

Expanded View Figures

Figure EV1. Kinetic characterization of sybodies by GCI.

- A RBD-vYFP and ECD were immobilized as indicated and the six top sybodies were injected at increasing concentrations ranging from 1.37 nM to 1 μ M. Data were fitted using a Langmuir 1:1 model.
- B In-depth affinity characterization of Sb#15 and Sb#68. RBD-vYFP and S-6P were immobilized as indicated and Sb#15 and Sb#68 were injected at concentrations ranging from 1.95 to 250 nM for Sb#15 and 3.9 to 500 nM for Sb#68. For RBD, data were fitted using a Langmuir 1:1 model. For S-6P, the data were fitted with the heterogeneous ligand model, because the 1:1 model was clearly not appropriate to describe the experimental data. Corresponding data for S-2P is shown in main Fig 1A.

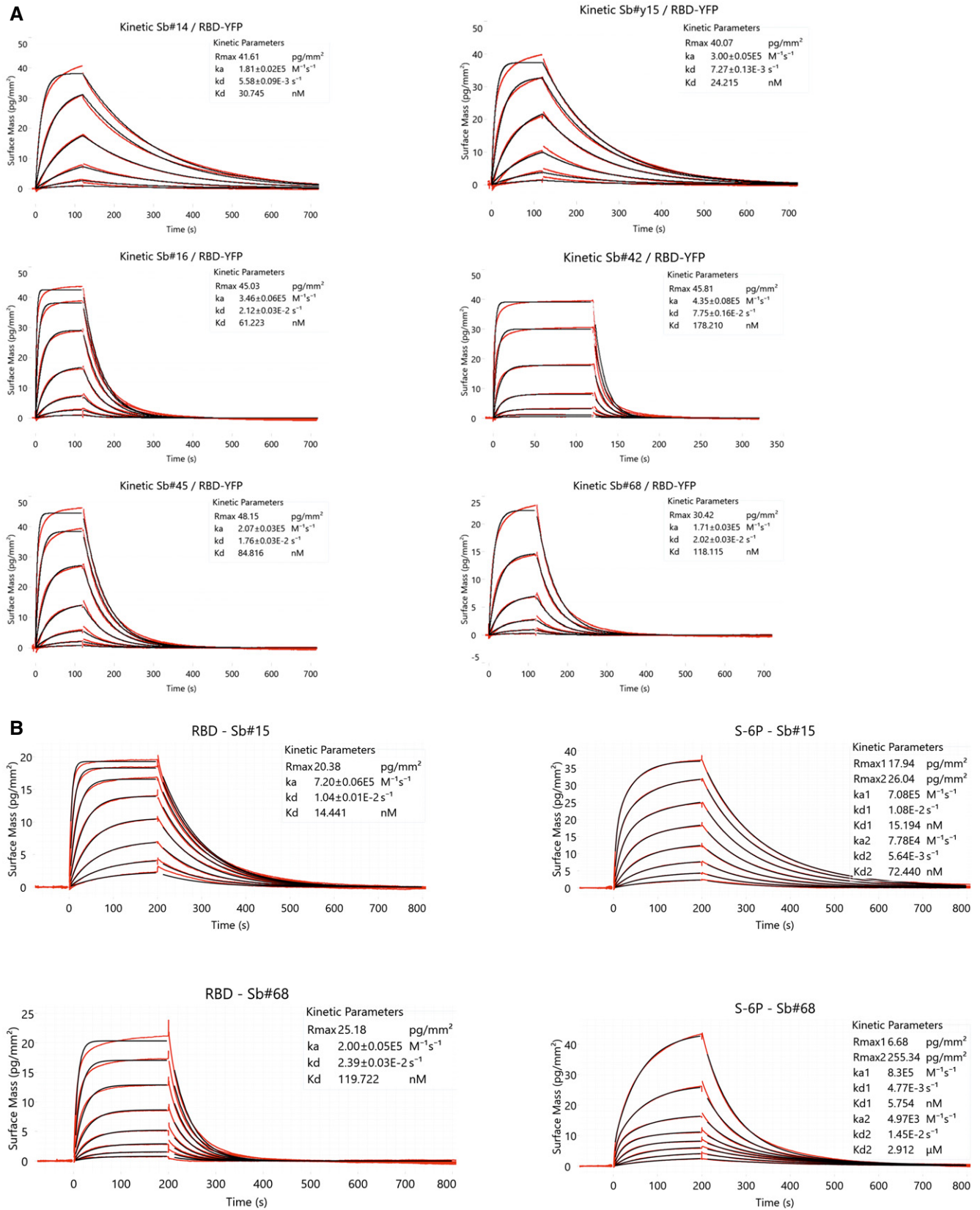


Figure EV1.

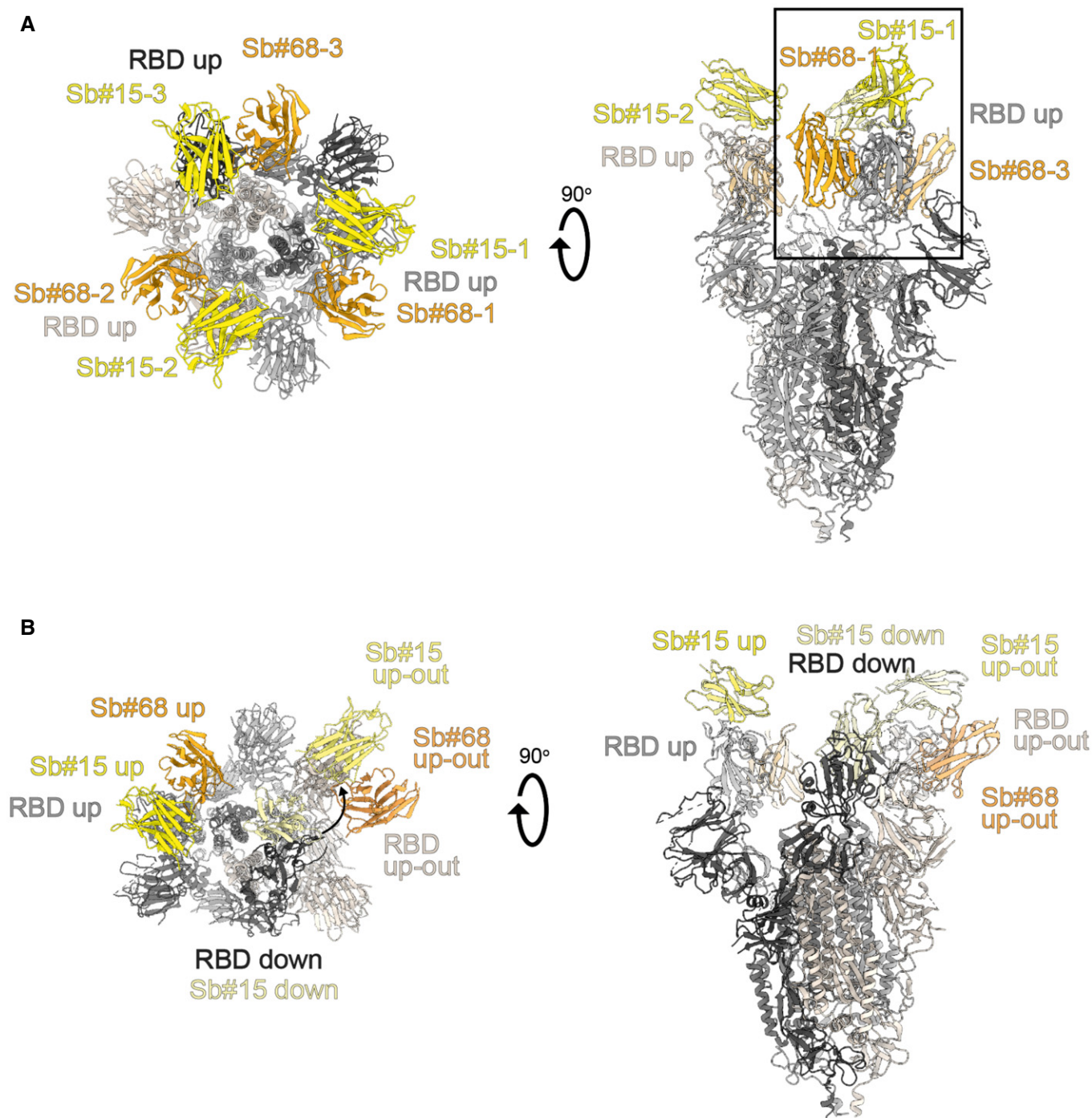


Figure EV2. Structures of S-2P spike in complex with both Sb#15 and Sb#68.

A Structure of S-2P with both Sb#15 and Sb#68 bound to each RBD adopting a symmetrical *3up* conformation. Based on the cryo-EM map shown in main Fig 5A, a model shown as ribbon was built using pre-existing structures (PDB ID:6X2B for S-2P; PDB ID:3K1K for Sb#15; PDB ID:5M13 for Sb#68).

B Structure of S-2P with the three RBDs adopting an asymmetrical *1up/1up-out/1down* conformation. Based on the cryo-EM map shown in Fig 5B, a model shown as ribbon was built using pre-existing structures (PDB ID:6X2B for S-2P; PDB ID:3K1K for Sb#15; PDB ID:5M13 for Sb#68). The *up-out* state is pushed outward by the adjacent RBD in a *down* state with bound Sb#15 (arrow). Spike protein is shown in shades of gray, Sb#15 in yellow, and Sb#68 in orange.

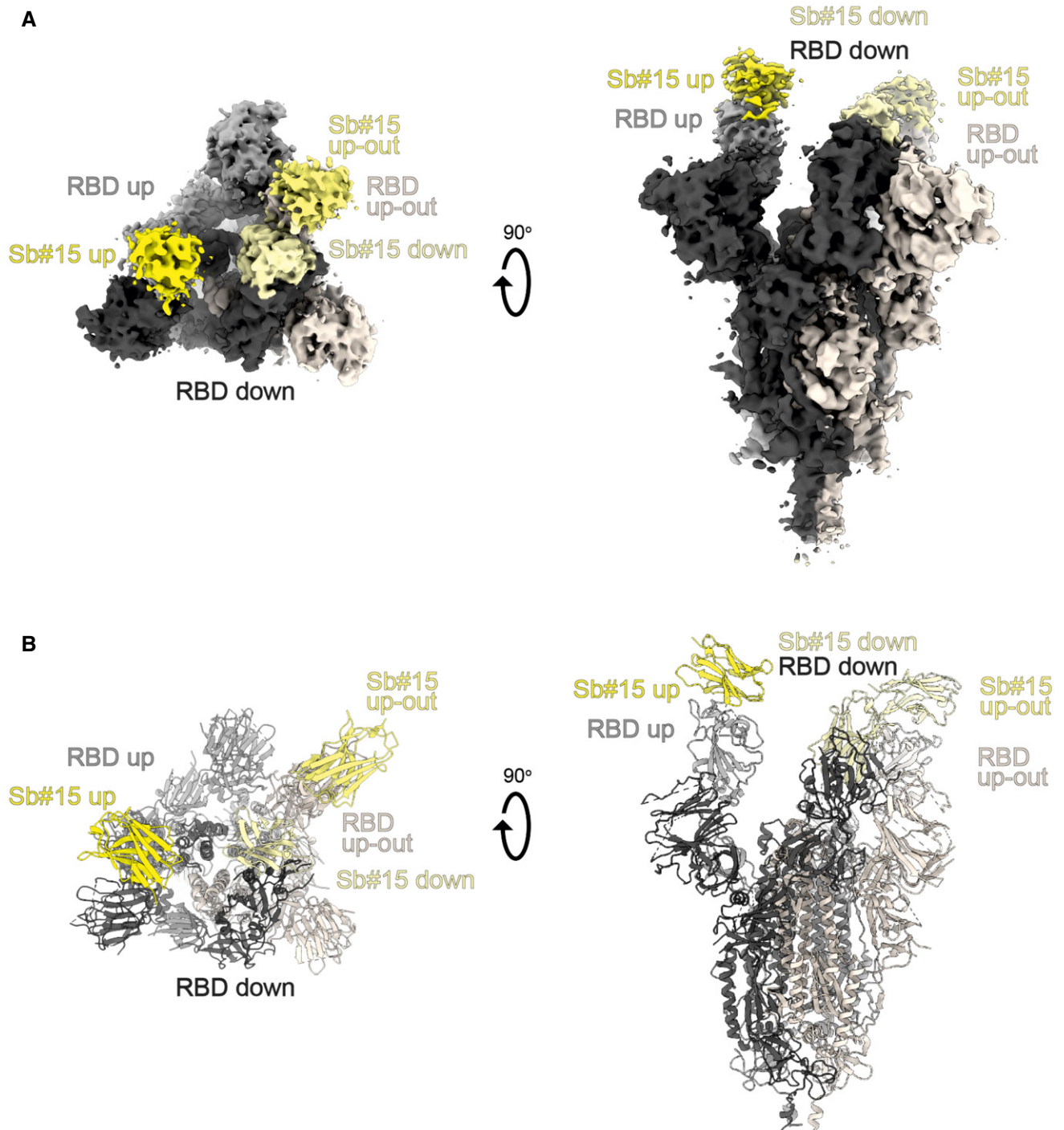


Figure EV3. Structural analysis of the S-2P/Sb#15 complex.

A Cryo-EM map of S-2P with Sb#15 bound to each RBD adopting an asymmetrical *1up/1up-out/1down* conformation.

B The corresponding model built using pre-existing structures (PDB ID:6X2B for S-2P; PDB ID:3K1K for Sb#15) is shown as ribbon. Final map blurred to a B factor of -30 \AA was used for better clarity of the less resolved RBDs and sybodies. Spike protein is shown in shades of gray and Sb#15 in yellow.

Figure EV4. Structural analysis of S-2P/Sb#68 complex.

- A Cryo-EM map of S-6P, with an *1up/2down* RBD conformation.
- B The corresponding model is shown as ribbon (PDB ID:6ZGG for S-6P). No densities for Sb#68 were observed.
- C Cryo-EM map of S-6P, with two Sb#68 bound to *up*-RBDs of the spike featuring a *2up/1flexible* conformation.
- D The corresponding model built on pre-existing structures (PDB ID:6X2B for S-6P; PDB ID:5M13 for Sb#68) is shown as ribbon.
- E Sb#68 cannot bind to *up*-RBD if the neighboring RBD exhibits a *down* conformation due to steric clashing. Final maps blurred to a B factor of -30 \AA were used for better clarity of the less resolved RBDs and sybodies. Spike protein is shown in shades of gray and Sb#68 in orange.

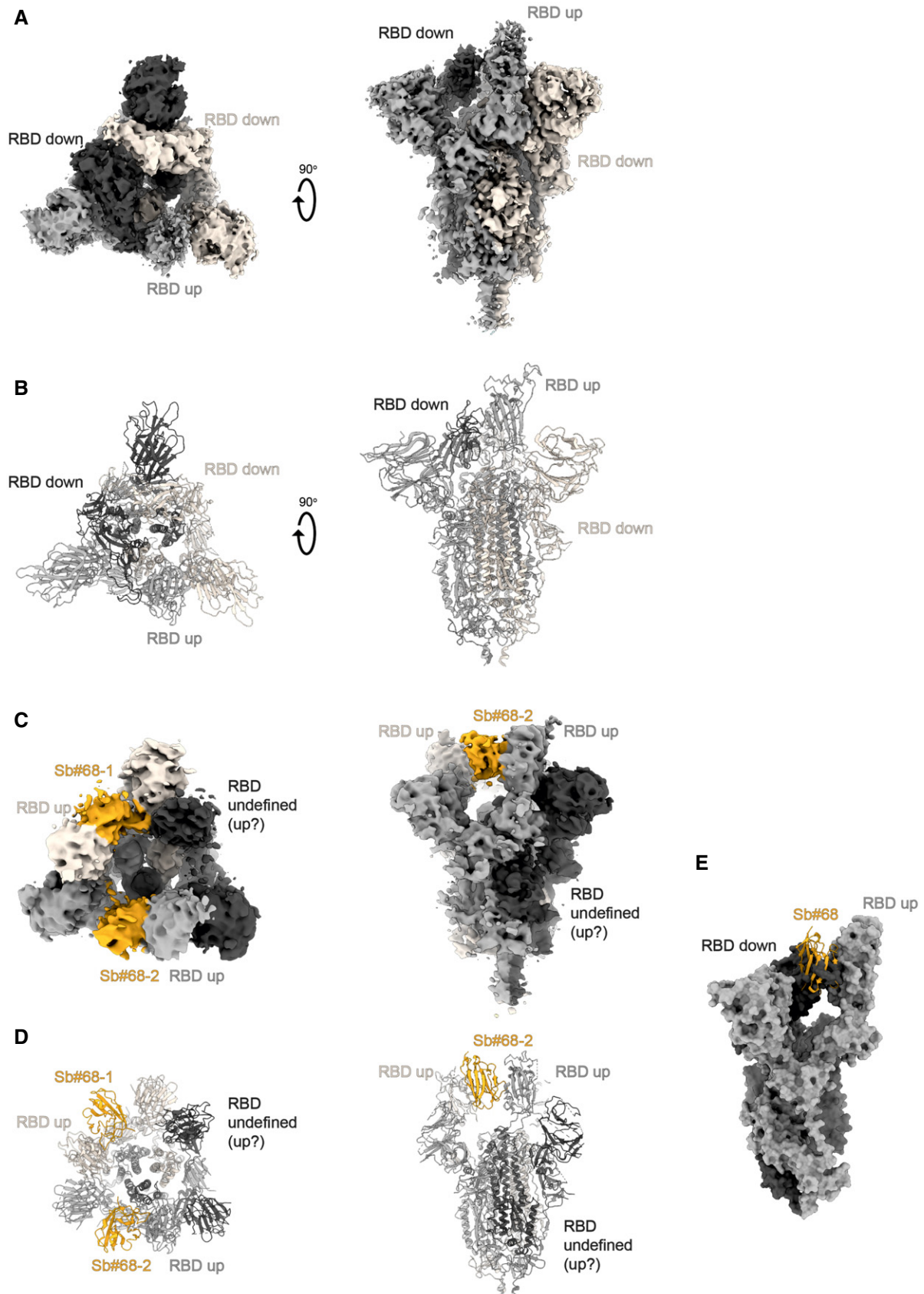


Figure EV4.

Figure EV5. Antibody, nanobody, and sybody binding to RBD epitopes.

- A Schematic representation of the ACE2 binding site and the cryptic epitope on the RBD.
- B Sb#15 binds to the top of RBD (the ACE2 epitope) and Sb#68 binds to the side of the RBD and recognizes a conserved cryptic epitope.
- C Superposition of the structures of binders recognizing the cryptic epitope: EY6A (PDB ID: 6ZCZ), CR3022 (PDB ID: 6W41), Nb12 (PDB ID:7MY3), Nb30 (PDB ID:7MY2), VHH-U (PDB ID: 7KN5), VHH-V (PDB ID: 7KN6), VHH-W (PDB ID: 7KN7), NM1226 (PDB ID: 7NKT), and WNb10 (PDB ID: 7LX5).
- D Superposition of the structures of binders recognizing the ACE2 epitope: WNb2 (PDB ID: 7LDJ), H11-D4 (PDB ID: 6YZ5), SR4 (PDB ID: 7C8V), Nb20 (PDB ID: 7JVB), VHH E (7KN5), NM1230 (PDB ID: 7B27), and MR17m (PDB ID: 7C8W). Structures are shown as surfaces.

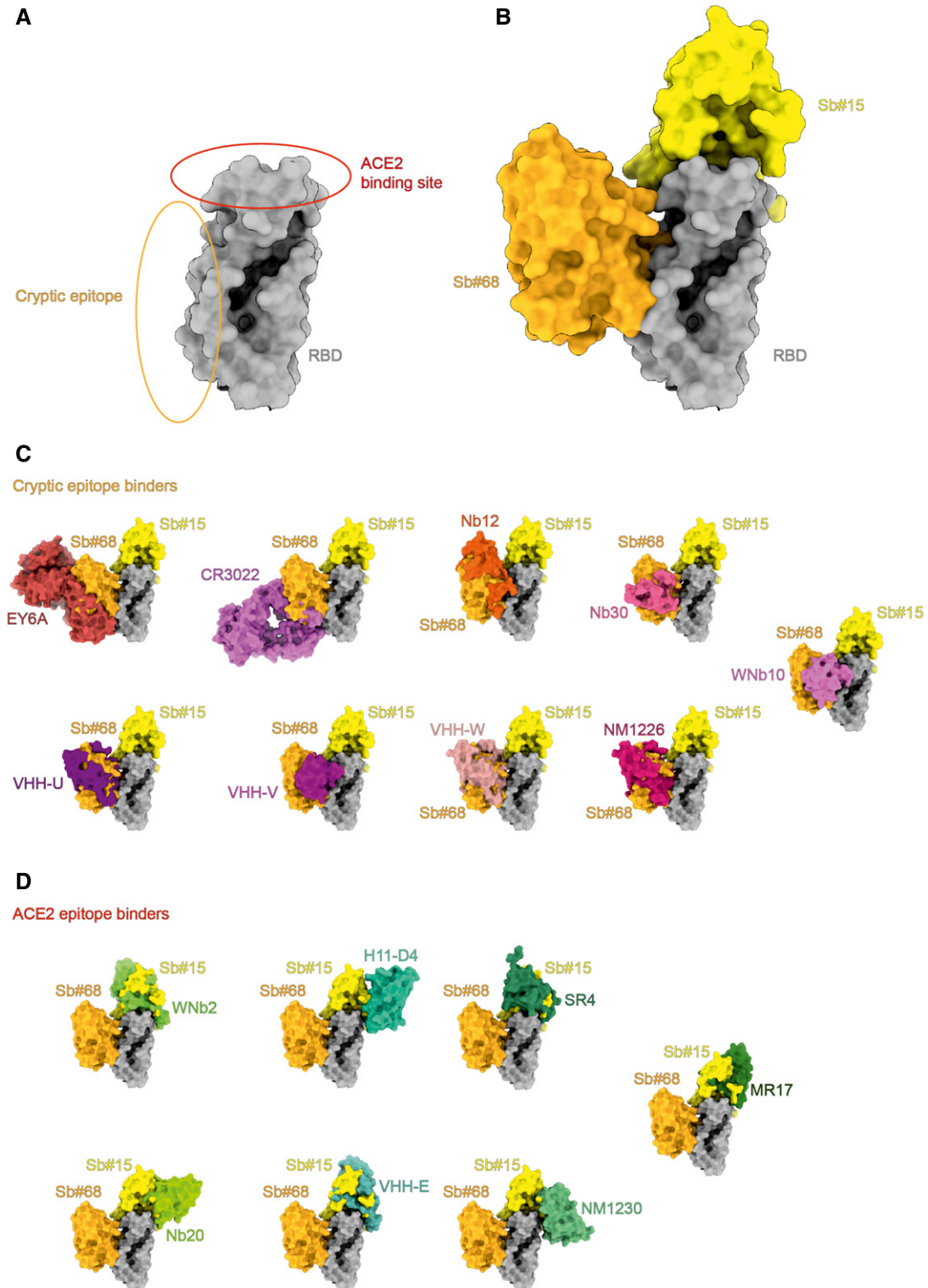


Figure EV5.