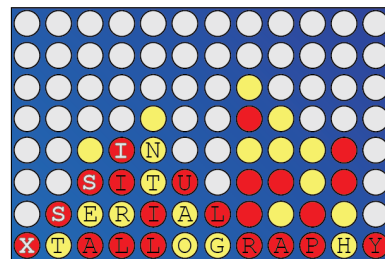


Serial crystallography data collection



Beamline and endstation:

X06SA-PXI

Tutors:

Vincent Olieric

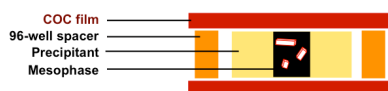
Shibom Basu

Chia-Ying Huang

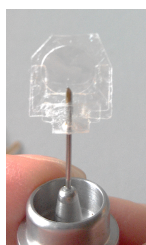
Meitian Wang

Description of the exercise:

Two samples (PepT_{St}_PDBID 5D58 and Lysozyme_PDBID 5D5F) were prepared on the IMISX plate and harvested on Y support for serial crystallography data collection.

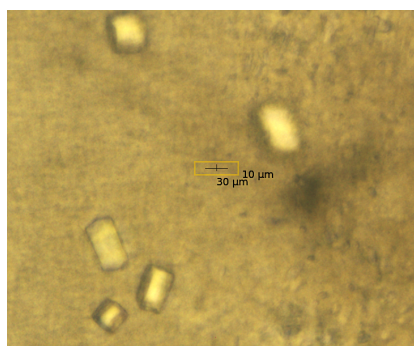


IMISX plate

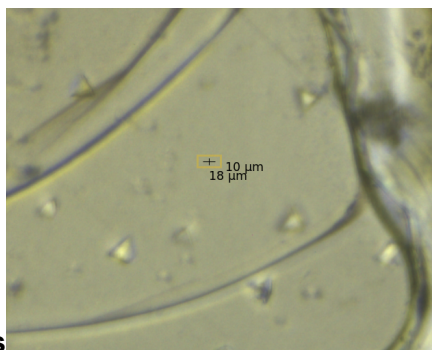


IMISX well on Y support

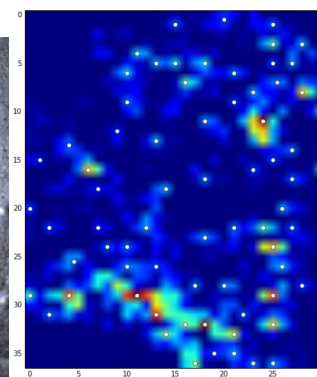
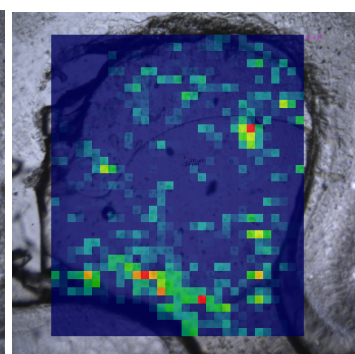
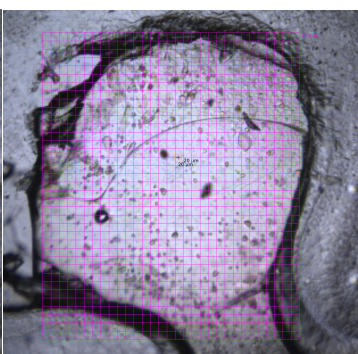
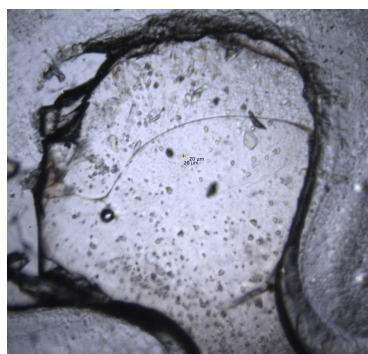
2. DA+ interface for screen the X-ray diffraction.



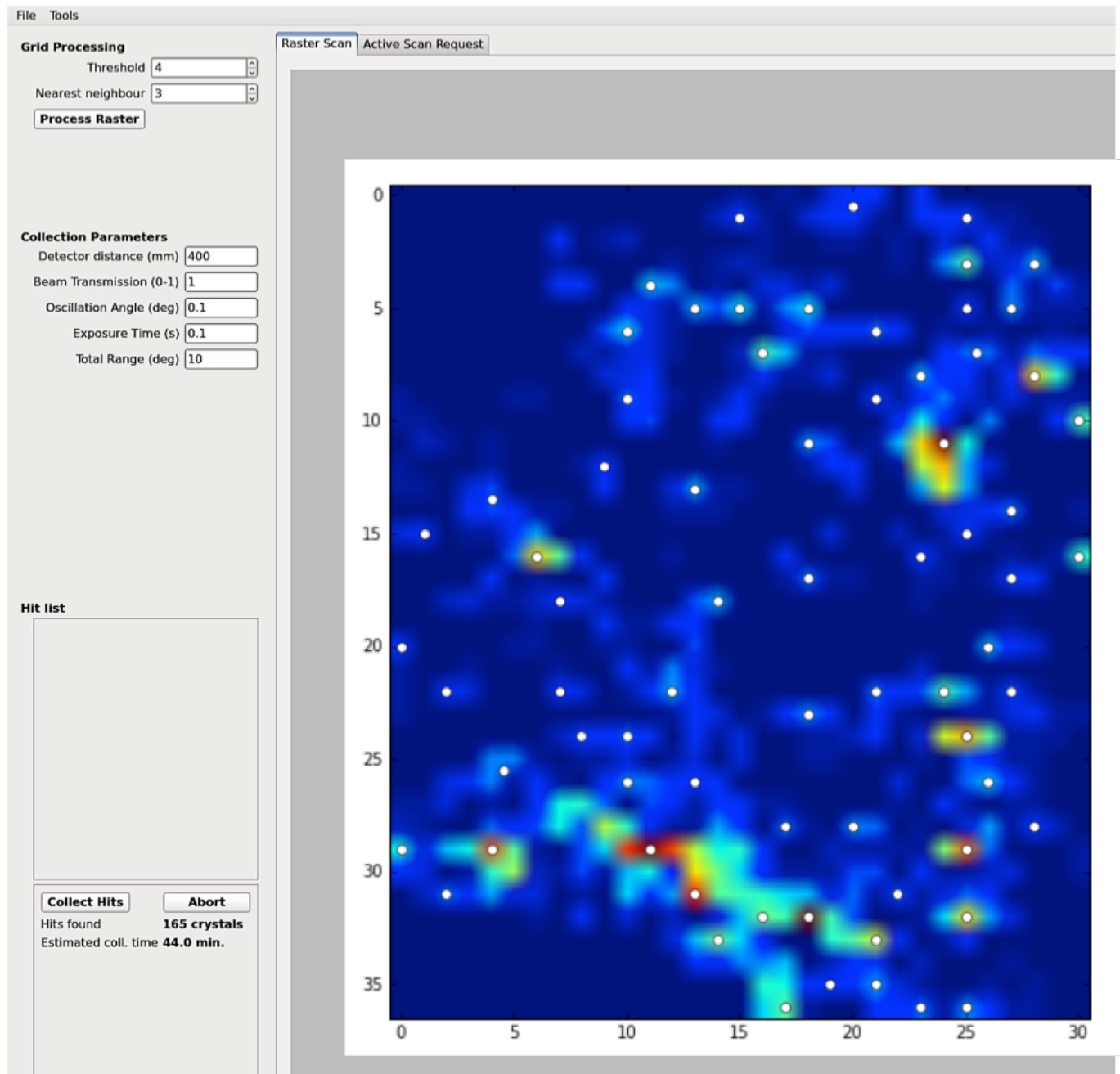
Lysozyme crystals



PepT_{St} crystals



3. CY+ interface for serial data collection



References:

1. Huang C.Y. *et al.* (2016) In meso in situ serial X-ray crystallography of soluble and membrane proteins at cryogenic temperatures. *ActaD* **72**, 93–112.