Supplementary information, Table S1: Data collection and refinement statistics

Data collection	SARS-CoV-2 HR121
Space group	**P 1 2 1**
Cell dimensions	
a, b, c (Å)	65.16, 51.73, 119.16
α, β, γ (°)	90.00, 95.33, 90.00
Wavelength (Å)	0.9791
Resolution (Å)	32.46 - 2.41 (32.55 - 2.41)
R_{merge}	0.02889 (0.9947)
$CC_{1/2}$	1 (0.434)
Mean I/σ(I)	10.62 (0.84)
Completeness (%)	99.46 (99.58)
Redundancy	2.0 (2.0)
Refinement	
Resolution (Å)	32.46-2.41
Total reflections	61592 (6140)
R_{work}/R_{free}	0.2489/0.2913 (0.4572/0.5382)
No. of atoms	
Protein	757
Water & ligands	0
Average B-factor (Å^2)	
Overall	91.01
Water & ligands	0
R.m.s. deviations	
Bond lengths (Å)	0.013
Bond angles (°)	1.53
Ramachandran outliers (%)	10.64
Ramachandran plot (%)	
Favored region	99.18
Allowed region	0.82
Disallowed region	0.00

*Highest resolution shell is shown in parentheses.