

## **eBIC: Applying over 10yrs of software automation and support of MX beamlines to CryoEM.**

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The Electron Bio-Imaging Centre (eBIC)[1] was established at Diamond Light Source, UK and now hosts four state of the art Titan Krios transmission electron microscopes for automated data collection along with a Talos Arctica and Scios cryo-FIB/SEM. One of the opportunities raised by co-locating eBIC with the UK synchrotron source and CCP-EM was the potential to utilise over 10yrs of developments made in automating, managing and supporting Macromolecular Crystallography (MX) experiments on Diamond beamlines and applying these to CryoEM.

As the improved accessibility to high-end CryoEM instruments inevitably attracts structural biologist familiar with using automated and integrated MX beamlines, there is a parallel drive to apply some of the software tools and potentially even integrate the experiments from this emerging domain. This presentation will describe the progress on how facility compute resources, data archive, software frameworks and the information management system ISPyB [2] and SynchWeb [3] are being extended to support the operation and automation of the eBIC facility.

[1] Clare, D.K. et al., *Electron Bio-Imaging Centre (eBIC): the UK national research facility for biological electron microscopy*. Acta Crystallogr D Struct Biol. 2017. **73**(Pt 6): p.488-495

[2] Delageniere, S., et al., *ISPyB: an information management system for synchrotron macromolecular crystallography*. Bioinformatics, 2011. **27**(22): p. 3186-92.

[3] Fisher, S.J., et al., *SynchWeb: a modern interface for ISPyB*. J Appl Crystallogr, 2015. **48**(Pt 3): p. 927-932.