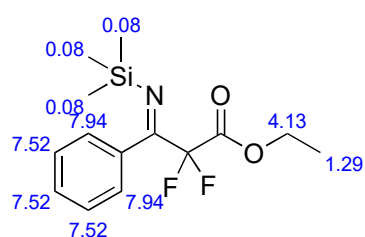
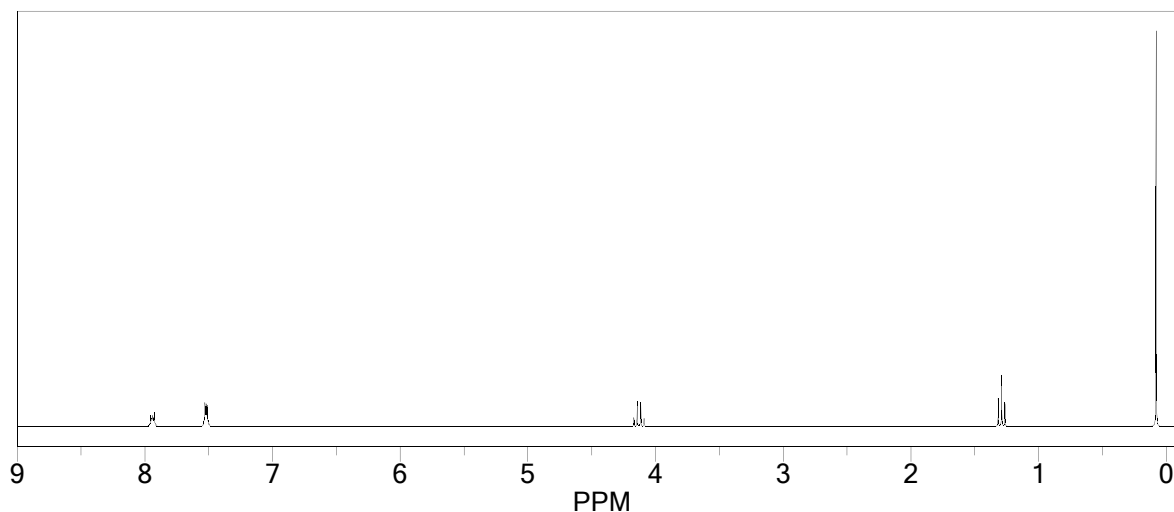


# ChemNMR <sup>1</sup>H Estimation



Estimation quality is indicated by color: **good**, **medium**, **rough**



Protocol of the H-1 NMR Prediction:

Node	Shift	Base + Inc.	Comment (ppm rel. to TMS)
CH	7.94	7.62	benzylidenimin
		?	1 unknown substituent(s)
		0.32	general corrections
CH	7.94	7.62	benzylidenimin
		?	1 unknown substituent(s)
		0.32	general corrections
CH	7.52	7.29	benzylidenimin
		?	1 unknown substituent(s)
		0.23	general corrections
CH	7.52	7.29	benzylidenimin
		?	1 unknown substituent(s)
		0.23	general corrections
CH	7.52	7.29	benzylidenimin
		?	1 unknown substituent(s)
		0.23	general corrections
CH3	0.08	0.86	methyl
		-0.78	1 alpha -Si(C)C
CH3	0.08	0.86	methyl
		-0.78	1 alpha -Si(C)C
CH3	0.08	0.86	methyl
		-0.78	1 alpha -Si(C)C
CH2	4.13	1.37	methylene
		0.00	1 alpha -C
		2.75	1 alpha -OC(=O)-C
		0.01	general corrections
CH3	1.29	0.86	methyl
		0.44	1 beta -OC(=O)C
		-0.01	general corrections

<sup>1</sup>H NMR Coupling Constant Prediction

shift atom index coupling partner, constant and vector

7.94	6	1	7.5	H-C*C-H
		4	1.5	H-C*C*C-H

7.94	4	4	1.5	H-C^C^C-H
		2	1.5	H-C*CH*C-H
7.52	3	3	7.5	H-C*C-H
		6	1.5	H-C*C*C-H
		2	1.5	H-C*CH*C-H
7.52	1	4	7.5	H-C*C-H
		2	7.5	H-C*C-H
		1	1.5	H-C*CH*C-H
7.52	2	6	7.5	H-C*C-H
		2	7.5	H-C*C-H
		3	1.5	H-C*CH*C-H
0.08	18	3	7.5	H-C*C-H
		1	7.5	H-C*C-H
		4	1.5	H-C*CH*C-H
		6	1.5	H-C*CH*C-H
0.08	19			
0.08	20			
4.13	13			
1.29	14	14	8.0	H-CH-CH2-H
		13	8.0	H-CH2-CH-H