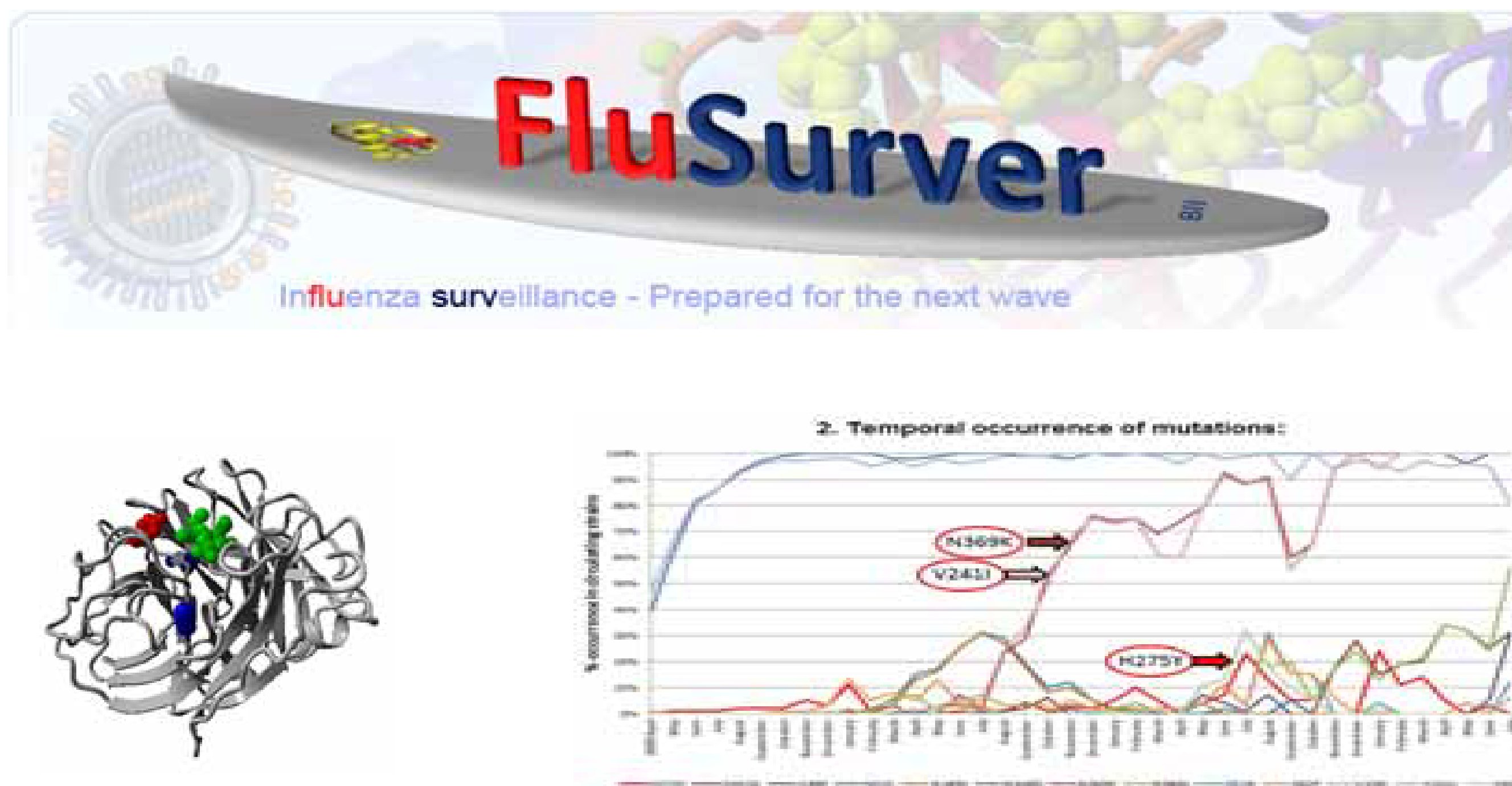


## FLUSURVER

ONLINE DATABASE FOR MONITORING FLU INFLUENZA



### CHALLENGES

(Clockwise from top)

1) FluSurver Banner

2) Temporal Occurrence of Mutations

3) A structure of the model, showing the position of mutations during drug binding

Increased interest in influenza due to the Swine flu pandemic and new Avian flu outbreaks combined with more generally available and cheaper sequencing methods gave rise to an increasing amount of influenza sequences. It became difficult for researchers and clinician scientists to rapidly and accurately screen their influenza sequences for potentially interesting mutations.

### OUR SOLUTION

The team from A\*STAR's Bioinformatics Institute (BII) developed the FluSurver, with the help of collaborators from all over the world<sup>1</sup>. The FluSurver is an online research tool developed to help the influenza research community to identify, analyze and interpret mutations in influenza sequences. By simply submitting the influenza sequence into the system, the FluSurver will then furnish details about the geographic and temporal frequency of the occurrence, along with any co-occurrence of mutations. Using its in-house database of curated literature annotations for mutation effects, FluSurver is able to provide details of phenotypic changes as well. In addition, FluSurver will show the position of the mutation in structural models, indicating if the location of the mutation is close to any common drug binding or functionally important sites.

### BENEFITS

Simply paste in a protein or nucleotide FASTA sequence(s), or upload the sequence FASTA file into the FluSurver. The FluSurver will instantly produce mutation annotation results, with details of the structure, epidemiology and associated published literature.

### APPLICATIONS

The FluSurver has already been instrumental in the discovery of new influenza strain variants with altered susceptibility, host specificity and antigenic properties.

<sup>1</sup>The BII Team collaborated with a few organizations that provided sequences for analysis, allowing the development of the FluSurver into a useful tool for the influenza research community. The collaborators include the Genome Institute of Singapore (GIS), INMEGEN Mexico City, National Public Health Laboratory (NPHL) of the Ministry of Health Singapore, IAL Sao Paulo, the WHO Collaborating Centre for Reference and Research on Influenza and the Global Initiative for Sharing All Influenza Data (GISAID).

