SUPPLEMENTARY TABLE

Table S1. Data collection and refinement statistics

	Csd4-Inhibitor 1
Data collection	
Space group	$P2_12_12_1$
Cell dimensions	
a, *b*, *c* (Å)	52.84, 66.61, 144.48
Resolution (Å)	39.03-1.90 (1.95-1.90)
R_{meas}	0.099 (0.898)
CC(1/2)	99.9 (77.7)
$I/\sigma I$	15.2 (2.6)
Completeness (%)	100.0 (100.0)
Redundancy	7.1
Refinement	
No. unique reflections	41021
R_{work} / R_{free}	0.18/0.22
No. atoms	
Protein	6850
Inhibitor 1	51
Iodide	19
Zinc	3
Water	284
Average *B*-factors (Å^2)	
Protein	37.8
Inhibitor 1	26.5
Iodide	41.9
Zinc	28.1
Water	38.1
R.M.S. deviations	
Bond lengths (Å)	0.009
Bond angles (°)	1.20
PDB Accession Code	5D2R

Figure S1. Plot of initial rate versus substrate concentration for the hydrolysis of the *N*-acetylated tripeptide substrate by Csd4. Data has been fit to the Michaelis-Menten equation.

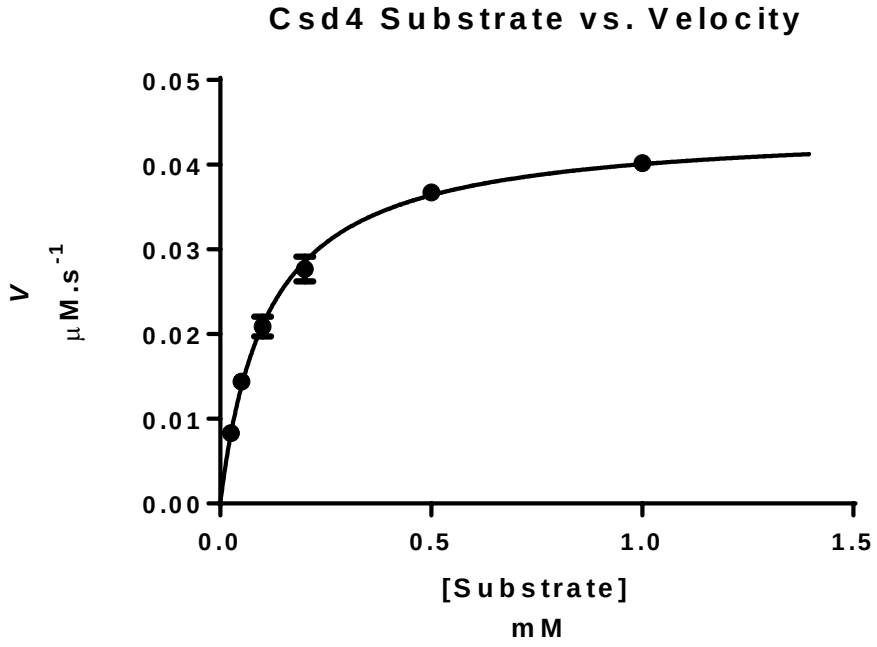


Figure S2 – S8. ^{1}H and ^{31}P NMR Spectra of selected compounds

Figure S2. ^{1}H NMR (400 MHz, $CDCl_3$) spectrum of compound **3**.

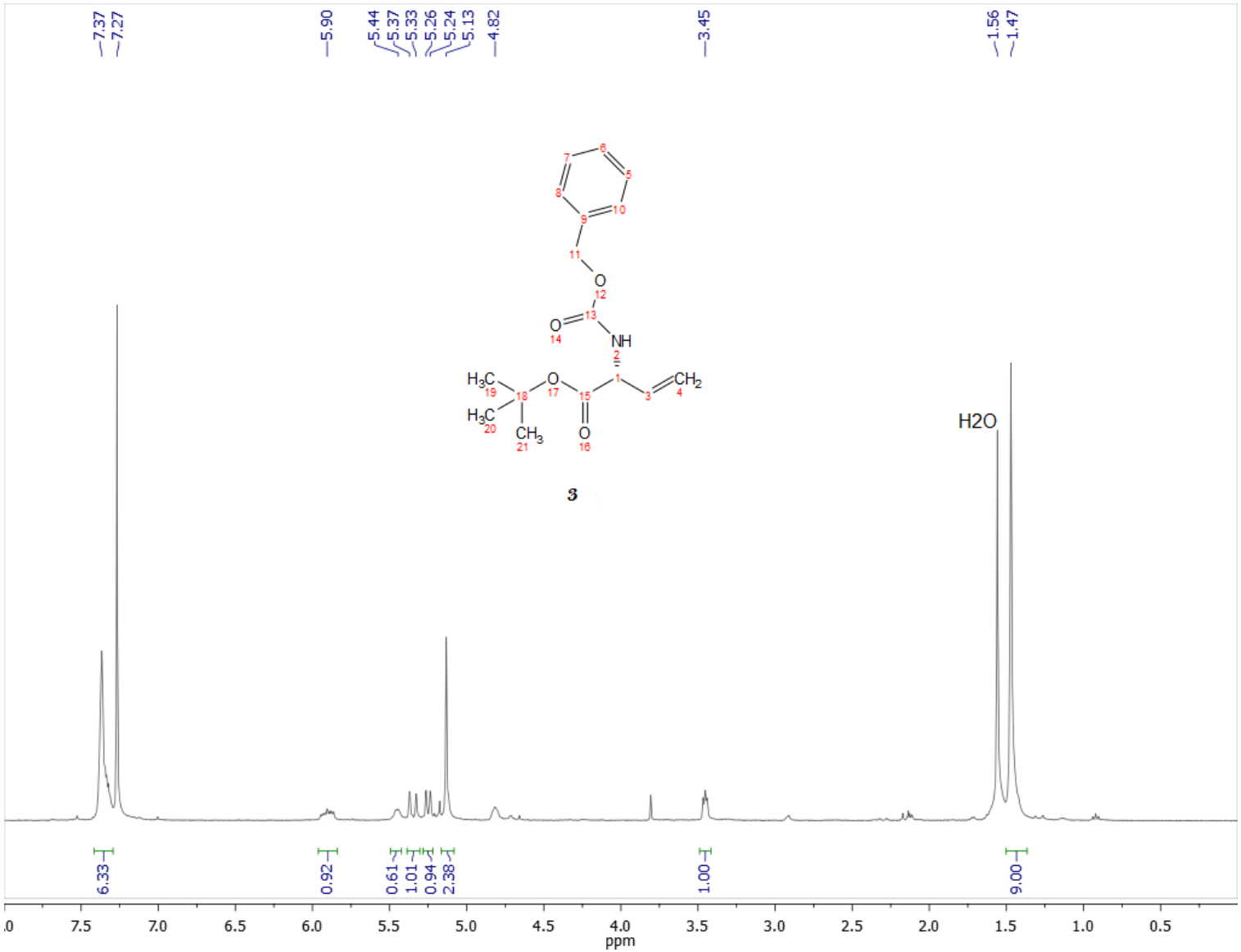


Figure S3. ^{1}H NMR (400 MHz, $CDCl_3$) spectrum of compound **7**.

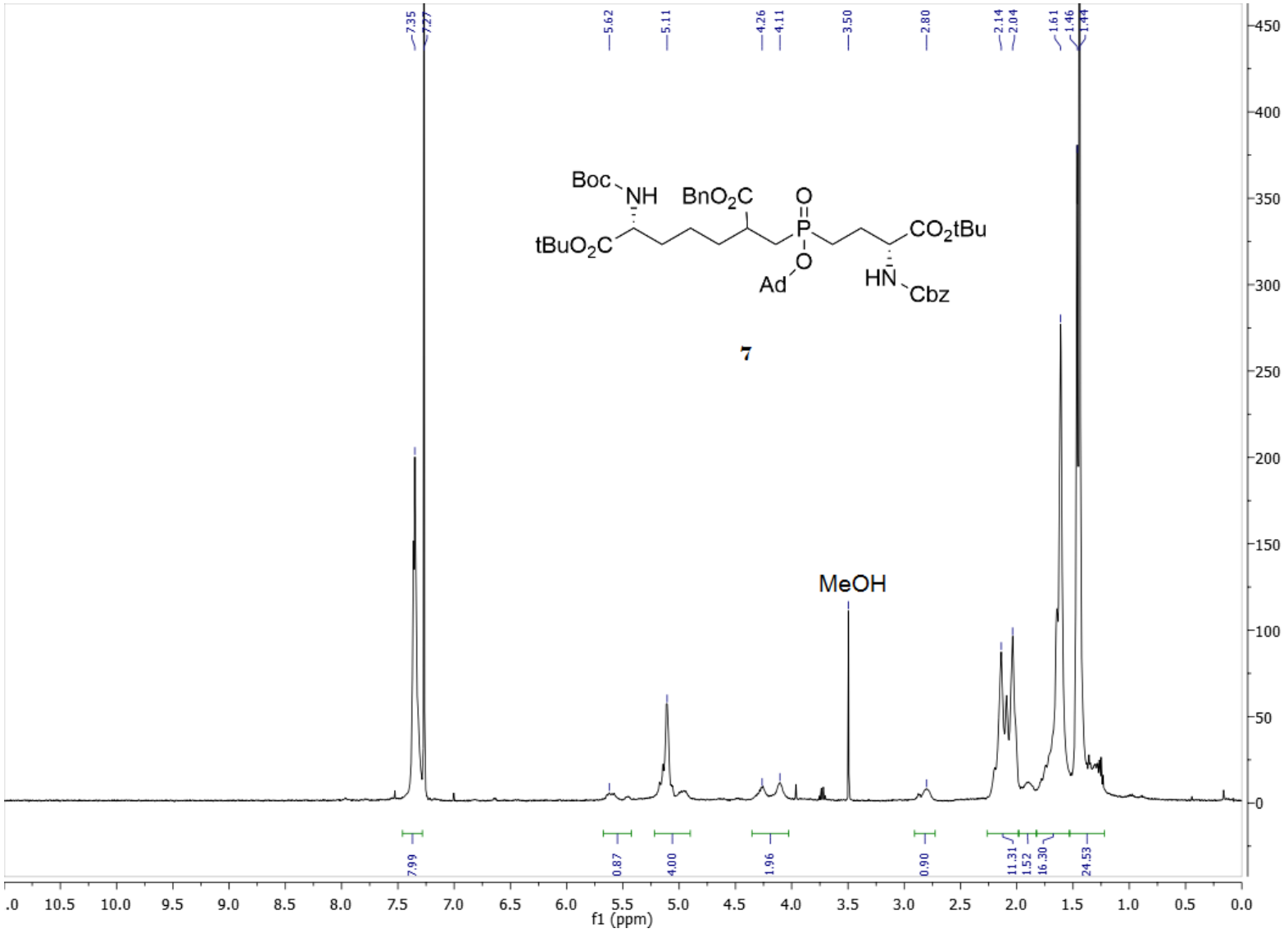


Figure S4. ^{31}P NMR (400 MHz, $CDCl_3$) spectrum of compound **7**.

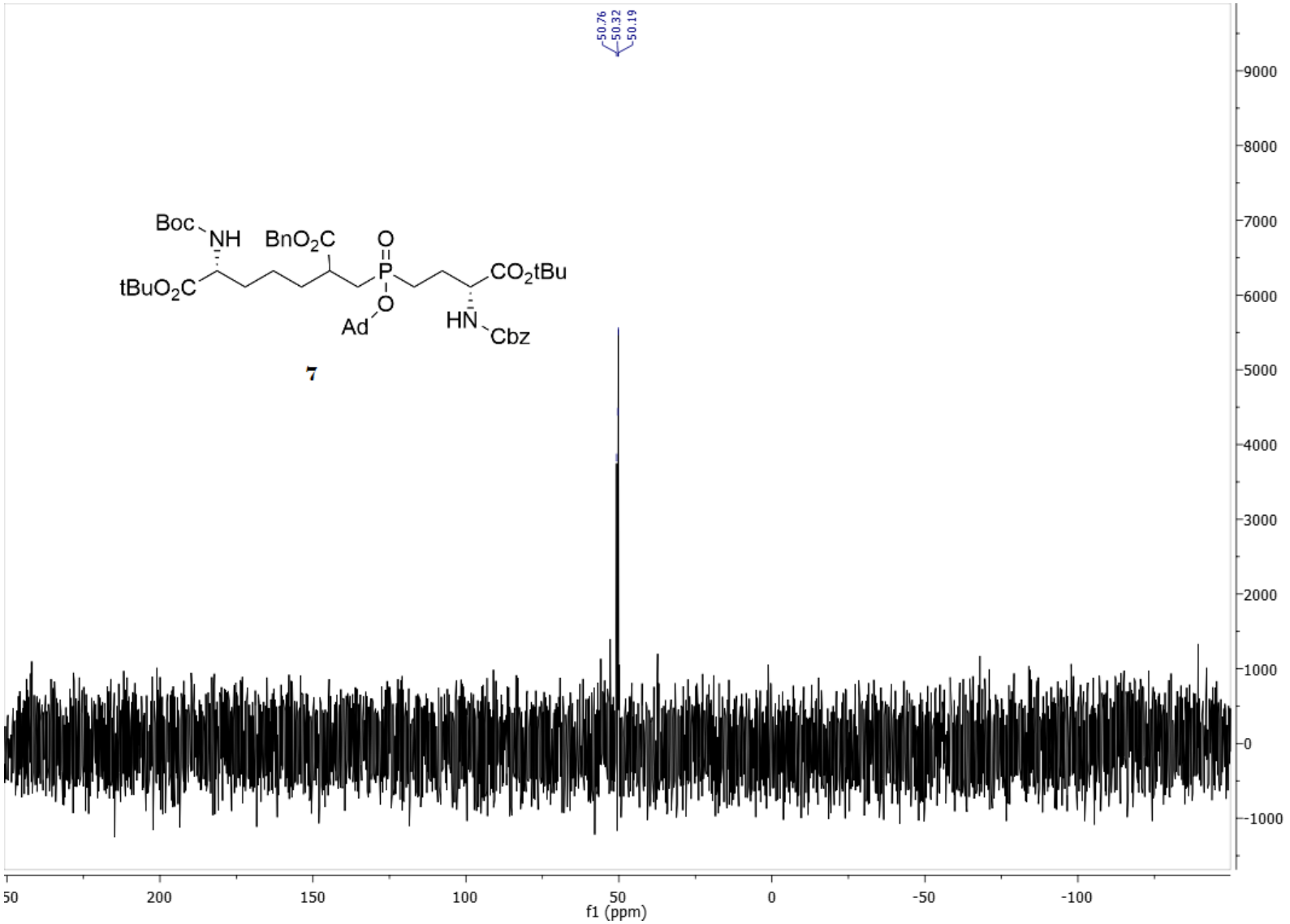


Figure S5. ^{1}H NMR (400 MHz, $CDCl_3$) spectrum of compound **8**.

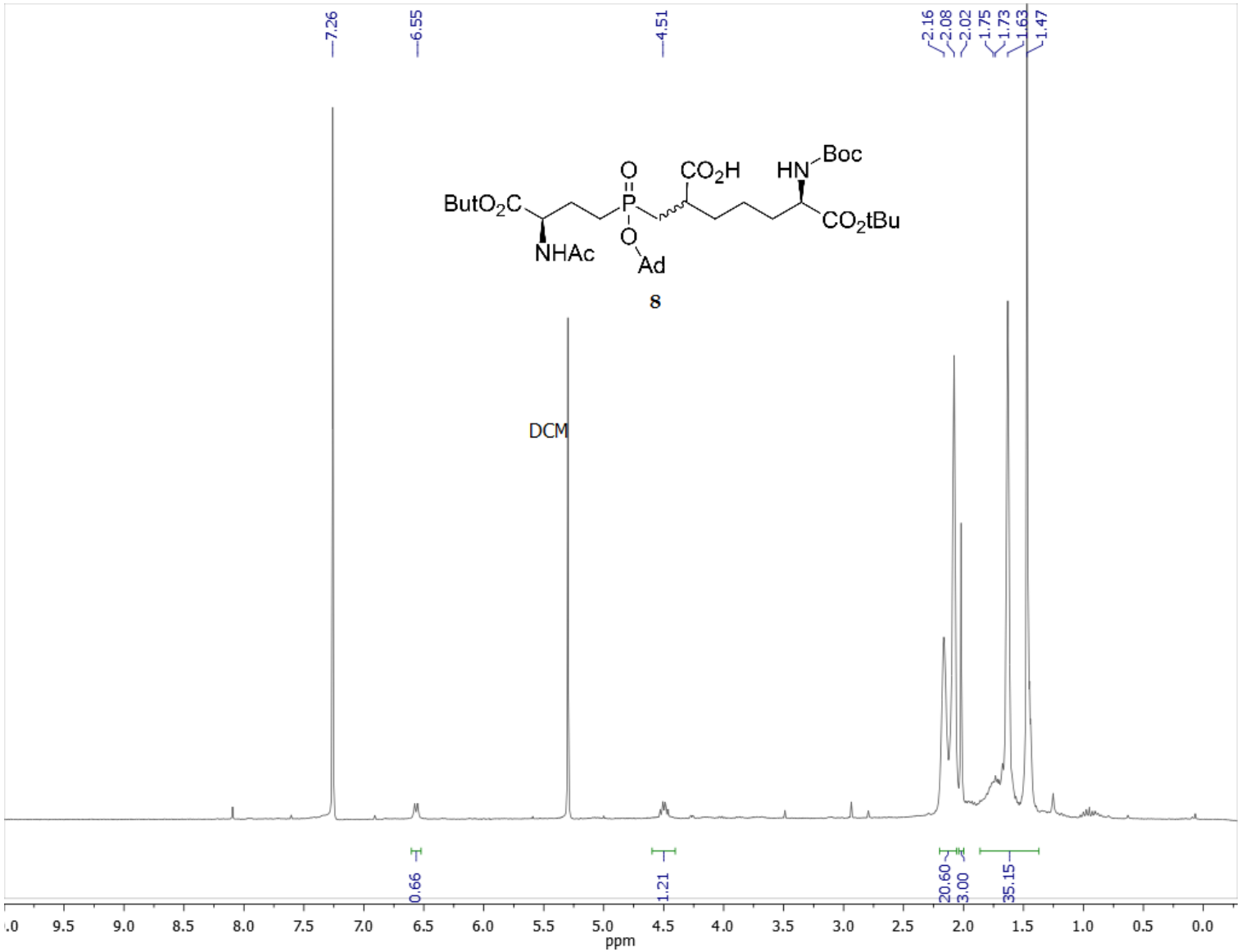


Figure S6. ^{31}P NMR (400 MHz, $CDCl_3$) spectrum of compound **8**.

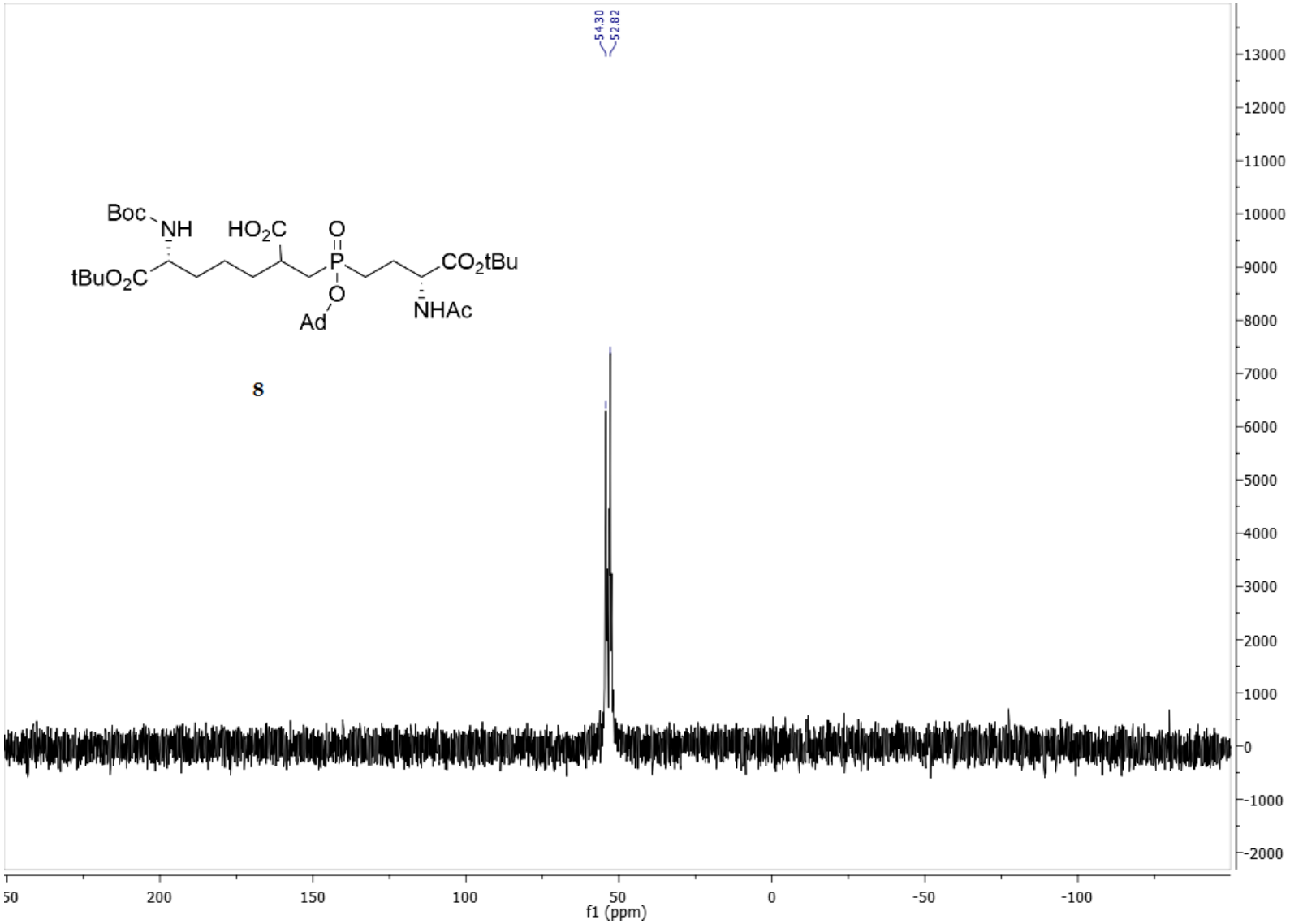


Figure S7. ^{1}H NMR (400 MHz, MeOH) spectrum of inhibitor **1.**

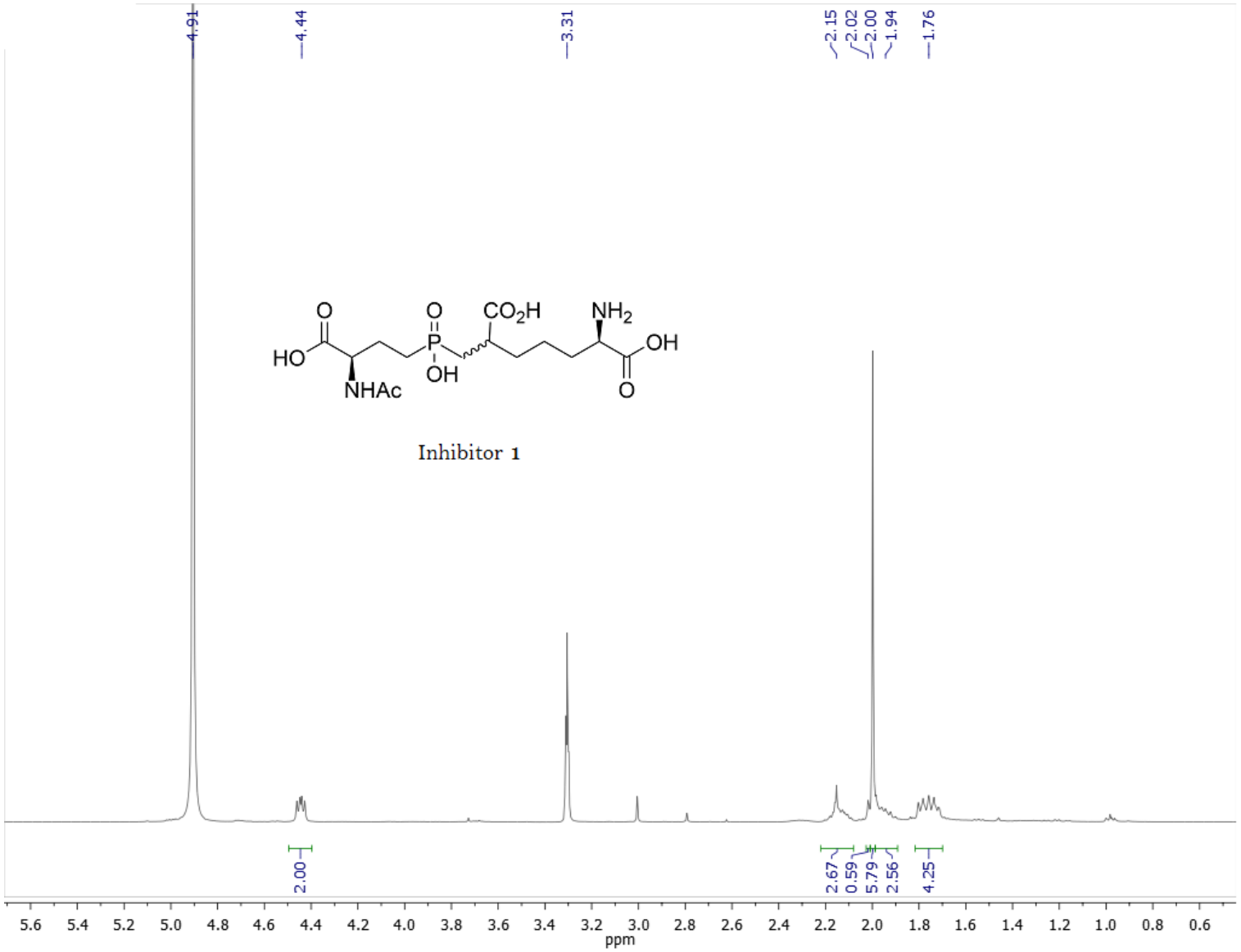


Figure S8. ^{31}P NMR (400 MHz, MeOH) spectrum of inhibitor **1.**

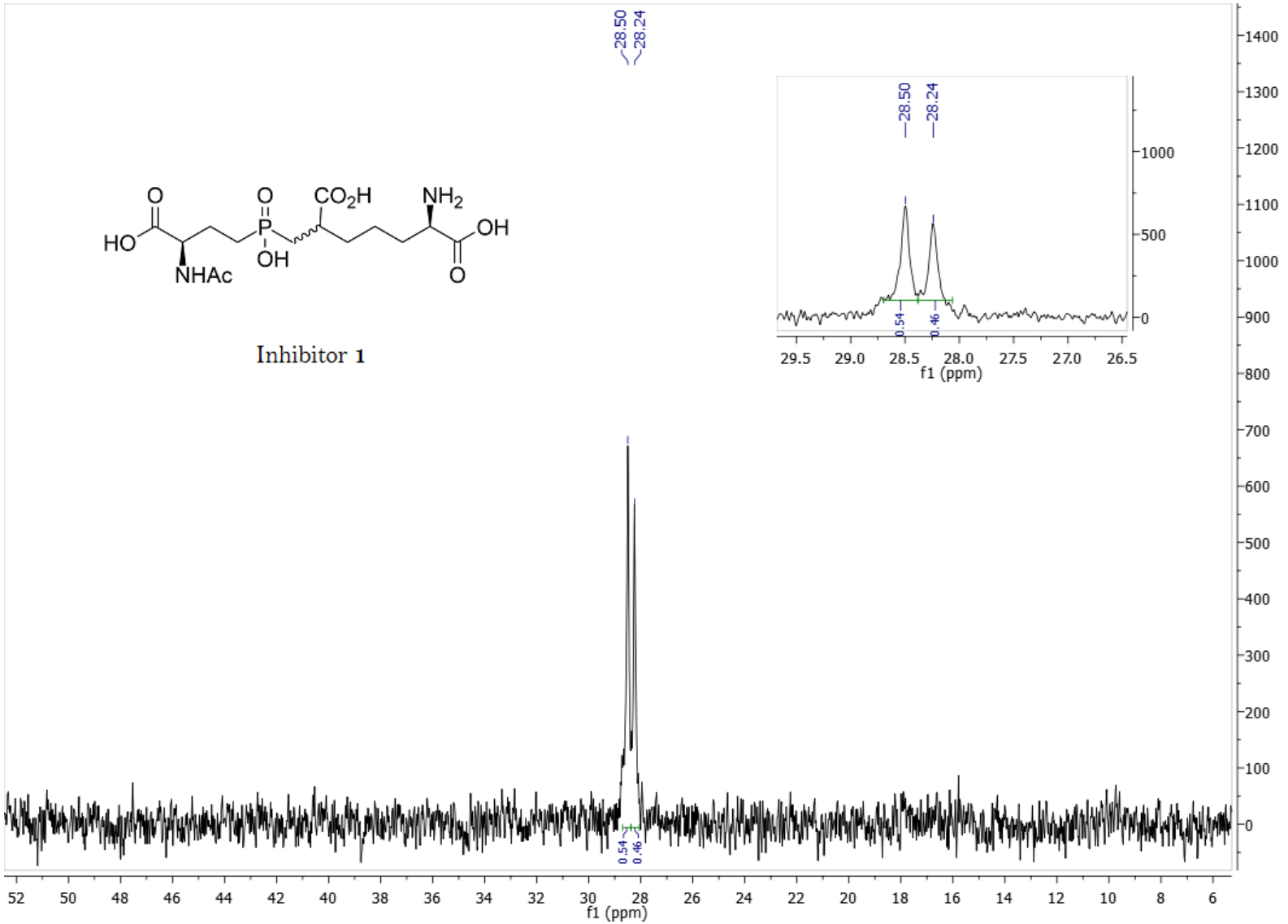
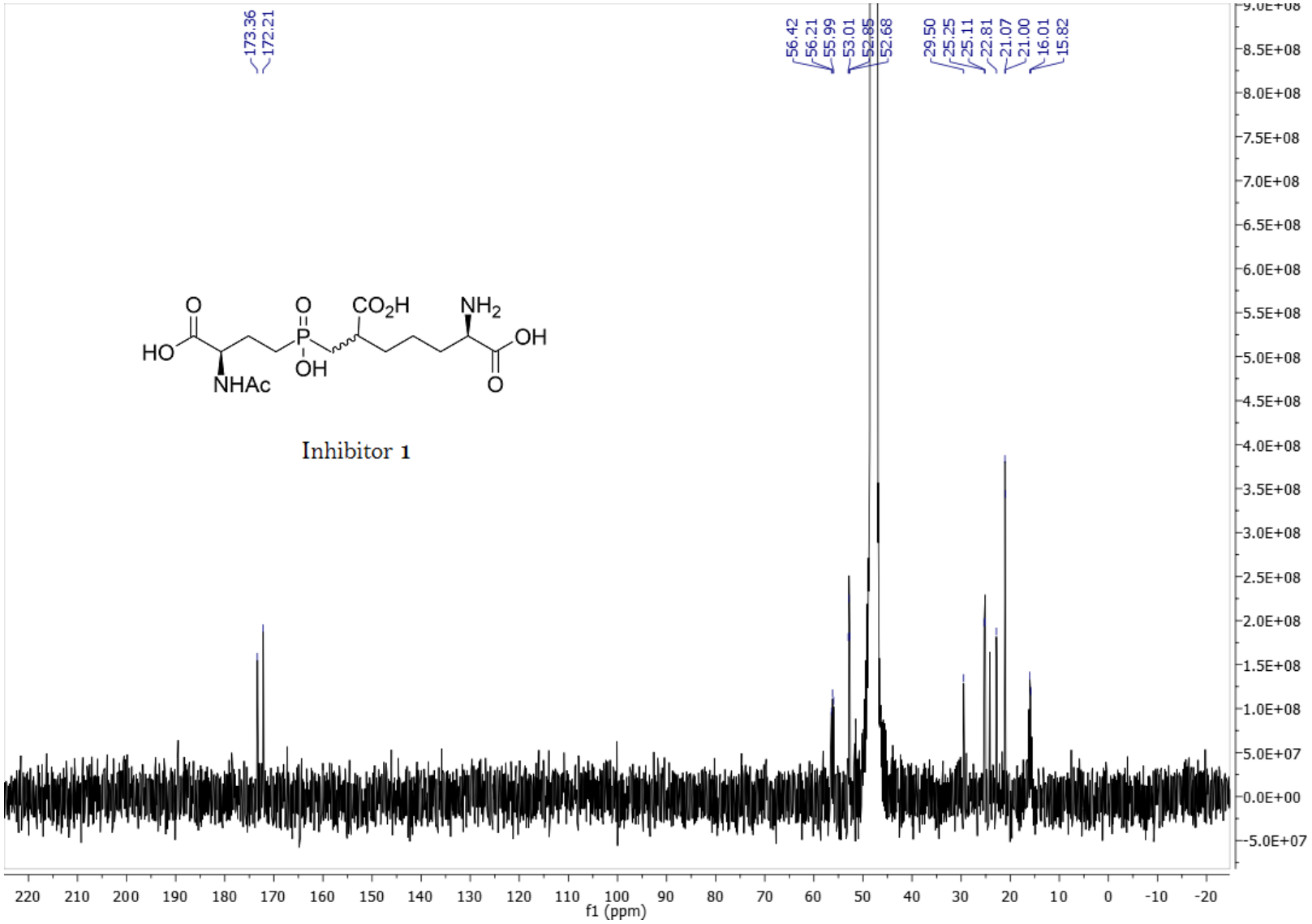


Figure S9. ^{13}C NMR (400 MHz, MeOH) spectrum of inhibitor **1.**



Supplementary Figure 10. Smooth histogram of population side curvature values for the starting culture and cells treated for 2.5, 5, 7.5, and 10 hours without (A) and with 2.1 mM inhibitor **1** (B). Treated cells have significantly lower side curvatures than untreated cells for all time points tested (2.5 hours, $p = 0.044$; 5, 7.5, and 10 hours, $p<0.00001$).