Supplementary Figure

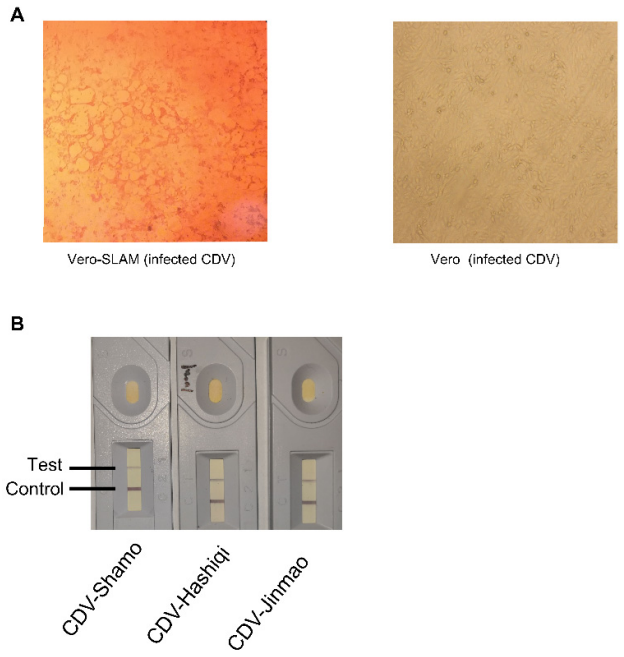


Figure S1. Cytopathic effects (CPE) induced by canine distemper virus (CDV) infection and colloidal gold immunochromatographic strip detection of viral antigen.

(A) Vero-SLAM cells infected with the wild-type CDV-Shamo strain, showing typical syncytium formation and cytopathic effects (CPE). Parental Vero cells inoculated with the same CDV-Shamo strain. No visible CPE was observed at 4 days post-infection. Consistent with the absence of CPE, the culture supernatant tested negative for CDV antigens using a colloidal gold immunochromatographic assay (data not shown), confirming the inability of the wild-type virus to replicate in the absence of the SLAM receptor.

(B) Colloidal gold-based rapid diagnostic test strips detecting CDV antigen in three different viral isolates. From left to right: CDV-Shamo, CDV-Hashidi, and CDV-Jinmao. All three samples show positive results with clear test (T) and control (C) lines visible, indicating successful detection of CDV antigen.

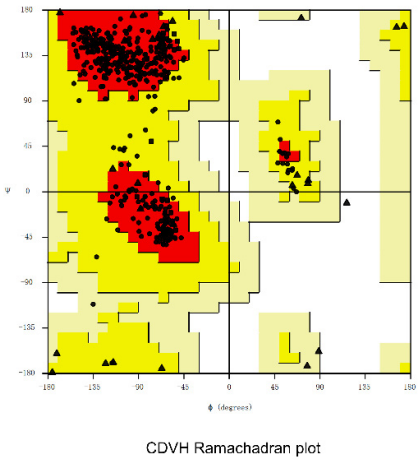


Figure S2. Ramachandran plot evaluating stereochemical quality of the CDV-H ectodomain model.
The model of the Canine Distemper Virus H protein ectodomain (472 residues) was constructed via homology modeling using the PDB entry 7ZNY (Chain C) as a template. Of 411 non-Gly and non-Pro residues, 373 (90.8%) reside in most favored regions, 36 (8.8%) in additional allowed regions, 2 (0.5%) in generously allowed regions, and 0 (0.0%) in disallowed regions. This analysis confirms excellent overall backbone geometry with all residues falling within acceptable conformational spaces.

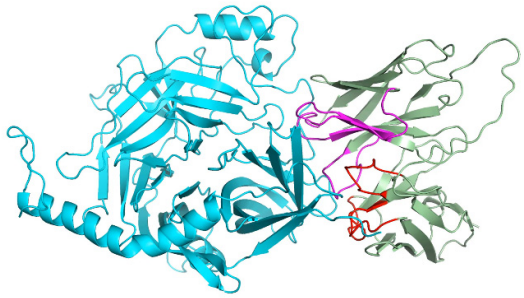


Figure S3. Molecular dynamics simulation trajectory of the CDV-H/scFv complex
Representative snapshot from the 100 ns MD simulation illustrates the binding interface between the Canine Distemper Virus Hemagglutinin (CDV-H) and the specific scFv. The CDV-H protein is shown in cyan, and the scFv is depicted in pale green. The Complementarity Determining Regions (CDRs), which are crucial for antigen recognition, are highlighted: CDR-L1, L2, and L3 are colored in red, while CDR-H1, H2, and H3 are colored in magenta. Throughout the 100 ns simulation, the scFv maintained a stable conformation, and the CDR loops (both light and heavy chains) exhibited sustained and robust interactions with the CDV-H antigen.