

SUPPLEMENTARY MATERIALS

Catalytic activity of halohydrin dehalogenases towards spiroepoxides

Maja Majerić Elenkov,^{*a} Ines Primožič,^b Tomica Hrenar,^b Ana Smolko,^a Irena Dokli,^a Branka Salopek Sondi,^a Lixia Tang^c

^a Ruđer Bošković Institute, Bijenička c. 54, 10000 Zagreb, Croatia. Fax: ++385 1 4680-108; Tel: +385 1 4560965; E-mail: majeric@irb.hr

^b Faculty of Science, University of Zagreb, Zagreb, Croatia. Fax: +385 1 4606 401; Tel: +385 1 4606 400; E-mail: ines.primozic@chem.pmf.hr

^c University of Electronic Science and Technology, No.4, Section 2, North Jianshe Road, Chengdu, China. Fax: +86 28 83208238; Tel: +86 28 83208232; E-mail: lixiatang@uestc.edu.cn

Content.

1. GC analyses	S2
2. Reaction profiles for the non-enzyme ring opening of spiroepoxides	S3
3. Docking studies of 1-oxaspiro[2.5]octane compounds 1b and 1d–1f in the active site of HheA and HheC	
3.1. Estimated lowest Gibbs energies of binding	S5
3.2. Overlay of equatorial and axial lowest energy conformers in the active site of HheA for 1d and 1f enantiomers	S6
3.3. Overlay of equatorial and axial lowest energy conformers in the active site of HheC for 1d and 1f enantiomers	S8
4. NMR spectra	S10

1. GC analyses

GC analyses for compounds were carried with β -DEX 225 column. Details are given in Table S1.

Table S1. GC analyses

Conditions	Retention time (min)		
	Epoxide	Azido alcohols	
100 °C 2 min, 10 °C/min to 150 °C, 10 min at 180 °C	3.7 (1a)	9.9 (2a)	9.6 (2a')
110 °C 2 min, 10 °C/min to 180 °C, 10 min at 180 °C	4.4 (1b)	10.2 (2b)	10.7 (2b')
120 °C 2 min, 10 °C/min to 200 °C, 10 min at 200 °C	5.2 (1c)	10.8 (2c)	11.4 (2c')
110 °C 5 min, 15 °C/min to 150 °C, 10 min at 150 °C	5.0 (1d)	13.1 (2d)	
110 °C 5 min, 15 °C/min to 150 °C, 10 min at 150 °C	4.5 (1e)	13.1, 13.3 (2e)	
110 °C 5 min, 15 °C/min to 150 °C, 10 min at 150 °C	5.4 (1f)	13.8 (2f)	

Determination of enantiomeric excesses was performed using different chiral columns, Table S2.

Table S2. Chiral GC analyses

Comp.	Column	Conditions	Retention time (min)
1d	β -DEX 225	80 °C	11.3 (3 <i>R</i> ,4 <i>S</i>)/11.5 (3 <i>S</i> ,4 <i>R</i>)
2d	Lipodex E	60 °C 0 min, 2 °C/min to 150 °C	37.2 (3 <i>S</i> ,4 <i>R</i>)/37.6(3 <i>R</i> ,4 <i>S</i>)
1e	CP Chirasil DEX	130 °C	5.1 (3 <i>R</i> ,5 <i>R</i>)/5.3 (3 <i>S</i> ,5 <i>S</i>)
2e	β -DEX 225	110 °C 5 min, 15 °C/min to 150 °C, 10 min at 150 °C	13.1 (3 <i>R</i> ,5 <i>R</i>)/13.3 (3 <i>S</i> ,5 <i>S</i>)
1f	Chiraldex G-TA	60 °C	32.9 (<i>S</i>)/35.8 (<i>R</i>)
2f	CP Chirasil DEX	140 °C 0 min, 5 °C/min to 170 °C	9.3(<i>S</i>)/9.5 (<i>R</i>)

2. Reaction profiles for the non-enzyme ring opening of spiroepoxides

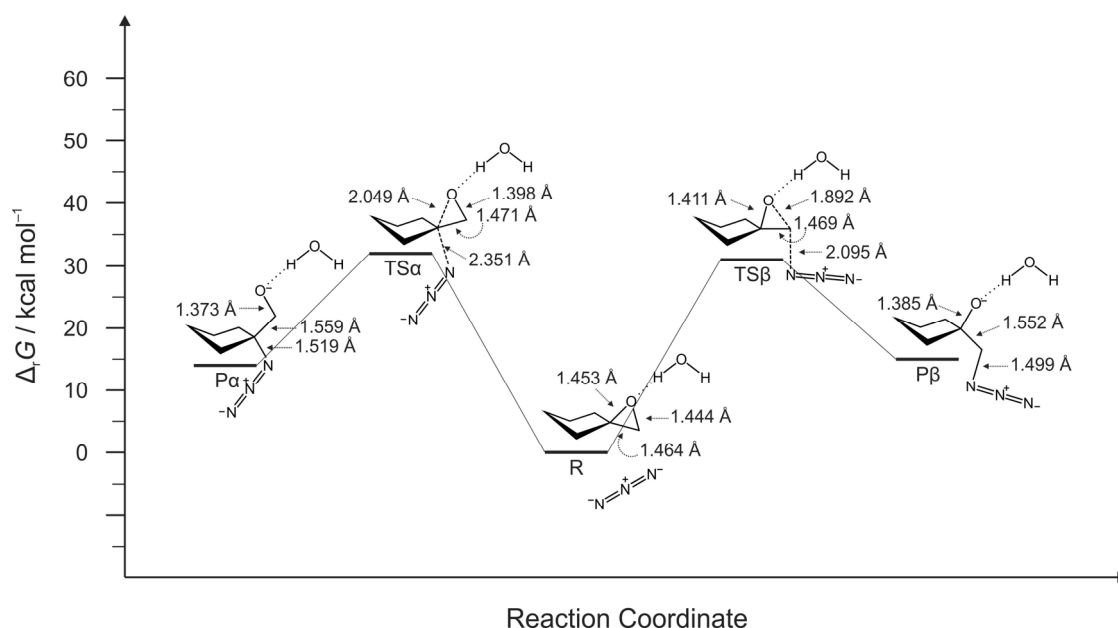


Figure S1. Calculated reaction profile for nucleophilic attack of azide on **1a**. R stands for reactants, TSα is the transition state for the attack on the Cα and TSβ for the attack on the Cβ carbon atom. Pα and Pβ are products, respectively. Calculations were carried out at the B3LYP/6-311++g(d,p) level with the polarizable continuum model using the integral equation formalism variant in H_2O ($\epsilon = 78.3553$). Gibbs energies were calculated at 298.15 K and 1 atm.

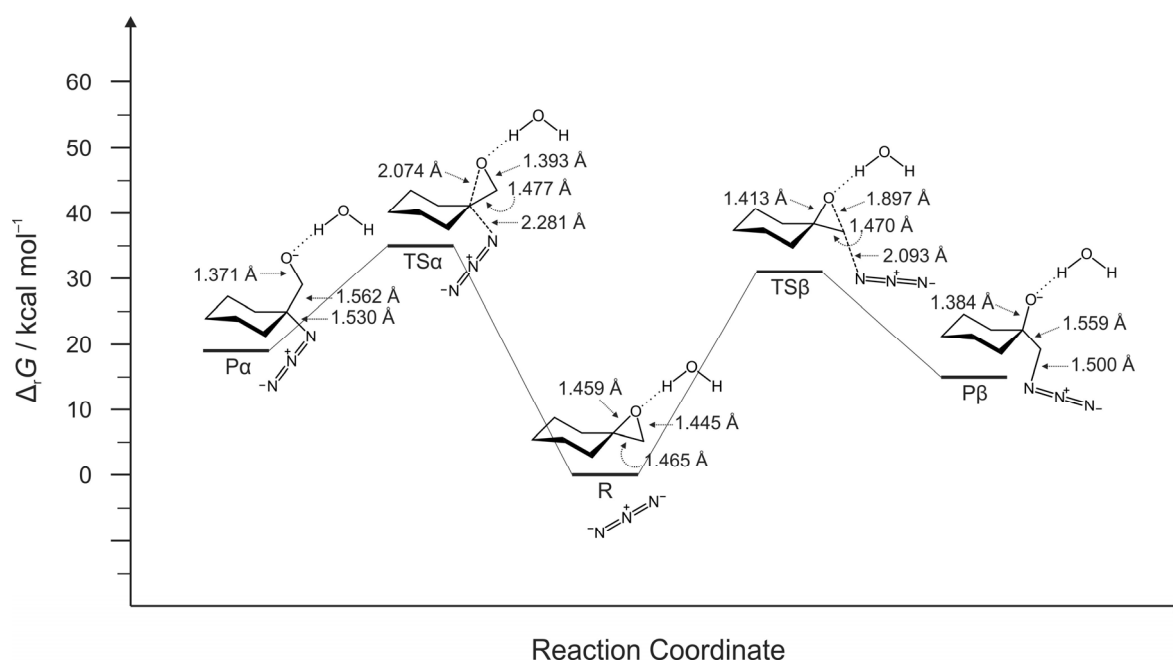


Figure S2. Calculated reaction profile for nucleophilic attack of azide on **1b**. R stands for reactants, TSα is the transition state for the attack on the Cα and TSβ for the attack on the Cβ carbon atom. Pα and Pβ are products, respectively. Calculations were carried out at the B3LYP/6-311++g(d,p) level with the polarizable continuum model using the integral equation formalism variant in H_2O ($\epsilon = 78.3553$). Gibbs energies were calculated at 298.15 K and 1 atm.

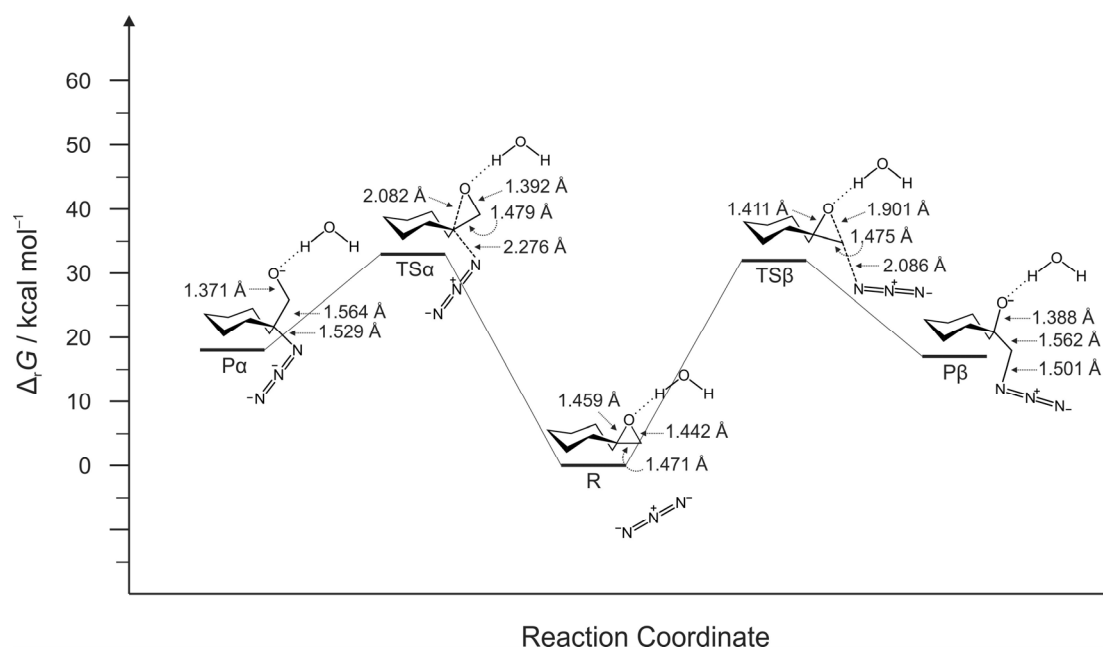


Figure S3. Calculated reaction profile for nucleophilic attack of azide on **1c**. R stands for reactants, TS α is the transition state for the attack on the C α and TS β for the attack on the C β carbon atom. P α and P β are products, respectively. Calculations were carried out at the B3LYP/6-311++g(d,p) level with the polarizable continuum model using the integral equation formalism variant in H₂O ($\epsilon = 78.3553$). Gibbs energies were calculated at 298.15 K and 1 atm.

3. Docking studies of 1-oxaspiro[2.5]octane compounds 1b and 1d–1f in the active site of HheA and HheC

3.1. Estimated lowest Gibbs energies of binding

Table S3. Estimated lowest Gibbs energy of binding for distinct conformational clusters of ligands (enzyme 1ZMO-HheA, rms tolerance for clustering was 0.5 Å) by the docking studies with the AutoDock 4.2 suite of programs. *O-ax* and *O-eq* stands for the *O*-axial and *O*-equatorial conformer respectively.

Comp. (3 <i>R</i>)-enantiomers	$\frac{\Delta G}{\text{kcal mol}^{-1}}$	Contribution in cluster / %	Comp. (3 <i>S</i>)-enantiomers	$\frac{\Delta G}{\text{kcal mol}^{-1}}$	Contribution in cluster / %
1a	−4.71	100			
1b_{O-ax}	−5.39	100			
1b_{O-eq}	−5.36	100			
1c	−6.06	100			
(3 <i>R</i> ,4 <i>S</i>)- 1d_{O-ax}	−5.78	100	(3 <i>S</i> ,4 <i>R</i>)- 1d_{O-ax}	−5.63	97
(3 <i>R</i> ,4 <i>S</i>)- 1d_{O-eq}	−5.70	100	(3 <i>S</i> ,4 <i>R</i>)- 1d_{O-eq}	−5.58	3
(3 <i>R</i> ,5 <i>R</i>)- 1e_{O-ax}	−5.90	100	(3 <i>S</i> ,5 <i>S</i>)- 1e_{O-ax}	−5.75	100
(3 <i>R</i>)- 1f_{O-ax}	−6.38	100	(3 <i>S</i> ,5 <i>S</i>)- 1e_{O-eq}	−5.71	1
(3 <i>R</i>)- 1f_{O-eq}	−5.87	100	(3 <i>S</i>)- 1f_{O-ax}	−5.70	99
			(3 <i>S</i>)- 1f_{O-eq}	−6.04	100
				−6.12	100

Table S4. Estimated lowest Gibbs energy of binding for distinct conformational clusters of ligands (enzyme 1ZMT-HheC, rms tolerance for clustering was 0.5 Å) by the docking studies with the AutoDock 4.2 suite of programs. *O-ax* and *O-eq* stands for the *O*-axial and *O*-equatorial conformer respectively.

Comp. (3 <i>R</i>)-enantiomers	$\frac{\Delta G}{\text{kcal mol}^{-1}}$	Contribution in cluster / %	Comp. (3 <i>S</i>)-enantiomers	$\frac{\Delta G}{\text{kcal mol}^{-1}}$	Contribution in cluster / %
1a	−5.44	100			
1b_{O-ax}	−5.90	100			
1b_{O-eq}	−5.65	100			
1c	−5.64	100			
(3 <i>R</i> ,4 <i>S</i>)- 1d_{O-ax}	−5.48	100	(3 <i>S</i> ,4 <i>R</i>)- 1d_{O-ax}	−5.62	100
(3 <i>R</i> ,4 <i>S</i>)- 1d_{O-eq}	−5.68	100	(3 <i>S</i> ,4 <i>R</i>)- 1d_{O-eq}	−5.54	100
(3 <i>R</i> ,5 <i>R</i>)- 1e_{O-ax}	−6.61	100	(3 <i>S</i> ,5 <i>S</i>)- 1e_{O-ax}	−5.69	100
(3 <i>R</i>)- 1f_{O-ax}	−6.78	100	(3 <i>S</i>)- 1f_{O-ax}	−5.81	100
(3 <i>R</i>)- 1f_{O-eq}	−5.95	100	(3 <i>S</i>)- 1f_{O-eq}	−6.36	100

3.2. Overlay of equatorial and axial lowest energy conformers in the active site of HheA for 1d and 1f enantiomers

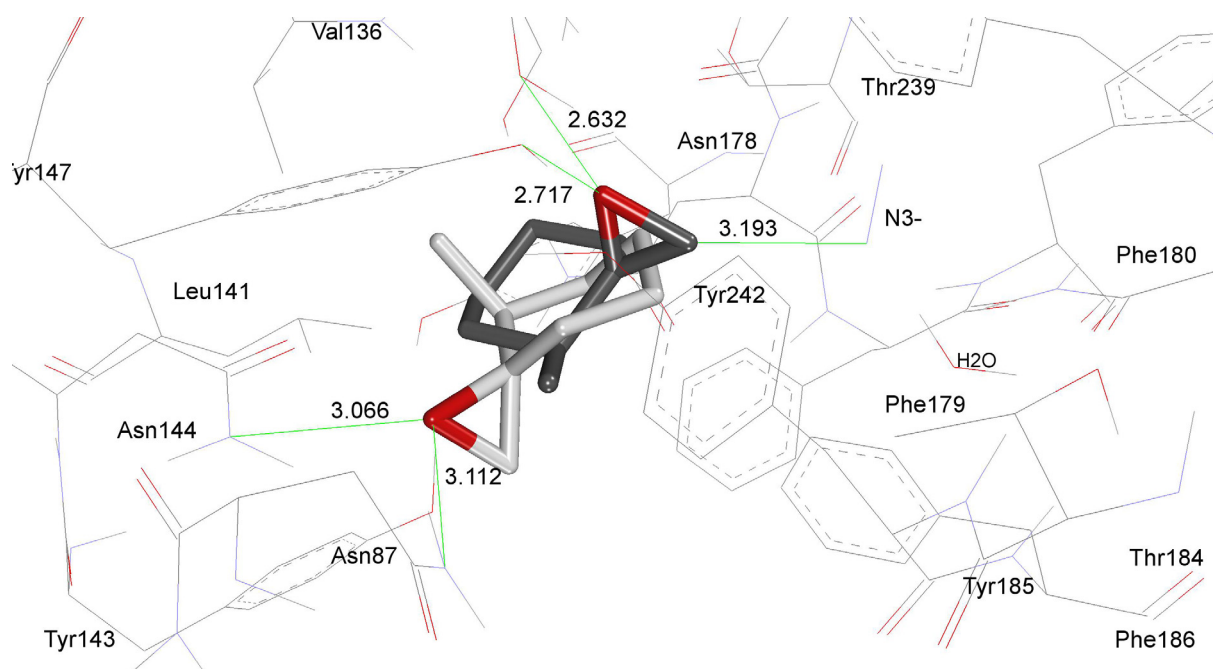


Fig. S4 (3R,4S)-1d-HheA complexes derived from docking studies: overlay of (3R,4S)-1d_{ax} (grey) and (3R,4S)-1d_{eq} (white). HheA active site is represented by some structurally important amino acids. Only polar hydrogen atoms are presented. Interatomic distances are given in Å.

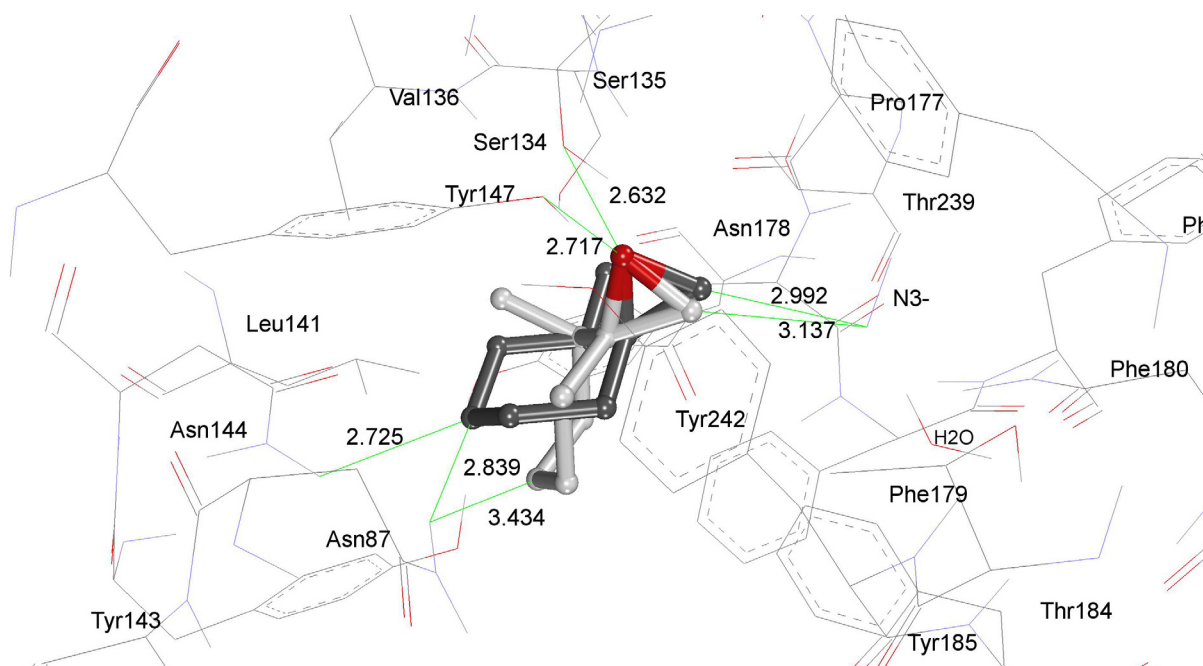


Fig. S5 (3S,4R)-1d-HheA complexes derived from docking studies: overlay of (3S,4R)-1d_{ax} (grey) and (3S,4R)-1d_{eq} (white). HheA active site is represented by some structurally important amino acids. Only polar hydrogen atoms are presented. Interatomic distances are given in Å.

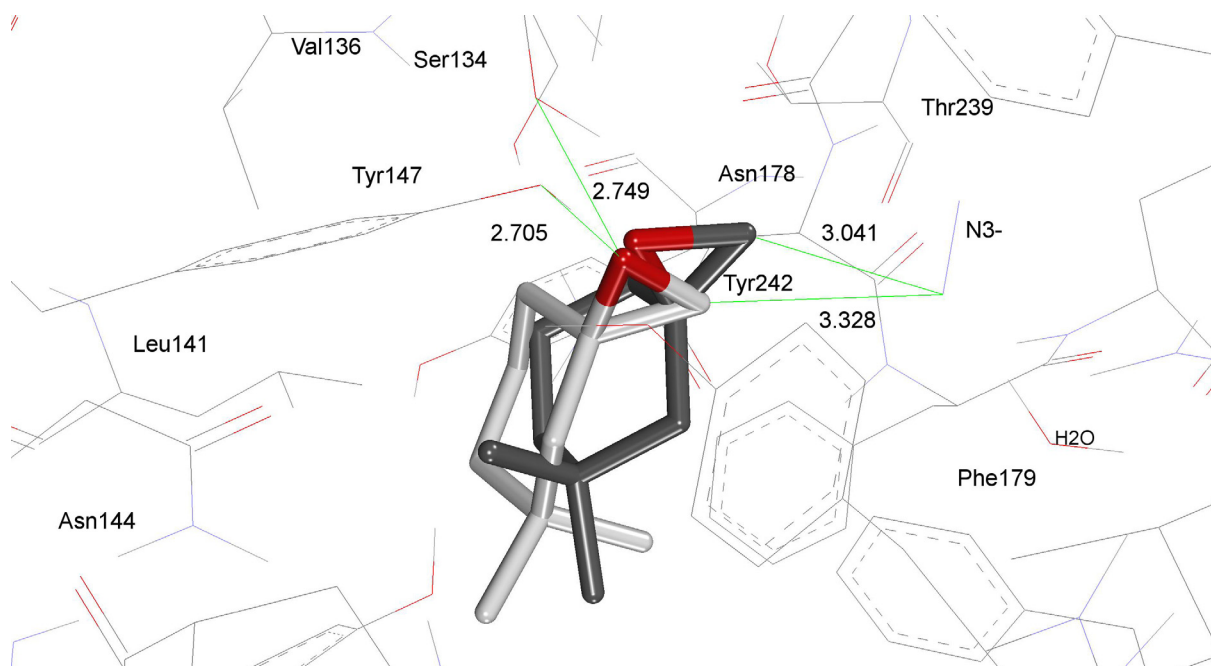


Fig. S6 (*R*)-**1f**-HheA complexes derived from docking studies: overlay of (*R*)-**1f**_{O-ax} (grey) and (*R*)-**1f**_{O-eq} (white). HheA active site is represented by some structurally important amino acids. Only polar hydrogen atoms are presented. Interatomic distances are given in Å.

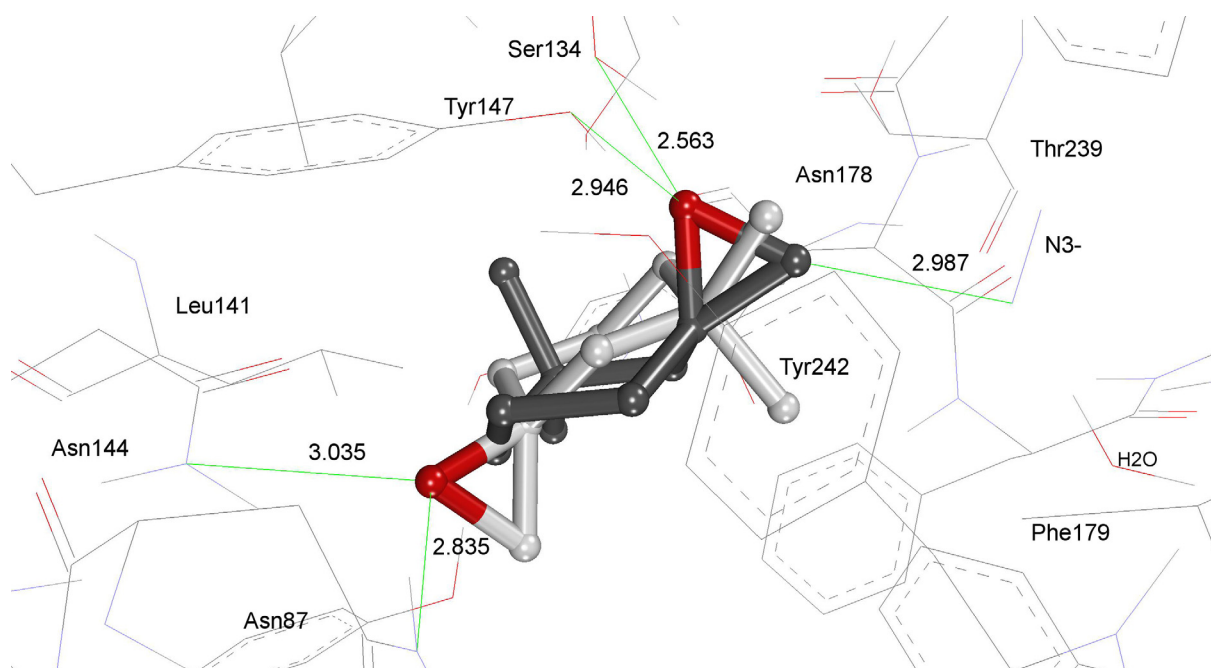


Fig. S7 (*S*)-**1f**-HheA complexes derived from docking studies: overlay of (*S*)-**1f**_{O-ax} (grey) and (*S*)-**1f**_{O-eq} (white). HheA active site is represented by some structurally important amino acids. Only polar hydrogen atoms are presented. Interatomic distances are given in Å.

3.3. Overlay of equatorial and axial lowest energy conformers in the active site of HheC for 1d and 1f enantiomers

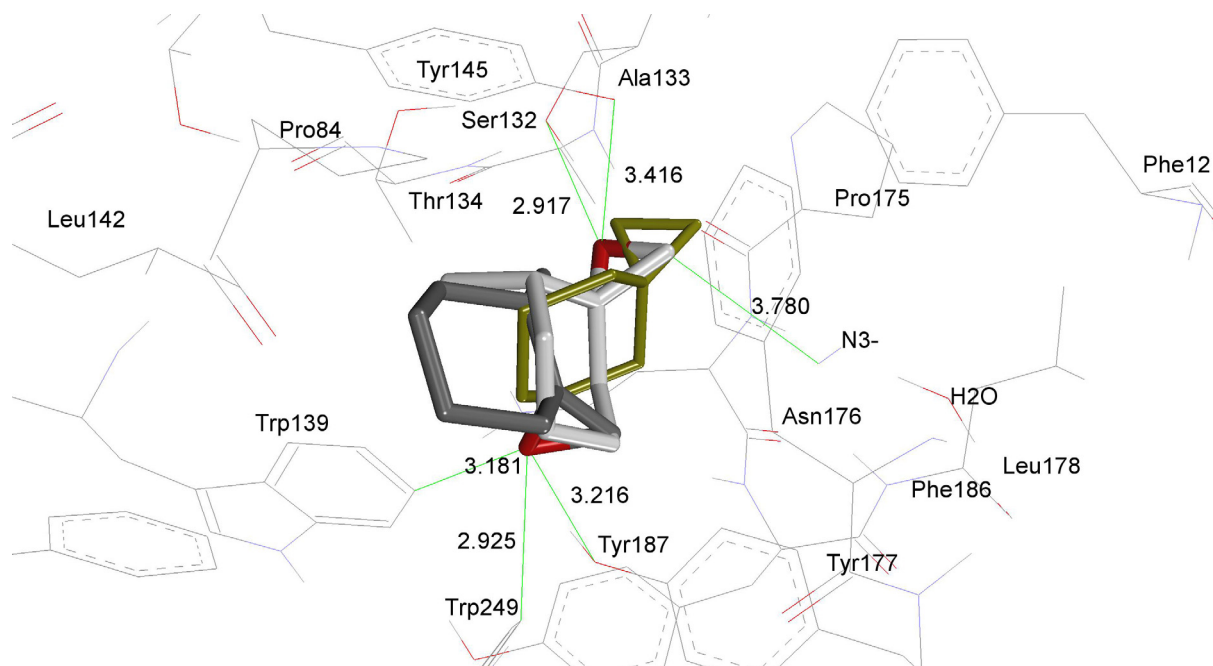


Fig. S8 (3R,4S)-1d-HheC complexes derived from docking studies: overlay of (3R,4S)-1d_{o-ax} (grey) and (3R,4S)-1d_{o-eq} (white). HheC active site is represented by some structurally important amino acids. Only polar hydrogen atoms are presented. Interatomic distances are given in Å.

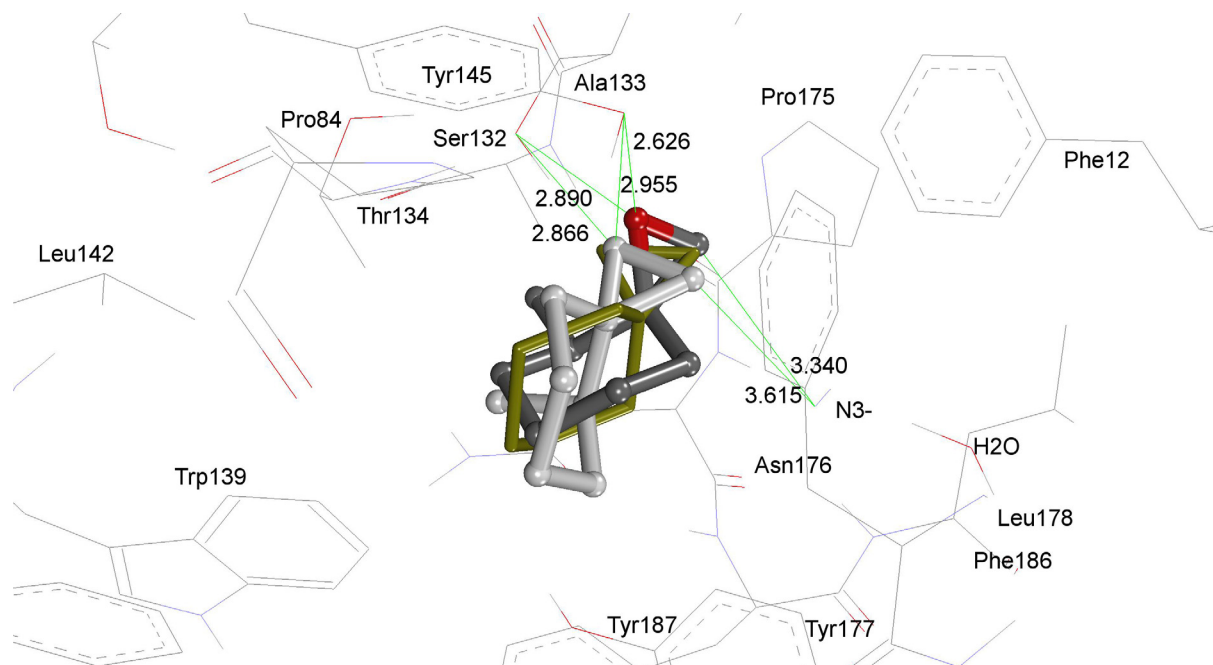


Fig. S9 (3S,4R)-1d-HheC complexes derived from docking studies: overlay of (3S,4R)-1d_{o-ax} (grey) and (3S,4R)-1d_{o-eq} (white). HheC active site is represented by some structurally important amino acids. Only polar hydrogen atoms are presented. Interatomic distances are given in Å.

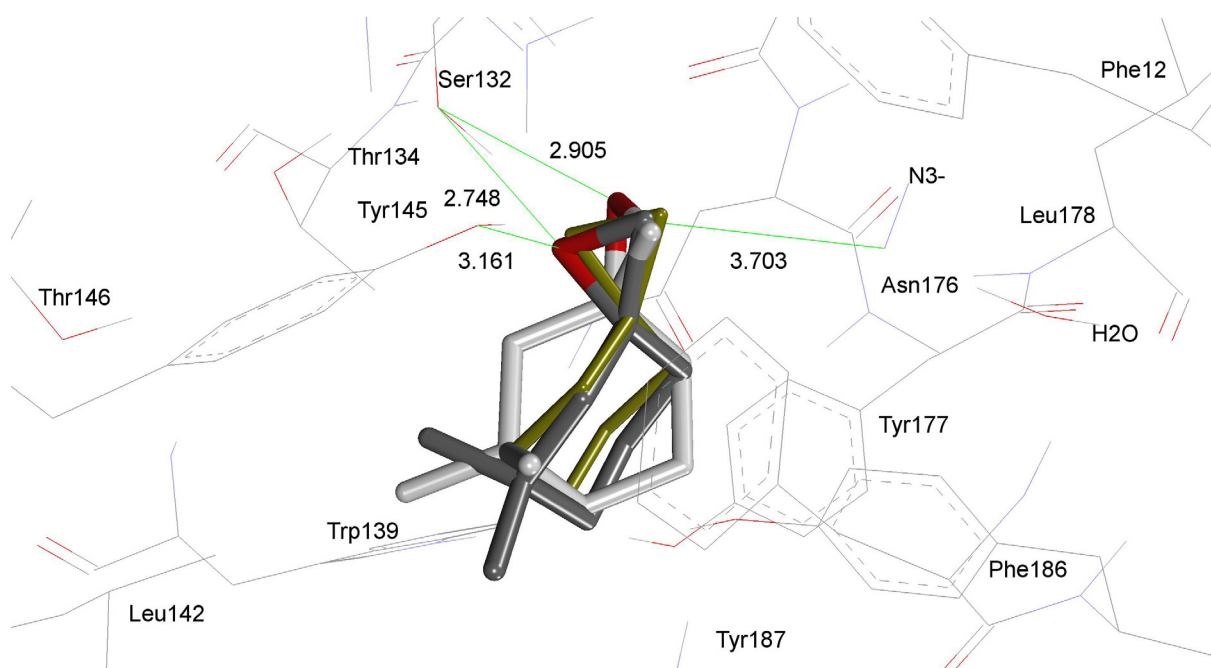


Fig. S10 *(R)*-1f-HhcC complexes derived from docking studies: overlay of *(R)*-1f_{O-ax} (grey) and *(R)*-1f_{O-eq} (white). HhcC active site is represented by some structurally important amino acids. Only polar hydrogen atoms are presented. Interatomic distances are given in Å.

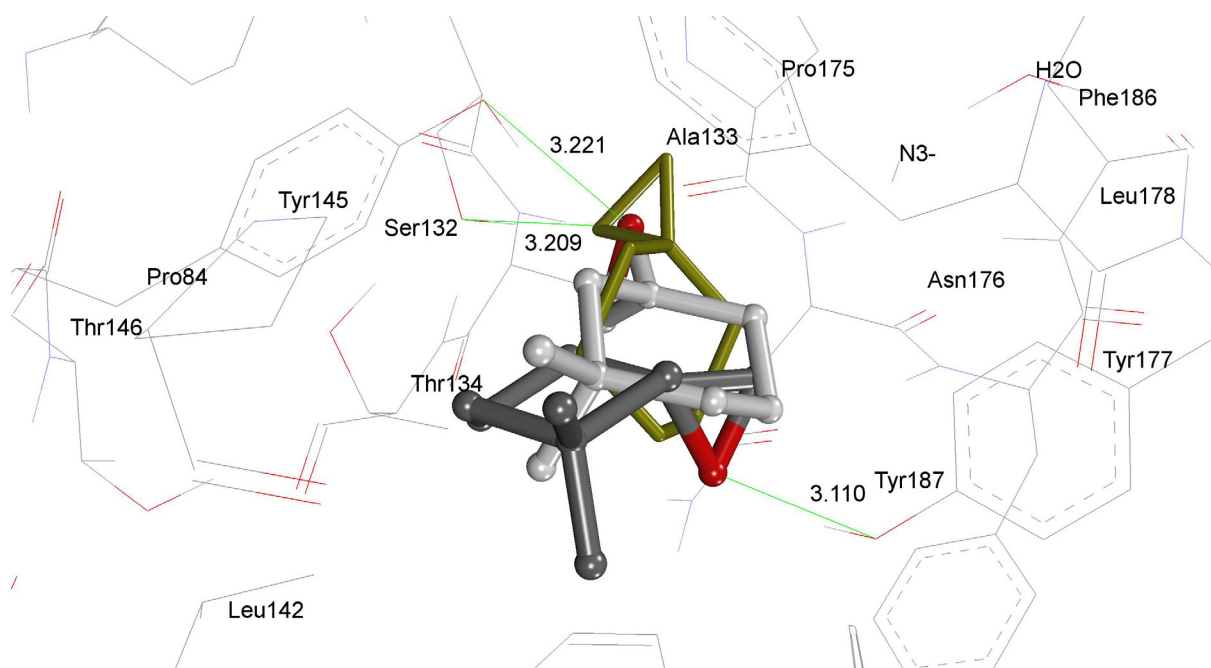
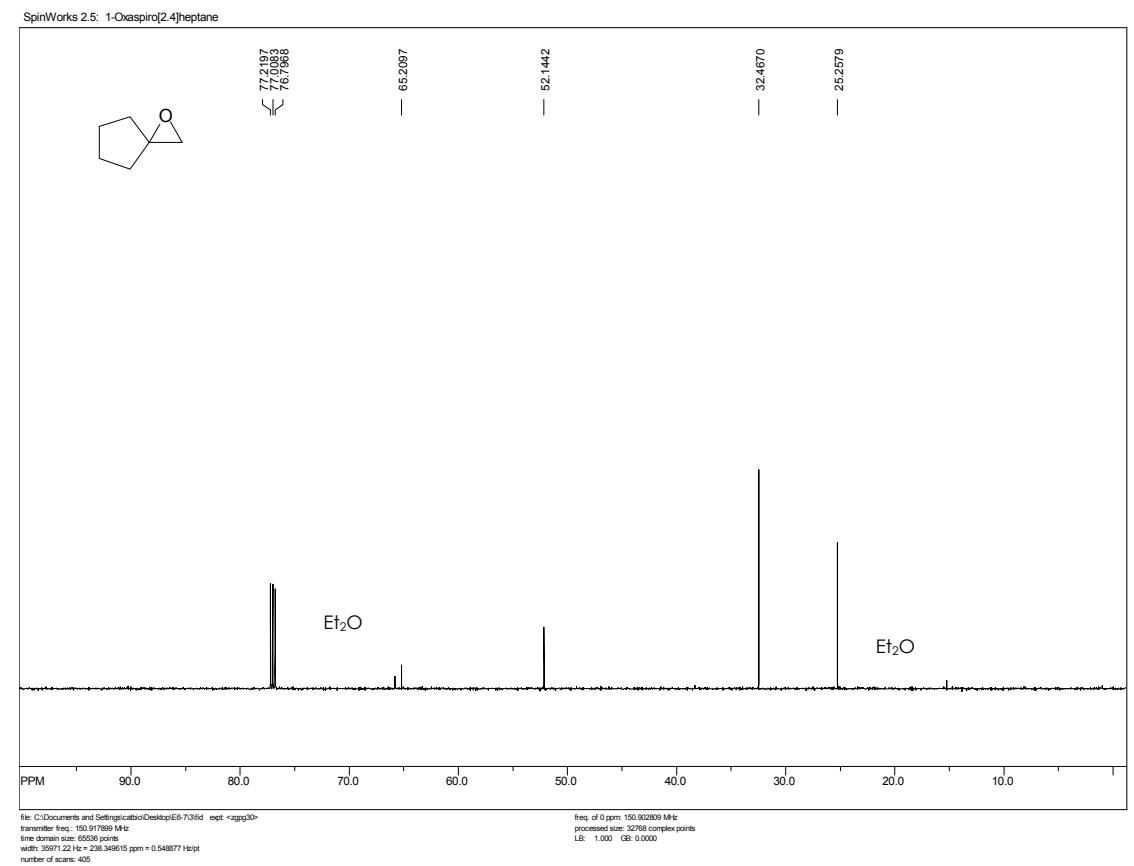
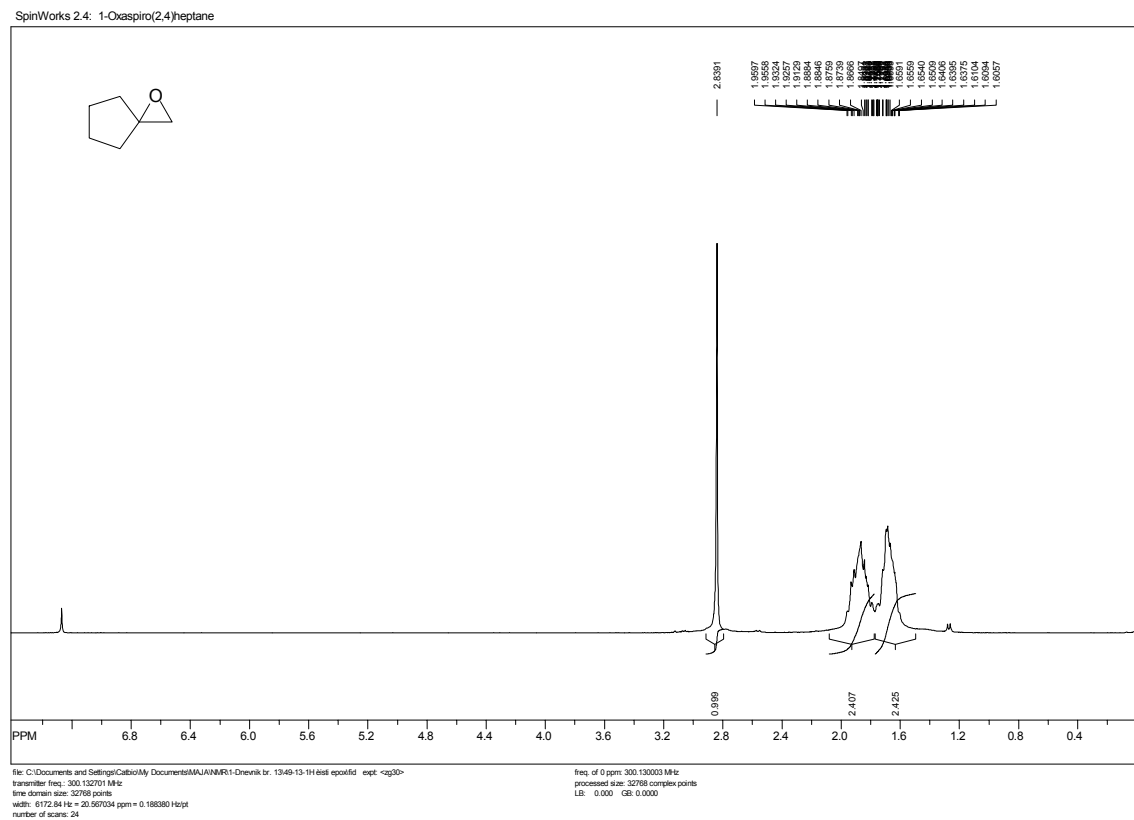
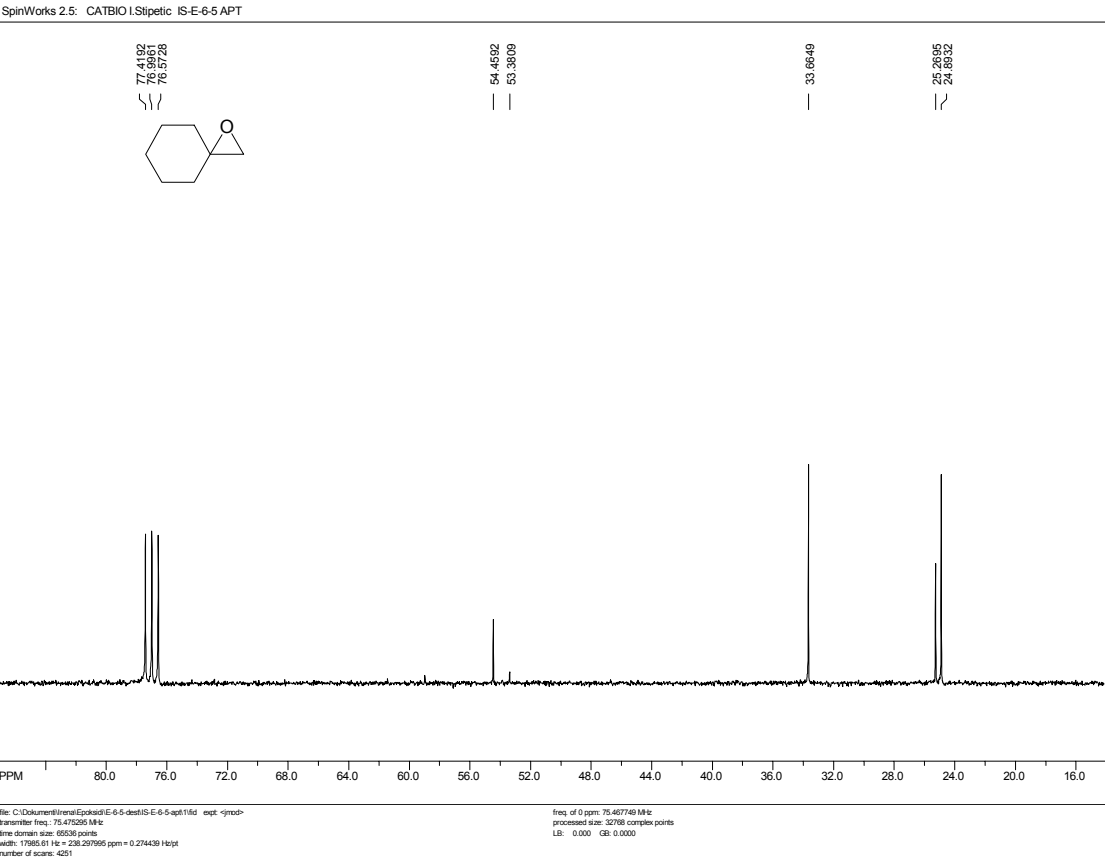
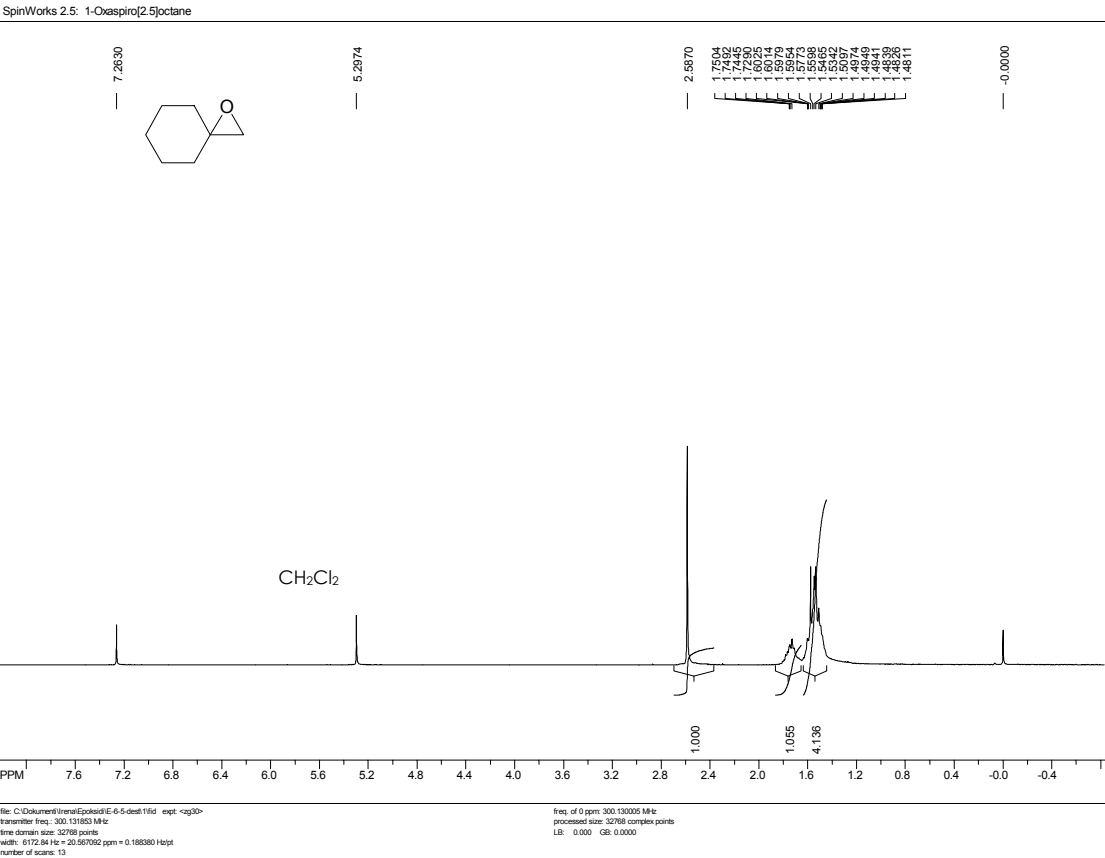


Fig. S11 *(S)*-1f-HhcC complexes derived from docking studies: overlay of *(S)*-1f_{O-ax} (grey) and *(S)*-1f_{O-eq} (white). HhcC active site is represented by some structurally important amino acids. Only polar hydrogen atoms are presented. Interatomic distances are given in Å.

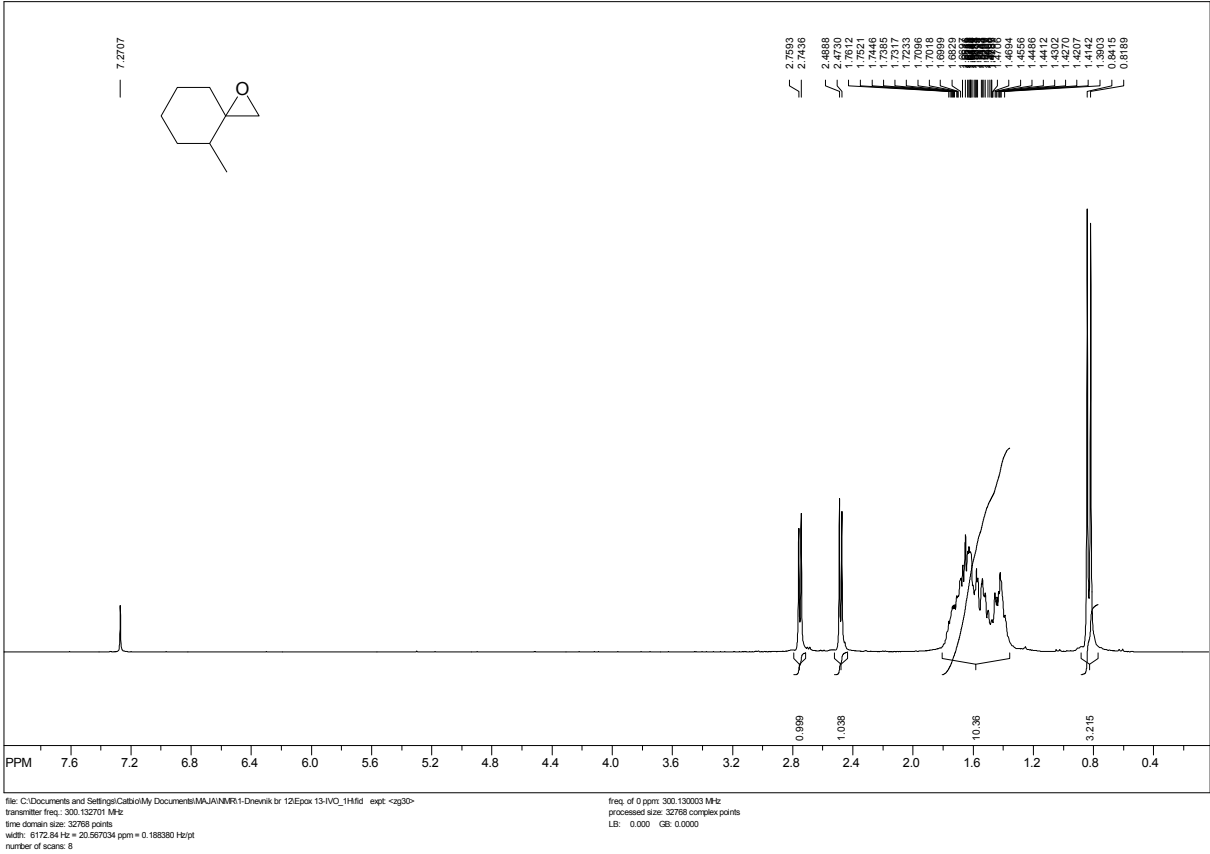
4. NMR spectra



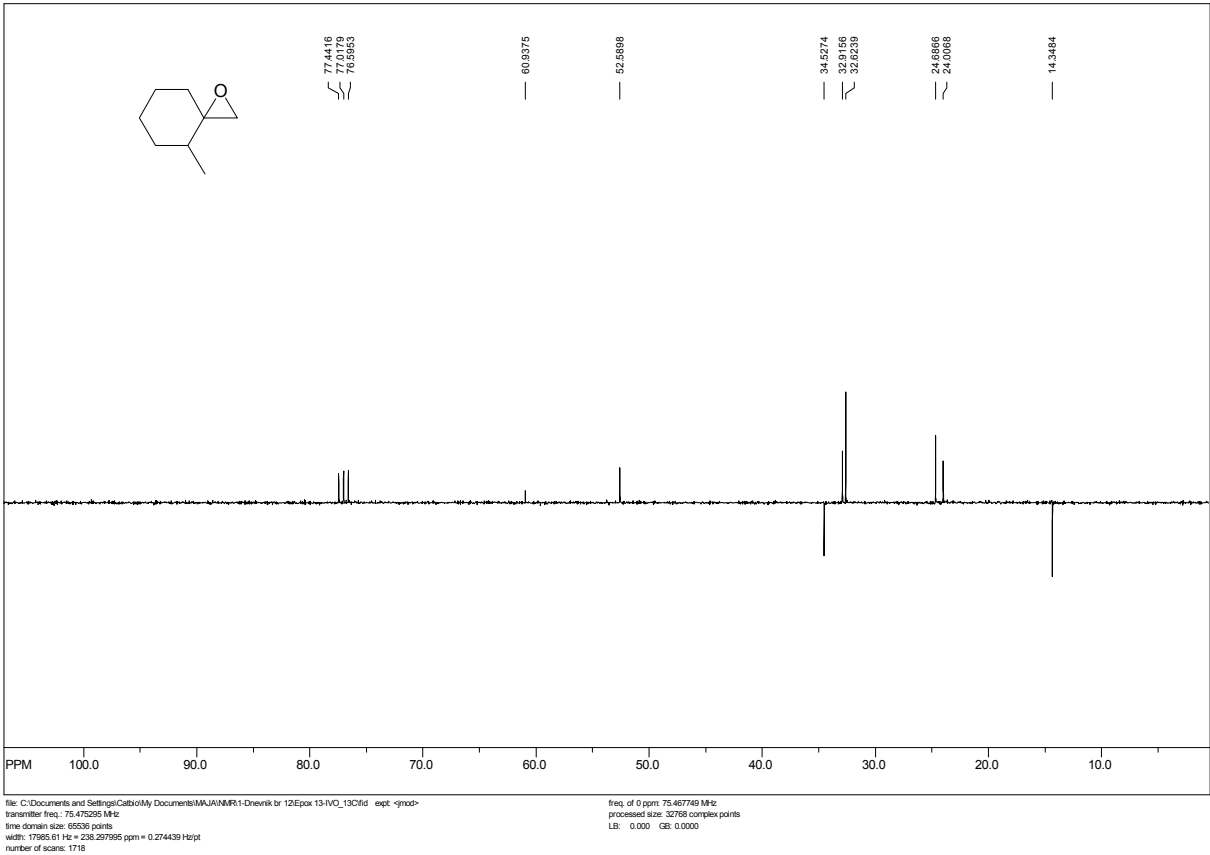




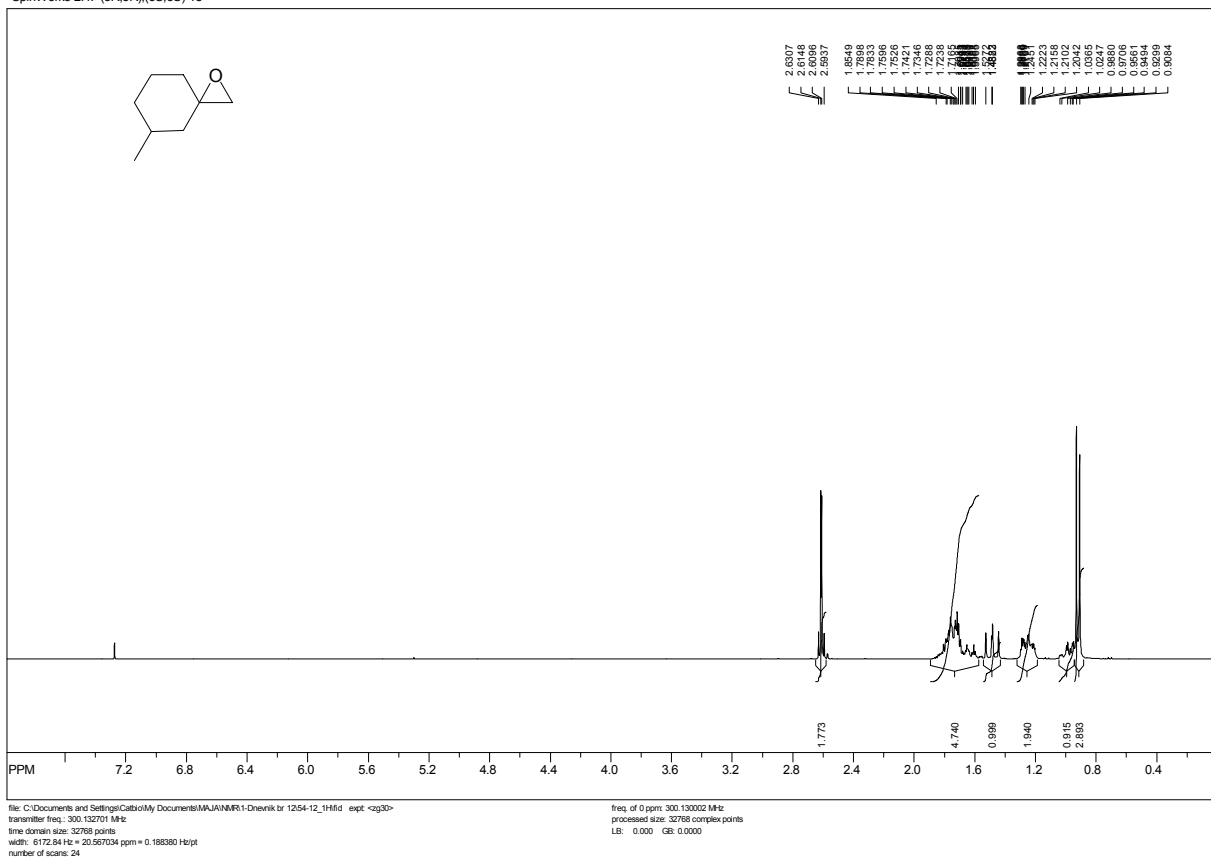
SpinWorks 2.4: (3R,4S),(3S,4R)-1d



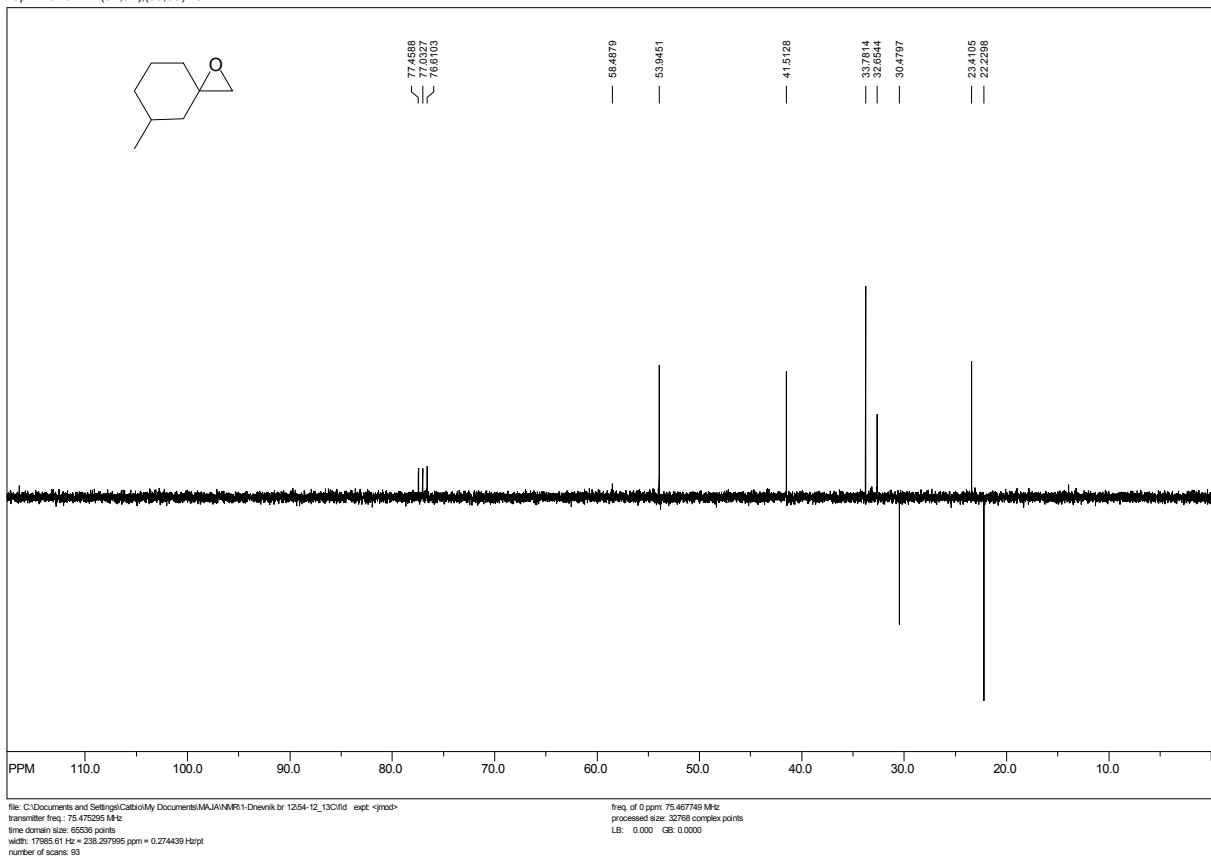
SpinWorks 2.4: (3R,4S),(3S,4R)-1d



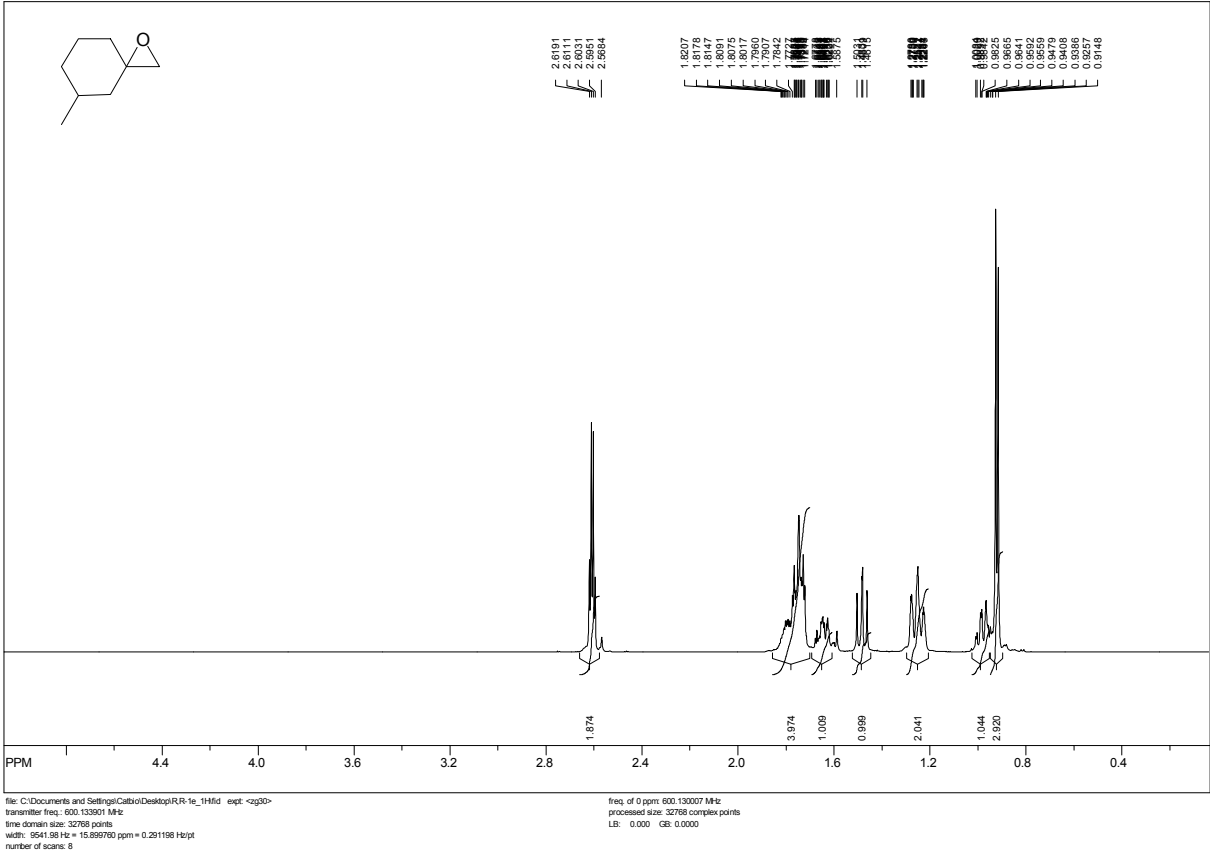
SpinWorks 2.4: (3R,5R),(3S,5S)-1e



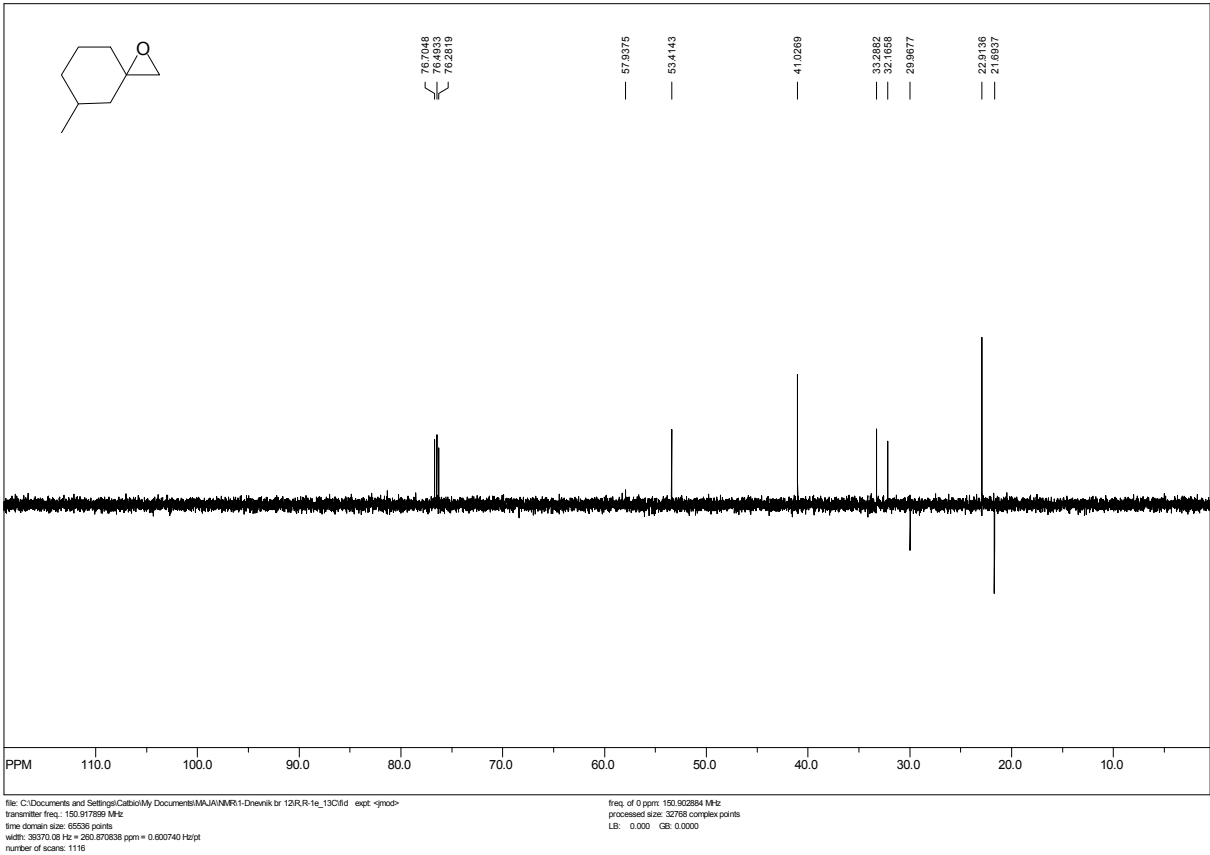
SpinWorks 2.4: (3R,5R),(3S,5S)-1e



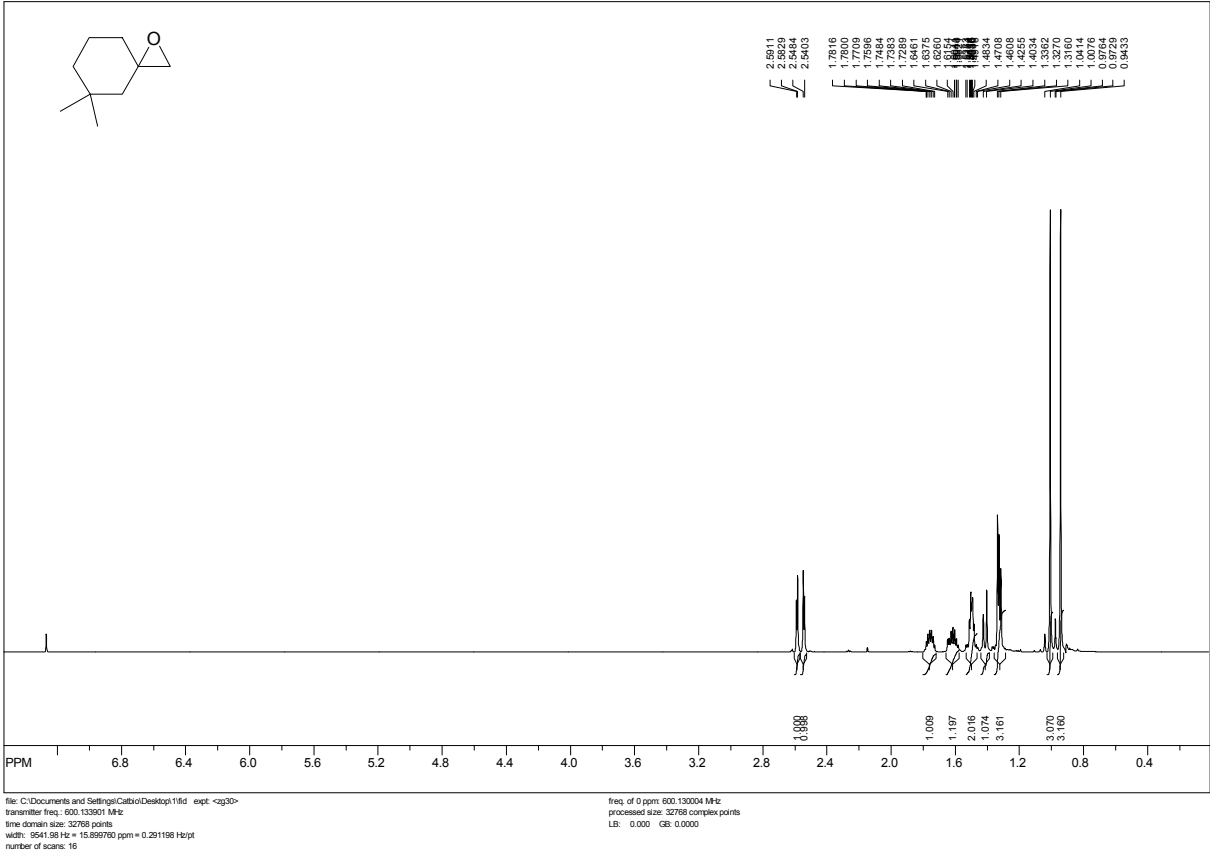
SpinWorks 2.4: (3R,5R)-1e



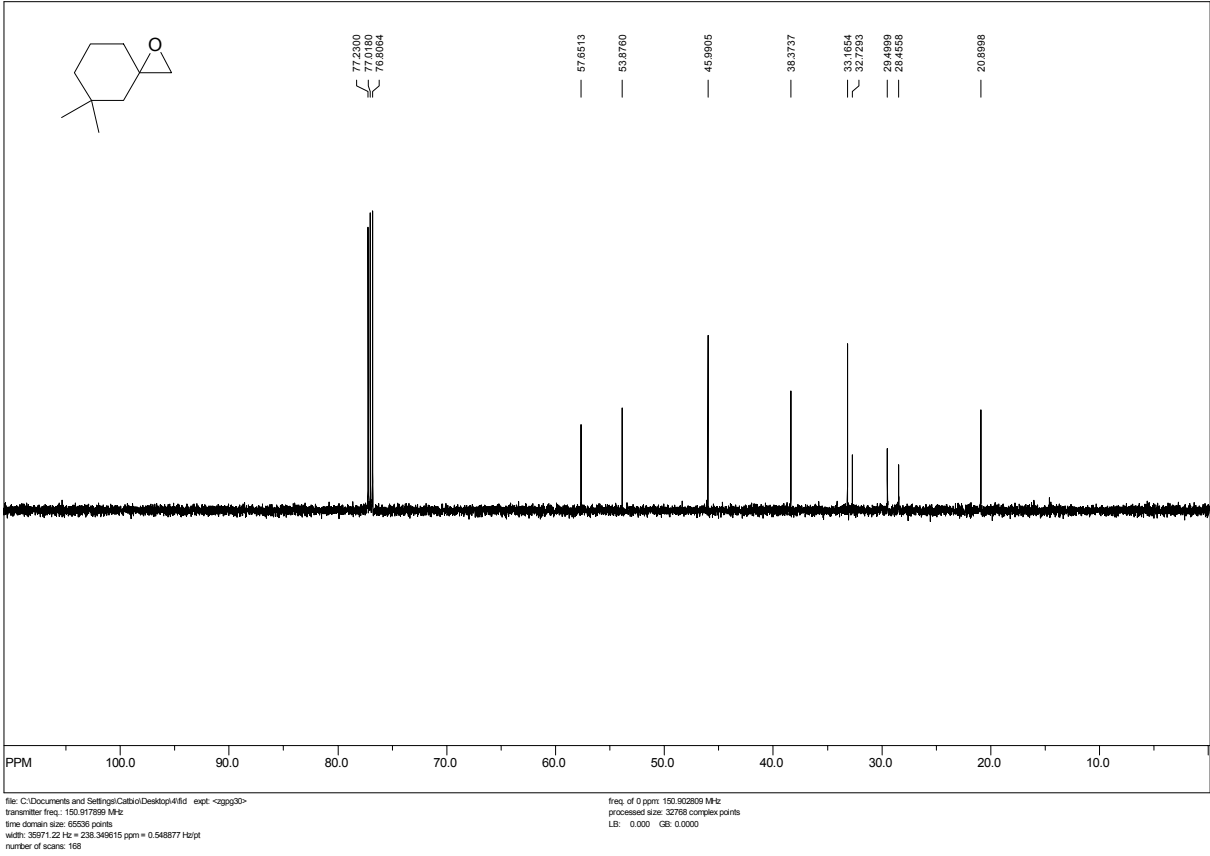
SpinWorks 2.4: (3R,5R)-1e



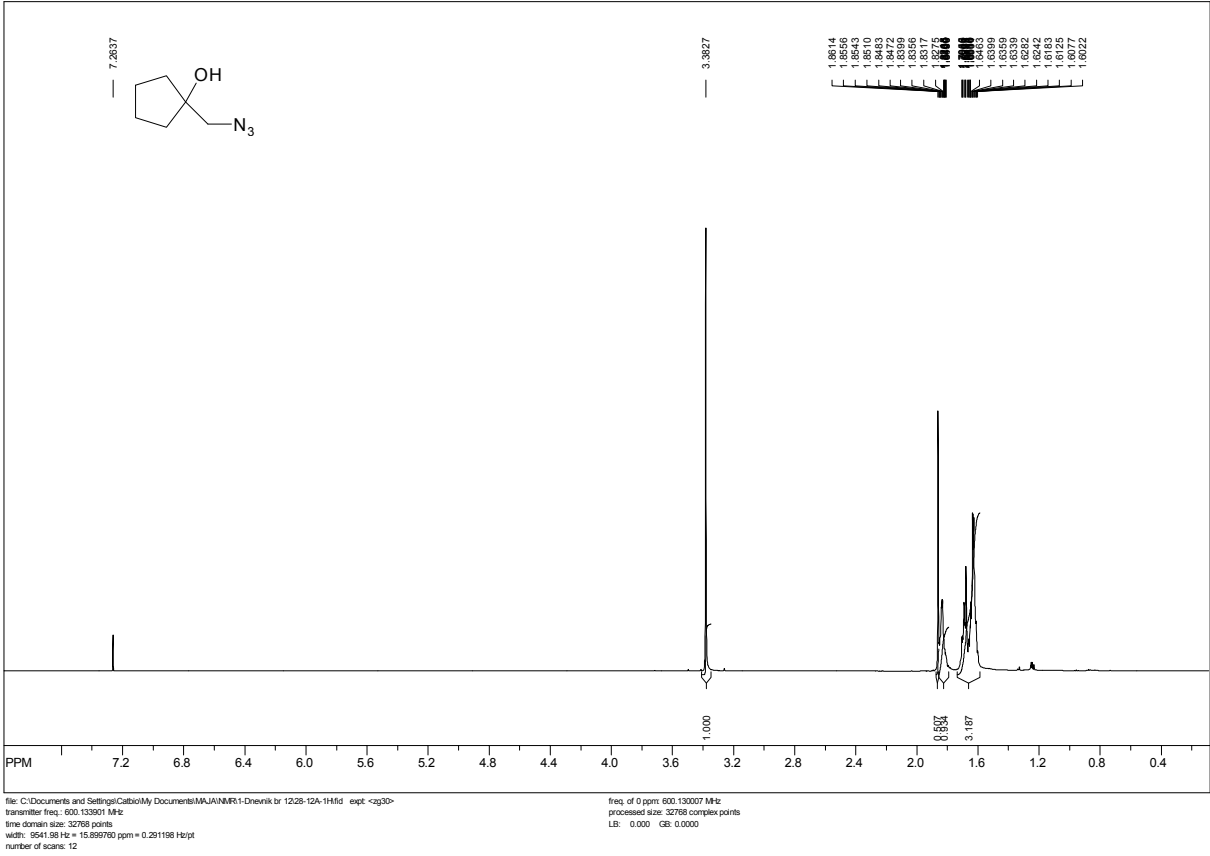
SpinWorks 2.4: (R,S)-1f



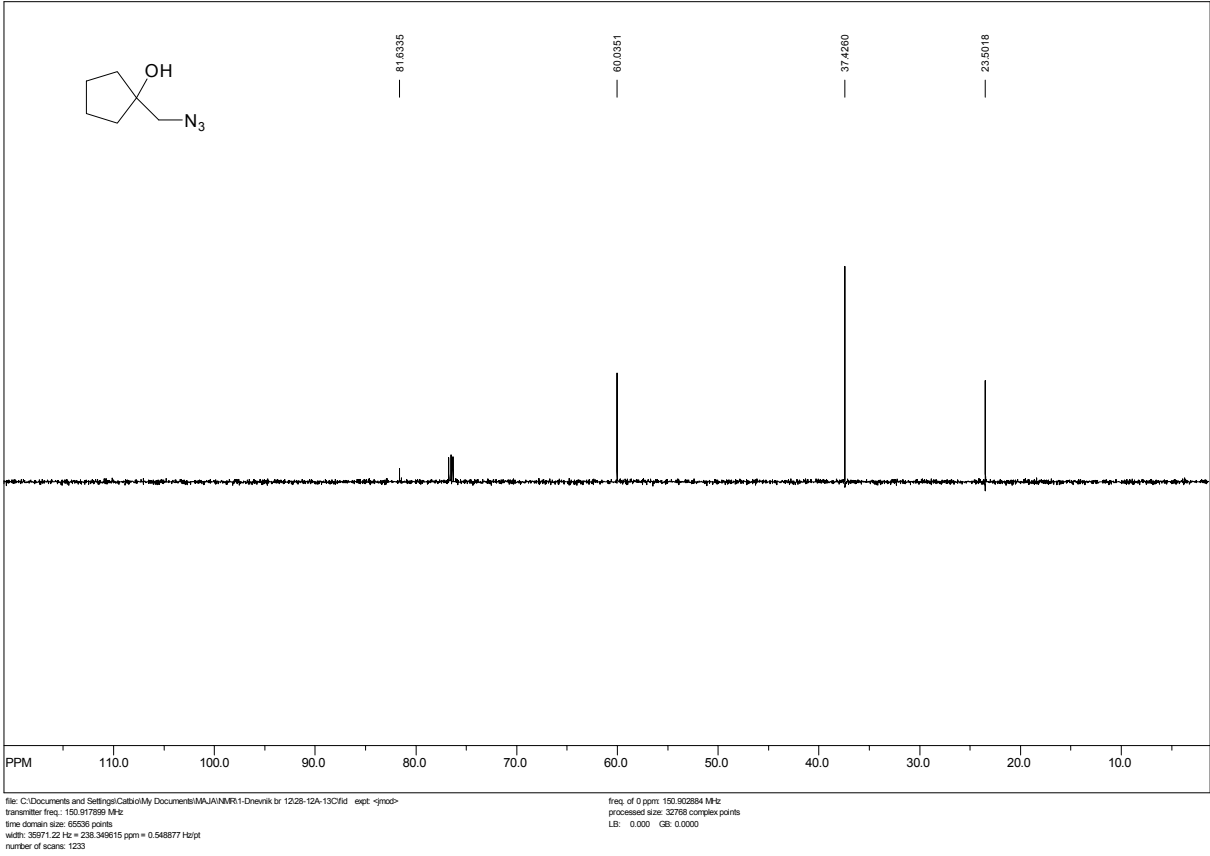
SpinWorks 2.4: (R,S)-1f



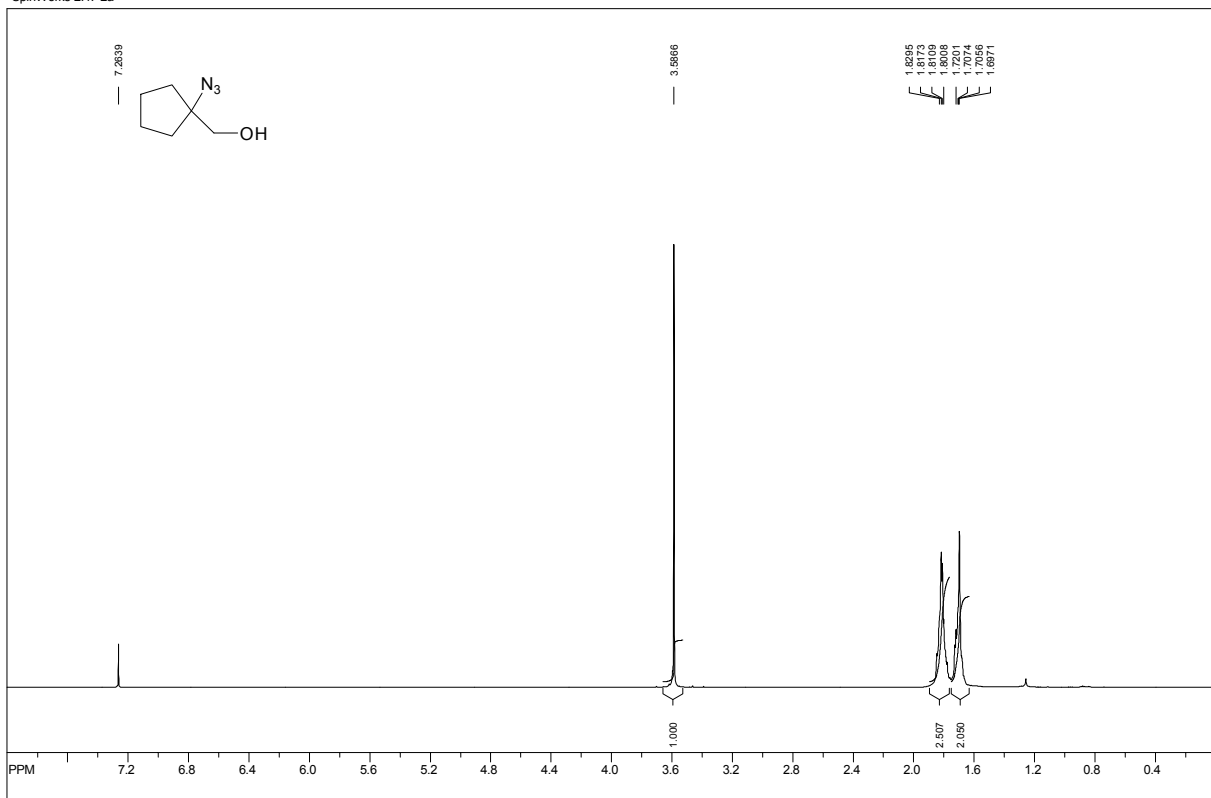
SpinWorks 2.4: 2a



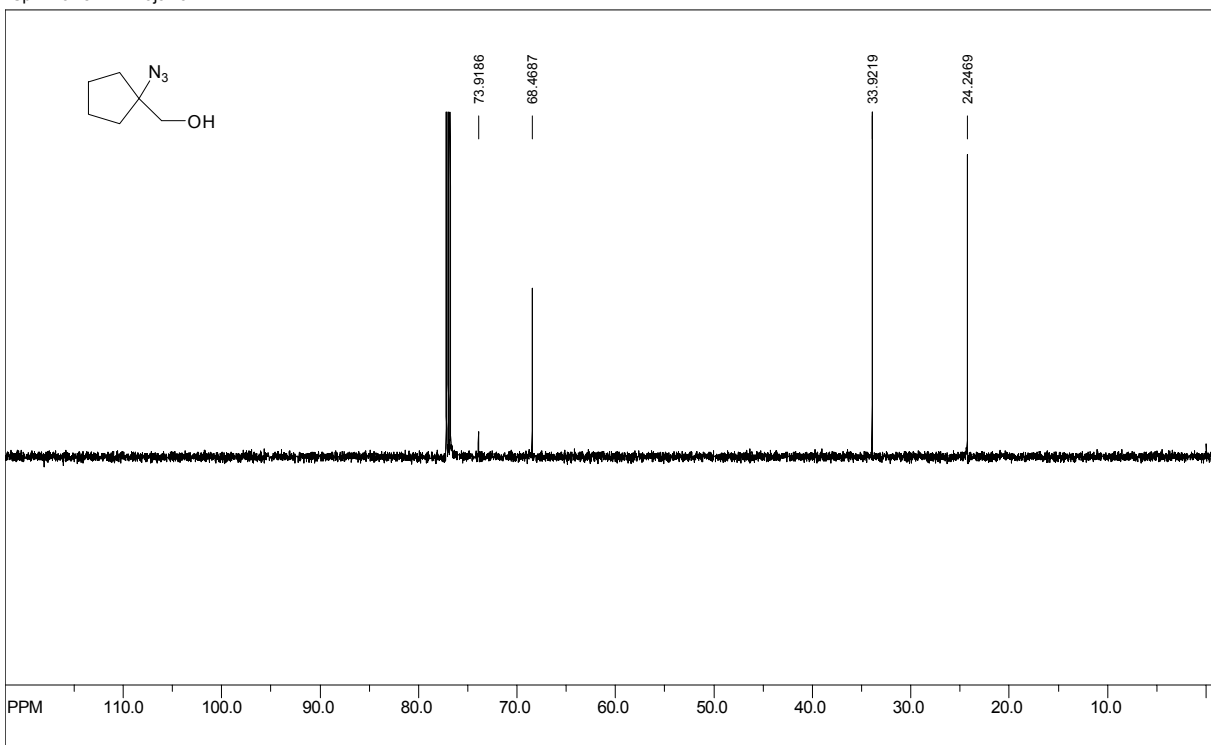
SpinWorks 2.4: 2a



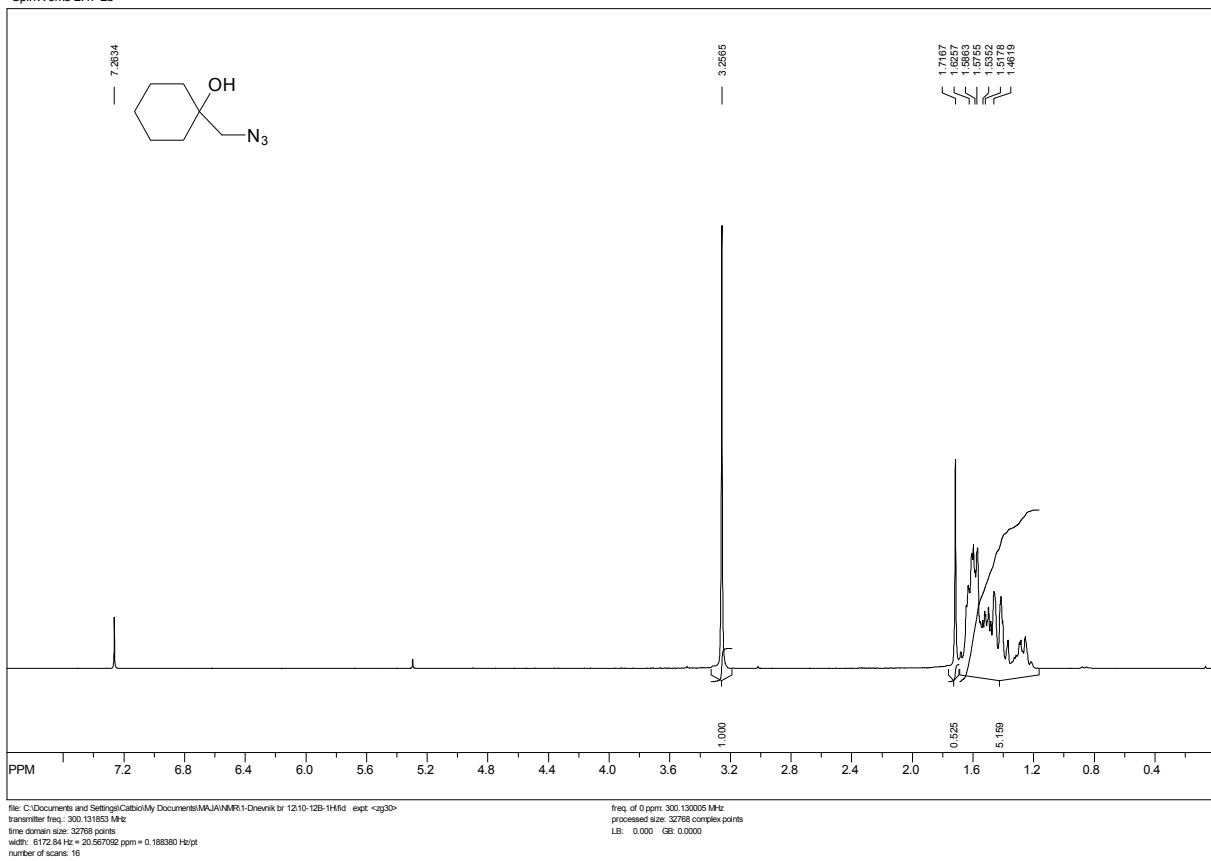
SpinWorks 2.4: 2a*



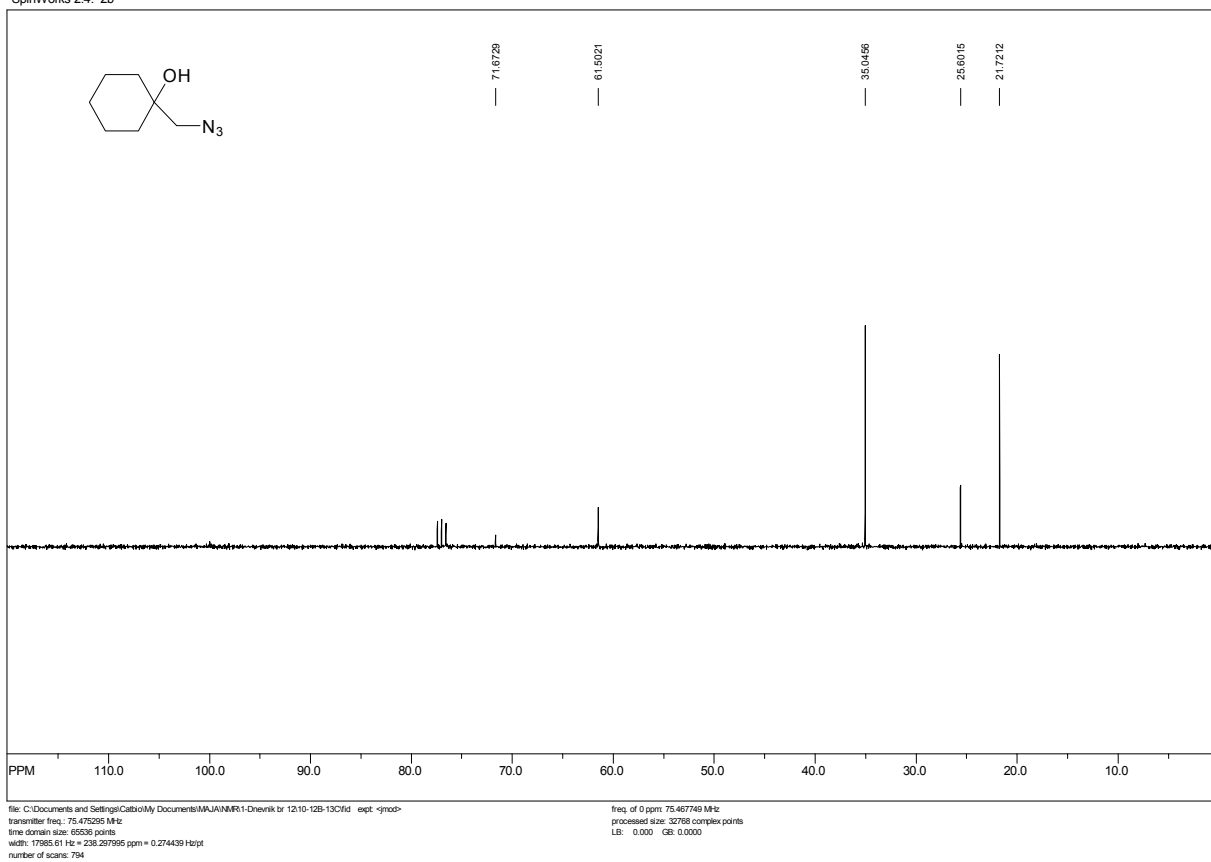
SpinWorks 2.4: Maja 2a*



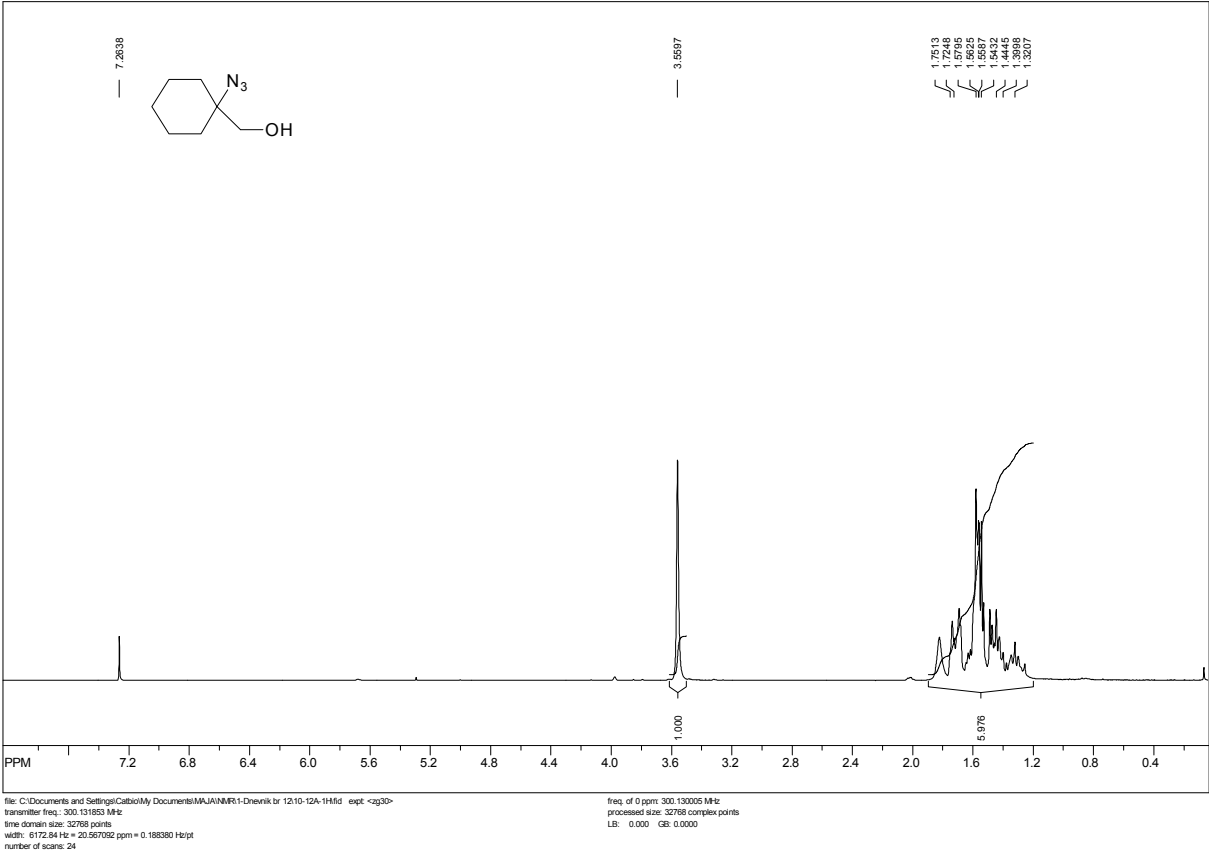
SpinWorks 2.4: 2b



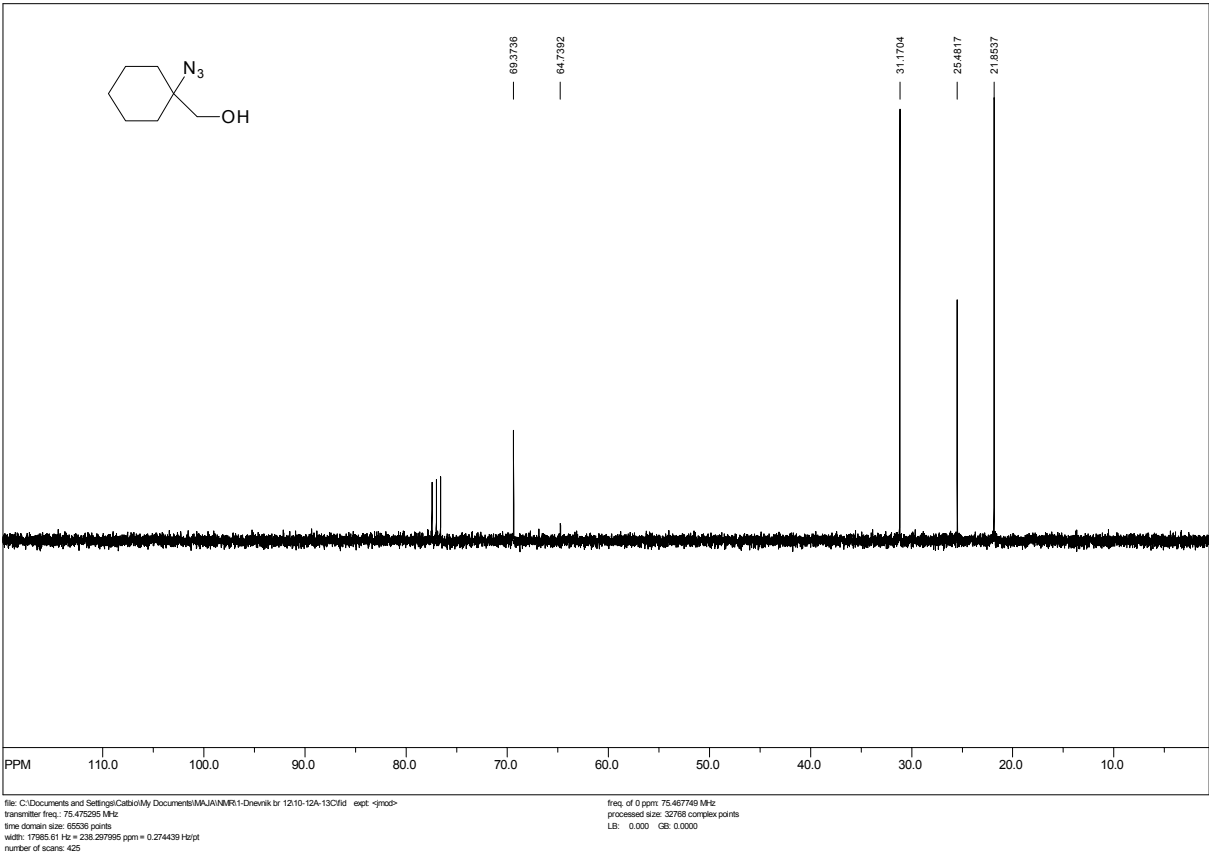
SpinWorks 2.4: 2b

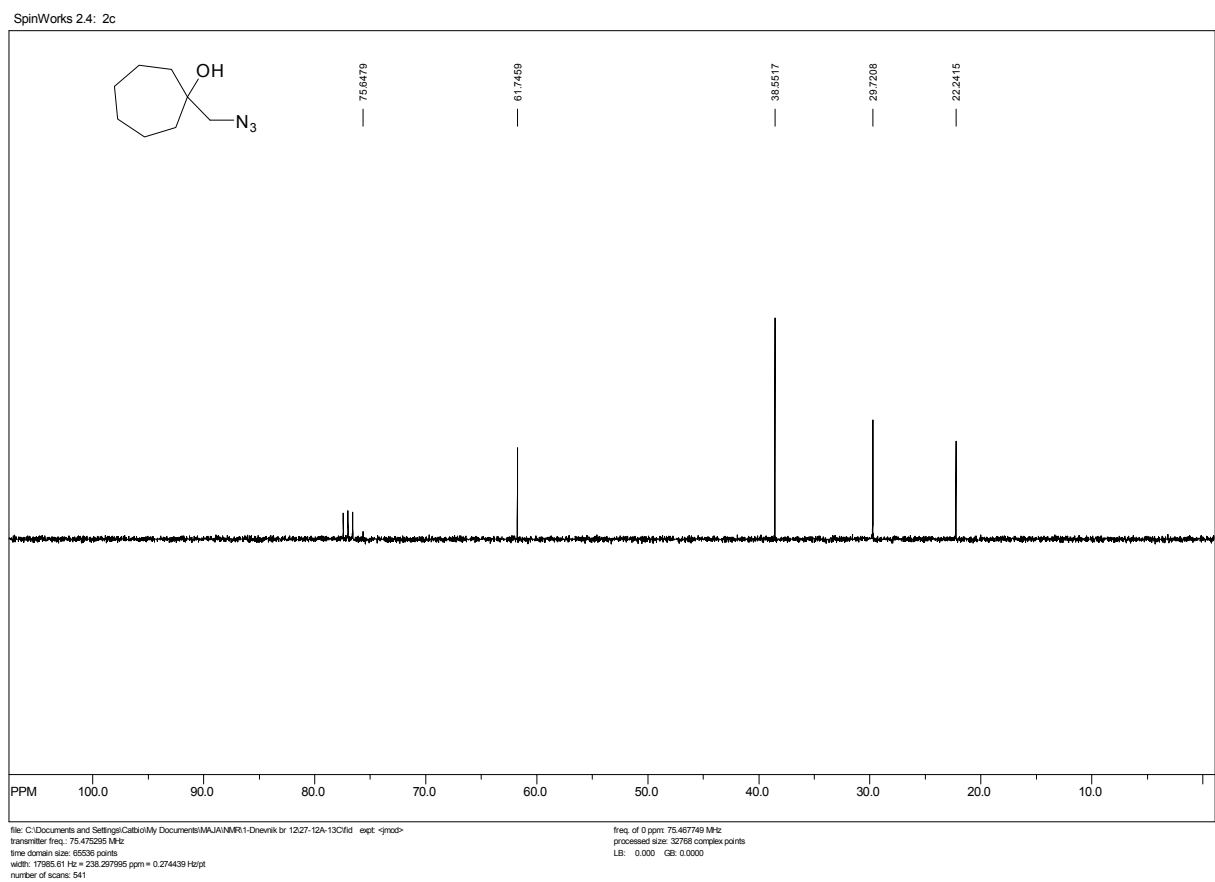
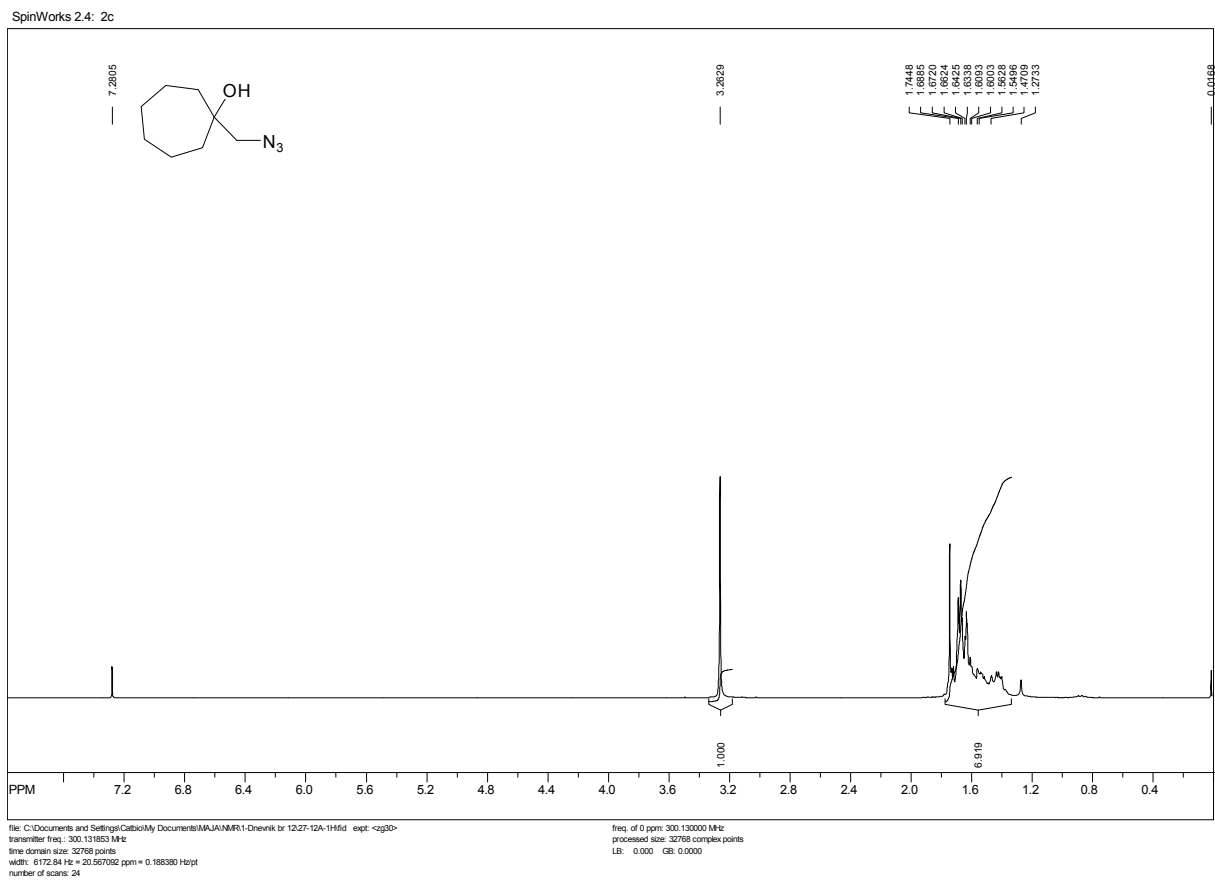


SpinWorks 2.4: 2b'

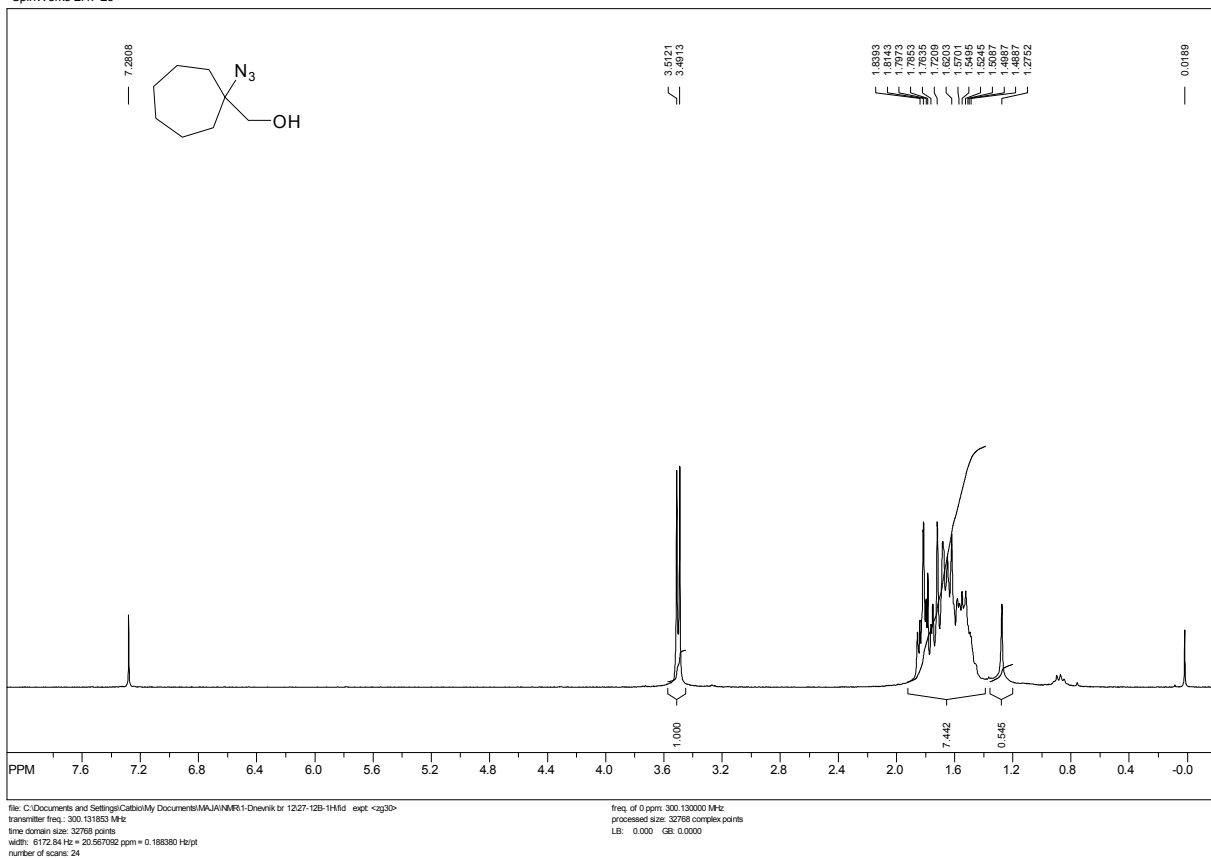


SpinWorks 2.4: 2b'

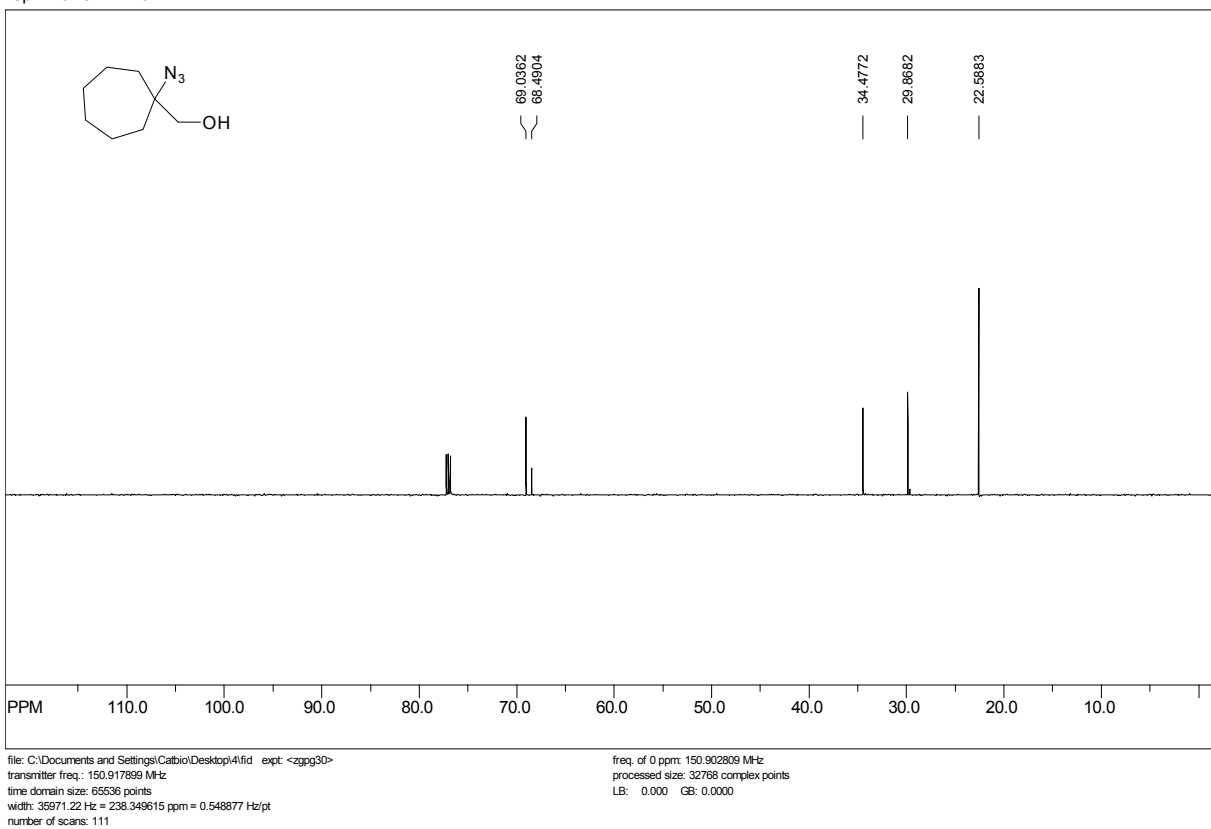




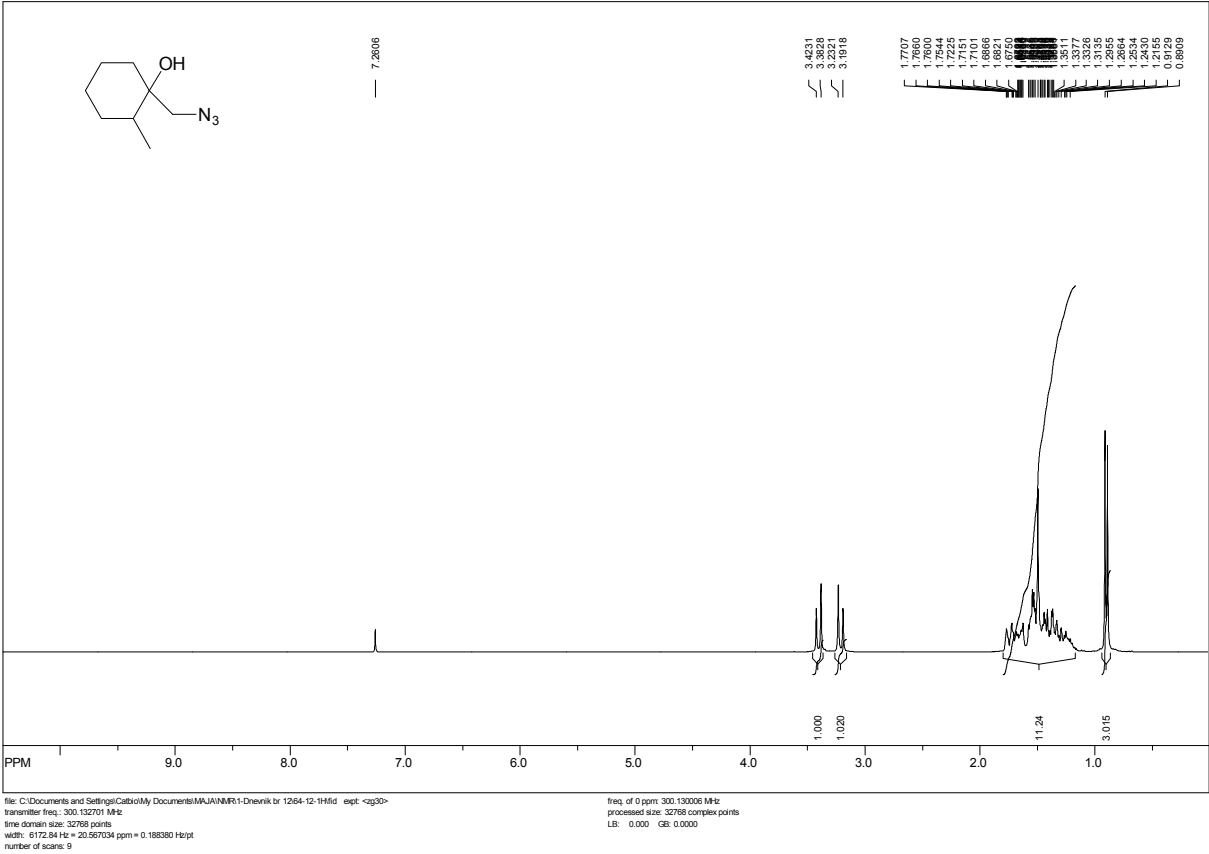
SpinWorks 2.4: 2c'



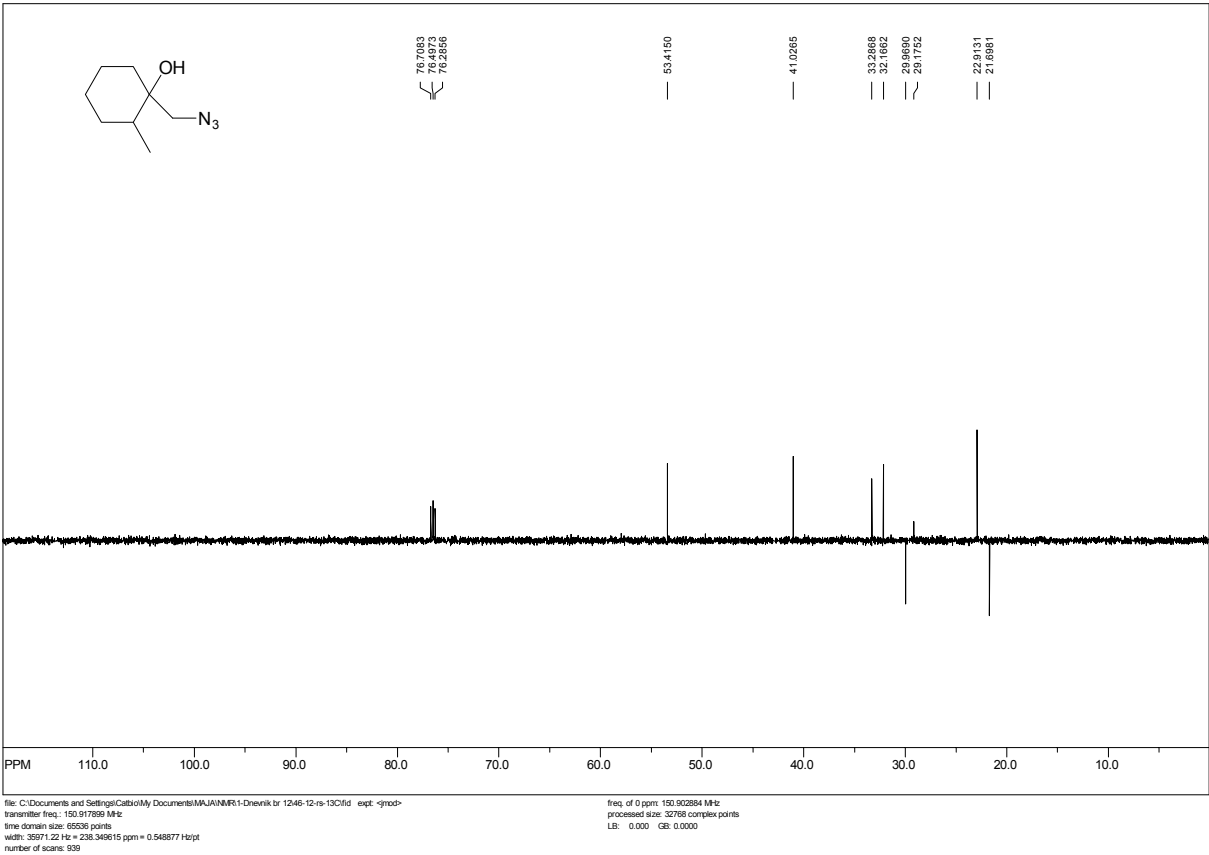
SpinWorks 2.4: 2c'



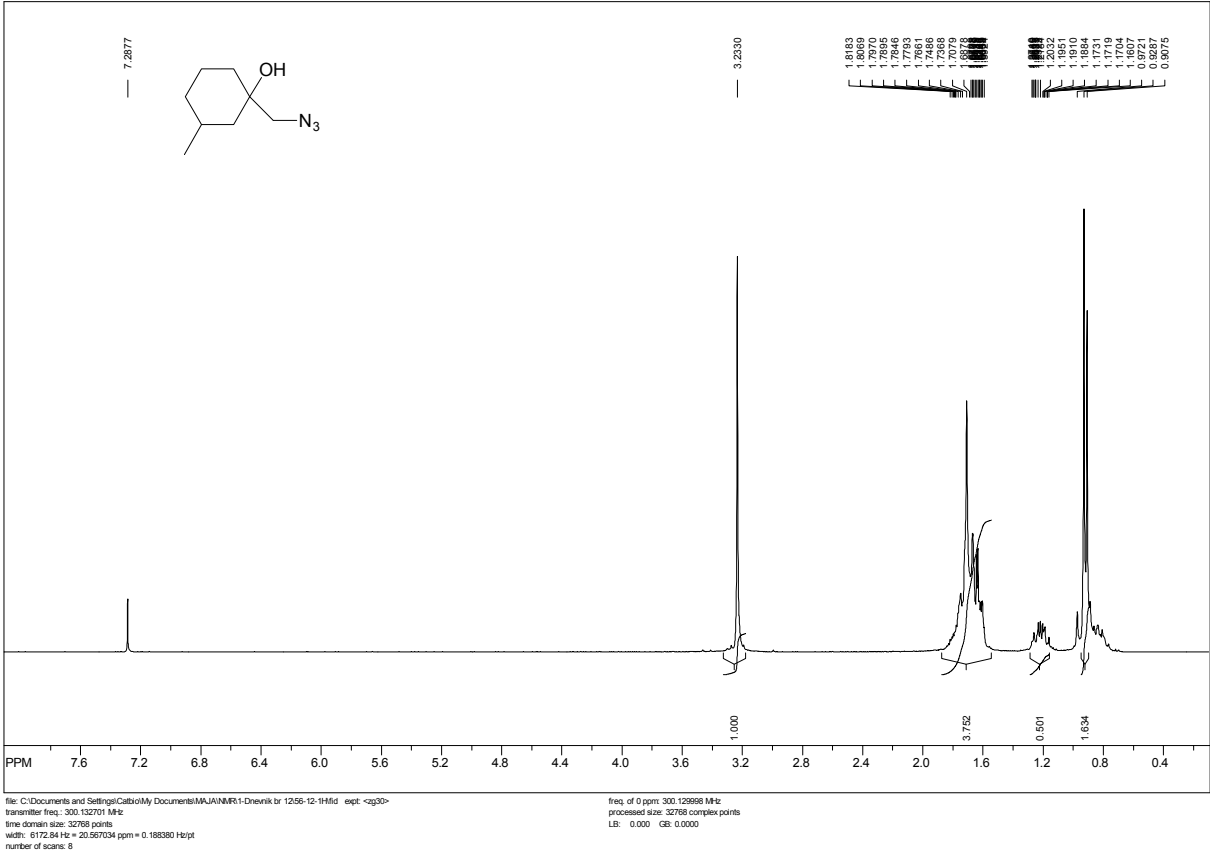
SpinWorks 2.4: 2d



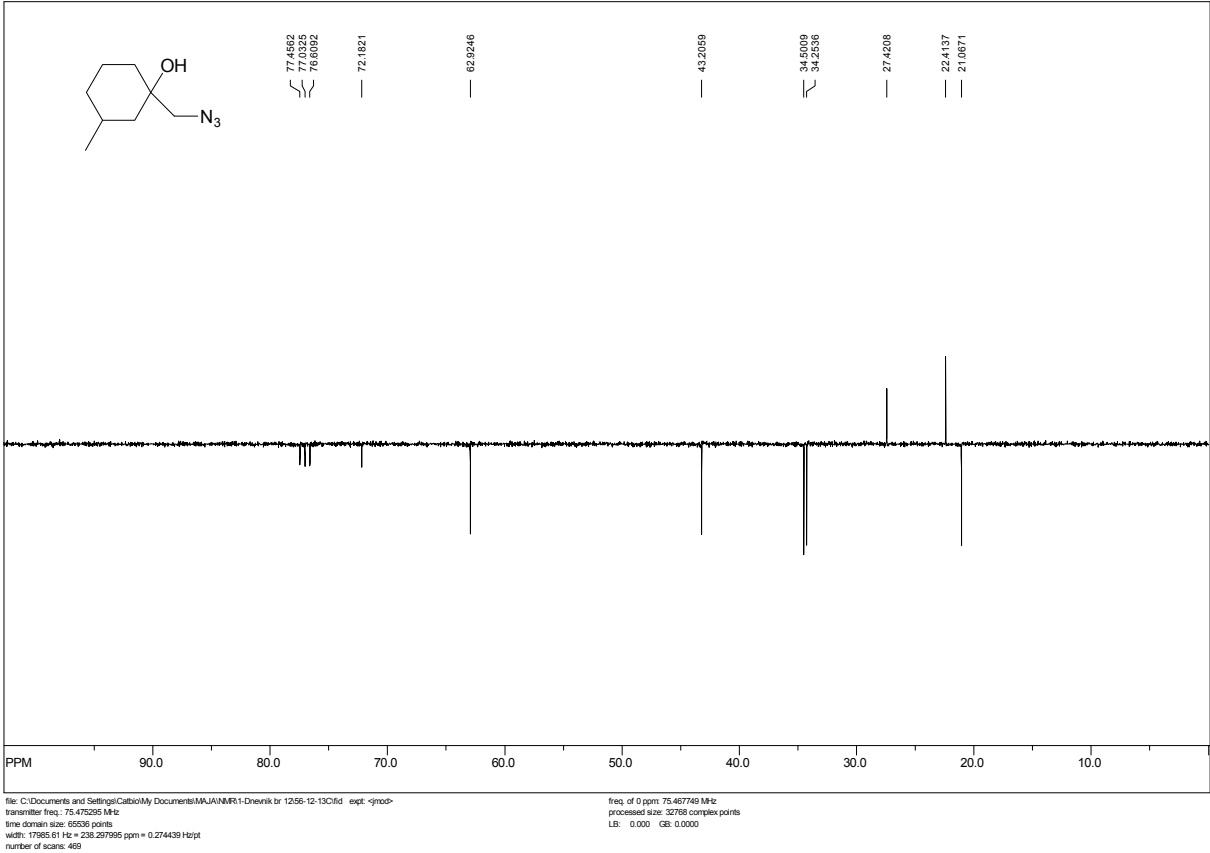
SpinWorks 2.4: 2d



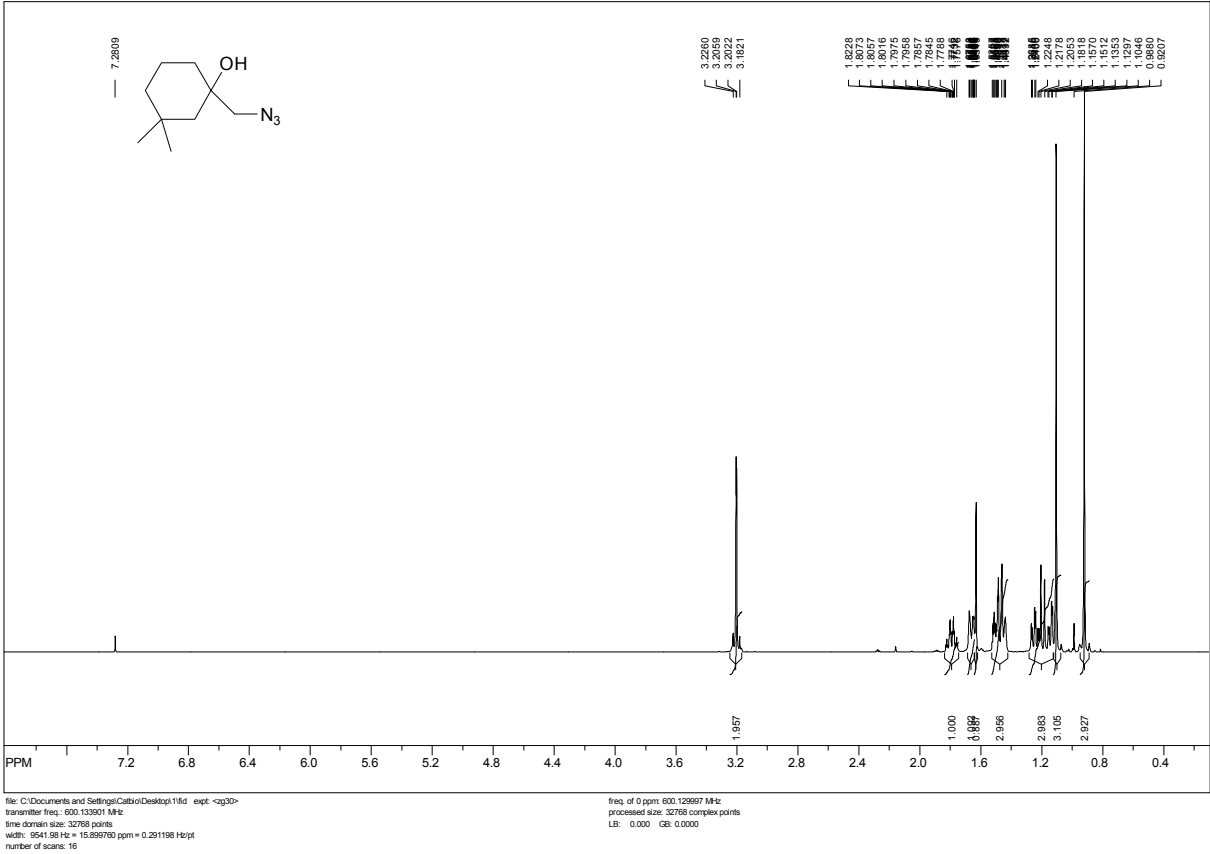
SpinWorks 2.4: 2e



SpinWorks 2.4: 2e



SpinWorks 2.4: 2f



SpinWorks 2.4: 2f

