Numerous improvements in the X-ray crystallographic methodology have promoted this technology which is the method of choice for the determination of the 3-dimensional structures of biological macromolecules. Current bottlenecks of this technique are the necessity to obtain relatively large amounts of chemically and structurally homogenous samples and to crystallise them. Protein crystallisation has mainly profited from automation in high-throughput crystallisation facilities which work more efficiently through the use of smaller volumes per experiment and a faster set-up of crystallisation plates. At the same time new methods which alter the crystallisation properties of biological samples as well as new sample characterisation technologies have been developed.

A 3 day practical workshop for students with a background in structural biology was held at the EMBL Hamburg outstation from 28th February until the 2nd March 2007. Experts from the US, Spain, England, France and Holland held a series of lectures and practicals which focused on sample preparation and characterization for microfluidic and high-throughput crystallisation. Time was evenly split between lectures and practicals in order to provide hands-on experience to 20 participants from Europe. They had been encouraged to bring own samples for the practicals which were supervised by experts in their respective fields. The course was very well received by the students. This workshop was part of a series of lectures and workshops sponsored by BioXhit and SPINE2, two large EU projects.