

Objectives of 3D visualization of influenza proteins:

Neuraminidase (NA): <https://www.rcsb.org/structure/1RU7>

Neuraminidase (NA) enables the release of new viral particles by cleaving sialic acid residues. In this 3D visualization, distinct orange regions on the surface likely represent active or antigenic sites critical for enzymatic function and immune evasion. These strategically positioned regions interact with sialic acid and host immune components, making them key areas for mutations that enhance drug resistance or immune escape. Understanding these structural and functional dynamics helps us NA's rapid evolution and its role in driving the need for annual flu vaccines.

Hemagglutinin (HA): <https://www.rcsb.org/structure/4N5Z>

Hemagglutinin (HA) facilitates the virus's entry into host cells by binding to receptors and initiating membrane fusion. In this 3D visualization, the orange regions represent the receptor-binding and fusion domains, while the purple highlights likely indicate antigenic sites where mutations occur to evade immune detection. These distinct regions illustrate the structural complexity of HA, emphasizing how small changes can impact its ability to interact with host cells and avoid antibodies. Seeing these mutation-prone areas helps us identify conserved regions critical for vaccine design

PB1 and PB2 Protein Complex: <https://www.rcsb.org/structure/3A1G>

PB1 serves as the catalytic core of the influenza virus RNA-dependent RNA polymerase complex. In this visualization, the green regions represent the conserved structural domains essential for RNA synthesis, while the orange sections highlight functional motifs involved in nucleotide binding. The purple spheres indicate interaction sites that coordinate with other polymerase subunits. The central reddish core houses the active site where RNA synthesis occurs. PB2 is responsible for recognizing and binding host cell mRNA caps. The 3D visualization reveals potential binding sites for antiviral compounds. The protein's structure reveals distinct functional domains: a cap-binding domain that recognizes host mRNA caps, and regions that interact with both PB1 and viral RNA.

Disclaimer: Our project primarily focused on analyzing white-tailed eagle influenza data. However, since the eagle data did not include specific accession IDs for individual proteins, we used the Human influenza protein structures as a reference. These visualizations help illustrate the structural features and evolutionary dynamics of these proteins, highlighting their progression and their critical role in viral adaptation and the need for annual vaccine updates.