

# 生物大分子国家重点实验室学术报告

## CryoEM for Multiscale Imaging - from Cells to Near Atomic Resolution

### 报告人简介：



Dr. Ludtke studied Physics at Caltech and Rice University, and is now a Professor of Biochemistry and Molecular Biology at Baylor College of Medicine, as well as co-directing both the National Center for Macromolecular Imaging (NCMI) and the Computational and Integrative Biomedical Research Center (CIBR). His group has been developing the EMAN software suite for CryoEM and CryoET analysis for the last 18 years, one of the most widely used packages in the field. In addition to developing computational methods, his group researches a wide range of biological topics including Ca<sup>++</sup> channels, chaperonins, LDL/HDL, and in-situ macromolecular CryoET.

### 报告内容：

The development of direct electron detectors has revolutionized the field of CryoEM, making it possible to achieve resolutions comparable to X-ray crystallography. This development has also had a significant impact on CryoET, producing tomograms with more detail and making subtomogram averaging possible down to ~1 nm resolution. Despite these massive improvements, a majority of macromolecule structures fail to achieve high resolution due to the internal motion which is an integral part of their function. Rather than viewing this as an impediment, we view this as an opportunity to directly study how macromolecular dynamics links to function. The challenges in these related fields are no longer achieving the next level of resolution, but in understanding macromolecules in a true in-situ environment and relating observed structural variations both in-situ and in-vitro to function. This talk will focus on the wide range of emerging computational methods for studying macromolecular variability and the capabilities and limitations of each technique.

邀请人：孙飞

主持人：张艳

时间：2016年6月23日10:00

地点：中科院生物物理研究所图书馆报告厅

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