BIOCHEMISTRY SEMINAR SERIES

Midstream Presentation - Fall 2020

"Design and Assembly of 3D Protein Crystals "

Kyle Meador

Yeates Group

Protein design has allowed researchers to create novel proteins to serve all manners of form and function. Our lab has been at the forefront of applying protein design towards large symmetric protein assemblies, increasing the size and complexity with which biotechnologies are built. Despite progress designing finite protein materials such as cubic or icosahedral capsid assemblies, the development of infinitely repeating materials, best characterized by 3D crystals, has lagged behind. Our group has laid out shared principles and geometric rules that apply to the construction of both finite and infinitely repeating materials; the essence is a requirement for rigidly orienting two oligomeric protein components with respect to one another. So far, this idea has not been demonstrated for protein crystals due to numerous challenges, both computational and biochemical. I will be discussing our work demonstrating conceptual advances towards creating such materials. An overview of the design challenge will be presented drawing from crystallization trials, followed by discussion of computational workflows to simultaneously constrain mathematical, physiochemical, and evolutionary observations to satisfy our design criteria. With continued effort, we hope to demonstrate that design of atomically precise, yet infinitely ordered materials is possible and will be the cornerstone of the next generation of biotechnological advances.

"Biochemical and structural analysis of *in vivo* Cry11Bs crystalline inclusions"

Natalie Schibrowsky

Rodriguez Group

Structural determination techniques are instrumental for proteins due to the immense amount of information elucidated from atomic to protein complex levels. One aspect of proteins that has eluded the structural field is self-assembly, from filaments to three-dimensional crystals. *Bacillus thuringiensis* is unusual due to its ability to form crystalline inclusions of proteins that are toxic upon activation and have specificity for vector species and organelles. *B. thuringiensis'* crystalline inclusions are of exceptional interest, since classical macromolecular crystallography consider a plethora of variables, which testing to exhaustion can still yield no crystals or results. This laborious process could be circumvented; however, by exploiting these crystalline inclusions' cellular self-assembly process. Since *B. thuringiensis'* crystalline inclusion self-assembly is not well-characterized or understood, our goal is to elucidate this information by characterizing the Cry11Bs toxin's self-assembly and functionality from the primary to quaternary structure through electron microscopy, *cryotomography,* and bioassays. We are currently gaining more insight into how the crystalline inclusions function, if this assembly is induced by environmental factors in vivo, and determining the ultrastructure of this crystalline self-assembly process *in vivo.*

Tuesday, November 10, 2020

via Zoom

4:00 pm

More information: marla@chem.ucla.edu

UCLA College | Physical Sciences Chemistry & Biochemistry