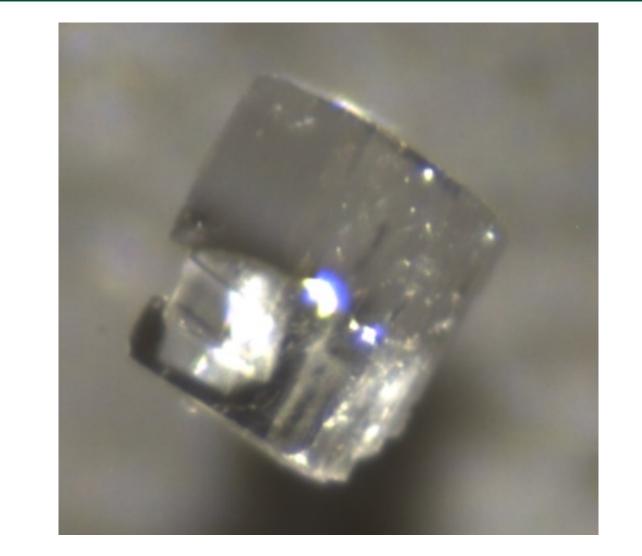


X-ray Diffraction (XRD) Bruker D8

XRD Single Crystal X-ray Diffraction

Single-crystal X-ray Diffraction, SXRD, is a non-destructive analytical technique which provides detailed information about the internal lattice of crystalline substances,





including unit cell dimensions, bond-lengths, bond-angles, as well as site-ordering.

The data generated from the X-ray analysis is interpreted and refined to obtain the crystal structure by single-crystal refinement. X-Rays are either transmitted through the crystal, reflected off the surface, or diffracted by the crystal lattice. Diffracted rays at the correct orientation for the configuration are then collected by the detector. Preferred size of crystals is between 100 nm and 200 nm.

Bruker Single Crystal Diffractometer

- Designed primarily to determine the crystal structure of single crystals. It can also be used for determining crystal orientation
- The diffractometer uses a two-dimensional CMOS detector for fast, high precision transmission diffraction through small single crystals.
- A cryostat is available to control the temperature of the sample between 100 and 400K under a nitrogen stream, which permits more structure determination under varied conditions even for air-sensitive crystals (Oxford Cryostream Cryosystem).

Structural Biology



A Lithium-OX single crystal before mounting on XRD

	191 -64 Min -64.0 Max 9132.0 Total 24667879 Time [s] 50.0	2Theta Omega Phi Chi <x> <y> <z> <zoom> Distance</zoom></z></y></x>	Common Commands 7.0000 deg -76.0000 deg 359.9999 deg 54.8293 deg 0.000 mm 0.000 mag 7.00000 cm	Temp C <u>-172.51</u> Target C <u>-173.15</u> Rate dpm 0 Hold s 0	ebug Debug Instrument hutters Safety / Main Timing / DetEn Attenuator Instrument Ready Generator Anode Cu kV 50.0 mA 1.000
Phi de-icing Activate auto de-ice feature	Interval time (s) n/a				Process
Frames taken: 0	Retakes 0	Time taken:	00:00:15	Start time:	5/13/2015 1:56:33 PM
Frames left: 0		Time left:	00:00:00	Estimated completion time:	done

Intensity data was collected on a small crystal of Vitamin C (40 µm x 100 µm x 100 μ m) using a D8 Quest with Cu radiation.

Bernal Institute possesses two Bruker D 8 Quest fixed Chi single crystal diffractometers

Crystallography is the most unambiguous method for characterisation of macromolecules, and SXRD provides the information required to understand structure and function of proteins and enzymes.

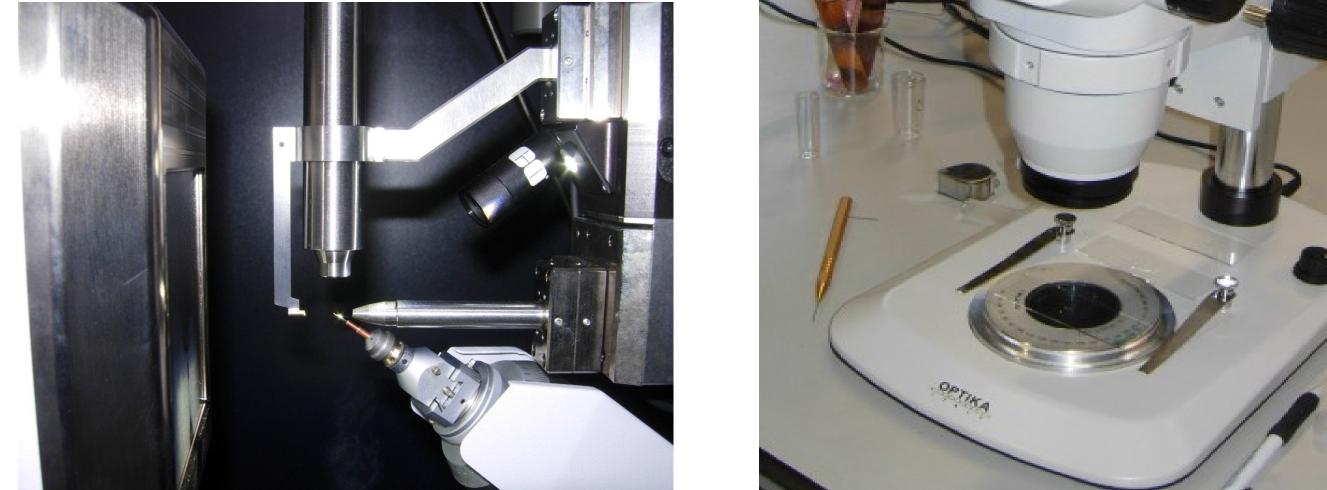


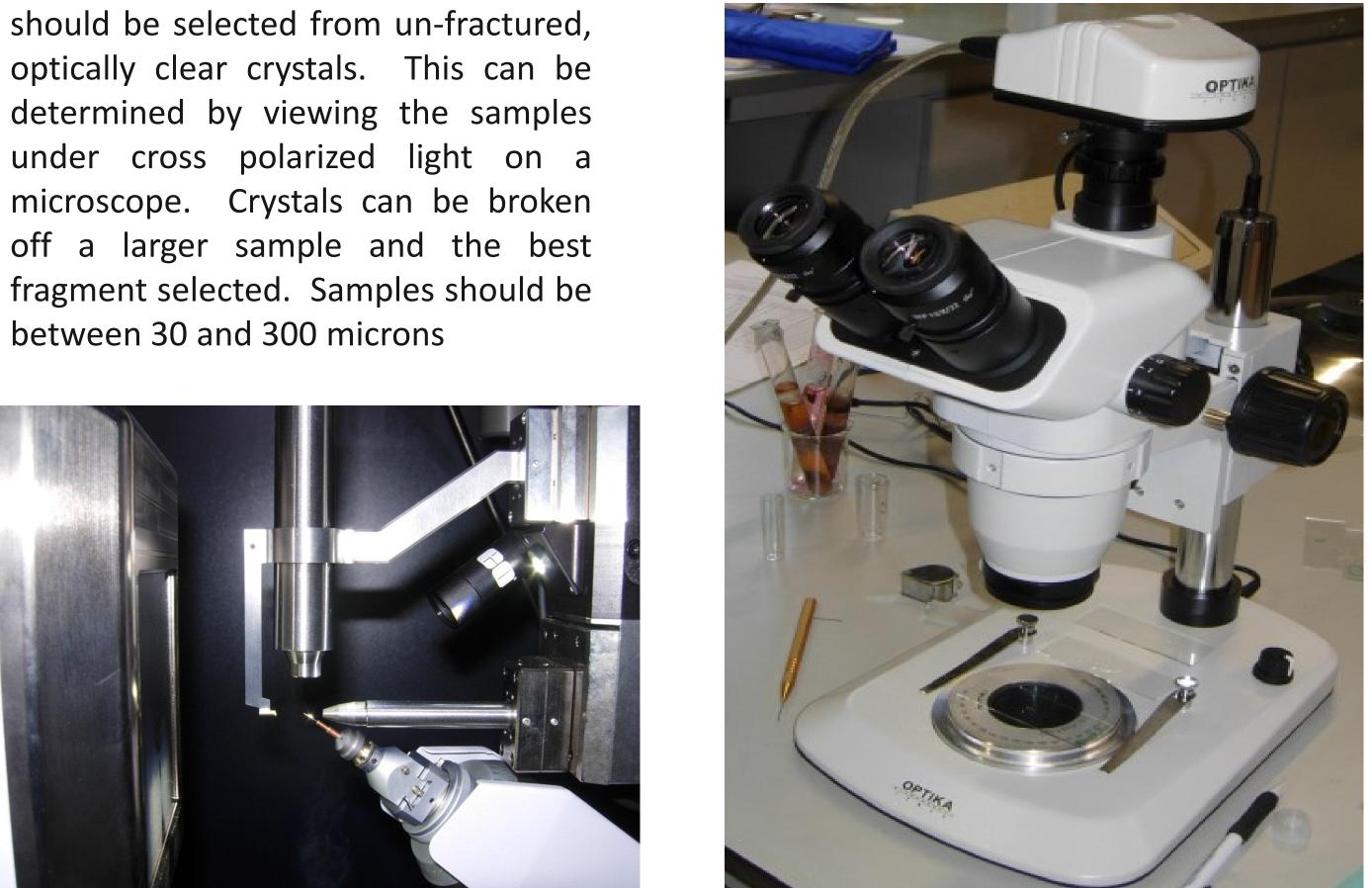
Samples are mounted on the tip of a thin glass or polymer fibre attached to a brass mounting pin, and the pin is then inserted into the goniometer head.

The Bruker Quest D8 has a 3-circle FIXED- X sample stage with open geometry has minimal obstruction and allows easy mounting of additional crystal-conditioning devices. It supports a 360° φ drive at the magic X angle of 54.7° and is efficient for data collection, using precise omega scans and "Easy-to-use" geometry. Apex software package allows structure determination.

1. Incoatec microfocus CuK α source (λ = 1.54178 Å) and Photon II detector. Due to the diameter of the incident beam (0.3 mm) the longest dimension of the crystal should be smaller than 0.3 mm. This setup is preferred for small crystals and crystals of compounds containing mostly light atoms (i.e. poorly diffracting organic compounds) 2. MoK α source λ = 0.71073 Å and Photon II detector The incident beam diameter (0.5) mm) allows measurement of crystals with the longest dimension of up to 0.5 mm. It is suitable for the study of crystals of compounds containing heavy metal atoms/ions or other strongly absorbing elements, and also to collect data of higher resolution

Samples for single-crystal diffraction should be selected from un-fractured, optically clear crystals. This can be determined by viewing the samples under cross polarized light on a microscope. Crystals can be broken off a larger sample and the best between 30 and 300 microns





Specific applications of single-crystal diffraction include:

- New mineral identification, crystal solution and refinement
- Determination of unit cell, bond-lengths, bond-angles and site-ordering
- Characterization of cation-anion coordination
- Variations in crystal lattice as function of chemical and physical environment



www.bernalinstitute.com

Contact Bernal Institute E: <u>bernal.institute@ul.ie</u>