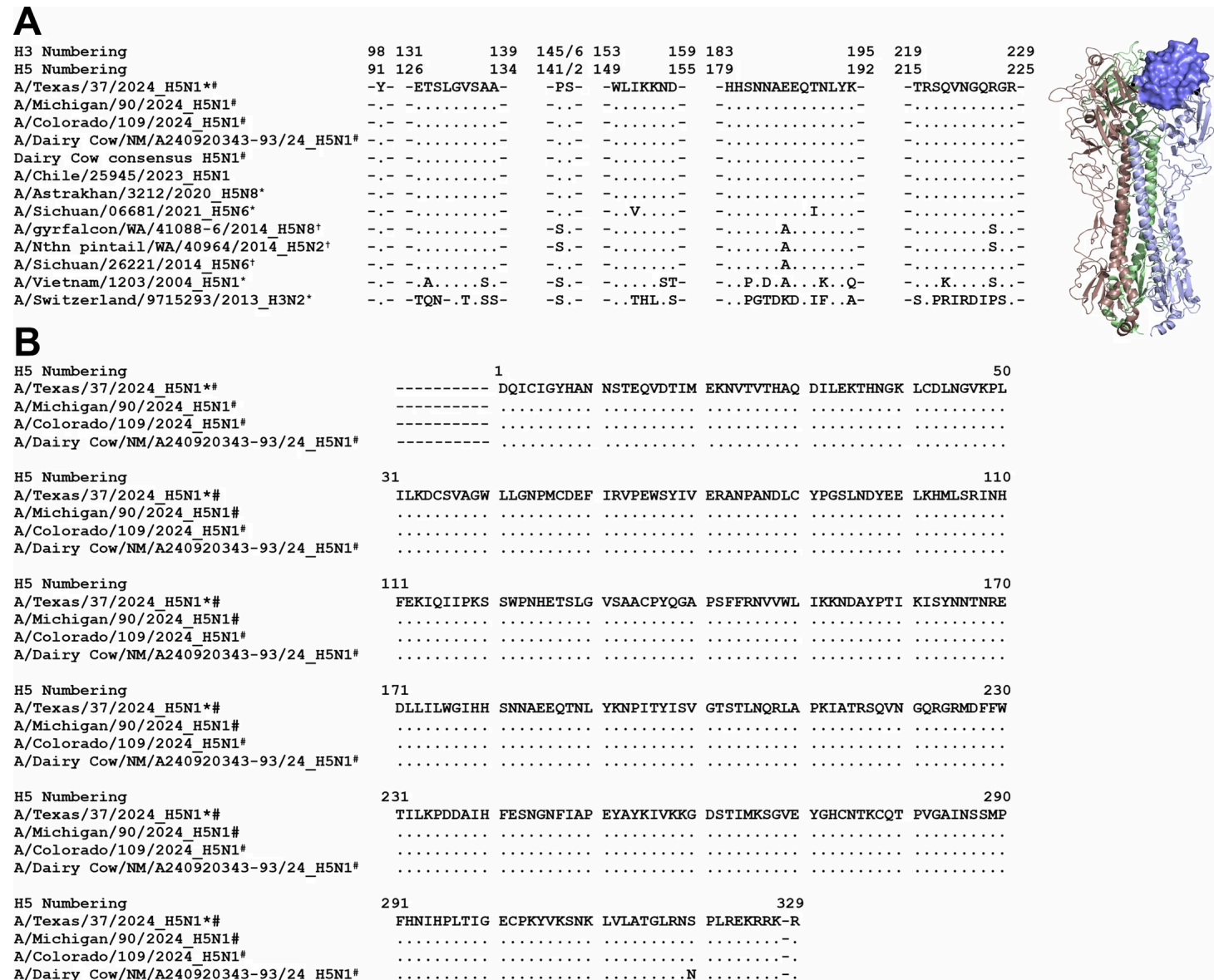


Extended Data Fig. 1: Comparison of receptor binding site residues in diverse H5 HAs.

From: [Transmission of a human isolate of clade 2.3.4.4b A\(H5N1\) virus in ferrets](#)



(A) Sequence residues that comprise the TX/37 HA receptor binding site (RBS) aligned with HA sequences from this and a previous study⁴⁴, as well as with a recent bovine A(H5N1) virus sequence that reported both human and avian receptor binding¹⁸. Alignments with amino acid positions (H3 and H5 numbering) are indicated above the alignment. Conserved residues are indicated as dots. The position of the RBS on the HA is illustrated on the TX/37 structural model. The HA is illustrated as a cartoon, while the receptor binding site residues listed in the alignment are shown as a surface representation. Figure was generated using PyMol 2.5.5. *Current data. †HAs with published glycan array binding results. #Isolates associated with dairy farm outbreaks including dairy cow isolate consensus sequence. (B) Full alignment of the HA for all viruses associated with dairy farm outbreaks included in A.

