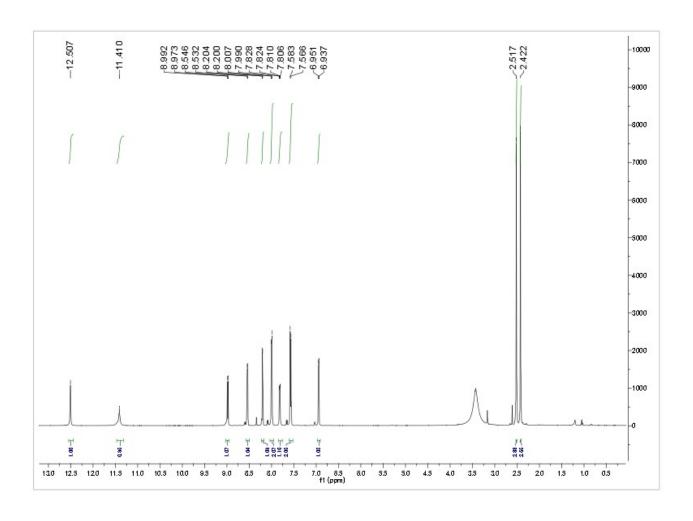
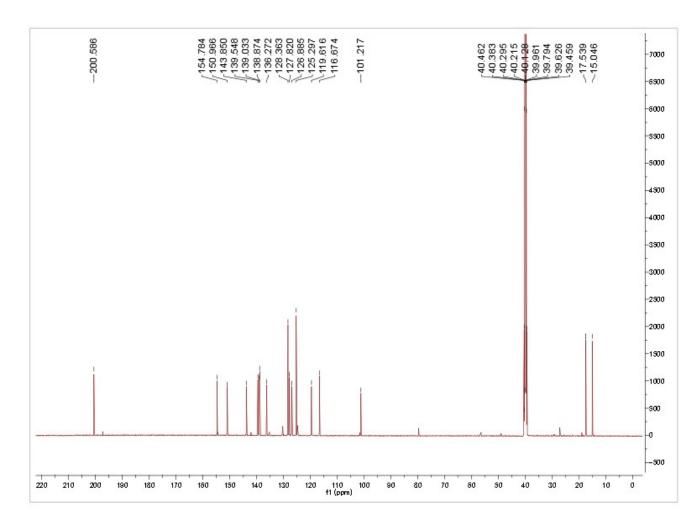
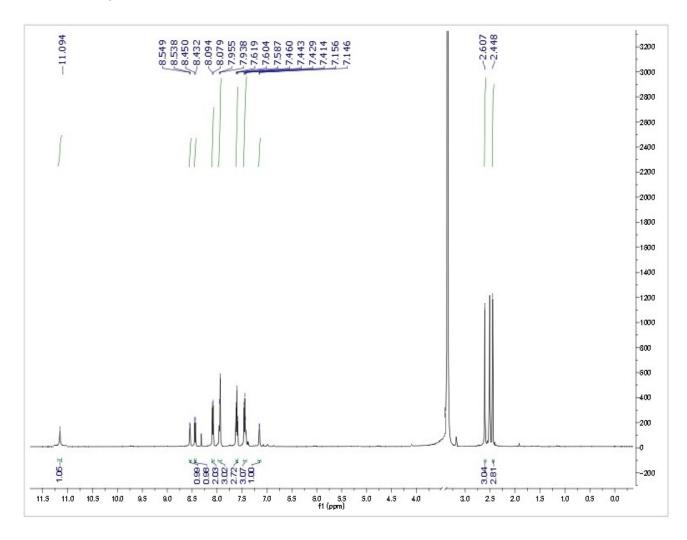
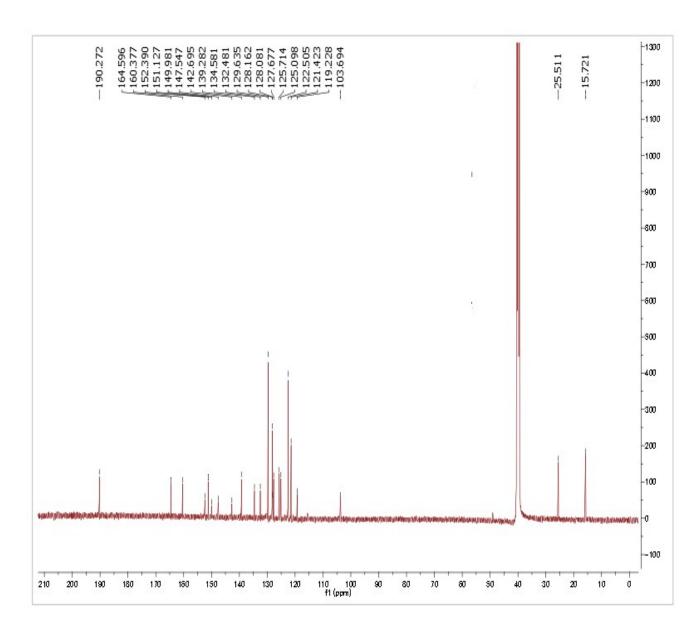
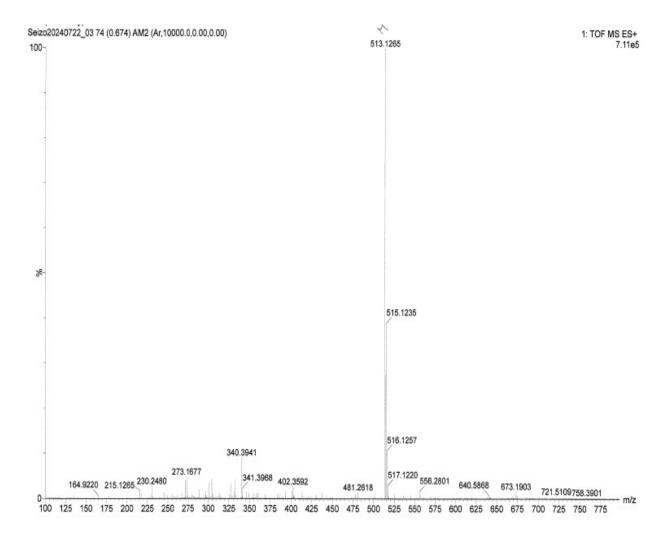
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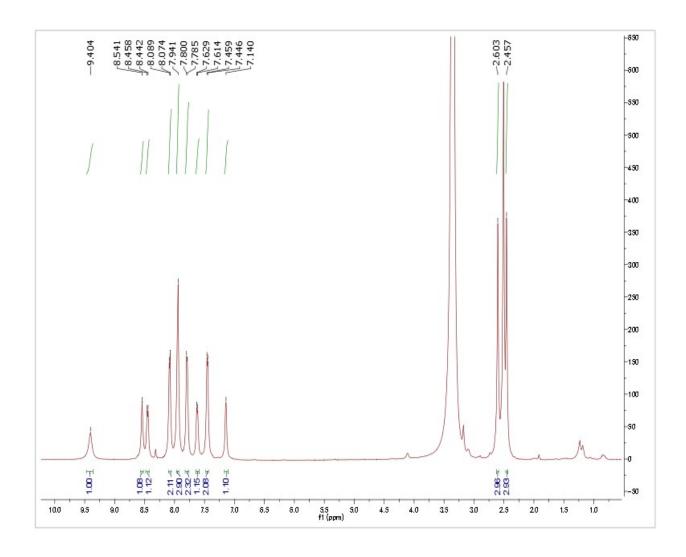


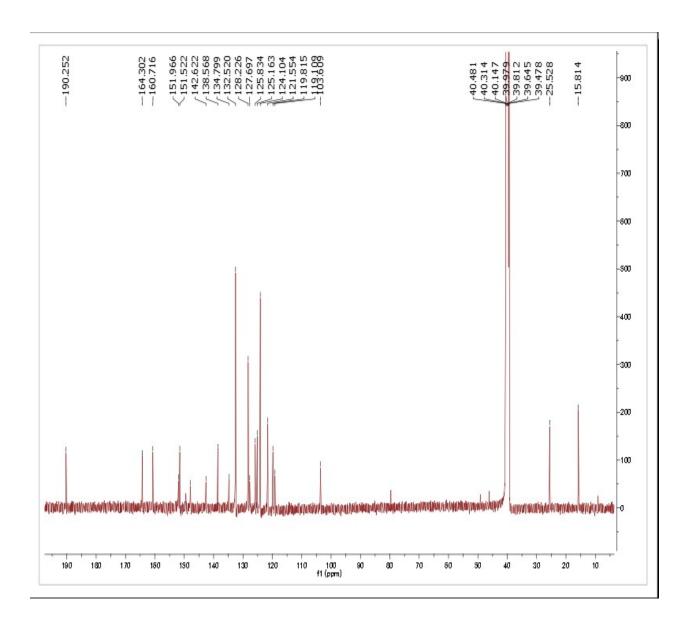


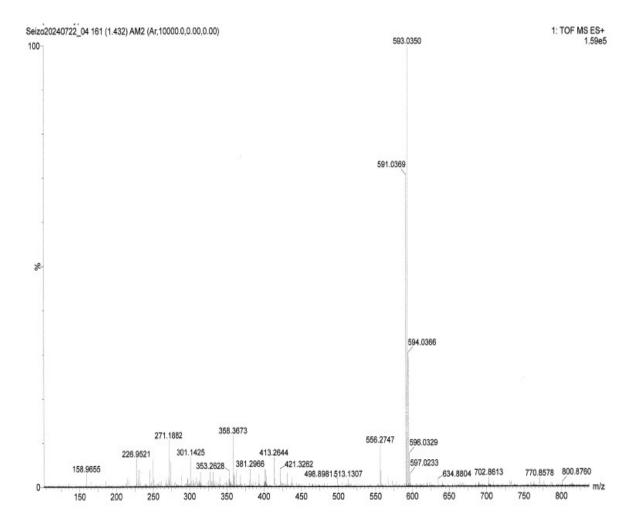




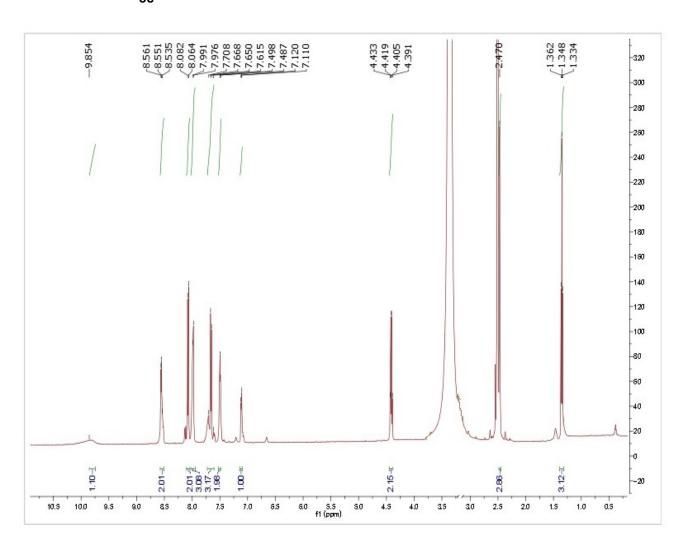


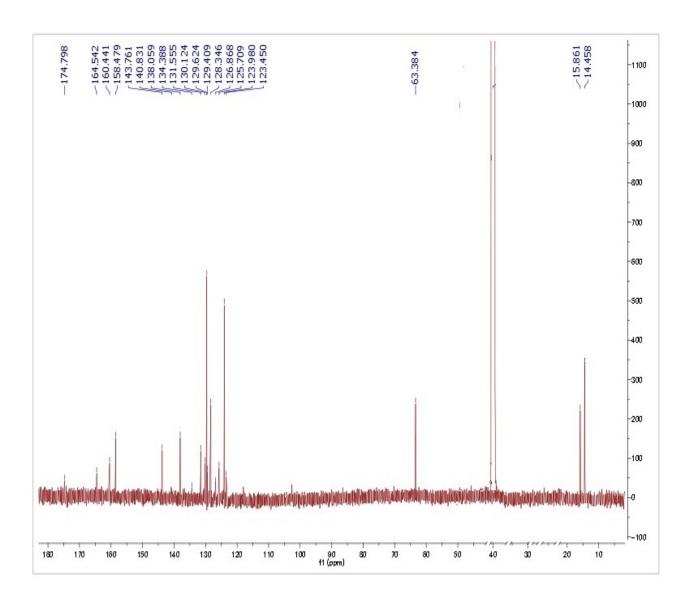


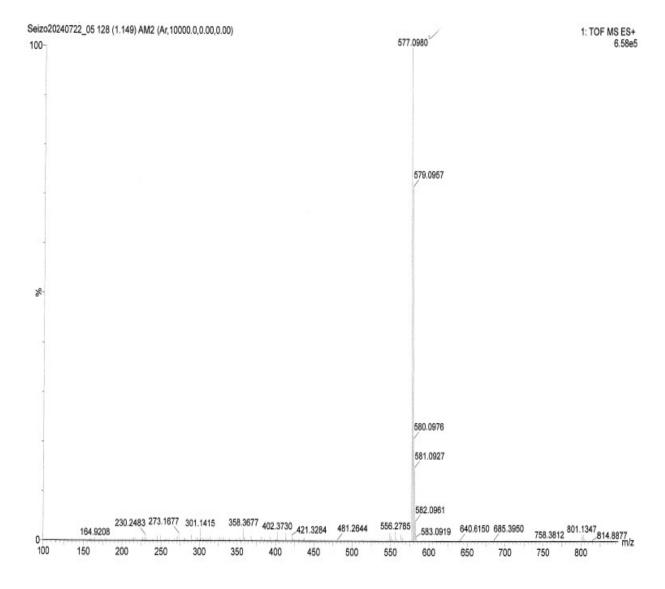


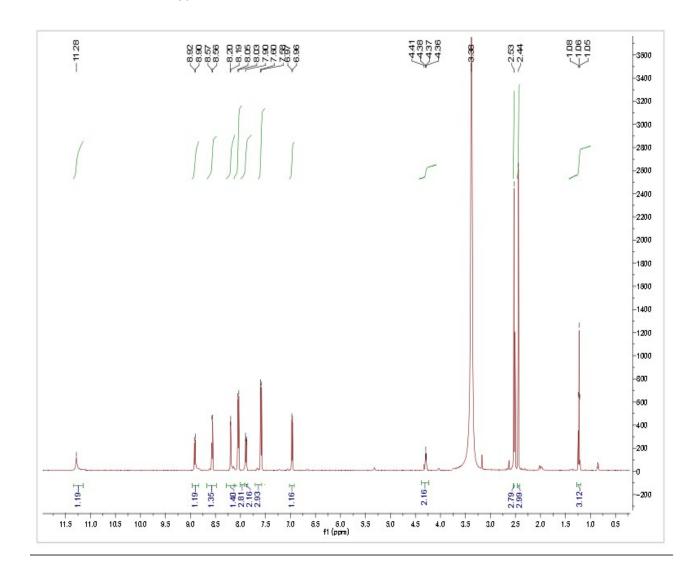


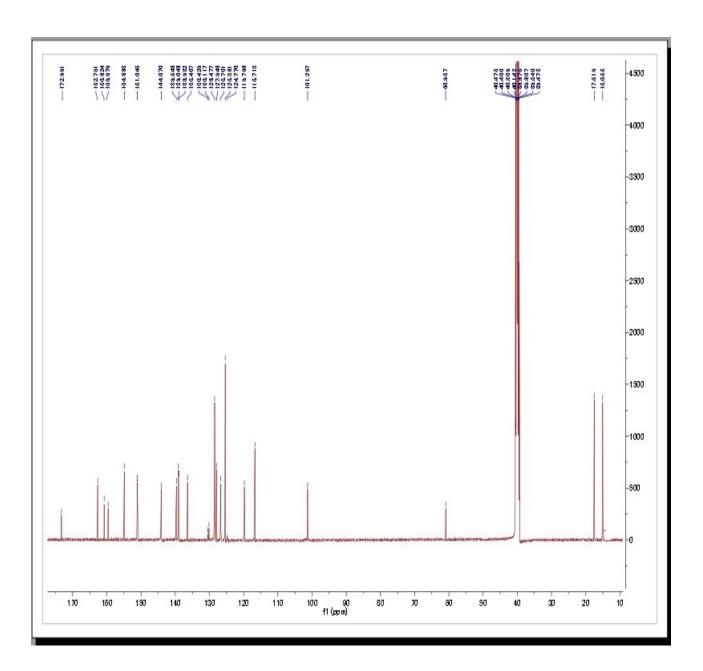
8c

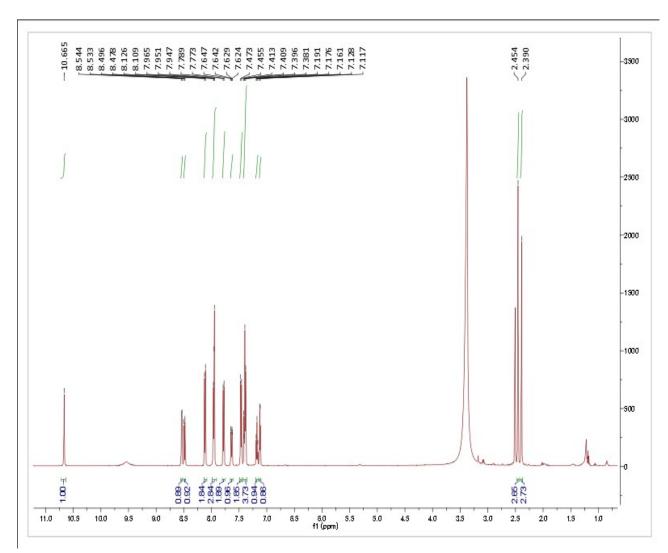


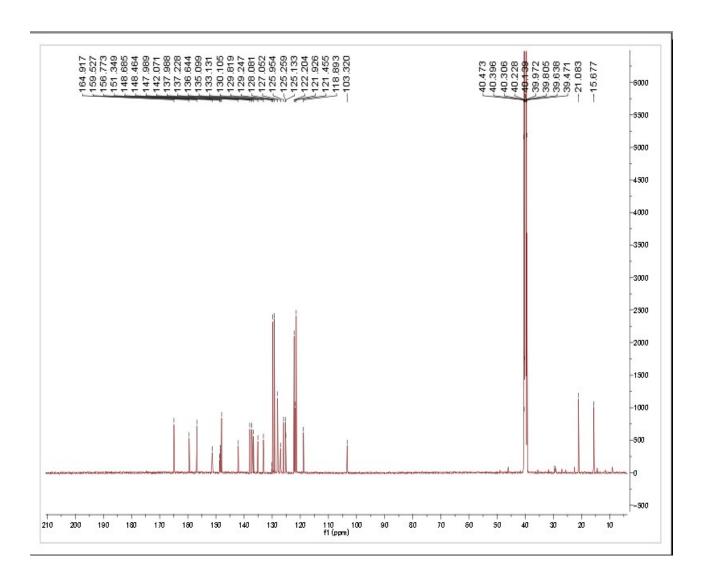


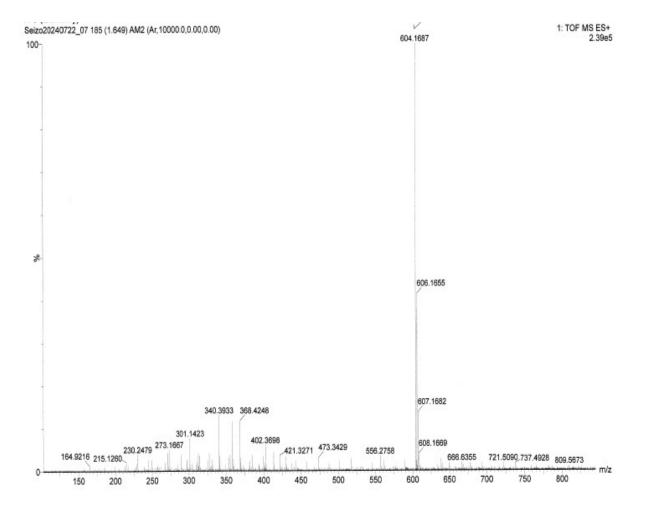




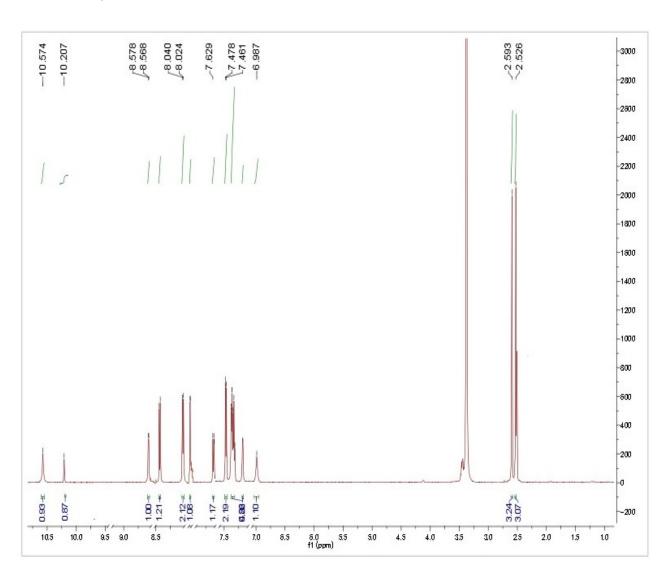


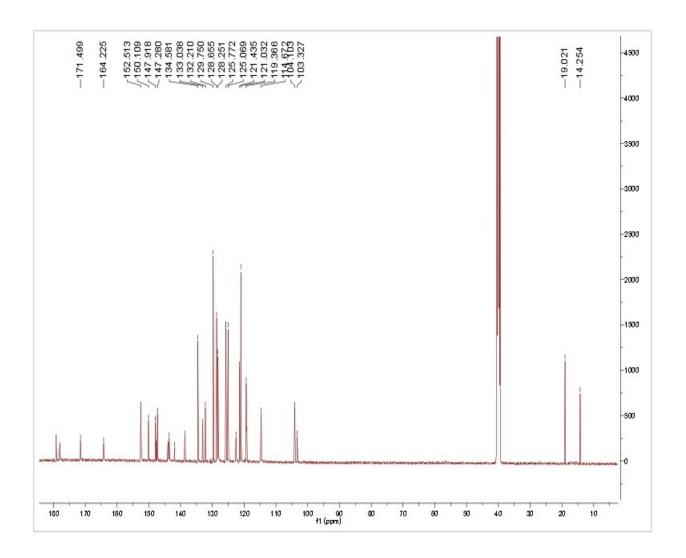


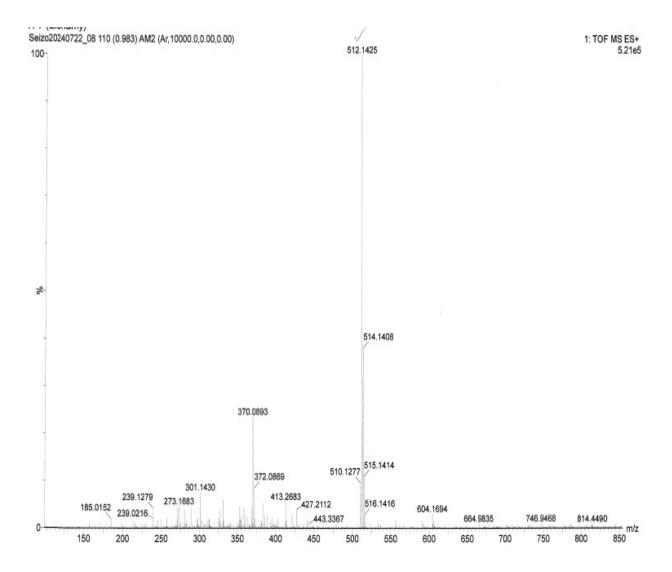




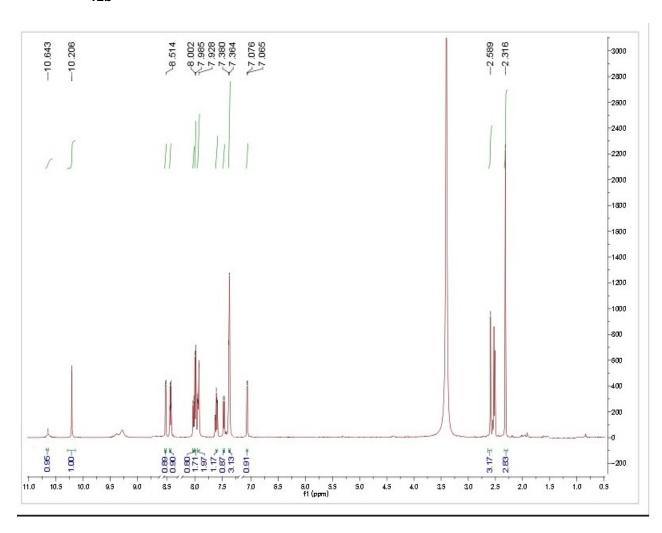
12a

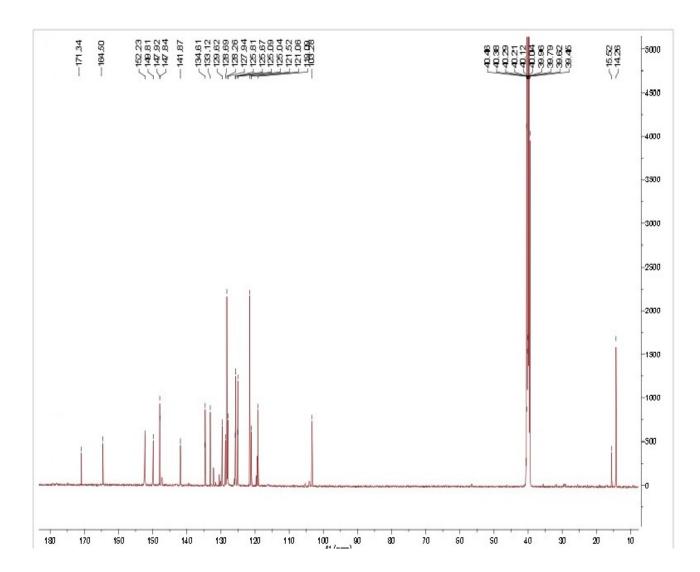


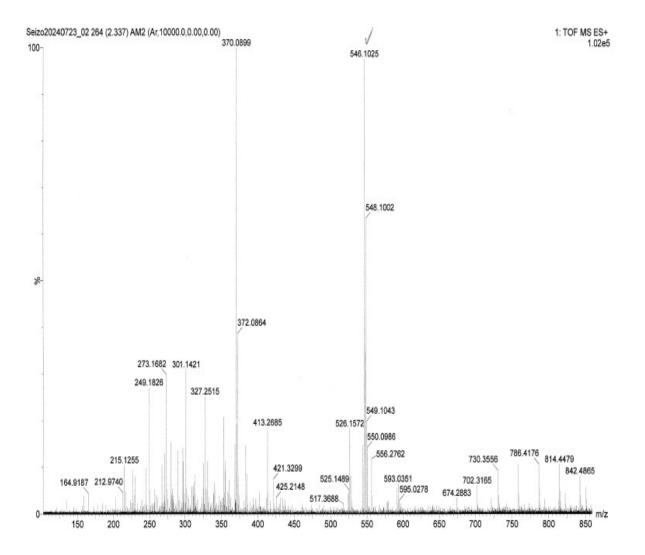




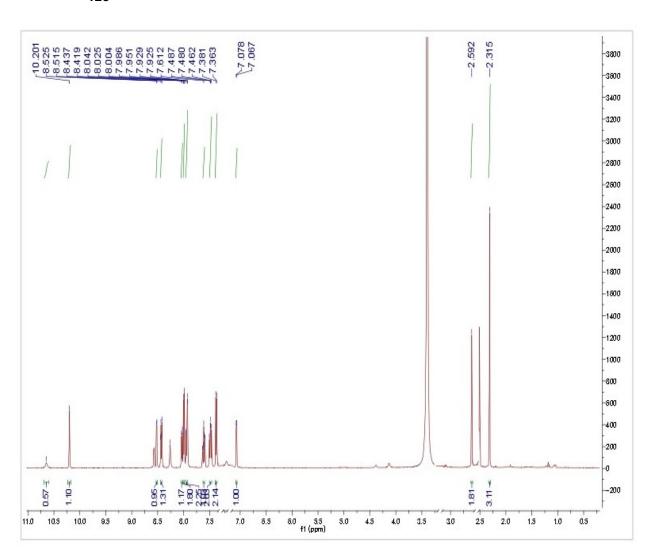
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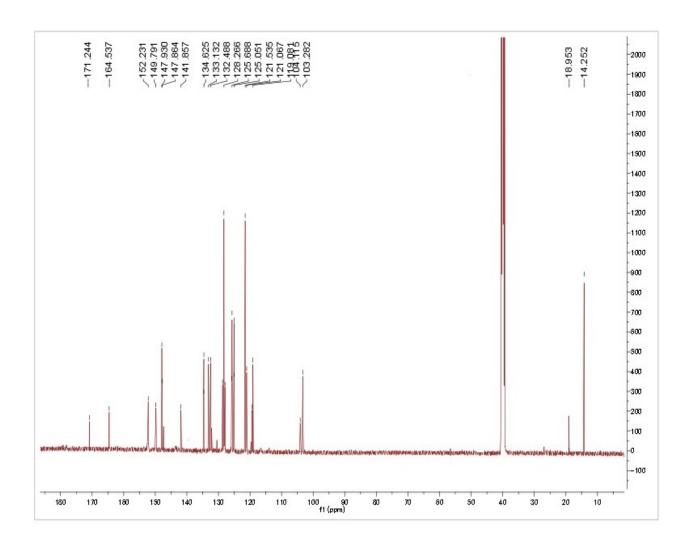


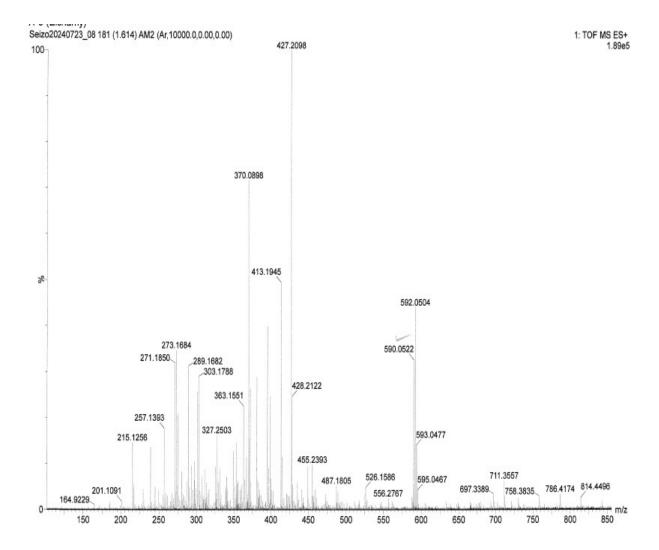




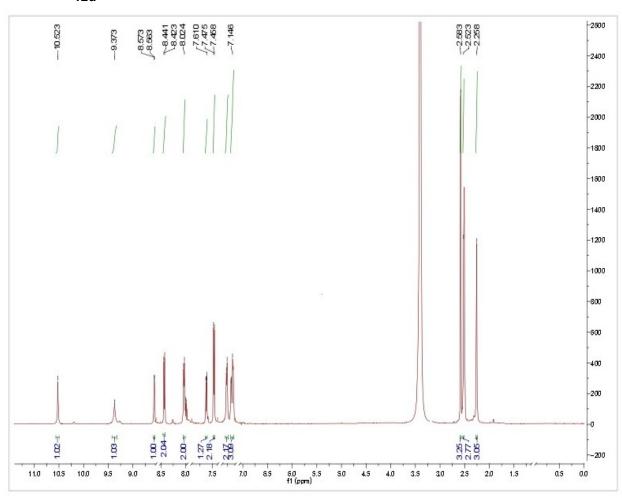
12c

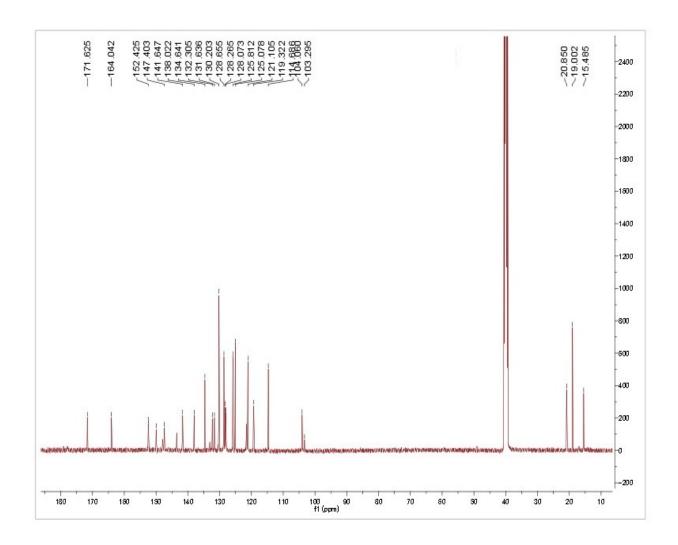


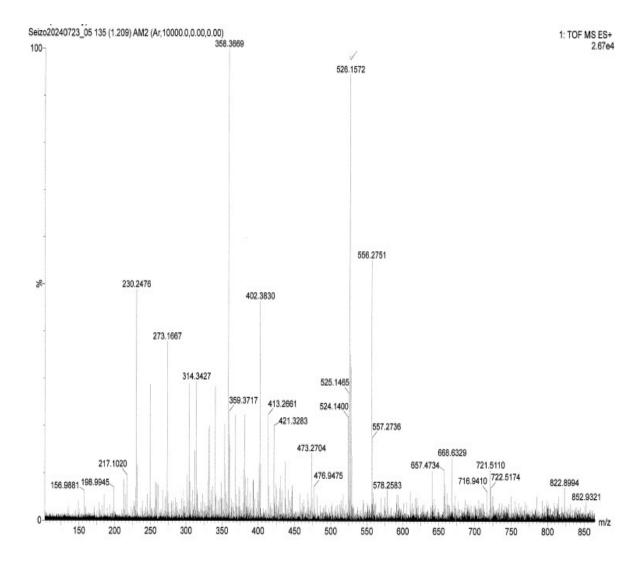




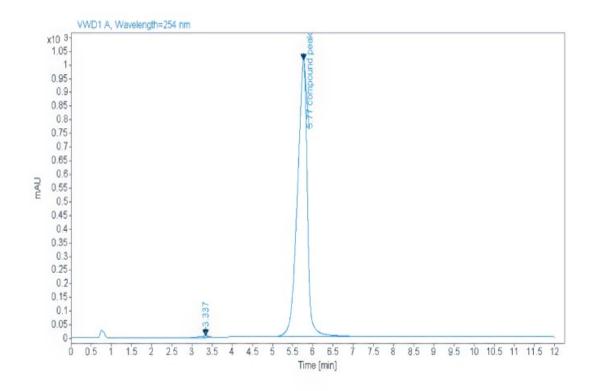
12d





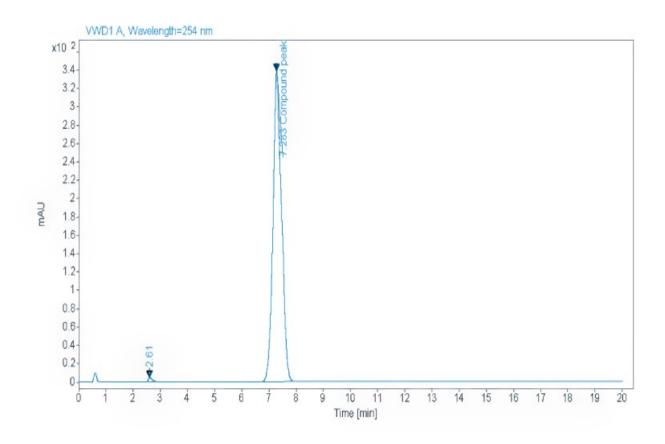


## **Charts of HPLC**



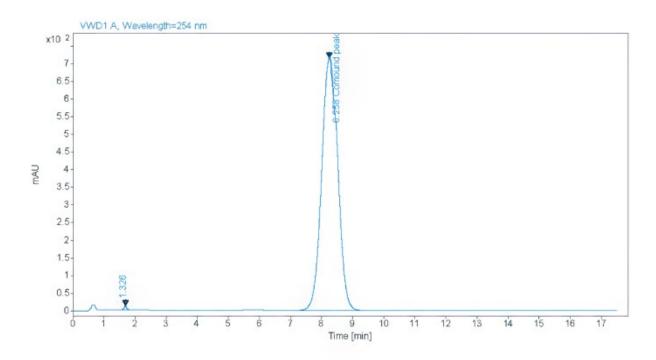
Signal:	VWE	01 A, Waveleng	th=254 nm		
RT [min]	Туре	Width [min]	Area	Height	Area% Name
3.337	BV	0.2564	101.3273	5.3740	0.5929
5.770	BB	0.2646	16991.2751	1011.5413	99.4071 compound peak
		Sum	17092.6024		

**HPLC** for compound 5



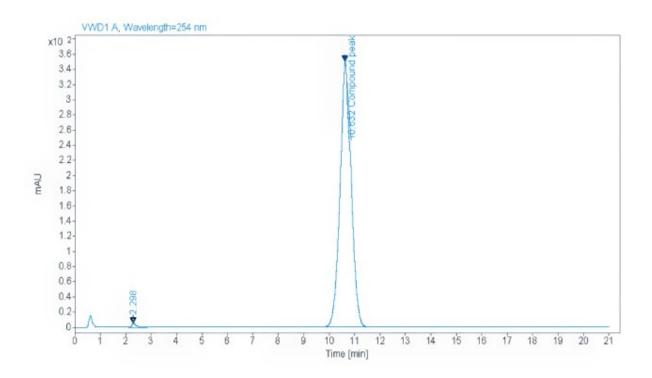
Signal:	VWD	1 A, Waveleng	th=254 nm			
RT [min]	Туре	Width [min]	Area	Height	Area%	Name
2.610	VV	0.1804	50.1489	4.5290	0.6038	
7.283	BV	0.3404	8255.9166	339.0104	99.3962	Compound peak
		Sum	8306.0655			

**HPLC** for compound 8b



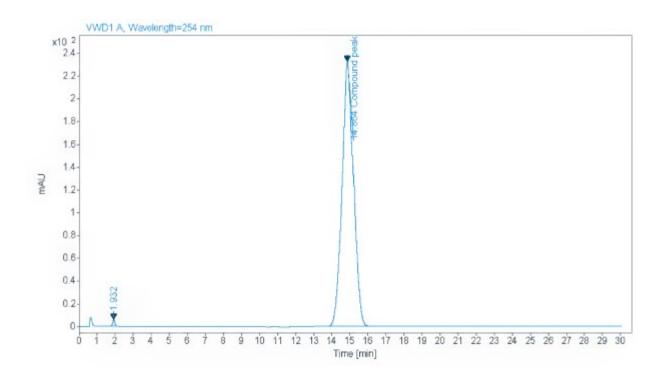
Signal:	VWD	1 A, Waveleng	th=254 nm			
RT [min]	Туре	Width [min]	Area	Height	Area% Name	
1.326	VB	0.0651	47.2621	11.1678	0.1562	
8.258	VB	0.6022	30221.1952	715.9852	99.8438 Comound peak	(
		Sum	30268.4573			

**HPLC** for compound 8d



Signal:	VWD	01 A, Waveleng	th=254 nm			
RT [min]	Type	Width [min]	Area	Height	Area%	Name
2.298	VV	0.1846	60.9981	5.2683	0.4273	
10.632	BV	0.5386	14214.2833	350.2096	99.5727	Compound peak
		Sum	14275.2814			

HPLC for compound 12a



Signal:	VWD	1 A, Waveleng	th=254 nm		
RT [min]	Туре	Width [min]	Area	Height	Area% Name
1.932	ВВ	0.5998	261.5290	5.3801	1.8811
14.864	ВВ	0.7763	13641.7191	230.5098	98.1189 Compound peak
		Sum	13903.2481		

HPLC for compound 12c

## **Biology part**

## **Culture conditions**

L. cultured in tissue flasks containing RPMI 1640 medium supplemented with 10% HIFCS and 100 IU penicillin and 100  $\mu$ gml-1 streptomycin solution at 26°C (Tariku et al., 2010; Habtemariam, 2003; Seifert et al., 2010). Stock solution and working concentration preparation All the compounds tested were dissolved in DMSO to a final concentration of 1 mg/ml Both test and standard solutions were serially diluted to appropriate concentrations using complete media. The test compounds were prepared by three-fold serial dilutions from 10  $\mu$ gml-1 to 0.04  $\mu$ g ml-1 Amphotericin B deoxycholate and miltefosine which were used as a positive control for comparison of the antileishmanial activities of the test compounds, were also made in three-fold serial dilutions (Foroumadi et al., 2005)

Tariku Y, Hymete A, Hailu A, Rohloff J (2010). Constituents, Antileishmanial Activity and Toxicity Profile of Volatile Oil from Berries of Croton macrostachyus. Nat. Prod. Commun. 5:975-980.

Habtemariam S (2003). In vitro antileishaminial effects of antibacterial diterpenes from two Ethiopian premna species: P.schimperi and P. oligotricha. BMC pharmacol 3:1-6.

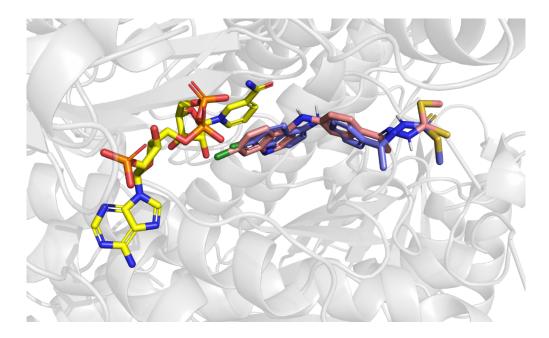
Seifert K, Escobar P, Croft SL (2010). In vitro activity of anti-leishmanial drugs against Leishmania donovani is host cell dependent. J. Antimicrob. Chemother. 3:508-11

Foroumadi A, Pournourmohammadi S, Soltani F, Asgharian-Rezaee M, Dabiri S, Kharazmi A, Shafiee A (2005). Synthesis and in vitro leishmanicidal activity of 2-(5-nitro-2-furyl) and 2-(5-nitro-2-thienyl)-5- substituted-1, 3, 4-thiadiazoles. Bioorg. Med. Chem. Lett. 15:1983-1985.

## **Docking part**

**Table S1**. RMSD values between the best-scoring binding mode obtained with CmDock and the best-scoring binding mode obtained with AutoDock Vina.

AutoDock Vina Compound 5 affinity to	CmDock Compound 5 affinity to	RMSD (Å)
Lm-PTR1 (kcal/mol)	Lm-PTR1 (kcal/mol)	
-8.4	-20.73	1.69



**Figure S1.** The binding mode of compound 5 obtained with CmDock (pink) in comparison with the binding mode of compound 5 obtained with AutoDock Vina (purple). The cofactor NADPH is presented in yellow.

The calculated RMSD value between the best-scoring docked poses, obtained with CmDock and AutoDock Vina equals 1.69 Å, which indicates that the binding modes obtained with both docking programs are indeed very simular. This additionally confirms the validity of the applied molecular docking protocol in CmDock.

To demonstrate the stability of the observed intermolecular interactions during 100 ns MD simulation, the occupancies of the observed intermolecular interactions in 25 ns intervals are presented in **Table S2**.

**Table S2.** Occupancy of intermolecular interactions throughout 100 ns MD simulation of compound 5-Lm-PTR1 complex.

Residue	Interaction type	Occupancy
	0-25 ns	
TYR194	H-bond	100.00%
PHE113	Hydrophobic	97.21%
HIS241	H-bond	88.45%
LEU229	Hydrophobic	76.10%
LEU226	Hydrophobic	70.60%
LEU188	Hydrophobic	62.67%
GLY225	Waterbridge	56.29%
PHE113	Pi-stack	50.77%
	26-50 ns	
PHE113	Hydrophobic	99%
TYR194	H-bond	97%
LEU229	Hydrophobic	77%
HIS241	H-bond	74%
LEU226	Hydrophobic	65%
LEU188	Hydrophobic	63%
GLY225	H-bond	52%
PHE113	Pi-stack	50.9%
	51-75 ns	
PHE113	Hydrophobic	98%
TYR194	H-bond	98%
LEU229	Hydrophobic	81%
HIS241	H-bond	78%
LEU226	Hydrophobic	68%
LEU188	Hydrophobic	65%
GLY225	H-bond	52%
PHE113	Pi-stack	50%
	76-100 ns	
PHE113	Hydrophobic	99%
HIS241	H-bond	98%
TYR194	H-bond	97%
LEU229	Hydrophobic	78%
LEU188	Hydrophobic	67%
LEU226	Hydrophobic	66%
GLY225	H-bond	57%
PHE113	Pi-stack	54%