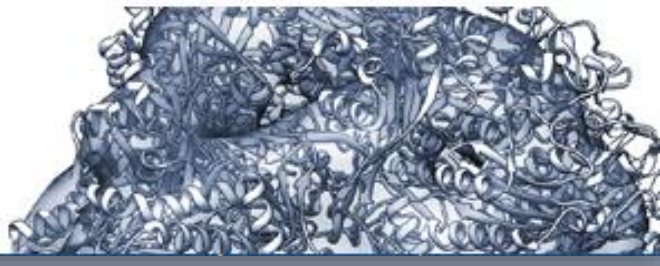
中央研究院冷凍電子顯微鏡中心

**ASCEM** Academia Sinica Cryo-EM Center



# Seminar 專題演講

## Micro-Electron Diffraction, Single Particle Analysis and Cryo-Electron tomography: A hybrid approach for structure determination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| ***Host 主持人*** | Dr. Ming-Daw Tsai 蔡明道特聘研究員 |
| ***Date 日期*** | **Tuesday, September 24, 2019** 2019年9月24日星期二 |
| ***Time 時間*** | 11:00 – 12:00 |
| ***Venue 地點*** | Rm. 209, Inst. of Biological Chemistry, Academia Sinica<br>院內生物化學研究所 209研討室 |


Despite great advances in X-ray crystallography, the requirement for large, well-ordered crystals remains a bottleneck for this technique. Growing protein crystals is difficult, requires a lot of time and effort and it is sometimes even not possible. However, quite often plenty of microcrystals and nanocrystals are produced during crystallization trials. Such crystals are regarded as useless for conventional X-ray diffraction experiments. However, these kind of small crystals could be used for high-resolution structure determination by electron microscopy methods.

Since, electrons interact strongly with matter and are less damaging per scattering event, electron diffraction is capable of producing high-resolution data from crystals that are an order of magnitude smaller. While this talk will dominate microED, I will also show results from our new project on structure based drug discovery with cryoEM facilitated by new developments in optical methods such as aberration free image shift (AFIS) and Fringe free imaging (FFI) and a new 6x faster camera with highest DQE, Faclon4, enabling 2.5Å resolution structure of membrane protein.

Finally, if time permits, I will show you the latest results combining cryoFIB and cryoET, to visualize and understand the formation of virus production factories inside the infected cells and first *in-situ* high resolution structures of virus life cycle in its native state.



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