Developments & challenges in managing large Cryo-EM facilities

M. Hons
ESRF, 71 avenue des Martyrs, CS 40220, FR - 38043 Grenoble Cedex 9, France, **mhons@embl.fr**

Cryo-Electron Microscopy has experienced a technical revolution followed by rising attention in recent years. Specifically, a new phase plate concept, new detector generations, fast automated data collection, dose fractionation and beam-induced motion correction, on-the-fly processing and more sophisticated GPU-accelerated computing algorithms increased the scientific impact of cryo-EM as a core technique in structural biology. With specialised cryo-EM facilities, access to this technology is granted to a broader community, thus increasing the collective scientific output.

Still many biological samples pose a challenge to modern EM routines. Using the example of small, elongated and flexible cohesin, I will show that biochemical procedures to stabilise and improve samples need to keep pace with the speed of the technical revolution. In future, difficult samples need to be brought into routine EM sample optimisation pipelines to limit sample effects in final image acquisition and data processing, with the aim to close the inaccessibility gap in structural biology. Development of new concepts for efficient sample optimisation and cryo preparation may be part of the work of future cryo-EM facilities.