Oral presentation

Macromolecular cryo-crystallography on the XtaLAB Synergy-ED

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The Rigaku XtaLAB Synergy-ED is a proven solution for microED with a seamless workflow from data collection to 3D structure determination. It features a JEOL electron source and optics, a Rigaku HyPix-ED detector, and Rigaku's CrysAlis^{Pro} software. Our previous treatment of macromolecular microED on the XtaLAB Synergy-ED used cryo focused ion beam (cryo-FIB) milling to obtain crystals thin enough for data collection[1]. Since cryo-FIB requires an expensive instrument, we investigated other methods to obtain suitable protein crystals for microED.

Here, we report a simpler method to preparing suitable protein crystals for 3D-ED/microED on the XtaLAB Synergy-ED. Briefly, a large crystal is crushed, transferred in its mother liquor to a tube, pipetted onto a TEM grid, blotted, and plunge cooled in liquid nitrogen. Example data collections and structure solutions will be presented.

Figure 1. XtaLAB Synergy-ED

[1] Truong, K.-N.; Ito, S.; Wojciechowski, J.M.; Göb, C.R.; Schürmann, C.J.; Yamano, A.; Del Campo, M.; Okunishi, E.; Aoyama, Y.; Mihira, T.; et al. (2023) *Symmetry*, **15**, 1555