Supplementary Information

Structural revision of the Mcl-1 inhibitor MIM1. Synthesis and biological studies on ovarian cancer cells with evaluation of designed analogues.

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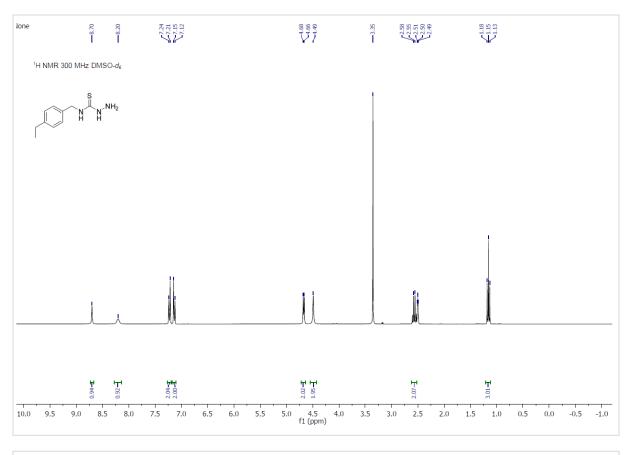
◆ Equal contribution to this work

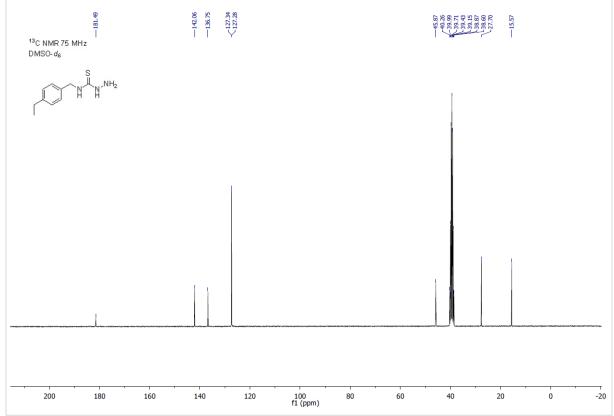
*co-corresponding authors

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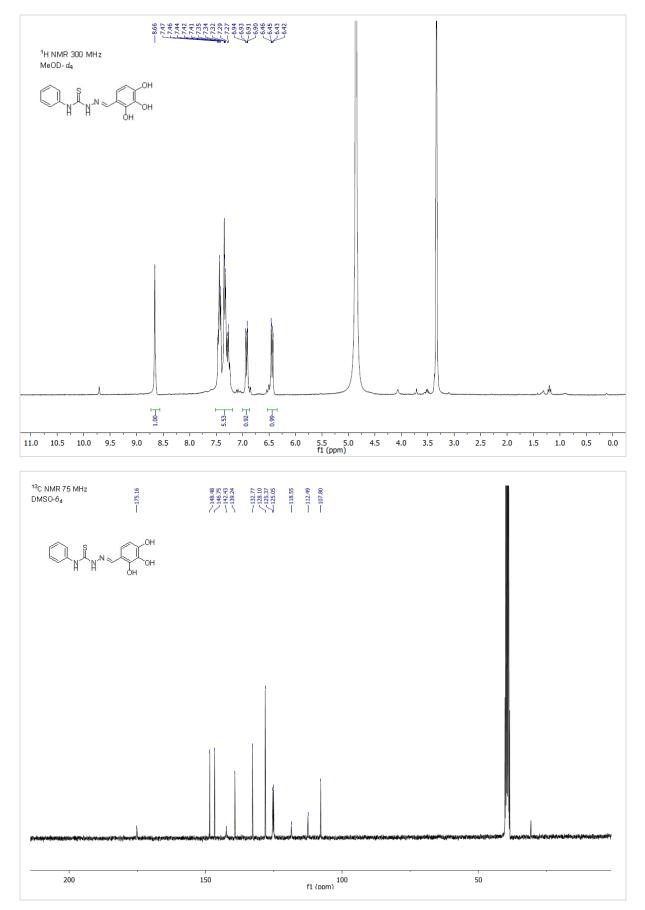
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Compound 21e

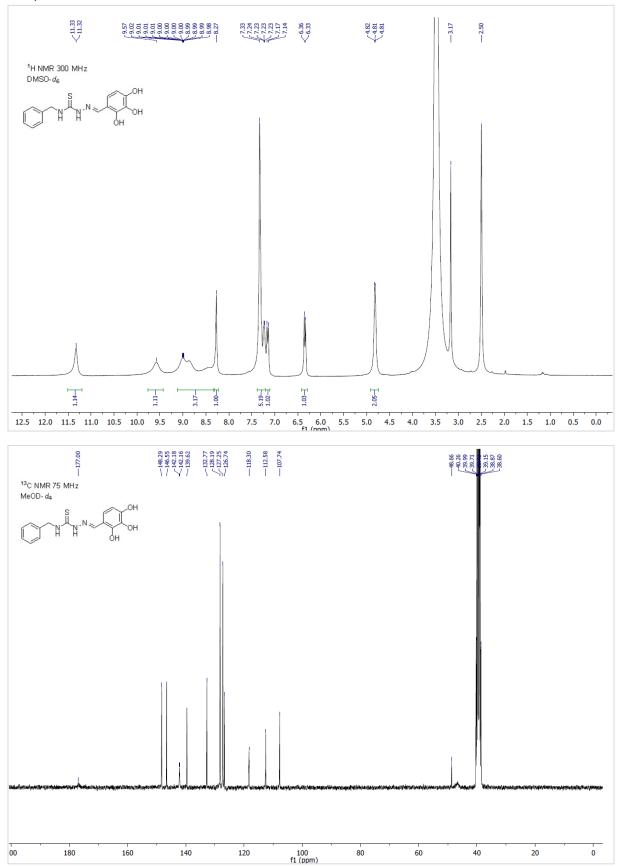




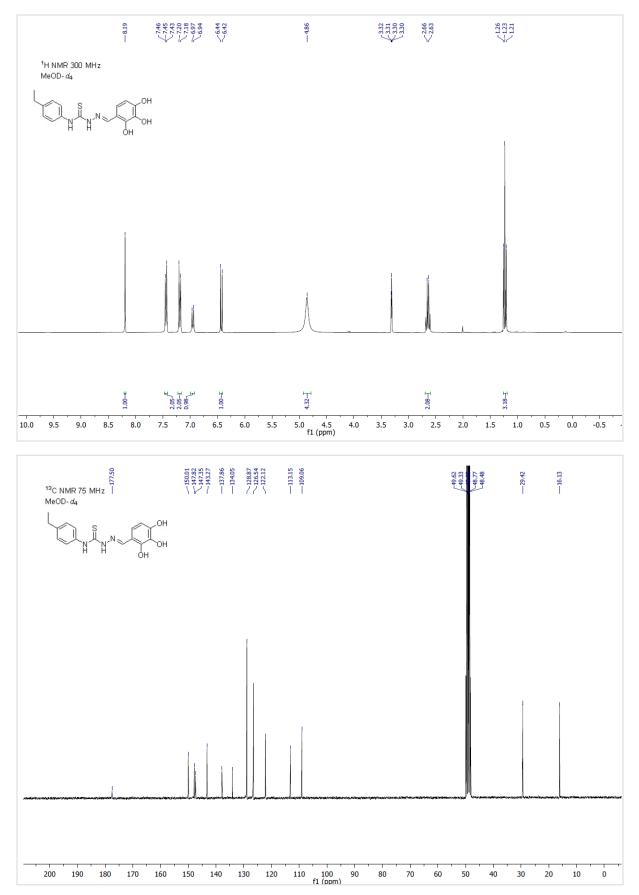
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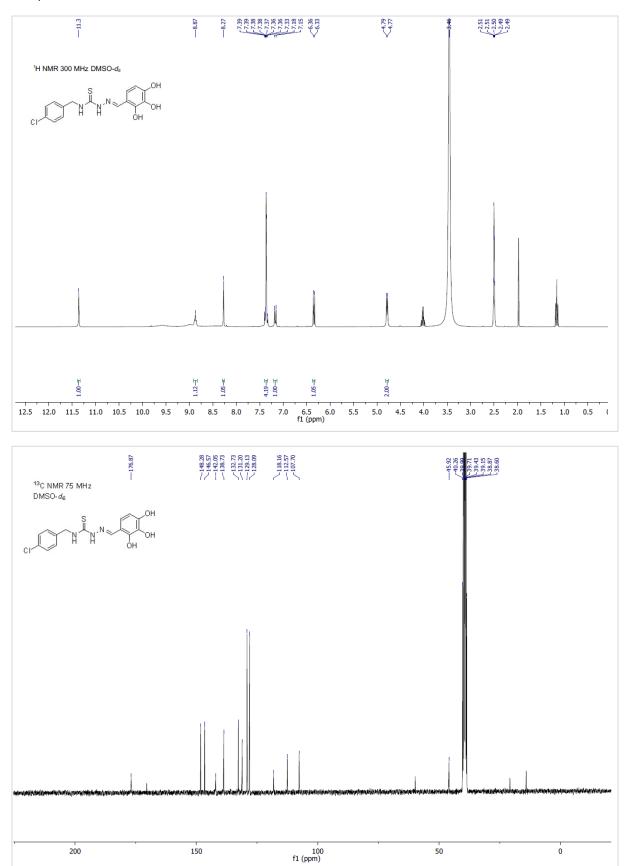
Compound 22b



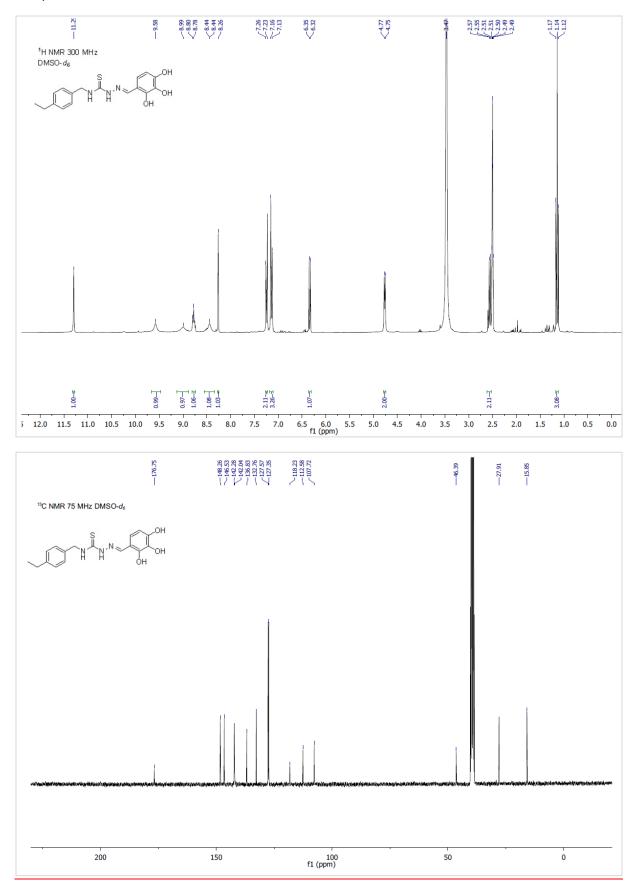
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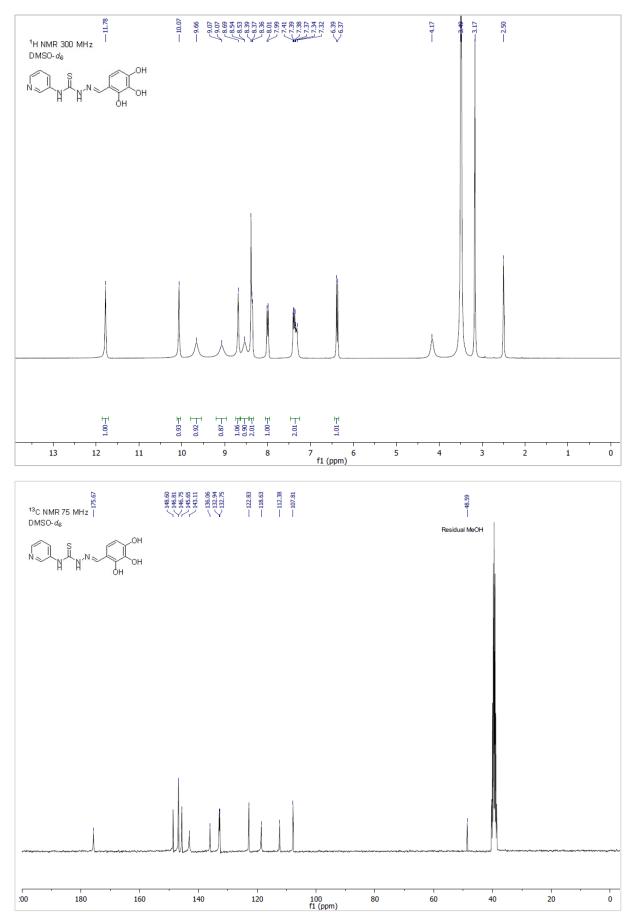
Compound 22d



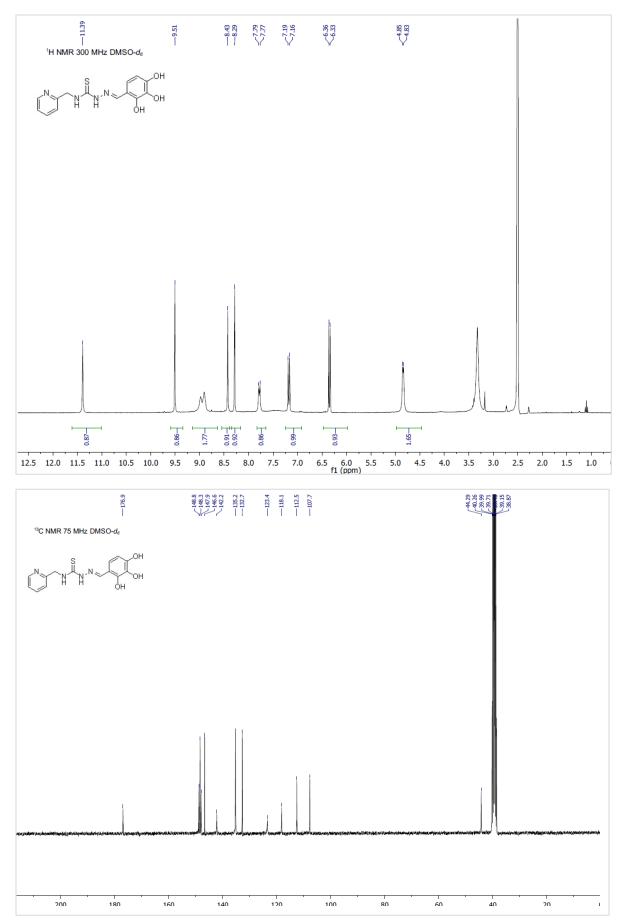
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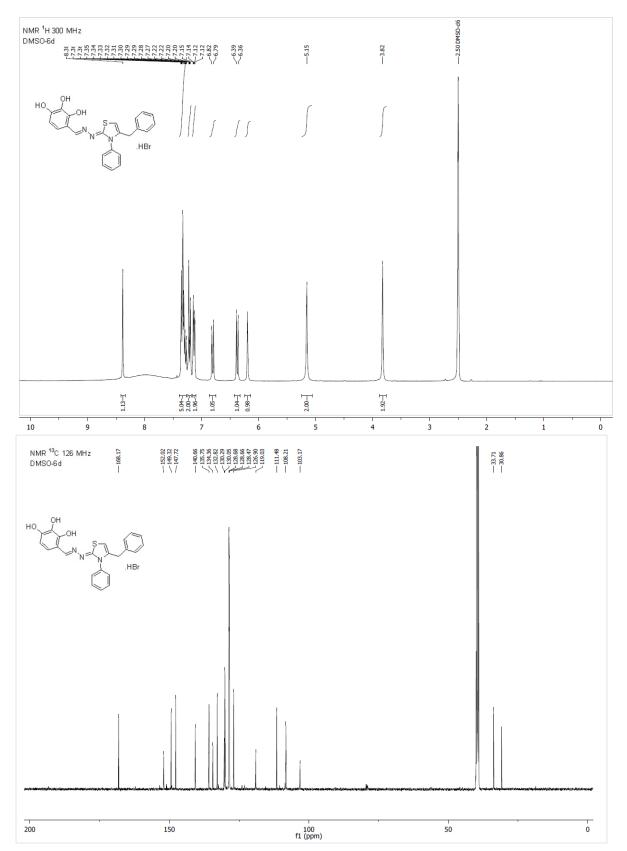


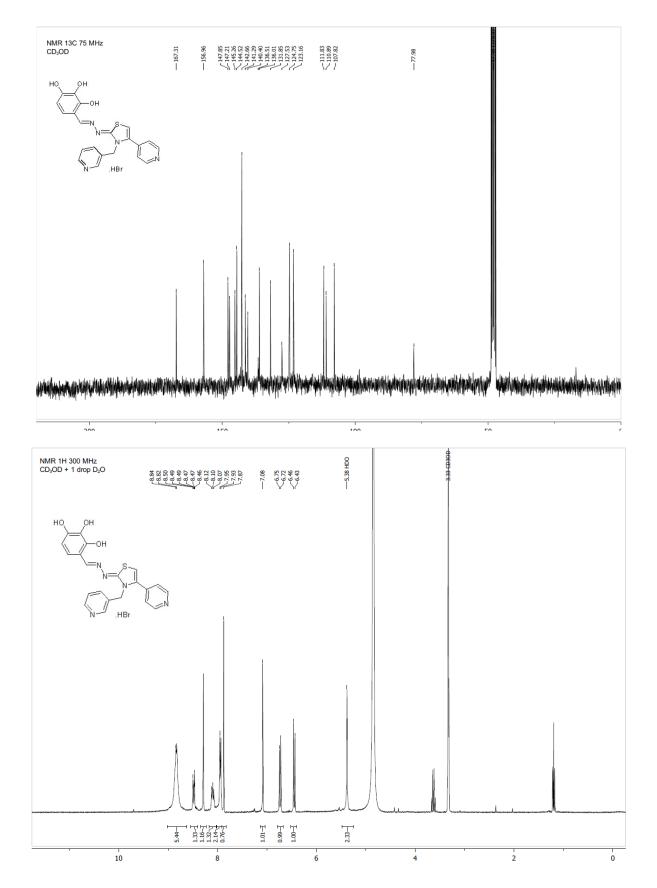
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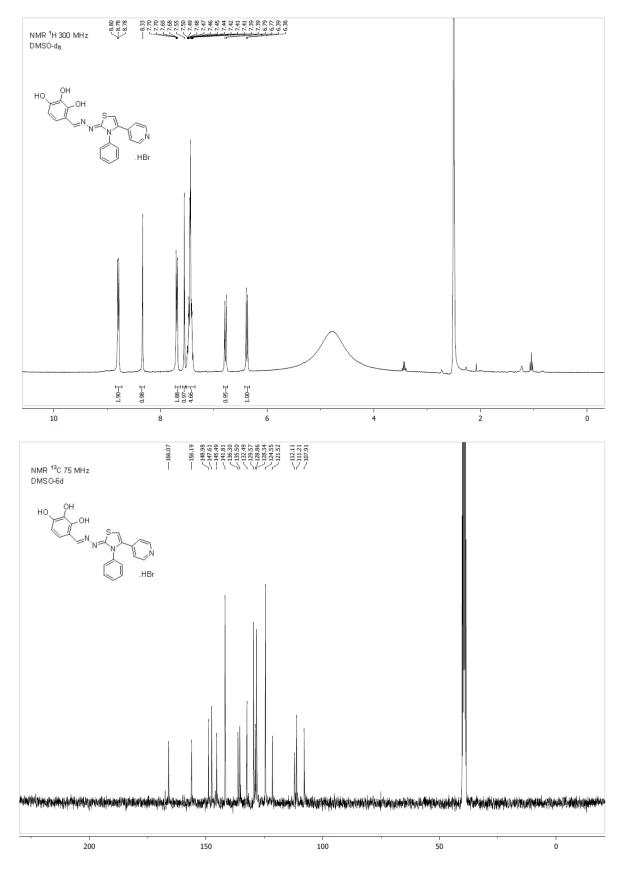


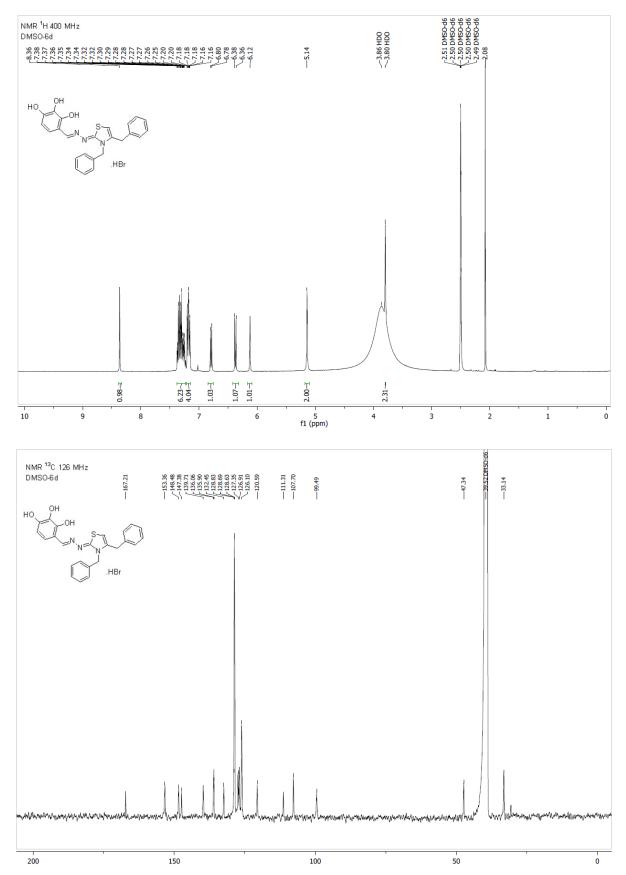
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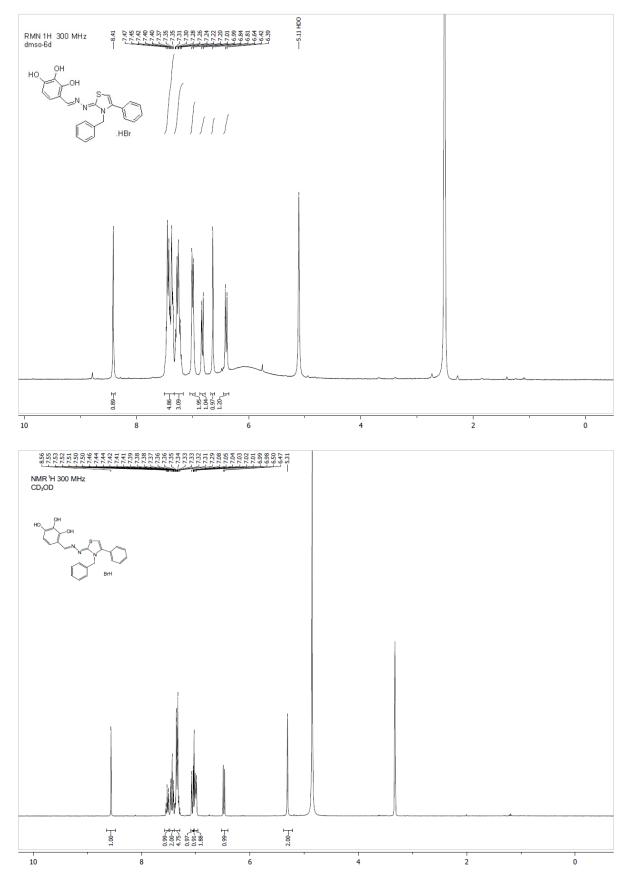


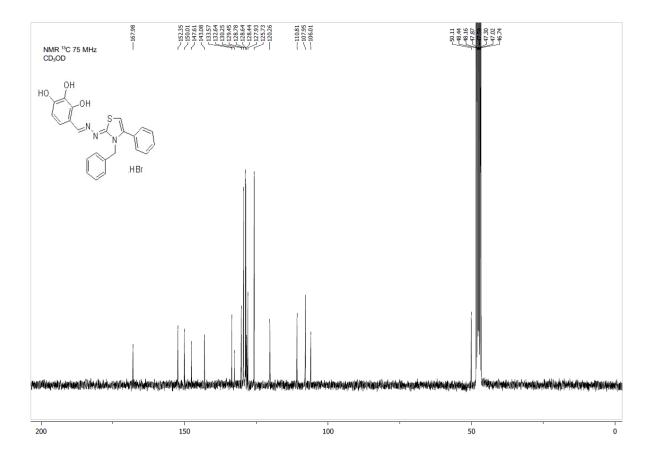


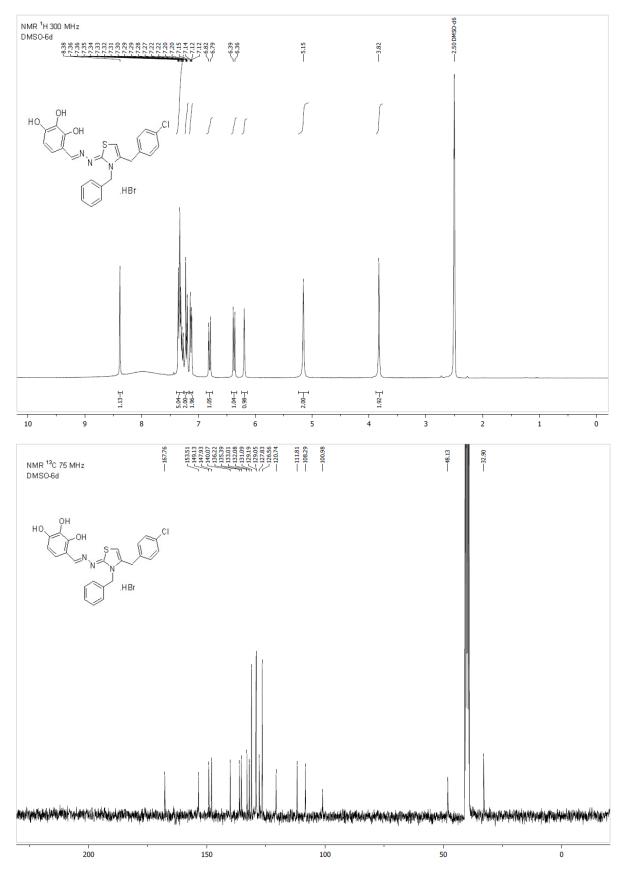


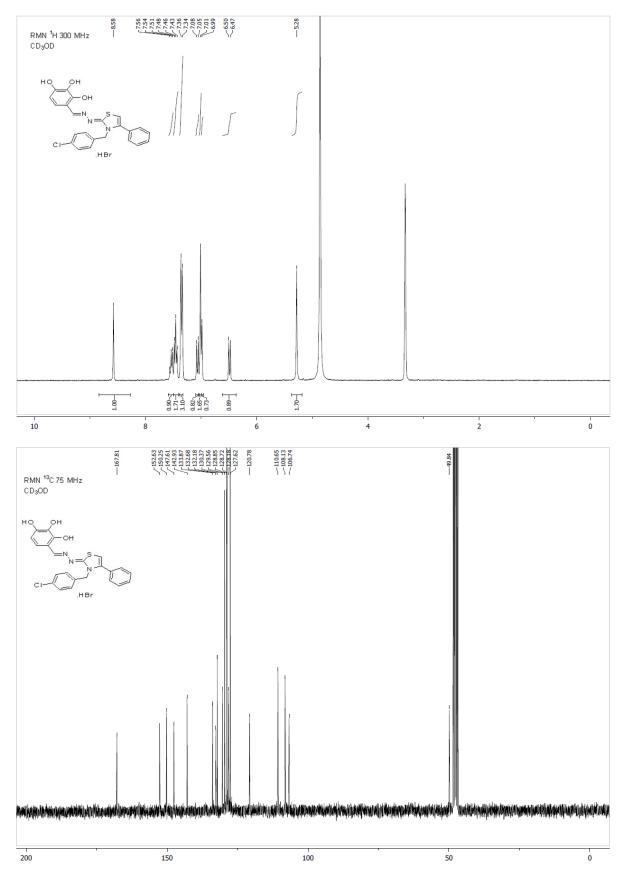


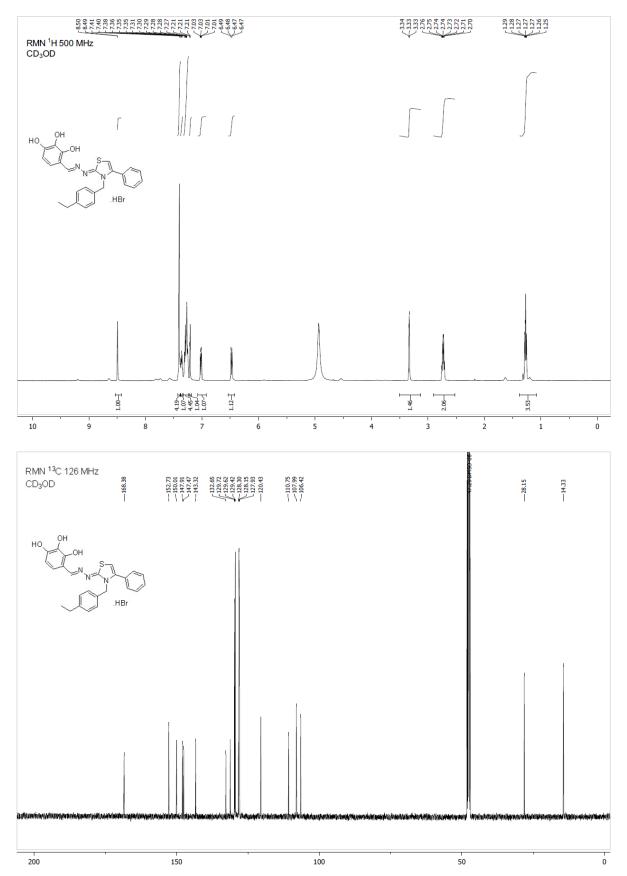


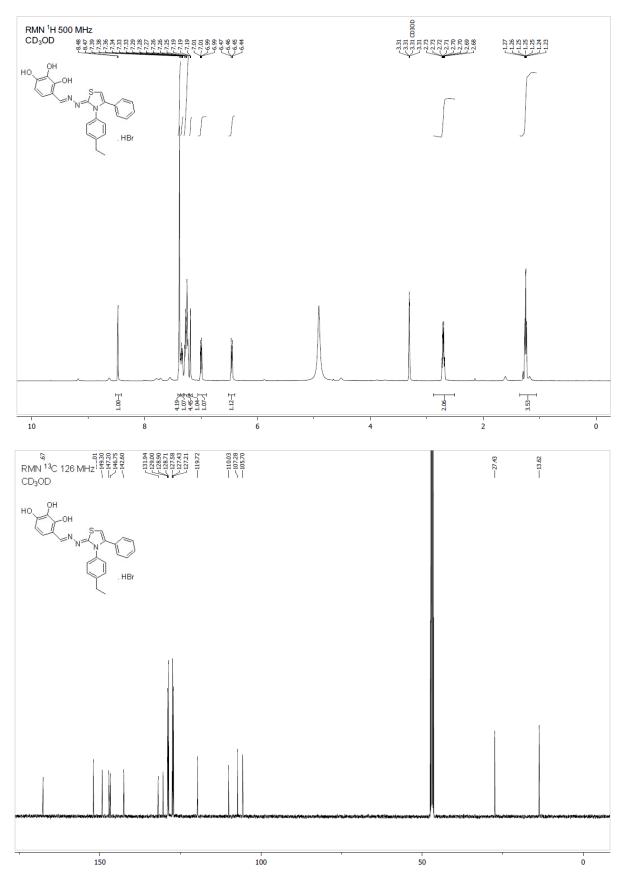


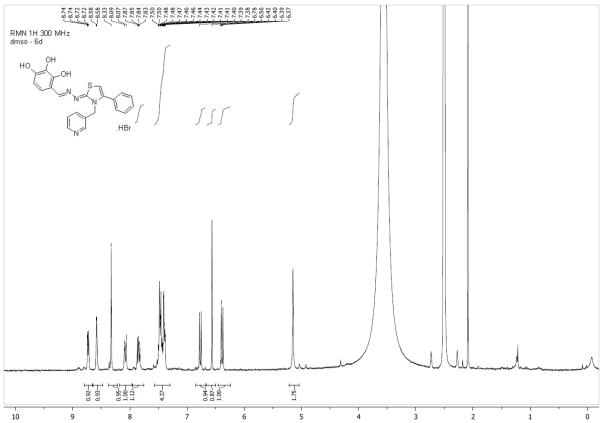


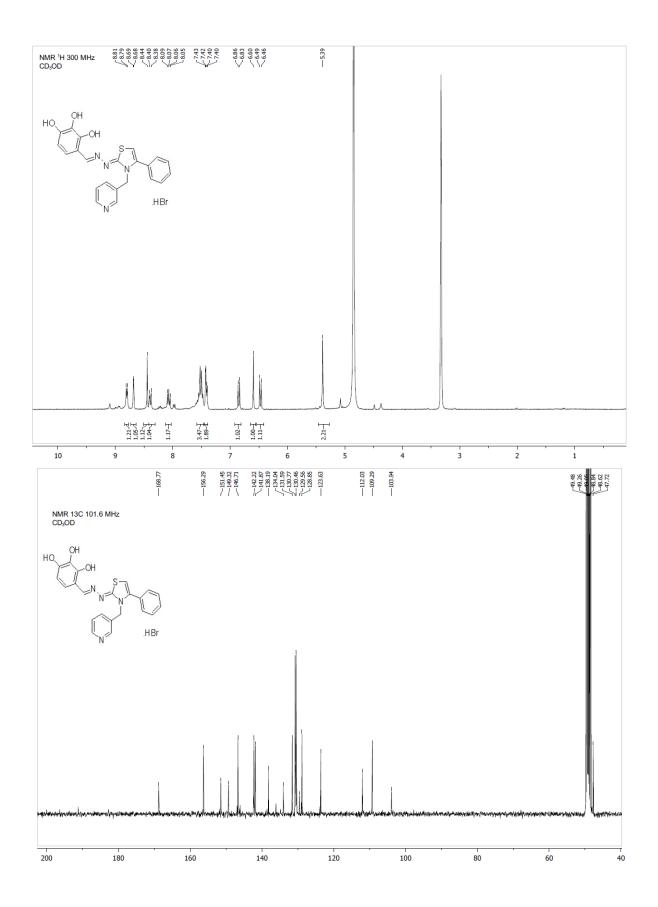


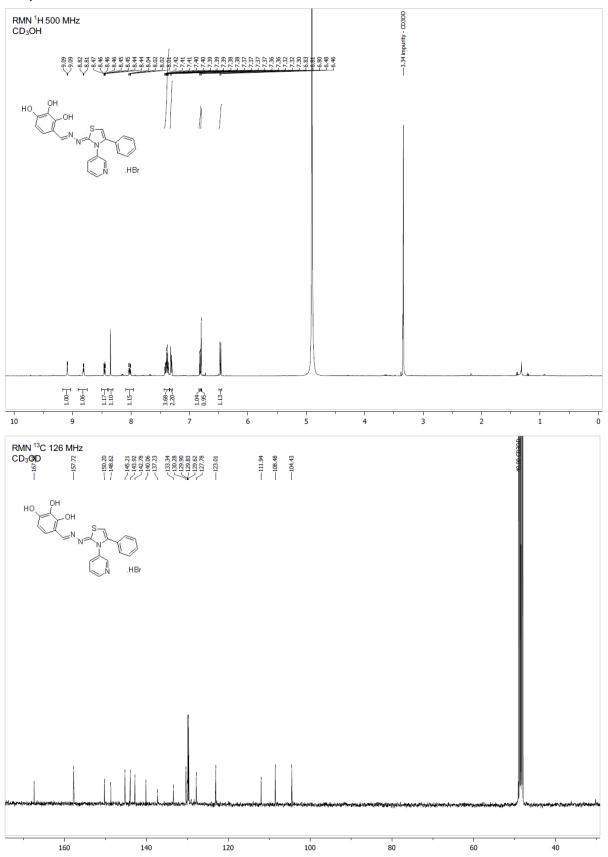


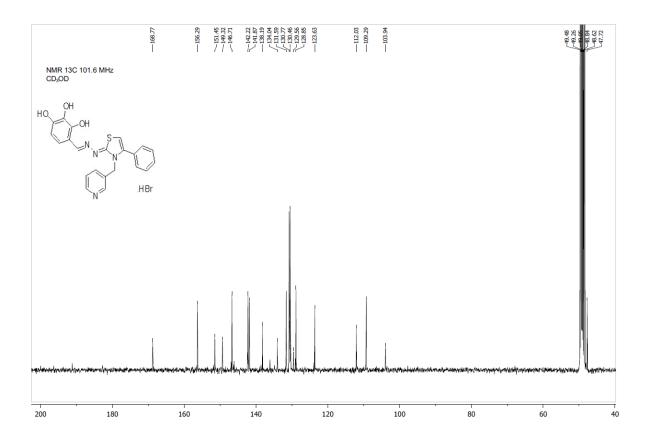


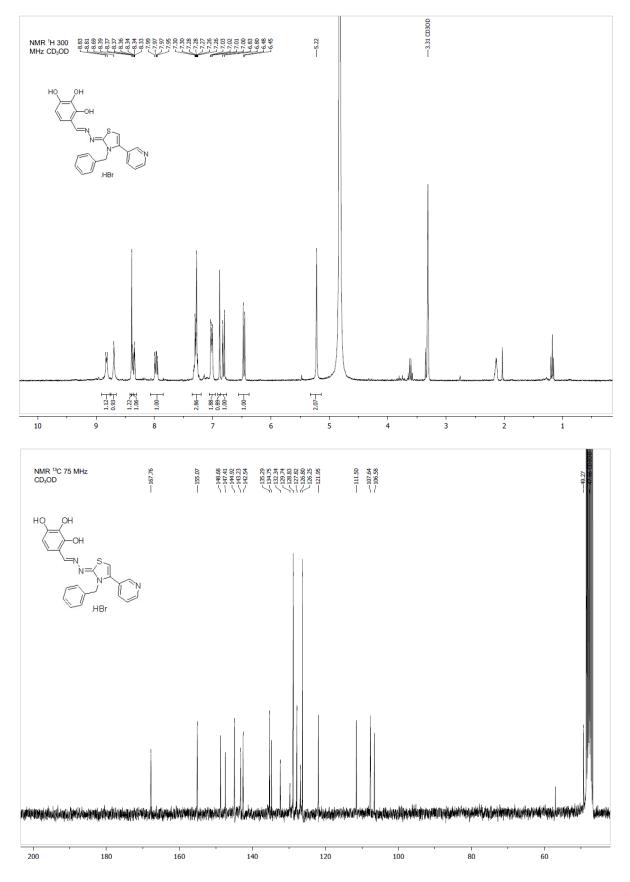


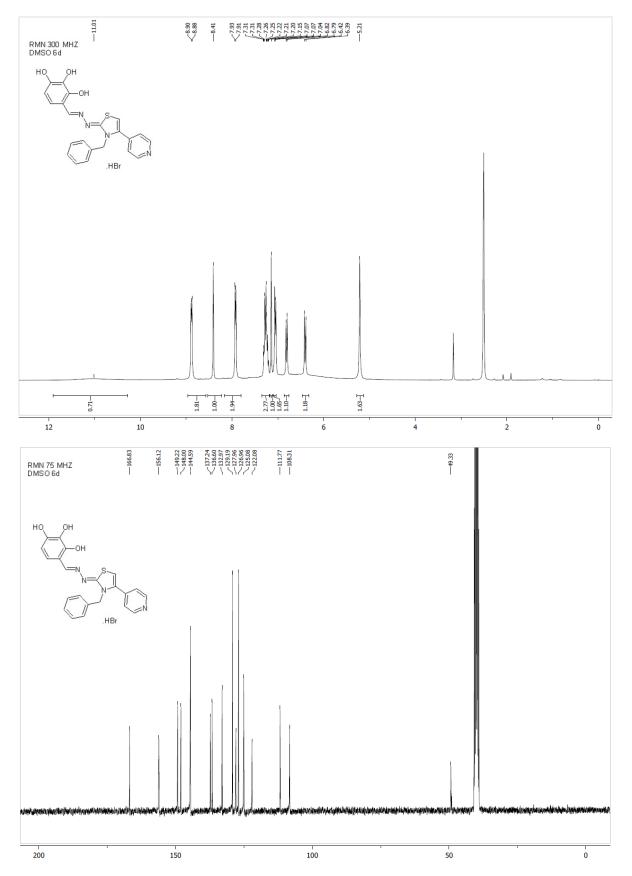




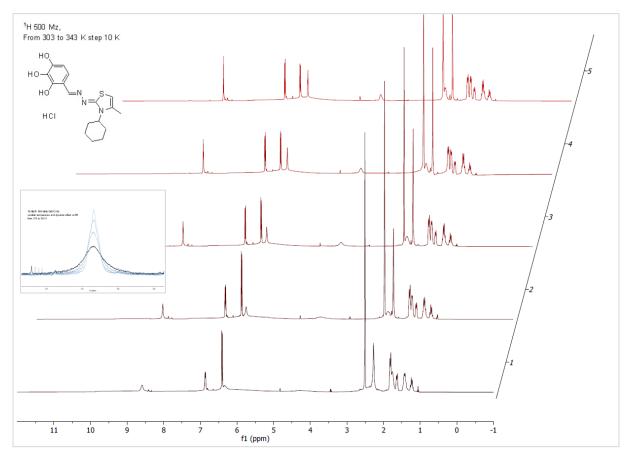




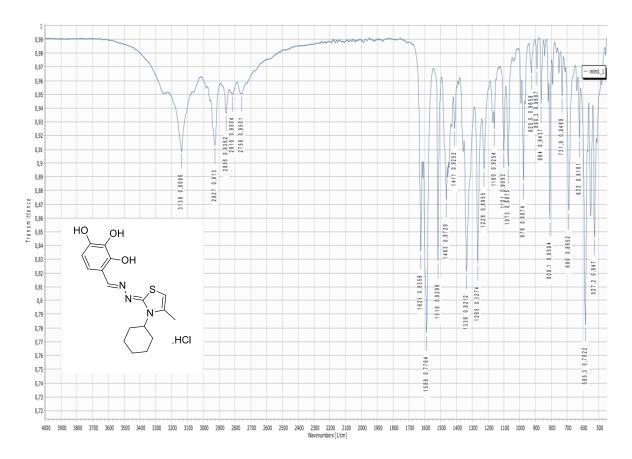




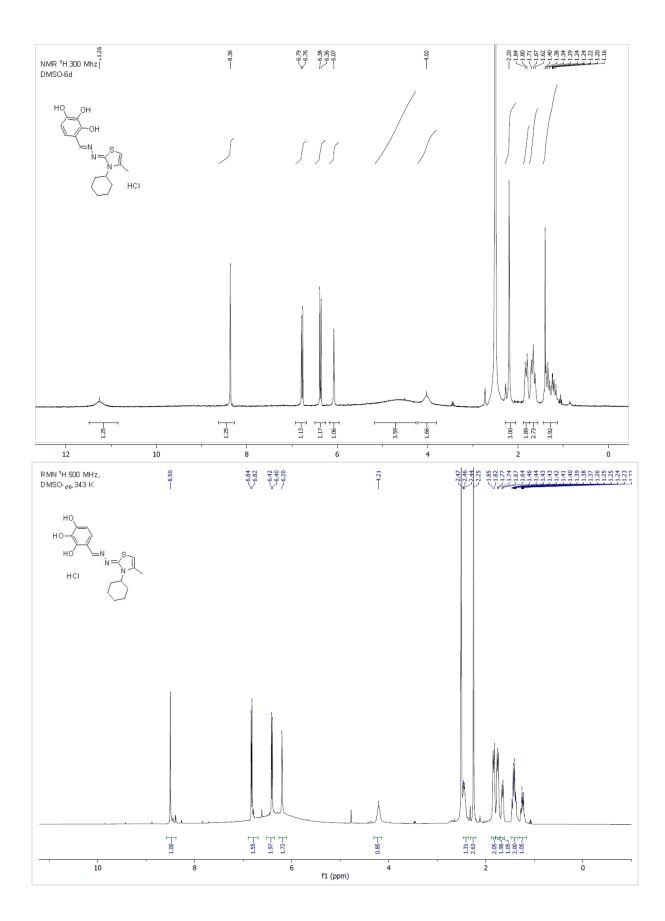
Compound 2 (MIM1 studies)

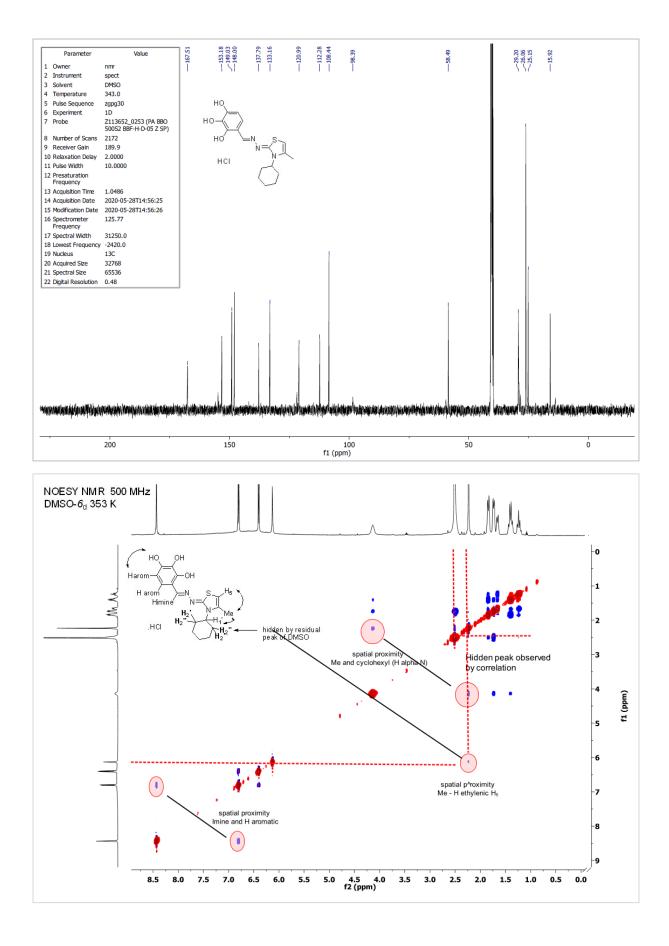


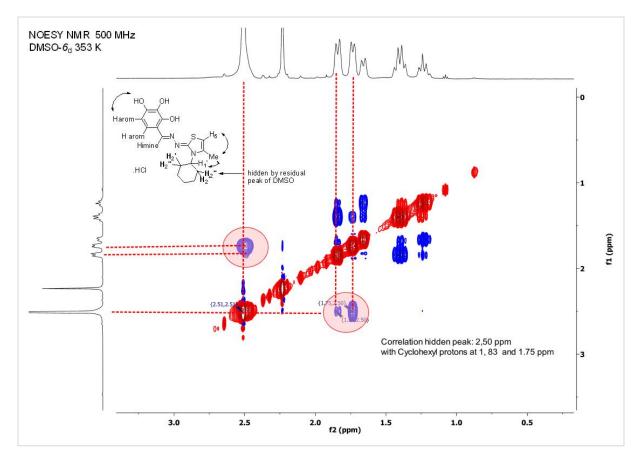
Supporting Information Figure 3: Dynamic Effect of ¹H NMR experiments with variations of temperature (step 10K)



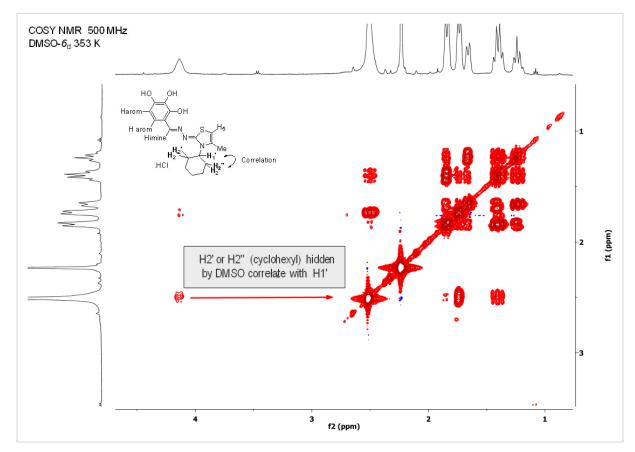
Supporting Information Figure 4: FT-IR of Compound 2

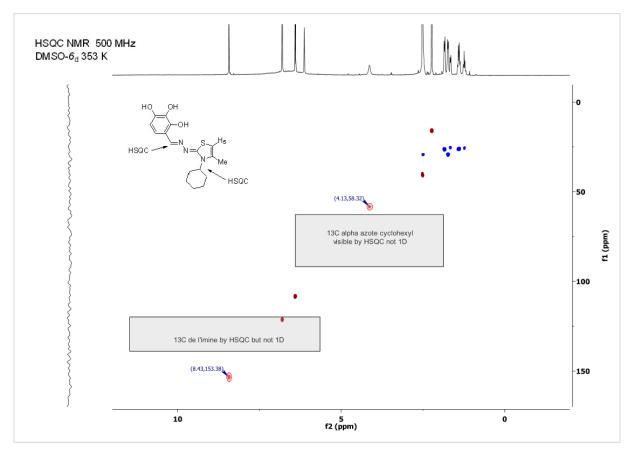




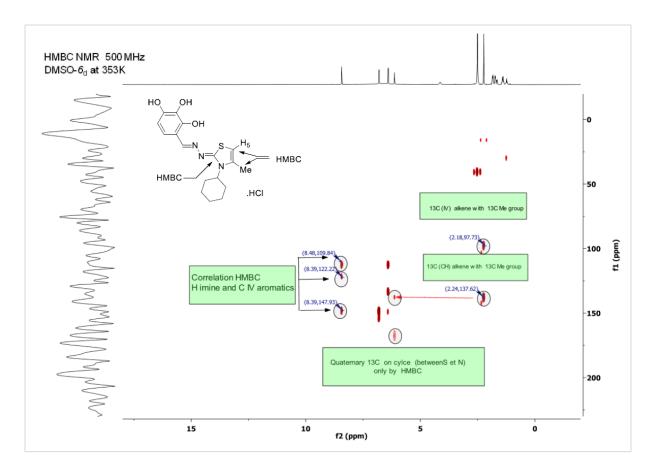


NOESY Experiment correlations: Me and H_5 , Me and $H_{1'}$, H2''/2' cyclohexyl (hidden by DMSO -6d) and H2'/H2'' (from cyclohexyl), Himine and Haromatic

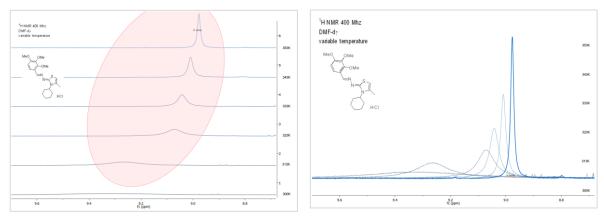




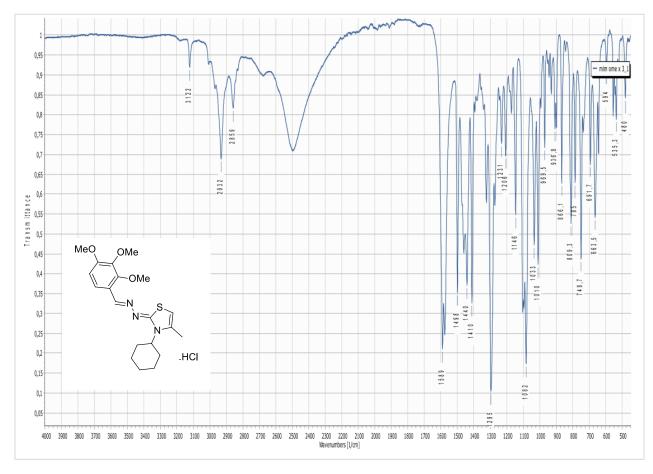
Correlation between $H_{1'}$ and $H_{2'}/H_{2''}$ cyclohexyl hidden by DMSO-6d. (second proof)



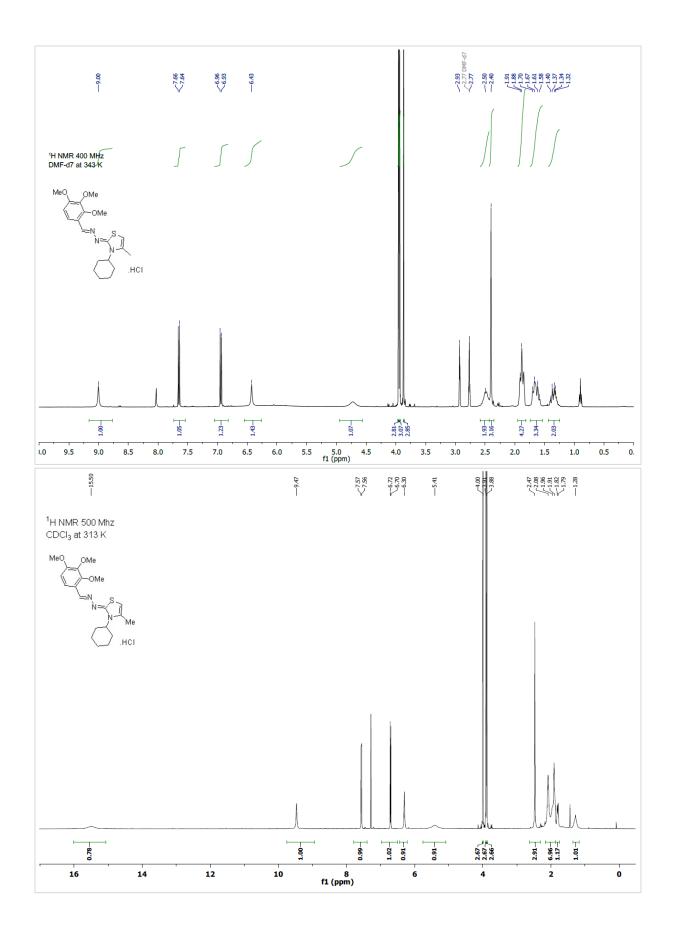
Compound 11 (analogue of MIM1 x OMe)

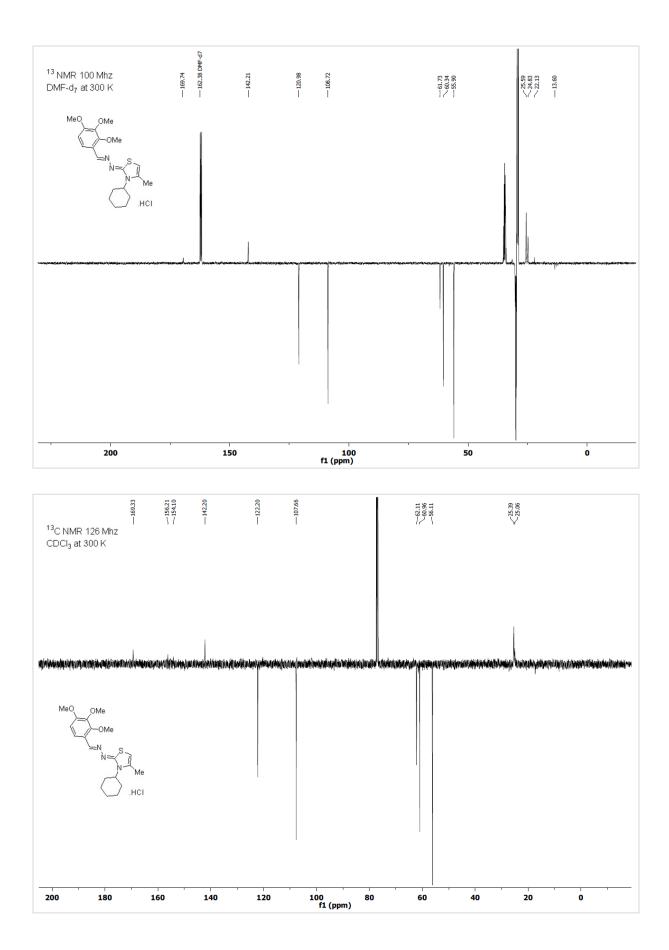


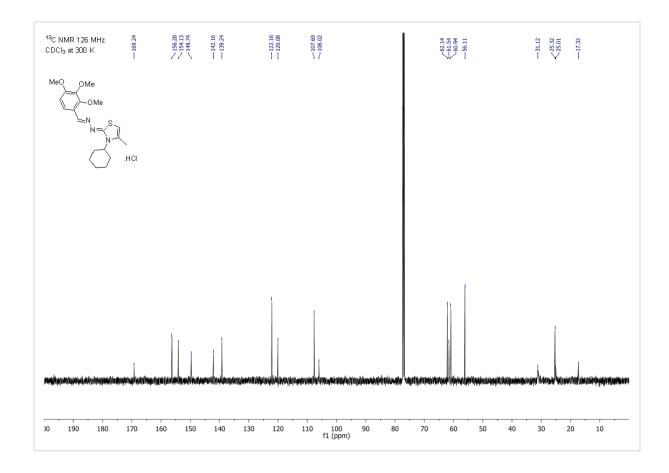
Supporting Information Figure 3: H imine proton of MIM1 (OMe x 3) relaxation upon temperature variation (copy of juxtaposition of ¹H NMR spectra)

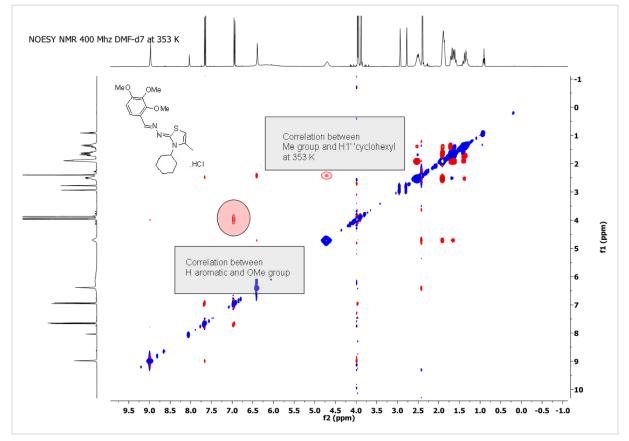


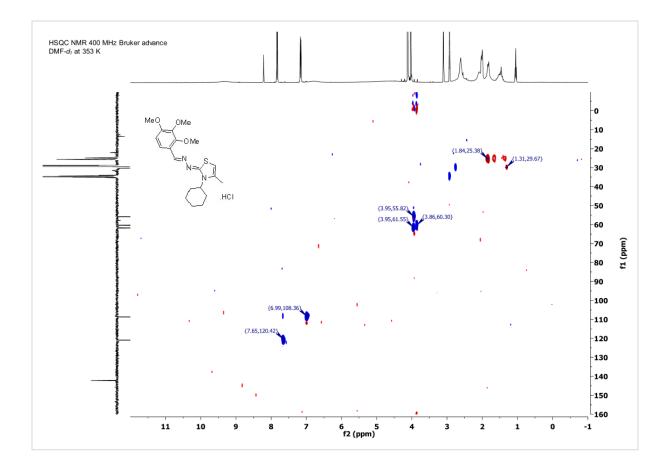
Supporting Information Figure 4: FT-IR compound 11

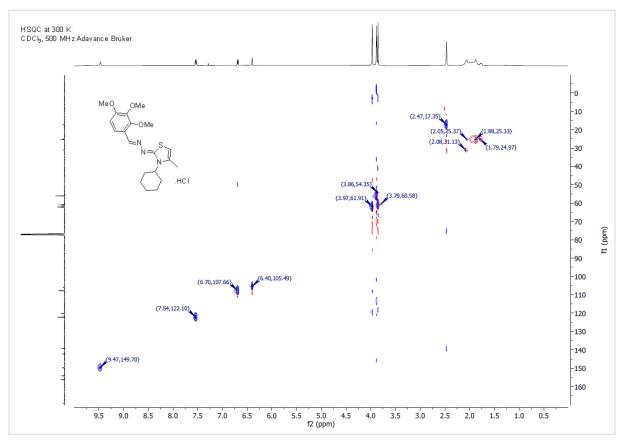


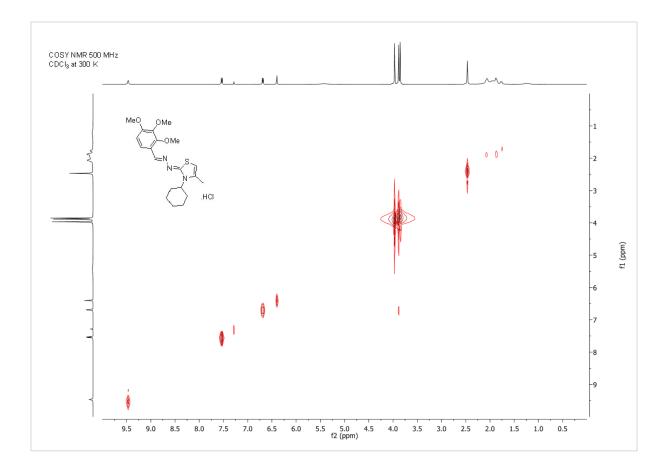


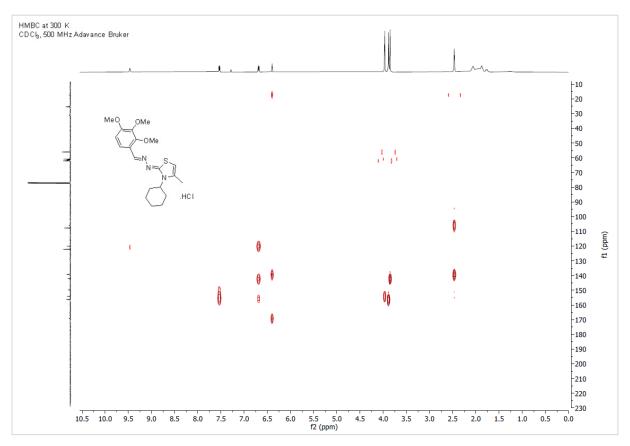




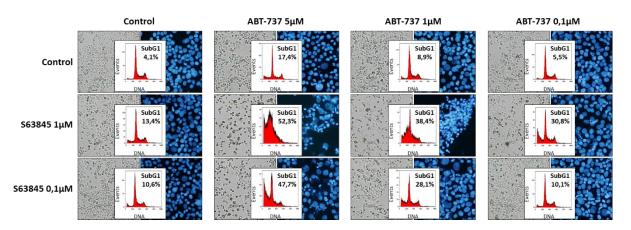




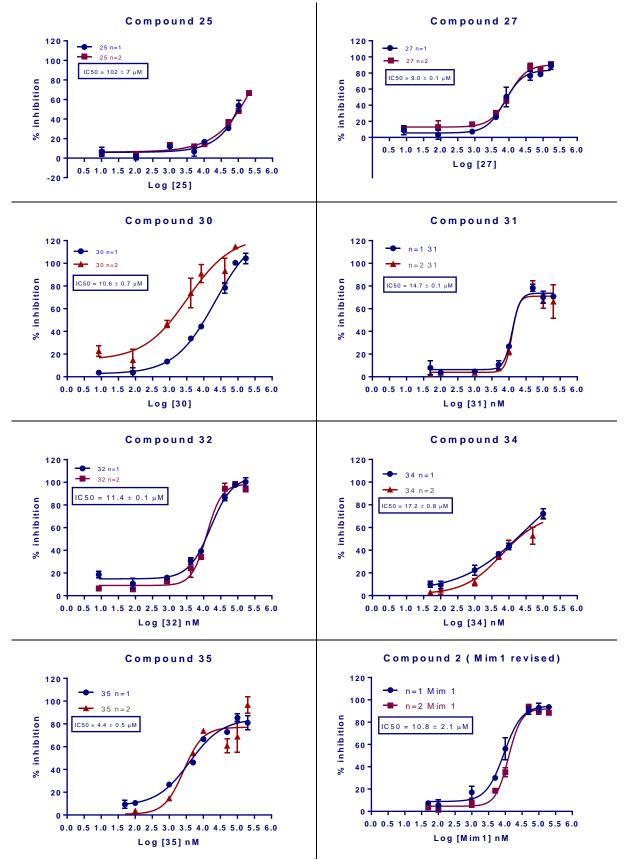




Supporting Information biological studies



Supporting Information Figure 5: Effect of ABT-737 and S63845 combination on IGROV1-R10 chemoresistant ovarian cancer cell line. Cellular morphology, DNA content and nuclear morphology were assessed after 24h exposure.



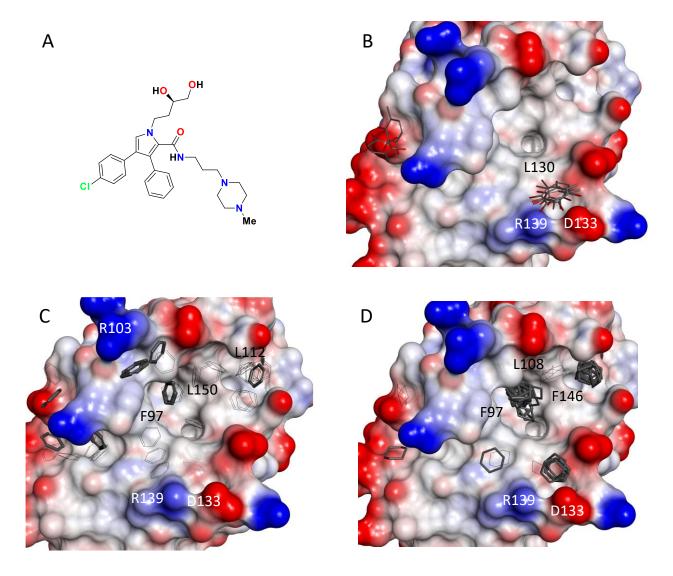
Supporting Information for Fluorescence Polarization Assays

Supporting Information, Table 1. Competitive inhibition binding curves of MIM1 analogues.

Supporting Information for molecular docking

Determination of $Bcl-x_{L}$ binding site by molecular modelling

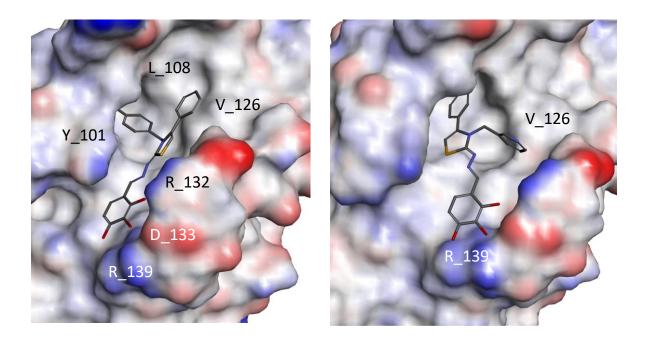
The structure of our compounds is, to our knowledge, completely new in the $Bcl-x_L$ area. So, their binding site had to be deciphered. To this end, we investigated the 82 Bcl- x_L complexes available in the PDB to find the most similar ligand to our molecules. We found a diphenyl-pyrrole derivative with a somewhat similarity to our diphenyl-thiazole compounds (PDB: 3SPF)



Supporting Information, Fig. 6. (A) Chemical structure of the closest $Bcl-x_L$ inhibitor found in the PDB. (B) Fragments docking at the surface of $Bcl-x_L$. Methyl-triphenol was mostly clustered in a cavity above R139/D133, with the highest calculated interaction energy: -44 kcal/mol. (C) Benzene was scattered on the protein surface, but much enriched in three cavities, one between F97 and L150 (-15.7 kcal/mol), the second beneath R103 (-14 kcal/mol), and the last near L112 (-11.6 kcal/mol). (D) Cyclohexane occupied essentially two deep cavities, the same as benzene (respectively -16.5 and -13.5 kcal/mol). The thickness of the fragments chemical bonds relates to the calculated interaction energy (the thickest, the highest).

To probe the possible binding sites and orientations of our ligands in this protein conformer, we first performed a multiple copy simultaneous search (MCSS) of different fragments: a triphenol and a benzene, directly related to our molecules, and a cyclohexane to identify the most hydrophobic binding site (more precisely, the site most prone to Van der Waals interactions). Clustering of the docked fragments and calculated interaction energy suggested that the triphenol might bind to a rather flat surface above L130, near the ionic pairs R139/D133 and R132/E129 (Fig. 6B). Benzene had more scattered binding sites, but the two most populated and highest affinity cavities were around F97, L150 and L112 (Fig. 6C). The cyclohexyl fragment predominated in the two central cavities (Fig. 6D). Interestingly, the predicted triphenol binding site corresponded to that of a co-crystallized glycerol (a trihydroxylated molecule), and the most favourable cyclohexane site to that of chlorophenyl of the co-crystallized inhibitor.

Independently of the MCSS experiment, we performed a flexible docking of compound **30**. The pose with the highest score suggests a binding mode where the triphenol forms extensive hydrogen bonds with ionic pairs R139/D133 and/or R132/E129 (Supporting Information Fig. 7). The thiazole is above V126, while the phenyl interacts with L108, V126 and L112, overhangs by Q111. The ethyl-benzyl is buried in the deep cavity, interacting with F146, L108, A104, Y101 and F97.

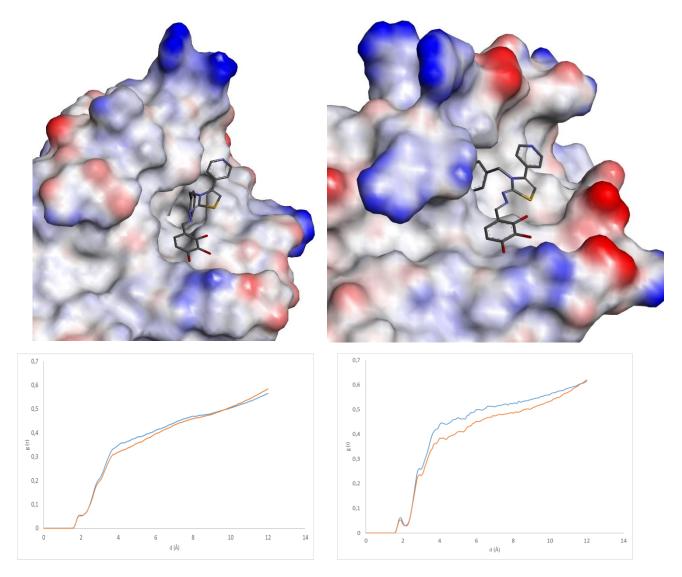


Supporting Information Fig. 7(left). Proposed binding mode of **30** in Bcl-xL. (B) (right) **32** docked in the same protein.

Computational studies of compound **35** onto Mcl-1 and Bcl-x_L

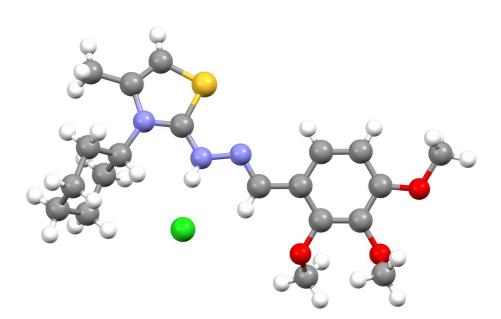
As already observed for Mcl-1, the ligand is able to flip in the binding site in order to minimize the solvent exposition of most hydrophobic parts. This was confirmed by molecular dynamics, showing that **35** is more solvated in Mcl-1 binding site than is Bcl- x_L (Supp. Info. Fig. 8), and explaining why **35** is selective for Mcl-1 in spite of a similar binding mode in both proteins.

This was confirmed by molecular dynamics, showing that **35** is more solvated in Mcl-1 binding site than is $Bcl-x_L$ (Supporting Information Fig. 8), and explaining why **35** is selective for Mcl-1 in spite of a similar binding mode in both proteins.



Supporting Information, Fig. 8. (top) Compound 35 docked onto Mcl-1 (left) and Bcl- x_{L} (right). One can observe that the pyridine is much more solvent-exposed in the former. Radial distribution function g(r) of water measured during molecular dynamics of full molecule 35 (bottom left) in Mcl-1 (blue) and Bcl- x_{L} (red), and only pyridine of 35 (bottom right).

Structure of **11** established by X-Ray analysis:



The details of X-Ray structural analysis of **11** have been deposited at CDDC with the number 2006656.

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Structure factors have been supplied for datablock(s) I

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0 ALERT level B = A potentially serious problem, consider carefully
8 ALERT level C = Check. Ensure it is not caused by an omission or oversight
5 ALERT level G = General information/check it is not something unexpected
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6 ALERT type 2 Indicator that the structure model may be wrong or deficient
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0 ALERT type 5 Informative message, check

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Alert level G

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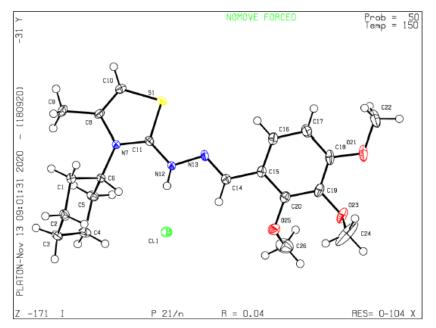
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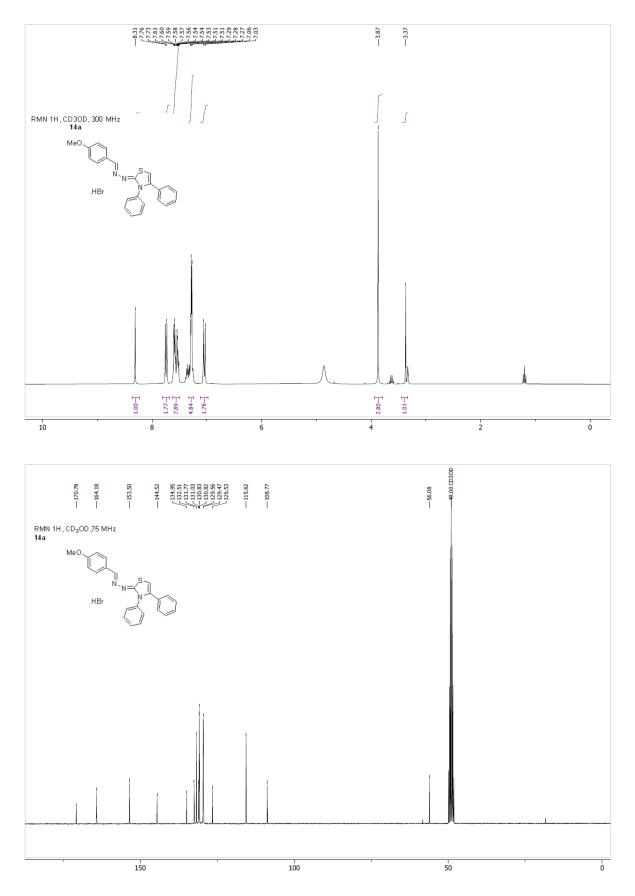
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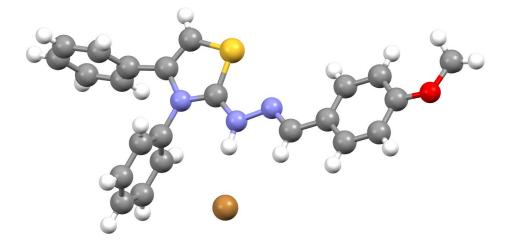
Datablock I - ellipsoid plot





NMR spectra of 14a

Structure of 14a established by X-Ray analysis:



The details of X-Ray structural analysis of **14a** have been deposited at CDDC with the number 2006657.

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Structure factors have been supplied for datablock(s) I

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No syntax errors found. CIF dictionary Interpreting this report

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Hall group	F 2 -2d		F 2 -2d	
Moiety formula	C23 H20 N3 O S, Bi solvent]	: [+	C23 H20	N3 O S, Br
Sum formula	C23 H20 Br N3 O S solvent]	[+	C23 H20	Br N3 O S
Mr	466.38		466.39	
Dx,g cm-3	1.348		1.348	
-	16		16	
Mu (mm-1)	1.897		1.897	
F000	3808.0		3808.0	
F000′	3806.57			
h,k,lmax			32,51,12	
	5275[2800]		5182	
Tmin,Tmax			0.548,0.	697
Tmin'	0.376			
Correction method= # Reported T Limits: Tmin=0.548 Tmax=0.697 AbsCorr = MULTI-SCAN				
Data completeness= 1.85/0.98 Theta(max) = 27.503				
R(reflections)=	0.0276(4943)	wR2(ref]	lections)	= 0.0664(5182)
S = 1.061	Npar= 2	67		

```
The following ALERTS were generated. Each ALERT has the format test-name_ALERT_alert-type_alert-level.
Click on the hyperlinks for more details of the test.
```

```
Alert level C
```

Alert level C	
PLAT431_ALERT_2_C Short Inter HLA Contact Br1S1 .	3.44 Ang.
x,y,1+z =	1 556 Check
PLAT911 ALERT 3 C Missing FCF Refl Between Thmin & STh/L= 0.600	
	_
Alert level G	
PLAT083_ALERT_2_G SHELXL Second Parameter in WGHT Unusually Large	15.24 Why ?
PLAT605 ALERT 4 G Largest Solvent Accessible VOID in the Structure	116 A**3
PLAT869 ALERT 4 G ALERTS Related to the Use of SQUEEZE Suppressed	! Info
PLAT910 ALERT_3_G Missing # of FCF Reflection(s) Below Theta(Min).	2 Note
PLAT912_ALERT_4_G Missing # of FCF Reflections Above STh/L= 0.600	2 Note
PLAT978_ALERT_2_G Number C-C Bonds with Positive Residual Density.	0 Info
0 ALERT level A = Most likely a serious problem - resolve or expl	
0 ALERT level B = A potentially serious problem, consider careful	•
2 ALERT level C = Check. Ensure it is not caused by an omission of	
6 ALERT level G = General information/check it is not something u	inexpected
0 ALERT type 1 CIF construction/syntax error, inconsistent or mis	-
3 ALERT type 2 Indicator that the structure model may be wrong or	deficient
2 ALERT type 3 Indicator that the structure quality may be low	
3 ALERT type 4 Improvement, methodology, query or suggestion	
0 ALERT type 5 Informative message, check	

checkCIF publication errors

🗣 Alert level A

Alert level G

7 ALERT level A = Data missing that is essential or data in wrong format 1 ALERT level G = General alerts. Data that may be required is missing

Publication of your CIF

You should attempt to resolve as many as possible of the alerts in all categories. Often the minor alerts point to easily fixed oversights, errors and omissions in your CIF or refinement strategy, so attention to these fine details can be worthwhile. In order to resolve some of the more serious problems it may be necessary to carry out additional measurements or structure refinements. However, the nature of your study may justify the reported deviations from journal submission requirements and the more serious of these should be commented upon in the discussion or experimental section of a paper or in the "special_details" fields of the CIF. *checkCIF* was carefully designed to identify outliers and unusual parameters, but every test has its limitations and alerts that are not important in a particular case may appear. Conversely, the absence of alerts does not guarantee there are no aspects of the results needing attention. It is up to the individual to critically assess their own results and, if necessary, seek expert advice.

If level A alerts remain, which you believe to be justified deviations, and you intend to submit this CIF for publication in a journal, you should additionally insert an explanation in your CIF using the Validation Reply Form (VRF) below. This will allow your explanation to be considered as part of the review process.

Validation response form

Please find below a validation response form (VRF) that can be filled in and pasted into your CIF.

start Validation Reply Form vrf_PUBL004_GLOBAL PROBLEM: The contact author's name and address are missing, RESPONSE: ... _vrf_PUBL005_GLOBAL PROBLEM: _publ_contact_author_email, _publ_contact_author_fax and RESPONSE: ... vrf PUBL006 GLOBAL PROBLEM: _publ_requested_journal is missing RESPONSE: ... vrf_PUBL008_GLOBAL , PROBLEM: _publ_section_title is missing. Title of paper. RESPONSE: ... _vrf_PUBL009_GLOBAL PROBLEM: _publ_author_name is missing. List of author(s) name(s). RESPONSE: ... vrf PUBL010 GLOBAL PROBLEM: _publ_author_address is missing. Author(s) address(es). RESPONSE: vrf_PUBL012_GLOBAL

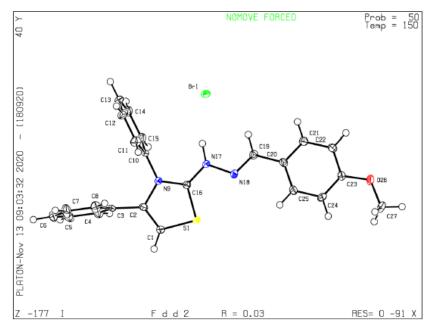
PROBLEM: _publ_section_abstract is missing. RESPONSE: ...

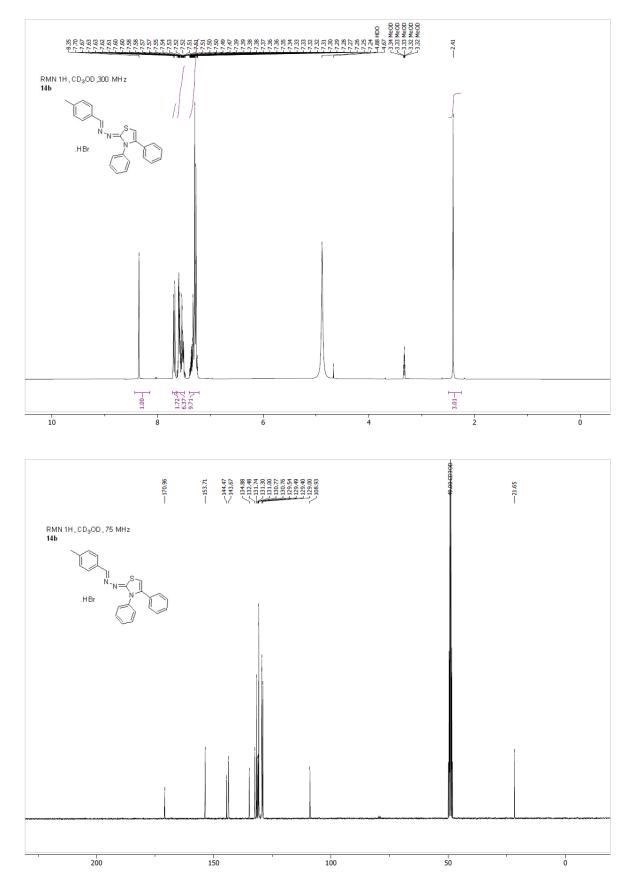
end Validation Reply Form

If you wish to submit your CIF for publication in Acta Crystallographica Section C or E, you should upload your CIF via the web. If you wish to submit your CIF for publication in IUCrData you should upload your CIF via the web. If your CIF is to form part of a submission to another IUCr journal, you will be asked, either during electronic submission or by the Co-editor handling your paper, to upload your CIF via our web site.

PLATON version of 18/09/2020; check.def file version of 20/08/2020

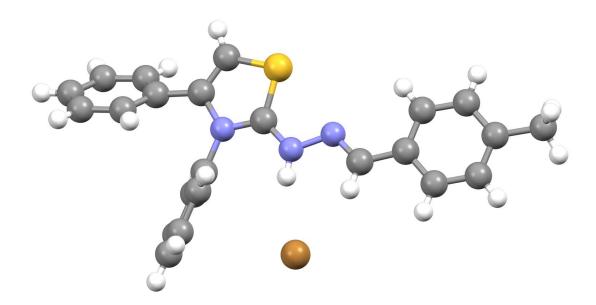
Datablock I - ellipsoid plot





NMR spectra of 14b

Structure of **14b** established by X-Ray analysis:



The details of X-Ray structural analysis of **14b** have been deposited at CDDC with the number 2006655.

checkCIF/PLATON report

Structure factors have been supplied for datablock(s) I

THIS REPORT IS FOR GUIDANCE ONLY. IF USED AS PART OF A REVIEW PROCEDURE FOR PUBLICATION, IT SHOULD NOT REPLACE THE EXPERTISE OF AN EXPERIENCED CRYSTALLOGRAPHIC REFEREE.

No syntax errors found. CIF dictionary Interpreting this report

Datablock: I

Bond precision: C-C = 0.0030 A		Wavelength=0.71073			
	a=9.087(1) alpha=80.956(4)				
Temperature:	-			-	
	Calculated		Reported	1	
Volume	1093.3(2)		1093.3(2	2)	
Space group	P -1		P -1		
Hall group			-P 1		
Moiety formula	C23 H20 N3 S, Br	, H2 O	C23 H20	N3 S, Br, H2 O	
Sum formula	C23 H22 Br N3 O 8	5	C23 H22	Br N3 O S	
Mr	468.40		468.40		
Dx,g cm-3	1.423		1.423		
Z	2		2		
Mu (mm-1)	1.994		1.994		
F000	480.0		480.0		
F000′	479.82				
h,k,lmax	11,13,17		11,13,1	7	
Nref	5042		4926		
Tmin,Tmax	0.555,0.772		0.592,0	.772	
Tmin'	0.437				
Correction meth AbsCorr = MULTI	od= # Reported T 1 -SCAN	Limits: Tn	nin=0.592	2 Tmax=0.772	
Data completeness= 0.977 Theta(max)= 27.539					
R(reflections) =	0.0264(4380)	wR2(ref	lections)= 0.0595(4926)	
S = 0.999	Npar=	272			

The following ALERTS were generated. Each ALERT has the format test-name_ALERT_alert-type_alert-level. Click on the hyperlinks for more details of the test.

<pre> Alert level B PLAT431_ALERT_2_B Short Inter HLA Contact Br1S1 .</pre>	-
Alert level C PLAT911_ALERT_3_C Missing FCF Refl Between Thmin & STh/L= 0.600	63 Report
● Alert level G PLAT154_ALERT_1_G The s.u.'s on the Cell Angles are Equal (Note) PLAT720_ALERT_4_G Number of Unusual/Non-Standard Labels PLAT910_ALERT_3_G Missing # of FCF Reflection(s) Below Theta(Min). PLAT912_ALERT_4_G Missing # of FCF Reflections Above STh/L= 0.600 PLAT911_ALERT_3_G Average HKL Measurement Multiplicity PLAT978_ALERT_2_G Number C-C Bonds with Positive Residual Density.	0.004 Degree 2 Note 1 Note 52 Note 4.3 Low 14 Info
<pre>0 ALERT level A = Most likely a serious problem - resolve or explai 1 ALERT level B = A potentially serious problem, consider carefully 1 ALERT level C = Check. Ensure it is not caused by an omission or 6 ALERT level G = General information/check it is not something une 1 ALERT type 1 CIF construction/syntax error, inconsistent or missi 2 ALERT type 2 Indicator that the structure model may be wrong or d 3 ALERT type 3 Indicator that the structure quality may be low 2 ALERT type 4 Improvement, methodology, query or suggestion 0 ALERT type 5 Informative message, check</pre>	, oversight expected ng data

checkCIF publication errors

7 ALERT level A = Data missing that is essential or data in wrong format 1 ALERT level G = General alerts. Data that may be required is missing

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start Validation Reply Form vrf_PUBL004_GLOBAL PROBLEM: The contact author's name and address are missing, RESPONSE: ... _vrf_PUBL005_GLOBAL PROBLEM: _publ_contact_author_email, _publ_contact_author_fax and RESPONSE: ... vrf PUBL006 GLOBAL PROBLEM: _publ_requested_journal is missing RESPONSE: ... vrf_PUBL008_GLOBAL , PROBLEM: _publ_section_title is missing. Title of paper. RESPONSE: ... _vrf_PUBL009_GLOBAL PROBLEM: _publ_author_name is missing. List of author(s) name(s). RESPONSE: ... vrf PUBL010 GLOBAL PROBLEM: _publ_author_address is missing. Author(s) address(es). RESPONSE: ... vrf_PUBL012_GLOBAL

PROBLEM: _publ_section_abstract is missing. RESPONSE: ...

, # end Validation Reply Form

If you wish to submit your CIF for publication in Acta Crystallographica Section C or E, you should upload your CIF via the web. If you wish to submit your CIF for publication in IUCrData you should upload your CIF via the web. If your CIF is to form part of a submission to another IUCr journal, you will be asked, either during electronic submission or by the Co-editor handling your paper, to upload your CIF via our web site.

PLATON version of 18/09/2020; check.def file version of 20/08/2020

Datablock I - ellipsoid plot

