

Poster Presentation

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Structure determination from in situ diffraction with the Rigaku PlateMate

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As crystallographers face increasing problems with crystallizing new proteins, in-situ screening in crystallization trays at room temperature is experiencing a renaissance. It saves a lot of time when screening large numbers of crystallization hits and it helps avoid crystal damage caused by human manipulation error (harsh manual handling, bad freezing) or changes in crystal properties (dehydration, wrong cryo-conditions). In certain cases, it is also possible to go beyond screening and collect enough data for structure solution, especially on an X-ray home source where a less intense beam helps minimize the devastations of radiation damage occurring at room temperature. The Rigaku PlateMate has proved itself as an efficient and easy-to-use in-situ screening tool on the field for the past two years. It is as easily mounted on a goniometer as a regular goniometer head and thanks to a plate adapter with SBS footprints, it accommodates most 96-wells plate types, from sitting and hanging drop to LCP plates. In addition, thanks to its narrow dimensions and aided by software to prevent collisions with the detector and the crystal viewing camera, the PlateMate can be used to easily collect data from crystals in situ. In this work, we present structure solution results obtained from data collected with the PlateMate on crystals from various proteins (native crystals or containing gold or iodine) and using one or multiple crystals to make up a complete data set.

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