Role of the water molecules in the structure and function of viral protein and virus infectivity.
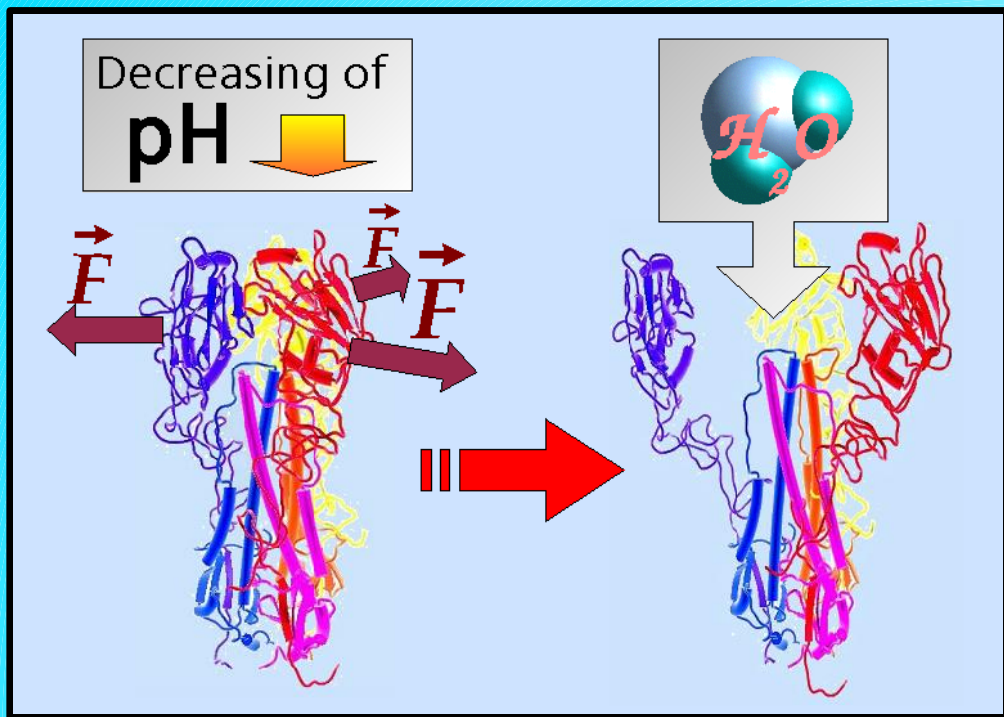
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of the Federal Service for Surveillance on Consumer Rights Protection and Human Well-being,
Koltsovo, Novosibirsk Region, Russia.
Novosibirsk State University,
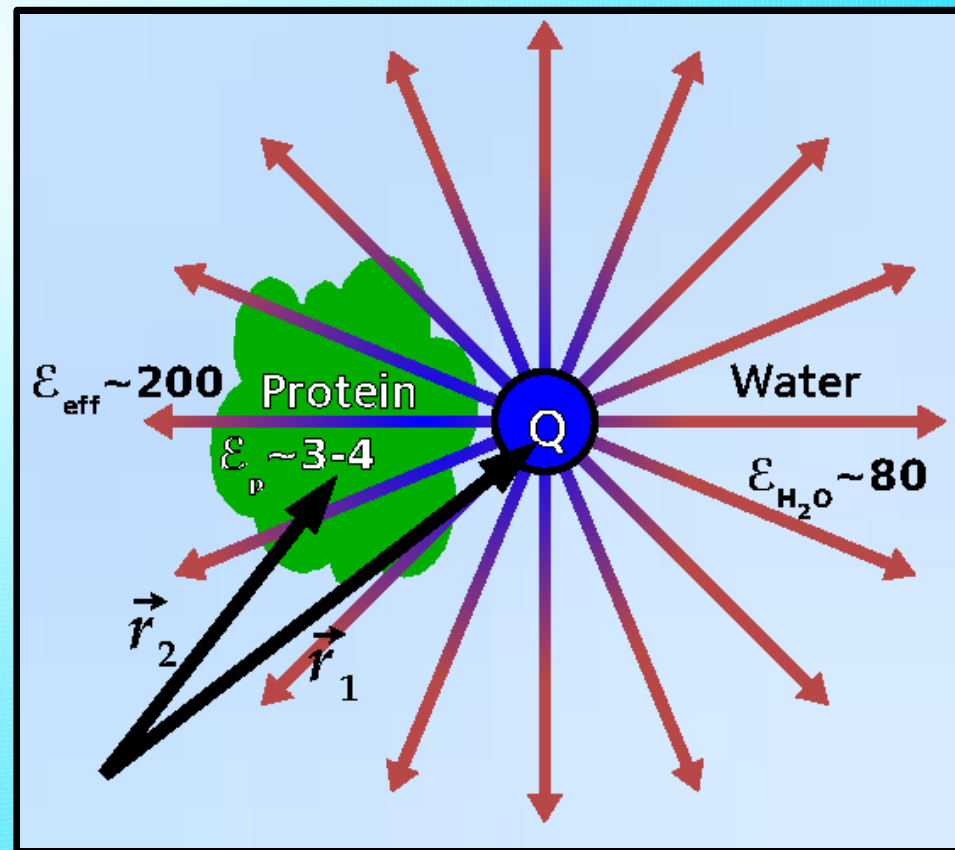Pirogova Street 2, Novosibirsk, Russia.

$$\vec{E}(\vec{r}_0) = \vec{E}_Q(\vec{r}_0 - \vec{r}_1) + \vec{E}_{\text{polarization effects}}(\vec{r}_0, \vec{r}_1, \vec{r}_2);$$

$$E_Q = \frac{Q}{\varepsilon_{H_2O} \cdot r^2}, \quad \vec{r} = \vec{r}_0 - \vec{r}_1;$$

$$E = \frac{Q}{\varepsilon(\vec{r}_1, \vec{r}_2) \cdot r^2}$$

Results

- The physical model for calculation of polarization effects for protein interactions was developed.
- The role of water molecules in the setting of threshold value of repulsive forces of hemagglutinin protein domains at the trigger stage of conformational changes was shown.
- Kinetics of virus-induced hemolysis for different influenza virus strain was experimentally measured.
- Trigger pH values for different influenza virus were both calculated with help of the program and measured experimentally.