

Fig S1. ACE2 Competition

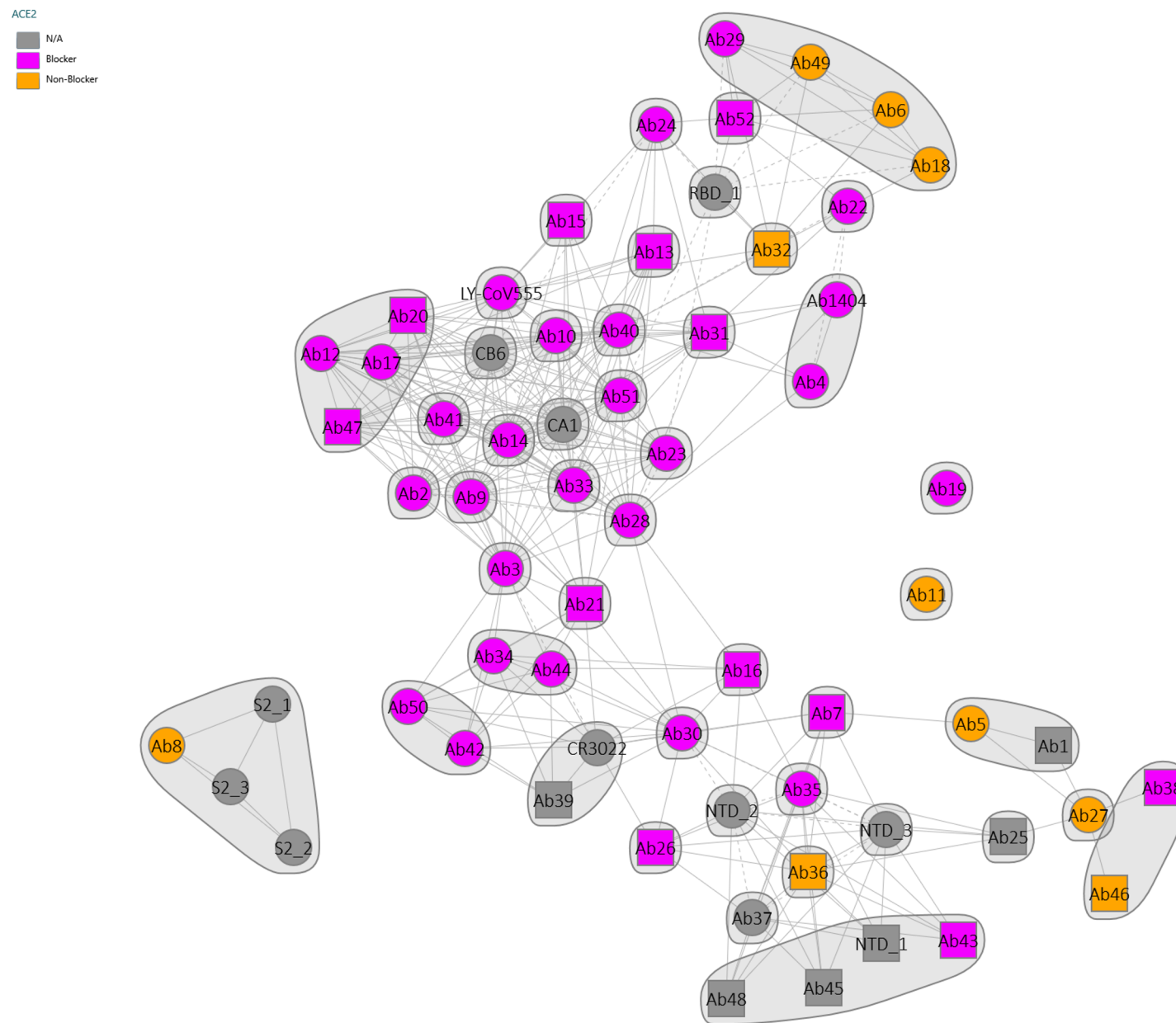


Fig S2. LY-CoV1404 binding to trimeric S protein

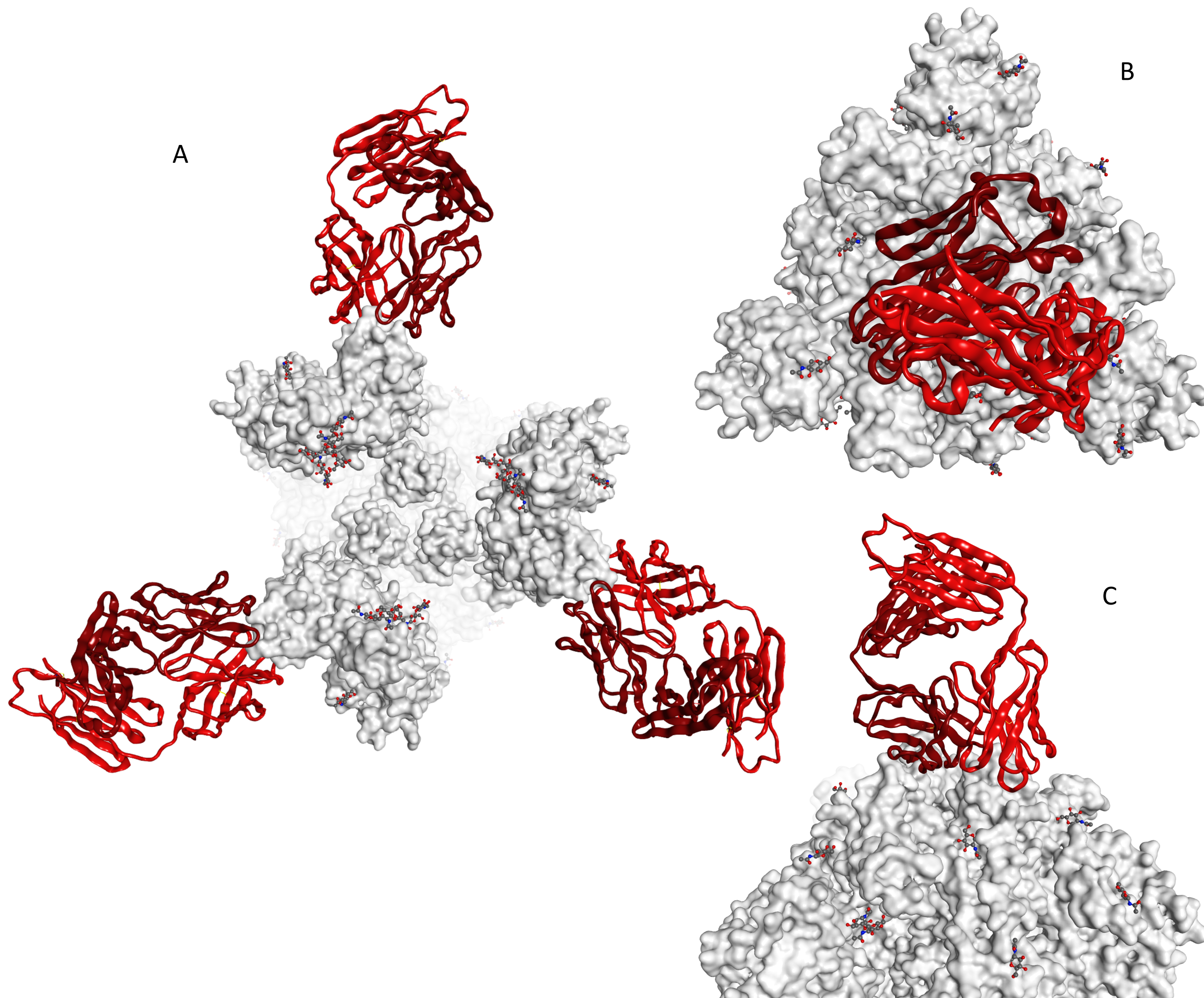


Table S1. Crystallographic statistics

	LY-CoV1404 + spike protein RBD
Data collection	
Space group	P2(1)2(1)2(1)
Cell dimensions a, b, c (Å)	73.09, 107.69, 190.47
Cell dimensions alpha, beta, gamma (°)	90, 90, 90
Resolution (Å)	94-2.43 (2.57-2.43)*
R-merge	0.069 (0.690)
I / sigma(I)	15.0 (2.5)
Completeness (%)	99.8 (99.9)
Redundancy	6.4 (6.8)
Refinement	
Resolution (Å)	94-2.43
No. of reflections	57431
R-work (%) / R-free (%)	23.5 / 26.4
No. of non-hydrogen atoms protein / ligand / water	9236 / 14 / 73
B-factors protein / ligand / water	60.2 / 72.8 / 44.8
Root mean squared deviations bond length (Å) / bond angle (°)	0.011 / 1.63
Ramachandran distribution phi-psi favored (%) / phi-psi allowed (%)	97.0 / 99.8

*Values in parenthesis denote highest resolution shell

Table S2. Summary of atomic interactions at the RBD epitope.

Antibody	PDB ID	atom-atom contacts	H-bonds	RBD contact surface area Å²
LY-CoV1404		198	12	584
REGN10987	6XDG	70	6	343
Fab 2-7	7LSS	156	10	496