

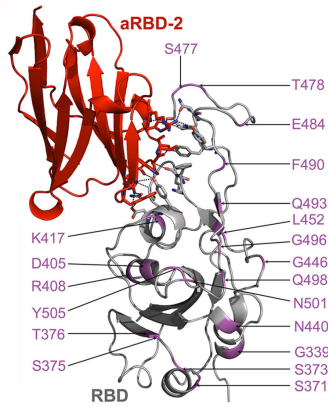
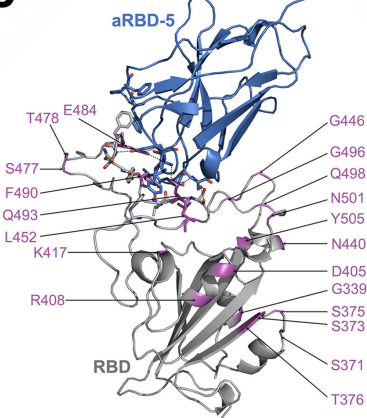
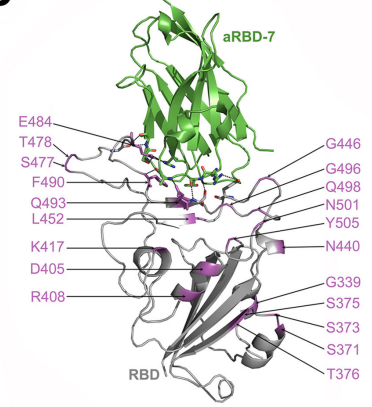
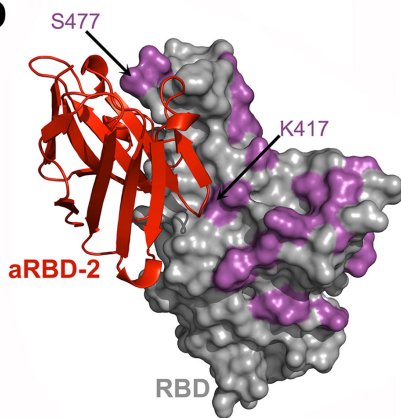
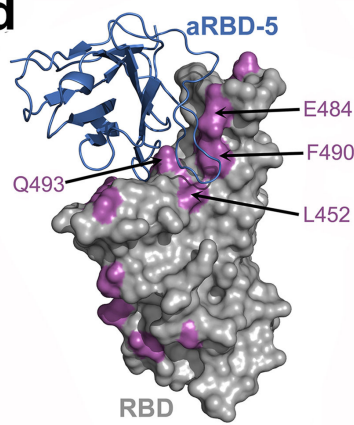
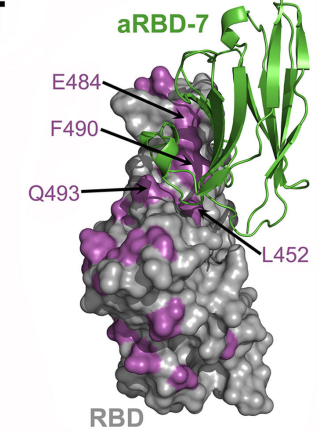
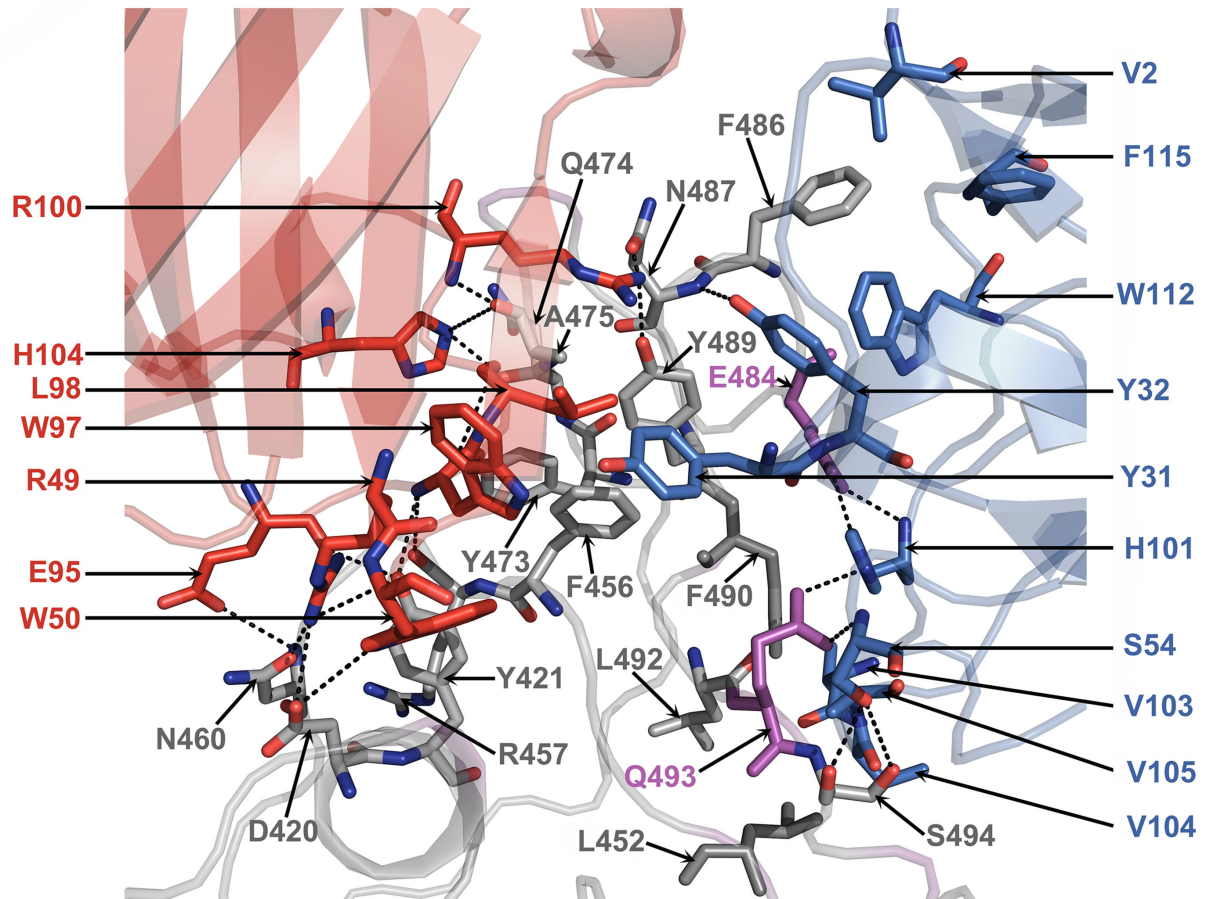
a**c****e****b****d****f****g**

Fig. S7 Display of mutation sites that affect the RBD binding of aRBD-2, aRBD-5, and aRBD-7. A total of 20 sites (magenta), including G339, S371, S373, S375, T376, D405, R408, K417, N440, G446, L452, S477, T478, E484, F490, Q493, G496, Q498, N501 and Y505, are mutated in the RBD of Alpha, Beta, Gamma, Delta, Delta plus, Kappa, Lambda, Omicron BA.1 and BA.2 variants. These mutation sites are displayed on the structures of aRBD-2: RBD (**a**), aRBD-5: RBD (**c**), and aRBD-7: RBD (**e**) complexes. Residues that form interactions are shown as sticks, and hydrogen bonds and salt bridges between the Nbs and RBD are shown as black dotted lines. Residues that may affect the RBD binding of the aRBD-2 (**b**), aRBD-5 (**d**) and aRBD-7 (**f**) are indicated by arrows. **g** Possible mechanism by which aRBD-5 contributes to the overall binding affinity of aRBD-2-5 for the Omicron RBD. The structure of aRBD-2: RBD complex is aligned with that of aRBD-5: RBD complex, interacting residues are shown as sticks, and hydrogen bonds and salt bridges between the Nbs and RBD are shown as black dotted lines. E484 and Q493 in magenta are two mutation sites in the Omicron variant.