

Table S3. Benchmarking results for three domain regions of the modeled Wuhan strain S-protein structure against each of three experimentally determined S-protein structures, which were identified using PDB accession codes. Three metrics are used to assess the quality of the modeled structure against the experimental references: Global Distance Test – Total Score (GDT-TS), Template Modeling Score (TM)(TM score/number of residues for L1 and L2), and Root Mean Square Deviation (RMSD)(Å/number of residues), with L1 and L2 representing the lengths of Wuhan WT segment or the length of the modeled segment, respectively.

	Closed state: 6VXX-A			Open state: 6VYB-A			Open state: 6VYB-B		
	GDT-TS	TM	RMSD < 5 Å	GDT-TS	TM	RMSD < 5 Å	GDT-TS	TM	RMSD < 5 Å
NTD	97.936	0.772/279 0.985/218	0.71/218	95.952	0.741/279 0.980/210	0.85/210	97.783	0.72050/279, 0.98701/203	0.62/203
RBD	93.063	0.832/223 0.956/193	1.01/189	93.878	0.853/223 0.958/198	0.95/193	81.18	0.70537/223 0.83950/186	0.90/156
S2	97.691	0.931/462 0.993/433	0.66/433	97.384	0.924/462 0.992/430	0.68/430	97.454	0.92770/462 0.99167/432	0.69/432