

*FROM DATA TO STRUCTURE*

Program

**Tuesday June 16<sup>th</sup>**

9H15 Denis Ptchelkine & Yves Bourne : Introduction to workshop

9H30 Denis Ptchelkine : CryoSparc best practices

10H15 Irfan Prabudiansyah: Cryo-EM and 3D variability analysis of membrane proteins and ligand-receptor complexes

11H00 Coffee break

11H15 Saikat Chowdhury : Going from 2D to 3D in single particle cryo-EM (remote)

12H00 Agathe Hubert: Understanding the role of VDAC2 in mitochondrial apoptosis

12H30 Lunch break

14H00 David Bhella: Breaking Symmetry to Reveal Hidden Entry Mechanisms in Icosahedral Viruses by Cryo-EM

15H00 CryoCloud : Cryo-EM data processing on the Cloud (remote)

15H45 Coffee break

16H00 Rhian Jones : Sorting out conformational heterogeneity in viral complexes

16H45 Round table

## **Wednesday June 17<sup>th</sup>**

9H15 Yves Bourne : Approaches to proteins multiple states analysis 3D variability

10H00 Adeline Goulet : Handling conformational variability: insights from a bacteriophage case study

11H00 Coffee break

11H15 Aurelien Fouillen: Structural characterization of the active and inactive conformations of the vasopressin V2 receptor using cryo-EM

12H00 Andrei Karpov: Helical reconstruction of Chikungunya virus NSP3 helical scaffolds

12H30 Lunch break

13H30 Laurent Terradot : Structural studies of Bacterial Secretion Systems and their effectors by cryoEM

14H30 Gaëtan Bellot : Design of DNA origami nanoscaffolds for cryo-TEM applications

15H15 Vidya Mangala Prasad : Cryo-electron tomography and subtomogram averaging

16H00 Coffee break

16H15 Denis Ptchelkine : Subtomogram averaging in Relion5 practical approach

17H00 Discussion & Conclusion remarks