

## **Supplemental Information**

### **Structures of Human Antibodies Bound to SARS-CoV-2 Spike Reveal Common Epitopes and Recurrent Features of Antibodies**

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## Supplemental Tables

**Table S1. Crystallographic data collection and refinement statistics for C105 Fab structure (related to Figure 5).**

<b>PDB ID</b>	<b>C105 Fab (12-I, SSRL) 6XCA</b>
<b>Data collection<sup>a</sup></b>	
Space group	I222
Unit cell (Å)	67.4, 120.1, 123.3
$\alpha, \beta, \gamma$ (°)	90, 90, 90
Wavelength (Å)	1.0
Resolution (Å)	38.9-1.80 (1.84-1.80)
Unique Reflections	46,713 (2752)
Completeness (%)	100 (99.8)
Redundancy	6.8 (6.5)
CC <sub>1/2</sub> (%)	98.8 (54.1)
$\langle I/\sigma I \rangle$	5.7 (1.2)
Mosaicity (°)	0.19
R <sub>merge</sub> (%)	18.1 (157)
R <sub>pim</sub> (%)	7.9 (70.5)
Wilson <i>B</i> -factor	16.8
<b>Refinement and Validation</b>	
Resolution (Å)	38.9 - 1.80
Number of atoms	
Protein	3,132
Ligand	10
Waters	477
R <sub>work</sub> /R <sub>free</sub> (%)	18.7/21.6
R.m.s. deviations	
Bond lengths (Å)	0.006
Bond angles (°)	0.853
MolProbity score	1.29
Clashscore (all atom)	4.2
Poor rotamers (%)	0
Ramachandran plot	
Favored (%)	97.6
Allowed (%)	2.4
Disallowed (%)	0
Average <i>B</i> -factor (Å)	27.1

<sup>a</sup>Numbers in parentheses correspond to the highest resolution shell

**Table S2. Cryo-EM data collection and refinement statistics for C105-S complex structure (related to Figure 5).**

	<b>C105 SARS-CoV-2 S 2P (state 1)</b>	<b>C105 SARS-CoV-2 S 2P (state 2)</b>
<b>PDB</b>	<b>6XCM</b>	<b>6XCN</b>
<b>EMD</b>	<b>22127</b>	<b>22128</b>
Microscope	Titan Krios	Titan Krios
Camera	Gatan K3 Summit	Gatan K3 Summit
Magnification	105,000x	105,000x
Voltage (kV)	300	300
Recording mode	counting	counting
Dose rate (e <sup>-</sup> /pixel/s)	22.1	22.1
Electron dose (e <sup>-</sup> /Å <sup>2</sup> )	60	60
Defocus range (μm)	1.0 - 2.5	1.0 - 2.5
Pixel size (Å)	0.418 (super resolution); 0.836 (binned)	0.418 (super resolution); 0.836 (binned)
Micrographs collected	5,940	5,940
Micrographs used	5,336	5,336
Total extracted particles	71,289	71,289
Refined particles	57,710	14,119
Symmetry imposed	C1	C3
Nominal Resolution (Å)		
FSC 0.5 (unmasked/masked)	3.90/3.60	4.00/3.60
FSC 0.143 (unmasked.masked)	3.40/3.20	3.50/3.40
Map sharpening <i>B</i> -factor		
<b>Refinement and Validation</b>		
Number of atoms		
Protein	25,973	27,798
Ligand	711	873
MapCC (global/local)	0.86/0.84	0.87/0.85
R.m.s. deviations		
Bond lengths (Å)	0.008	0.011
Bond angles (°)	0.812	0.893
MolProbity score	2.17	2.26
Clashscore (all atom)	13.6	14.8
Poor rotamers (%)	0.04	1.1
Ramachandran plot		
Favored (%)	90.9	89.9
Allowed (%)	9	10.1
Disallowed (%)	0.1	0

**Table S3. S protein mutations found in different SARS-CoV-2 isolates (related to Figure 6).**

<b>Mutation</b>	<b>Count</b>	<b>Frequency(%)</b>	<b>Location</b>
D614G	9688	63.2	S1 domain D
P1263L	115	0.7	S2 cytoplasmic tail
L5F	91	0.6	signal sequence
D936Y	88	0.6	S2 HR1
L54F	58	0.4	S1 domain A
G1124V	56	0.4	S2
N439K	38	0.2	S1 domain B (RBD)
H49Y	35	0.2	S1 domain A
L18F	31	0.2	S1 domain A
L8V	30	0.2	signal sequence
A831V	29	0.2	S2
D839Y	28	0.2	S2
V483A	28	0.2	S1 domain B (RBD)
Q675H	24	0.2	S1 domain D
S50L	24	0.2	S1 domain A
S943P	22	0.1	S2 HR1
A1078S	21	0.1	S2
R21I	19	0.1	S1 domain A
V367F	18	0.1	S1 domain B (RBD)
T29I	18	0.1	S1 domain A

List of SARS-CoV-2 spike mutations with a frequency  $\geq 0.1\%$  in a set of 15335 isolates downloaded from the Global Initiative for Sharing All Influenza Data (GISAID) SARS-CoV-2 sequence database on 5/3/20 (Elbe and Buckland-Merrett, 2017; Shu and McCauley, 2017).

The genomes were processed with the nextstrain augur pipeline

(<https://github.com/nextstrain/augur>) (Hadfield et al., 2018), using MAFFT v7.464 (Kato and Standley, 2013) for sequence alignment and FastTree (Price et al., 2010) to generate a phylogenetic tree. The resulting data were then analyzed with a custom Swift program.