ABSTRACT
This seminar aims to provide guidance to current and future practitioners on how to undertake macromolecular powder diffraction studies in a thorough, precise and accurate manner and with a careful understanding of core principles. Several cases studies will be described, following a general survey of examples. Synchrotron beamline options and home laboratory studies will be described including their respective advantages and disadvantages. A wide variety of software exists for powder diffraction data processing and analyses, some of which have been adapted to large unit cell studies, and will be briefly presented. Over a period of hardly more than 10 years, macromolecular powder diffraction has moved from an impossible dream to a reality as exemplified by characterising bulk pharmaceuticals, the molecular replacement structure determination of the protein ponsin, the moving forward of a Trinidadian virus which will not yield sizeable single crystals, the high throughput screening of pharmaceutical proteins creating phase diagrams and even the discovery of new polymorphs. Current developments include more robust structure refinement procedures. Future prospects move towards structure determination using multiple techniques in a synergistic manner. Combining methods include electron diffraction as well as femto-second X-ray laser time-resolved powder diffraction studies.