

Table S1. Diffraction data and model refinement statistics

Protein / Ligand	M ^{pro} with boceprevir	M ^{pro} with telaprevir	M ^{pro} with MG-78	M ^{pro} with MG-131	EV-A71-3C ^{pro} with MG-78	CVB3-3C ^{pro} with MG-78
PDB entry	7NBR	7NBS	7QL8	7Z0P	7QUB	7QUW

Data collection statistics

X-ray source	DESY P11	DESY P11	DESY P11	DESY P11	DESY P11	DESY P11
Wavelength [Å]	1.0332	1.0332	1.0332	1.0332	1.0332	1.0332
Vm [Å ³ /Da]	2.02	2.10	2.27	2.32	2.32	2.22
Solvent content [%]	39.1	41.4	45.8	47.0	47.0	44.5
Space group	C2	C2	P2 ₁ 2 ₁ 2	C2	P432	C2

Unit cell dimensions [Å]	$a = 113.77$, $b = 53.37$, $c = 45.95$	$a = 109.69$, $b = 54.63$, $c = 48.28$	$a = 45.52$, $b = 64.04$, $c = 105.38$	$a = 113.72$, $b = 51.67$, $c = 45.45$	$a = b = c = 122.34$	$a = 78.27$, $b = 64.29$, $c = 39.85$
Unit cell dimensions [°]	$\alpha = \gamma = 90$, $\beta = 101.83$	$\alpha = \gamma = 90$, $\beta = 101.40$	$\alpha = \beta = \gamma = 90$	$\alpha = \gamma = 90$, $\beta = 103.33$	$\alpha = \beta = \gamma = 90$	$\alpha = \gamma = 90$, $\beta = 115.52$
Resolution range ^a [Å]	48.13 - 2.40 (2.53 - 2.40)	48.70 - 1.70 (1.79 - 1.70)	41.79 - 1.80 (1.90 - 1.80)	46.81 - 2.52 (2.62 - 2.52)	43.25 - 2.07 (2.19 - 2.07)	35.95 - 1.65 (1.74 - 1.65)
Number of observations	71,648 (10,224)	206,145 (28,922)	195,279 (30,344)	168,983 (25,182)	771,011 (123,429)	141,834 (20,568)
Number of unique reflections	10,684 (1,563)	30,908 (4,476)	29,378 (4,548)	49,867 (7,839)	19,792 (3,098)	43,026 (6,281)
Completeness [%]	99.9 (100.0)	100.0 (100.0)	99.4 (97.0)	99.0 (98.3)	99.9 (99.8)	98.1 (98.0)
Mean I/σ(I)	15.6 (1.7)	15.6 (1.8)	18.9 (3.5)	16.2 (1.0)	14.4 (1.0)	15.4 (1.9)
Multiplicity	6.7 (6.5)	6.7 (6.5)	5.6 (6.6)	3.5 (3.6)	38.9 (39.8)	6.7 (6.8)

R _{merge} ^b [%]	0.093 (1.179)	0.073 (1.089)	0.042 (0.480)	0.040 (0.167)	0.043 (0.282)	0.047 (0.797)
R _{pim} ^c [%]	0.039 (0.496)	0.030 (0.462)	0.025 (0.297)	0.039 (0.156)	0.010 (0.063)	0.020 (0.326)
CC _{1/2} ^d	0.999 (0.663)	0.999 (0.688)	0.991 (0.693)	0.990 (0.392)	0.999 (0.522)	0.999 (0.874)
Wilson <i>B</i> -factor [Å ²]	48	23	44	53	46	51

Refinement statistics

R _{cryst} ^e /R _{free} ^f [%]	18.5/26.4	21.3/26.7	23.4/30.0	20.3/28.9	19.1/21.8	21.9/27.9
r.m.s.d. in bond lengths [Å]	0.008	0.009	0.007	0.007	0.012	0.007
r.m.s.d. in bond angles [°]	1.9	1.7	1.8	1.6	1.7	1.6
Clashscore ^g	4	5	3	8	5	4

Average <i>B</i> -factor for protein atoms [\AA^2]	58	29	55	47	45	53
Average <i>B</i> -factor for ligand atoms [\AA^2]	51	25	51	40	38	66
Average <i>B</i> -factor for water molecules [\AA^2]	49	35	51	37	46	57
Number of protein atoms	2320	2352	2331	2347	1413	1393
Number of ligand atoms	37	49	39	40	39	39
Number of water molecules	48	155	75	37	52	51

Ramachandran plot

Preferred regions [%]	93	97	93	88	93	92
Allowed regions [%]	6	2	6	10	6	8
Outlier regions [%]	1	1	1	2	1	0

^a The highest resolution shell is shown in parentheses.

$$^b R_{merge} = \sum_{hkl} \sum_{i=1}^n |I_i(hkl) - \bar{I}(hkl)| / \sum_{hkl} \sum_{i=1}^n I_i(hkl)$$

$$^c R_{pim} = \sum_{hkl} \sqrt{1/(n-1)} \sum_{i=1}^n |I_i(hkl) - \bar{I}(hkl)| / \sum_{hkl} \sum_{i=1}^n I_i(hkl) [34]$$

^d CC_{1/2} is the correlation coefficient determined by two random half data sets [35]

$$^e R_{cryst} = \sum_{hkl} |F_o(hkl) - F_c(hkl)| / \sum_{hkl} |F_o(hkl)|$$

^f Rfree was calculated for a test set of reflections (5%) omitted from the refinement.

^g Clashscore is defined as the number of clashes calculated for the model per 1000 atoms (including hydrogens) of the model. Hydrogens were added by MolProbity [36]

Figure S1: Inhibitory activities of boceprevir-derived compounds vs. the SARS-CoV-2 M^{pro}

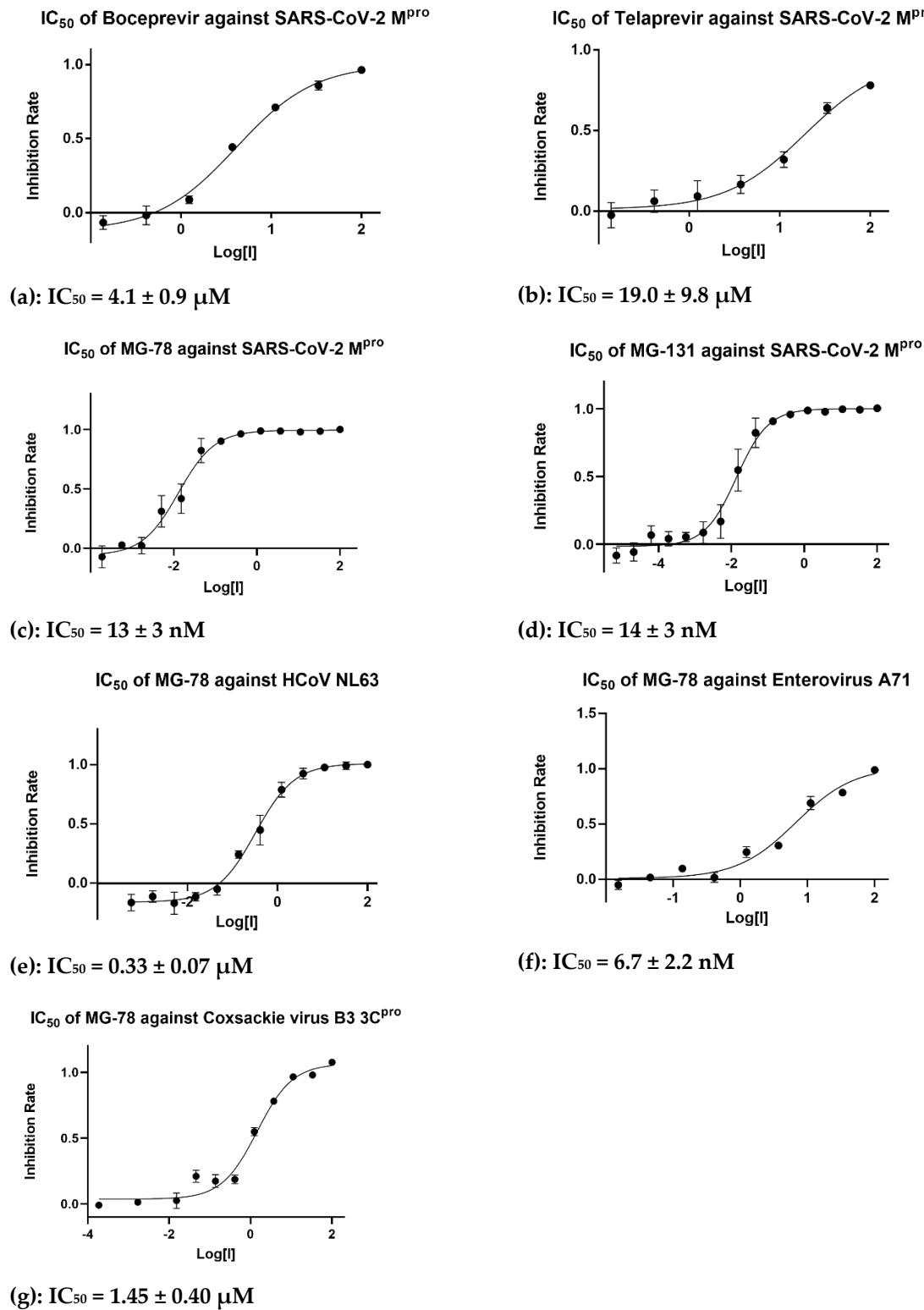
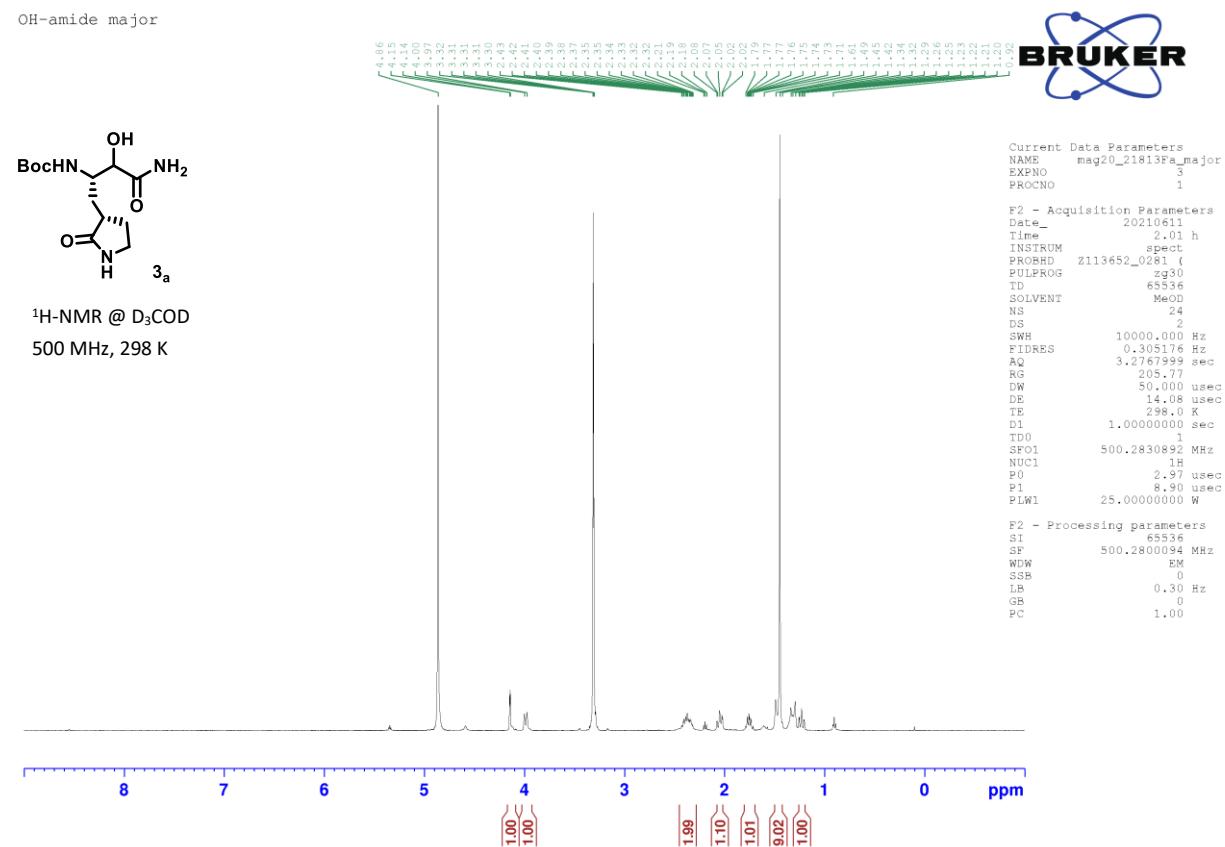
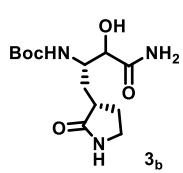
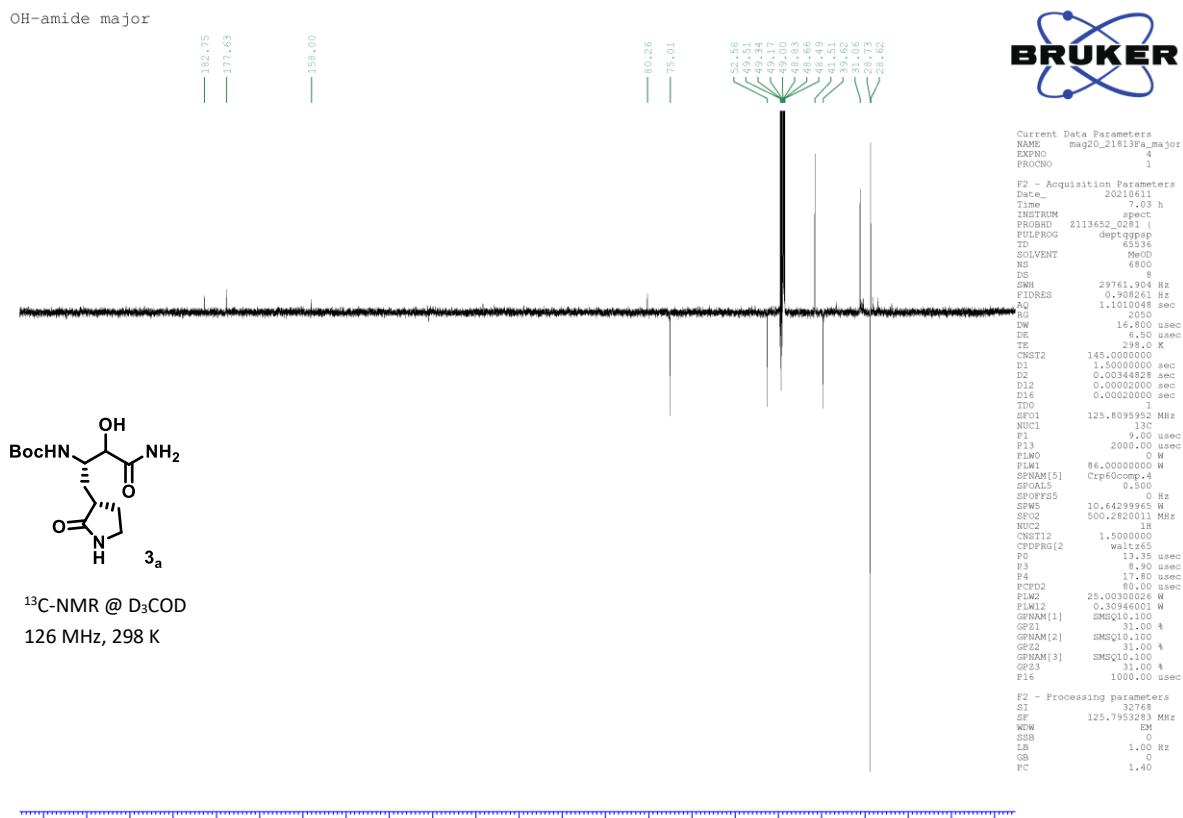


Figure S1. Inhibitory activities against the SARS-CoV-2 M^{pro} of boceprevir (a), telaprevir (b), MG-78 (c), and MG-131 (d); inhibitory activities of compound MG-78 against HCoV-NL63 M^{pro} (e), EV-A71 3C^{pro} (f), and CVB3 3C^{pro} (g). IC₅₀ values have been derived from FRET-based enzymatic assays described in the main text.

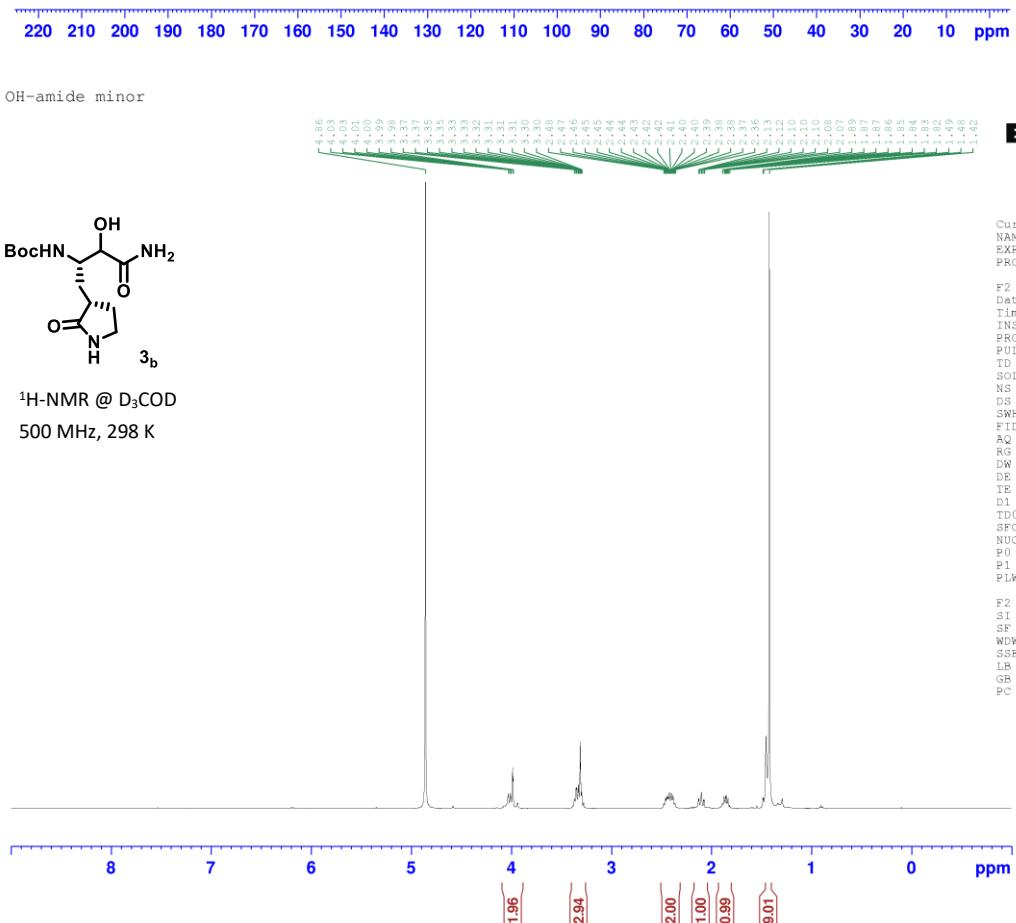
Figure S2. NMR spectra

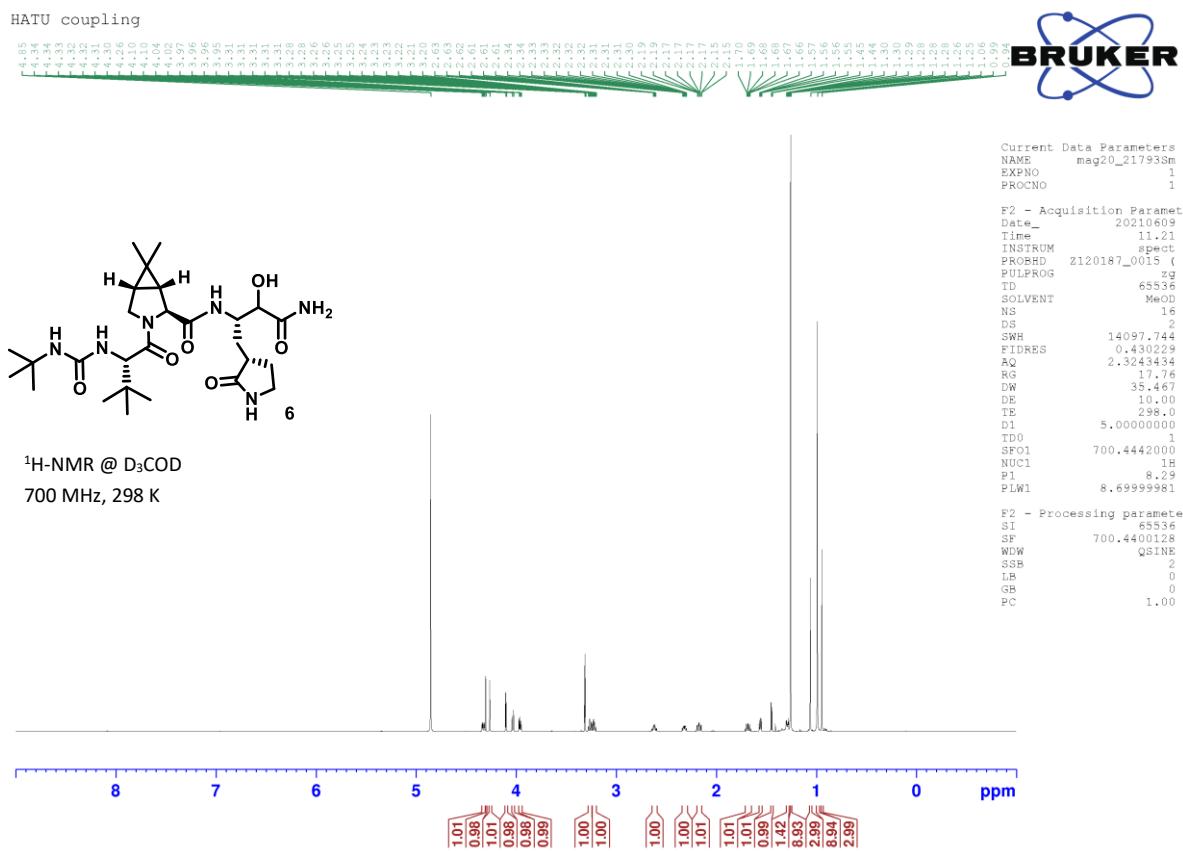
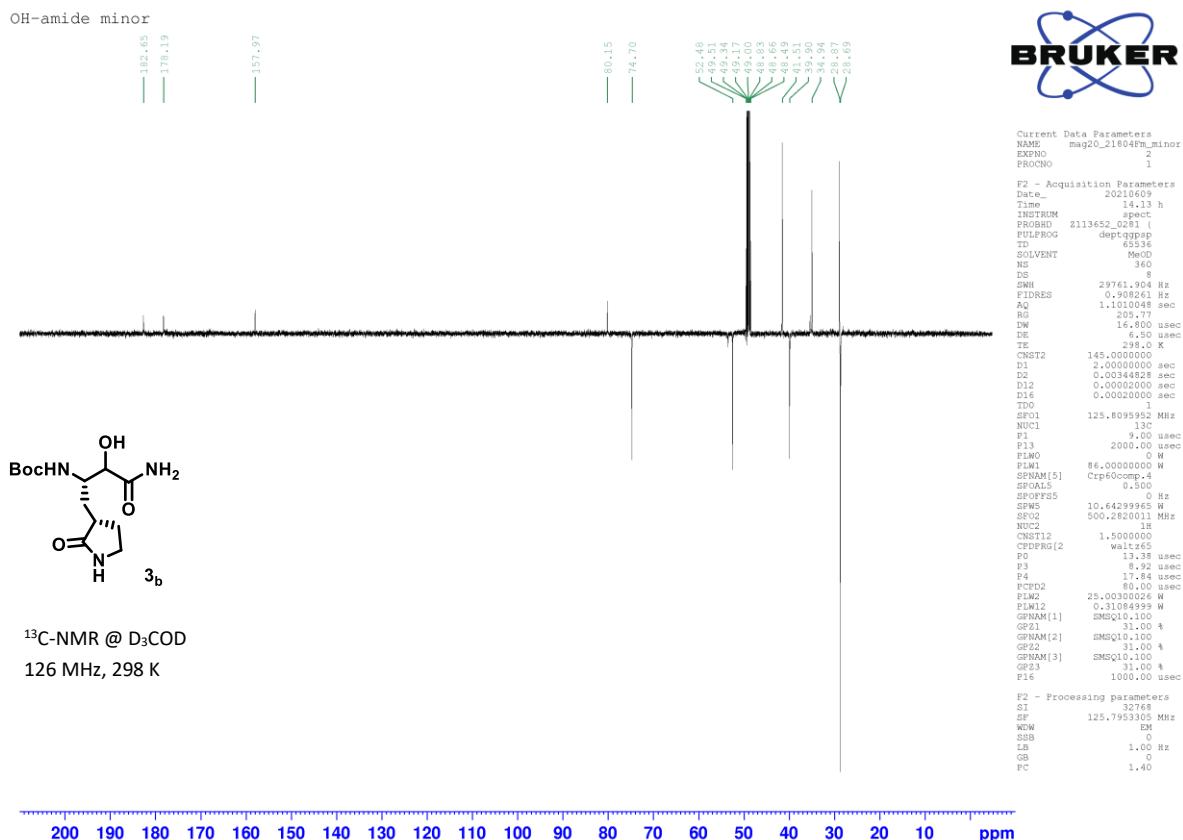
NMR spectra of MG-78 and its intermediates

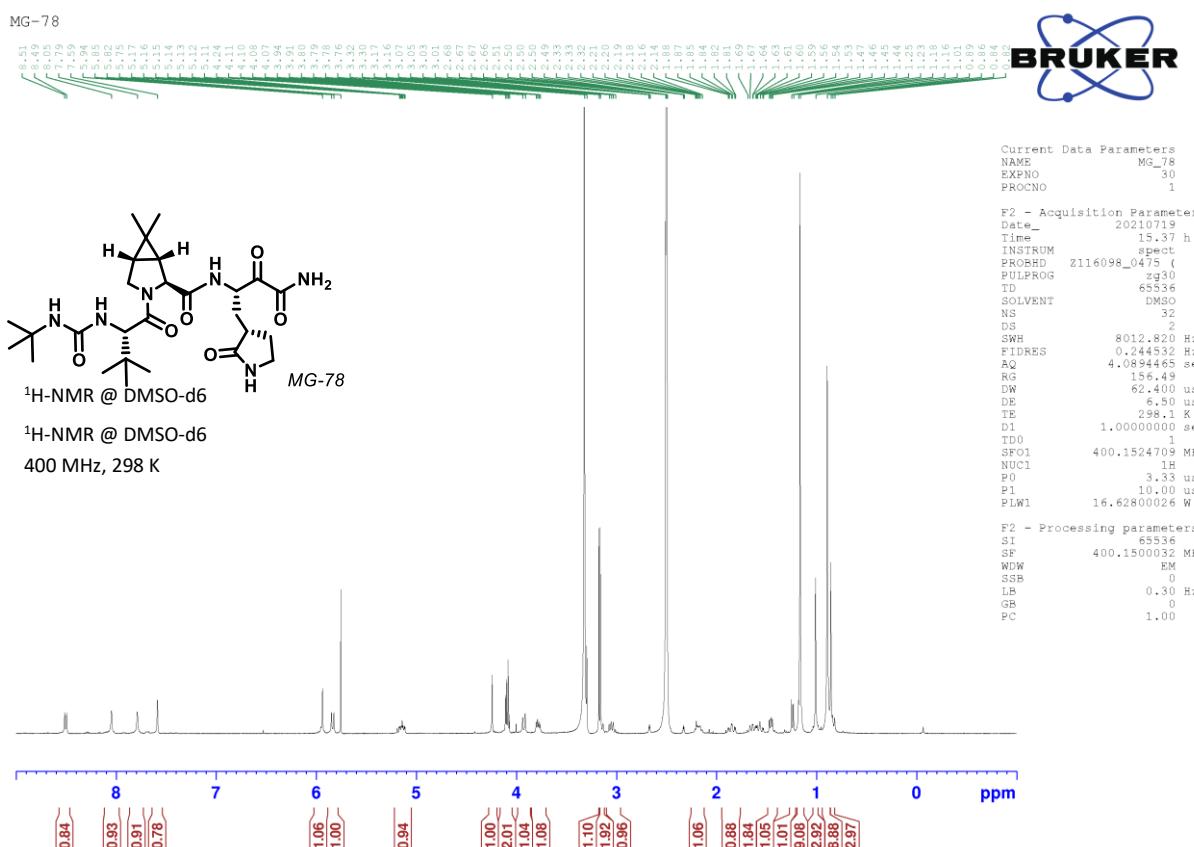
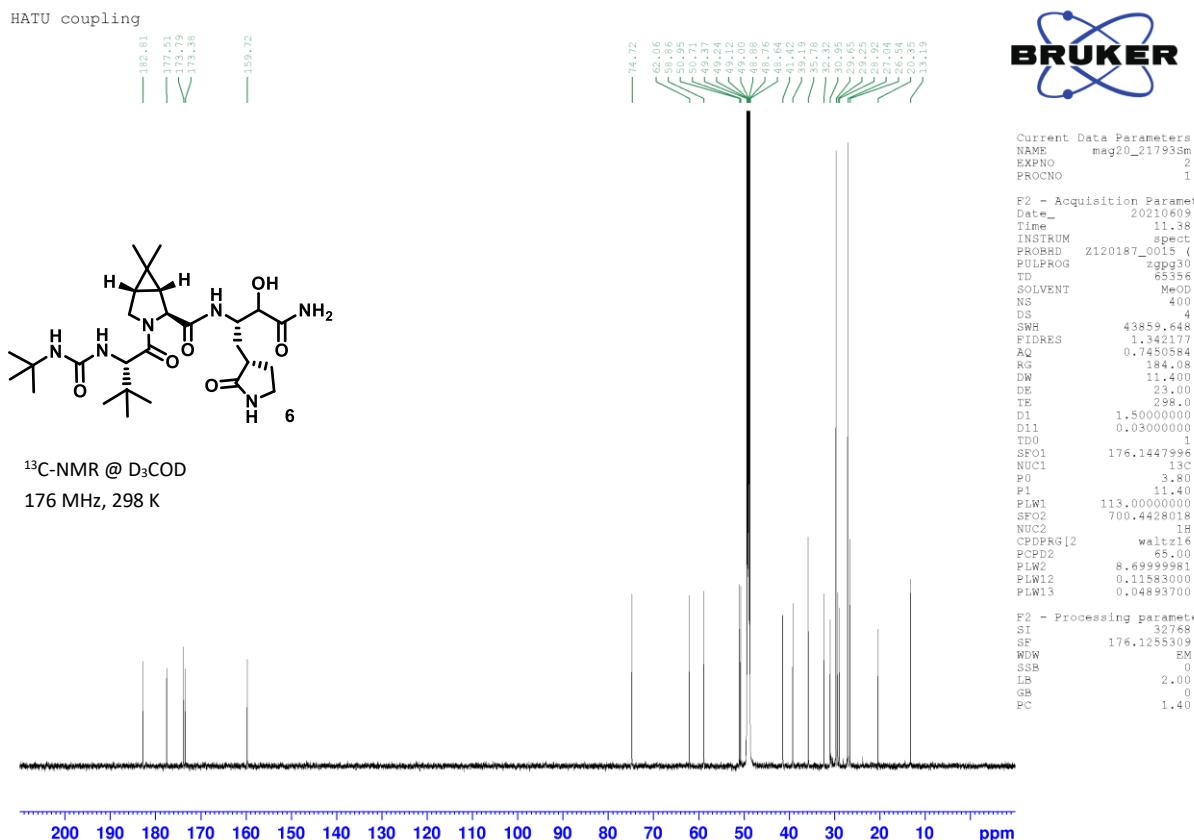




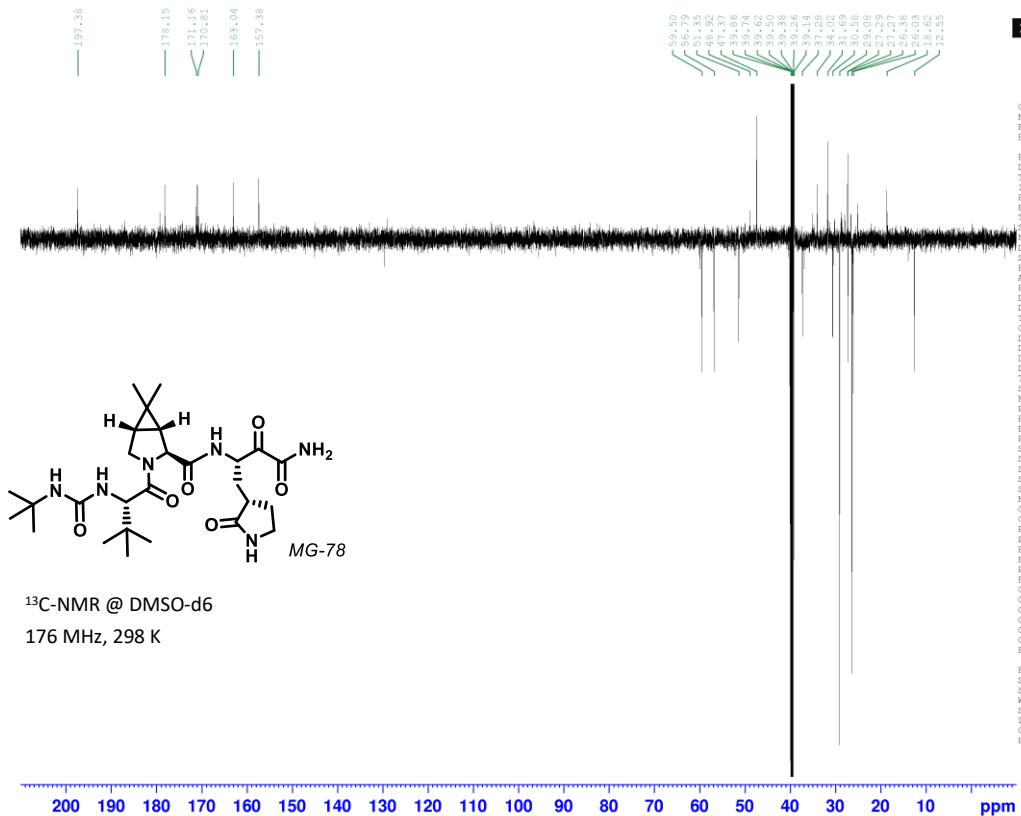
¹H-NMR @ D₃COD
500 MHz, 298 K







MG-78



Current Data Parameters
NAME: mg78_21900s

EXPNO: 2

PROCNO: 1

F2 - Acquisition Parameters

Date: 20210623

Time: 10:45:00 h

INSTRUM: spect

PROBHD: Z120187_0015 (

FULPROG: dept90fpi

T1: 1.35E0

SOLVENT: DMSO

NS: 4144

SWH: 42613.637 Hz

ETR: 1.300465 Hz

AQ: 0.768955 sec

RG: 1.08

DW: 11.733 usec

DE: 15.00 usec

TE: 29.400 K

CNST2: 145.0000000

D1: 1.5000000 sec

D2: 0.00344828 sec

D3: 0.0002000 sec

D4: 0.00020000 sec

TDO: 1

SP1: 176.144271 MHz

NUCL: 13C

P1: 11.40 usec

P3: 2000.00 usec

PL1W0: 0 W

PL1W1: 113.0000000 W

SP1W1L: Crp80comp.4

SP1W1S: 0.500000

SP1P2S: 0 Hz

SP1W2S: 29.91699982 W

SP1F02: 700.4428018 MHz

NUCL2: 13C

CNST12: 1.5000000

CPDPFG[2]: Wait265

P6: 11.00 usec

P3: 7.80 usec

P4: 15.60 usec

CPDPD2: 65.00 usec

PL1W1: 5.70982000 W

PL1W12: 0.12542000 W

GENAM[1]: SMSQ10.100

GENAM[2]: SMSQ10.100 %

GENAM[3]: SMSQ10.100 %

GENAM[4]: SMSQ10.100 %

P16: 1000.00 usec

F2 - Processing parameters

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SF: 176.1258642 MHz

WDW: 0

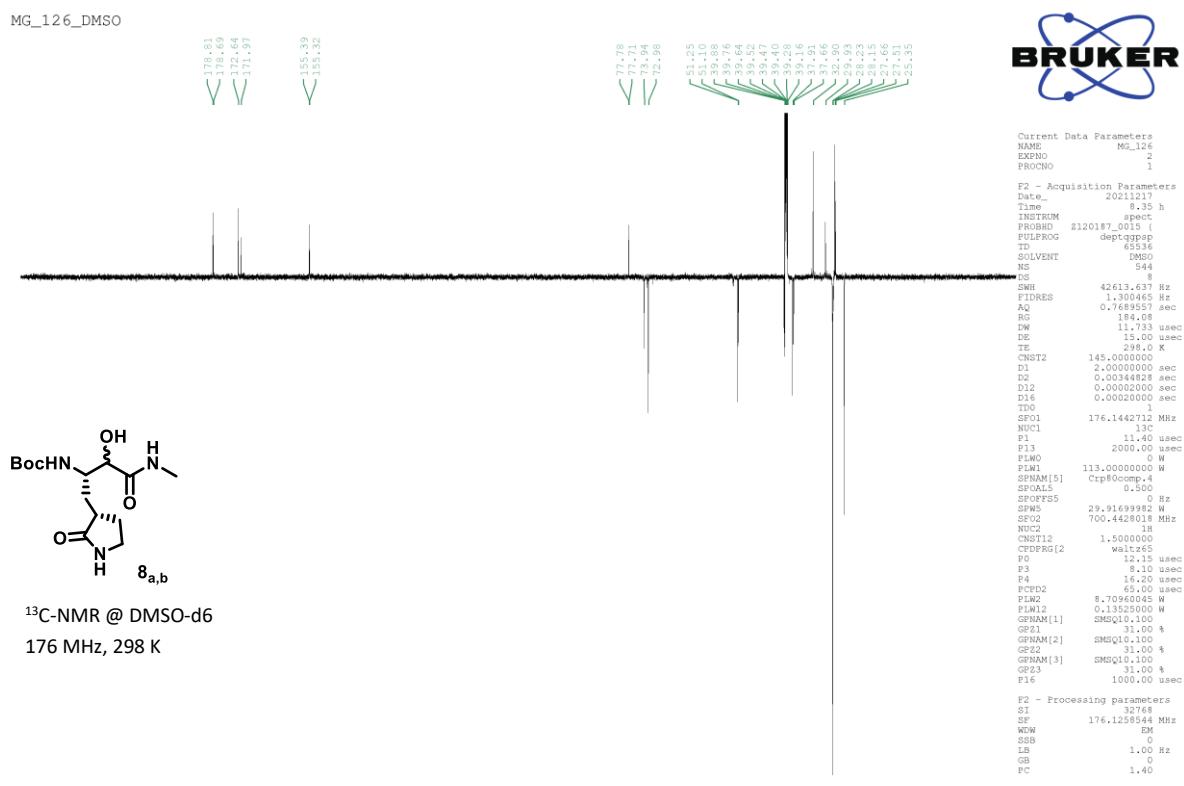
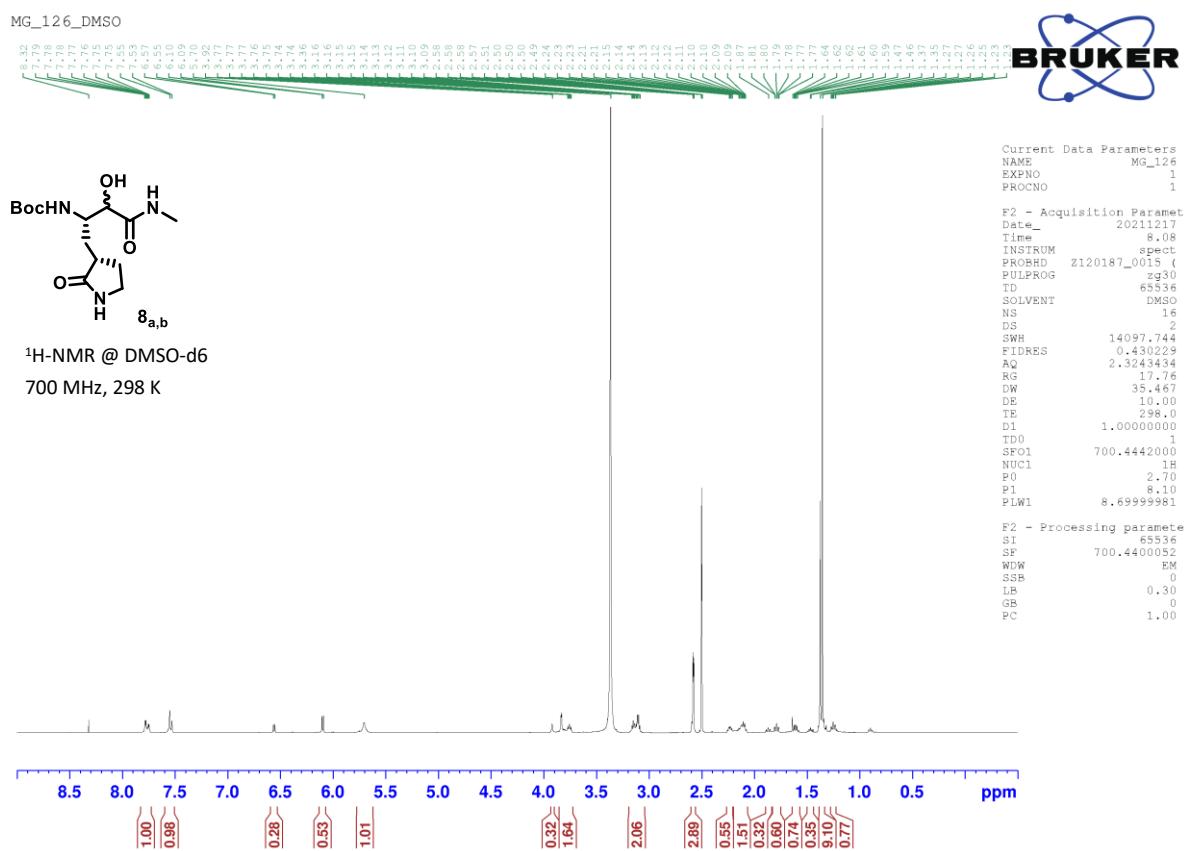
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LB: 1.00 Hz

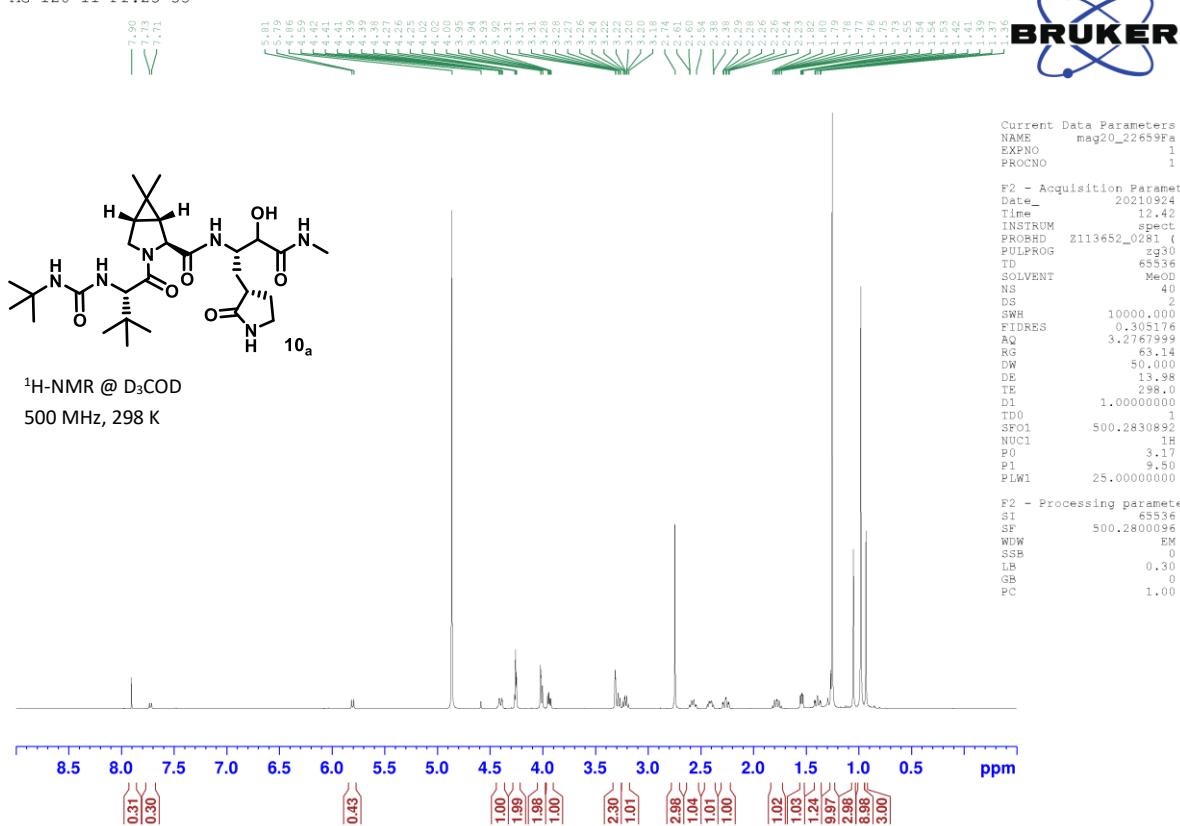
GB: 0

PC: 1.40

NMR spectra of MG-131 and its intermediates



MG-128-II-Fr.23-35



MG-128-II-Fr.23-35

