, Even Electron Ions

1011 formula(e) evaluated with 5 results within limits (up to 50 closest results for each mass)

Elements Used:

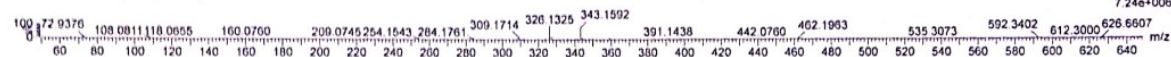
C: 0-60 H: 0-100 N: 0-5 O: 0-20 S: 0-1 Cl: 0-2

series: O1

10HR721 140 (1 123) Cm (140 167)

1: TOF MS ES+

7.24e+006



Mass	Calc. Mass	mDa	PPM	DBE	i-FIT	Norm	Conf (%)	Formula
343.1592	343.1593	-0.1	-0.3	9.5	2239.9	0.208	81.24	C18 H23 H4 O S
	343.1595	-0.3	-0.9	4.5	2254.9	15.212	0.00	C19 H29 O Cl2
	343.1604	-1.2	-3.5	0.5	2251.1	11.400	0.00	C13 H27 O10
	343.1579	1.3	3.8	4.5	2241.4	1.674	18.76	C17 H27 O5 S
	343.1577	1.5	4.4	9.5	2253.3	13.589	0.00	C20 H24 N2 O Cl

Fig. 4S. HRMS spectrum of compound 4a

Compound 4b

¹H
O2
500.13MHz

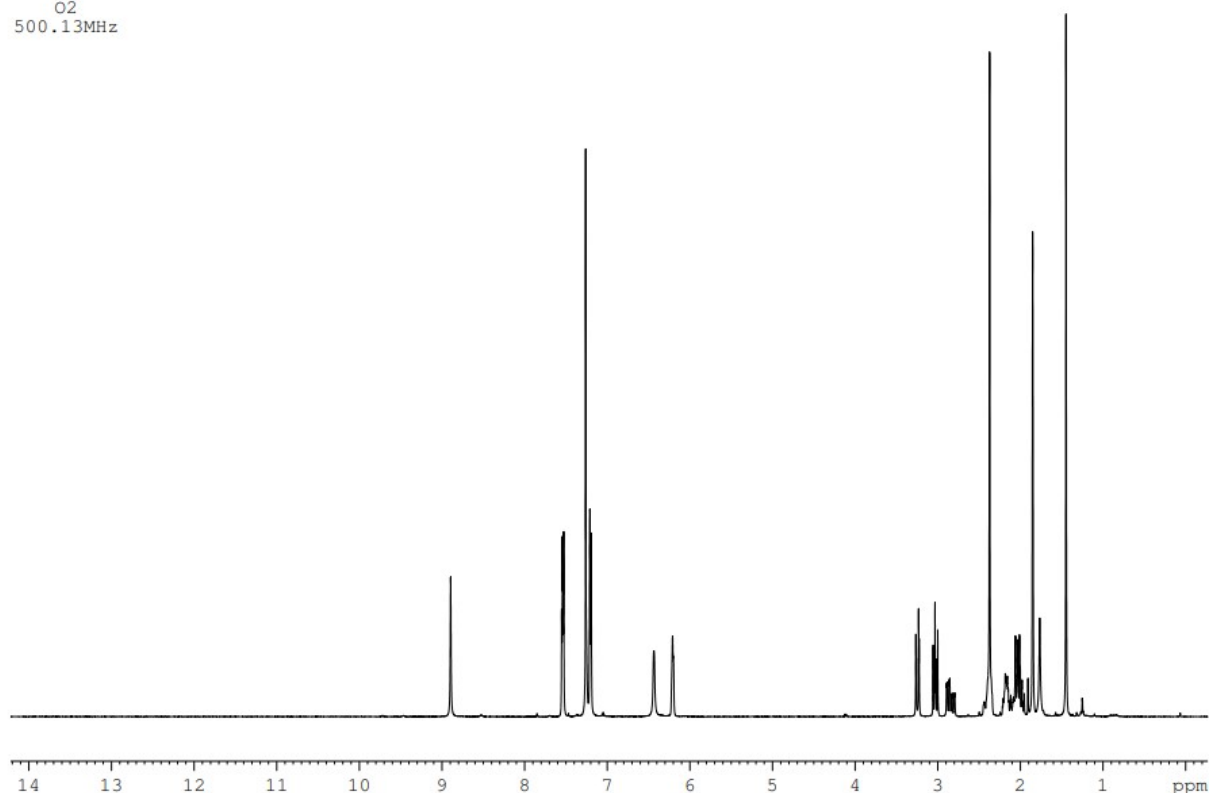


Fig. 5S. ¹H-NMR spectrum of compound 4b (500 MHz, CDCl₃)

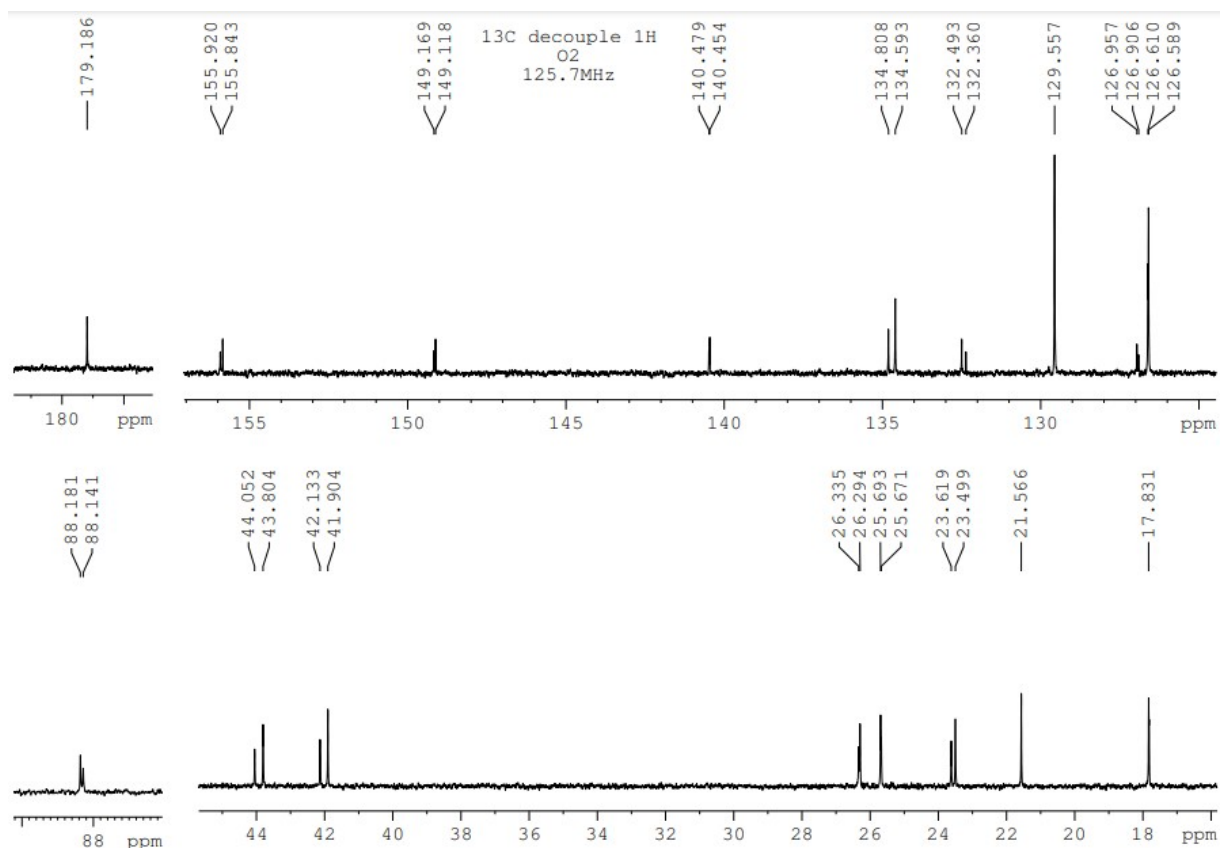


Fig. 6S. ¹H-NMR spectrum of compound **4b** (500 MHz, CDCl₃ “Zoom”)

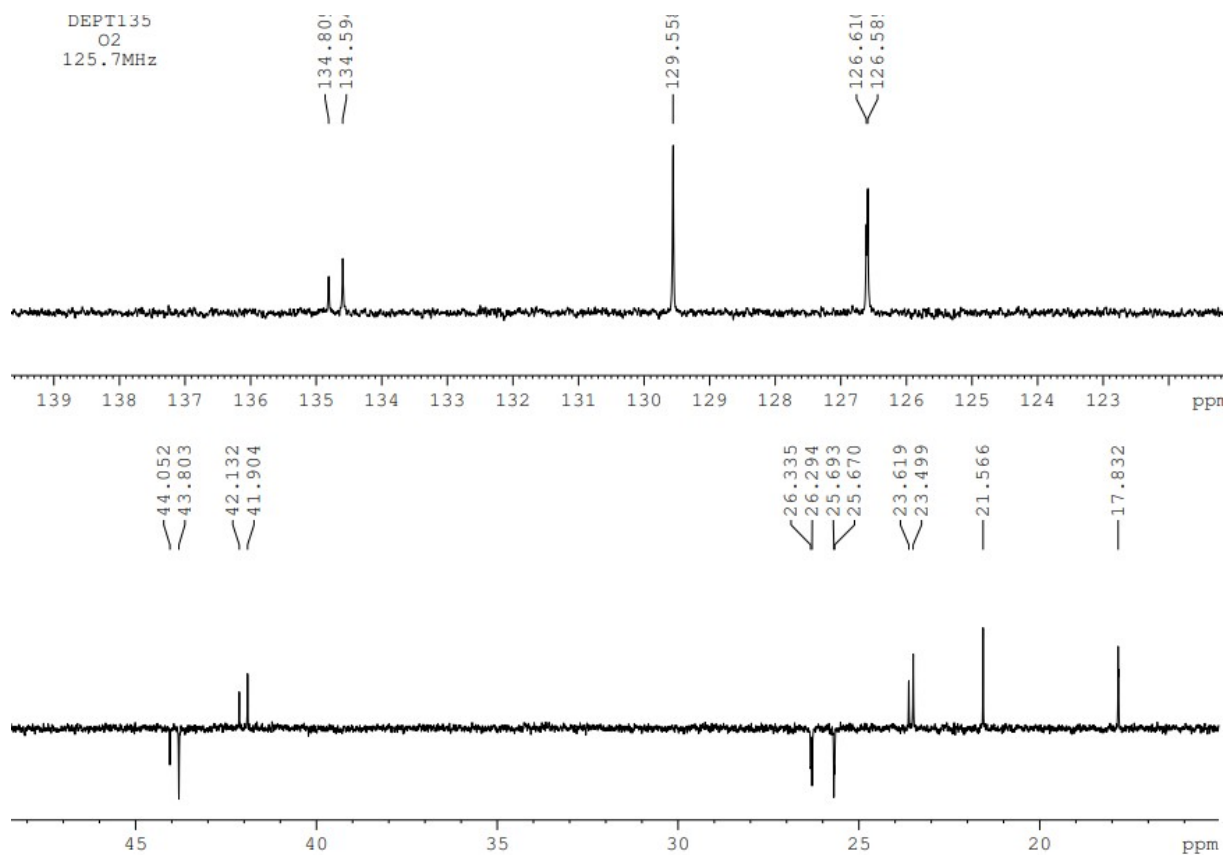


Fig. 7S. ¹³C Decoupled ¹H-NMR spectrum of compound **4b** (DEPT 135 Mode)

Single Mass Analysis

Tolerance = 4.0 PPM / DBE: min = -1.5, max = 50.0

Element prediction: Off

Number of isotope peaks used for i-FIT = 3

Monoisotopic Mass, Even Electron Ions

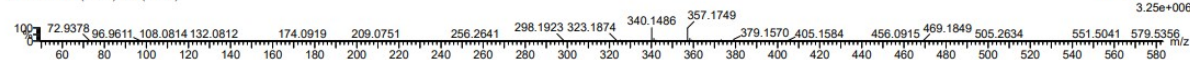
231 formula(e) evaluated with 1 results within limits (up to 15 closest results for each mass)

Elements Used:

C: 0-25 H: 0-100 N: 0-6 O: 0-3 S: 0-1

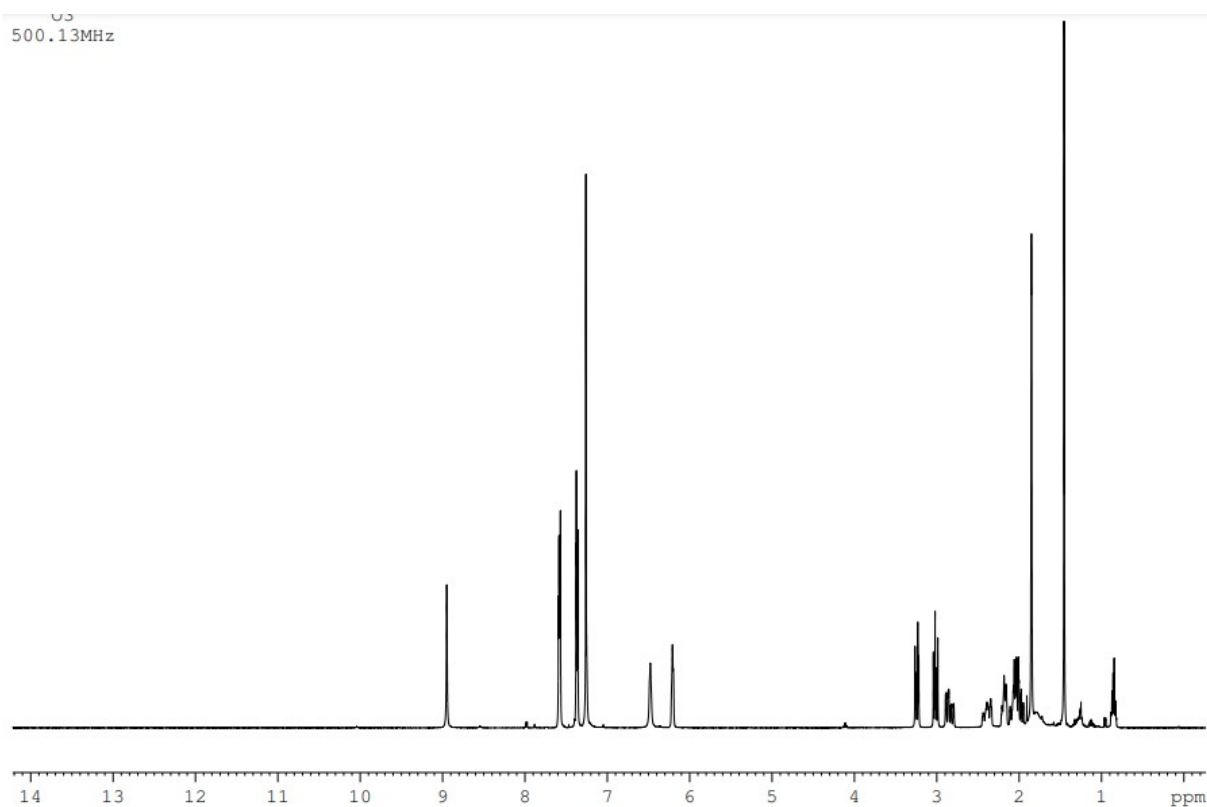
AR_O2

21HR263 53 (0.411) Cm (53.59)

1: TOF MS ES+
3.25e+006Minimum: -1.5
Maximum: 30.0 4.0 50.0

Mass	Calc. Mass	mDa	PPM	DBE	i-FIT	Norm	Conf (%)	Formula
357.1749	357.1749	0.0	0.0	9.5	931.0	n/a	n/a	C19 H25 N4 O S

Fig. 8S. HRMS spectrum of compound 4b

Compound 4cFig. 9S. ¹H-NMR spectrum of compound 4c (500 MHz, CDCl₃)

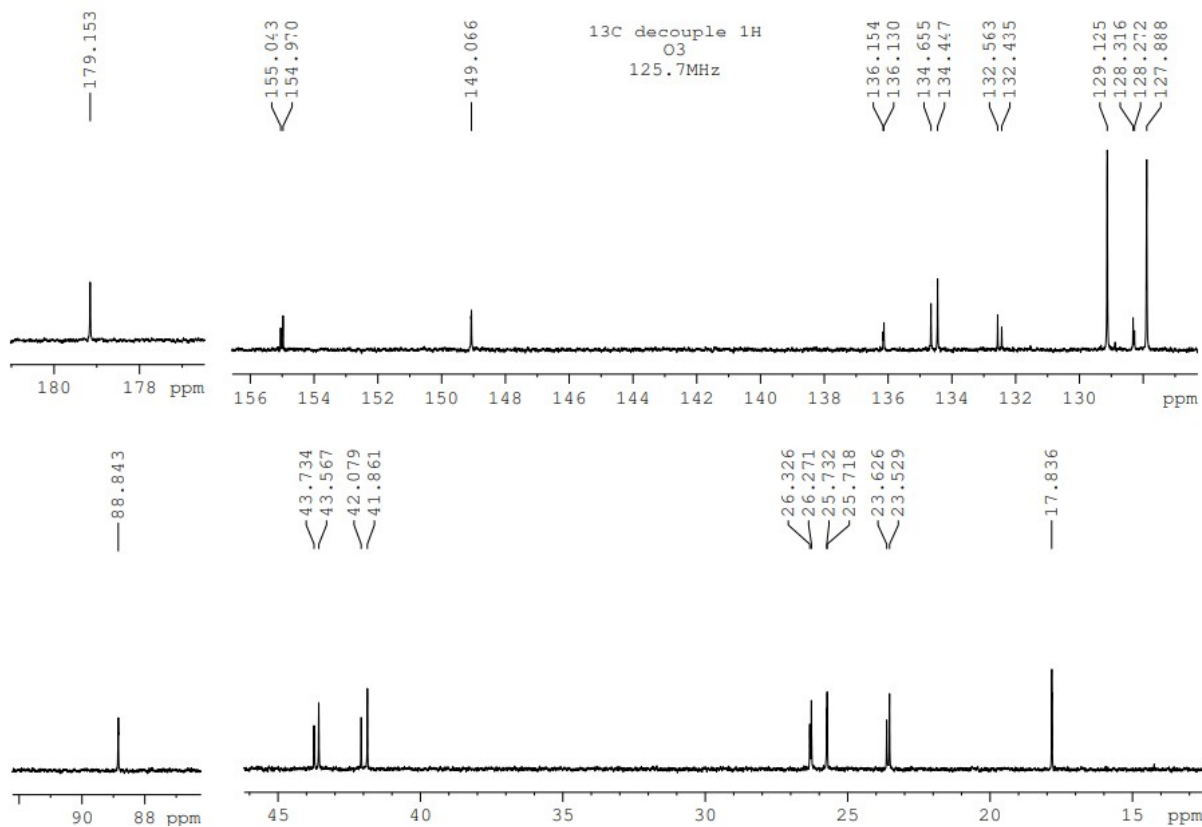


Fig. 10S. ¹³C Decoupled ¹H-NMR spectrum of compound **4c**

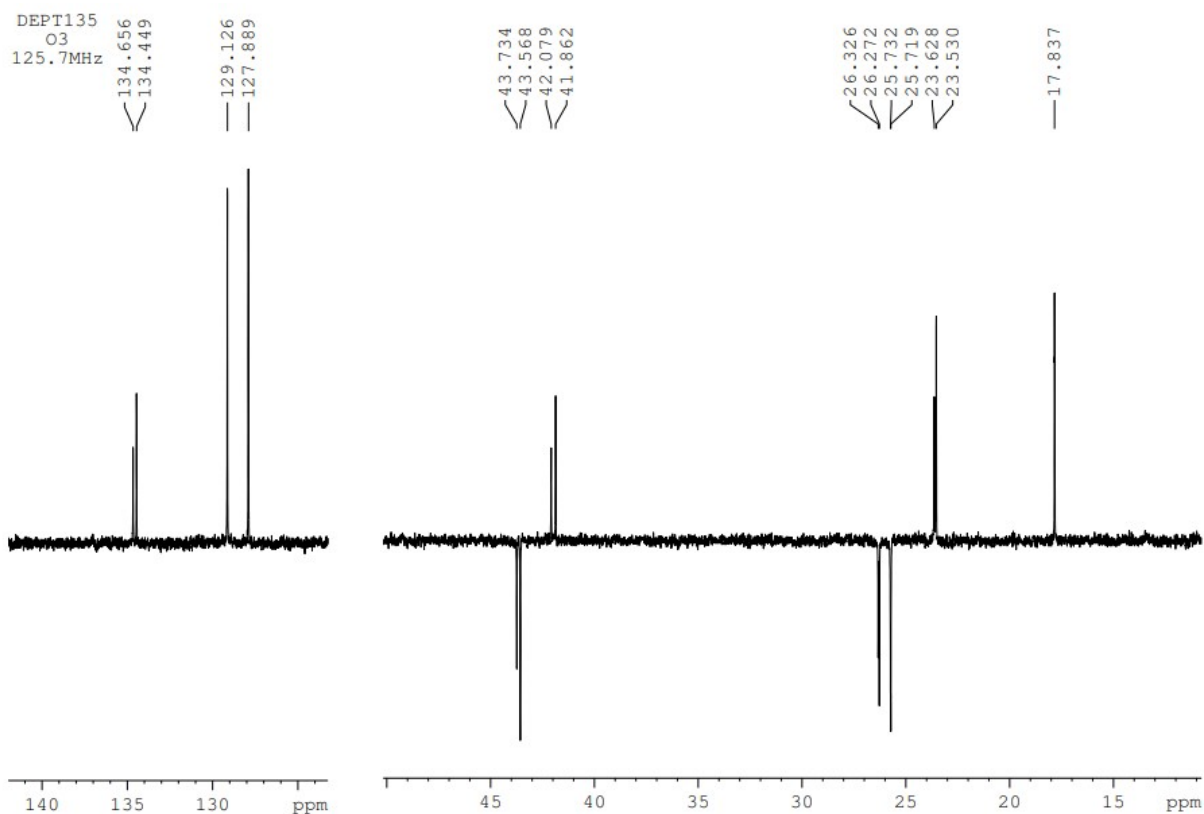


Fig. 11S. ¹³C Decoupled ¹H-NMR spectrum of compound **4c** (DEPT 135 Mode)

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 = 3

Monoisotopic Mass, Even Electron Ions

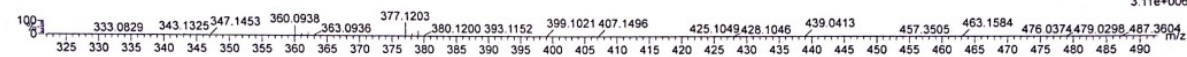
1946 formula(e) evaluated with 7 results within limits (up to 50 closest results for each mass)

Elements Used:

C: 0-60 H: 0-100 N: 0-5 O: 0-20 S: 0-1 Cl: 0-2

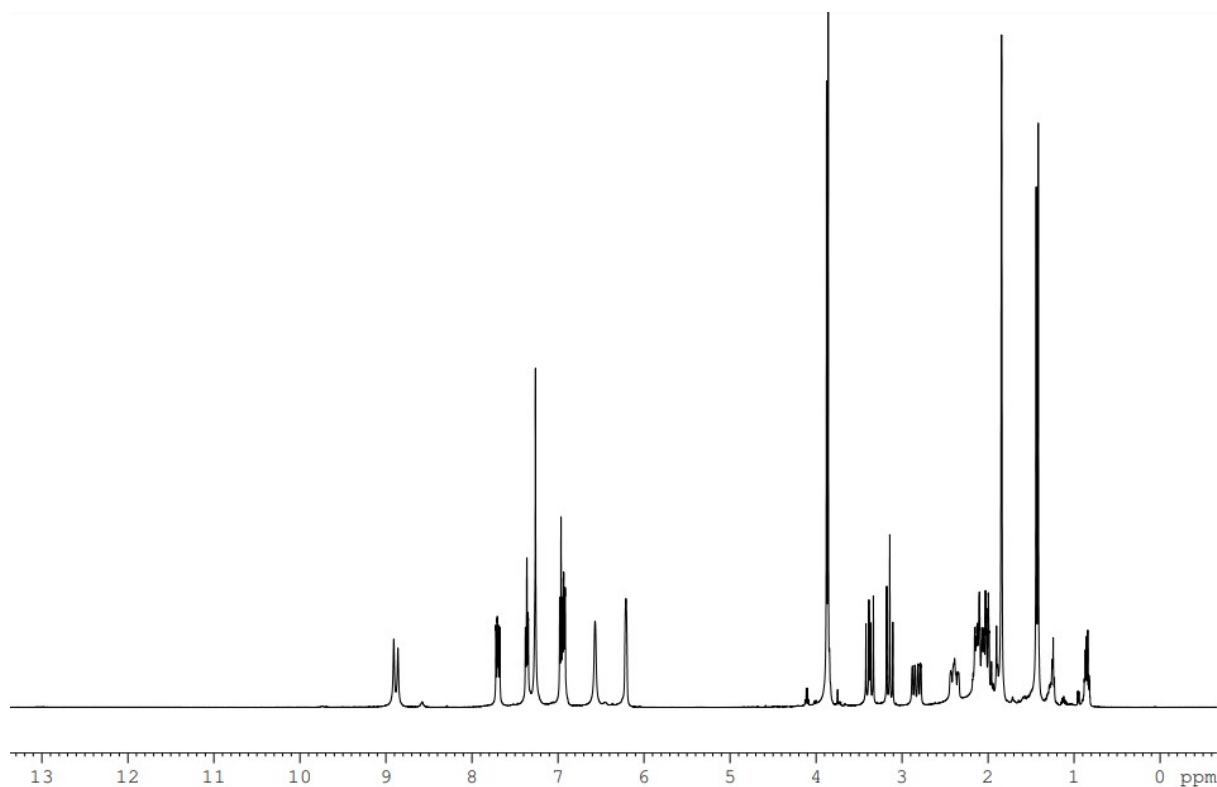
sene2_O3

19HR722 181 (1.364) Cm (176.194)

1: TOF MS ES+
3.11e+006

Mass	Calc. Mass	mDa	PPM	DBE	i-FIT	Norm	Conf(%)	Formula
377.1203	377.1203	0.0	0.0	9.5	2196.5	0.362	69.65	C18 H22 N4 O S Cl
	377.1196	0.7	1.9	5.5	2216.1	20.005	0.00	C14 H21 N2 O10
	377.1211	-0.8	-2.1	13.5	2212.4	16.278	0.00	C23 H21 O3 S
	377.1214	-1.1	-2.9	0.5	2201.8	5.672	0.34	C13 H26 O10 Cl
	377.1189	1.4	3.7	4.5	2197.3	1.204	30.00	C17 H26 O5 S Cl
	377.1187	1.6	4.2	9.5	2205.6	9.491	0.01	C20 H23 N2 O Cl2
	377.1221	-1.8	-4.8	4.5	2207.2	11.083	0.00	C17 H27 N2 O S Cl2

Fig. 12S. HRMS spectrum of compound 4c

Compound 4dFig. 13S. ¹H-NMR spectrum of compound 4d (500 MHz, CDCl₃)

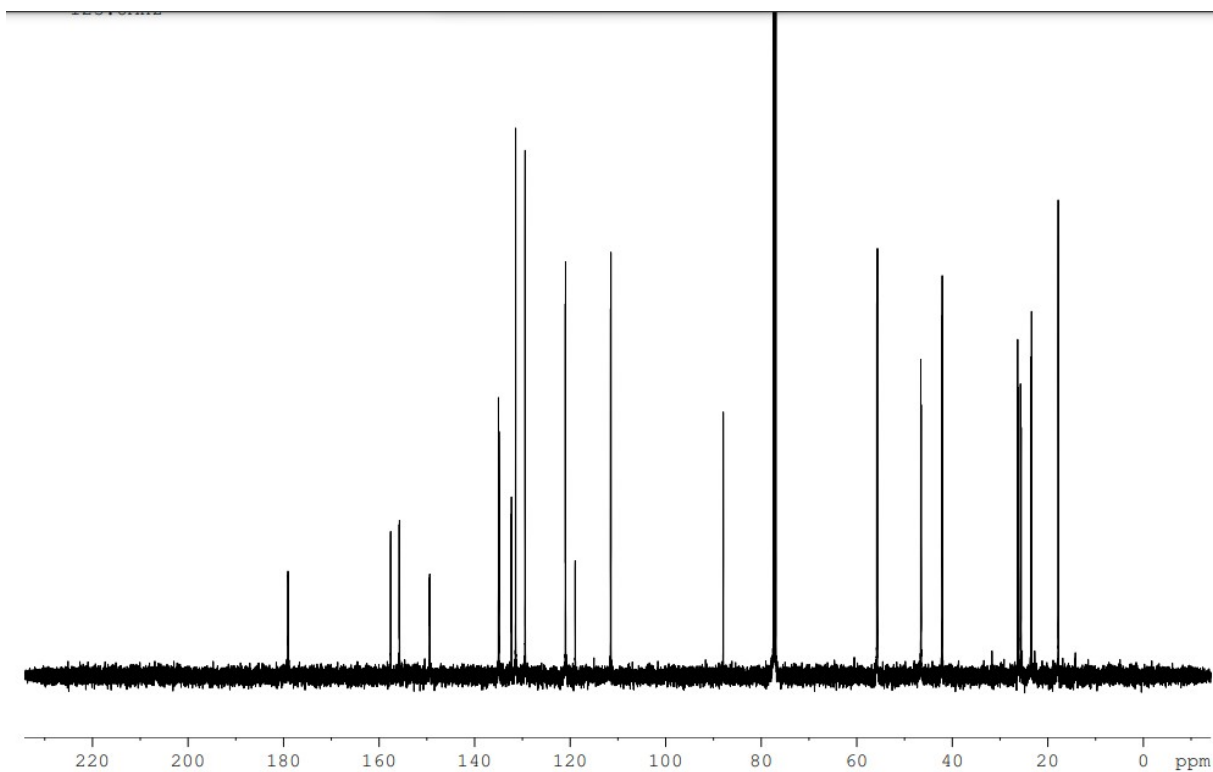


Fig. 14S. ^{13}C Decoupled ^1H -NMR spectrum of compound **4d**

Elemental Composition Report

Page 1

Single Mass Analysis

Tolerance = 4.0 PPM / DBE: min = -1.5, max = 50.0

Element prediction: Off

Number of isotope peaks used for i-FIT = 3

Monoisotopic Mass, Even Electron Ions

217 formula(e) evaluated with 1 results within limits (up to 15 closest results for each mass)

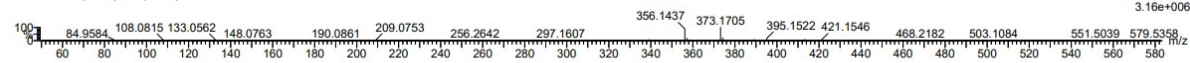
Elements Used:

C: 0-25 H: 0-100 N: 0-6 O: 0-3 S: 0-1

AR_O5

21HR264 52 (0.404) Cm (52.56)

1: TOF MS ES+
3.16e+006



Mass	Calc. Mass	mDa	PPM	DBE	i-FIT	Norm	Conf (%)	Formula
373.1705	373.1698	0.7	1.9	9.5	945.1	n/a	n/a	C ₁₉ H ₂₅ N ₄ O ₂ S

Fig. 15S. HRMS spectrum of compound **4d**

Compound 5



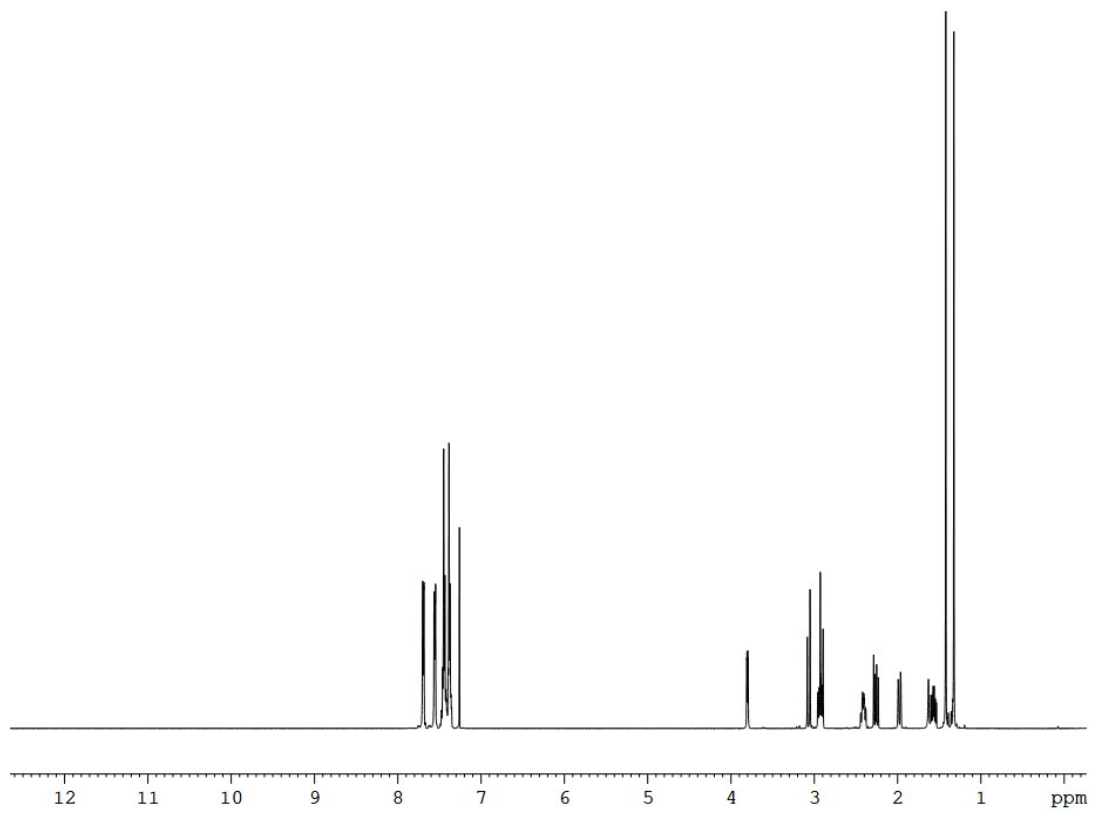


Fig. 16S. $^1\text{H-NMR}$ spectrum of compound 5

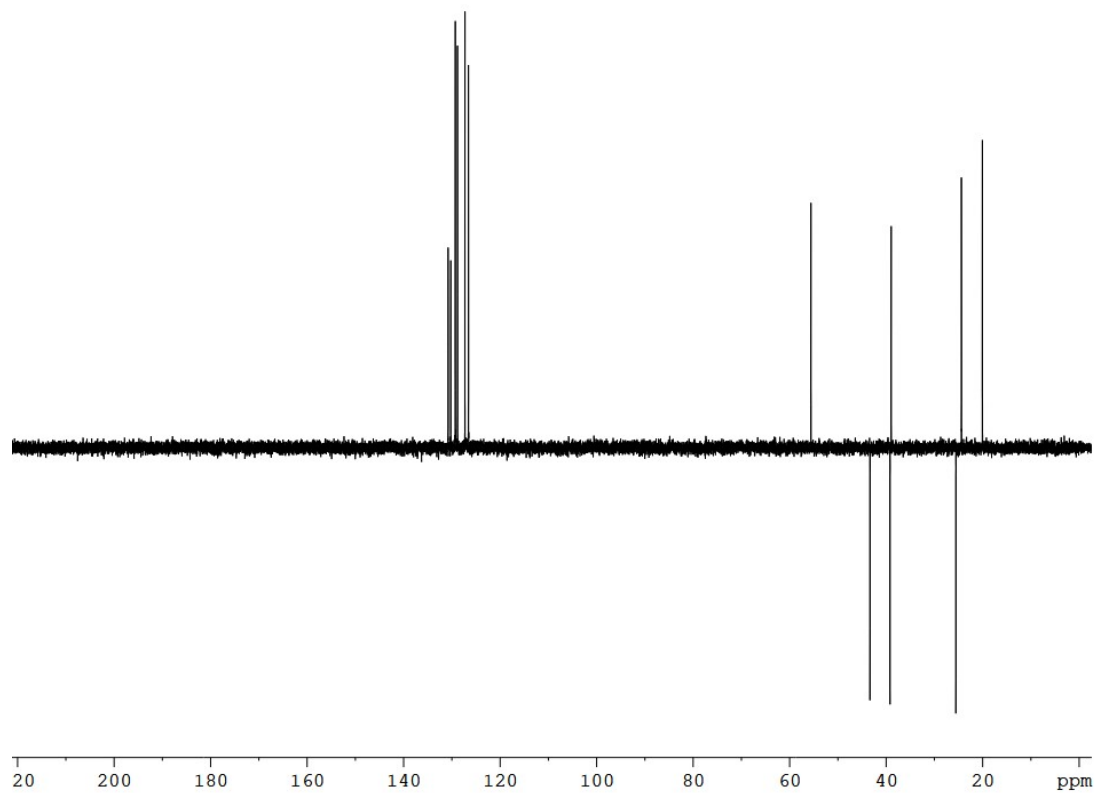


Fig. 17S. $^{13}\text{C-NMR}$ spectrum of compound 5

Single Mass Analysis

Tolerance = 5.0 PPM / DBE: min = 0.0, max = 18.0

Element prediction: Off

Number of isotope peaks used for i-FIT = 4

Monoisotopic Mass, Even Electron Ions

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

Elements Used:

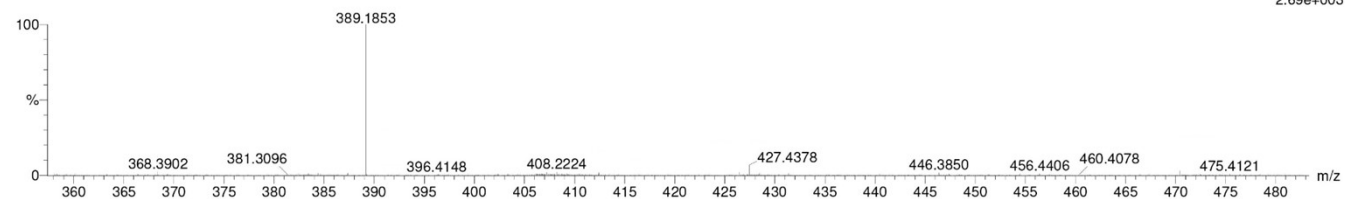
C: 0-500 H: 0-1000 N: 0-10 O: 0-4

A9

2:36

23-Dec-2020

1912037 628 (3.807) Cm (628:637:544:551)

1: TOF MS ES+
2.69e+003

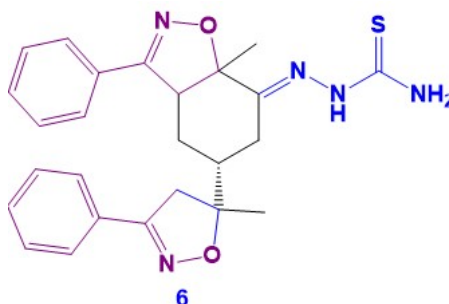
Minimum:

Maximum: 5.0 5.0 0.0 18.0

Mass	Calc. Mass	mDa	PPM	DBE	i-FIT	i-FIT (Norm)	Formula
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389.1853	389.1849	-0.4	-0.8	14.5	298.2	0.0	C24 H25 N2 O3
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Fig. 18S. HRMS spectrum of compound 5

Compound 6

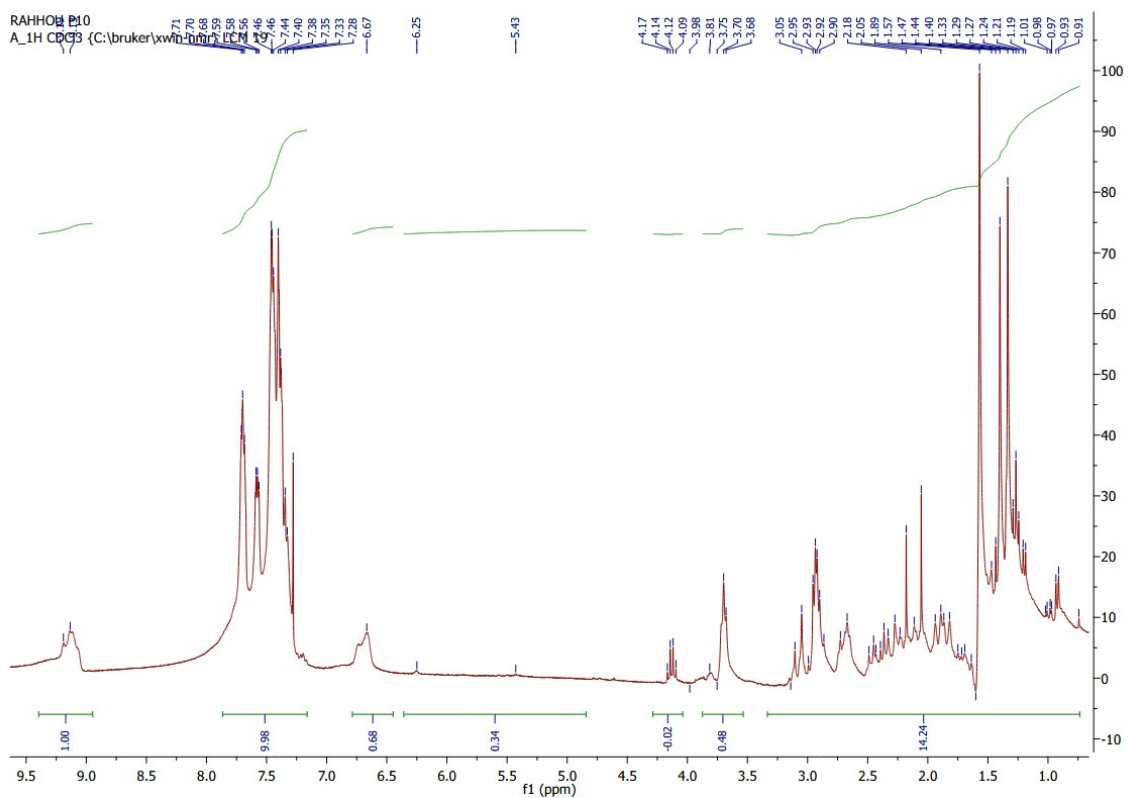


Fig. 19S. ^1H NMR spectrum of compound **6**

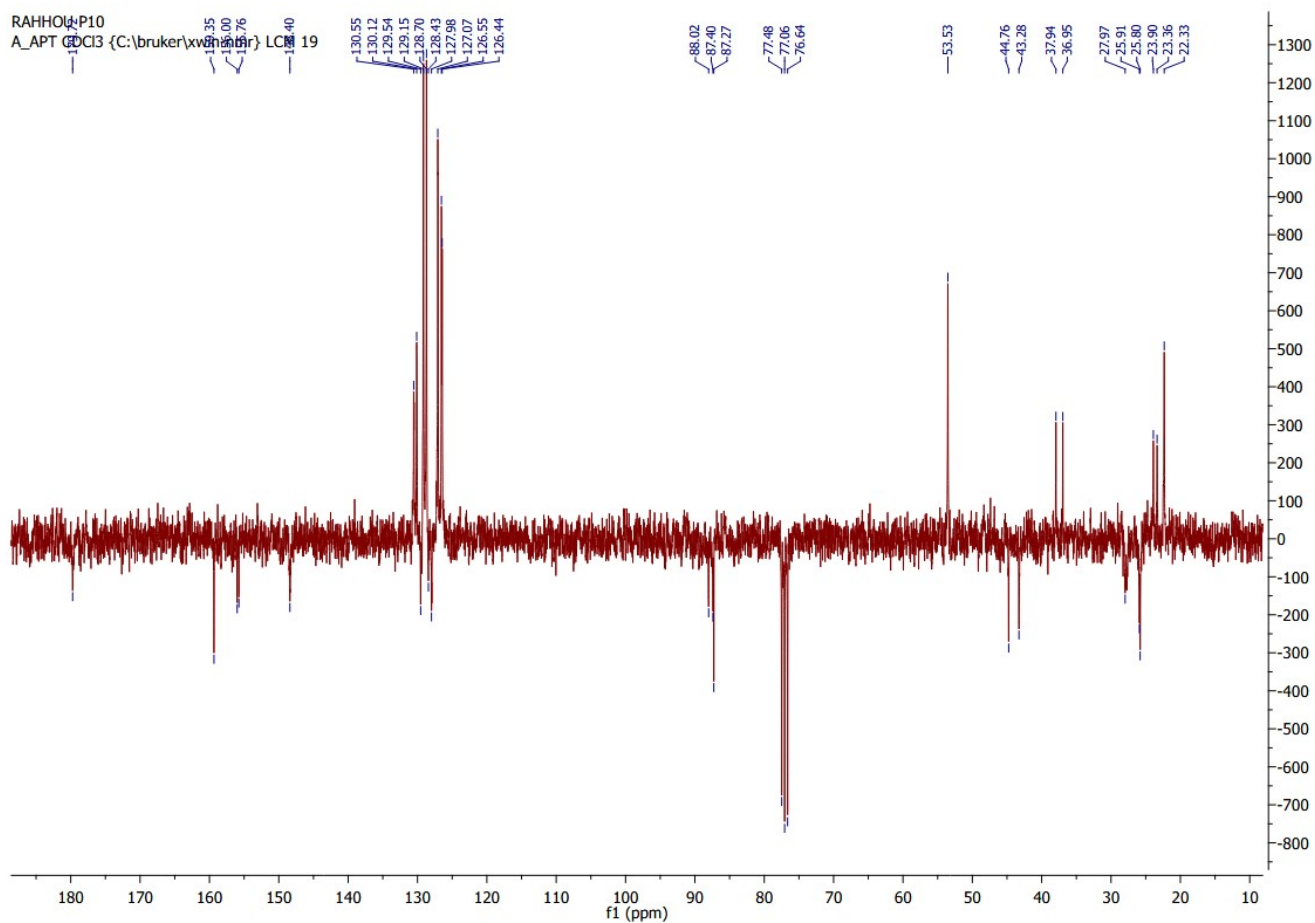


Fig. 20S. ¹³C NMR spectrum of compound 6

Elemental Composition Report

Single Mass Analysis

Tolerance = 5.0 PPM / DBE: min = -2.0, max = 20.0

Element prediction: Off

Number of isotope peaks used for i-FIT = 4

Monoisotopic Mass, Even Electron Ions

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

Elements Used:

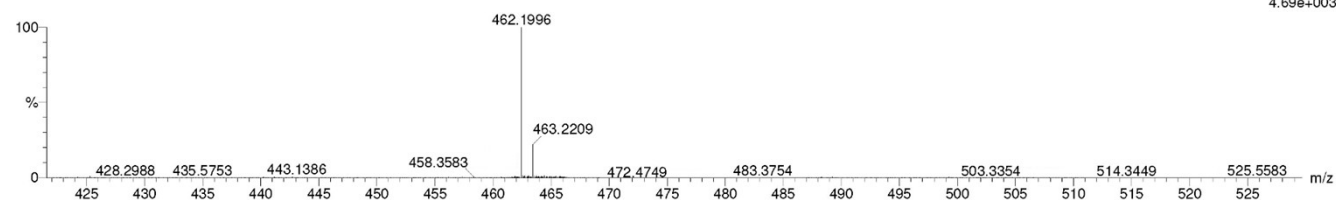
C: 0-500 H: 0-1000 N: 1-6 O: 0-5 S: 0-1

25-Jan-2023

2001023 225 (4.390) Cm (725:729-(657:662+777:779))

1:28

1: TOF MS ES+
4.69e+003



Minimum:

Maximum:

5.0 5.0 -2.0 20.0

Mass	Calc. Mass	mDa	PPM	DBE	i-FIT	i-FIT (Norm)	Formula
462.1996	462.1905	0.0	0.0	15.5	346.4	0.0	C25 H27 N5 O2 S

Fig. 21S. HRMS spectrum of compound 6

