

# Identification of a Dual Inhibitor of Secreted Phospholipase A<sub>2</sub> (GIIA sPLA<sub>2</sub>) and SARS-CoV-2 Main Protease

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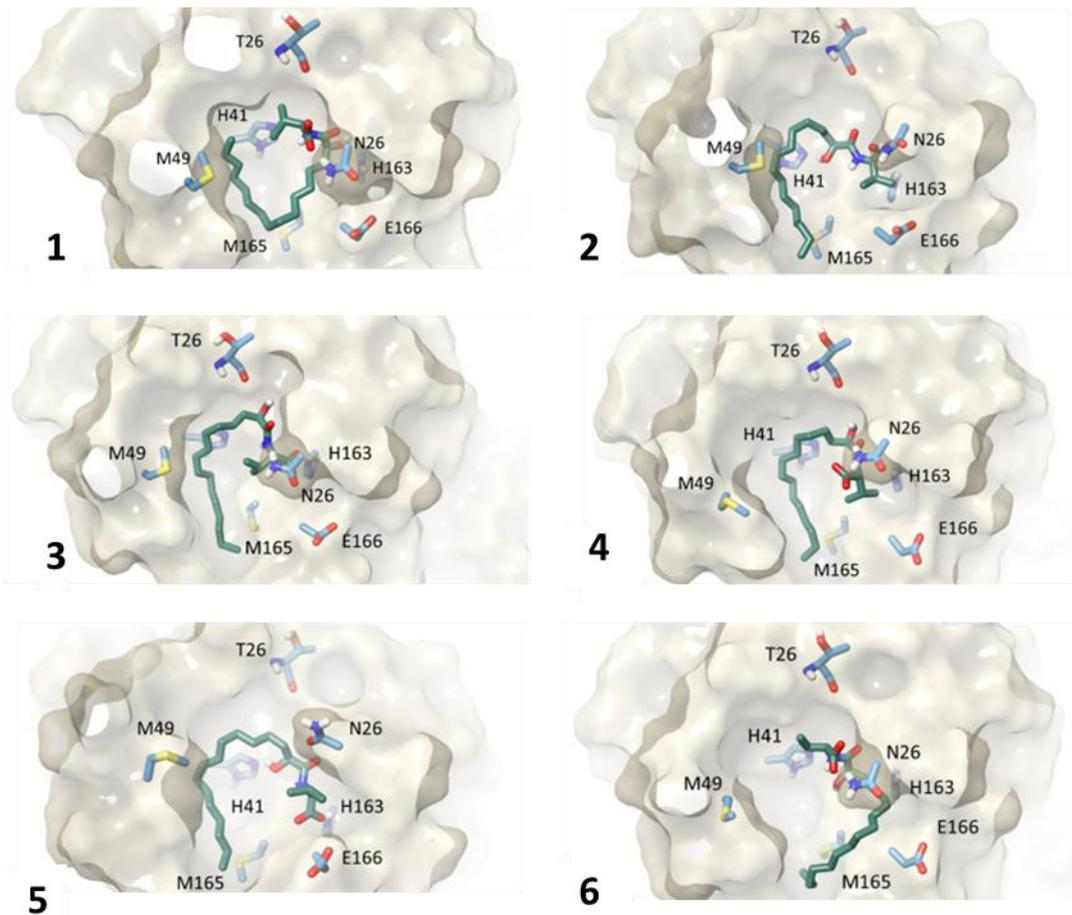
## SUPPLEMENTARY MATERIALS

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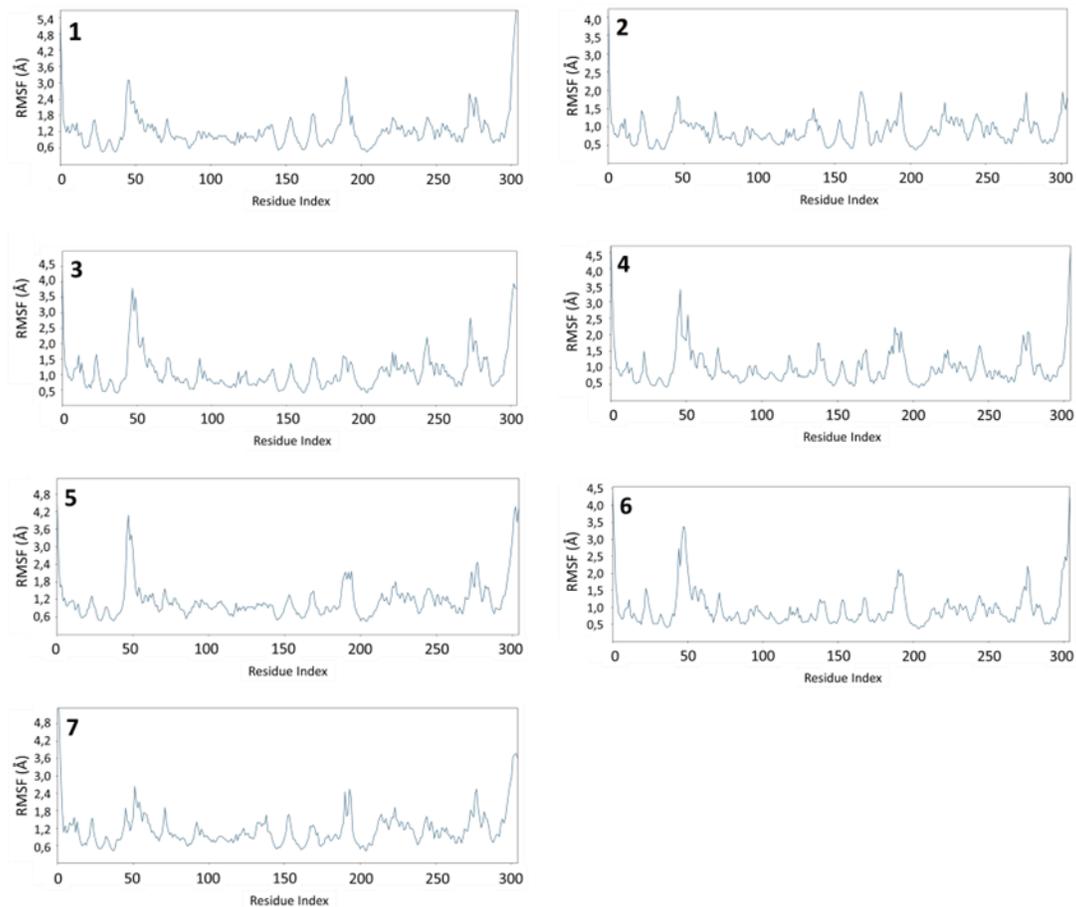
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**Table S1.** Structural details of structures 1-7 concerning the configuration of 2-carbon and the dihedral angle  $C\beta_{C145}-S_{C145}-C2-O2$  related to the covalent bond formatted between Cys145 and 2-oxoamide moiety. Molecular Dynamics RMSDs for the protein and the ligand along with MM-GBSA Binding Energy.

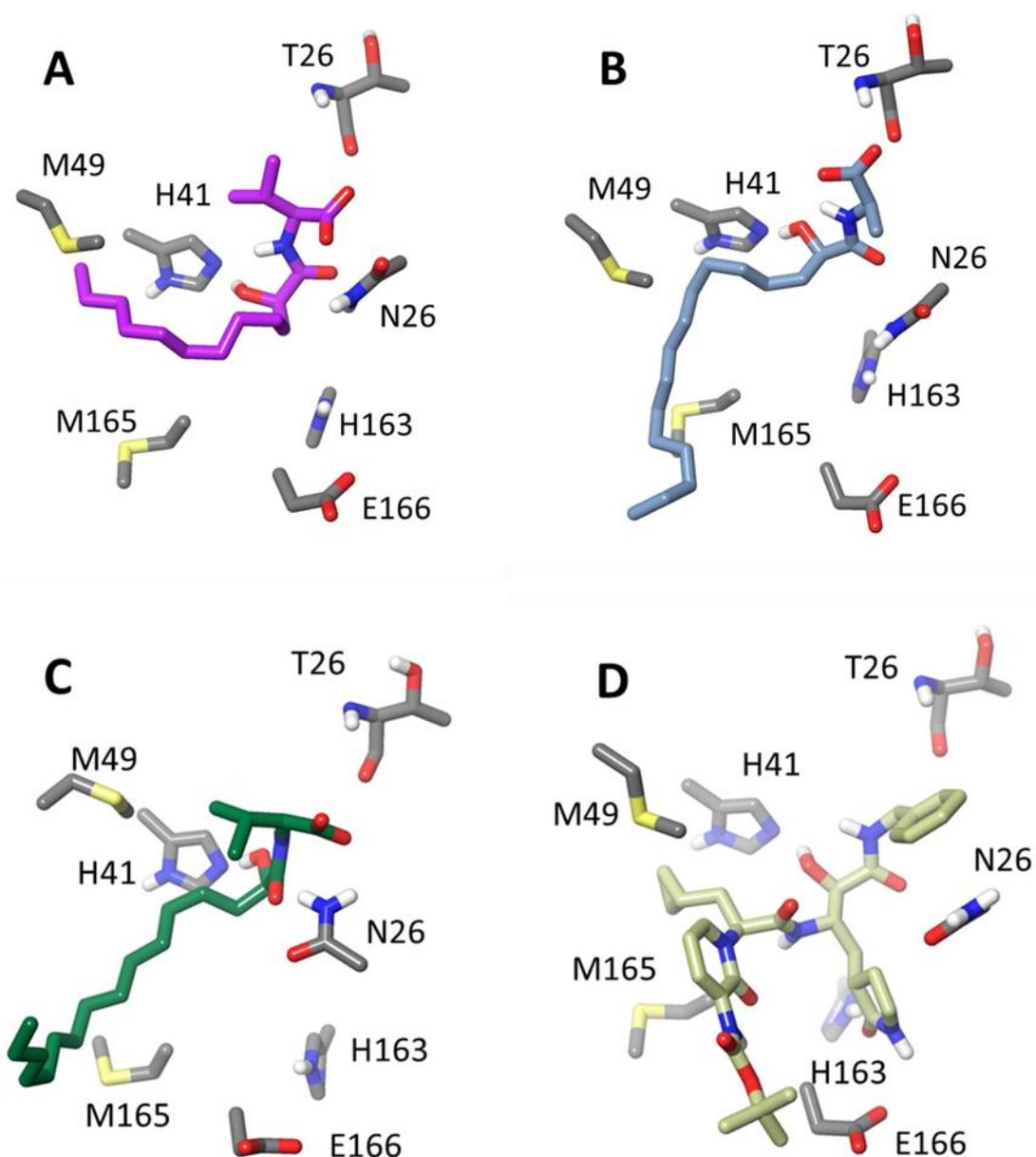
Structure	Configuration of 2-carbon	MM-GBSA Binding Energy (kcal/mol)	Average Protein RMSD $\pm$ StDev	Average Ligand RMSD $\pm$ StDev	Major Interactions	Dihedral Angle $C\beta-S-C2-O2$
1	<i>R</i>	-58.69	2.84 $\pm$ 0.48	3.36 $\pm$ 0.95	S144	-73.68
2	<i>R</i>	-56.37	1.77 $\pm$ 0.24	4.63 $\pm$ 0.70	E166	-175.218
3	<i>S</i>	-54.51	1.73 $\pm$ 0.28	7.36 $\pm$ 3.73	-	86.525
4	<i>S</i>	-47.03	2.29 $\pm$ 0.35	5.53 $\pm$ 0.89	T26, T24	-45.037
5	<i>R</i>	-46.41	2.00 $\pm$ 0.32	3.97 $\pm$ 1.10	H41, E166	-50.033
6	<i>S</i>	-45.17	1.95 $\pm$ 0.31	5.05 $\pm$ 0.95	H41, N142, H164	134.808
7	<i>S</i>	-43.26	1.79 $\pm$ 0.26	3.22 $\pm$ 0.79	T26, H41, N142	-55.195



**Figure S1.** Structural details for the M<sup>Pro</sup>-GK241 interactions in structures 1-6 resulted by covalent docking calculations.

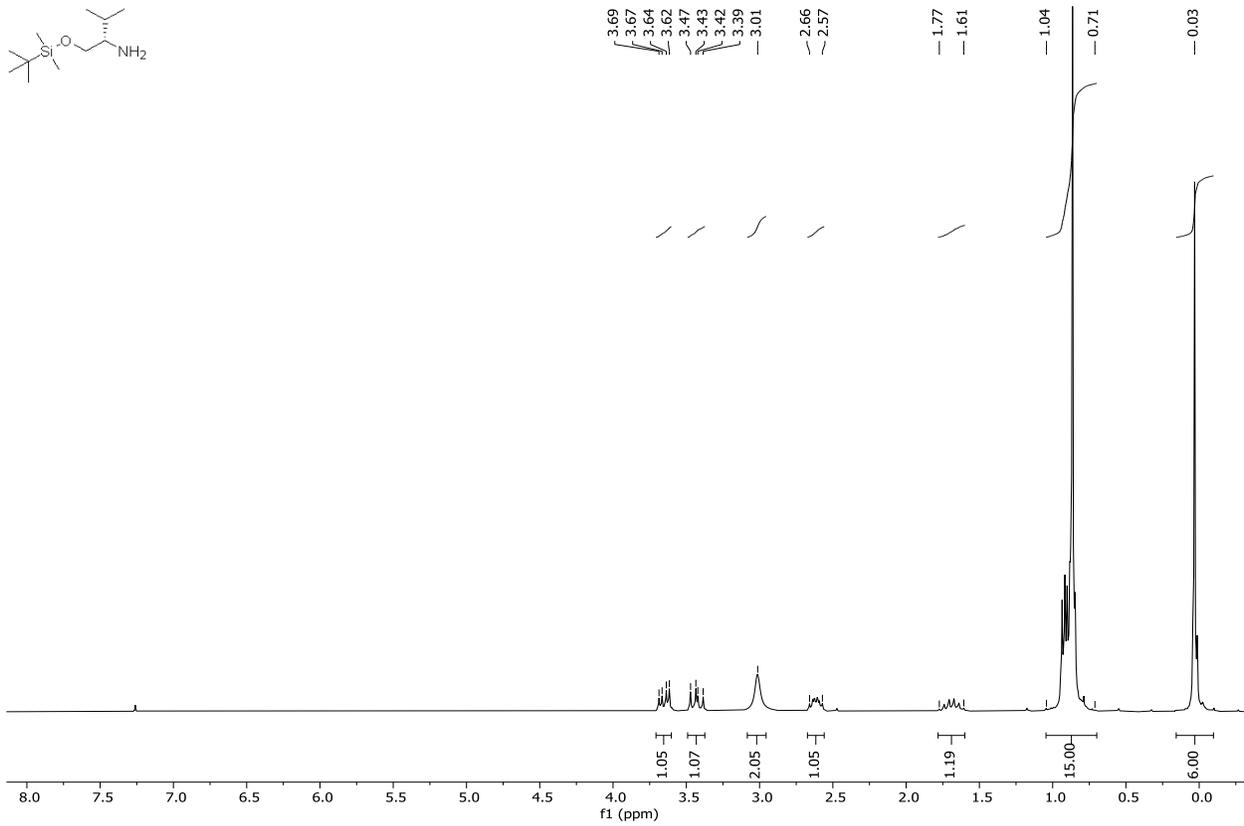
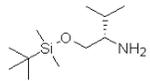


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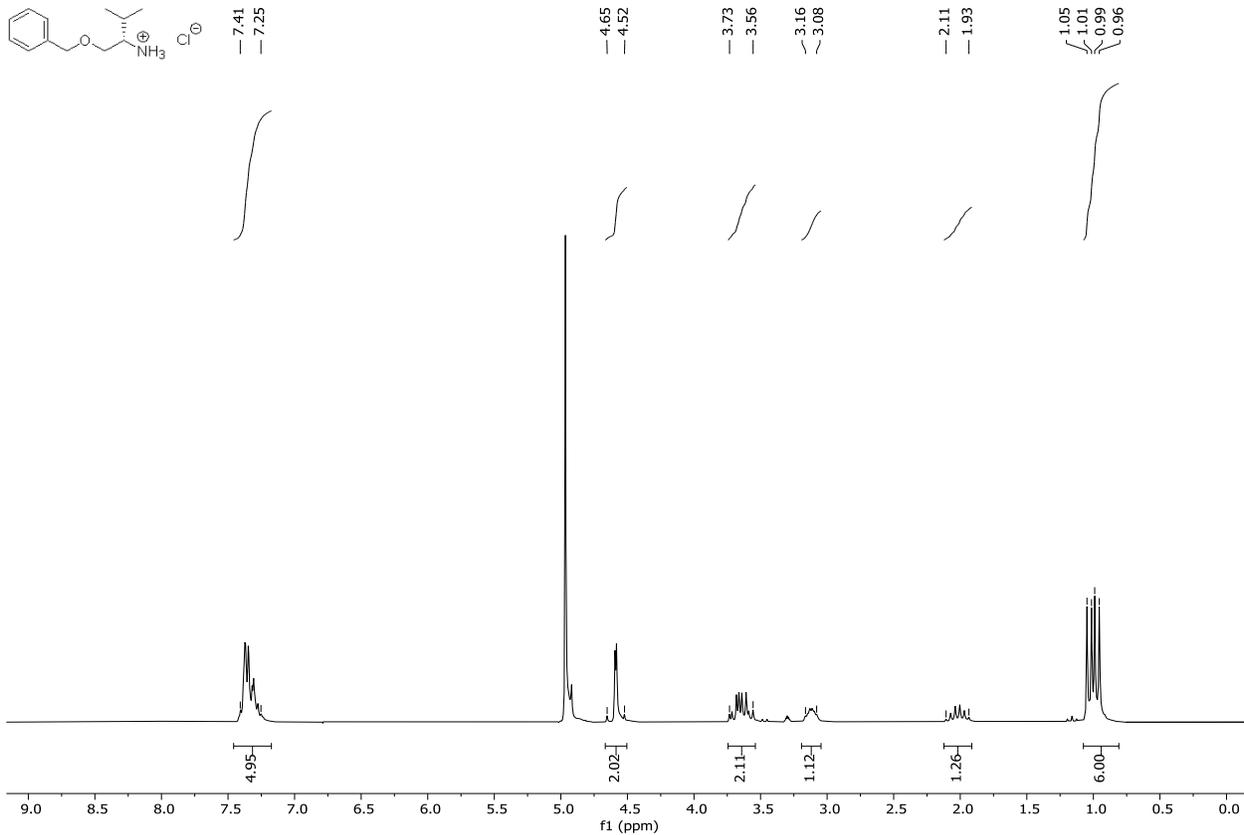
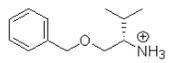


**Figure S3.** Structures of **8d** (A) in magenta and **8a** (B) in blue bound to M<sup>pro</sup> in comparison with GK241 (C) in green and crystal structure PDB 6Y2F (D) in chaki. The side chain in derivative **8d** adopts a curved conformation exploring part of S1 and S2 protease cavities. Derivative **8a** aliphatic chain adopts a very similar structural arrangement to GK241, however the alanine moiety appears to interact weakly with N142 and T26.

# NMR Spectra



<sup>1</sup>H NMR spectrum of **5b**.



<sup>1</sup>H NMR spectrum of **5c**.

