

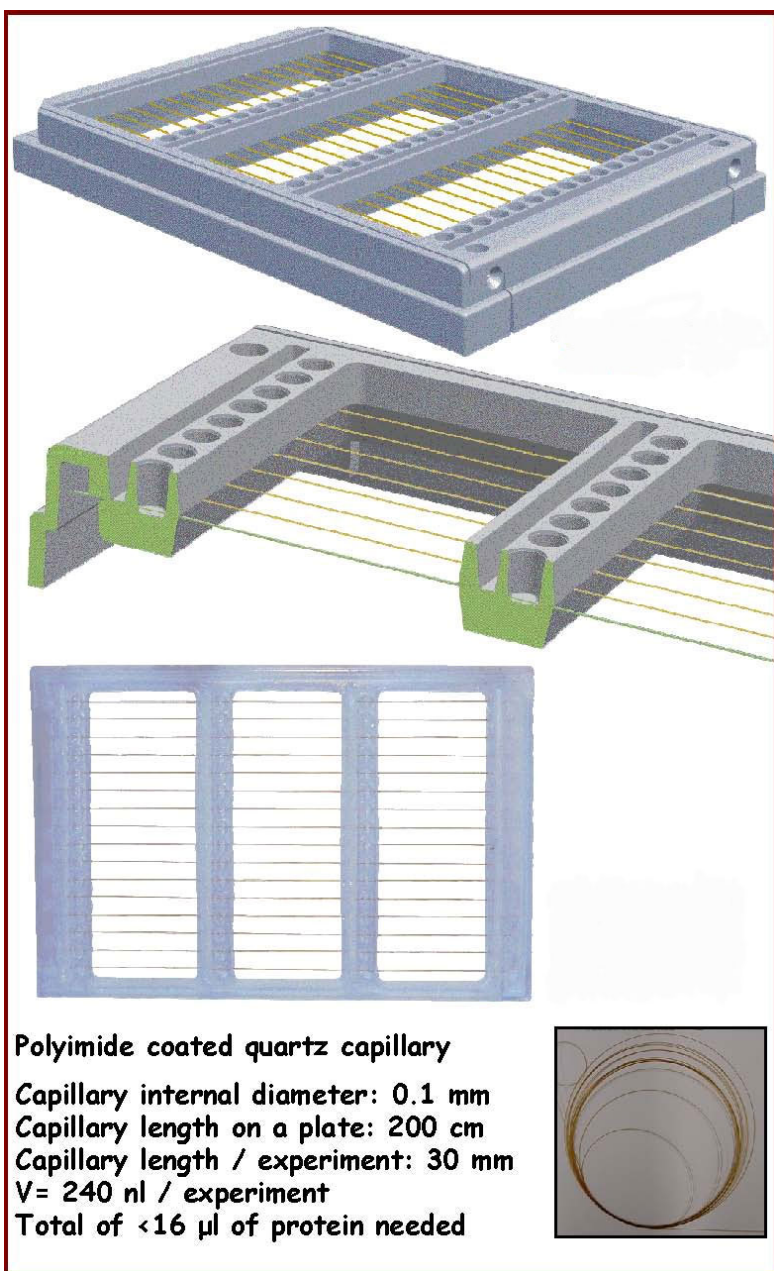
Molecular
Dimensions

New Product

CrystalHarp™



Advanced high throughput **capillary plate** for protein crystal growth and data collection

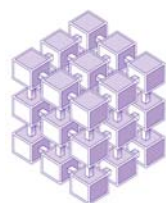


Polyimide coated quartz capillary

Capillary internal diameter: 0.1 mm
Capillary length on a plate: 200 cm
Capillary length / experiment: 30 mm
V= 240 nl / experiment
Total of <16 µl of protein needed

Features of CrystalHarp™:

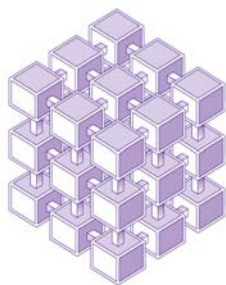
- Capillary based plate based on the successful counter diffusion method
- 48 channels of proven optimal length (30mm) sampling large amounts of protein phase space
- No scale up needed - *in-situ* diffraction – shoot through the plate or mount individual capillaries in standard CryoCaps
- Unique capillary material allows data collection at RT and/or flash-frozen in a liquid nitrogen stream (with or without the use of cryo protectants)
- SBS format suitable for high throughput screening
- Simple set up and analysis, seal with everyday crystallography tape
- Easy addition of cryo protectants or derivatives for phasing studies
- Compatible with all storage and imaging systems – no additional holders needed
- Room for labelling – by hand or with barcodes



Molecular
Dimensions

moleculardimensions.com



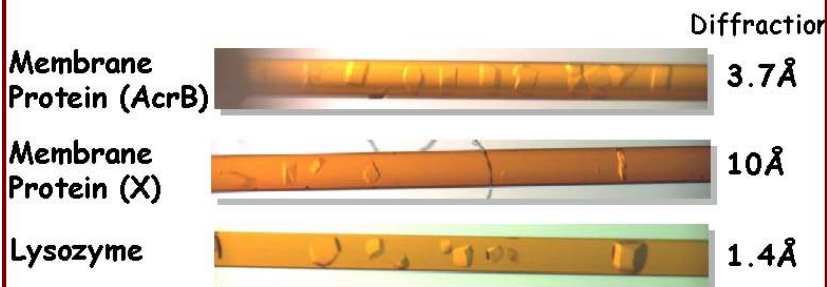


Molecular
Dimensions

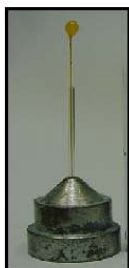
CrystalHarp™



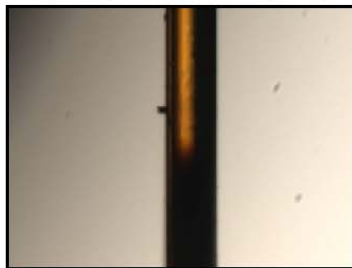
Crystallization using CrystalHarp
Plates tested on different proteins
Crystals were taken to the SLS for diffraction analysis



Capillaries used in a cryo stream - no ice formation

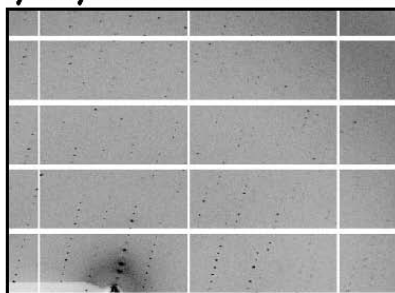


Capillaries are sealed and mounted in a glass sleeve on a standard magnetic CrystalCap.

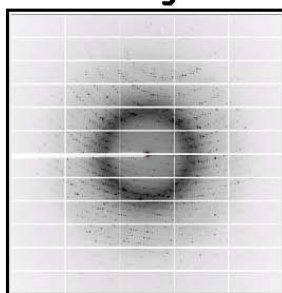


Cryo solution diffused partly through the capillary, cryo-protected part stays clear, non cryo-protected part turns intransparent on freezing.

Data collection was performed under cryocooling in a N₂-gas stream at the PX(X06SA) beamline at the SLS (Villigen, CH). Using the data collected from crystals grown in capillary the structures of lysozyme⁽²⁾ and AcrB⁽³⁾ could be solved using MR.



AcrB 3.7 Å



lysozyme 1.4 Å

Results with CrystalHarp™

Beat Blattmann, Mareike Kurz and Markus G. Grütter
Institute of Biochemistry, University of Zürich,
Winterthurerstrasse 190, CH-8057 Zürich

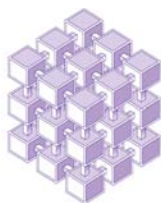
Counter diffusion crystallization⁽¹⁾ of macromolecules in capillaries is an easy, cost-effective, and practical procedure for obtaining protein crystals suitable for *in-situ* X-ray data analysis. The counter diffusion process has been used to simultaneously screen for optimal conditions for protein crystal growth, and mix in cryogenic solutions in a single capillary tube. Problems harvesting crystals and difficulties in transportation are reduced to a bare minimum. We can show, that crystals grown in capillaries diffract to at least the same resolution as the ones grown by vapour diffusion. A 1.4 Å dataset for Lysozyme and a 3.7 Å dataset for AcrB were collected and the structures solved by molecular replacement. Additionally, we observed that capillary grown crystals can be flash-frozen without the need of a cryo protectant. The observation of ice rings was reduced to a bare minimum.

(1) Garcia-Ruiz JM, Methods in Enzymology, 1997, Vol. 368

(2) Cianci M, Helliwell JR, Suzuki A., Acta Crystallogr D, 2008 Dec;64

(3) Pos KM, Schiefner A, Seeger MA, Diederichs K., FEBS Lett. 2004 Apr 30;564(3)

Individual kits available to order
now under product code
MD11- 57



Molecular
Dimensions

moleculardimensions.com

