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RESEARCH INSTITUTE FOR FUNDAMENTAL SCIENCES

*Frontiers of Science*

# Biological Sciences Seminar Series

## Protein Structure Prediction

***Virtual Venue: December 10 2020, 19:00 - 20:00 (GMT +3), Zoom Meeting ID: 914 4127 4679***


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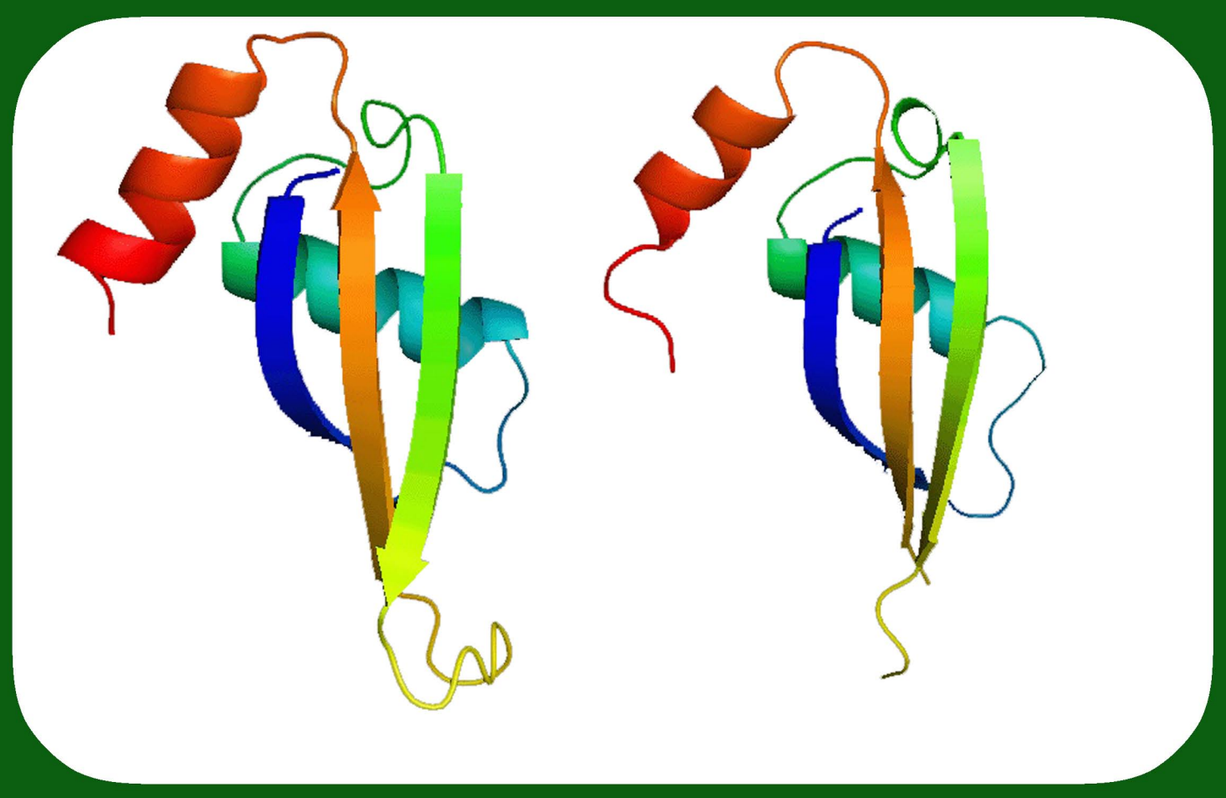

Protein structure prediction aims to determine the spatial location of every atom in protein molecules from the amino acid sequence by computational simulations. In this talk, we first review recent progress in computer-based protein structure prediction and show that the problem can be solved in principle by template-based modeling in case that threading could recognize the best structural templates from the Protein Data Bank. Next, we discuss the results of protein structure prediction in the most recent community-wide blind CASP experiments, and show that new approaches combining ab initio folding and deep neural-network contact and distance predictions can break through the barrier of physics-based protein folding, which resulted in successful folding of protein domains with length longer than 350 amino acids. Finally, we summarize the major challenges faced by the community in ab initio folding, deep neural-network learning, and membrane protein structure prediction.

YouTube

Live Stream:

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