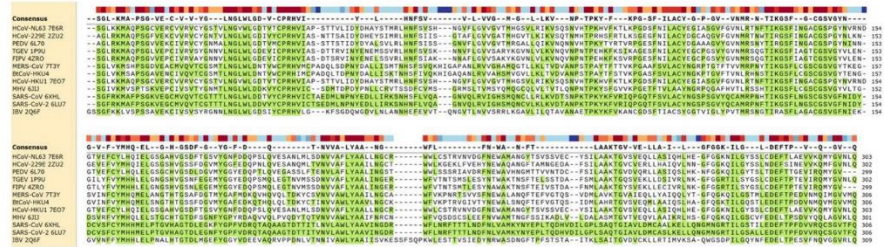


A



B

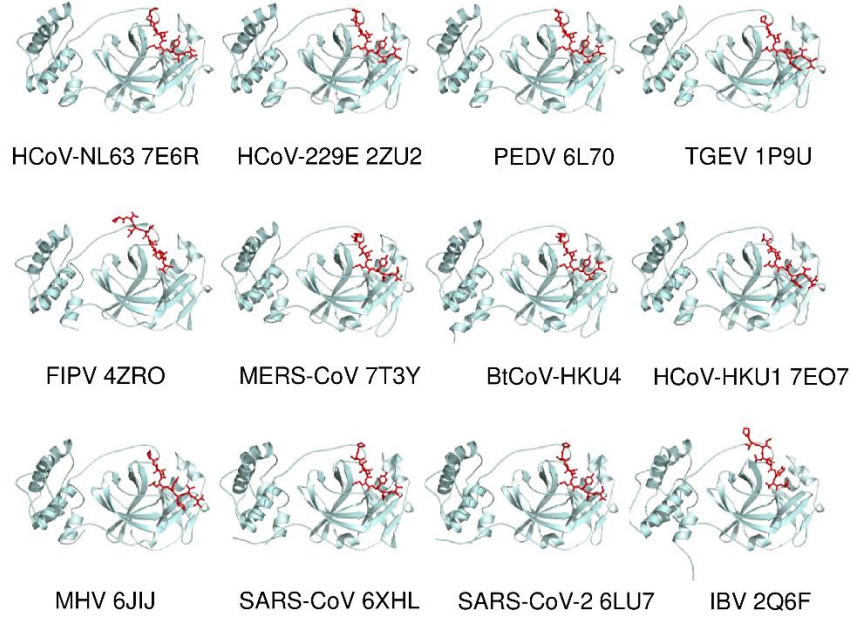


Figure S1. The multi-sequence alignment and structural binding modes of 3CLpro among different viral strains. (A) Multi-sequence alignment of 3CLpro. (B) Conservation of the P1 peptide binding modes within the active pockets of twelve 3CLpro strains.