PX Scanner
In-Situ X-ray Diffraction: Initial Results

Application Note

X-ray Crystallography

The PX Scanner is a revolutionary product from Agilent Technologies which has been designed specifically for the *in-situ* identification and analysis of protein crystals within multi-well crystallisation plates.

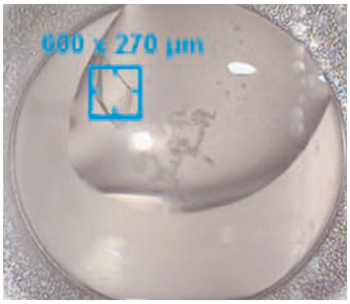
Within this application note we present a collection of experimental results obtained using the PX Scanner.

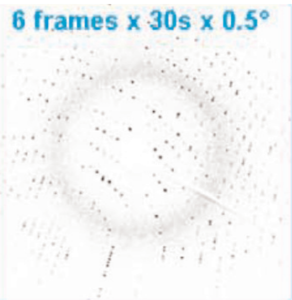
Agilent Technologies

Model Protein Benchmarks

Thaumatin

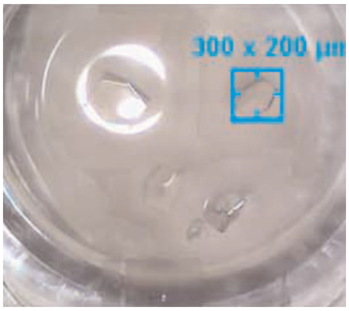
- Strong diffraction to 2.0 Å using 30 second frames
- Easily indexed: Tetragonal form: a = 58.6 Å c = 151.9 Å





Lysozyme

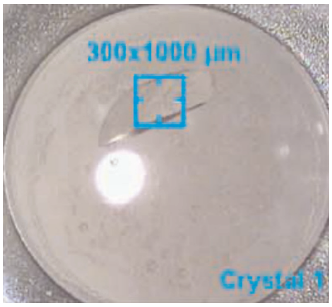
- Strong diffraction to 2.0 Å using 10 second frames
- Easily indexed: Tetragonal form: a = 78.9 Å c = 38.7 Å

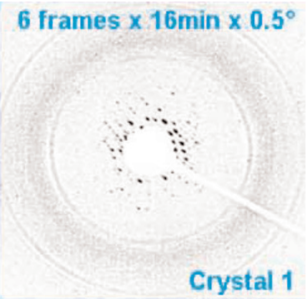


Intrinsic Membrane Protein (Imperial College London)

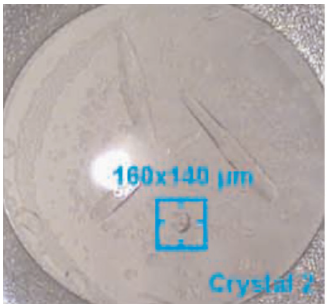
Intrinsic membrane protein crystals generally give weak, low resolution diffraction. The crystals studied here may grow up to 1mm long, and diffract to 8 Å on average at the synchrotron. The PX Scanner gave the following results:

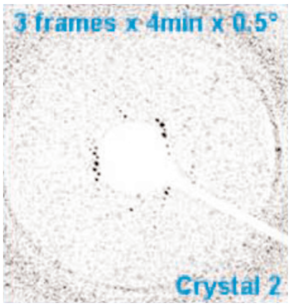
	Angular resolution (Å)
Crystal 1	9 Å
Crystal 2	11 Å





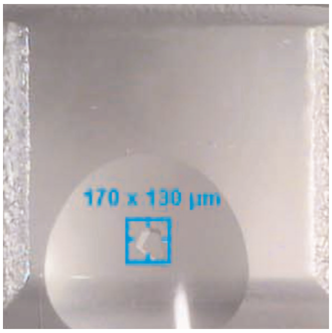
Surprisingly it was possible to detect protein diffraction, even with crystals of less than 200 µm length. These results indicate that the PX scanner is a useful tool for screening small crystals of challenging proteins.

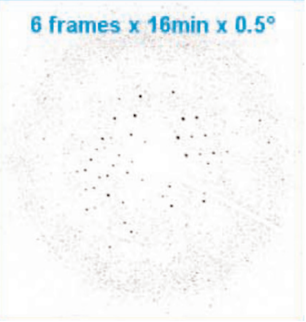




A Typical Weakly Diffracting Protein (Laboratory of Molecular Biophysics, Oxford University)

A more typical example of a weakly diffracting crystal than the membrane protein, is that of the soluble protein provided by a group at the Laboratory of Molecular Biophysics at Oxford University. This protein was found to diffract to 4.5 Å on the PX Scanner using 16 min exposures compared to 4 Å when measured at the synchrotron.



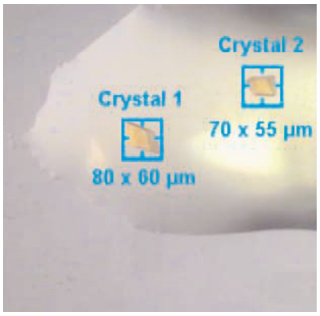


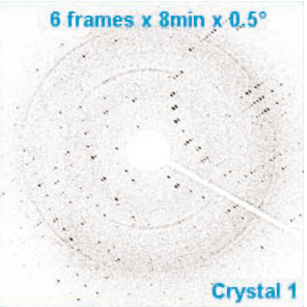
Protein Kinase – Crystal Comparison (GlaxoSmithKline, Stevenage)

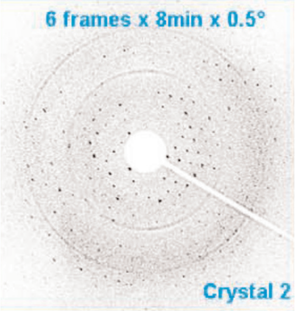
The PX Scanner allows crystal diffraction properties to be assessed *in-situ*. This allows comparison and ranking of a set of crystals within a crystallisation plate. In this example:

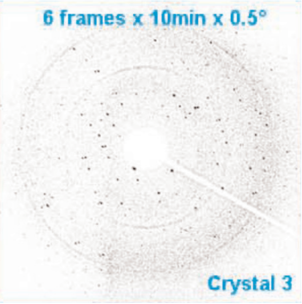
Crystal 1	2.7 Å
Crystal 2	3.2 Å
Crystal 3	3.5 Å

The identical trigonal cell was indexed for each crystal









▢ *Indicates the crystal x-rayed*

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Printed in the USA
November 1, 2010
SI-A-0381

Agilent Technologies