

2017 ISGC cryoEM workshop

6-8 March 2017

Instructors

Chi-Yu Fu, Institute of Cellular and Organismic Biology, Academia, TW

Wei-Hau Chang, Institute of Chemistry, Academia Sinica, TW

Shang-Rung (Sunny) Wu, Institute of Oral Medicine, National Cheng Kung University, TW

Jose Maria Carazo, Spanish National Center for Biotechnology, ES

Alexandre Bonvin, Bijvoet Center, Utrecht University, NL

Organizers

Shang-Te Danny Hsu, Institute of Biological Chemistry, Academia Sinica, TW

Academia Sinica Grid Computing (ASGC)

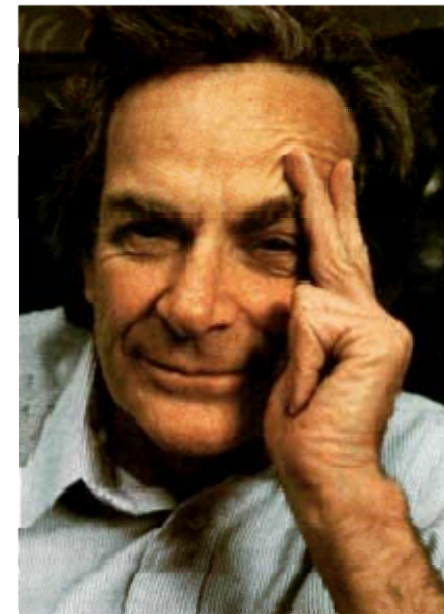


“It is very easy to answer many of these fundamental biological questions; you just *look at the thing!*”

***There's Plenty of Room at the Bottom -
An Invitation to Enter a New Field of Physics***

Richard P. Feynman

December 29th 1959 at the annual meeting of the American Physical Society at the California Institute of Technology (Caltech)



(Reprinted from Nature, Vol. 217, No. 5124, pp. 130-134, January 13, 1968)

Reconstruction of Three Dimensional Structures from Electron Micrographs

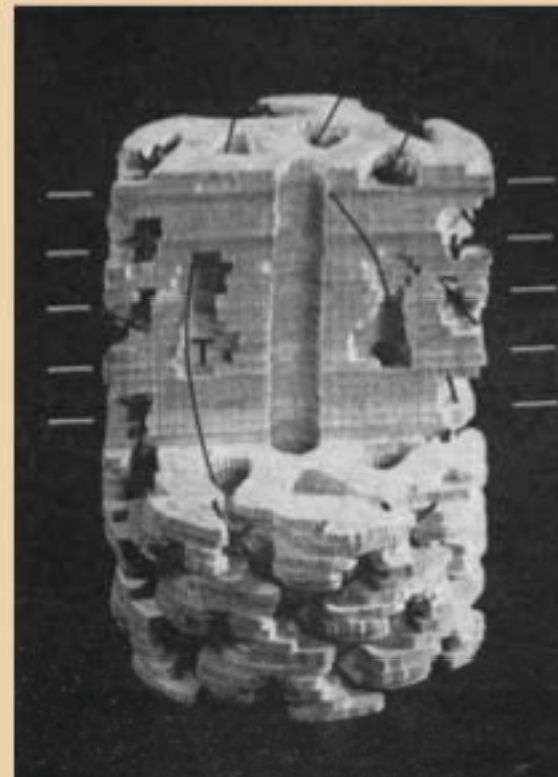
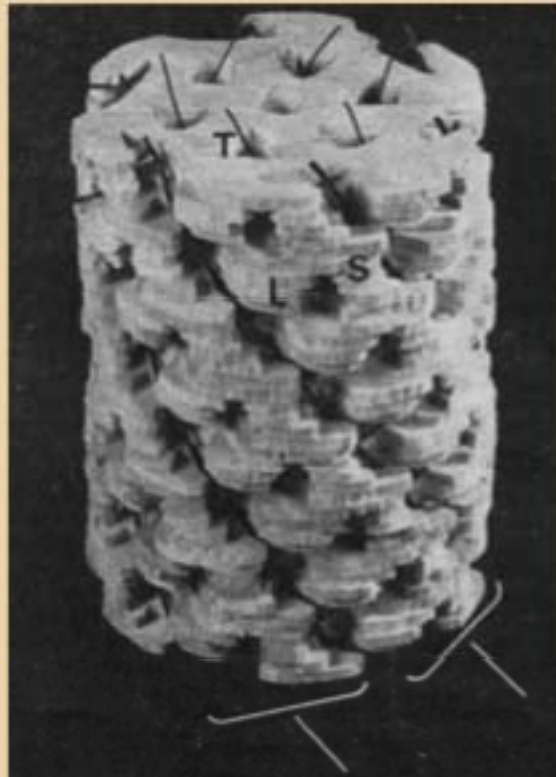
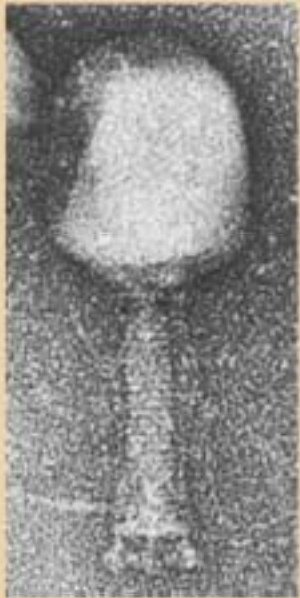
by

D. J. DE ROSIER

A. KLUG

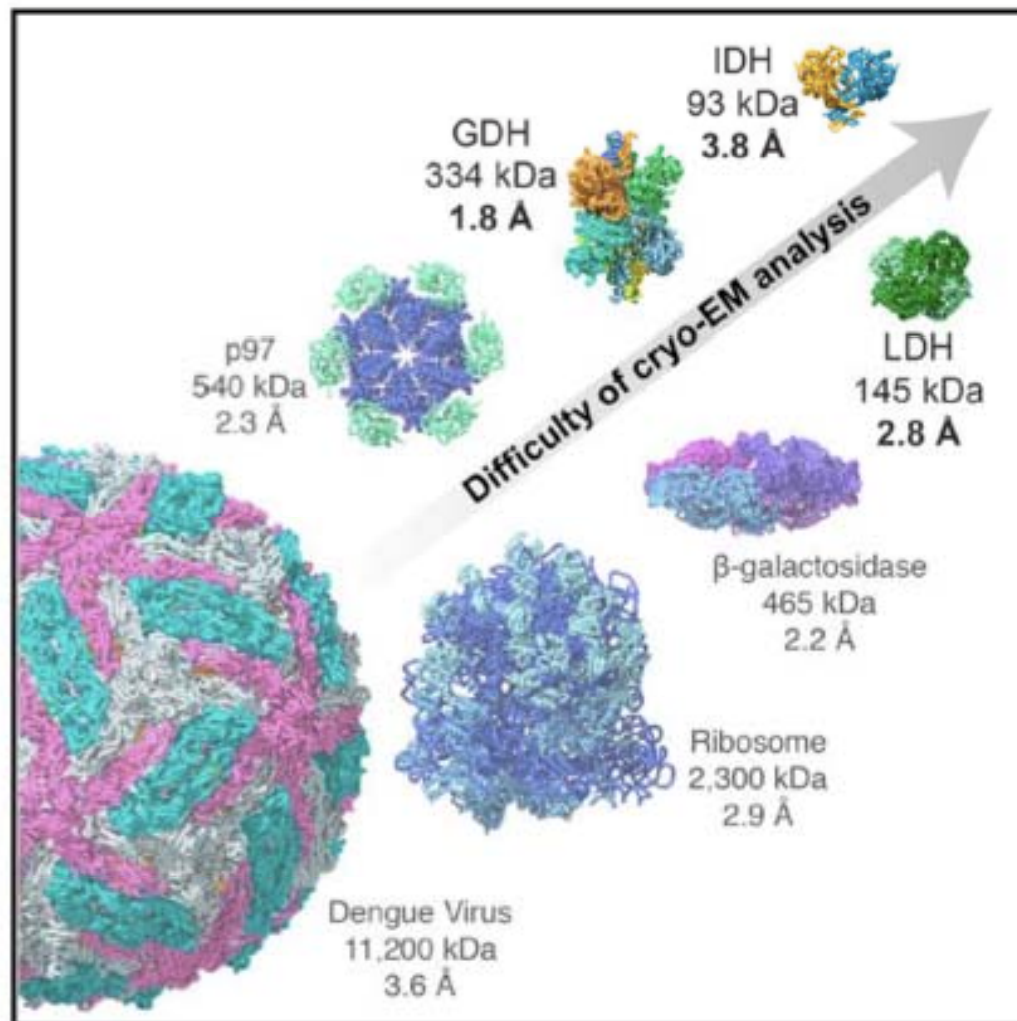
MRC Laboratory of Molecular Biology,
Hills Road, Cambridge

General principles are formulated for the objective reconstruction of a three dimensional object from a set of electron microscope images. These principles are applied to the calculation of a three dimensional density map of the tail of bacteriophage T4.



Breaking Cryo-EM Resolution Barriers to Facilitate Drug Discovery

Graphical Abstract



Authors

Alan Merk, Alberto Bartesaghi, Soojay Banerjee, ..., Lesley A. Earl, Jacqueline L.S. Milne, Sriram Subramaniam

Correspondence

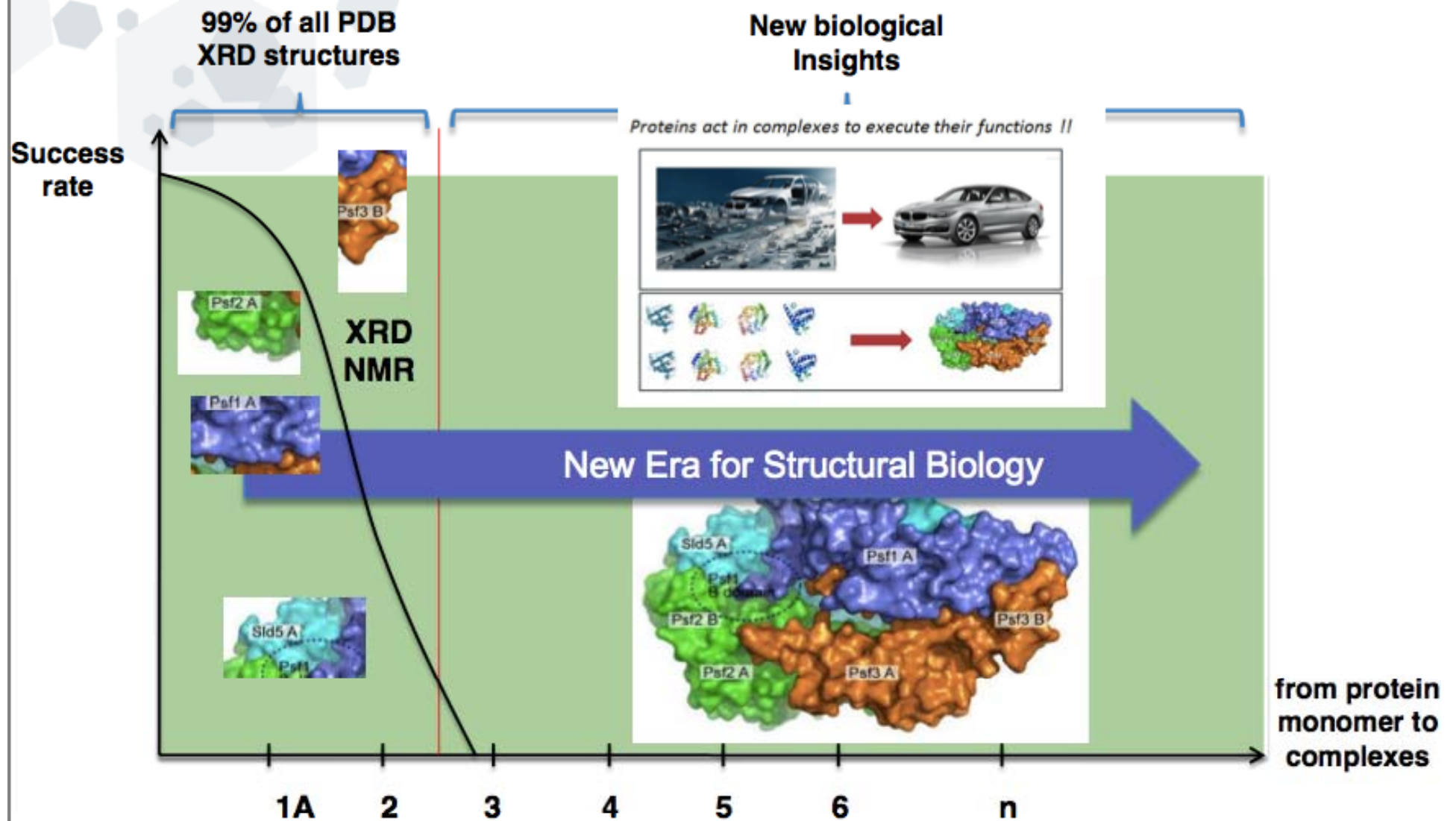
ss1@nih.gov

In Brief

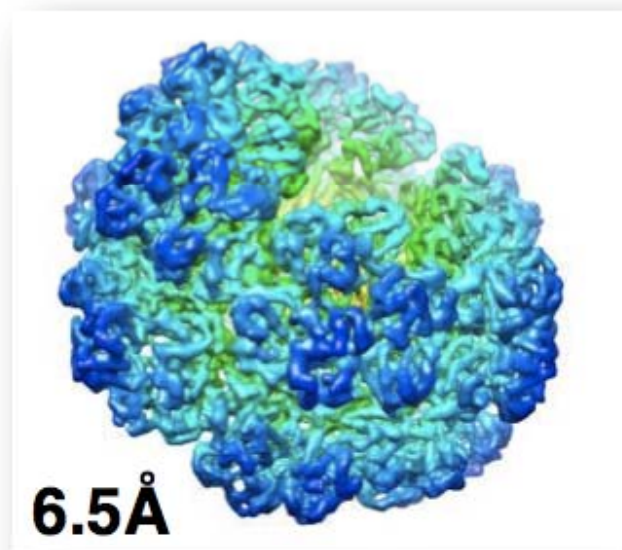
By using cryo-EM methods, the structure of small metabolic enzymes as well as the localization of small-molecule inhibitors that bind to them can be determined at near-atomic resolution.

Structure – Function Relationship

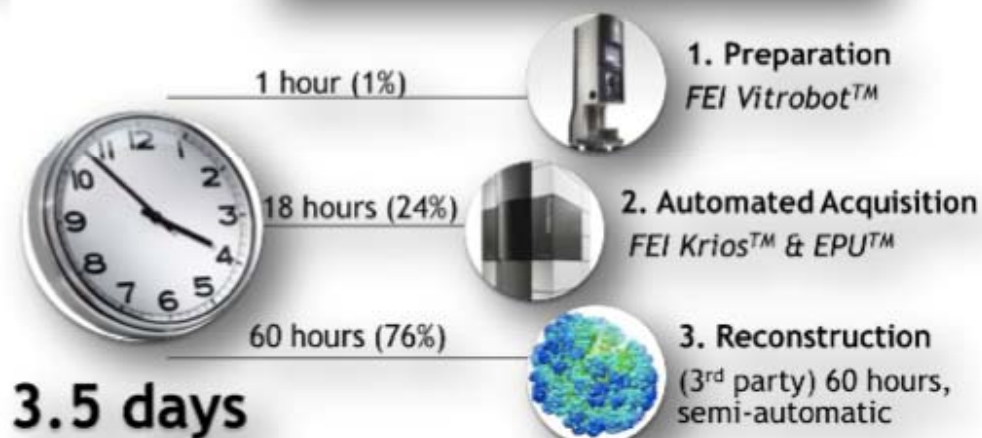
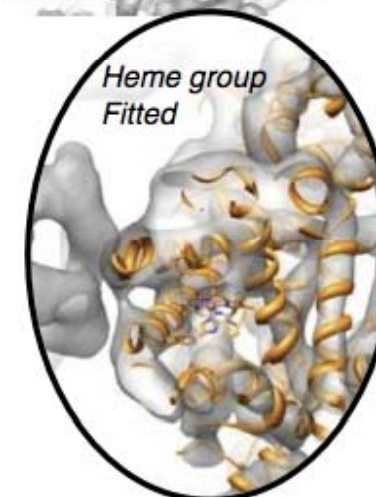
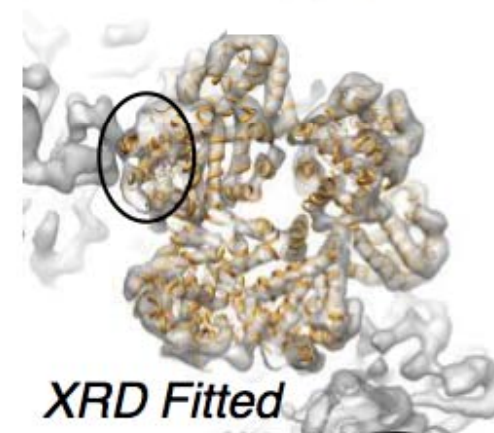
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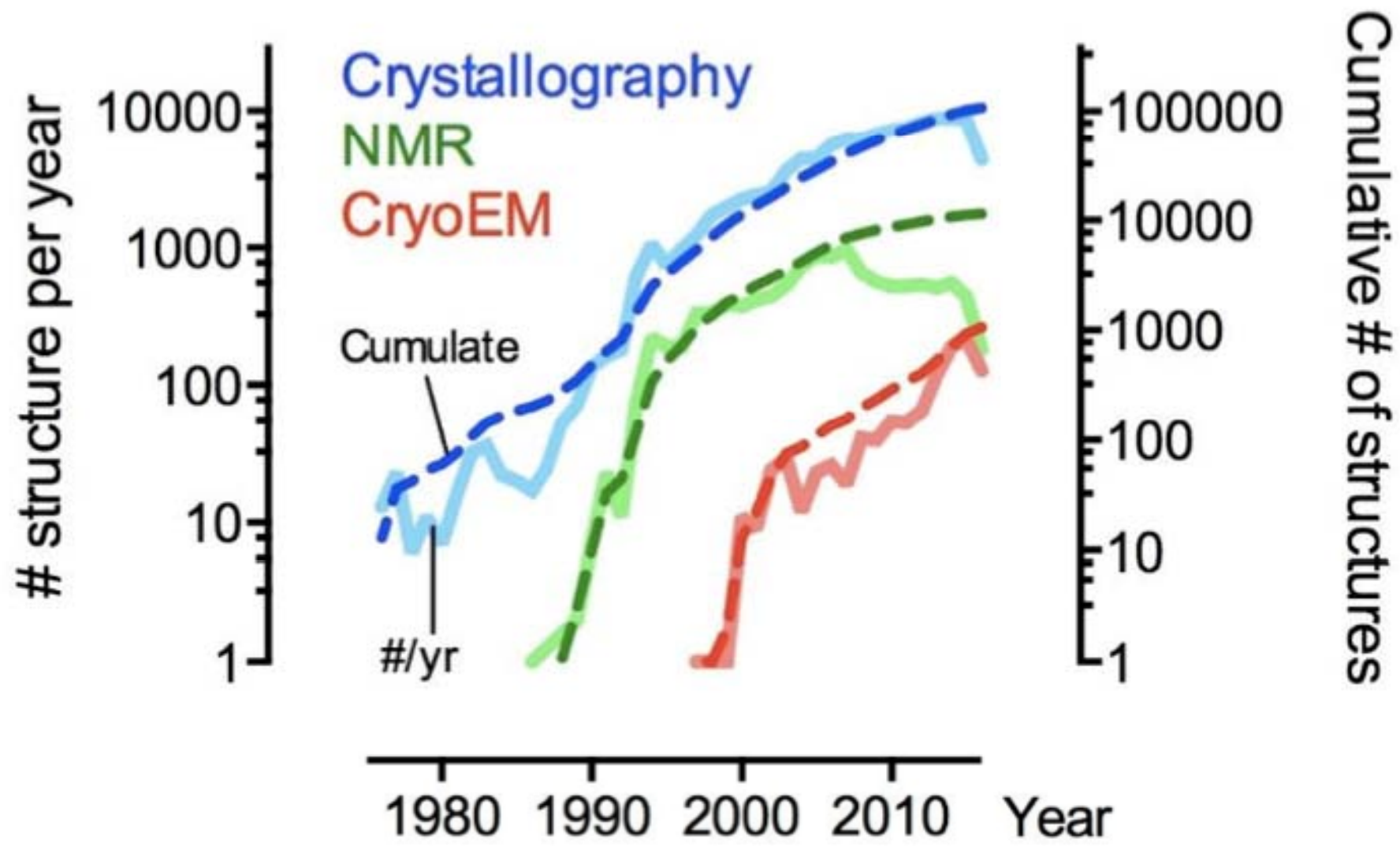


Suspension of Worm Hemoglobin in our FEI Titan Krios with workflow software for acquisition and analysis (EPU, Xplore3D, ARGOS)



NeCEN





Cryo-EM Workshop

Date: Monday~Wednesday, 6~8 March 2017

Venue: 3F, Building for Humanities and Social Science, Academia Sinica

AGENDA

Monday 6 March 2017

08:30-09:00 Registration

09:00-09:45 General introduction to biological cryoEM / Chi-Yu Fu / Scientific talk

09:45-10:30 Three key breakthroughs that enable cryo-EM to become a routine density map generator / Wei-Hau Chang / Scientific talk

10:30-11:00 Coffee break

11:00-12:30 Relion (part 1) / Wei-Hau Chang / Tutorial

12:30-13:30 Lunch

13:30-15:00 Relion (part 2) / Wei-Hau Chang / Tutorial

15:00-15:30 Coffee break

15:30-17:30 Legion and Appion / Chi-Yu Fu / Tutorial

Tuesday 7 March 2017

11:00-11:45 Image Processing in cryoEM: Open problems and current perspectives / Jose Maria Carazo / Scientific talk

11:45-12:30 Applications of cryo-electron microscopy to understand complex structures / Sunny Wu / Scientific talk

12:30-13:30 Lunch

13:30-15:00 EMAN 2 (part 1) / Sunny Wu / Tutorial

15:00-15:30 Coffee break

15:30-17:30 EMAN 2 (part 2) / Sunny Wu / Tutorial

Wednesday 8 March 2017

09:45-10:30 High-resolution integrative modelling of biomolecular complexes from fuzzy data / Alexandre Bonvin / Scientific talk

10:30-11:15 POWERFIT and DISVIS (part 1) / Alexandre Bonvin / Tutorial

11:15-11:30 Coffee break

11:30-13:00 POWERFIT and DISVIS (part 2) / Alexandre Bonvin / Tutorial

13:00-13:45 Lunch

13:45-15:15 Scipion (part 1) / Jose Maria Carazo / Tutorial

15:15-15:30 Coffee break

15:30-17:15 Scipion (part 2) / Jose Maria Carazo / Tutorial

17:15-17:30 Closing remark/round table discussion