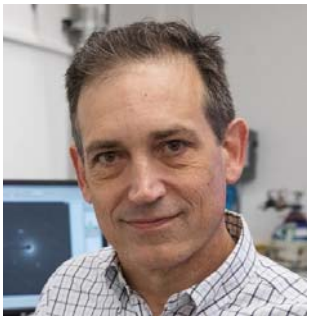

Yeates earned his Bachelor's degree at UCLA in 1983 and then his PhD in 1988 while doing research under the direction of Prof. Douglas Rees. There he helped determine the crystal structure of the bacterial photosynthetic reaction center as part of a team racing to determine the first crystal structures of membrane proteins. He moved to The Scripps Research Institute to do postdoctoral research on the structure of poliovirus with Prof. James Hogle. Yeates returned to UCLA in 1990 to join the Faculty in the Department of Chemistry and Biochemistry. His interdisciplinary research, combining molecular biology with computing and mathematics, has focused on macromolecular structure, computational genomics, and protein design. In the area of cell biology, the Yeates laboratory elucidated the structures and biochemical mechanisms of extraordinary protein-based organelles in bacteria, including the carboxysome and other metabolic microcompartments whose shells are assembled from thousands of protein subunits. In the area of bioengineering, the Yeates laboratory pioneered principles and methods for designing novel geometrically sophisticated protein assemblies, originally dubbed 'nanohedra', ranging in form from cubic cages to extended materials. Designed protein cages are currently being exploited in diverse applications, including most recently as a framework for cryo-electron microscopy scaffolding to allow the visualization of individual protein molecules at near-atomic detail. Yeates is currently the Director of the UCLA-DOE Institute for Genomics and Proteomics. He has published approximately 200 research papers.

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Principles and Preferences: Proteins as Soft Matter Assemblies in the Solid State

For atoms and simple shapes, the solid state is often understood in simple terms, such as cubic packing of spheres. In contrast, highly complex molecules such as proteins offer many potential outcomes in terms of the kinds of assemblies they form, both as finite aggregates and as extended materials. This presentation will begin by revisiting the theoretical ideas laid out in 1995 (Wukovitz and Yeates) to explain the profound preferences that macromolecules exhibit for forming specific spatial arrangements (space groups) when they crystallize. Predictions from that theory and connections to racemic crystallography will be examined. The idea of minimum contact number, central to the W&Y theory of space group preferences, has also played a critical role in laying the foundation for the design of novel self-assembling protein architectures, from cages to layers and crystals (Padilla, Colovos, Yeates, 2001). Those ideas have begun to reach maturation with the atomic level validation of numerous novel materials created in the laboratory by redesigning protein molecules. The ability to create highly geometric and atomically precise protein assemblies by design is opening up diverse applications in medicine and nanotechnology, ranging from vaccines to machines for molecular encapsulation and delivery. A new and unique application will be discussed where we have developed designed protein assemblies as modular scaffolds for arraying small proteins in a rigid fashion for imaging by cryo-electron microscopy, thereby breaking through the lower size barrier for that powerful emerging structural technique (Liu, Huynh, Yeates, 2019).