



Do you want to explore the fun side of structural biology?

**Join us to learn more about protein structure prediction and design
and how Rosetta and Foldit can be used to tackle COVID-19!**



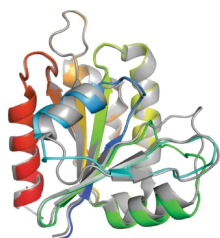
Dr. David Baker



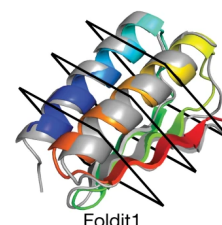
Dr. Brian Koepnick



**Experience the world's first protein-folding game
and join an open round-table discussion after a captivating talk.**



March 30th
9.30 am-11.15 am PST
18.30 pm - 20.15 pm CET



Register here:
<https://tinyurl.com/register-proteindesign> or



iubmb.org/iubmb-trainee-initiative

Webinar Part 1: The Coming of Age of De Novo Protein Design

Professor David Baker is the Director of the Institute for Protein Design at the University of Washington. The Baker lab seeks to understand the fundamental principles underlying protein structure and function, to encode these principles in the Rosetta computer program, and to use them to create a new world of de novo designed proteins to address 21st-century challenges in health and technology. The Baker Lab can be found here: <https://www.bakerlab.org/>



Talk Abstract:

Proteins mediate the critical processes of life and beautifully solve the challenges faced during the evolution of modern organisms. Our goal is to design a new generation of proteins that address current-day problems not faced during evolution. In contrast to traditional protein engineering efforts, which have focused on modifying naturally occurring proteins, we design new proteins from scratch based on Anfinsen's principle that proteins fold to their global free energy minimum. We compute amino acid sequences predicted to fold into proteins with new structures and functions, produce synthetic genes encoding these sequences, and characterize them experimentally. In this talk, I will describe the de novo design of SARS-CoV-2 candidate therapeutics, synthetic antagonists and agonists of cellular receptors, molecular machines, and recent advances in deep learning-based structure modeling and design.

Talk start time: 9:30 am PST, 18.30 CET

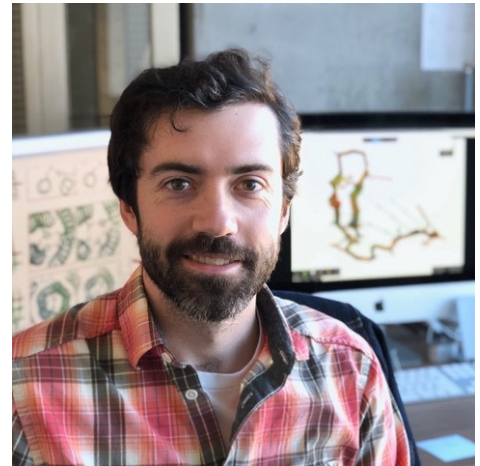


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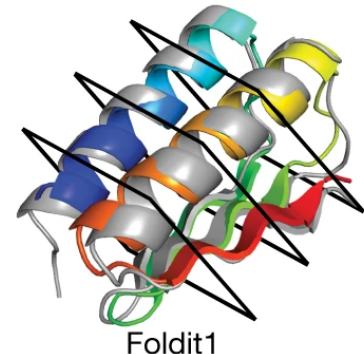
Webinar Part 2: Learn how to solve puzzles for science with Foldit

Dr. Brian Koepnick is currently a research scientist in the laboratory of Dr. David Baker. He works on Foldit, a computer game that they use to crowdsource problems in protein modeling. He sets up protein puzzles that are relevant to the lab's research, then analyzes and tests Foldit players' solutions in the lab. Foldit players are especially good at exploring creative and diverse solutions to protein design problems. Foldit is free to play at <https://fold.it>!



Talk Abstract:

Jumping off from Foldit's previous successes in protein design, I'll talk about how we can now directly challenge Foldit players to design drugs and therapeutics. Then I can describe specifically how we were able to start designing COVID-19 inhibitors as early as February 2020. Finally I'll demo a little Foldit puzzle about the SARS-CoV-2 spike to show the audience how it works and get them engaged with the software.



Talk start time: 10:15 am PST, 19.15 CET

Foldit overview and figure reference: Koepnick B, Flatten J, Husain T, et al. De novo protein design by citizen scientists. *Nature*. 2019; 570(7761):390-394. doi:10.1038/s41586-019-1274-4

Rosetta overview and figure reference: Leman, J.K., Weitzner, B.D., Lewis, S.M. et al. Macromolecular modeling and design in Rosetta: recent methods and frameworks. *Nat Methods* 17, 665–680 (2020). <https://doi.org/10.1038/s41592-020-0848-2>