Supplementary information Table S2: Table of Crystallization Statistics

Data Collection	**PDB ID 6WTT**
Structure	SARS-CoV-2 M^{pro} + GC-376
Space Group	P $3_2$21
Cell Dimension	
a, b, c (Å)	101.82, 101.82, 160.01
α, β, γ (°)	90, 90, 120
Resolution (Å)	50.00 - 2.15
	(2.19 - 2.15)
R_{merge}	0.110 (0.889)
<I>/σ<I>	28.6 (1.9)
Completeness (%)	100.0 (99.7)
Redundancy	9.5 (7.3)
Refinement	
Resolution (Å)	45.64 - 2.15
	(2.22 - 2.15)
No. reflections/free	52574 / 2714
R_{work}/R_{free}	0.22 /0.30
No. Atoms	7430
Protein	6963
Ligand/Ion	107
Water	340
B-Factors (Å^2)	
Protein	66.75
Ligand/Ion	67.17
Solvent	63.79
RMS Deviations	
Bond Lengths (Å)	0.014
Bond Angles (°)	1.93
Ramachandran Favored (%)	94.78
Ramachandran Allowed (%)	5.22
Ramachandran Outliers (%)	0.00
Rotameric Outliers (%)	2.33

***** Numbers in parentheses represent the highest resolution shell.