School of Molecular Sciences
Arizona State University

SMS Fall 2021 Seminar Series

Friday Aug 27 | 2:30pm | Biodesign Auditorium*

Computational Protein Design with Natural and Unnatural Amino Acids

Proteins play a fundamental role in essentially all biological processes. The ability to rationally alter protein function (a field known as protein engineering) would have far-reaching implications on human health; however, this represents a very challenging problem. In recent years, computational protein modeling methods have been developed that have dramatically accelerated protein engineering efforts. Despite this, certain protein engineering goals (e.g., rationally designing new enzymes or imbuing proteins with completely novel functions) remain difficult to achieve even with these powerful computational tools. To circumvent these challenges, we have developed a unique approach in which amino acids that are not found in nature serve as starting points for our protein engineering efforts. By combining these "non-canonical amino acids" with the Rosetta computational protein design software, we engineer proteins that have properties that would be difficult to achieve with naturally occurring amino acids alone. Two of the major focuses of our research, the rational design of fluorescent, protein-based sensors of a variety of important cellular process and the development of enhanced computational enzyme design methods, will be discussed in this presentation.

Jeremy Mills, PhD

Assistant Professor, Arizona State University

Jeremy Mills is an assistant professor in the School of Molecular Sciences and the Center for Molecular Design and Biomimetics in the Biodesign Institute. He obtained his undergraduate degree in chemistry from Vanderbilt University where he studied free radical atom transfer reactions with Professor Ned Porter. He then carried out graduate studies focused on protein engineering with natural and unnatural amino acids at The Scripps Research Institute under the guidance of Professor Peter Schultz. He then carried out postdoctoral studies in the field of computational protein design with Professor David Baker at the University of Washington.

Research in the Mills group focuses on the use of computational protein design methods to engineer proteins in which non-canonical amino acids carry out important functions.

**ZOOM option available: https://asu.zoom.us/j/87081218152*