Cryo-EM Seminar

2026年5月22日 (金) 14:00 – 15:00

生命機能研究科 生命システム棟 2Fセミナー室

The Cryo-EM Revolution: A Story in Four Acts

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Grigorieff教授は2017年ノーベル化学賞受賞者のR. Hendersonと共にクライオ電子顕微鏡による生体分子構造解析への道筋をつけたパイオニアの一人であり、特に高分解能な構造解析を確立させる上で数多くの成果を残しています。
本講演では歴史的な背景から最新の研究成果までご紹介いただきます。

Almost fifteen years ago, single-particle electron cryo-microscopy (cryo-EM) emerged as one of the most powerful methods for determining the atomic structures of biomolecules. Today, it is a routine technique that produces high-resolution structures of molecules and molecular assemblies, rivaling those obtained by X-ray crystallography. Unlike crystallography, however, single-particle cryo-EM can visualize multiple conformational states within a single sample, offering snapshots of the functional cycles of the molecules and complexes under study.

At the same time, electron cryo-tomography (cryo-ET) is being developed to visualize molecules inside cells and tissues, revealing the three-dimensional cellular context in which they function. Despite major advances in sample preparation and image processing, cryo-ET is still typically limited to resolutions of approximately 2 nm unless averaging techniques can be applied. At this resolution, it often remains difficult to identify specific molecules and determine their functional states.

In this presentation, I will offer a brief historical perspective on cryo-EM’s rise to prominence, discuss the strengths and current limitations of cryo-ET, and introduce 2D template matching, a new technique for placing molecules of known structure precisely into cellular environments.

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