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Talk Title *TBA*

For the last 24 years, Ludtke's group has focused on CryoEM/CryoET and structural biology, applying these techniques to a wide range of biological systems, including: nuclear receptor complexes, nuclear pore complexes, ion channels, RNA/DNA, chaperonins, and a variety of other systems. Much of this work has been focused around development of the EMAN software suite. This software has been used in solving a significant fraction of the structures in the EMDatabank, and remains widely used in the field. In addition to developing new methods within EMAN, his group engages in a wide range of biological collaborations, through the CryoEM Core at BCM which he directs, and previously, through the National Center for Macromolecular Imaging, the CryoEM P41 center he codirected for 15 years. The core has recently expanded under a CPRIT core facility award, allowing us to update our equipment and begin moving more aggressively into cellular CryoET. Recent developments include deep-learning techniques to improve CryoET capabilities (now achieving 0.5 nm resolution within cells) new mathematical techniques for studying biomolecule flexibility in solution and many others.