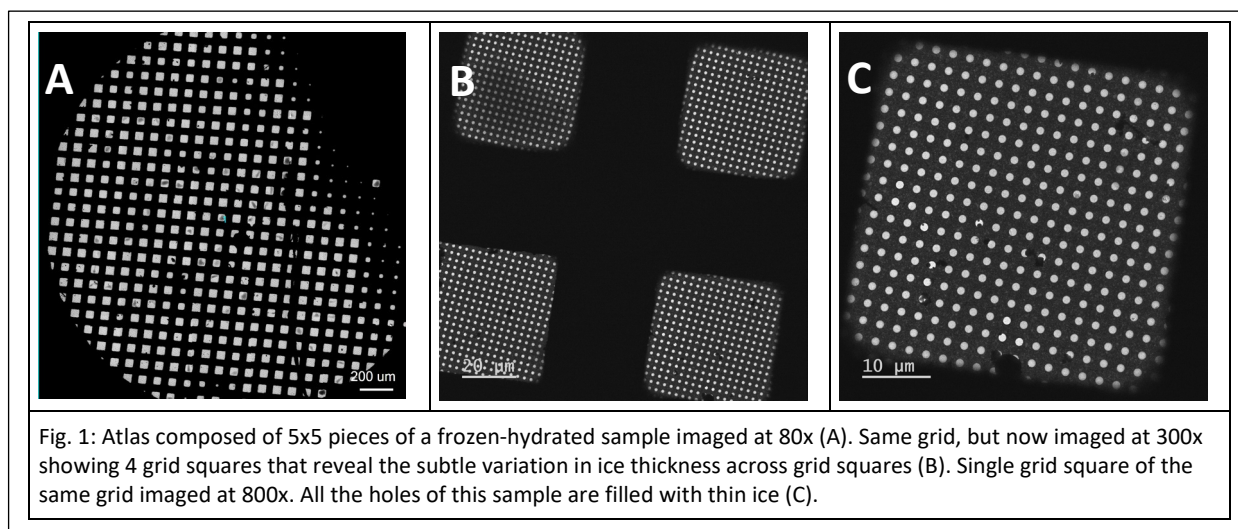


# JEOL CRYO ARM™ achieves top resolution!

The field of single particle structure analysis (SPA) by cryo-electron microscopy reached new highs with the publication of a 1.19Å structure of apo-ferritin by Maki-Yonekura et al. obtained using a JEOL CRYO ARM™ 300 model 3300<sup>1</sup>. This electron cryo-microscope was specifically designed for highly automated workflows capable of the unattended acquisition thousands of images of vitrified specimens. Workflow support of the JEOL CRYO ARM™ is available for SPA, batch tomography and microED. The specimen used in the study, apo-ferritin, is a conveniently available benchmark protein used for determining the performance of these highly automated cryo microscopes. In instances where a single chain version is used, 24-fold non-crystallographic averaging can be applied, which vastly improves the signal-to-noise in cryo-EM images.



SPA workflows rely on atlases or maps of the specimen, which allow stage navigation to be used in targeting regions/holes of interest (Fig. 1). Maps taken at successive higher mags allow for precise targeting of holes in the support film using a combination of stage shift and deflector-based shift.

A total of 7900 movies were acquired on a K3 camera at 0.5Å/pixel yielding a total of 2,000,000 particles that were subjected to processing in Relion-3.1. The final map was computed at 1.19Å resolution (Fig. 2). The data was deposited in the EMDB under accession number EMD-35984.

## References:

1. S. Maki-Yonekura, K. Kawakami, K. Takaba, T. Hamaguchi and K. Yonekura (2023), Comm. Chemistry 6, 98

