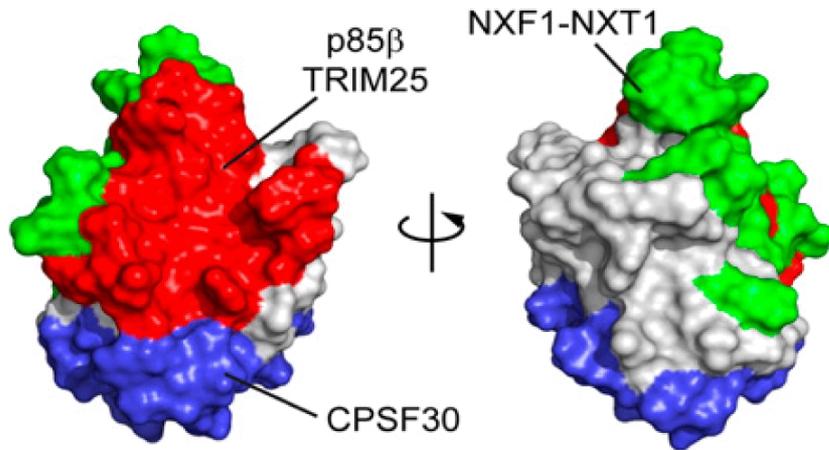


Pandemic Influenza is Dynamic



Surface representation of the NS1 protein from the 1918 influenza virus with its binding interfaces. The pandemic NS1 protein was found to be highly dynamic, whereas seasonal NS1 is mostly static.

J.-H. Cho, B. Zhao, J. S. hi, N. Savage, Q. Shen, J. Byrnes, L. Yang, W. Hwang, P. Li. *Proc Natl Acad Sci USA* **117** (12), 6550-6558 (2020).

Work was performed in part at Brookhaven National Laboratory

Scientific Achievement

Scientists discovered a drastically different binding mechanism for the protein, NS1, in the pandemic and seasonal influenza, explaining the higher severity in the pandemic strain.

Significance and Impact

Understanding the difference between the 1918 influenza pandemic and seasonal outbreaks can offer a new pathway to different drug targets for influenza.

Research Details

- Nonstructural protein 1 (NS1) increased the severity of the influenza by activating a host protein through binding to p85 β .
- Comparison between the binding mechanism between NS1 and p85 β in the seasonal vs. pandemic influenza showed that pandemic NS1 is highly dynamic, whereas seasonal NS1 is mostly static.
- X-ray scattering data collected at the LiX beamline at NSLS-II were instrumental in this work.