

MX at KEK

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Self-introduction



Fig. 1 Sweden.

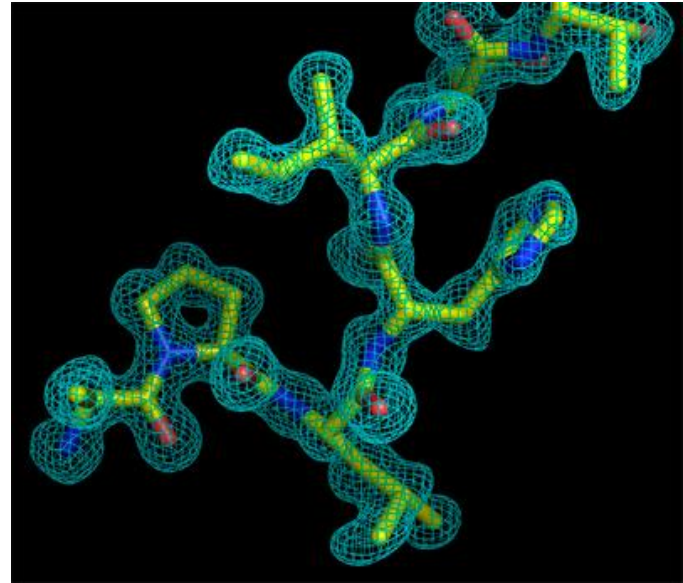
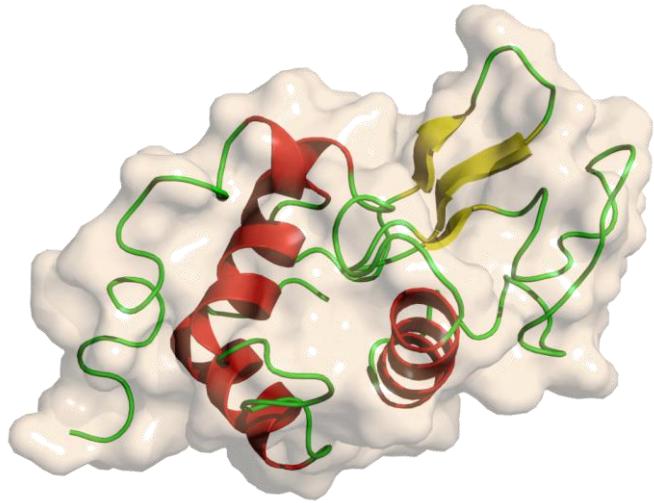


Fig. 2 My cat Lotus :)

Experimental theme:

Material & life science,
Basics of Structural Biology
Research,
X-ray Crystallography.

Macromolecular Crystallography (MX)



Crystallisation

- A purified protein solution and a stock solution are prepared and mixed.
- After becoming supersaturated, if successful the protein molecules will join together to form a stable nucleus.
- As it grows, a crystal is created.
- Since it is thermodynamically unlikely due to a decrease in entropy, for most proteins the process has a success rate of about 30%.
- Therefore usually an initial screening and further refinement are performed.

Sample holders



Research group

- Since MX experiments at PF are automated, a 2d barcode sample identification system is used.
- However, frost reduced legibility.
- Thus a two-step uni-puck identification system is being developed

My assignment

Based on existing Python scripts for the barcode and RFID readers, I

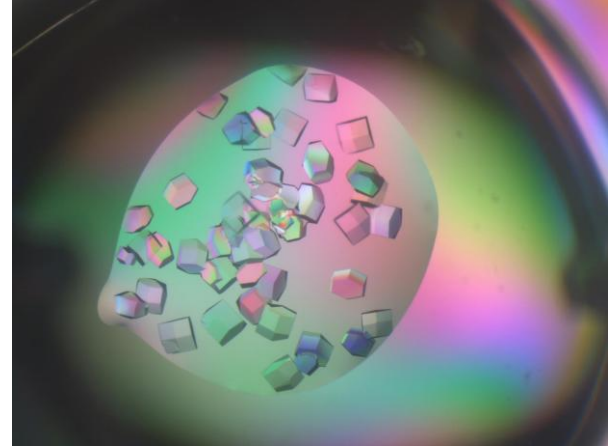
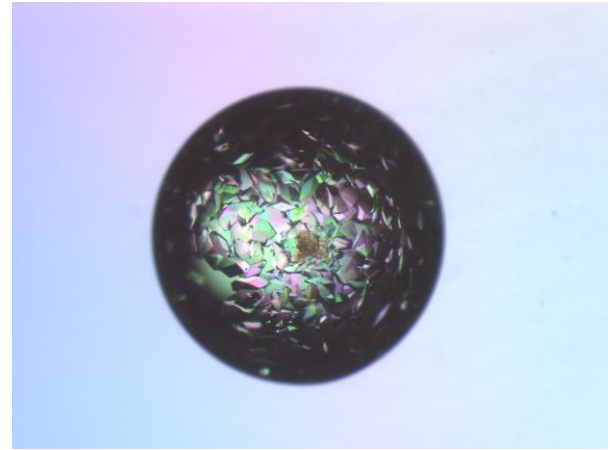
- updated the commands according to the parameters of the new barcode reader model,
- combined both programs into one that reads both,
- made it save the read data into a text file.

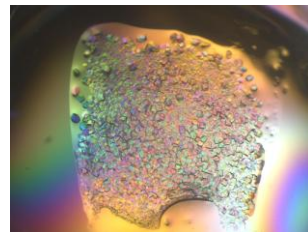
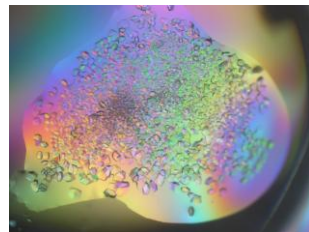
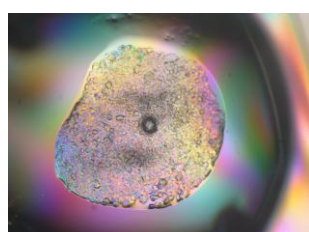
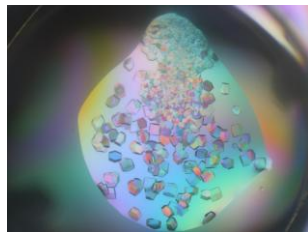
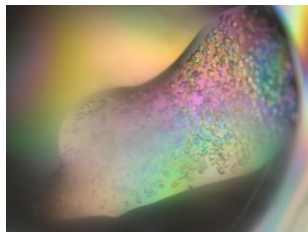
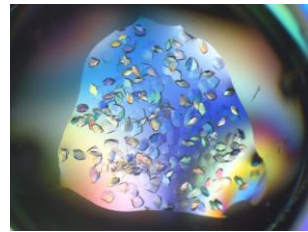
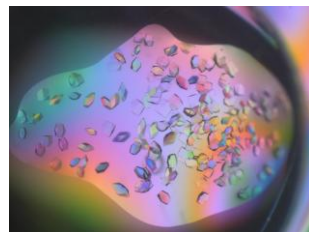
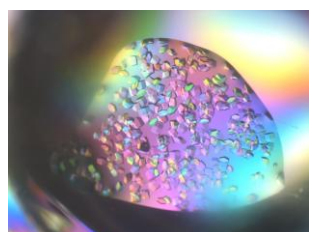
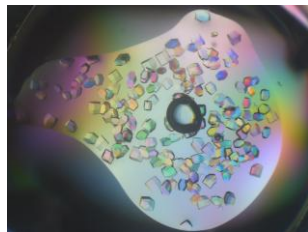
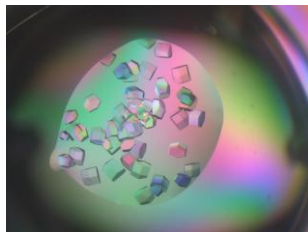
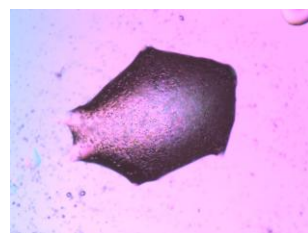
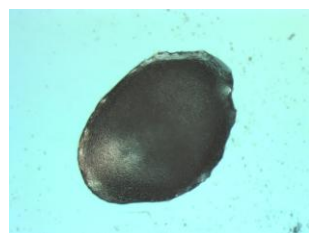
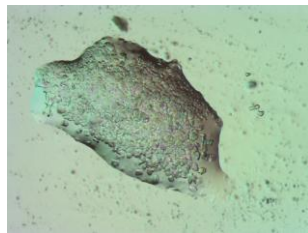
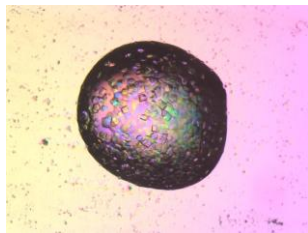
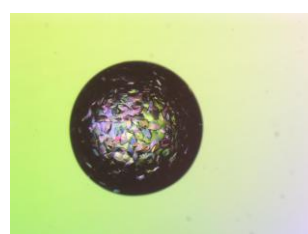
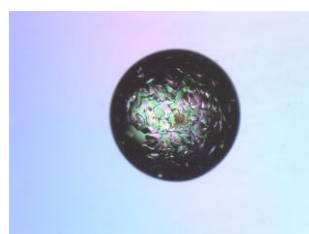
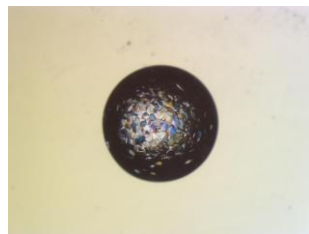
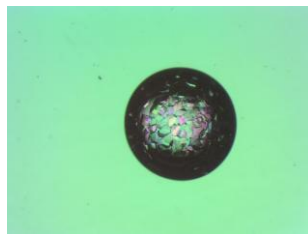
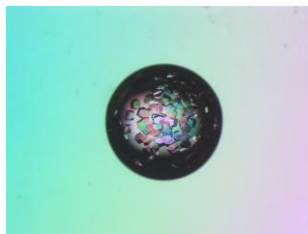
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Barcode B: C0901AB030:002  
Barcode C: C0304AA683:003  
Barcode D: C0102AD693:004
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Protein crystallisation

Additionally, I practiced protein crystallisation on lysozyme crystals.

This week, we will screen mutant BphA4 (Ferredoxin reductase) crystals using an automated crystallisation robot.





Thank you!
