

Supporting Information
for
**Chemoenzymatic Synthesis of Optically Active
Ethereal Analog of *iso*-Moramide –
a Novel Potentially Powerful Analgesic**

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Table S1. List of commercial enzyme preparations employed in these studies.

Enzyme and its origin (microorganism/tissue)	Enzyme preparation ^[a] (brand name)	Usage form of enzyme preparation	Enzyme specified activity	Commercial supplier
Lipase from <i>Candida antarctica</i> B (CAL-B)	Novozym 435	immobilized on macroporous acrylic resin [poly (methyl methacrylate-co-butyl methacrylate)]	>10000 U/g or 10 PLU/mg, water content 1.4%	Novozymes A/S
	Chirazyme L-2, c.-f., C2, Lyo.	immobilized on the carrier-fixed (carrier 2)	150 kU	Roche
	Chirazyme L-2, c.-f., C3, Lyo.	immobilized on the carrier-fixed (carrier 3)	150 kU	Roche
Lipase from <i>Candida antarctica</i> A (CAL-A)	Chirazyme L-5	native	unspecified	Boehringer Mannheim ^[b]
Lipase from <i>Burkholderia cepacia</i> (formerly <i>Pseudomonas cepacia</i>)	Amano PS	native	>23.000 U/g	Amano Pharmaceutical Co., Ltd.
	Amano PS-IM	immobilized on diatomite	500 U/g	Amano Pharmaceutical Co., Ltd.
	PS-Immobead 150	immobilized on Immobead 150	≥900 U/g	Sigma-Aldrich
Lipase from <i>Pseudomonas fluorescens</i>	Amano AK	native	>20.000 U/g	Amano Pharmaceutical Co., Ltd.

[a] All commercial formulations of enzymes studied herein were used without pre-treatment.

[b] Currently: Roche Diagnostics.

Table S2. The results of specific rotation values for optically active products.

Compound	ee [%]	Measured specific rotation $[\alpha]_D$	Literature specific rotation $[\alpha]_D^{\text{lit.}}$
 (S)-(+)-3	>99	$[\alpha]_D^{27.5} = +50.40$ (c 1.3, CHCl ₃)	Lack of data
 (R)-(-)-3	98	$[\alpha]_D^{22} = -73.03$ (c 1.8, CHCl ₃)	Lack of data
 (R)-(-)-4a	99	$[\alpha]_D^{27.5} = -4.66$ (c 1.2, CHCl ₃)	Lack of data
 (R)-(-)-5	>99	$[\alpha]_D^{22} = -19.87$ (c 2.3, CHCl ₃)	Lack of data
 (S)-(+)-5	98	$[\alpha]_D^{22} = +23.00$ (c 1.3, CHCl ₃)	Lack of data
 (R)-(-)-10	89	$[\alpha]_D^{22} = -22.6$ (c 1.9, CHCl ₃)	Lack of data
 (S)-(+)-10	87	$[\alpha]_D^{22} = +19.2$ (c 1.8, CHCl ₃)	Lack of data

Table S3. Analytical separation conditions of studied compounds by GC column.

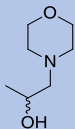
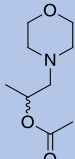
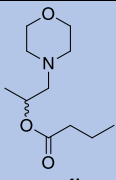
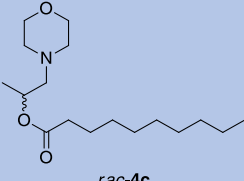
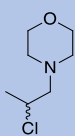
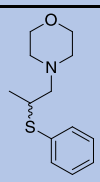
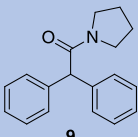
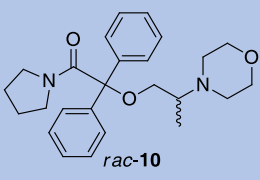
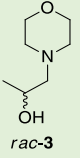
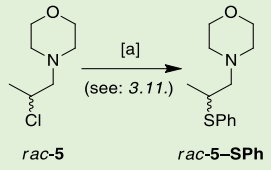
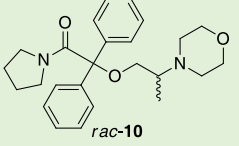
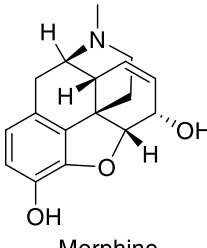
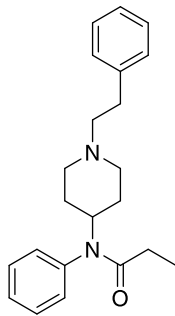
Compound	Temperature program [°C]	Retention time [min]
 <i>rac-3</i>	80–260 (10 °C/min)	4.43
	120–260 (10 °C/min)	2.20
 <i>rac-4a</i>	80–260 (10 °C/min)	6.39
	120–260 (10 °C/min)	3.28
 <i>rac-4b</i>	120–260 (10 °C/min)	4.98
 <i>rac-4c</i>	120–260 (10 °C/min)	11.15
 <i>rac-5</i>	80–260 (10 °C/min)	4.66
 <i>rac-5-SPh</i>	80–260 (10 °C/min)	15.24
 9	150–260 (10 °C/min)	14.83
 <i>rac-10</i>	250–260 (10 °C/min) and then 15 min at 260 °C	30.45

Table S4. HPLC analytical separation conditions of racemic compounds.

Compound	HPLC Column	Mobile Phase	Flow Rate [mL/min] / Pressure [MPa]	Detection [nm] / Temperature [°C]	Retention Time [min]
 <chem>C[C@H](O)CN1CCOCC1</chem> <i>rac-3</i>	Chiralpak AD-H	<i>n</i> -hexane/EtOH (90:10, v/v)	0.6 / 2.7	208 / 30	14.611 (<i>R</i>) and 16.213 (<i>S</i>)
 <chem>CC1(C)CCN2CCOCC2CC1Cl</chem> $\xrightarrow{\text{[a]}}$ <chem>CC1(C)CCN2CCOCC2CC1SPh</chem> <i>rac-5</i> \rightarrow <i>rac-5-SPh</i> (see: 3.11.)	Chiralcel OJ-H	<i>n</i> -hexane/ <i>tert</i> - ButOH/Et ₃ N (96.5:3.0:0.5, v/v/v)	1.0 / 4.4	254 / 30	19.417 (<i>R</i>) and 20.940 (<i>S</i>)
 <chem>CC1(C)CCN2CCOCC2CC1C(=O)C(=O)C3=CC=CC=C3C4=CC=CC=C4C5=CC=CC=C5C6=CC=CC=C6C7=CC=CC=C7C8=CC=CC=C8C9=CC=CC=C9C10=CC=CC=C10</chem> <i>rac-10</i>	Chiralcel OD-H	<i>n</i> -hexane/2-PrOH (90:10, v/v)	0.8 / 3.0	222 / 30	9.026 (<i>S</i>) and 19.519 (<i>R</i>)

[a] Derivatization of *rac-5* into *rac-5-SPh* was performed using thiophenol (10 equiv) in EtONa (10 equiv)/EtOH, 12 h at 25 °C.

Table S5. Docking scoring of the respective ligands complexed with opioid receptors (ORs).

Entry	Ligand	OR	Pose ^[a]	Affinity (kcal/mol)	Distance from best mode ^[b]	
					rmsd l.b.	rmsd u.b.
1	 Morphine	μ -OR (PDB ID: 4DKL)	S1	-7.9	0.000	0.000
2			S2	-7.7	8.375	10.081
3			S3	-7.5	2.560	4.445
4			S4	-7.1	8.092	10.366
5			S5	-6.9	9.020	10.999
6			S6	-6.9	9.524	11.945
7			S7	-6.9	8.563	11.057
8			S8	-6.8	8.938	11.097
9			S9	-6.7	8.338	10.729
10		δ -OR (PDB ID: 4EJ4)	S1	-7.6	0.000	0.000
11			S2	-7.3	2.561	4.265
12			S3	-6.1	2.275	4.311
13			S4	-6.1	15.622	17.950
14			S5	-6.1	12.937	15.126
15			S6	-6.0	16.654	18.709
16			S7	-6.0	11.256	13.364
17			S8	-6.0	11.356	13.831
18			S9	-6.0	3.416	5.155
19		κ -OR (PDB ID: 4DJH)	S1	-7.8	0.000	0.000
20			S2	-7.8	3.145	4.663
21			S3	-7.8	11.398	12.939
22			S4	-7.8	2.638	4.239
23			S5	-7.6	2.110	2.888
24			S6	-7.6	1.824	3.964
25			S7	-7.5	1.516	2.032
26			S8	-7.4	10.564	12.414
27			S9	-7.0	3.386	5.235
28	 Fentanyl	μ -OR (PDB ID: 4DKL)	S1	-8.4	0.000	0.000
29			S2	-8.4	0.062	1.510
30			S3	-8.3	0.081	1.510
31			S4	-8.3	0.142	1.076
32			S5	-8.1	1.673	7.375
33			S6	-8.1	1.691	7.473
34			S7	-7.8	2.203	8.255
35			S8	-7.5	3.108	4.614
36			S9	-7.5	1.260	1.769
37		δ -OR (PDB ID: 4EJ4)	S1	-7.0	0.000	0.000
38			S2	-6.9	3.035	5.002
39			S3	-6.8	14.751	16.236
40			S4	-6.8	2.156	3.990
41			S5	-6.8	1.602	2.427
42			S6	-6.8	2.894	8.772
43			S7	-6.7	2.248	9.467
44			S8	-6.7	2.221	3.584
45			S9	-6.7	2.409	3.288
46		κ -OR (PDB ID: 4DJH)	S1	-7.7	0.000	0.000
47			S2	-7.7	11.001	12.666
48			S3	-7.6	12.524	15.704
49			S4	-7.6	0.223	1.520
50			S5	-7.5	12.552	15.802
51			S6	-7.3	4.340	8.252
52			S7	-7.3	11.202	14.990
53			S8	-7.3	4.132	8.022
54			S9	-7.3	13.137	16.068

[a] The pose S1 represents the lowest value of ΔG_{calc} (kcal/mol), which means that ligand-binding affinity to receptor is the highest, and in contrary, the S9 mode represent the lowest ligand-binding affinity.

[b] The values <2.000 rmsd represent the closest distance between the ligand and the opioid receptor binding site.

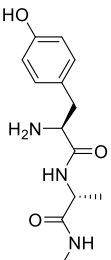
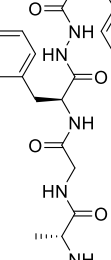
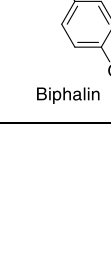
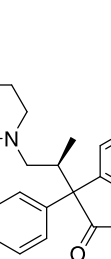


Table S5. Docking scoring of the respective ligands complexed with opioid receptors (ORs) – continued.

Entry	Ligand	OR	Pose ^[a]	Affinity (kcal/mol)	Distance from best mode ^[b]	
					rmsd l.b.	rmsd u.b.
55		μ -OR (PDB ID: 4DKL)	S1	-9.3	0.000	0.000
56			S2	-8.6	1.192	1.574
57			S3	-8.6	2.731	3.870
58			S4	-8.5	1.368	1.562
59			S5	-8.1	2.264	3.451
60			S6	-7.9	3.486	7.660
61			S7	-7.8	1.808	2.161
62			S8	-7.8	3.288	6.639
63			S9	-7.8	2.963	3.857
64		δ -OR (PDB ID: 4EJ4)	S1	-9.1	0.000	0.000
65			S2	-8.8	1.155	1.388
66			S3	-8.8	2.185	3.462
67			S4	-8.6	1.678	2.752
68			S5	-8.6	2.685	3.212
69			S6	-7.7	1.899	3.232
70			S7	-7.6	2.481	4.227
71			S8	-7.4	14.717	17.865
72			S9	-7.3	15.226	18.108
73		κ -OR (PDB ID: 4DJH)	S1	-7.9	0.000	0.000
74			S2	-7.9	3.539	7.041
75			S3	-7.9	13.462	16.581
76			S4	-7.9	7.479	10.610
77			S5	-7.9	16.239	19.390
78			S6	-7.9	3.626	7.199
79			S7	-7.8	14.123	16.680
80			S8	-7.7	13.193	16.407
81			S9	-7.7	1.413	1.797
82		μ -OR (PDB ID: 4DKL)	S1	-9.2	0.000	0.000
83			S2	-9.2	2.075	10.006
84			S3	-9.1	2.934	10.105
85			S4	-8.9	3.228	4.971
86			S5	-8.9	2.877	4.179
87			S6	-8.8	5.779	10.009
88			S7	-8.8	2.862	3.947
89			S8	-8.7	2.939	10.007
90			S9	-8.6	4.945	9.454
91		δ -OR (PDB ID: 4EJ4)	S1	-8.7	0.000	0.000
92			S2	-8.6	3.481	8.576
93			S3	-8.4	3.717	6.056
94			S4	-8.3	4.658	5.353
95			S5	-8.2	4.137	8.592
96			S6	-8.2	4.434	9.199
97			S7	-8.1	11.821	16.216
98			S8	-8.0	10.812	13.721
99			S9	-8.0	4.637	5.631
100		κ -OR (PDB ID: 4DJH)	S1	-9.6	0.000	0.000
101			S2	-9.2	3.905	7.474
102			S3	-9.0	1.990	2.768
103			S4	-9.0	4.308	7.534
104			S5	-8.8	3.909	6.425
105			S6	-8.8	11.291	14.030
106			S7	-8.8	3.722	5.290
107			S8	-8.7	4.169	6.220
108			S9	-8.7	4.369	7.899

[a] The pose S1 represents the lowest value of ΔG_{calc} (kcal/mol), which means that ligand-binding affinity to receptor is the highest, and in contrary, the S9 mode represent the lowest ligand-binding affinity.

[b] The values <2.000 rmsd represent the closest distance between the ligand and the opioid receptor binding site.

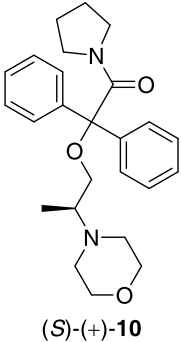
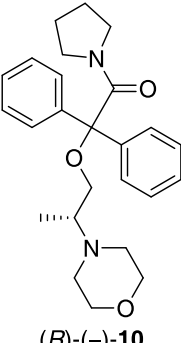
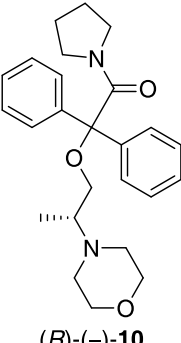
Table S5. Docking scoring of the respective ligands complexed with opioid receptors (ORs) – continued.

Entry	Ligand	OR	Pose ^[a]	Affinity (kcal/mol)	Distance from best mode ^[b]	
					rmsd l.b.	rmsd u.b.
109		μ -OR (PDB ID: 4DKL)	S1	-9.3	0.000	0.000
110			S2	-9.3	2.443	5.912
111			S3	-9.2	2.533	8.272
112			S4	-9.2	2.641	7.153
113			S5	-9.1	2.229	7.540
114			S6	-9.0	2.367	4.987
115			S7	-9.0	2.183	6.312
116			S8	-8.9	2.653	6.808
117			S9	-8.9	2.708	6.123
118		δ -OR (PDB ID: 4EJ4)	S1	-9.9	0.000	0.000
119			S2	-9.6	3.459	5.022
120			S3	-9.5	3.034	12.152
121			S4	-9.5	2.363	4.021
122			S5	-9.4	1.626	2.563
123			S6	-9.3	1.822	14.672
124			S7	-9.3	2.252	3.463
125			S8	-9.2	5.071	8.288
126			S9	-9.2	3.160	5.744
127		κ -OR (PDB ID: 4DJH)	S1	-9.6	0.000	0.000
128			S2	-9.6	2.070	7.564
129			S3	-9.5	2.074	8.131
130			S4	-9.2	2.168	7.994
131			S5	-9.0	2.156	7.687
132			S6	-8.9	1.637	2.271
133			S7	-8.9	2.058	8.762
134			S8	-8.9	2.345	6.662
135			S9	-8.8	2.307	9.438
136		μ -OR (PDB ID: 4DKL)	S1	-8.0	0.000	0.000
137			S2	-7.8	1.461	4.753
138			S3	-7.7	1.695	4.147
139			S4	-7.7	2.330	5.998
140			S5	-7.6	2.177	5.119
141			S6	-7.5	1.580	2.295
142			S7	-7.5	5.479	8.762
143			S8	-7.5	1.816	6.490
144			S9	-7.4	3.921	6.438
145		δ -OR (PDB ID: 4EJ4)	S1	-8.0	0.000	0.000
146			S2	-7.8	2.128	6.156
147			S3	-7.3	1.561	2.200
148			S4	-7.3	2.018	5.746
149			S5	-7.3	1.745	4.636
150			S6	-7.2	2.038	5.665
151			S7	-7.2	1.823	5.618
152			S8	-7.2	1.921	4.642
153			S9	-7.2	2.032	5.358
154		κ -OR (PDB ID: 4DJH)	S1	-7.8	0.000	0.000
155			S2	-7.8	11.083	13.749
156			S3	-7.8	1.632	4.633
157			S4	-7.7	1.728	2.729
158			S5	-7.7	1.910	4.492
159			S6	-7.7	10.839	13.325
160			S7	-7.6	3.406	7.119
161			S8	-7.6	1.643	4.711
162			S9	-7.6	11.332	14.262

[a] The pose S1 represents the lowest value of ΔG_{calc} (kcal/mol), which means that ligand-binding affinity to receptor is the highest, and in contrary, the S9 mode represent the lowest ligand-binding affinity.

[b] The values <2.000 rmsd represent the closest distance between the ligand and the opioid receptor binding site.

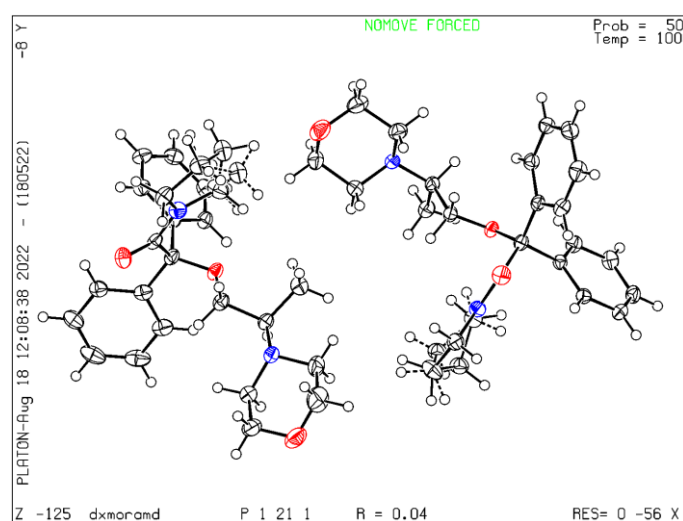
Table S5. Docking scoring of the respective ligands complexed with opioid receptors (ORs) – continued.

Entry	Ligand	OR	Pose ^[a]	Affinity (kcal/mol)	Distance from best mode ^[b]	
					rmsd l.b.	rmsd u.b.
163		μ -OR (PDB ID: 4DKL)	S1	-7.8	0.000	0.000
164			S2	-7.7	1.553	4.319
165			S3	-7.7	1.543	2.597
166			S4	-7.7	1.953	4.992
167			S5	-7.6	2.011	4.739
168			S6	-7.6	2.036	4.956
169			S7	-7.5	2.313	5.442
170			S8	-7.5	5.419	8.322
171			S9	-7.5	1.832	4.660
172		δ -OR (PDB ID: 4EJ4)	S1	-7.6	0.000	0.000
173			S2	-7.6	1.411	2.113
174			S3	-7.5	1.531	2.193
175			S4	-7.4	1.299	4.468
176			S5	-7.4	1.637	2.355
177			S6	-7.4	1.829	4.822
178			S7	-7.4	1.816	4.790
179			S8	-7.3	1.811	4.398
180			S9	-7.2	1.533	2.076
181		κ -OR (PDB ID: 4DJH)	S1	-7.7	0.000	0.000
182			S2	-7.7	1.147	1.947
183			S3	-7.7	10.819	12.732
184			S4	-7.7	1.360	4.496
185			S5	-7.7	11.720	14.686
186			S6	-7.6	12.036	14.375
187			S7	-7.6	1.981	3.482
188			S8	-7.4	12.248	14.632
189			S9	-7.4	11.912	14.636
190		μ -OR (PDB ID: 4DKL)	S1	-8.1	0.000	0.000
191			S2	-7.8	1.411	4.303
192			S3	-7.7	2.084	4.910
193			S4	-7.7	1.393	1.982
194			S5	-7.6	1.553	4.359
195			S6	-7.6	1.915	4.698
196			S7	-7.6	1.508	4.437
197			S8	-7.6	1.856	4.381
198			S9	-7.4	2.197	5.312
199		δ -OR (PDB ID: 4EJ4)	S1	-8.3	0.000	0.000
200			S2	-8.1	2.388	5.043
201			S3	-8.0	2.173	4.981
202			S4	-7.9	2.107	4.966
203			S5	-7.9	2.413	5.153
204			S6	-7.8	2.303	5.990
205			S7	-7.8	1.683	2.551
206			S8	-7.7	2.156	3.143
207			S9	-7.7	2.326	5.235
208		κ -OR (PDB ID: 4DJH)	S1	-8.8	0.000	0.000
209			S2	-8.8	10.483	12.202
210			S3	-8.8	10.190	12.758
211			S4	-8.7	10.406	12.386
212			S5	-8.7	1.382	4.591
213			S6	-8.6	11.920	14.495
214			S7	-8.5	12.094	14.633
215			S8	-8.5	2.035	6.436
216			S9	-8.5	1.776	2.540

[a] The pose S1 represents the lowest value of ΔG_{calc} (kcal/mol), which means that ligand-binding affinity to receptor is the highest, and in contrary, the S9 mode represent the lowest ligand-binding affinity.

[b] The values <2.000 rmsd represent the closest distance between the ligand and the opioid receptor binding site.

Table S6. Crystal data and structure refinement parameters for (*R*)-(-)-10.



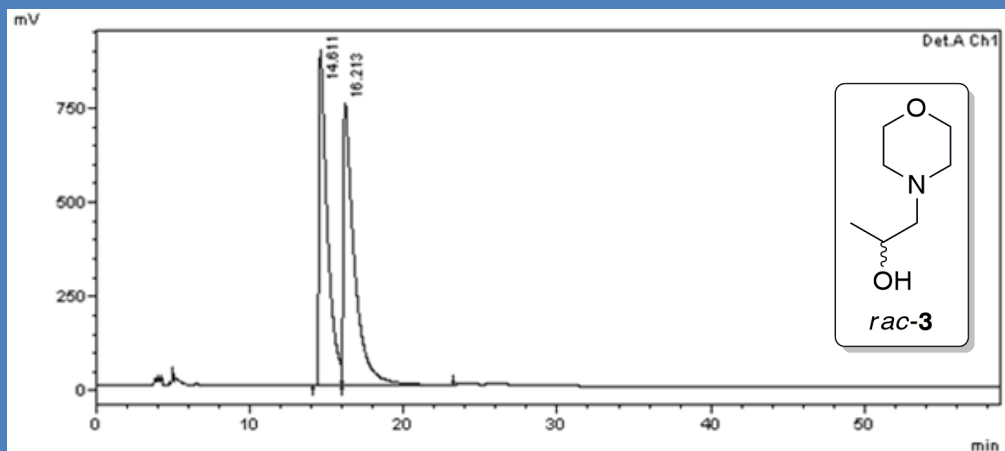
Compound	(<i>R</i>)-(-)-10
Chemical formula	C ₂₅ H ₃₂ N ₂ O ₃
<i>M</i> /g·mol ⁻¹	408.52
<i>T</i> /K	100.0(1)
Crystal system	monoclinic
Space group	<i>P</i> 2 ₁
<i>a</i> /Å	11.4651(1)
<i>b</i> /Å	9.1043(1)
<i>c</i> /Å	21.3925(2)
β /°	98.324(1)
<i>V</i> /Å ³	2209.46(4)
<i>Z</i>	4
<i>D</i> _{calc} /g·cm ⁻³	1.228
μ /mm ⁻¹	0.638
<i>F</i> (000)	880.0
Crystal size/mm ³	0.67 × 0.42 × 0.251
Radiation, λ / Å	CuK α (λ = 1.54184)
2 θ Range /°	7.794 to 134.06
Reflections collected	93508
Independent reflections	7903
<i>R</i> _{int}	0.0550
Data/restraints/parameters	7903/5/552
<i>S</i> (<i>F</i> ²) ^[a]	1.030
<i>R</i> 1, <i>wR</i> 2 (<i>I</i> > 2 σ (<i>I</i>)) ^[b]	0.0354, 0.0923
<i>R</i> 1, <i>wR</i> 2 (all data)	0.0361, 0.0929
$\Delta\rho_{\text{min/max}}$ /eÅ ⁻³	+0.46/−0.26
Flack parameter	0.01(6)

[a] Goodness-of-fit $S = \{\sum[w(F_o^2 - F_c^2)^2]/(n-p)\}^{1/2}$ where *n* is the reflections number and *p* is the parameters number.

[b] $R1 = \sum||F_o| - |F_c||/\sum|F_o|$, $wR2 = \{\sum[w(F_o^2 - F_c^2)^2]/\sum[w(F_o^2)^2]\}^{1/2}$.

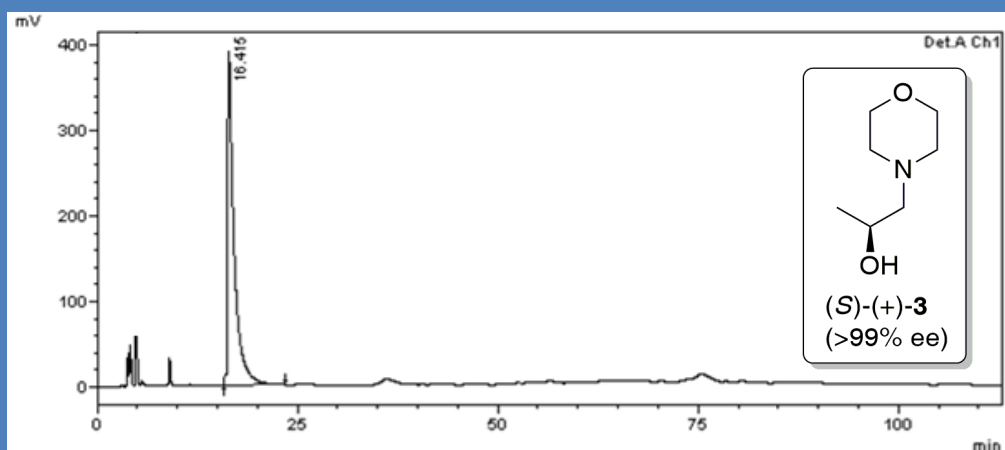
HPLC of *rac*-3 on Chiralpak AD-H at 30 °C

Conditions: *n*-hexane-EtOH (90:10, v/v); *f*=0.6 mL/min; λ =208 nm



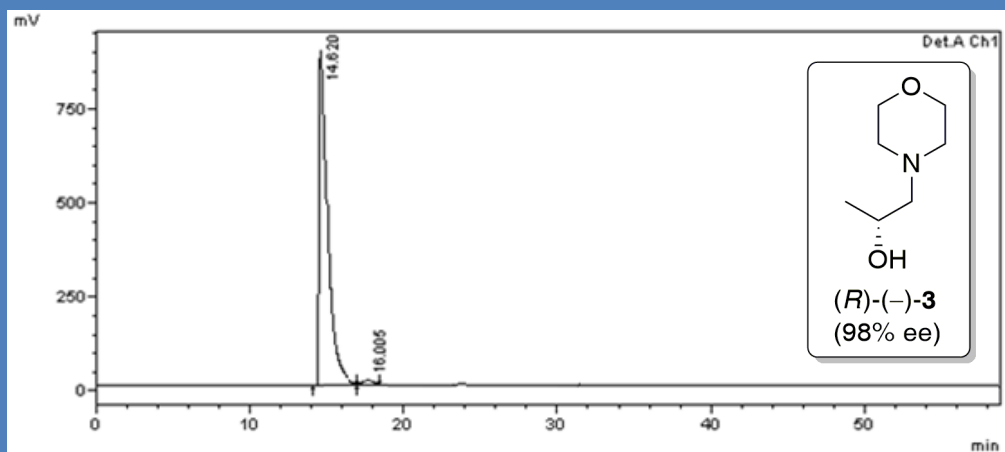
HPLC of (*S*)-(+)-3 on Chiralpak AD-H at 30 °C

Conditions: *n*-hexane-EtOH (90:10, v/v); *f*=0.6 mL/min; λ =208 nm



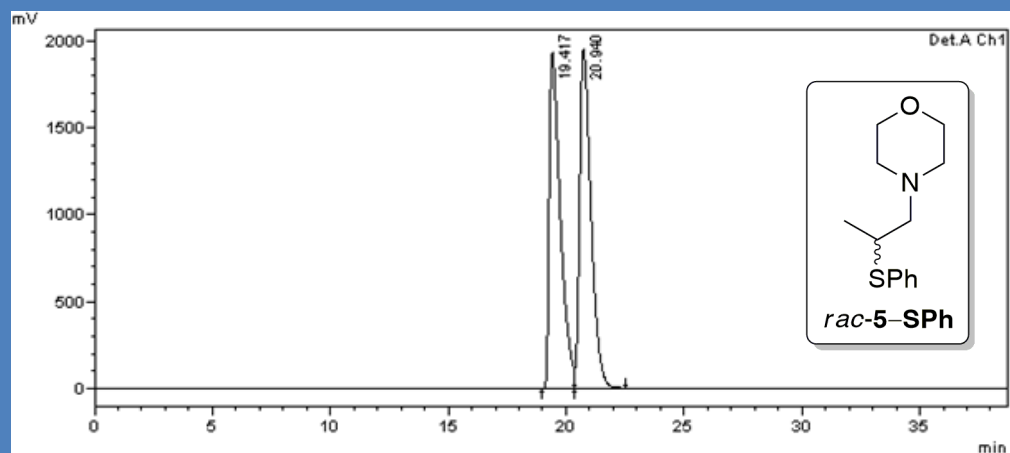
HPLC of (*R*)-(-)-3 on Chiralpak AD-H at 30 °C

Conditions: *n*-hexane-EtOH (90:10, v/v); *f*=0.6 mL/min; λ =208 nm



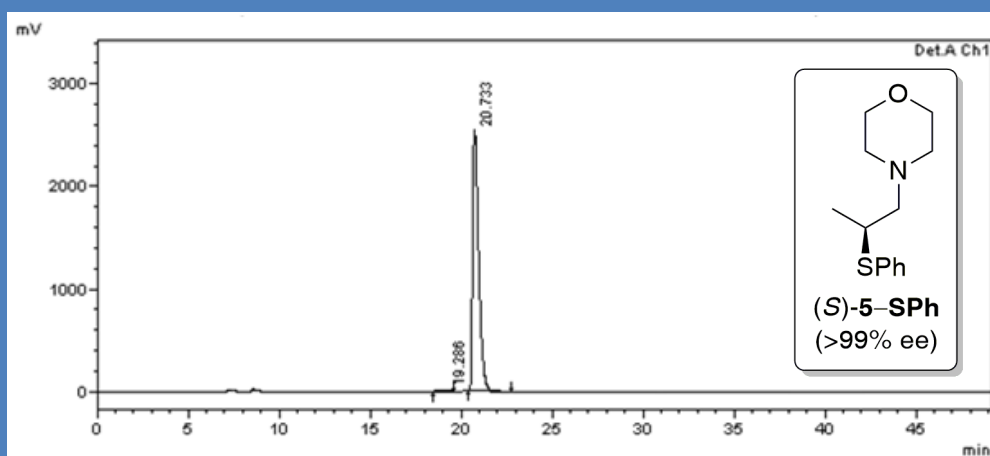
HPLC of *rac*-5-SPh (obtained from *rac*-5) on Chiralcel OJ-H at 30 °C

Conditions: *n*-hexane/*tert*-ButOH/Et₃N (96.5:3.0:0.5, v/v/v); *f*=1.0 mL/min; λ =254 nm



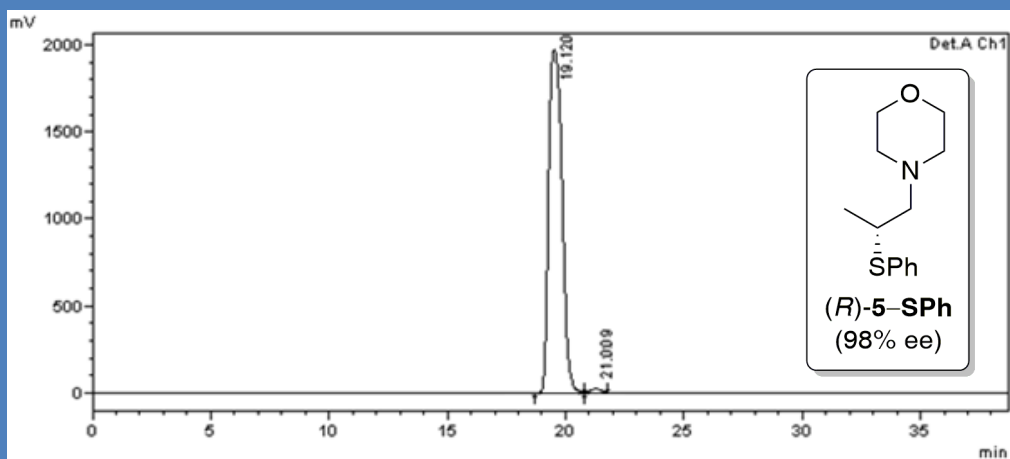
HPLC of (*S*)-5-SPh [obtained from (*R*)-(-)-5] on Chiralcel OJ-H at 30 °C

Conditions: *n*-hexane/*tert*-ButOH/Et₃N (96.5:3.0:0.5, v/v/v); *f*=1.0 mL/min; λ =254 nm



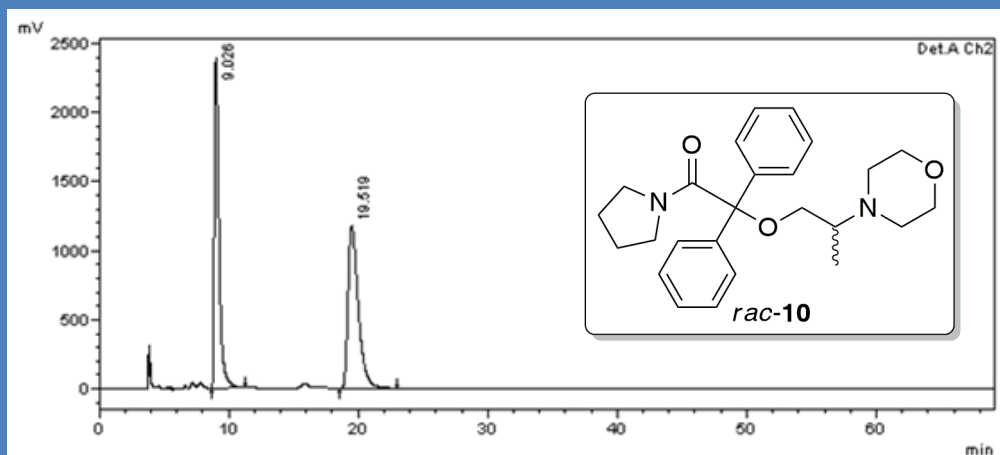
HPLC of (*R*)-5-SPh [obtained from (*S*)-(+)-5] on Chiralcel OJ-H at 30 °C

Conditions: *n*-hexane/*tert*-ButOH/Et₃N (96.5:3.0:0.5, v/v/v); *f*=1.0 mL/min; λ =254 nm



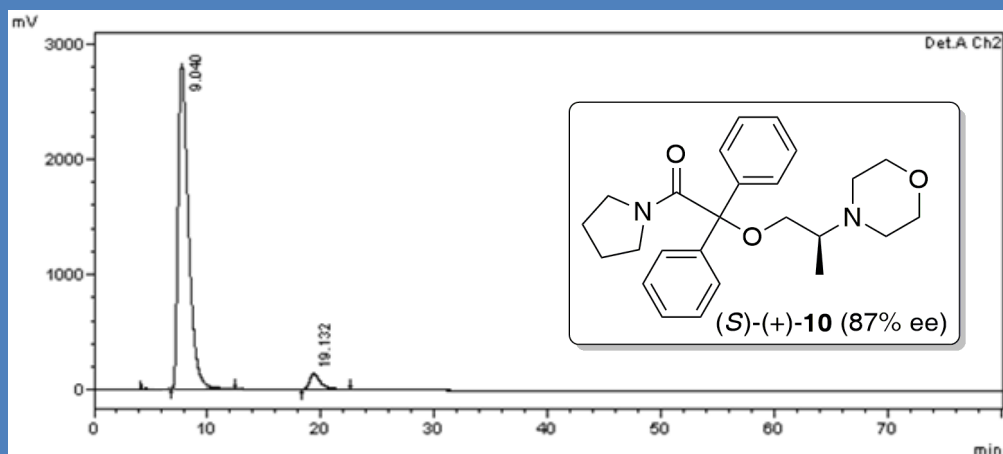
HPLC of *rac*-10 on Chiralcel OD-H at 30 °C

Conditions: *n*-hexane-2-PrOH (90:10, v/v); f=0.8 mL/min; λ =222 nm



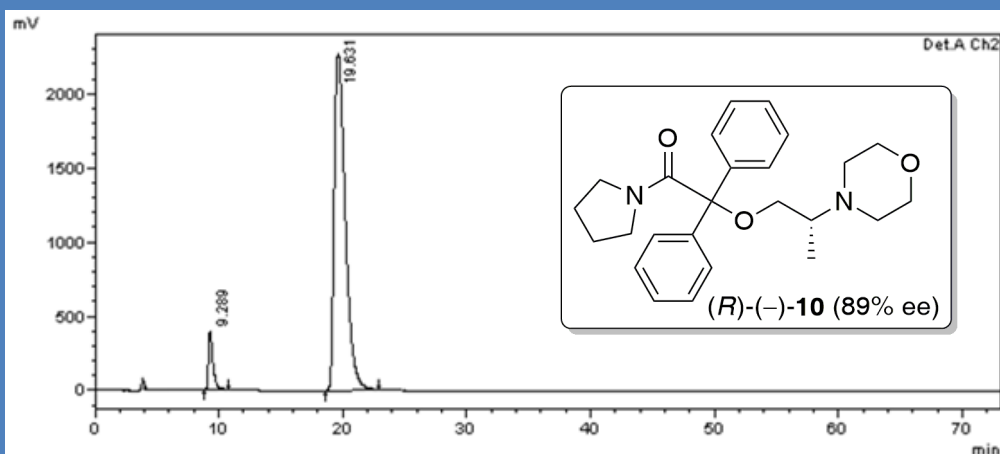
HPLC of (*S*)-(+)-10 on Chiralcel OD-H at 30 °C

Conditions: *n*-hexane-2-PrOH (90:10, v/v); f=0.8 mL/min; λ =222 nm



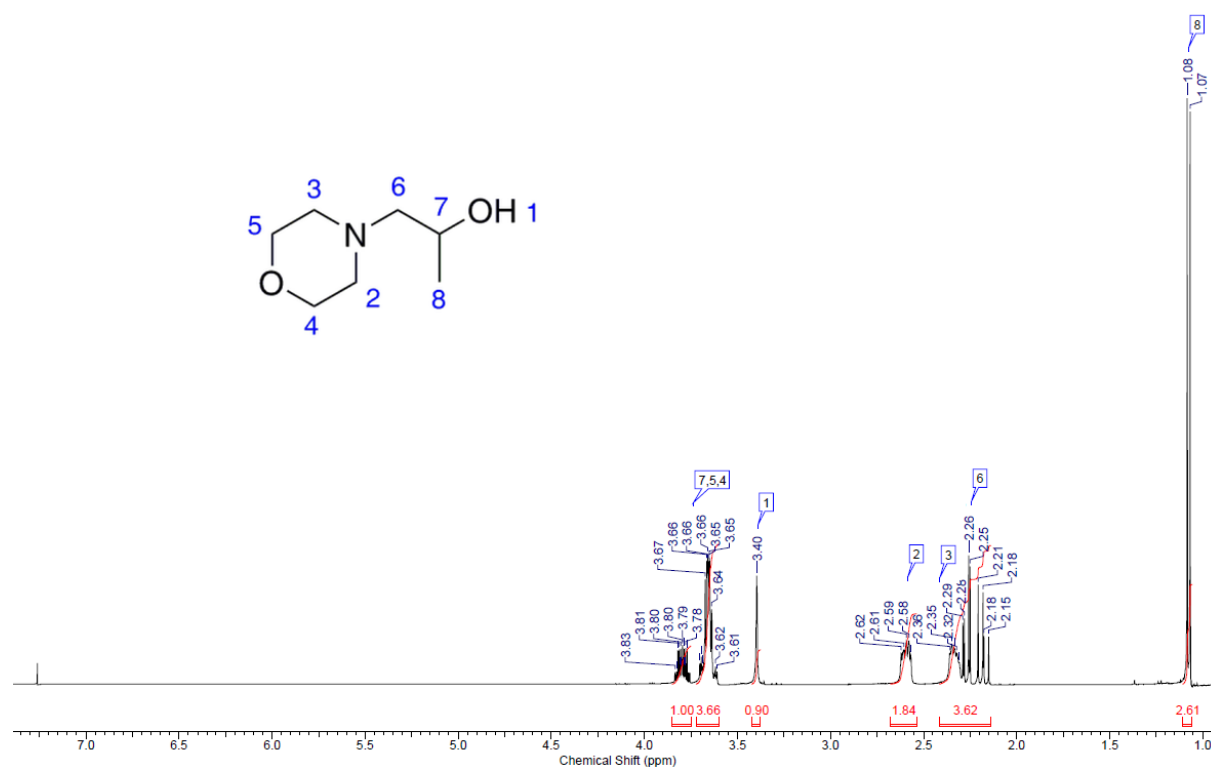
HPLC of (*R*)-(-)-10 on Chiralcel OD-H at 30 °C

Conditions: *n*-hexane-2-PrOH (90:10, v/v); f=0.8 mL/min; λ =222 nm

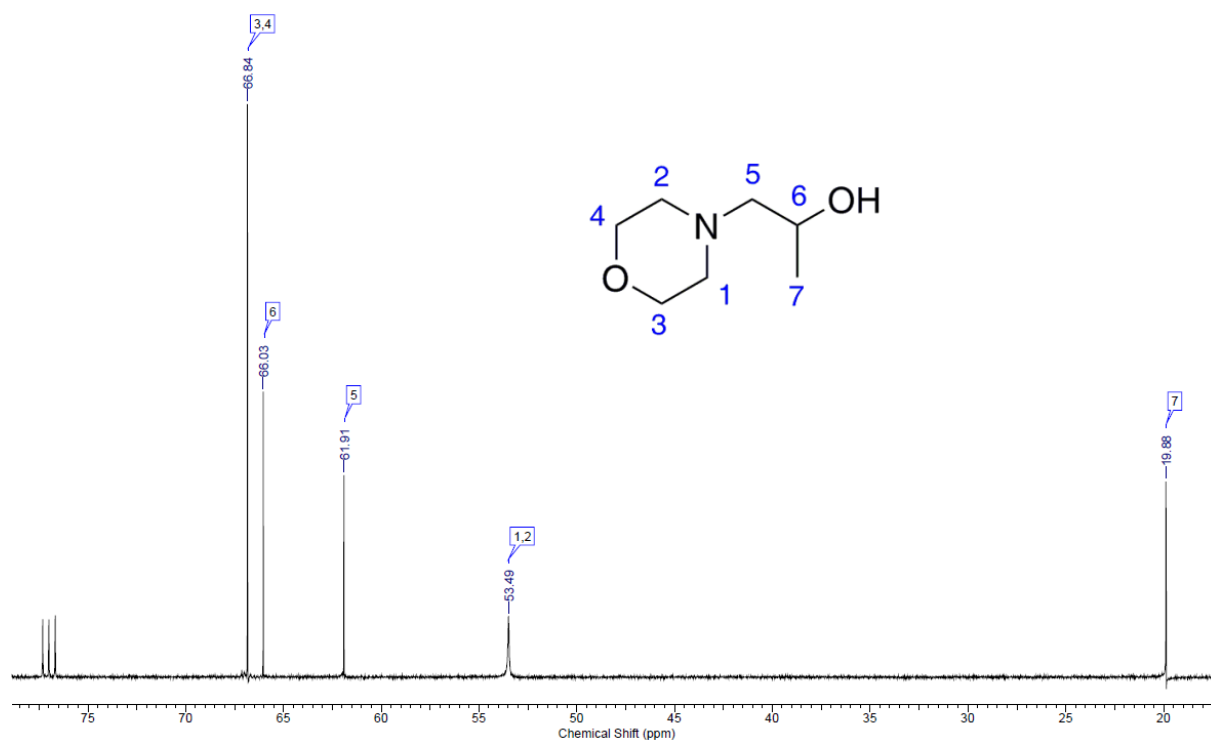


1-(Morpholin-4-yl)propan-2-ol (*rac*-**3**)

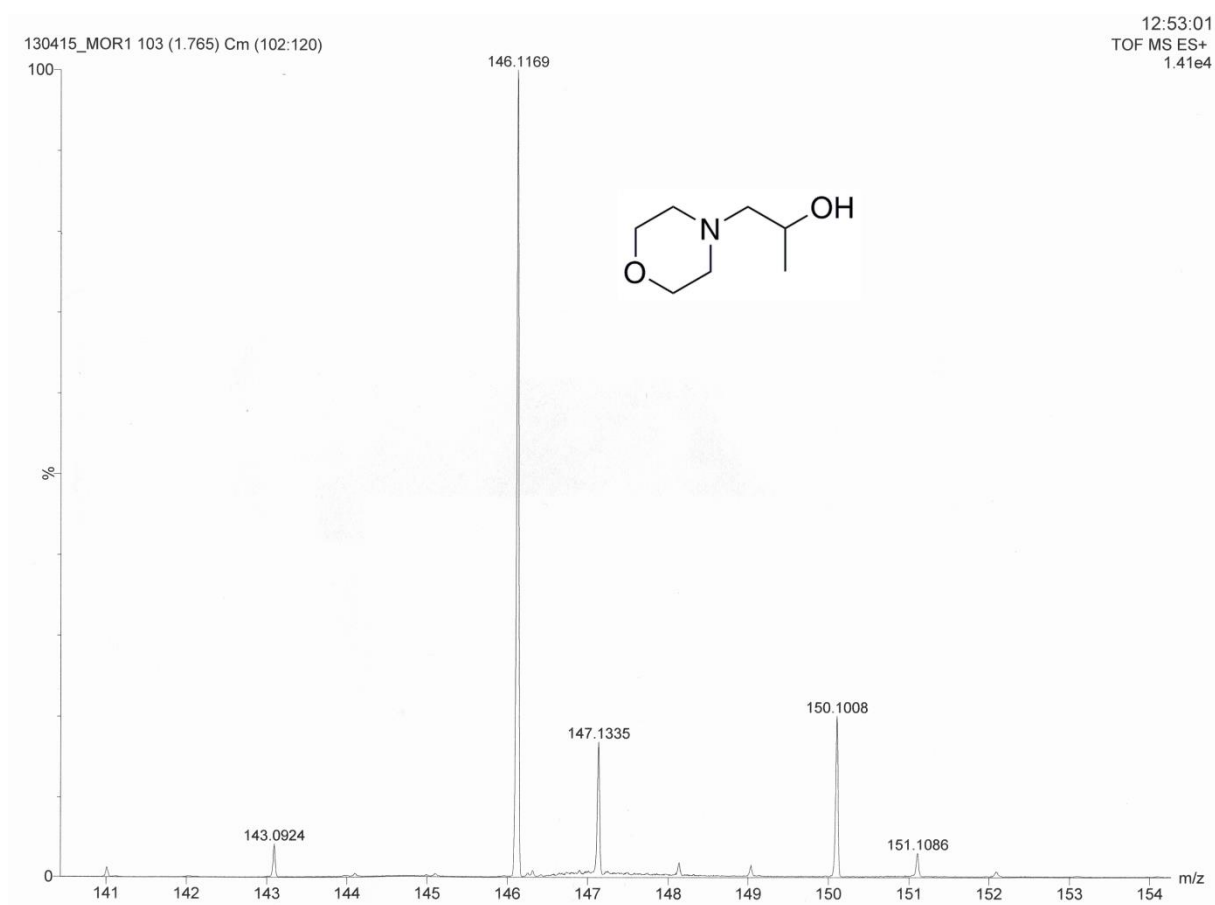
^1H NMR spectrum of *rac*-**3** (400 MHz, CDCl_3)



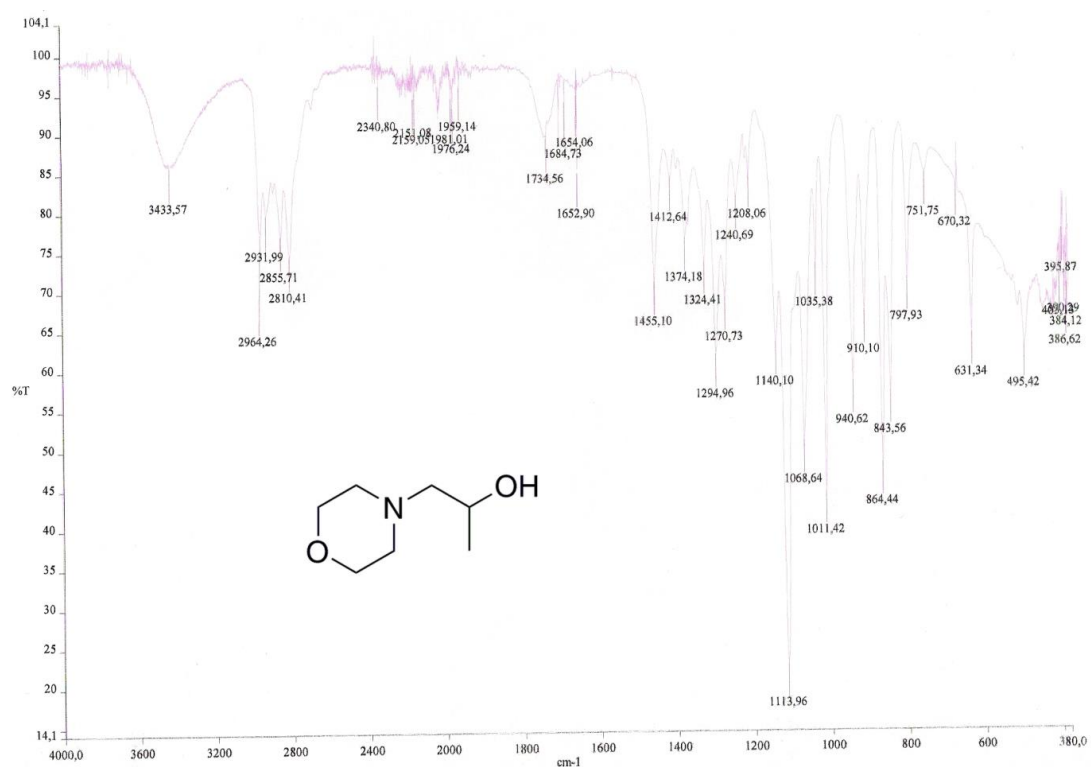
^{13}C NMR spectrum of *rac*-**3** (100 MHz, CDCl_3)



MS spectrum of *rac*-**3** (ESI-TOF)

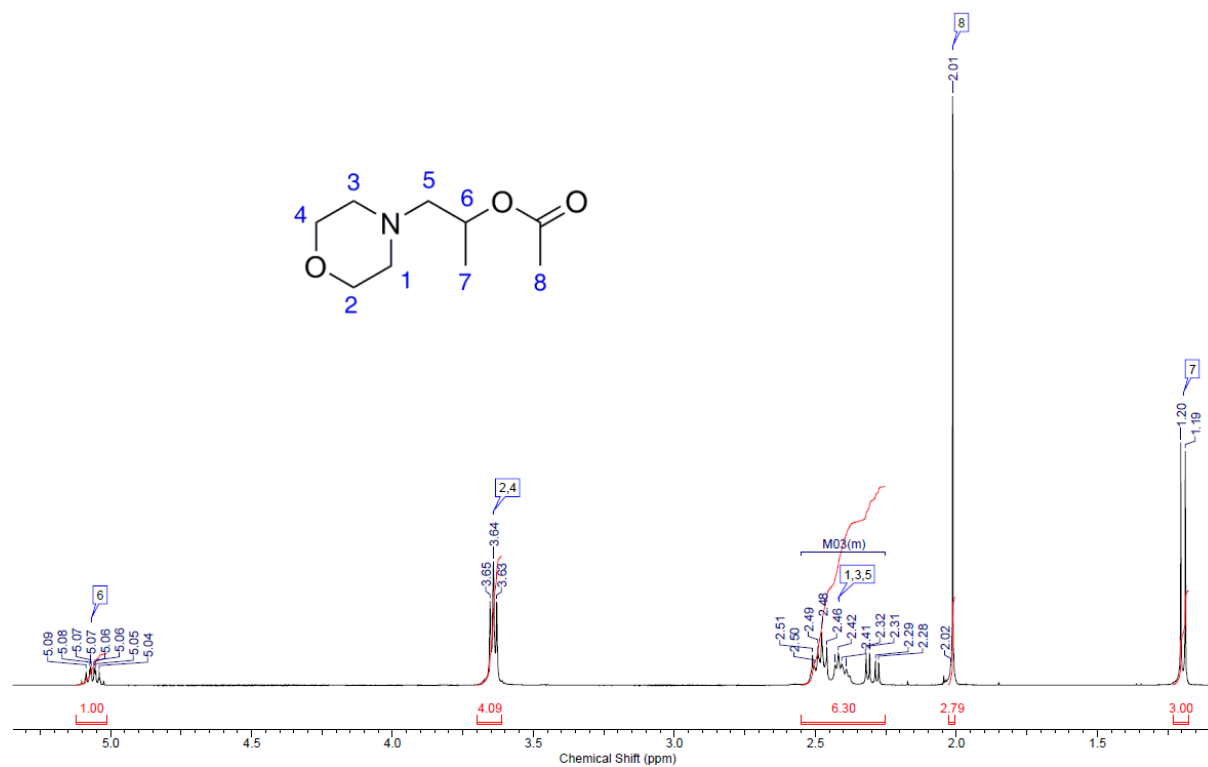


FT-IR spectrum of *rac*-**3** (neat)

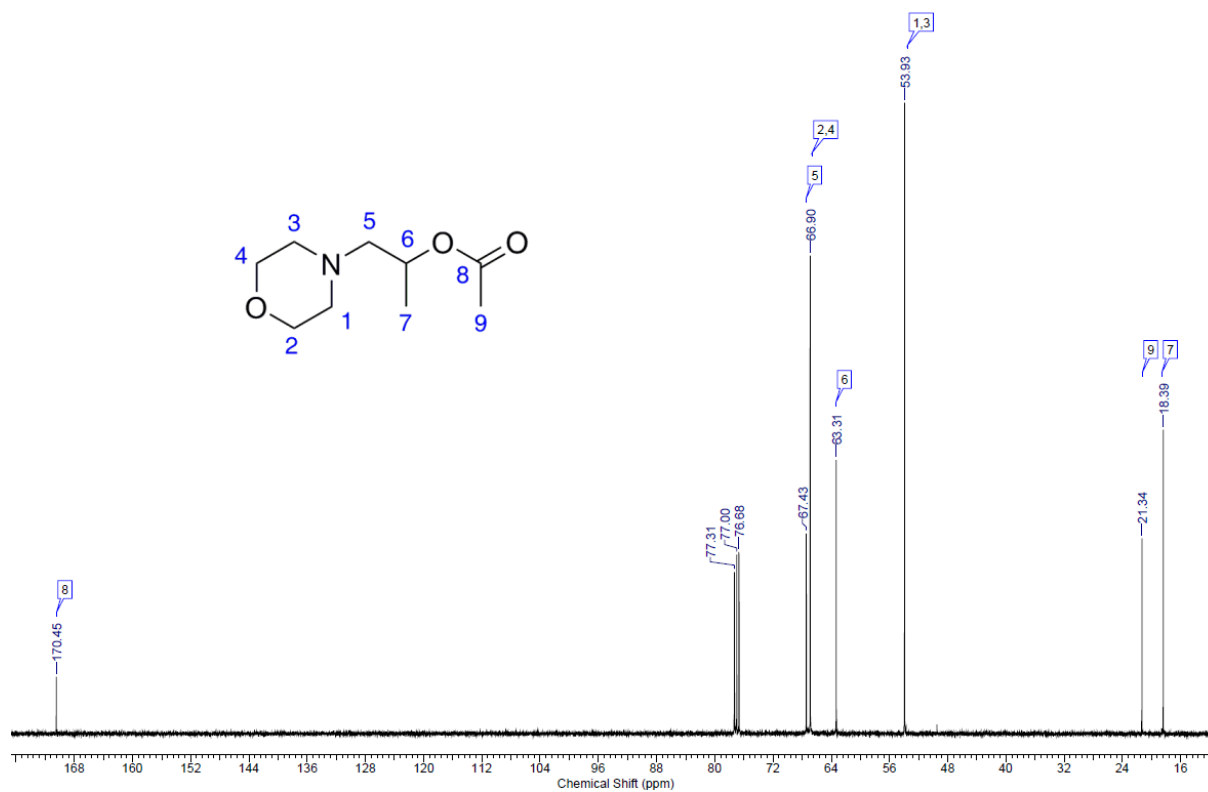


1-(Morpholin-4-yl)propan-2-yl acetate (*rac*-**4a**)

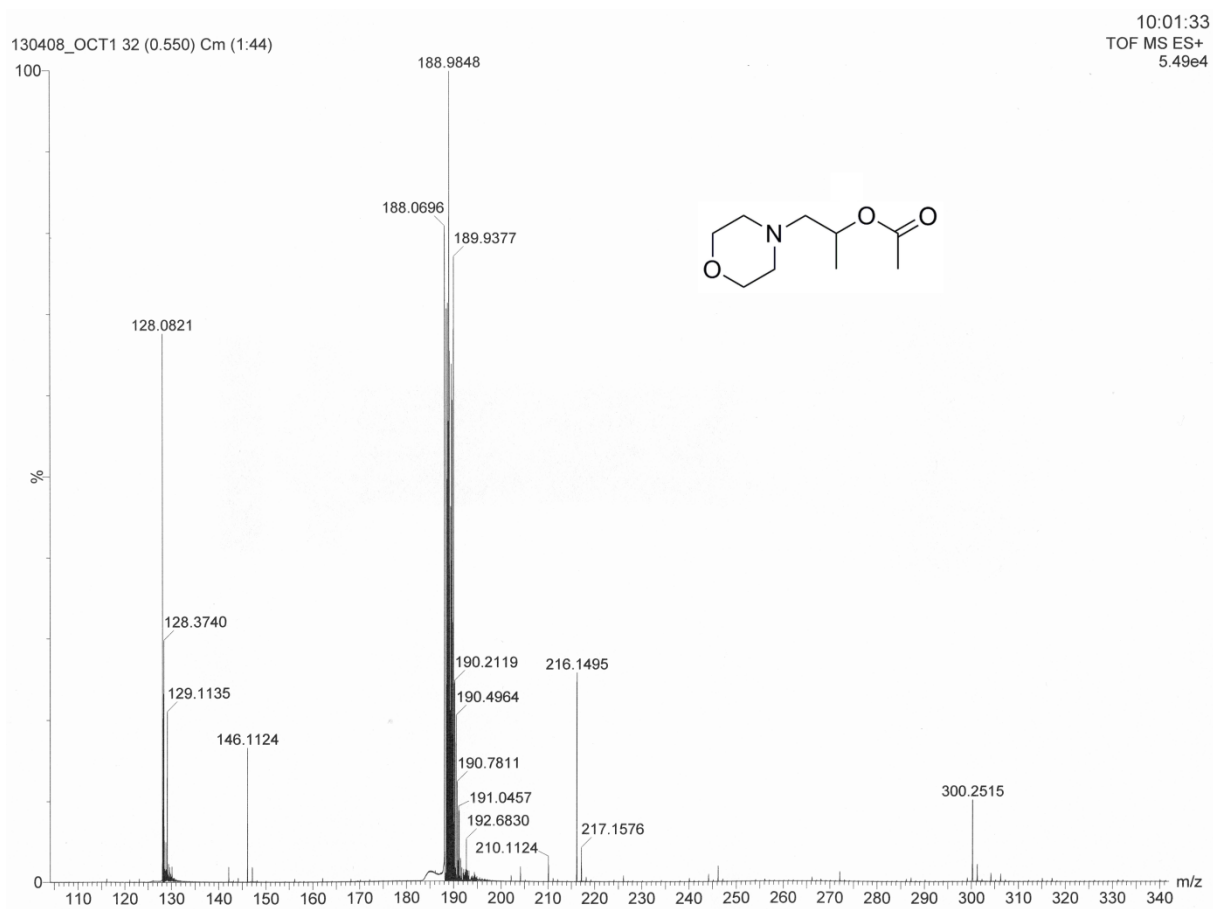
^1H NMR spectrum of *rac*-**4a** (400 MHz, CDCl_3)



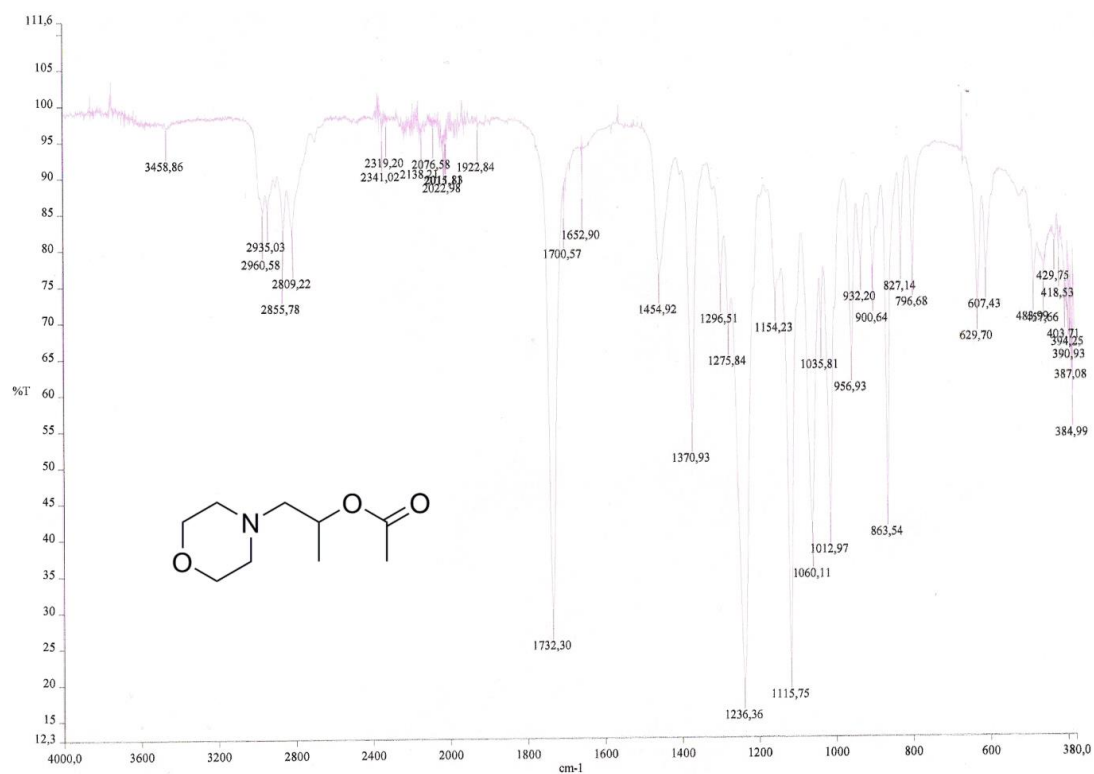
^{13}C NMR spectrum of *rac*-**4a** (100 MHz, CDCl_3)



MS spectrum of *rac*-**4a** (ESI-TOF)

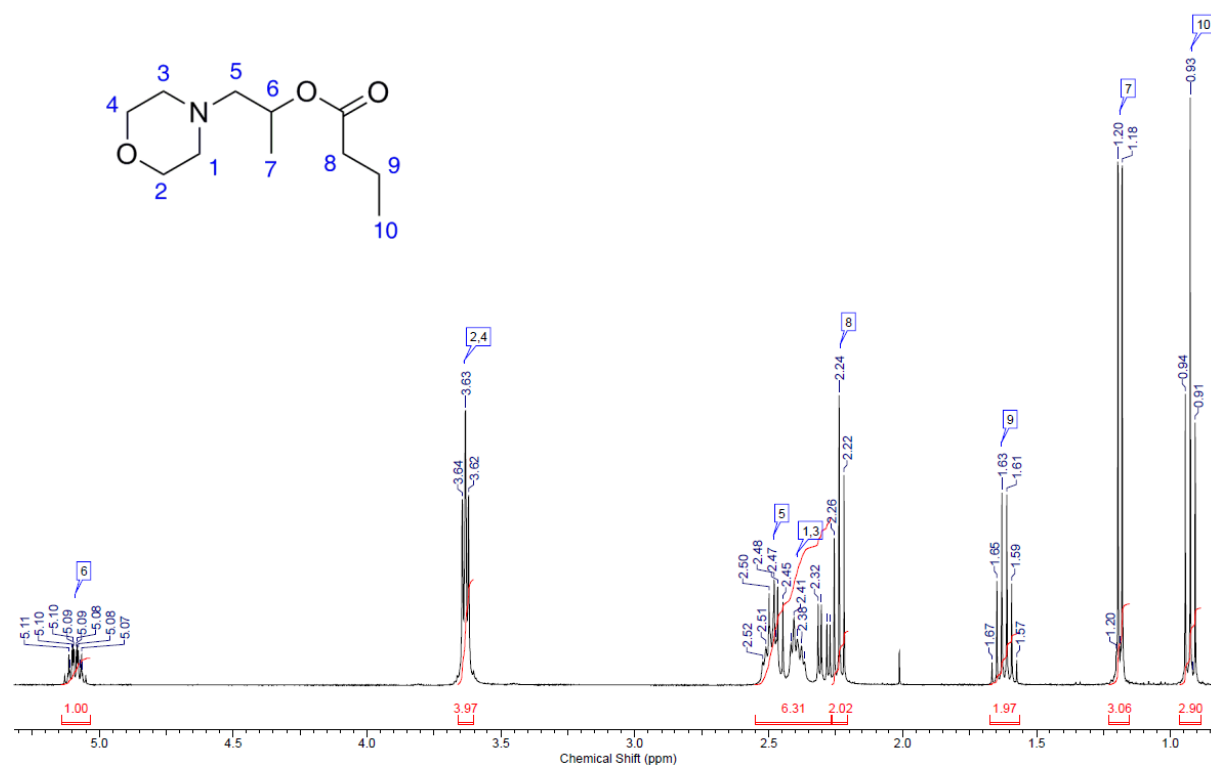


FT-IR spectrum of *rac*-**4a** (neat)

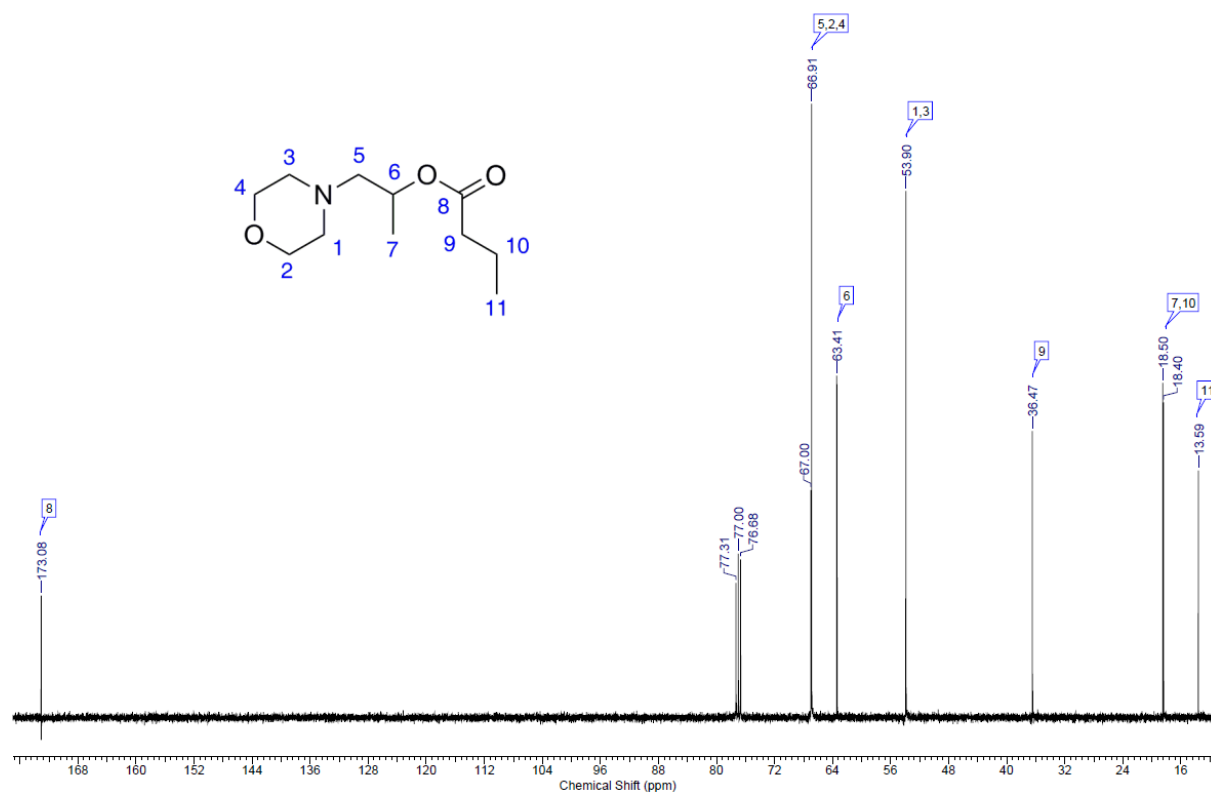


1-(Morpholin-4-yl)propan-2-yl butanoate (*rac*-4b**)**

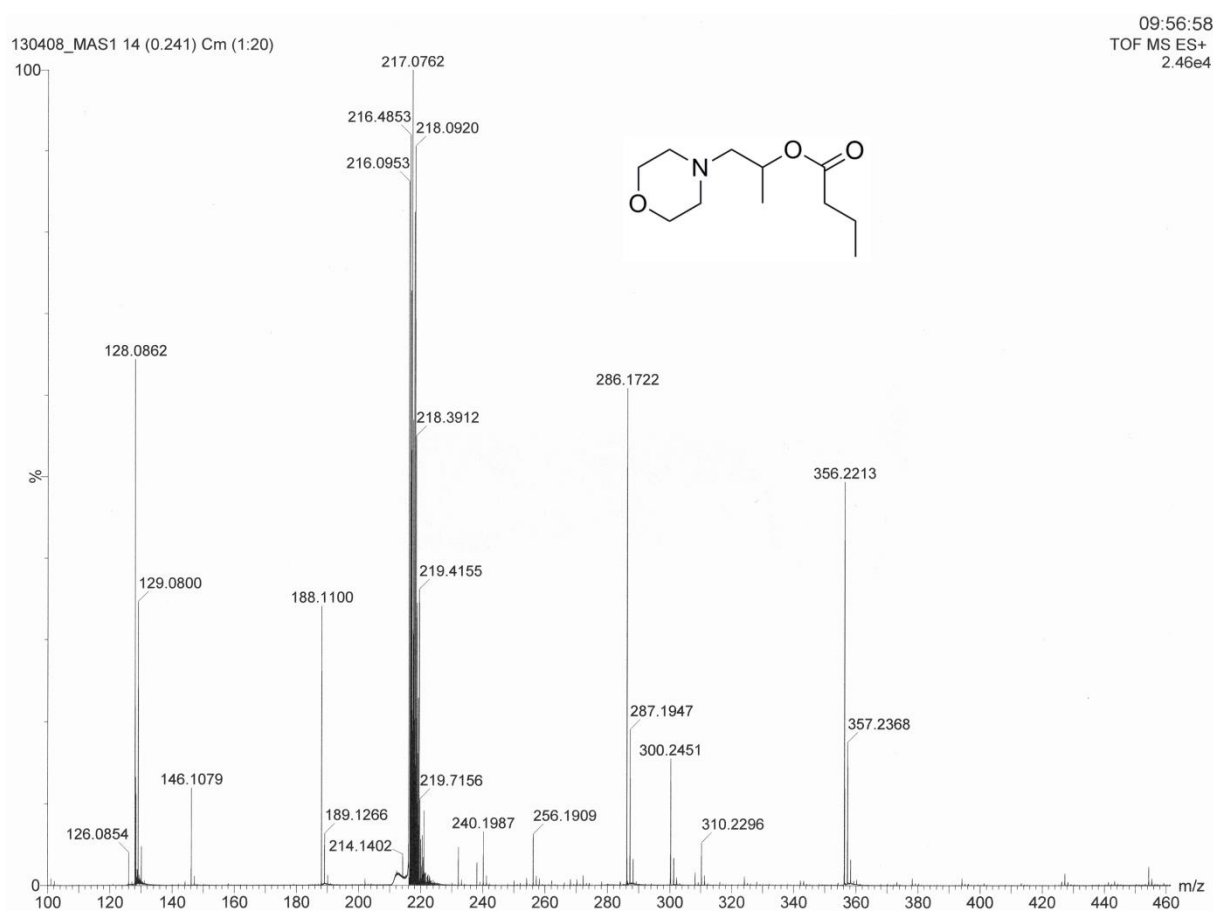
¹H NMR spectrum of *rac*-**4b** (400 MHz, CDCl₃)



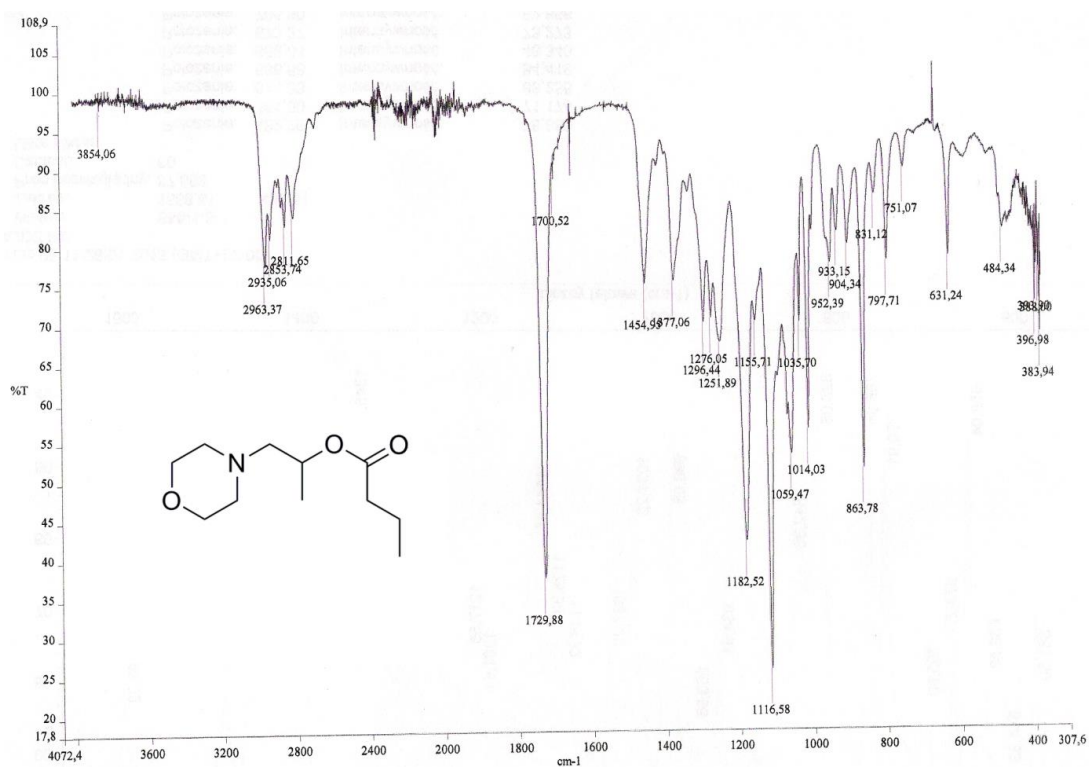
¹³C NMR spectrum of *rac*-**4b** (100 MHz, CDCl₃)



MS spectrum of *rac*-**4b** (ESI-TOF)

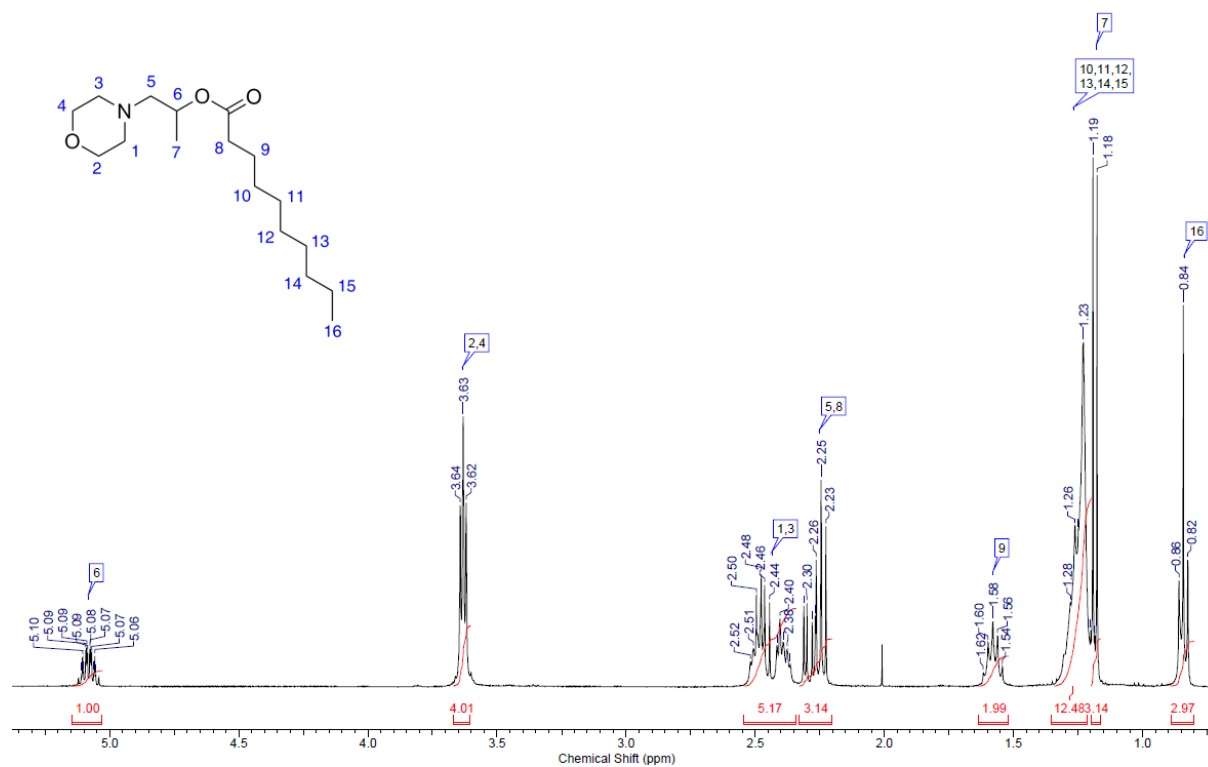


FT-IR spectrum of *rac*-**4b** (neat)

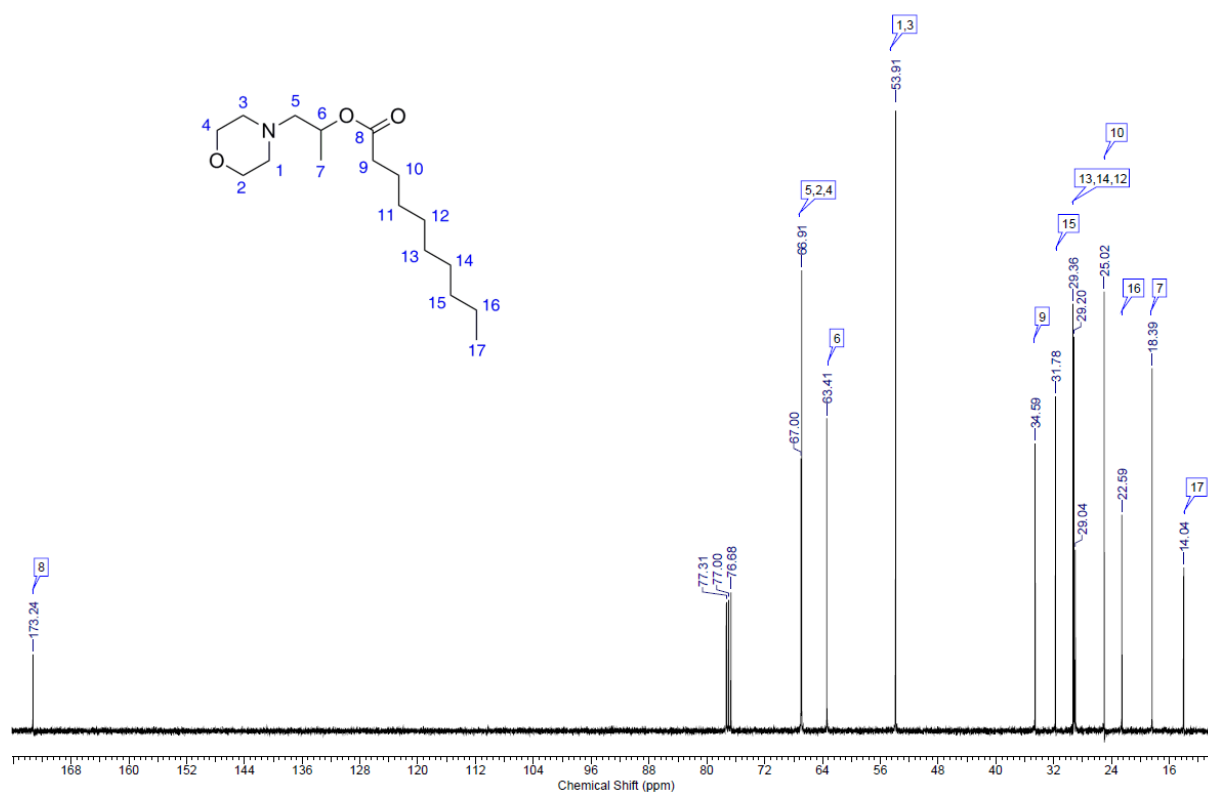


1-(Morpholin-4-yl)propan-2-yl decanoate (*rac*-**4c**)

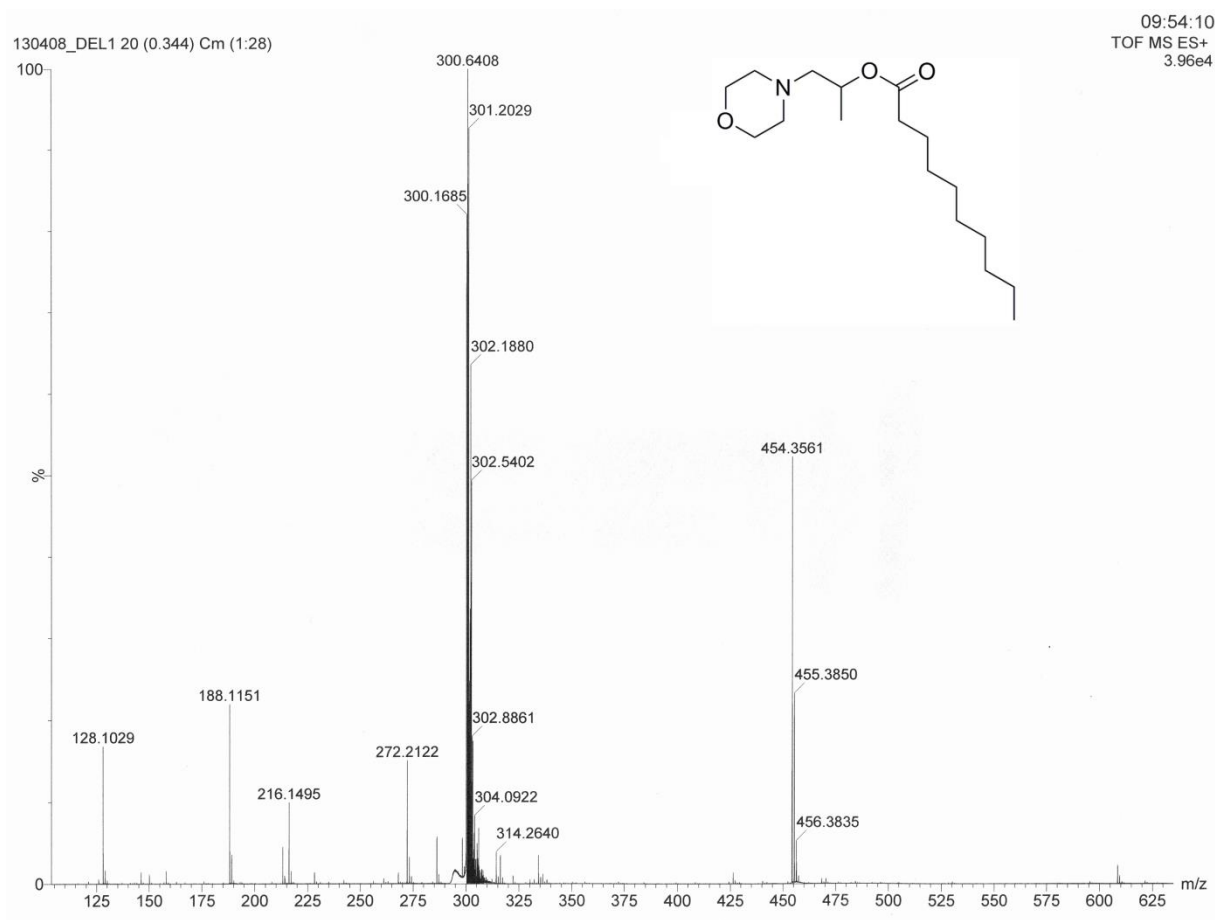
^1H NMR spectrum of *rac*-**4c** (400 MHz, CDCl_3)



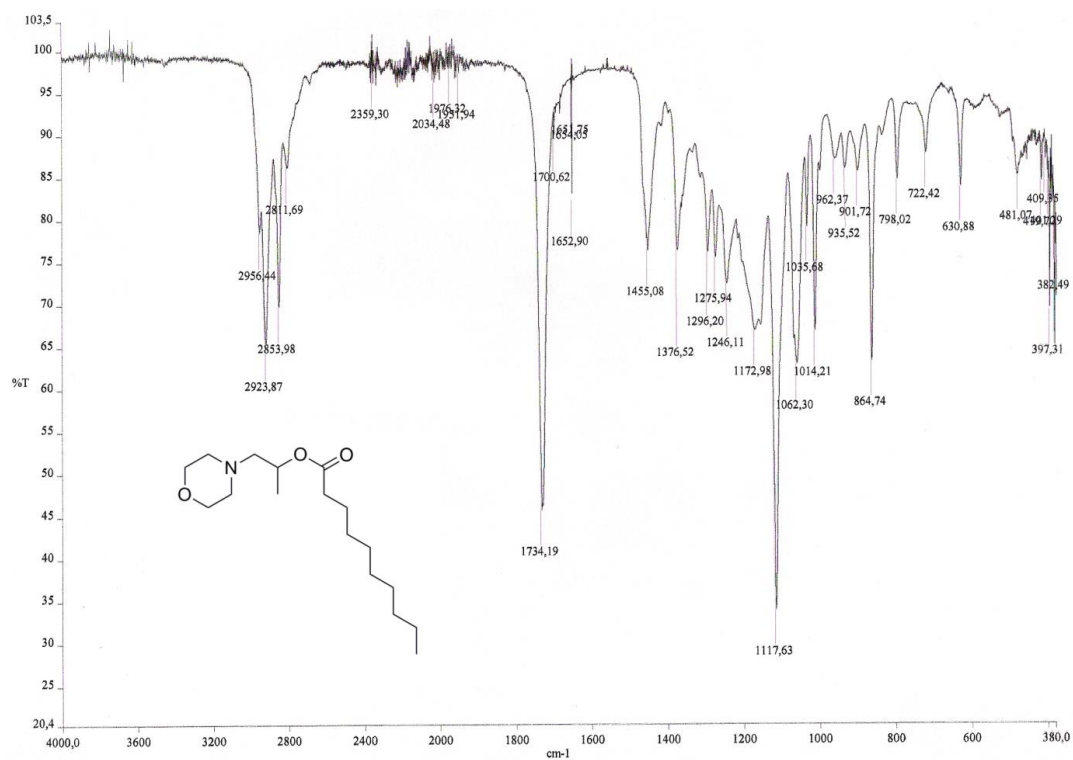
^{13}C NMR spectrum of *rac*-**4c** (100 MHz, CDCl_3)



MS spectrum of *rac*-**4c** (ESI-TOF)

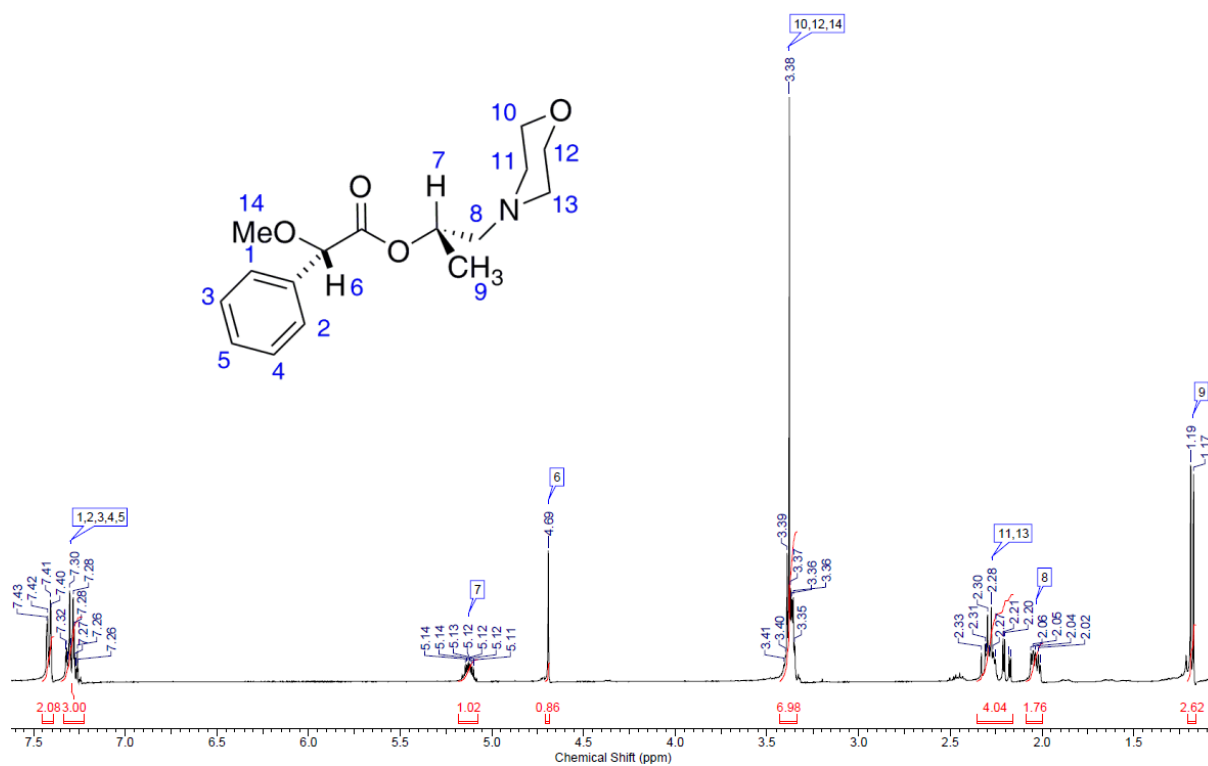


FT-IR spectrum of *rac*-**4c** (neat)

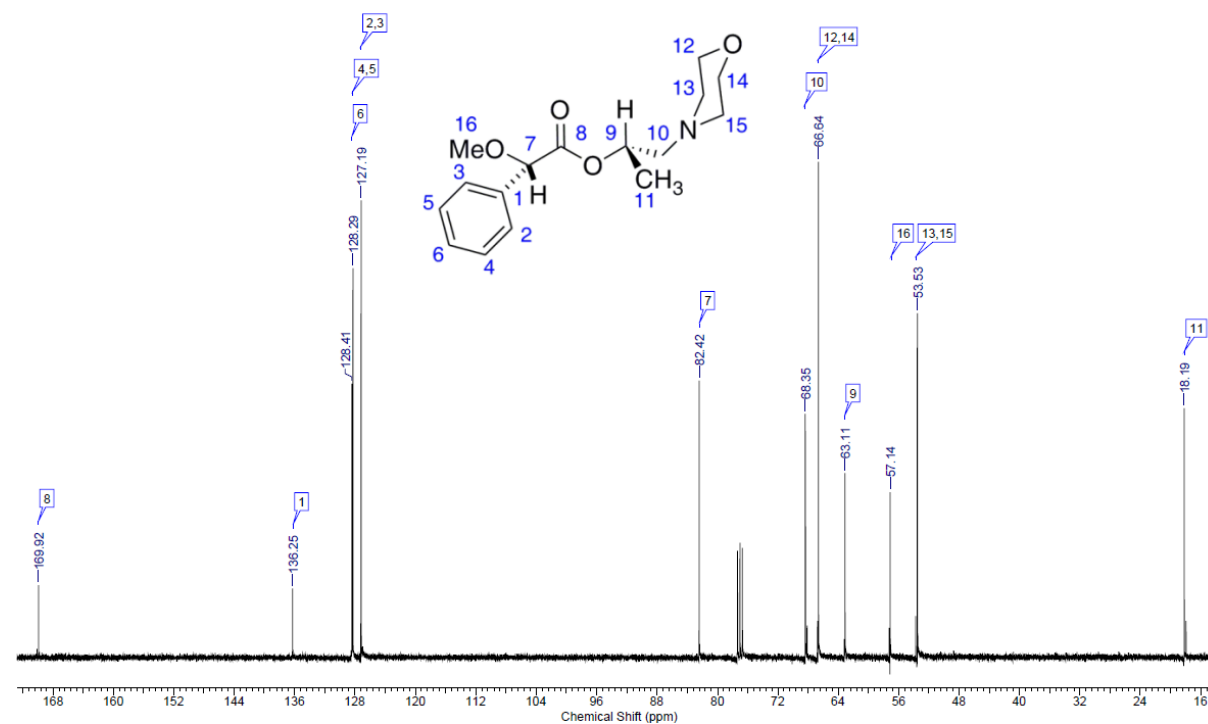


(2S)-1-(Morpholin-4-yl)propan-2-yl (2R)-methoxy(phenyl)acetate [(S)-(+)-3-(R)-MPA]

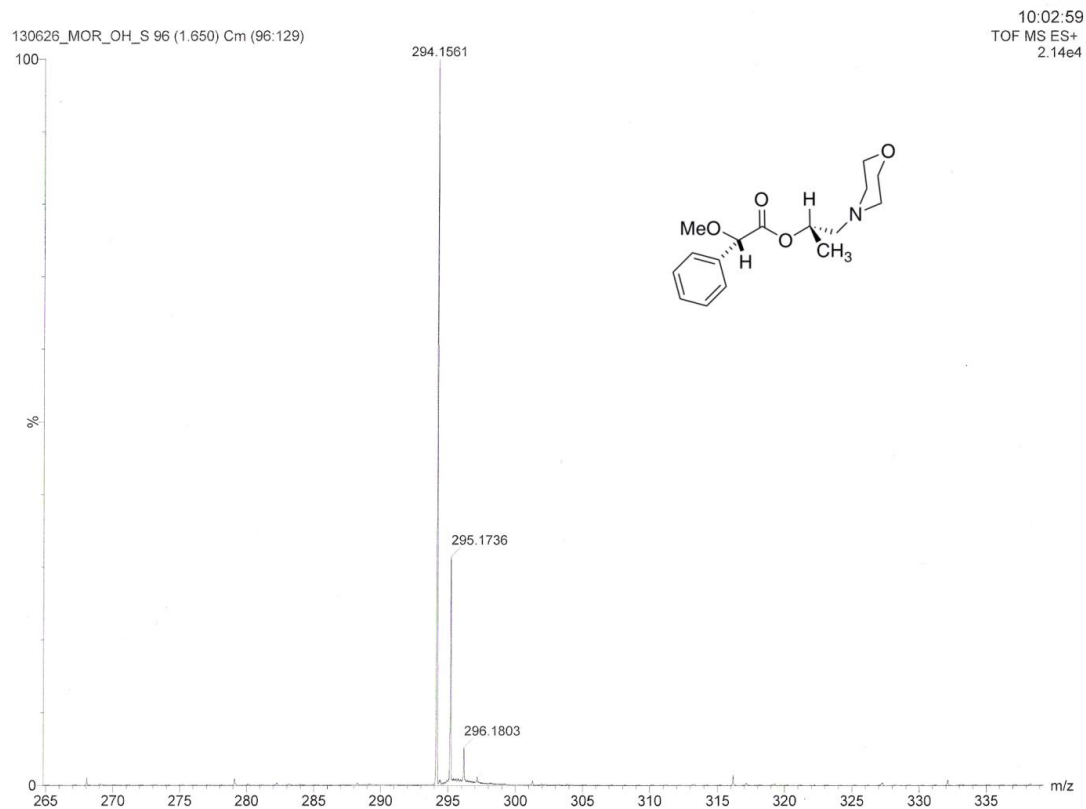
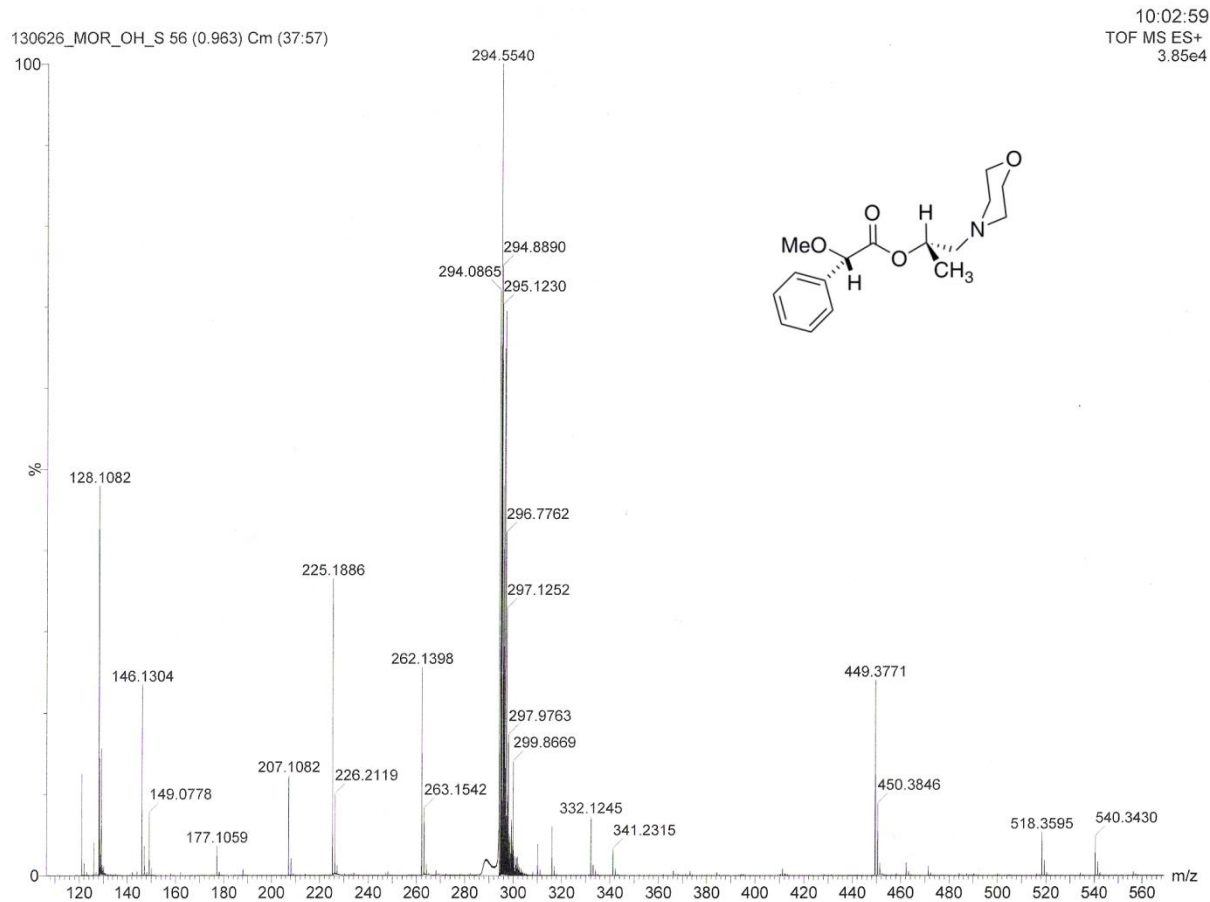
^1H NMR spectrum of (S)-(+)-3-(R)-MPA (400 MHz, CDCl_3)



^{13}C NMR spectrum of (S)-(+)-3-(R)-MPA (100 MHz, CDCl_3)

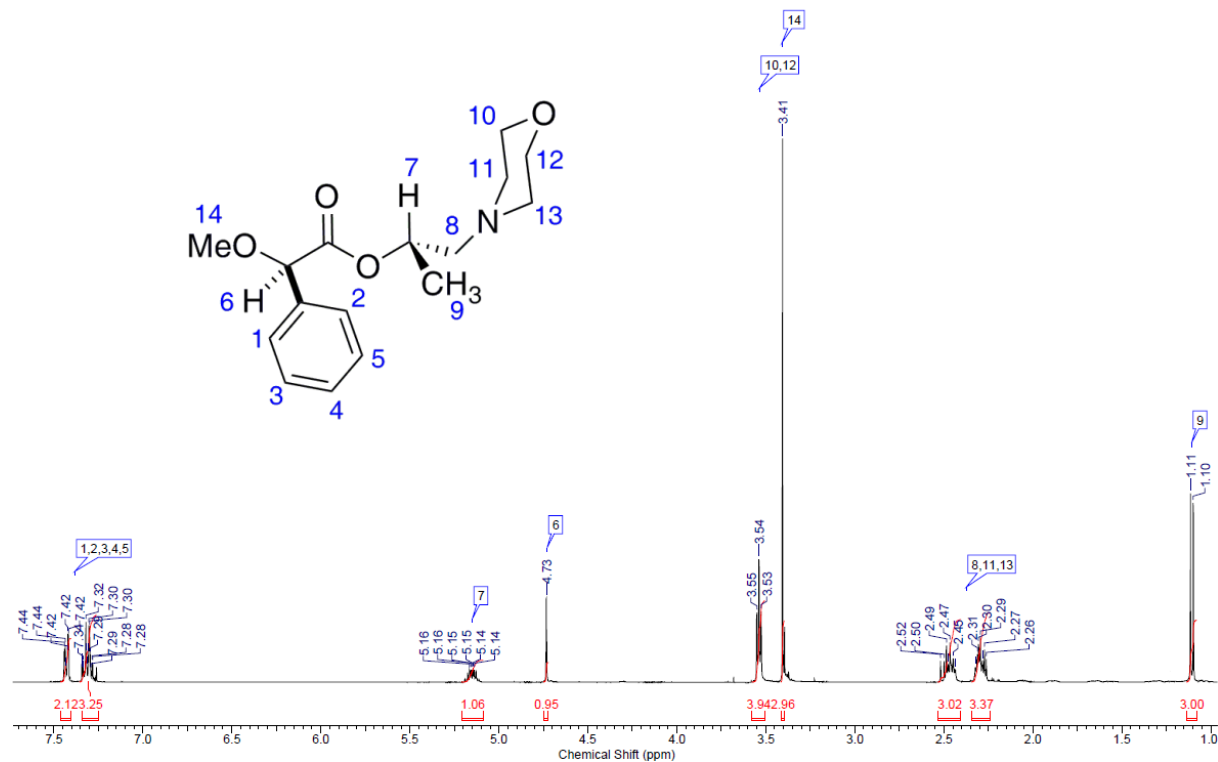


MS spectrum of (S)-(+)-3-(R)-MPA (ESI-TOF)

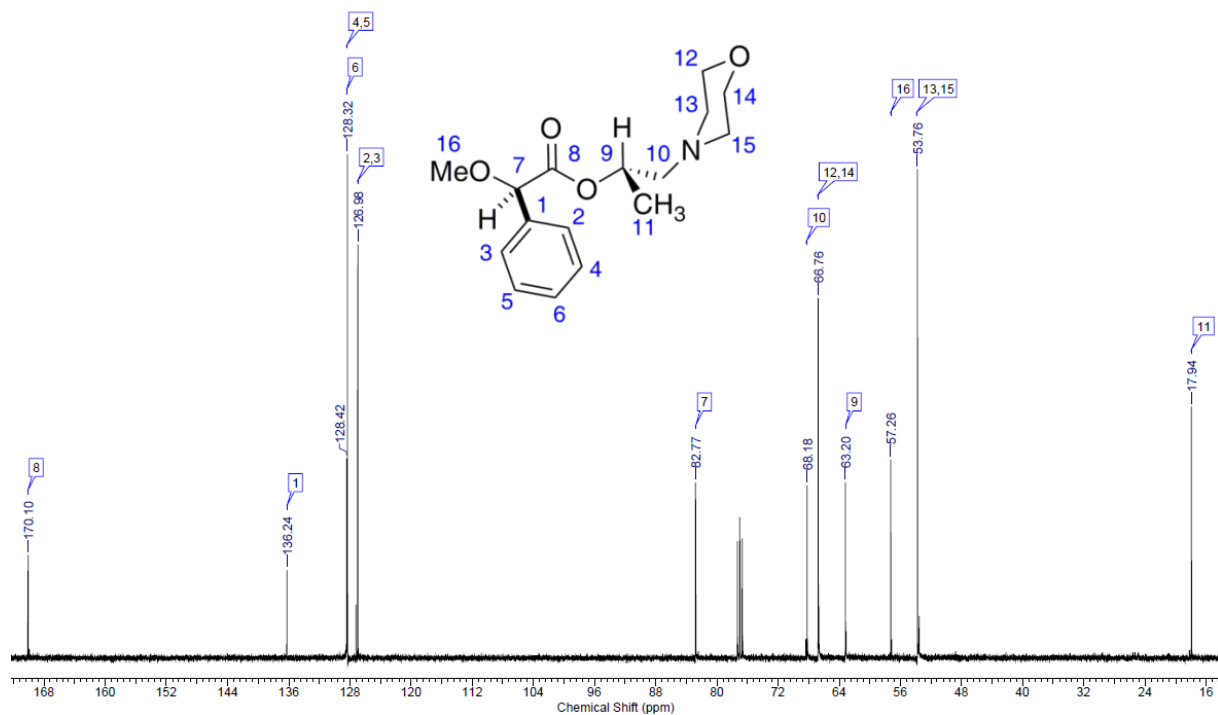


(2S)-1-(Morpholin-4-yl)propan-2-yl (2S)-methoxy(phenyl)acetate [(S)-(+)-3-(R)-MPA]

^1H NMR spectrum of (S)-(+)-3-(R)-MPA (400 MHz, CDCl_3)



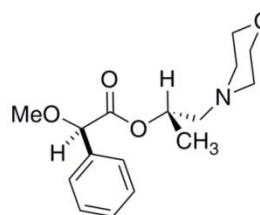
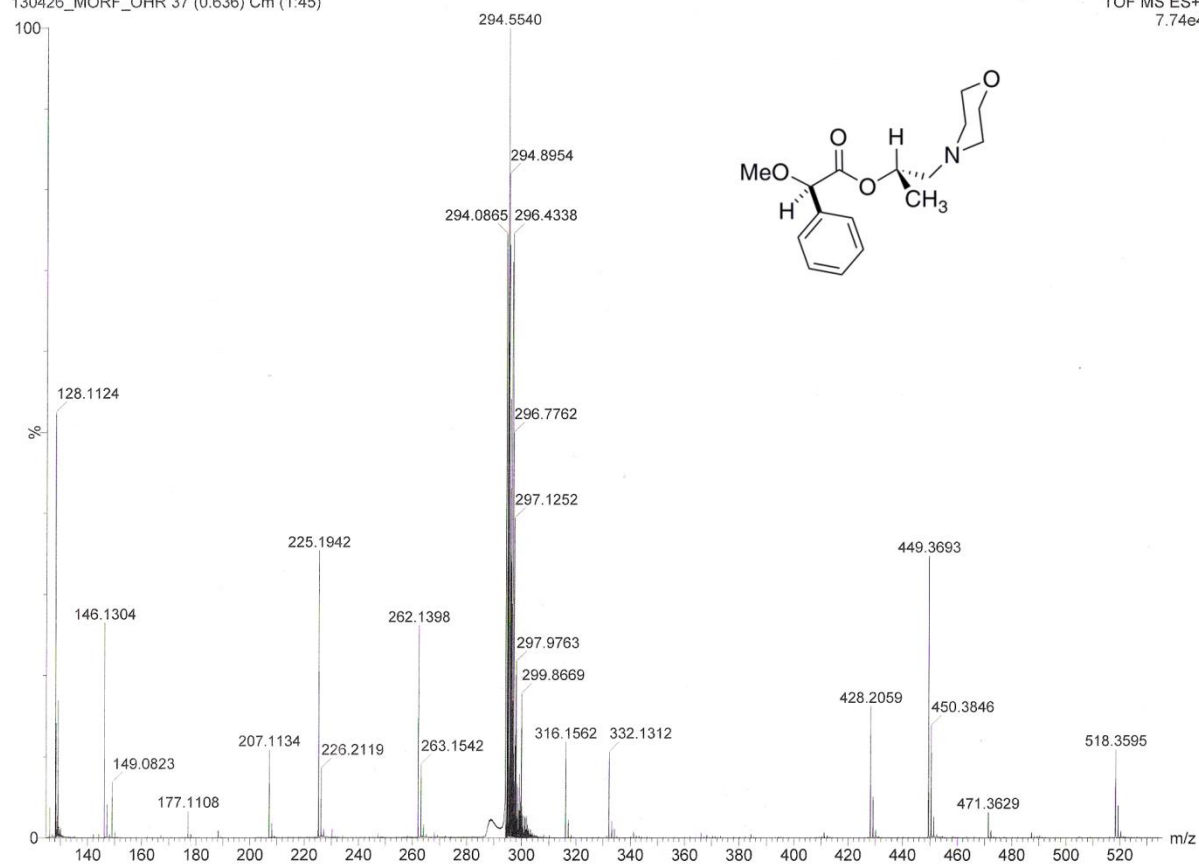
^{13}C NMR spectrum of (S)-(+)-3-(R)-MPA (100 MHz, CDCl_3)



MS spectrum of (S)-(+)-3-(R)-MPA (ESI-TOF)

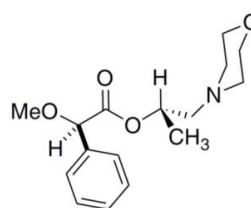
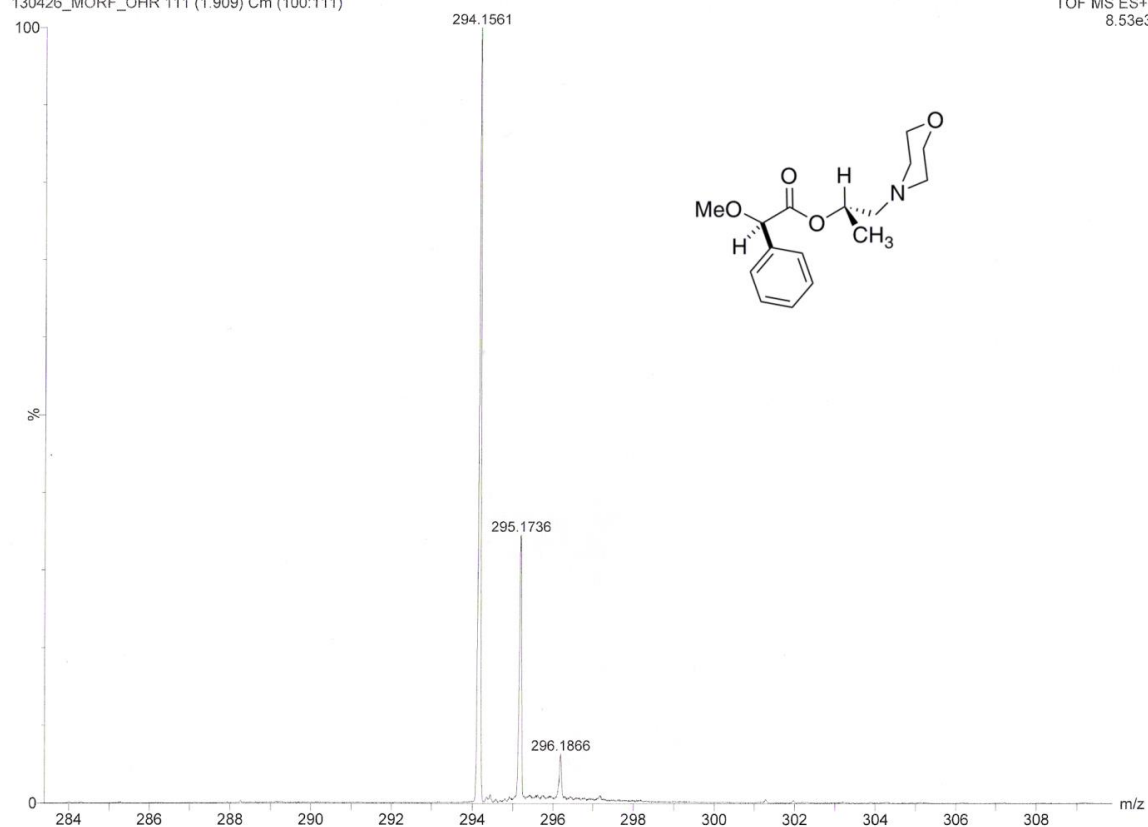
130426_MORF_OHR 37 (0.636) Cm (1.45)

10:19:04
TOF MS ES+
7.74e4



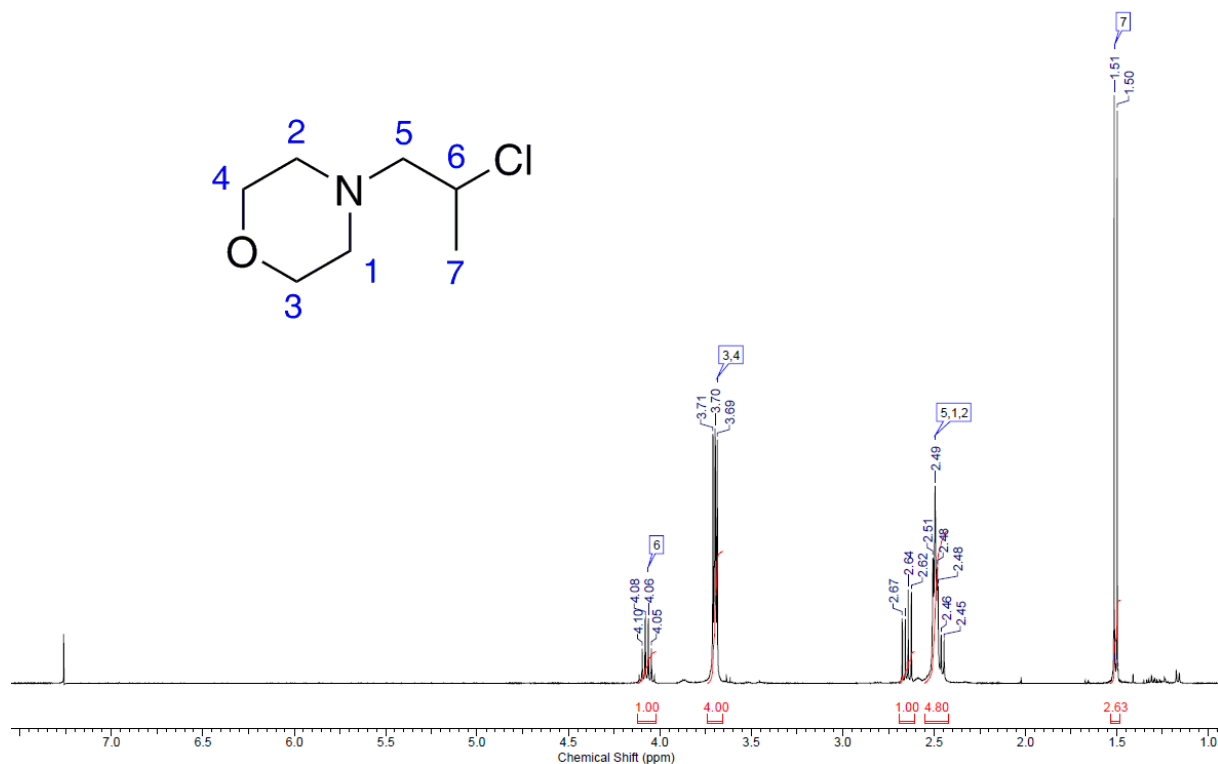
130426_MORF_OHR 111 (1.909) Cm (100:111)

10:19:04
TOF MS ES+
8.53e3

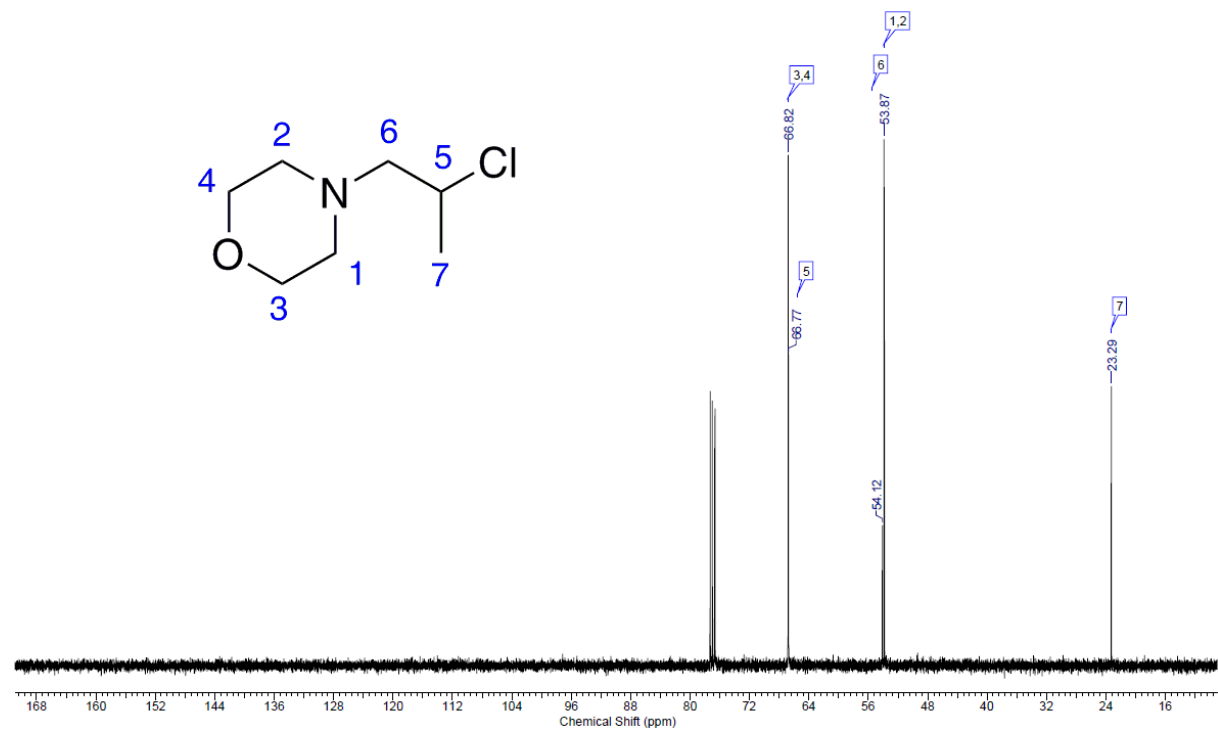


4-(2-Chloropropyl)morpholine (*rac*-**5**)

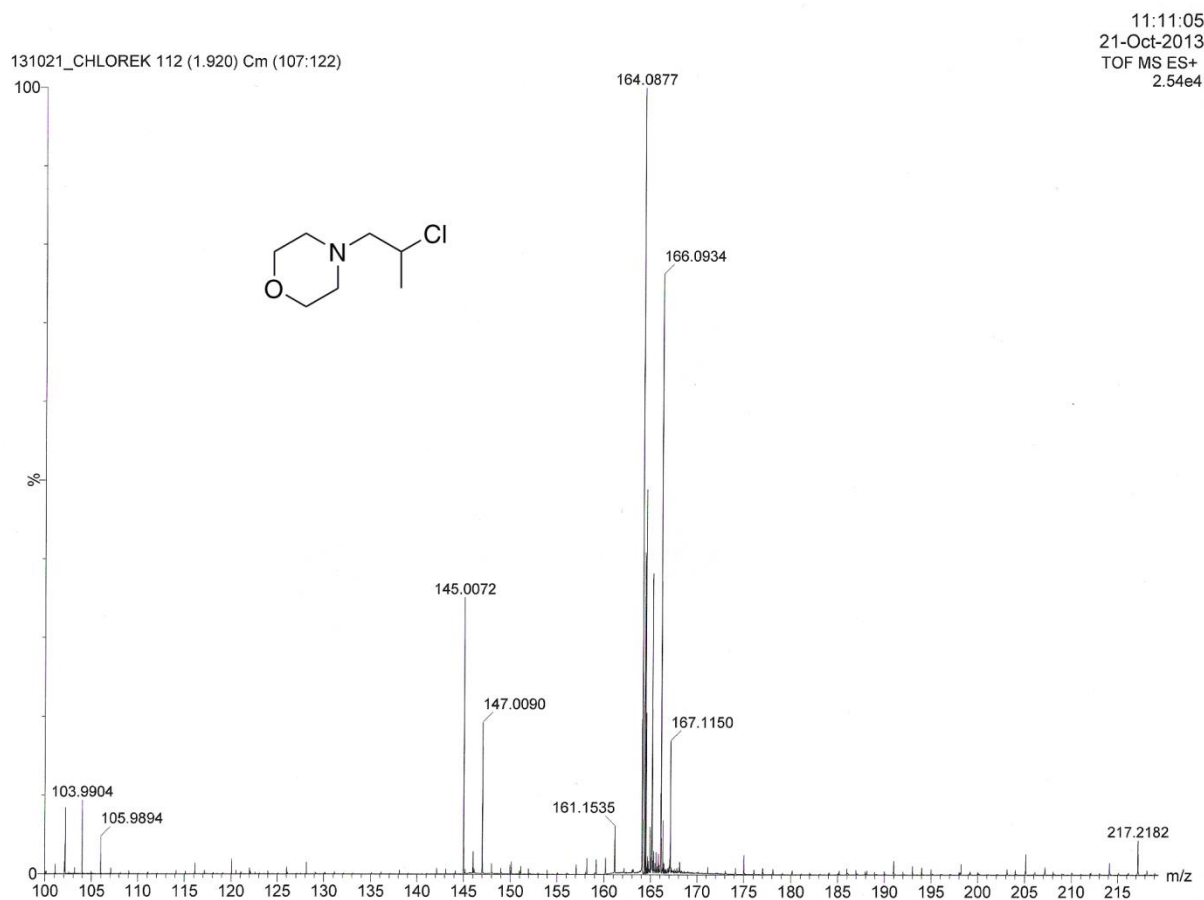
^1H NMR spectrum of *rac*-**5** (400 MHz, CDCl_3)



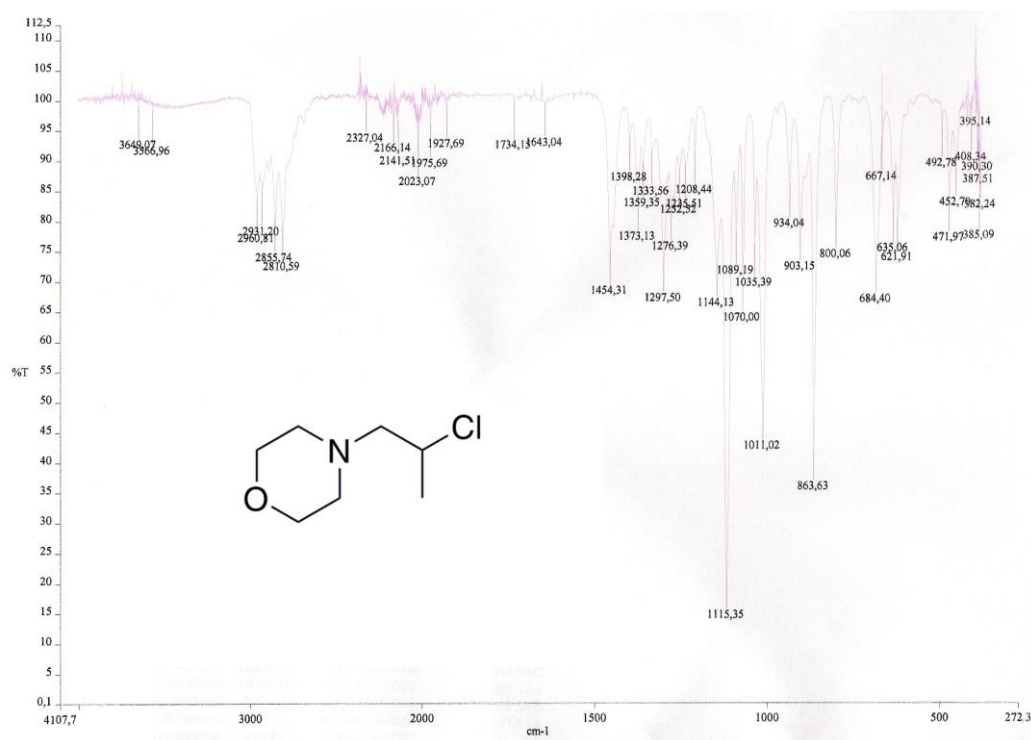
^{13}C NMR spectrum of *rac*-**5** (100 MHz, CDCl_3)



MS spectrum of *rac*-**5** (ESI-TOF)

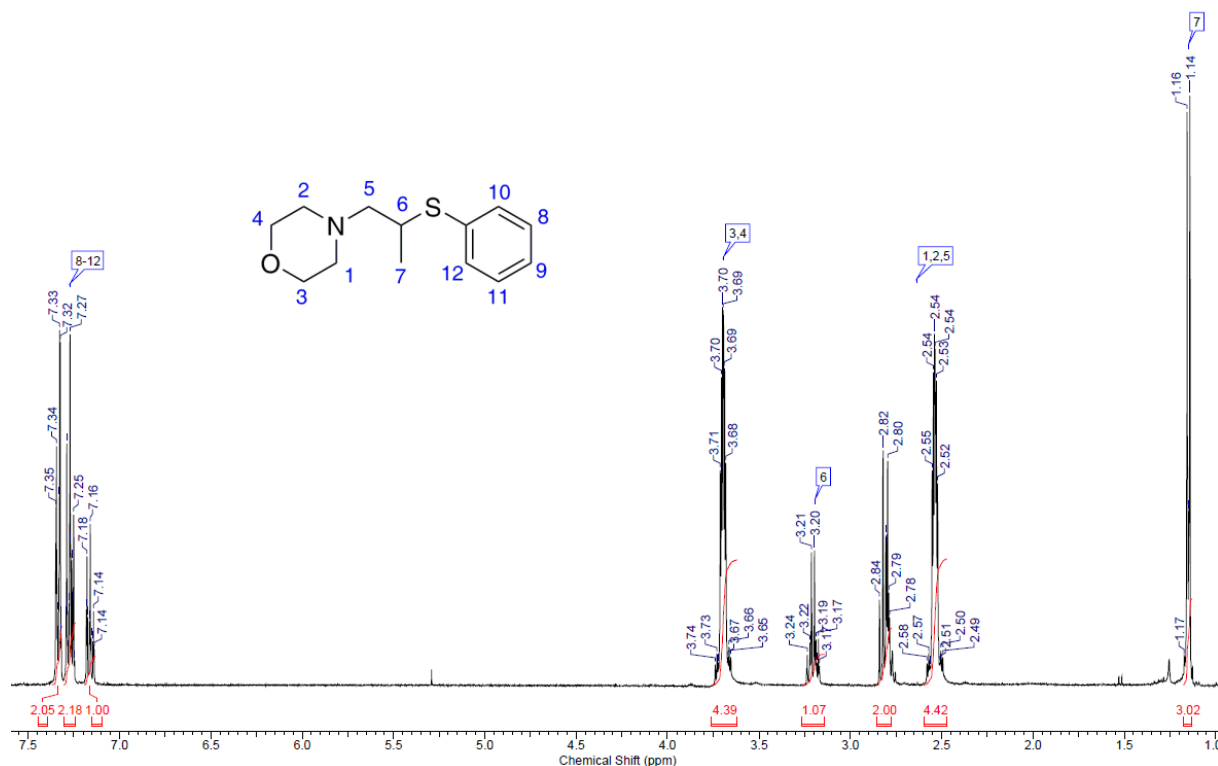


FT-IR spectrum of *rac*-**5** (neat)

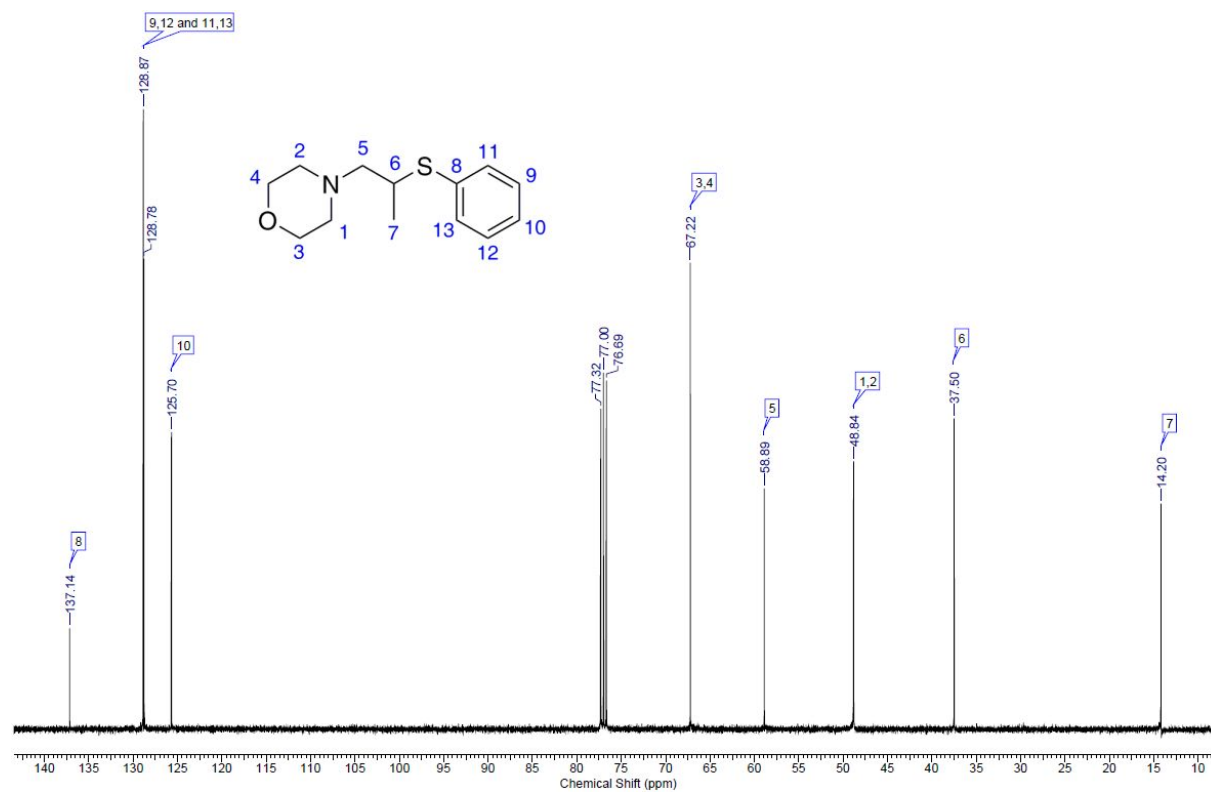


4-[2-(Phenylsulfanyl)propyl]morpholine (*rac*-5-SPh)

^1H NMR spectrum of *rac*-5-SPh (400 MHz, CDCl_3)



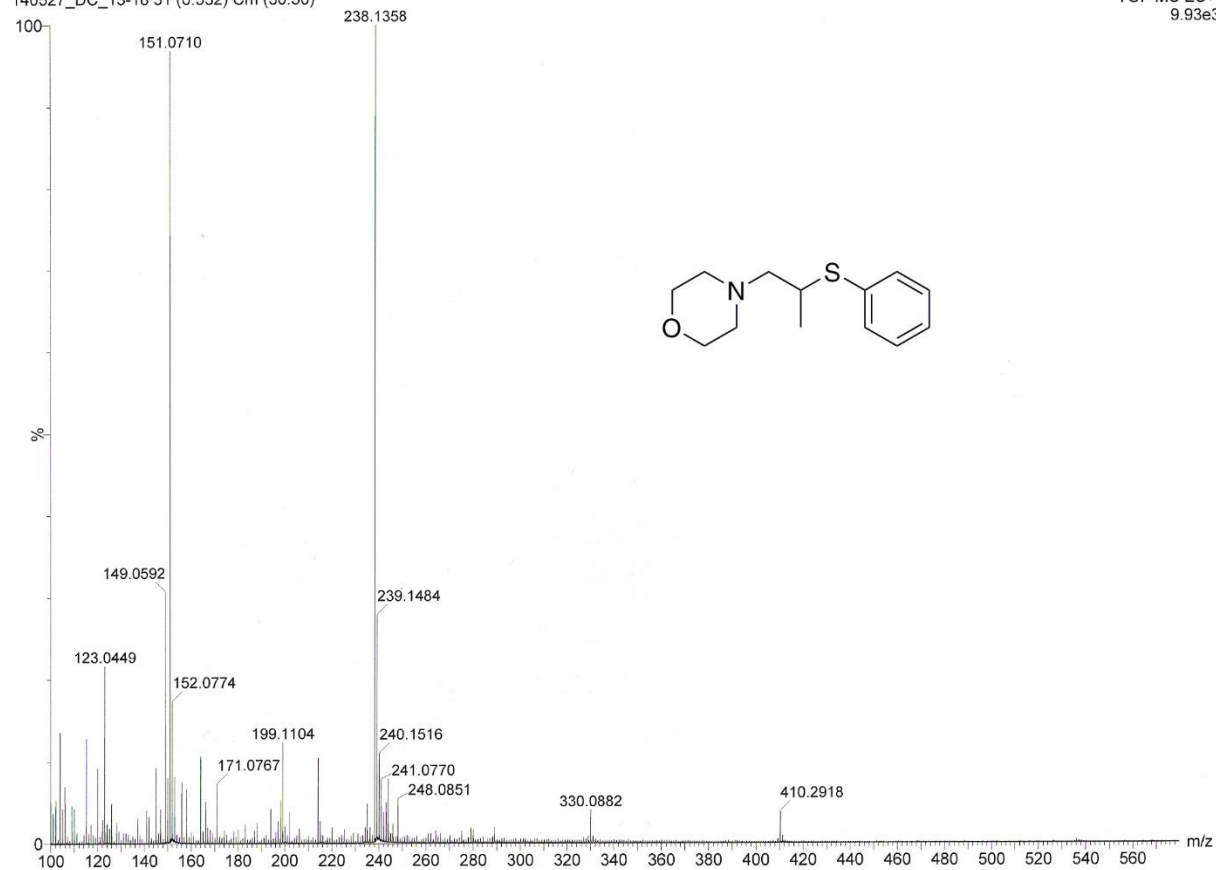
^{13}C NMR spectrum of *rac*-5-SPh (100 MHz, CDCl_3)



MS spectrum of *rac*-**5-SPh** (ESI-TOF)

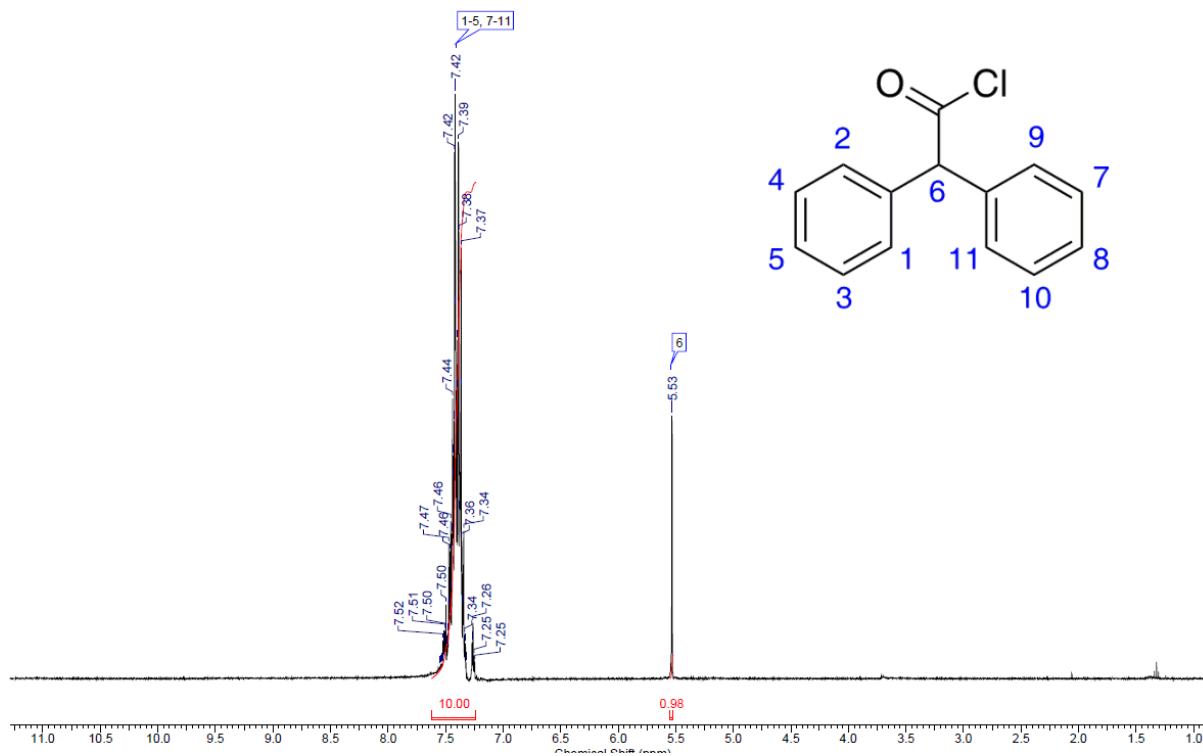
140527_DC_13-18 31 (0.532) Cm (30:50)

TOF MS ES+
9.93e3

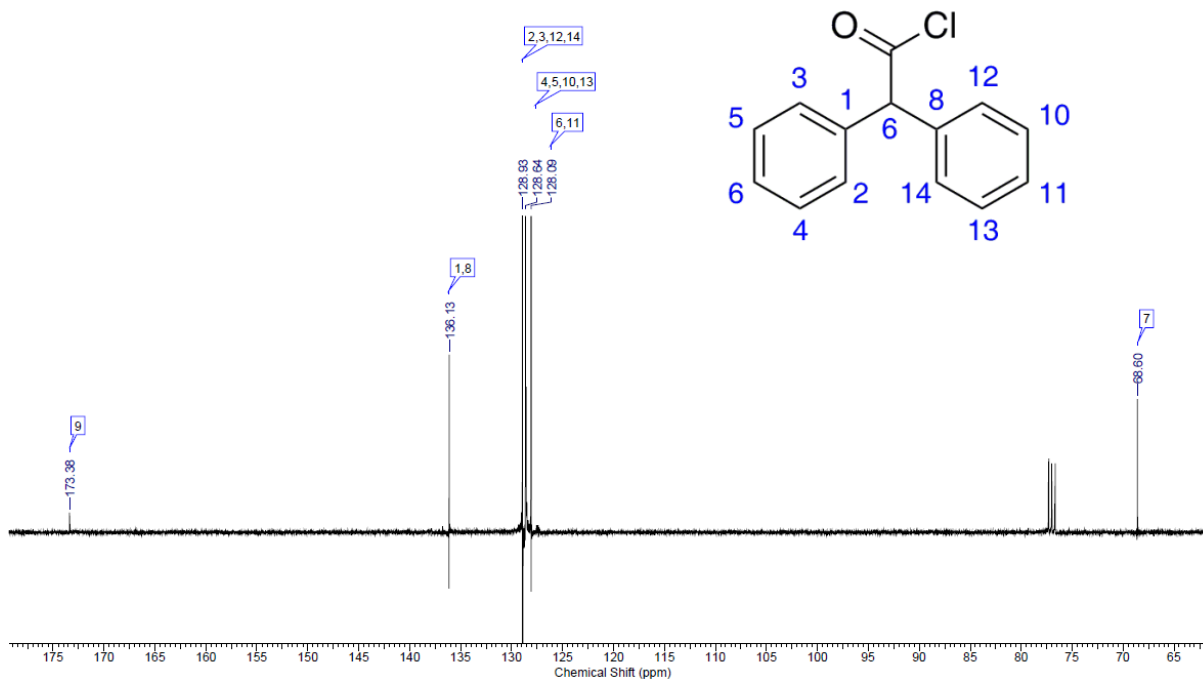


Diphenylacetic acid chloride (**8**)

^1H NMR spectrum of **8** (400 MHz, CDCl_3)

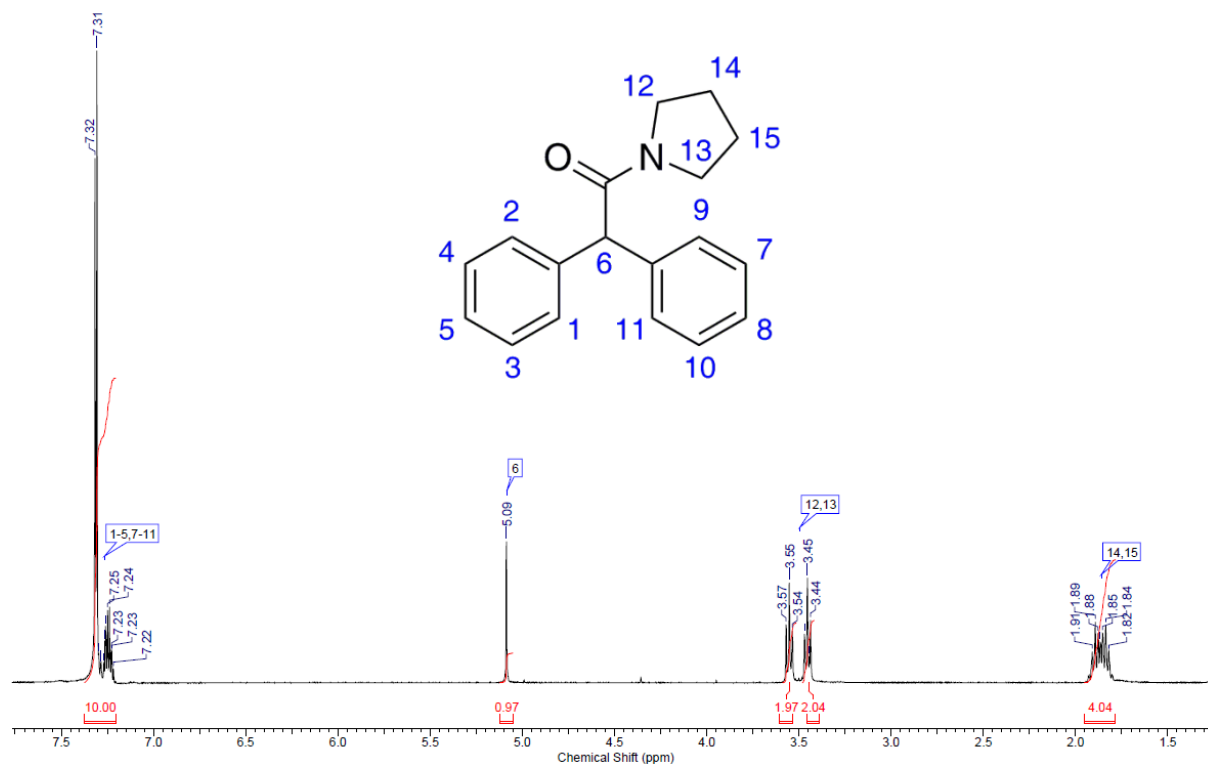


^{13}C NMR spectrum of **8** (100 MHz, CDCl_3)

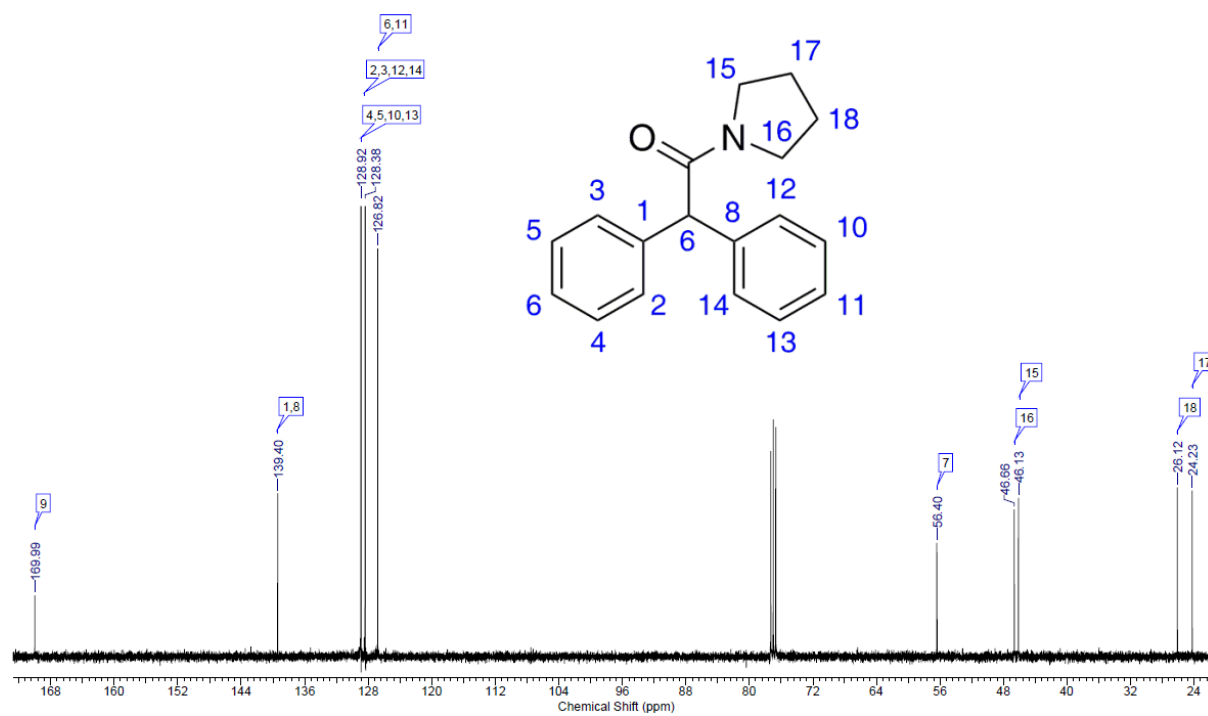


N-diphenylacetyl-1-pyrrolidine (**9**)

^1H NMR spectrum of **9** (400 MHz, CDCl_3)

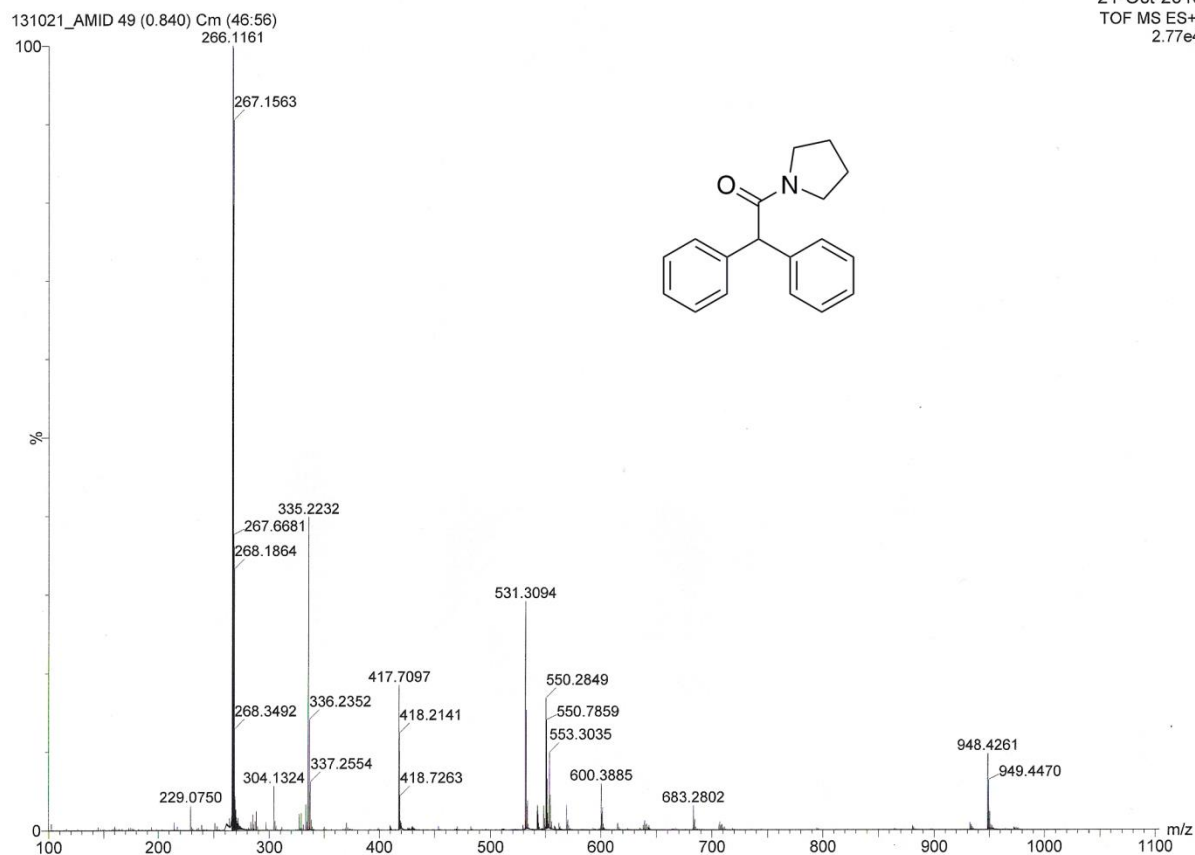


^{13}C NMR spectrum of **9** (100 MHz, CDCl_3)

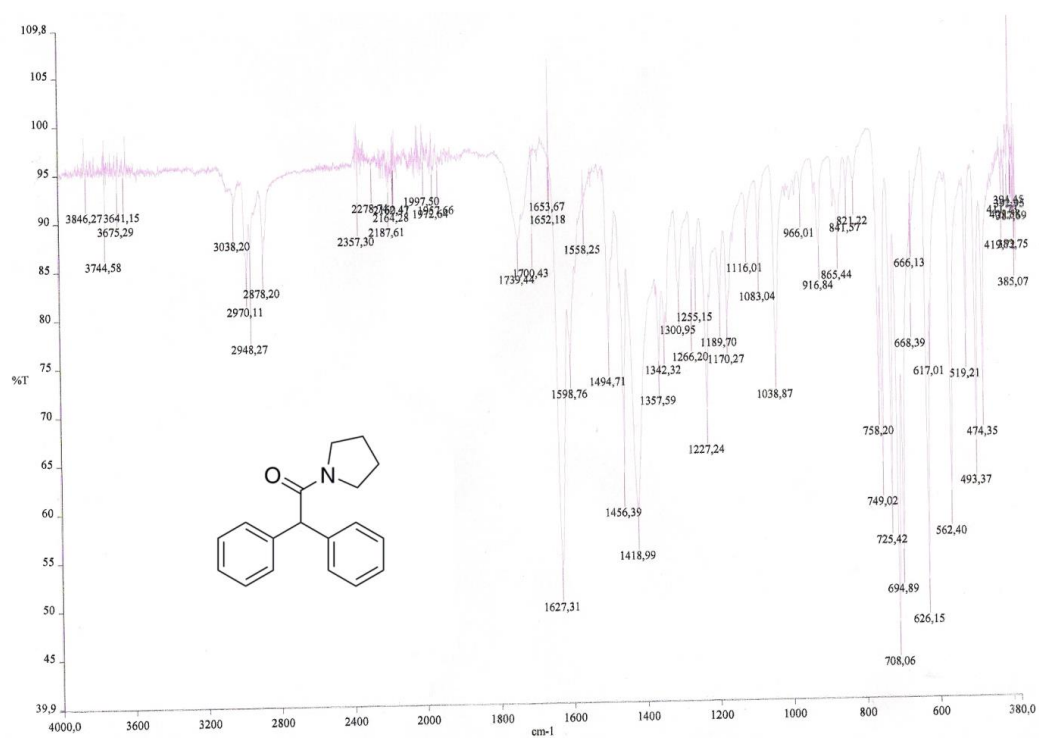


MS spectrum of **9** (ESI-TOF)

11:01:33
21-Oct-2013
TOF MS ES+
2.77e4

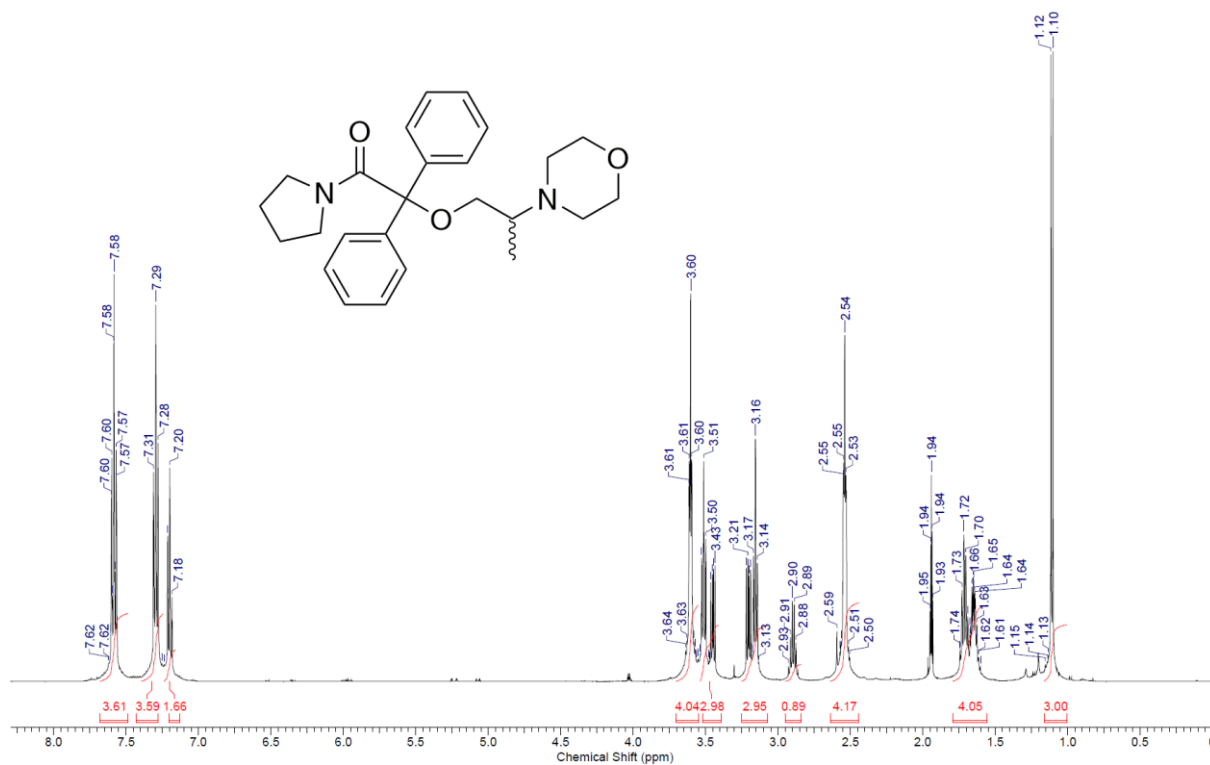


FT-IR spectrum of **9** (neat)

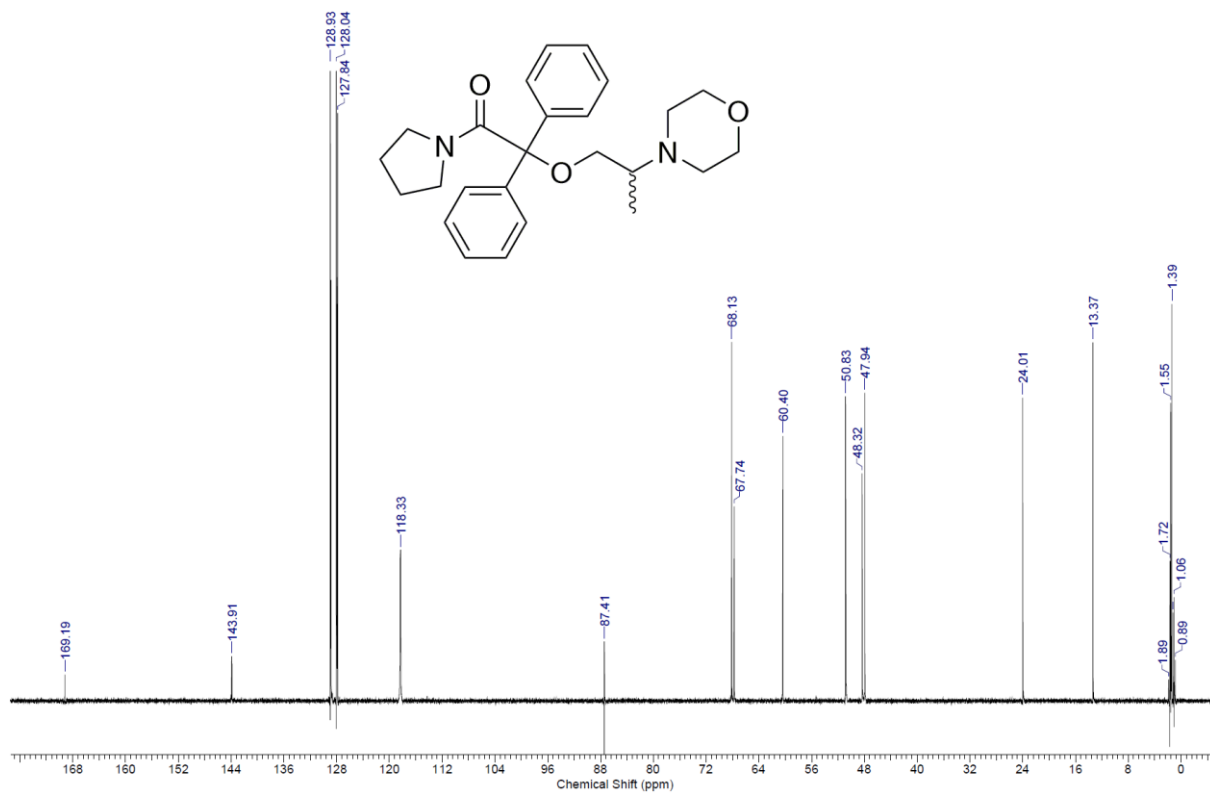


2-[2-(Morpholin-4-yl)propoxy]-2,2-diphenyl-1-(pyrrolidin-1-yl)ethan-1-one (*rac*-10**)**

^1H NMR spectrum of *rac*-**10** (500 MHz, CD_3CN)



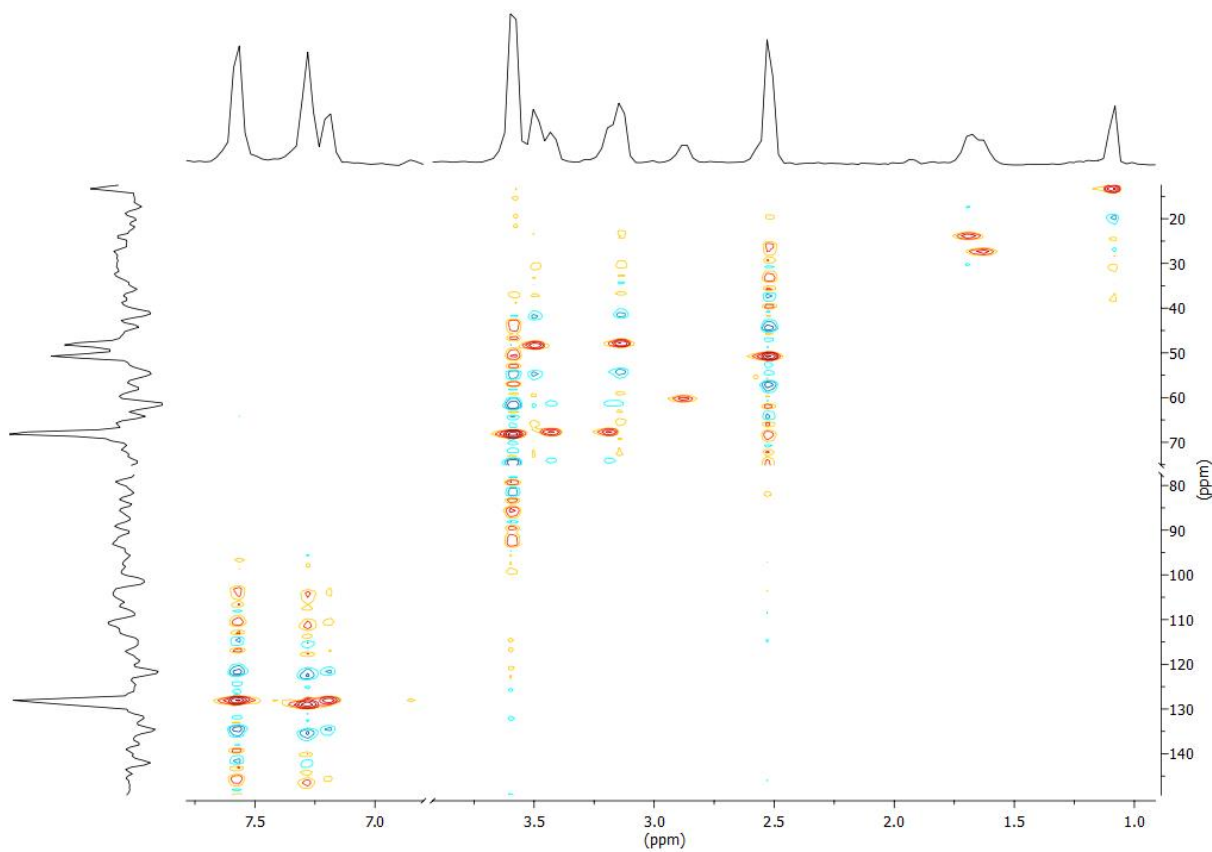
^{13}C NMR spectrum of *rac*-**10** (126 MHz, CD_3CN)

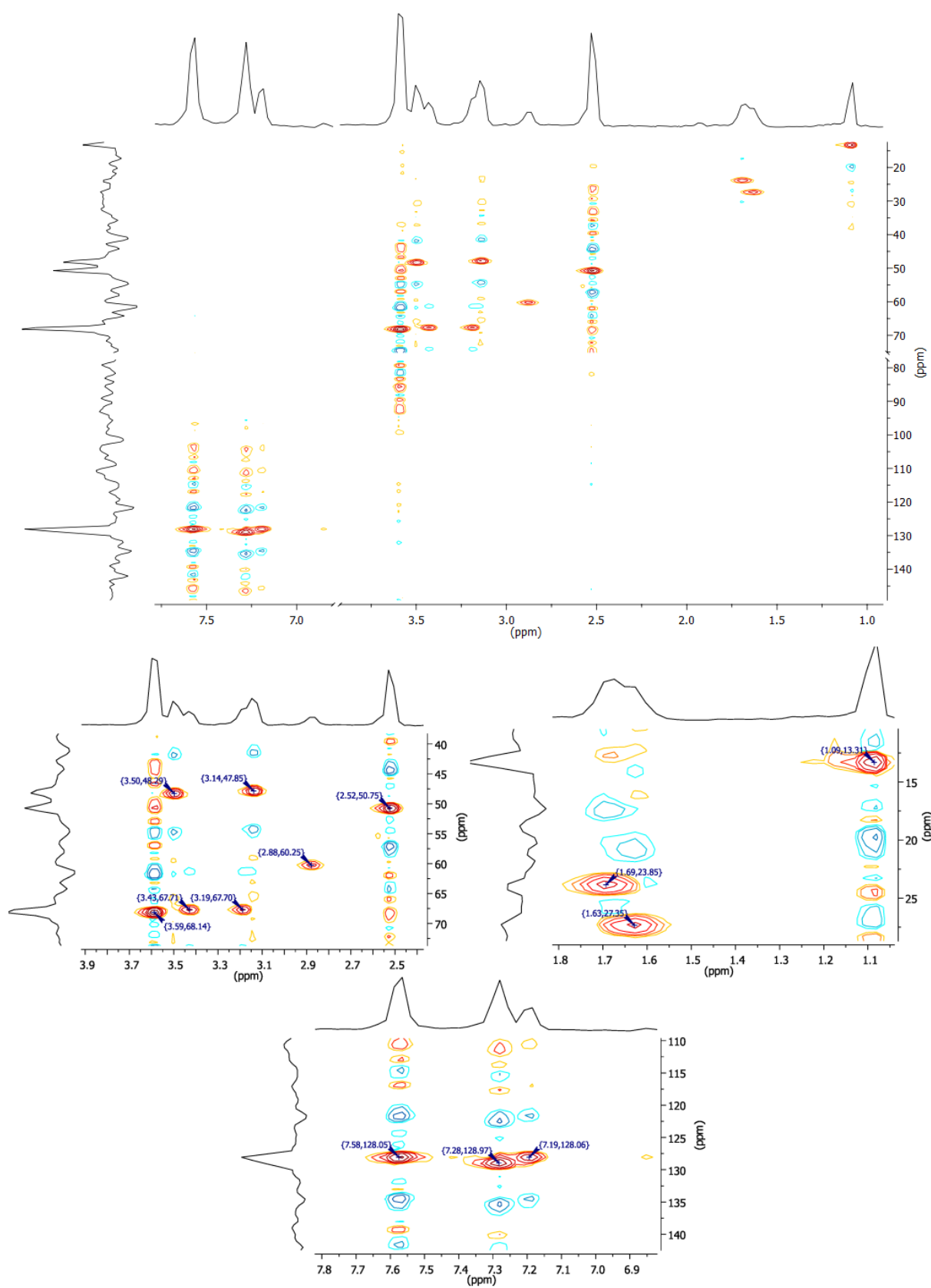


^{13}C DEPT-135 NMR spectrum of *rac*-**10** (126 MHz, CD_3CN)

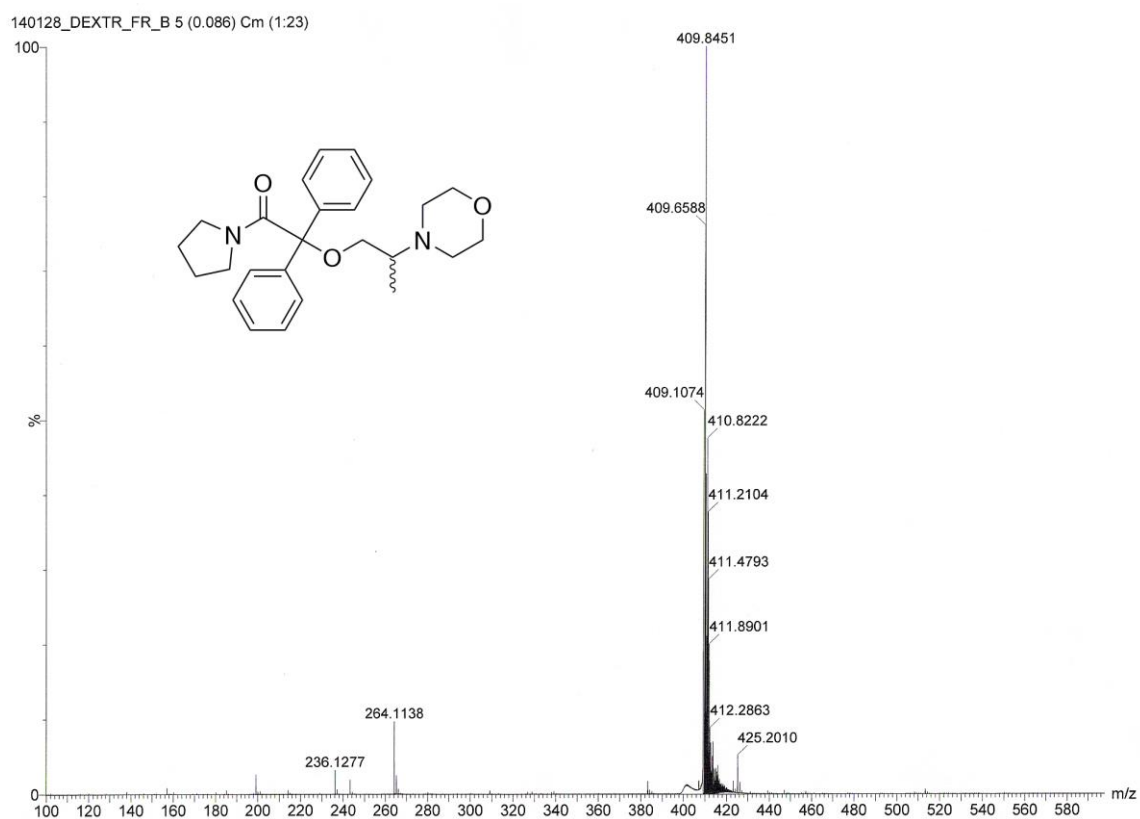


2D NMR (HSQC) spectrum of *rac*-**10** (126 MHz, CD_3CN)

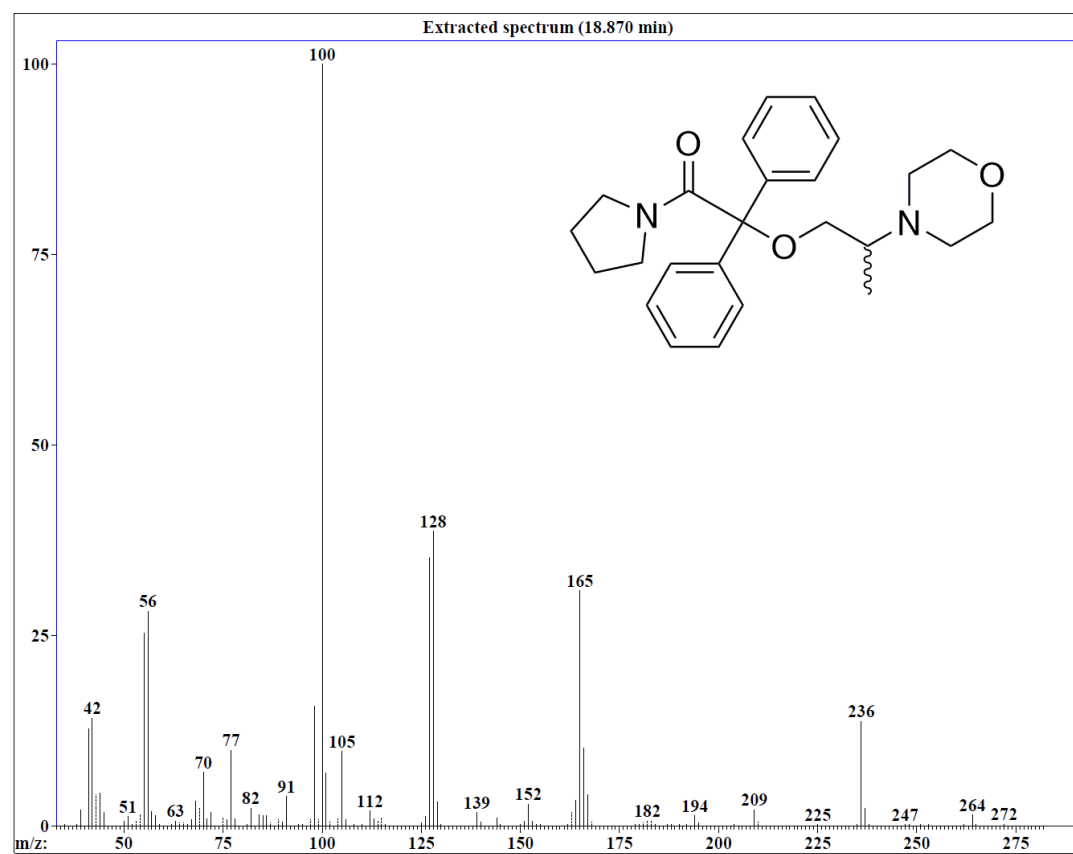




MS spectrum of *rac*-**10** (ESI-TOF)



GC-MS spectrum of *rac*-**10** (EI)



FT-IR spectrum of *rac*-**10** (neat)

