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VISITING PROGRAM

TSVP TALK

What Could Become a Protein? From Early Amino Acid Alphabets to Random Sequence Space

2026 WED. Dec. 2

15:00–16:00

HYBRID L5D23, ZOOM

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Proteins are products of billions of years of evolution, but neither their earliest forms nor the routes by which entirely new proteins emerge are directly accessible. My group uses experimental models to approach these questions using synthetic biology. We explore what structures and functions may be supported by limited amino acid alphabets that serve as models of possible early stages of protein evolution, and what molecular behaviors arise from random sequences built from the modern alphabet but lacking evolutionary history. Using large, compositionally controlled libraries together with biochemical, biophysical, cellular, and computational analyses, we ask how amino acid composition and sequence shape folding, assembly, and function, and what these constraints may reveal about possible protein beginnings.

Charles University

Klára Hlouchová

Klára Hlouchová is a biochemist studying the origins and evolution of proteins. She studied biochemistry at Charles University, completed her PhD at the Institute of Organic Chemistry and Biochemistry of the Czech Academy of Sciences, and conducted postdoctoral research on enzyme and metabolic pathway evolution at the University of Colorado Boulder. She now leads the interdisciplinary Synthetic Biology Group at the Faculty of Science, Charles University in Prague. Her research explores early amino acid alphabets, random protein sequence space, protein–RNA interactions, and the emergence of new proteins.

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