Structural basis for the neutralization of MERS-CoV by a human monoclonal antibody MERS-27

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Figure S1. Gel filtration profiles and SDS-PAGE gels of purified MERS-CoV RBD, MERS-27 Fab, and the RBD-Fab complex.

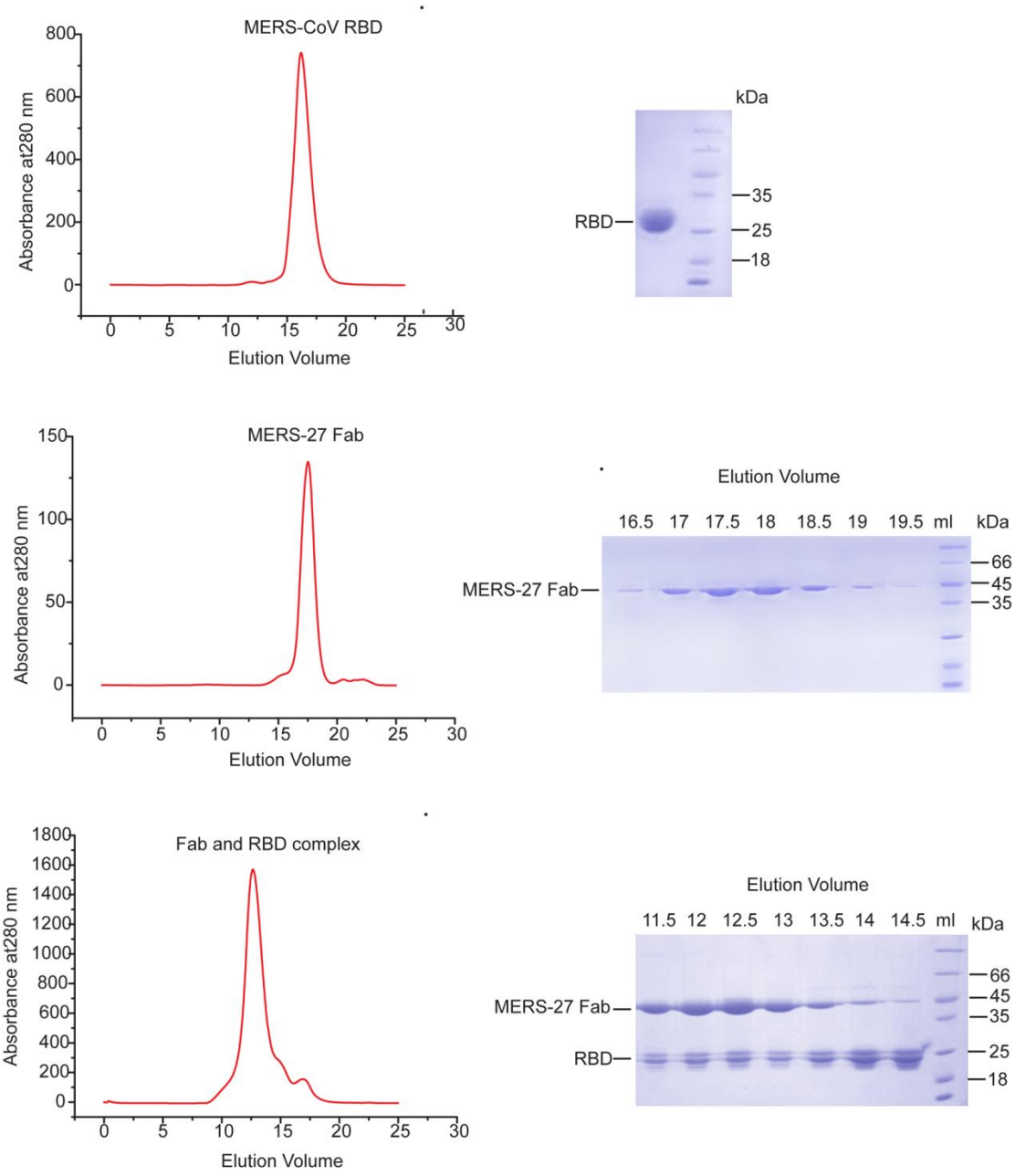

Figure S2. Stereo view of the two complexes of MERS-CoV RBD with MERS-27 Fab in the crystallographic asymmetric unit.

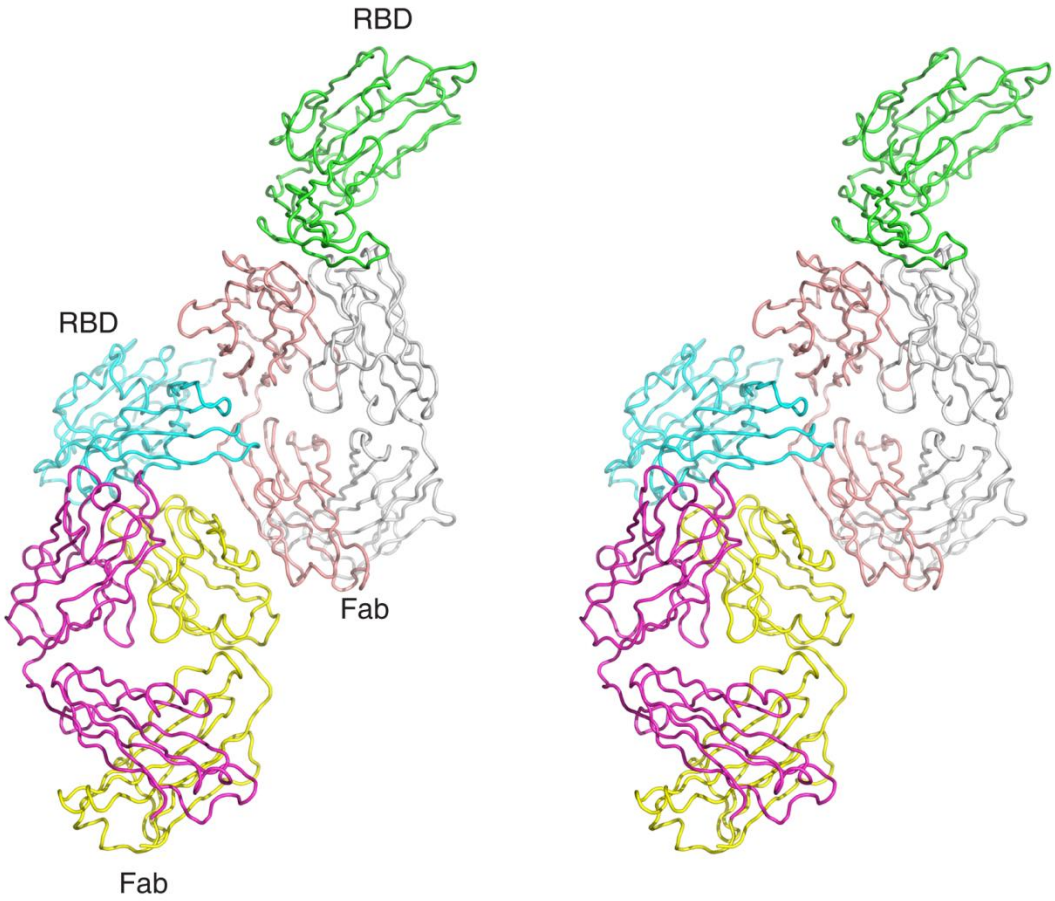

Figure S3. Structural superimposition of RBD in unbound (blue), DPP4-bound (orange), and MERS-27-bound (green) states.

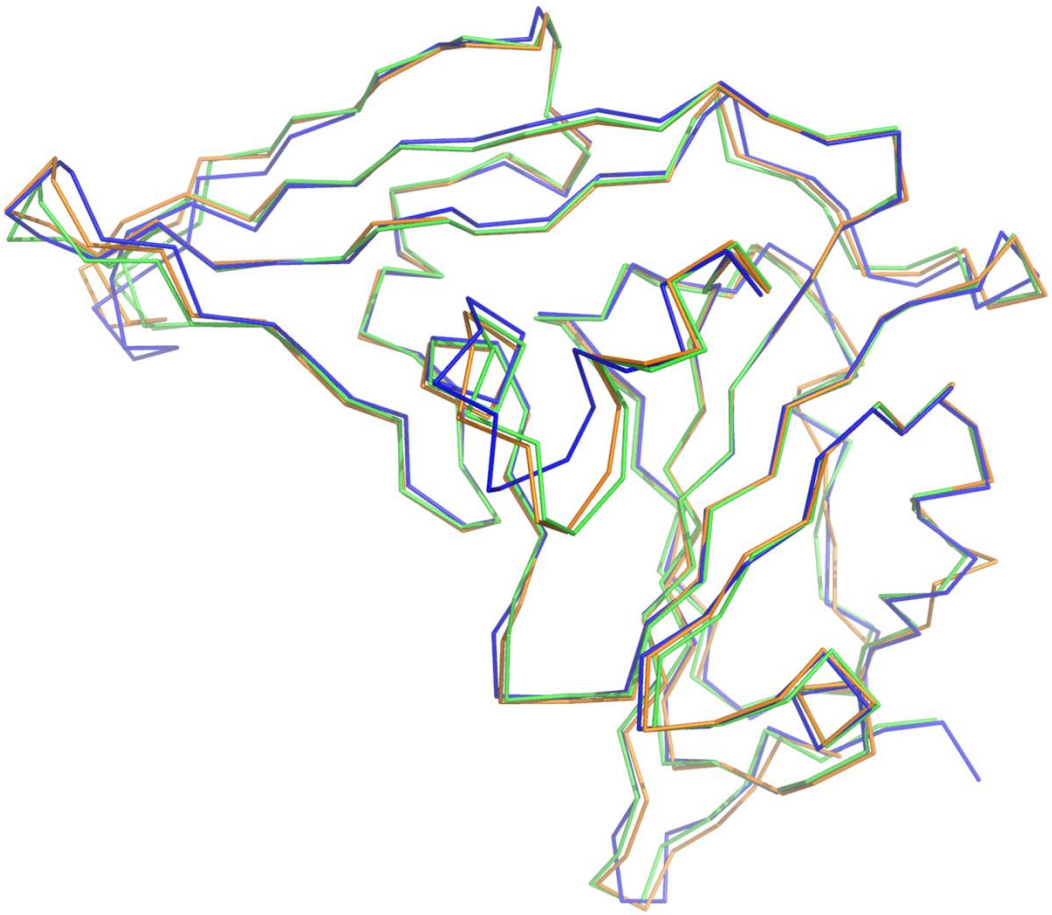

Figure S4. The MERS-CoV RBD residue Asp539 forms a hydrogen bond with Tyr33 of heavy chain upon MERS-27 binding (**A**). This RBD residue forms a salt bridge with Lys267 upon receptor DPP4 binding (**B**).