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**Supplemental Information**

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pharmacophore targeting the SARS-CoV-2 main protease**

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## Structure-guided design of a perampanel-derived pharmacophore targeting the SARS-CoV-2 main protease

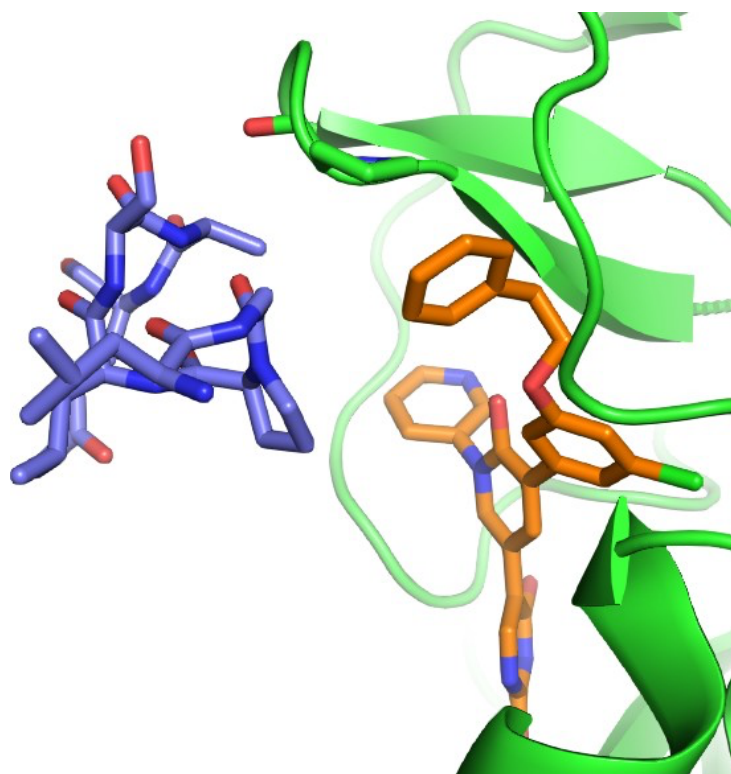
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### Supplementary Information



**Figure S1. Crystal structure of the complex of M<sup>pro</sup> with compound 15.** M<sup>pro</sup>:15 is shown with M<sup>pro</sup> in green, 15 in orange, and Leu<sup>250</sup>-Gln<sup>256</sup> of a symmetry-related molecule that packs in close proximity to Pro<sup>168</sup> shown in blue. Related to Figure 4.

Complex	Mpro: Mpro-6	Mpro: Mpro-11	Mpro: Mpro-29	Mpro: Mpro-15	Mpro: Mpro-16	Mpro: Mpro-19	Mpro: Mpro-50	Mpro: Mpro-25	Mpro: Mpro-23
PDB ID	7M8X	7M8M	7M8Z	7M8Y	7M8N	7M8O	7M90	7M91	7M8P
<b>Data collection</b>									
X-Ray Source	APS 24ID-E	APS 24ID-E	APS 24ID-E	APS 24ID-E	NSLS-II17-ID-1	NSLS-II17-ID-1	NSLS-II17-ID-1	APS 24ID-E	APS 24ID-E
Wavelength, Å	0.97918	0.97918	0.97918	0.97918	0.920106	0.920106	0.920106	0.97918	0.97918
Space Group	C2	P212121	C2	C2	P212121	P212121	C2	C2	P212121
Cell dimensions									
a, b, c (Å)	96.831, 81.325, 54.553	67.790, 100.292, 103.036	97.711, 81.57, 54.567	115.371, 53.545, 44.719	67.306, 100.947, 104.137	67.841, 101.922, 103.797	96.807, 82.660, 54.667	97.9, 81.1, 54.7	68.18, 100.61, 104.35
$\alpha, \beta, \gamma$ (°)	90, 116.827, 90	90, 90, 90	90, 116.678, 90	90, 103.198, 90	90, 90, 90	90, 90, 90	90, 117.53, 90	90, 116.6, 90	90, 90, 90
Resolution (Å)	48.652-1.751 (1.85-1.74)	103.036-1.786 (1.88-1.78)	48.758-1.8000 (1.90-1.79)	56.162-1.761 (1.86-1.75)	29.582-1.966 (2.07-1.96)	29.503-2.449 (2.58-2.44)	27.158-2.279 (2.40-2.27)	48.781-1.961 (2.07-1.95)	72.482-2.237 (2.36-2.23)
Rmerge	0.074 (0.834)	0.077 (0.813)	0.092 (0.478)	0.069 (0.440)	0.136 (0.732)	0.170 (0.710)	0.063 (0.173)	0.14 (0.465)	0.064 (0.344)
$I / \sigma I$	9.88 (1.41)	14.60 (2.52)	7.87 (1.93)	8.37 (1.98)	6.24 (1.35)	11.93 (3.19)	11.77 (4.83)	10.85 (4.34)	10.52 (2.82)
Completeness (%)	94.7 (98.0)	99.6 (98.1)	97.1 (90.8)	96.7 (91.8)	98.3 (97.7)	99.5 (97.8)	97.1 (98.1)	96.9 (94.0)	97.9 (92.3)
Redundancy	3.440278 486	6.802257 804	3.374860 441	2.660227 318	3.074058 904	13.37499 545	3.046290 425	3.317307 692	3.117139 85
<b>Refinement</b>									
Resolution (Å)	48.65-1.74	71.87-1.78	48.76-1.79	56.16-1.75	29.50-1.96	29.50-2.44	27.15-2.19	48.78-1.95	72.43-2.23
No. reflections	38,050	68,032	35,331	26,375	51,467	27,418	19,273	52,859	66,457
Rwork / Rfree	0.229/0.273	0.206/0.234	0.198/0.240	0.195/0.228	0.197/0.229	0.211/0.288	0.216/0.273	0.198/0.233	0.185/0.231
No. atoms									
Protein	2313	4669	2294	2357	4669	4756	2285	2342	4660
Inhibitor	53	51	58	58	116	55	61	51	55
Water	145	296	192	242	323	191	172	163	231
<b>B-factors</b>									
Protein	35.91	31.24	34.91	29.91	24.74	45.19	33.04	26.86	45.53
Inhibitor	34.69	33.07	36.24	34.08	24.81	44.14	31.3	28.45	49.67

Water	40.91	37.04	41.01	38.08	31.39	44.21	34.54	30.93	52.19
R.m.s deviations									
Bond lengths (Å)	0.007	0.006	0.007	0.007	0.007	0.007	0.009	0.007	0.007
Bond angles(°)	0.82	0.89	0.84	0.88	0.88	0.94	0.93	0.84	0.87
Ramach andran									
Favored (%)	97.99	97	98.63	98.67	97.17	92.48	95.41	97.32	97.01
Allowed (%)	2.01	2.83	1.37	1	2.33	7.17	4.24	2.68	2.82
Outliers (%)	0.00	0.17	0	0.33	0.5	0.35	0.35	0	0.17

**Table S1. Diffraction data and refinement statistics.** Related to Figures 4, 5, and STAR Methods.

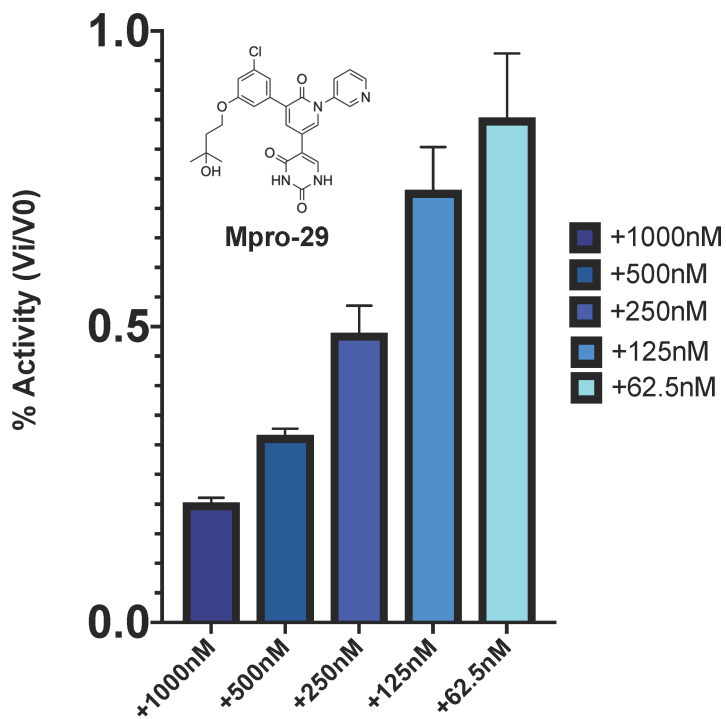
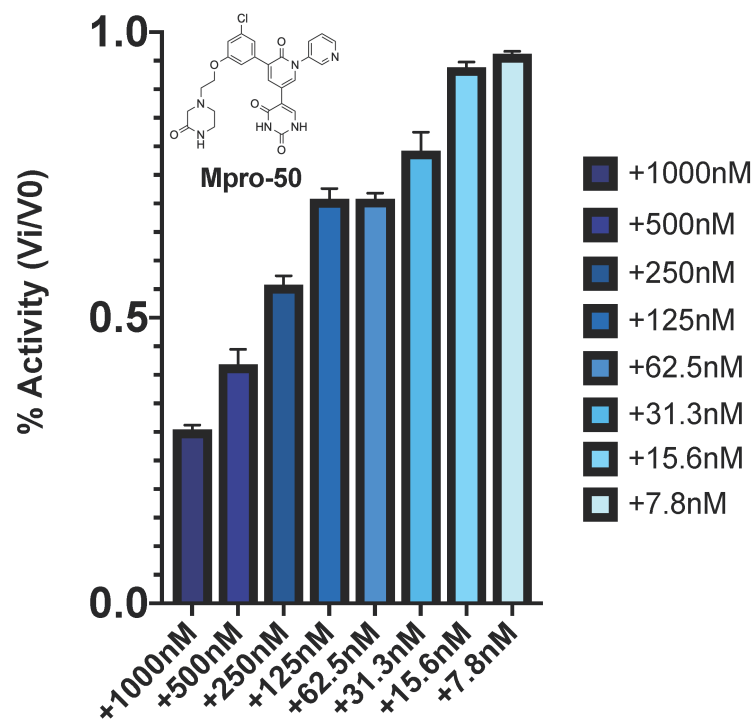


Figure S2. %Activity (Vi/V0) of M<sup>pro</sup> with compounds 50 (top) and 29 (bottom). Related to Table 1.

## NMR spectral data for synthesis of compounds 29 and 50

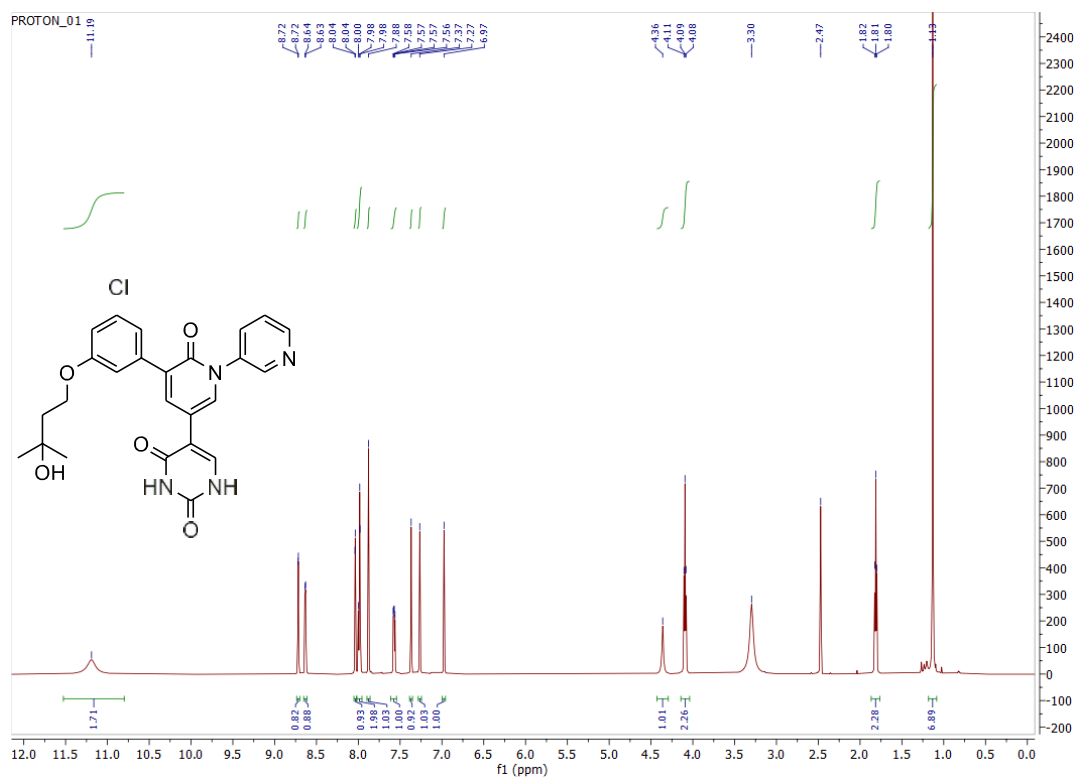


Figure S3. 29,  $^1\text{H}$  NMR (600 MHz,  $\text{DMSO-}d_6$ ). Related to STAR Methods.



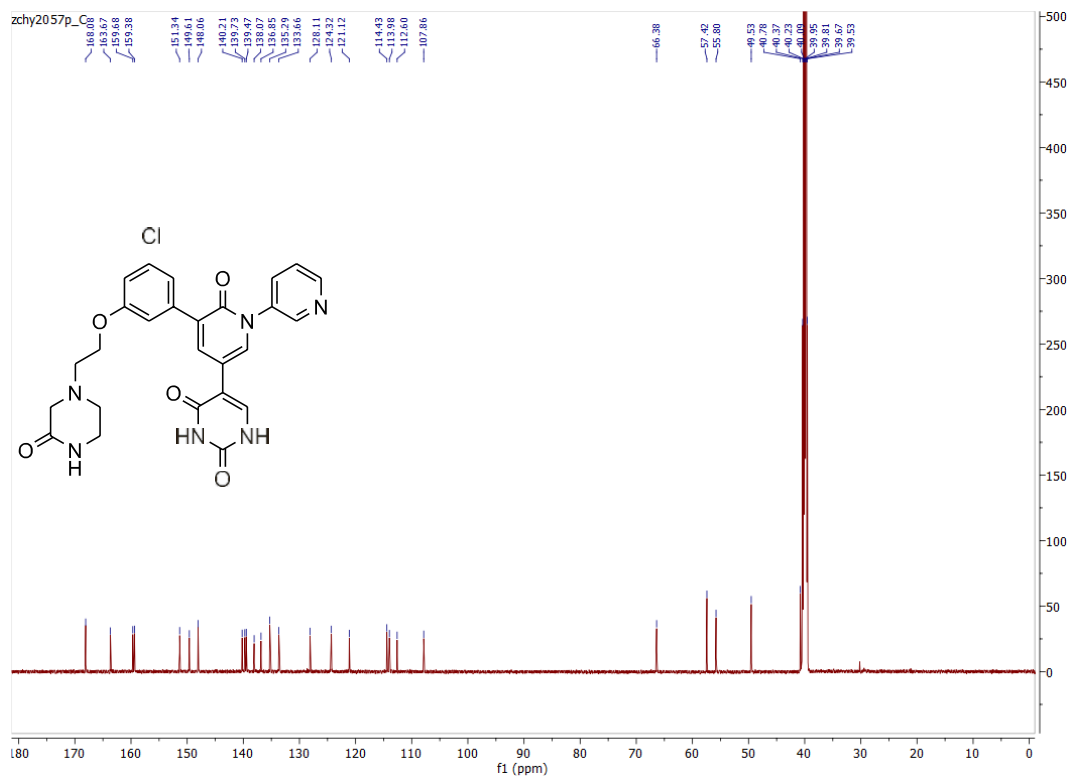


Figure S6. 50,  $^{13}\text{C}$  NMR (151 MHz,  $\text{DMSO-}d_6$ ). Related to STAR Methods.