

Abstract

The contribution of synchrotron radiation to the understanding of fundamental biological questions continues to be of importance for the European life science community. The current trend towards studying ever more complex biological systems requires that future macromolecular crystallography (MX) beamlines are capable of rapidly screening and collecting optimal diffraction data from ever smaller crystals or the best part(s) of larger ones. The UPBL10 project, part of the ESRF upgrade program, will provide a modern suite of MX beamlines for structural biology users in Europe to facilitate such experiments. In order to maximise the potential of this new suite of beamlines the EMBL-Grenoble and ESRF are developing the associated instrumentation and software technologies needed. Here, I will present some of the current beamline specifications and further improvements envisaged.