

Supplemental information

An infectivity-enhancing site on the SARS-CoV-2 spike protein targeted by antibodies

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Table S1. Cryo-EM data collection and processing statistics, related to Figure 5.

Sample	Spike protein			Spike protein with 8D2 Fab			Spike protein with COV2-2490 Fab		
Data collection									
Microscope	Titan Krios			Titan Krios			Titan Krios		
Acc. Voltage (kV)	300			300			300		
Total electron dose (e ⁻ /Å)	50			50			50		
Pixel size (Å)	0.88			0.88			0.88		
Defocus range (µm)	-0.8 – -2.0 (0.15)			-0.8 – -2.0 (0.15)			-0.8 – -2.0 (0.15)		
Magnification	81,000			81,000			81,000		
Corrected Cs (mm)	0.0452			0.059			0.0355		
Data processing									
Software	CryoSparc v3.0.1			CryoSparc v3.0.1			CryoSparc v3.0.1		
# of Micrographs	5,075			2,135			5,177		
# of particles	74,756	161,974	161,524	99,745	743,99	137,974	104,069	33,092	
Symmetry				C1					
# of antibody	-	1	1	1	1	1	3	2	
Resolution (Å, GS-FSC=0.143)	3.36	3.46	3.53	3.82	4.16	3.74	3.15	4.06	
EMDB ID	30915	30916	30117	30918	30919	30920	30921	30922	
Model building									
Method	Homology modeling & Rigid body fitting			Homology modeling & Rigid body fitting			Homology modeling & Rigid body fitting		
Template model (spike)	7KEB			7K8W			7K8W		
Template model (Fab)				5K8M*1			5K8M*1		
Fitting software				MODELL ER v9.23			MODELL ER v9.23		
Fitting Criteria				UCSF Chimera v1.14			UCSF Chimera v1.14		
Correlation after fitting				0.829			0.780		
Modeling software (Fab)				Repertoire Builder			Repertoire Builder		
# of Atoms	13,452			15,212			18,708		
Ramachandran Favored (%)	93			95			95		
Allowed (%)	5			4			4		
Outlier (%)	2			1			1		
Clash score	2			3			1		
RMSZ bound length (Å)	0.87			0.93			0.94		
RMSZ bound angle (°)	0.95			0.91			0.91		
PDBID	7DZW			7DZX			7DZY		
Related figure	Figure 5D Figure S4D	Figure S4E	Figure S4F	Figure 5D Figure S4G	Figure S4H	Figure S4I	Figure 5D Figure S4J	Figure S4K	

*1 The variable region of Fab was modelled by Repertoire Builder. See details in Methods.