**Suppl 9.** A single glutamine to leucine mutation at residue 226 of the virus hemagglutinin was sufficient to enact the change from avian to human specificity.

(**A**) The three dimensional structure of Texas H5 HA was determined at 2.80-Å resolution. One HA monomer is highlighted in gray for 220-loop. The receptor binding site is composed of the 220-loop. Key residues and additional mutations analyzed in this study are shown as red and lavender dots, respectively. (**B**) Sequence comparison of 220-loop of WT Texas with human pandemic H1, H2, and H3 HA and human-infecting H5N1 HA. The hallmark residues for switch of receptor binding preference in 220-loop are highlighted in red. For HA-receptor analogs complexes, we used LSTa (Neu5Acα2-3Galβ1-3GlcNAcβ1-3Galβ1-4Glc), and LSTc (Neu5Acα2-6Galβ1-3GlcNAcβ1 3Galβ1-4Glc).

**ダイアグラム

AI によって生成されたコンテンツは間違っている可能性があります。(A)**

**(B)**

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | 220-loop | | | | | | | | Binging efficiency with 2.6SA |
| Strain | 221 | 222 | 223 | 224 | 225 | 226 | 227 | 228 |  |
| A/Texas/37/2024 H5N1 | S | Q | V | N | G | Q | R | G | NO |
| Bovine-A/Texas/37/2024 H5N1 | S | Q | V | N | G | L | R | G | Strong |
| A/California/06/2009/H1N1 | S | Q | V | R | G | L | R | G | Strong |