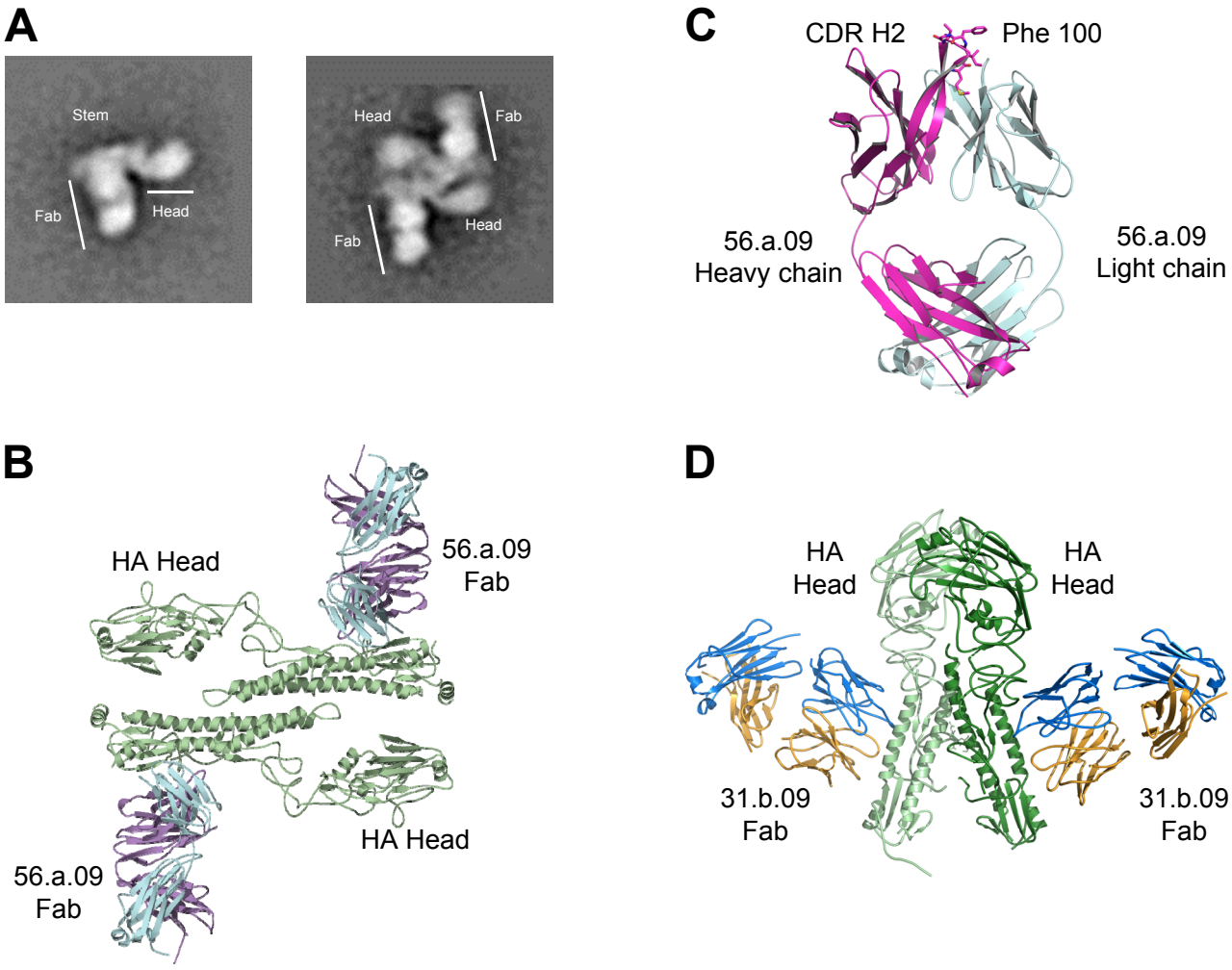

Figure S5. Negative-stain microscopy and crystal structure of the antigen-binding fragment (Fab) for antibody, 56.a.09, alone and in complex with HA0, and for the complex of 31.b.09 with HA0, related to Figures 2 and 3. (A) Negative-stain electron microscopy of monomeric and head-to-stem dimeric complex of 56.a.09 and the HA0 of A/Hong Kong/1-4-MA21-1/1968 (H3N2). **(B)** Crystal packing of the 56.a.09 and HA0 A/Hong Kong/1-4-MA21-1/1968 (H3N2) complex closely resembles the head-to-stem dimer observed by negative-stain electron microscopy. The 56.a.09 heavy chain is depicted in purple and the light chain is depicted in light blue. The HA0 is depicted in pale green. A complex and its nearby crystallographic symmetry mate are shown. **(C)** Crystal structure of 56.a.09. The antibody structure is depicted in ribbon conformation with the heavy chain colored in light purple and light chain in pale cyan. The CDR H3 residues that are part of the conserved recombination sequence (Met-Ile-Phe-Gly-Ile) are shown in stick representation. The Phe residue points out away from the antibody while the conserved Met residue stacks against the antibody light chain. **(D)** Crystal packing of the 31.b.09 Fab and HA0 A/California/04/2009 (H1N1). The 31.b.09 Fab heavy chain is colored blue and the light chain is colored orange with the HA molecules colored in pale and dark green.