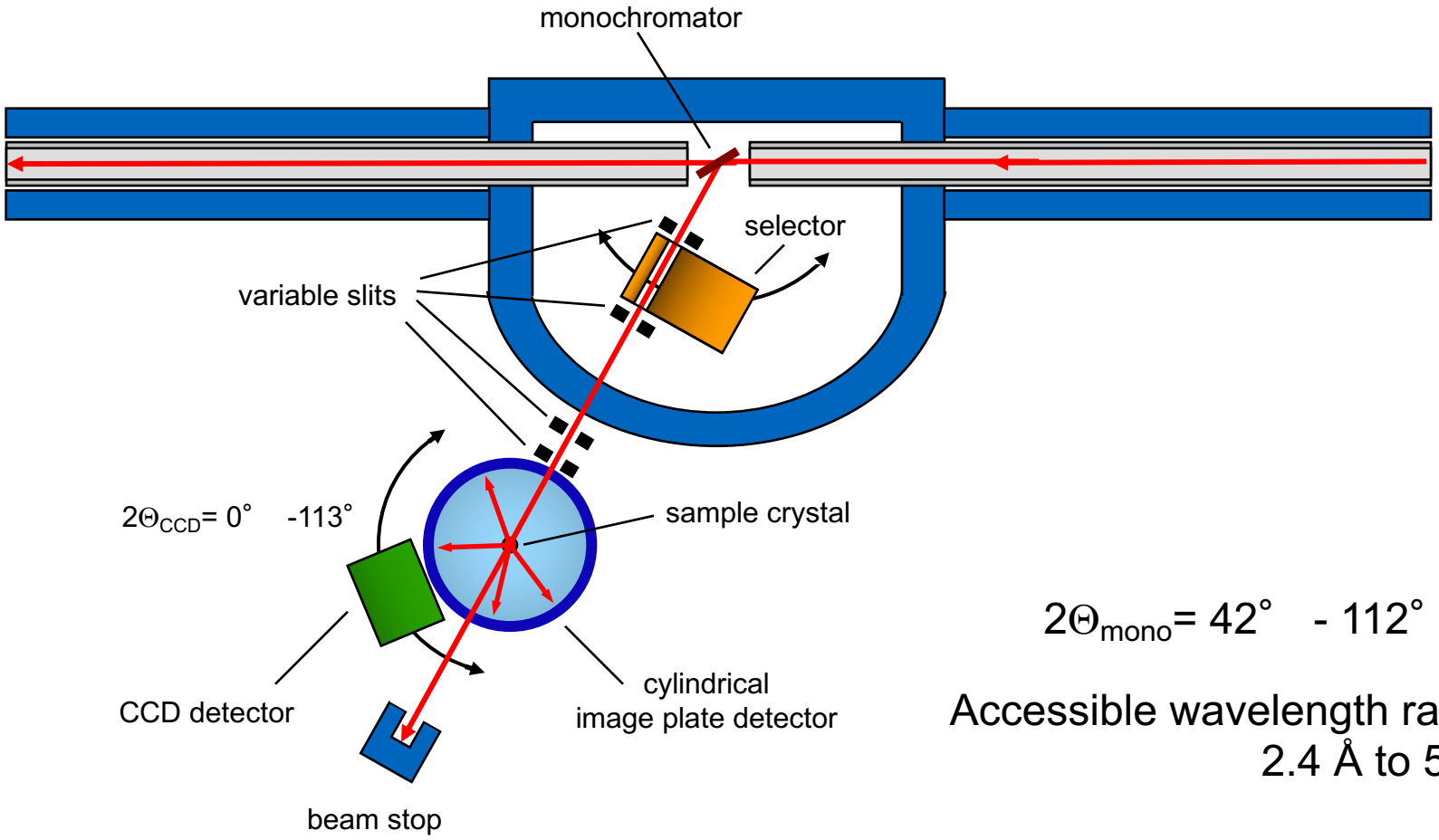
Real-time investigation of Lysozyme crystallization kinetics: a neutron diffraction study

M. Longo, R. J. Heigl, and T. E. Schrader

Forschungszentrum Jülich

MLZ is a cooperation between:

Schematic Overview over the Instrument BIODIFF

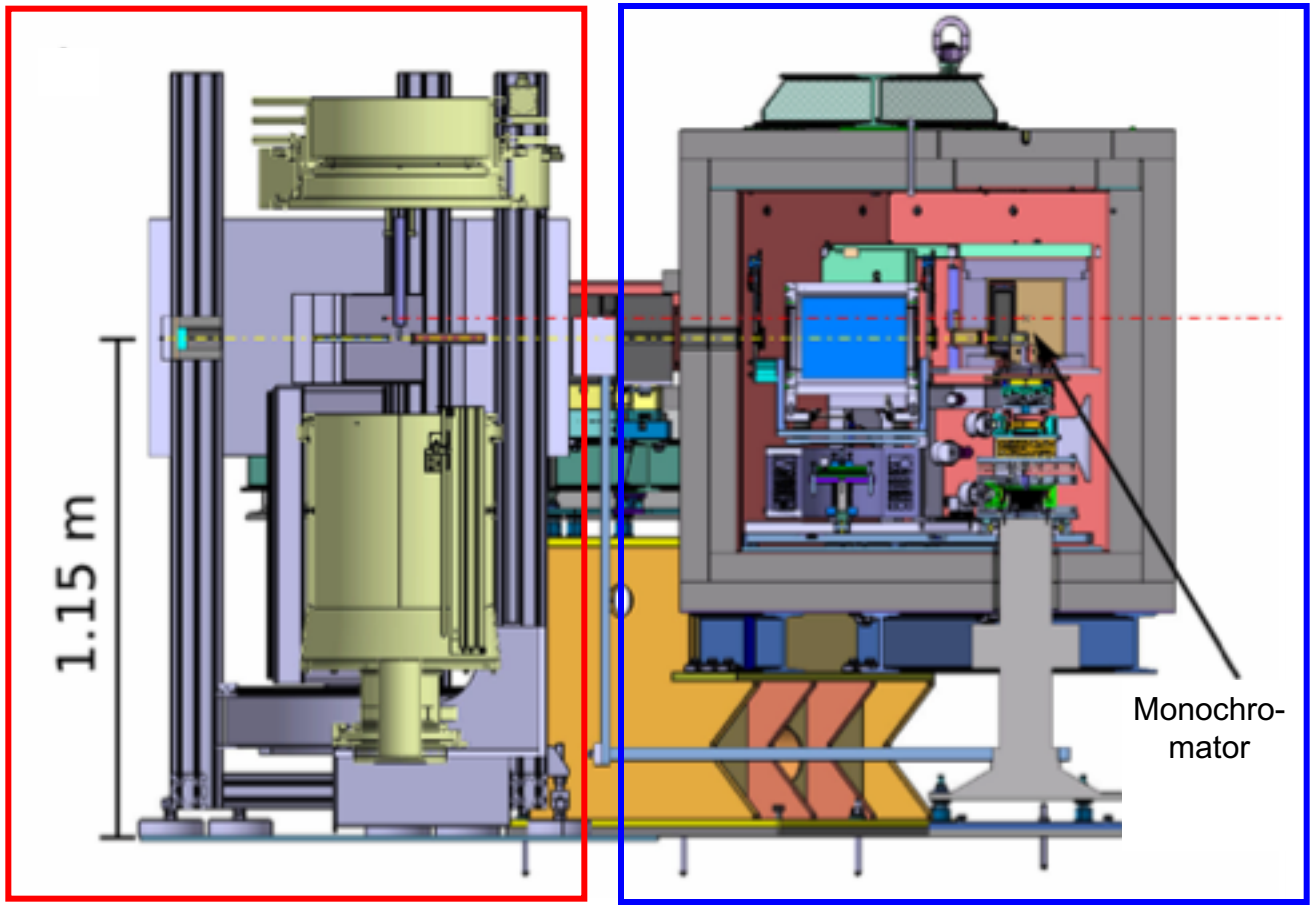


$2\Theta_{mono}$= 42° - 112°

Accessible wavelength range:
2.4 Å to 5.6 Å

Wavelength can be adapted to unit cell size and resolution needs.

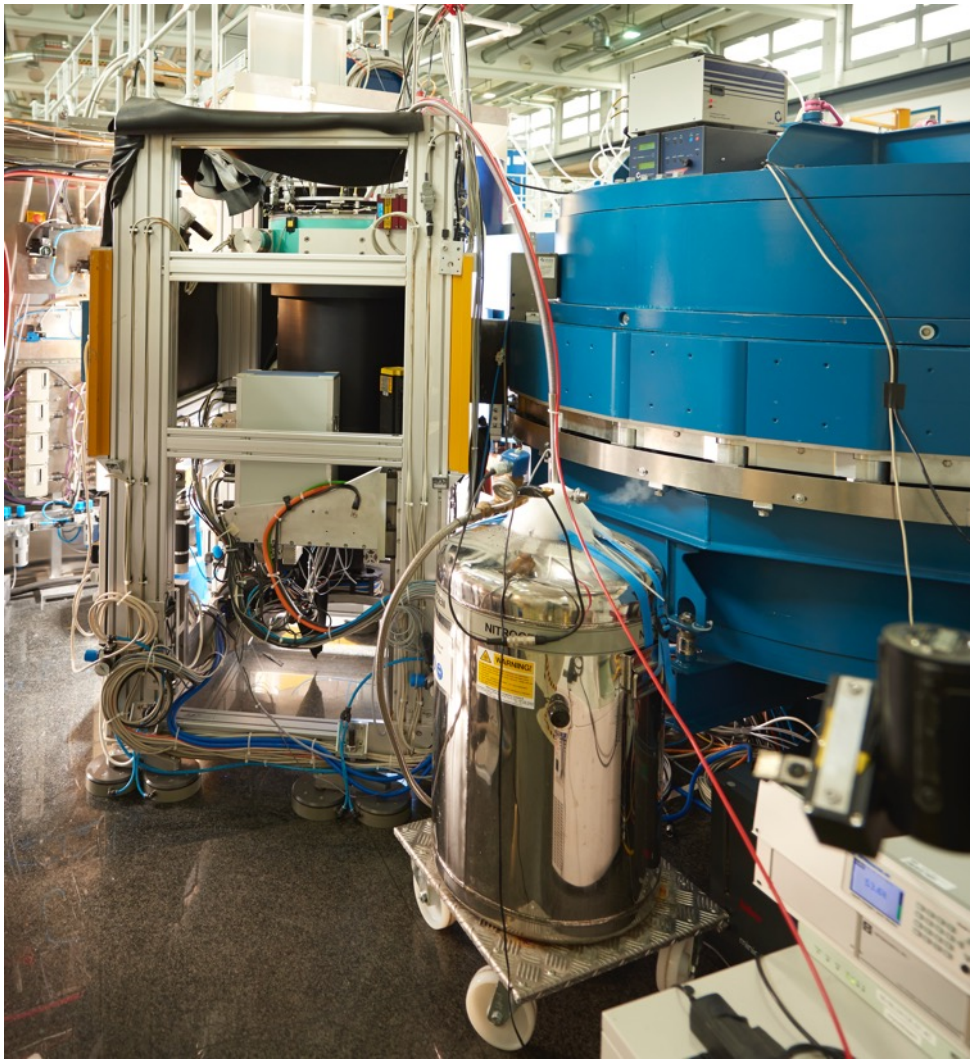
The Simultaneous Construction Phase in Garching and Jülich



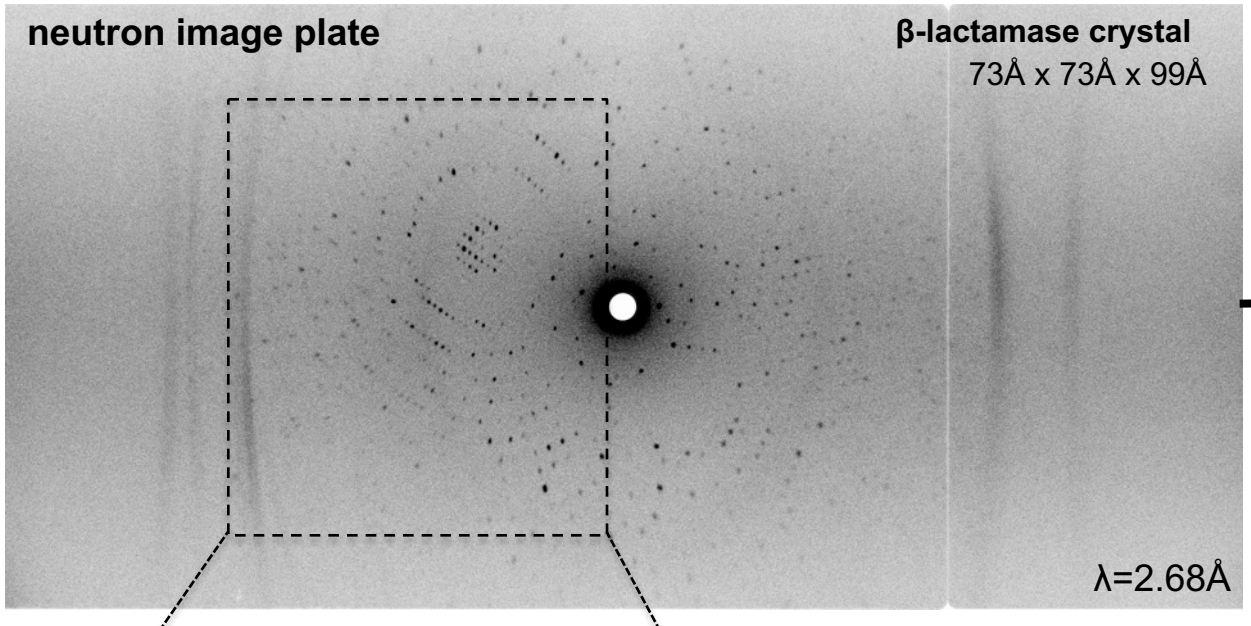
Detector unit, constructed and built in Garching (Ph. Jüttner, MLZ)

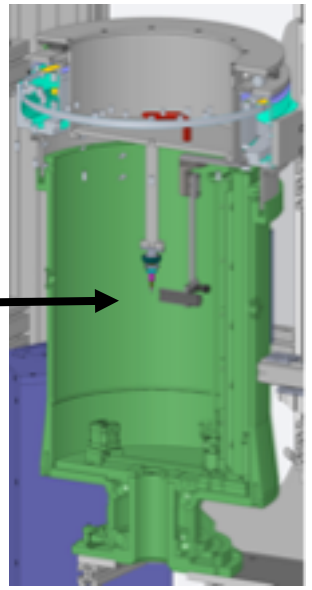
Monochromator-shielding, constructed and built in Juelich (B. Laatsch, ZEA-1 Engineering)

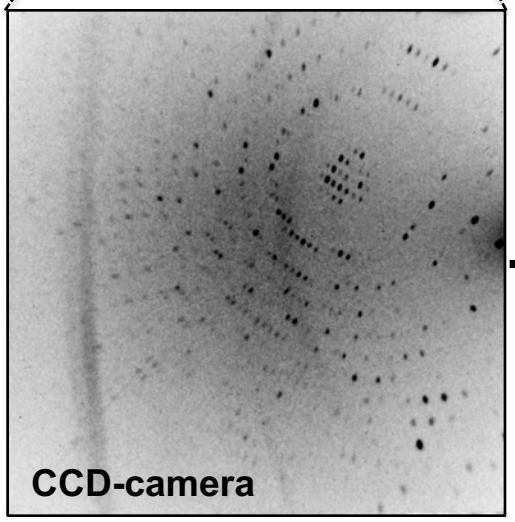
A Most Recent View of the Instrument BIODIFF

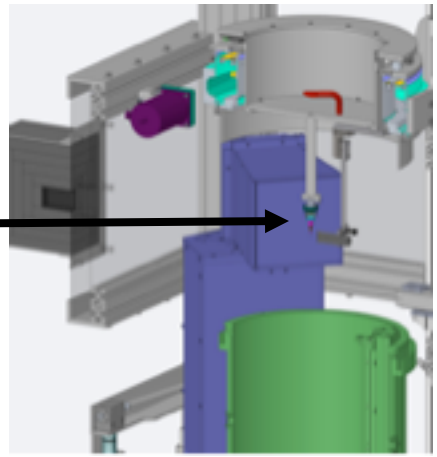


The Two Detectors of BIODIFF









NIP-scanner

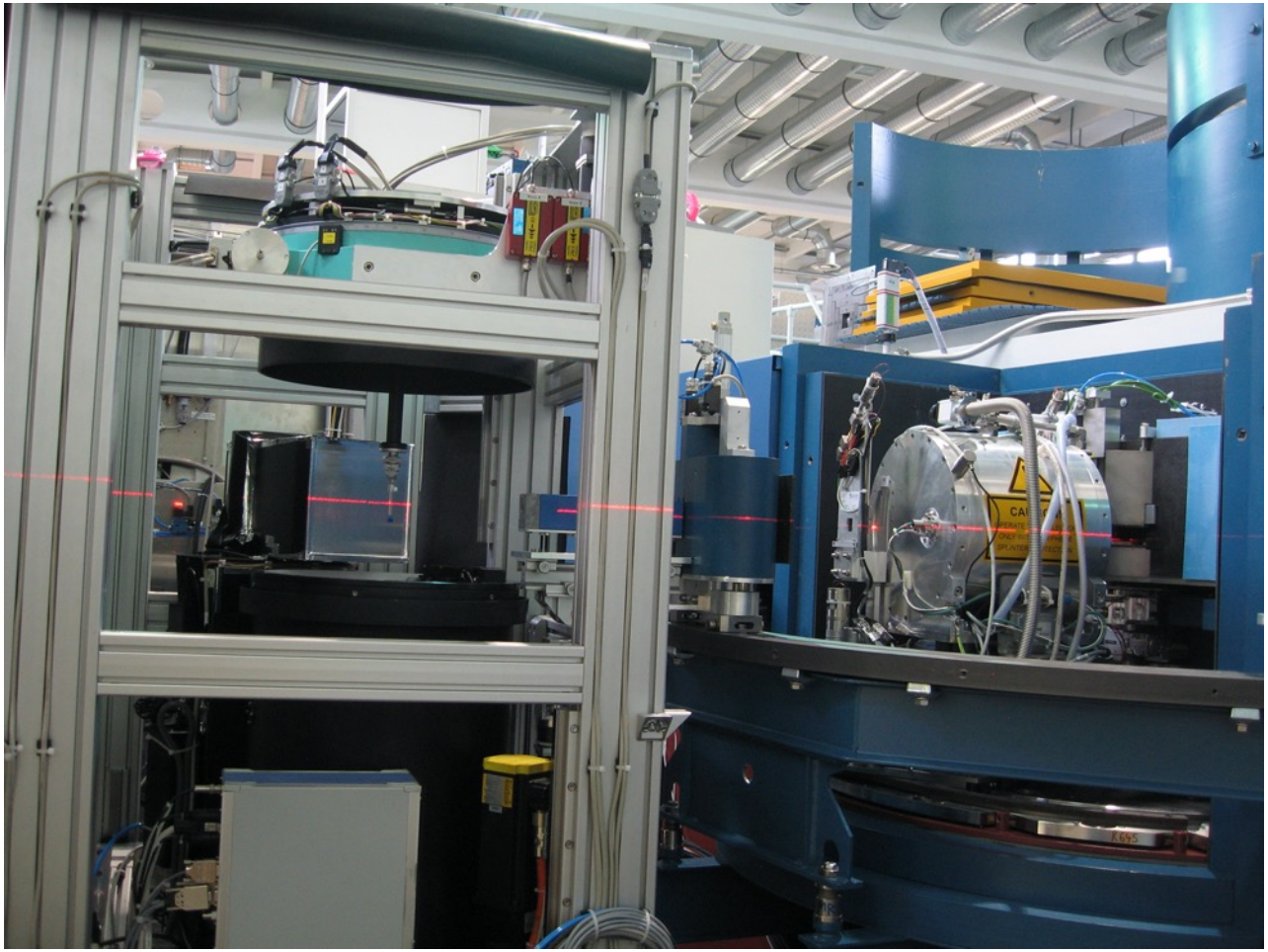
- larger solid angle
- readout time ≥ 4 min

CCD-camera

- smaller solid angle
- readout time ≥ 1 sec

Room temperature set- up of the instrument BioDiff

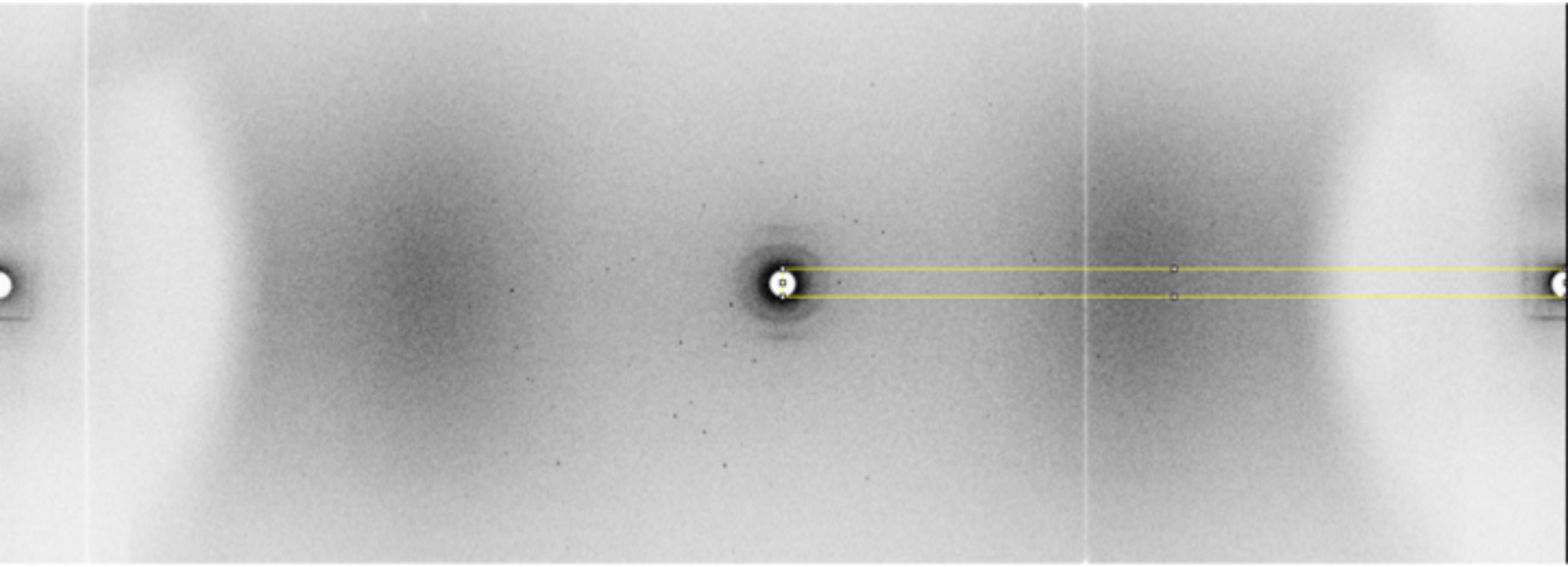
- a bit an old picture, but it shows all necessary parts



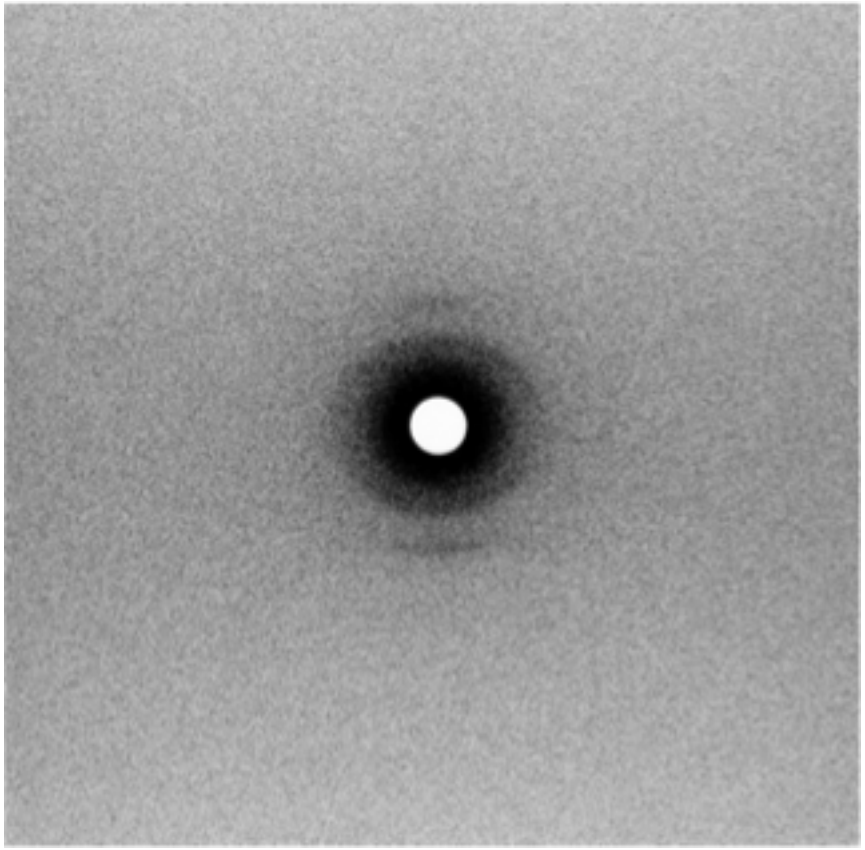
Questions

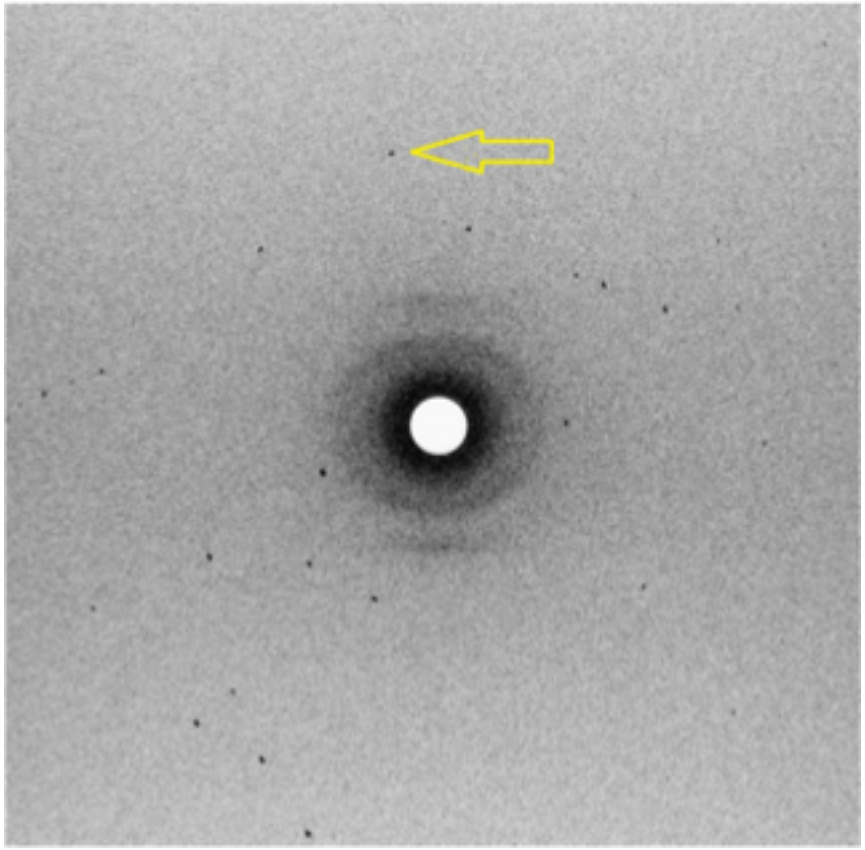
- Do proteins crystallize in the neutron beam?
- Can we learn something from the crystallization kinetics?

Area of the detector which was averaged for SANS signal

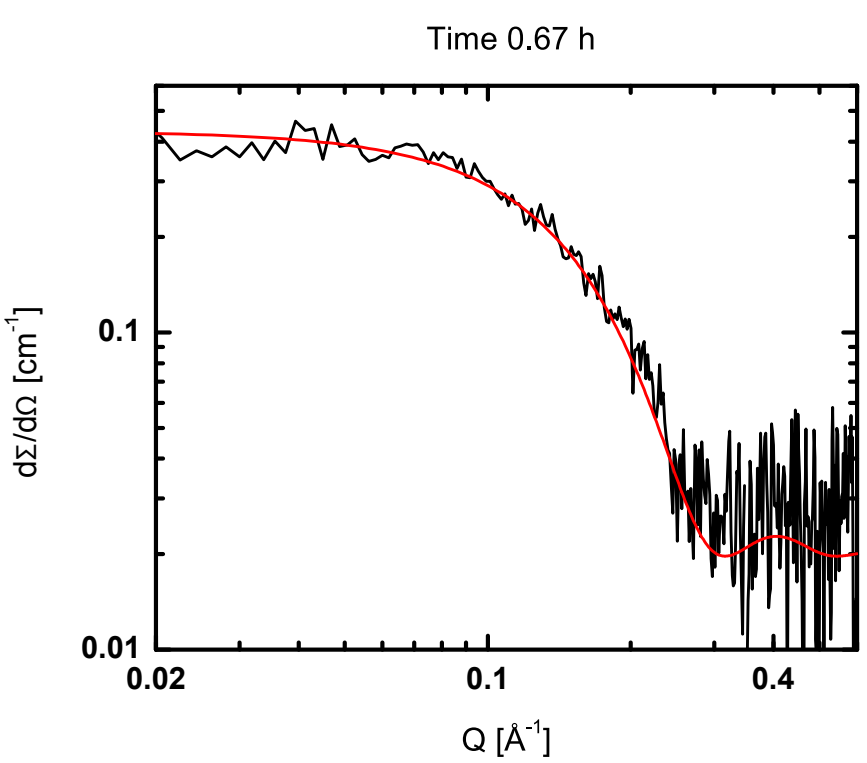


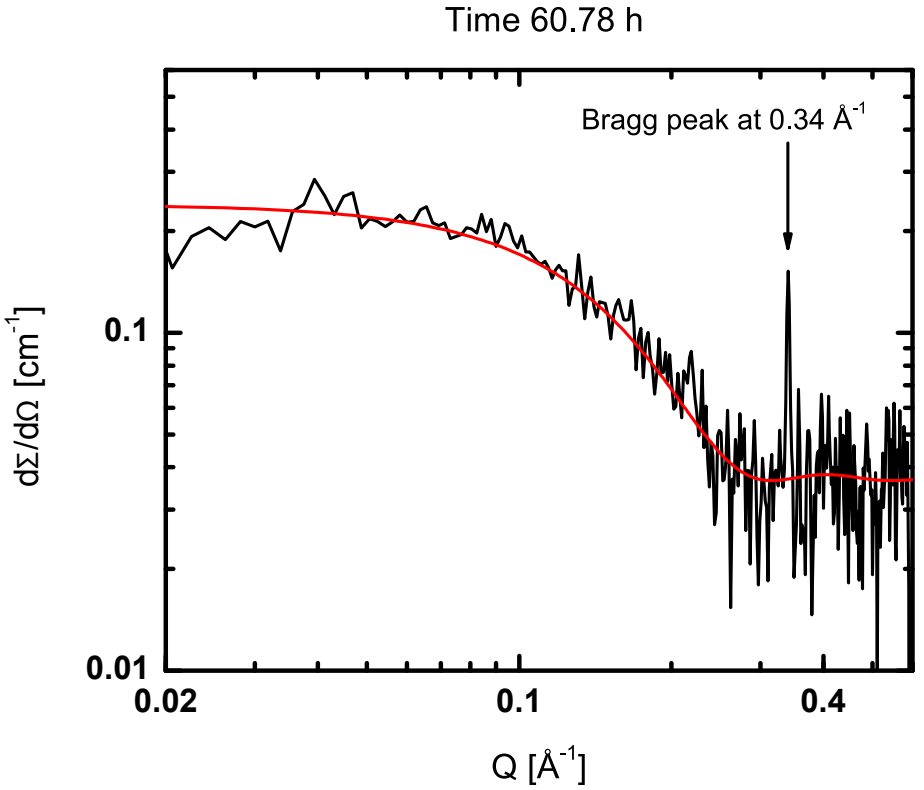
First Bragg reflexes appearing

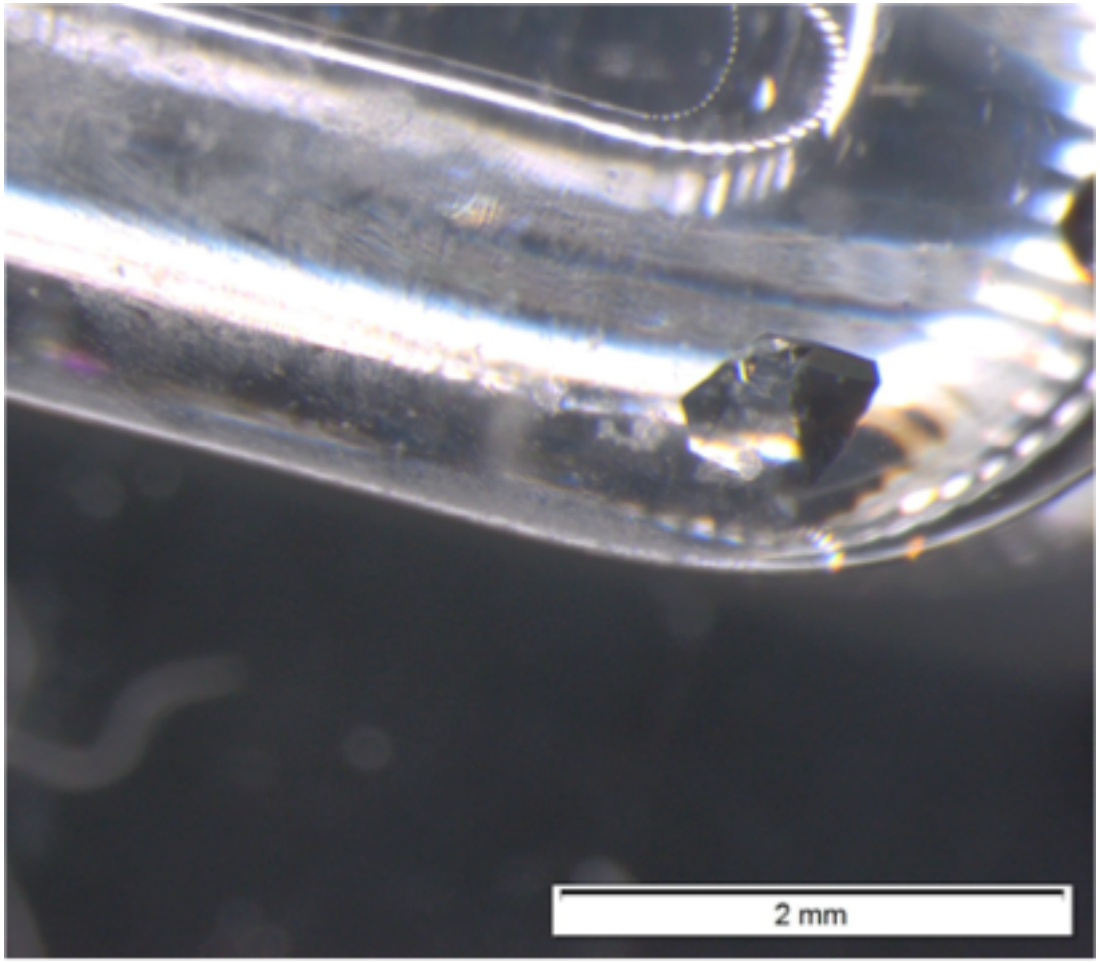




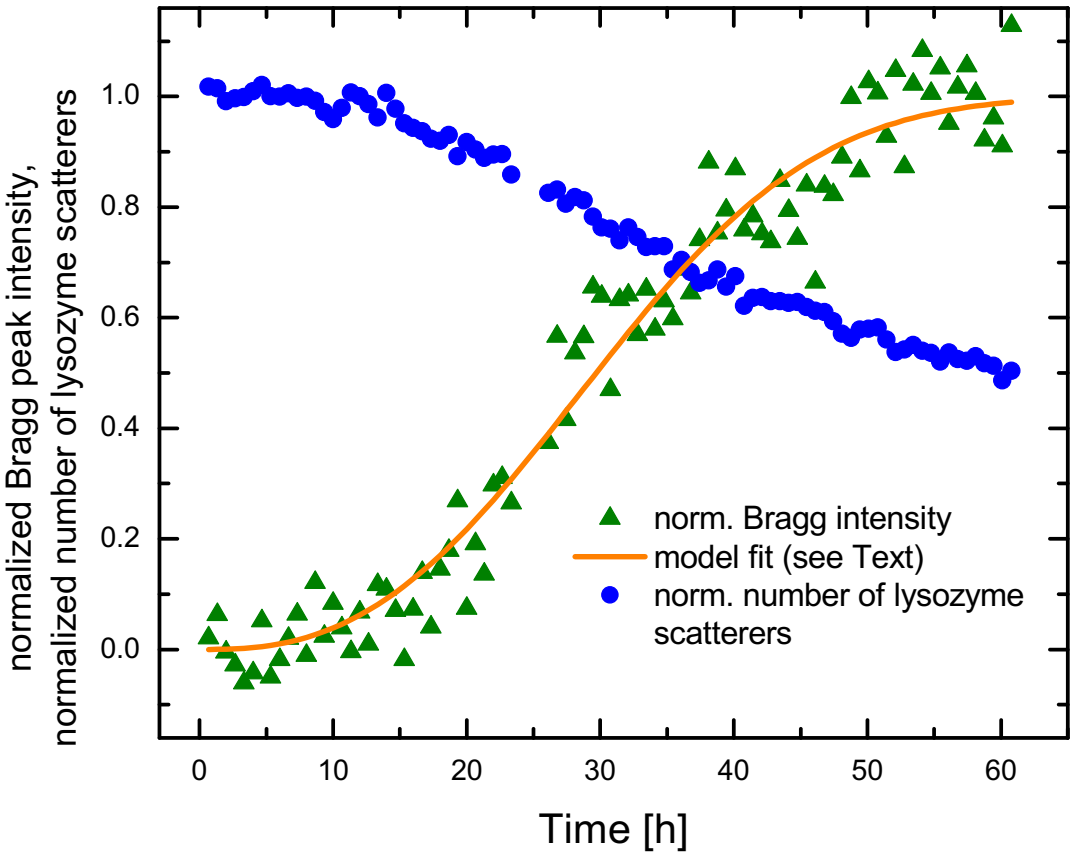
SANS curves


Time 0.67 h
dΣ/dΩ [cm^{-1}]
0.1
0.01
0.02
0.1
0.4
Q [Å^{-1}]


Time 60.78 h
Bragg peak at 0.34 Å^{-1}
dΣ/dΩ [cm^{-1}]
0.1
0.01
0.02
0.1
0.4
Q [Å^{-1}]


2 mm

SANS and WANS data in one graph



Conclusions

- Lysozyme crystals grow in the neutron beam
- One can learn things about the crystallization process from the combination of the Small angle neutron scattering signal and the increase in the intensity of Bragg peaks.