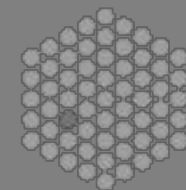


Aspects of Instrumentation at the European Molecular Biology Laboratory

Thomas R. Schneider, EMBL Hamburg

EIROforum School on Instrumentation
ESO (Garching, Germany) 15/06/2015

EMBL



EMBL's Five Missions



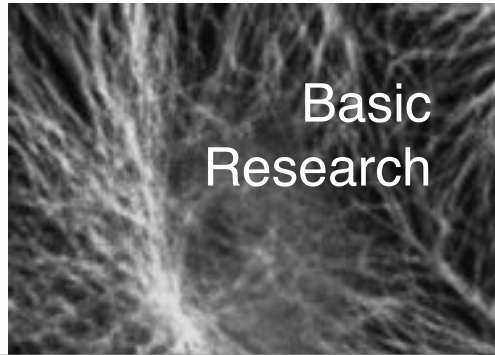
Core Facilities

Services

Synchrotron beamlines



Advanced
Training



Basic
Research

Nuclear Pore Complex



Technology
Development
& Transfer

EMBL-EM

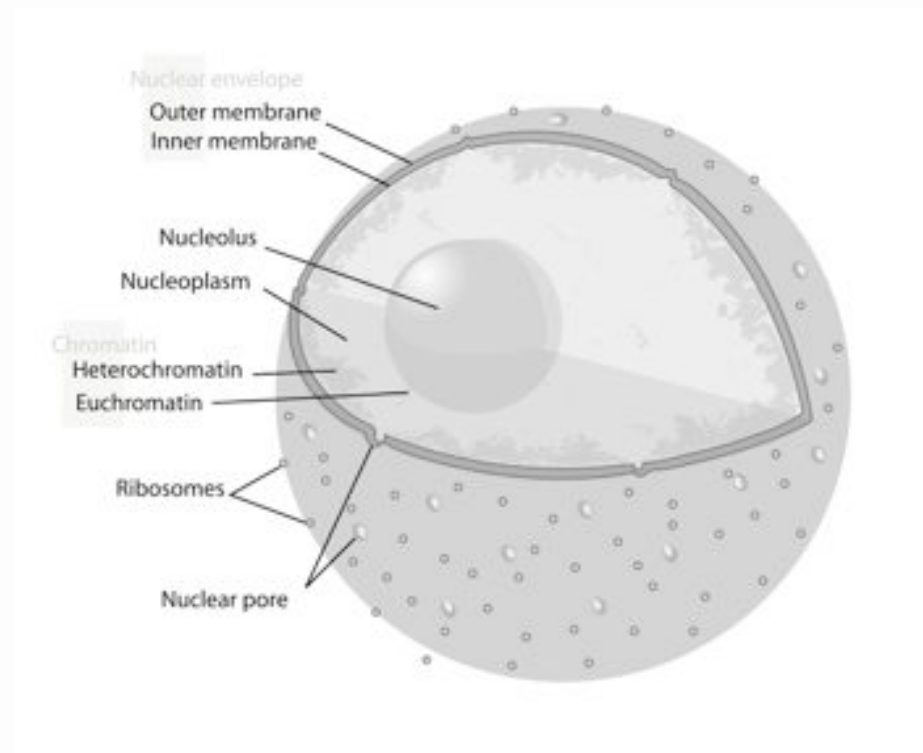
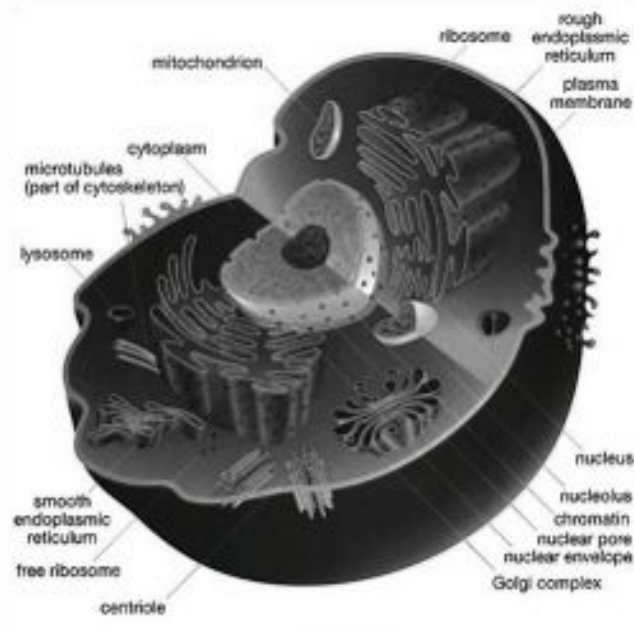


Integration of
life science
research

The Nuclear Pore Complex

- An example of multi-scale 'hybrid' structural biology

The Nuclear Pore Complex ('NPC')

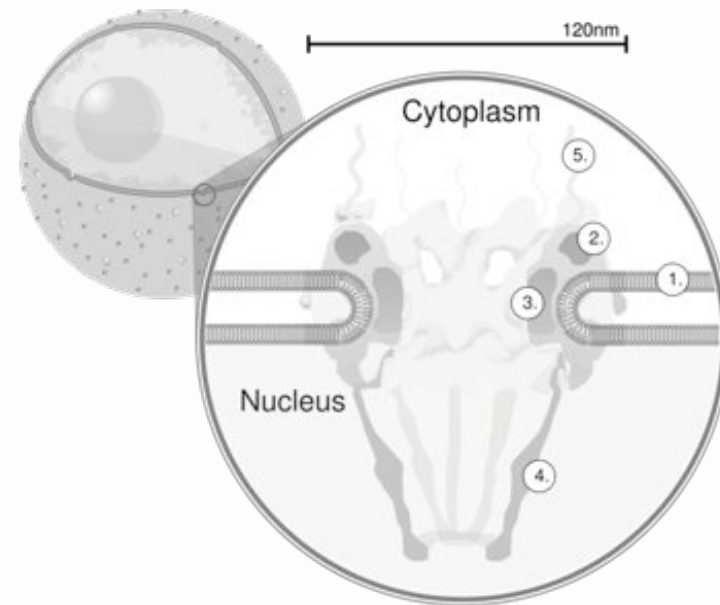
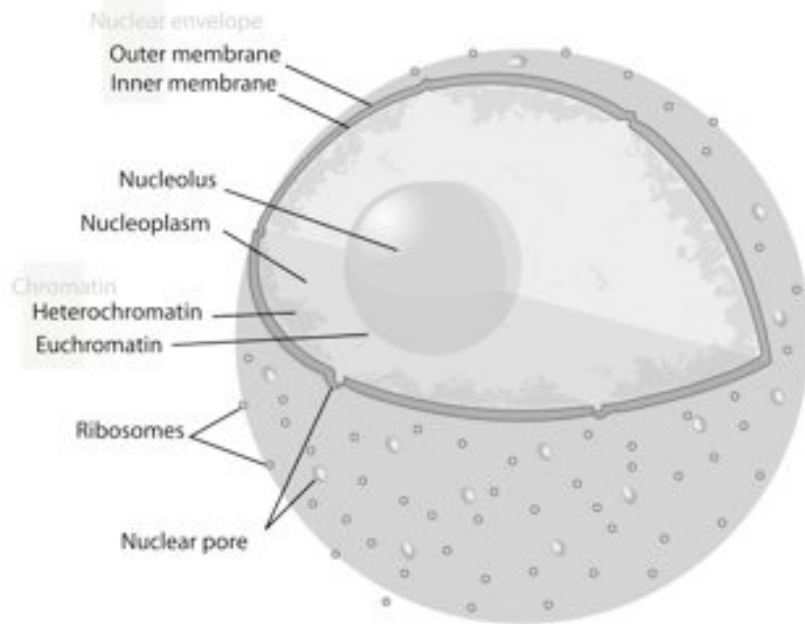


Linear dimensions: 3 – 100 μm

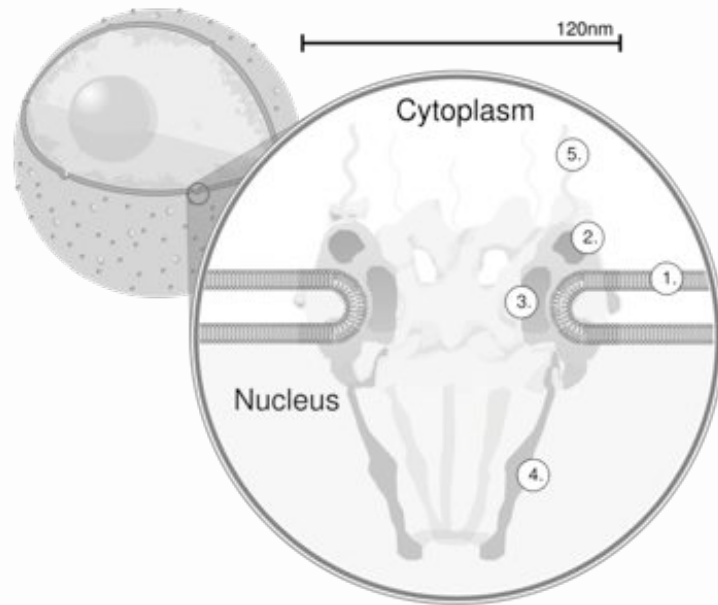
https://en.wikipedia.org/?title=Nuclear_pore

<http://book.bionumbers.org/how-big-is-a-human-cell/>

The Nuclear Pore Complex ('NPC')

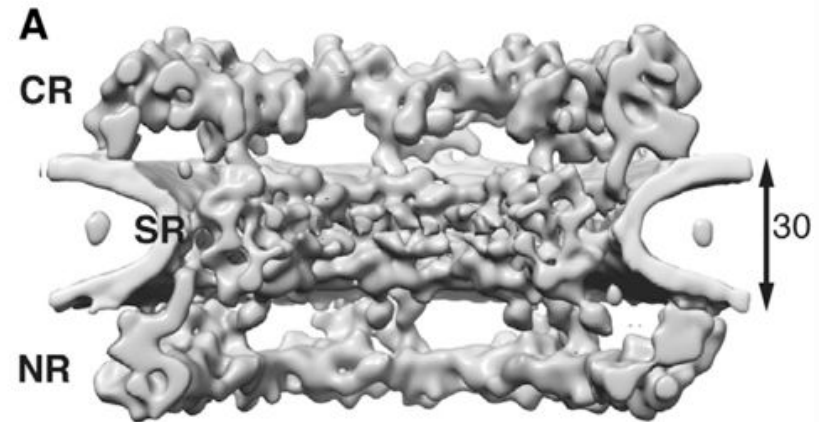


The Nuclear Pore Complex ('NPC')



~ 1000 protein molecules of 30 kinds

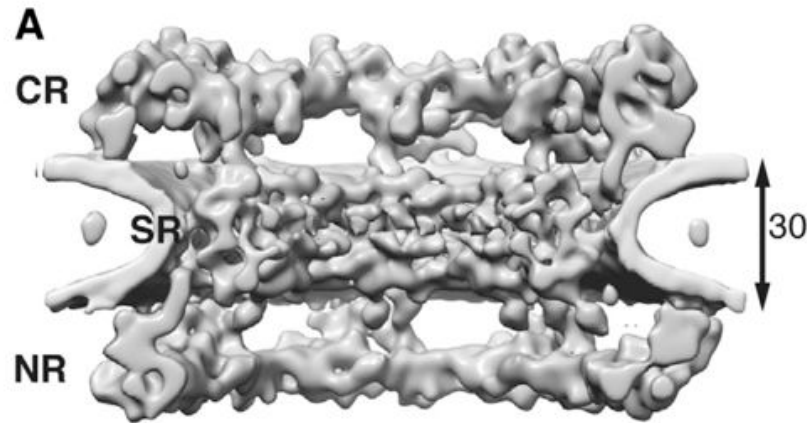
assemble / disassemble



**NPC by Cryo Electron Tomography:
3.2 nm**

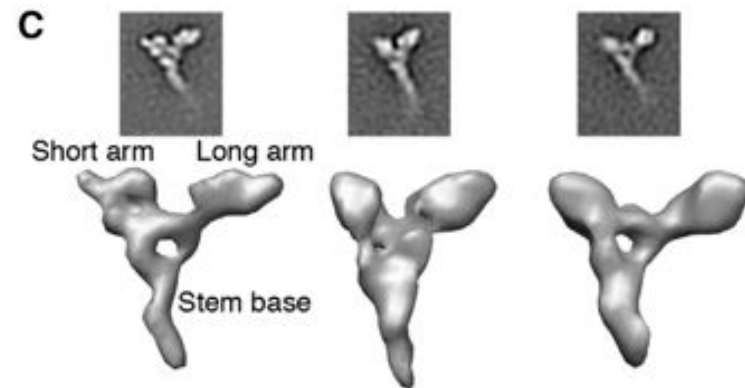
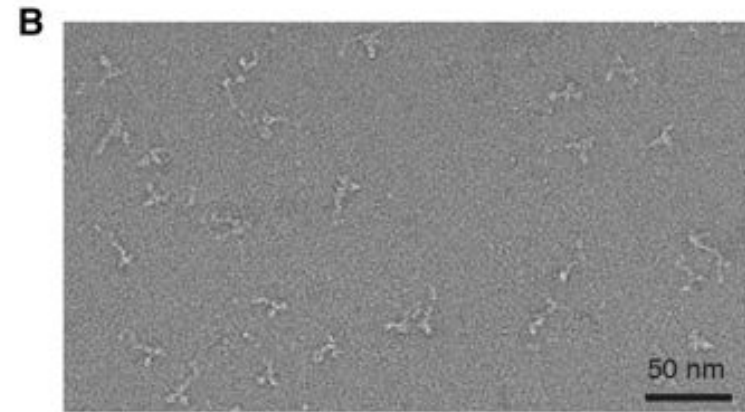
Bui et al. (2013). Integrated Structural Analysis of the Human Nuclear Pore Complex Scaffold. *Cell*, 155:1233

Bui et al



Composition

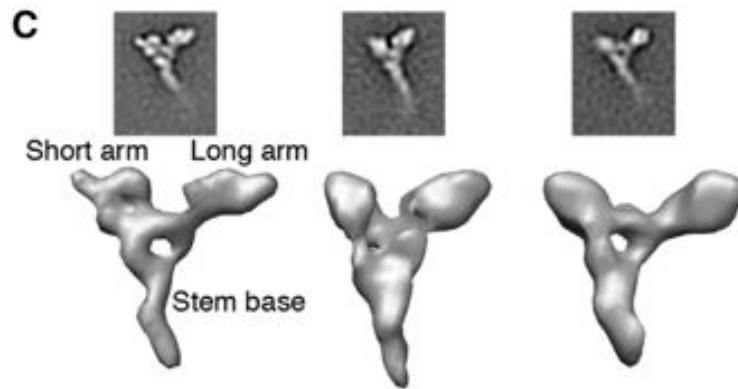
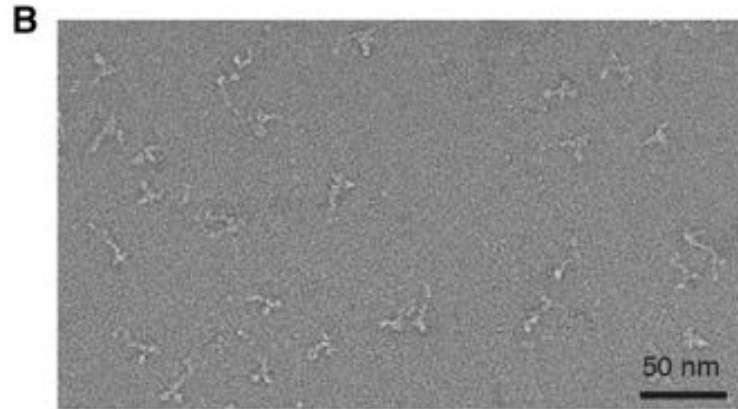
Numerous proteins: e.g. hNup107, Nup358, Nup214, Nup88, Aladin, hCG1, Nup153, Nup50



CNC by Single Particle Cryo Electron Microscopy: ~1 nm

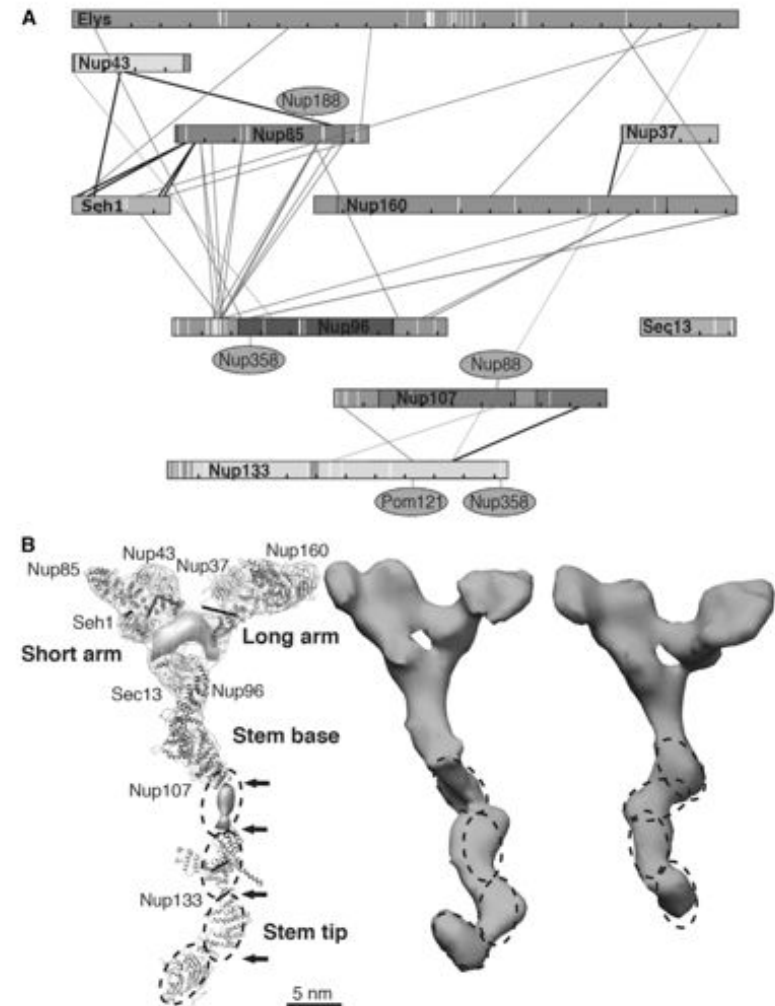
Bui et al. (2013). Integrated Structural Analysis of the Human Nuclear Pore Complex Scaffold. *Cell*, 155:1233

Nuclear Pore Complex



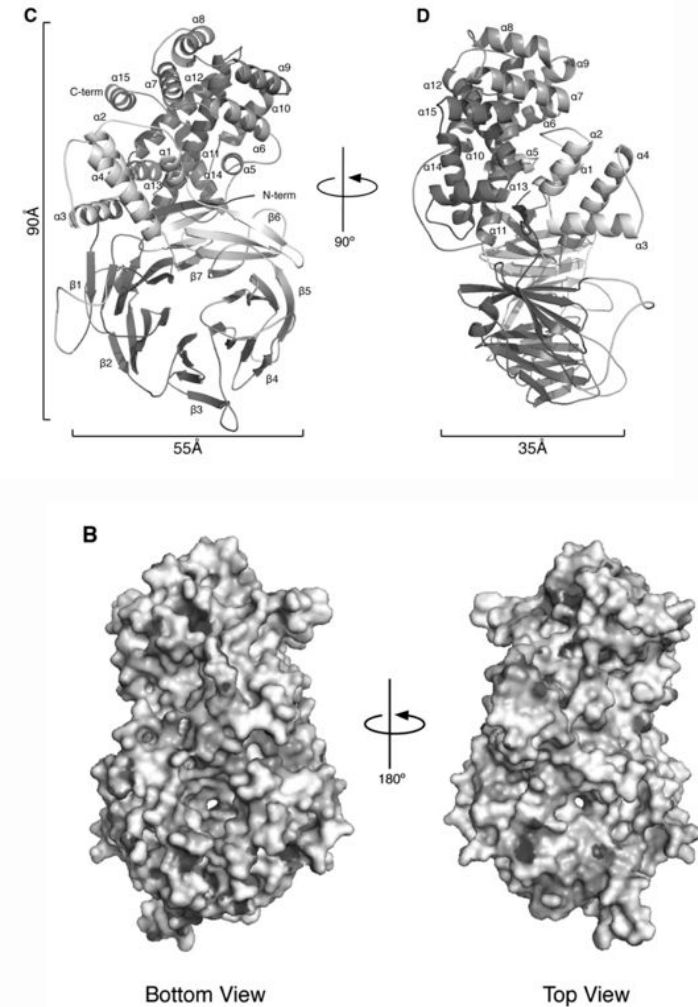
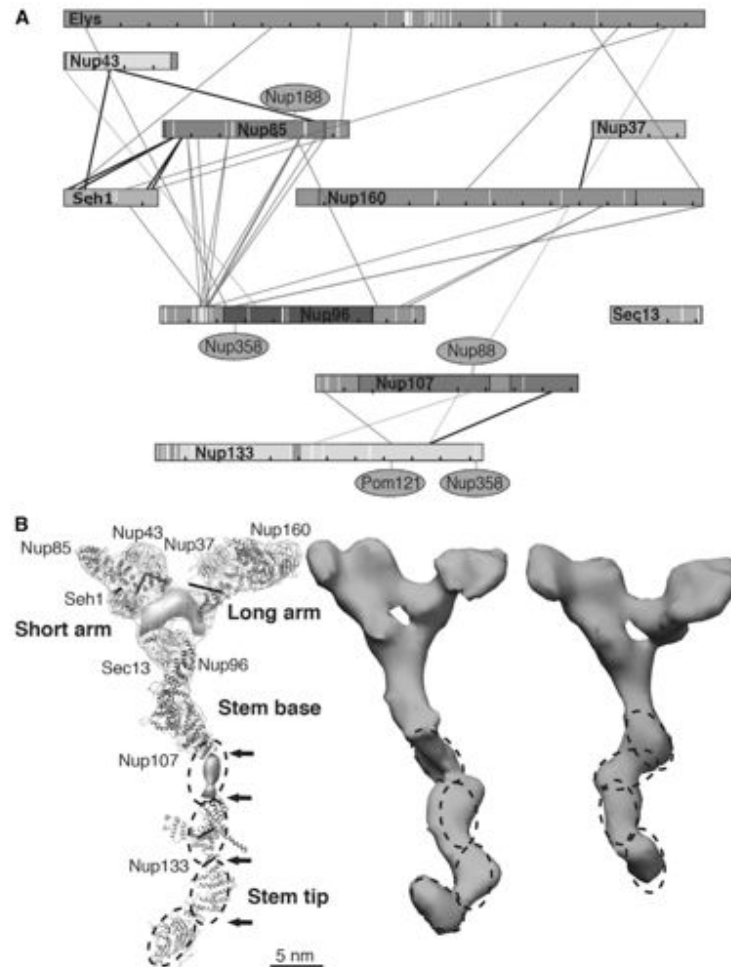
Nup107 Composition

Nup107 consists of 10 proteins



Spatial arrangement by cross-linking mass spectrometry

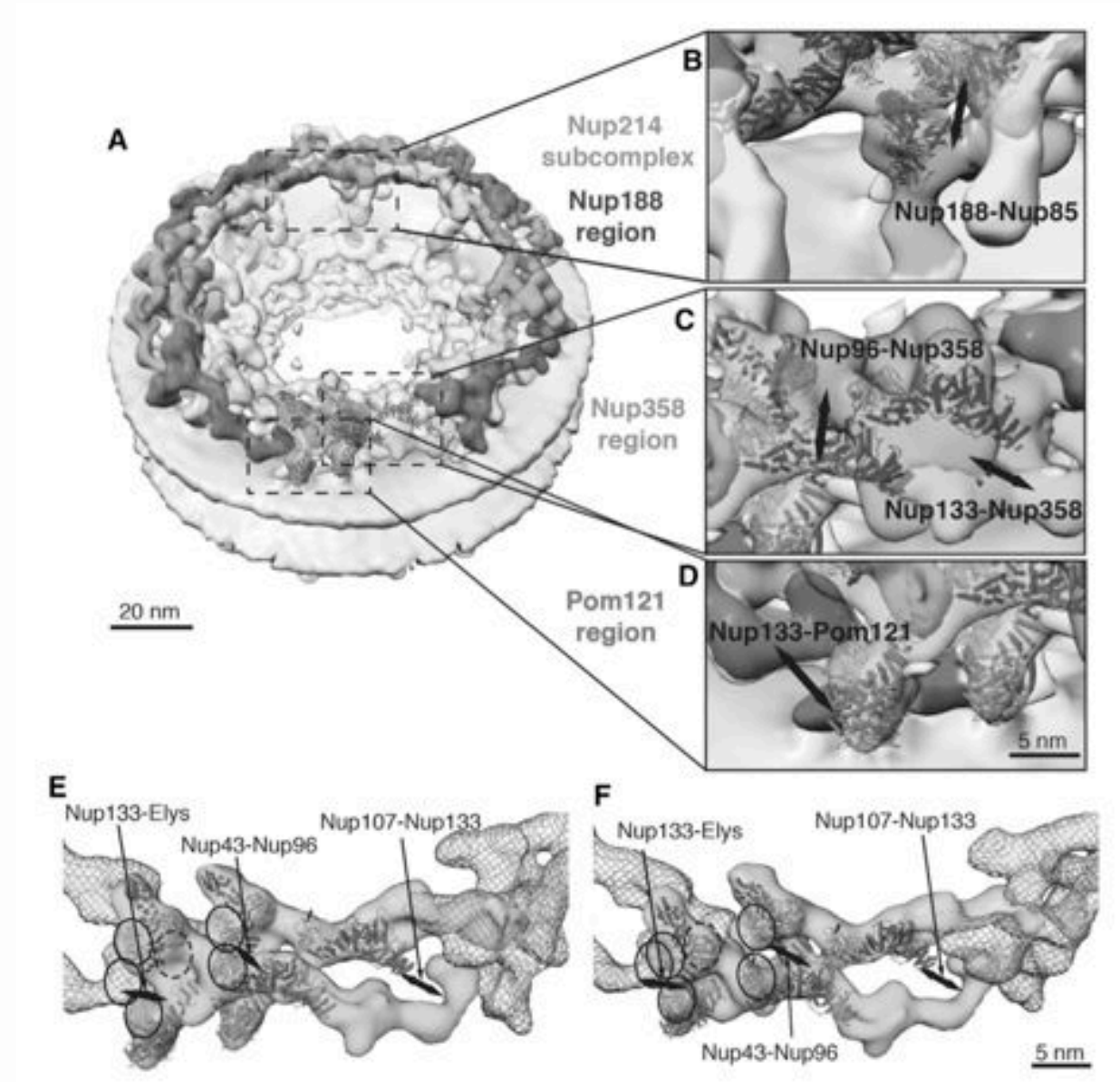
Nuclear Pore Complex



Nup120 by X-ray Crystallography: 3.0 Å

Leksa et al. (2009). The Structure of the Scaffold Nucleoporin Nup120 Reveals a New and Unexpected Domain Architecture. *Structure*, 17:1082

Putting things back together



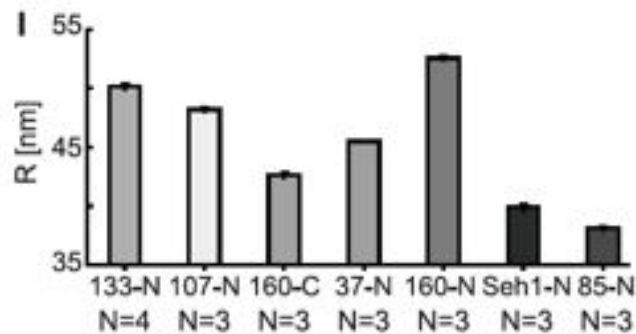
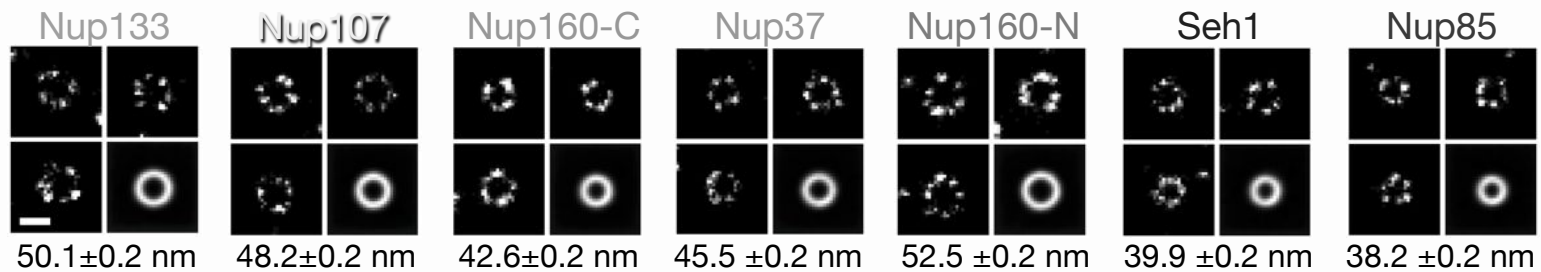
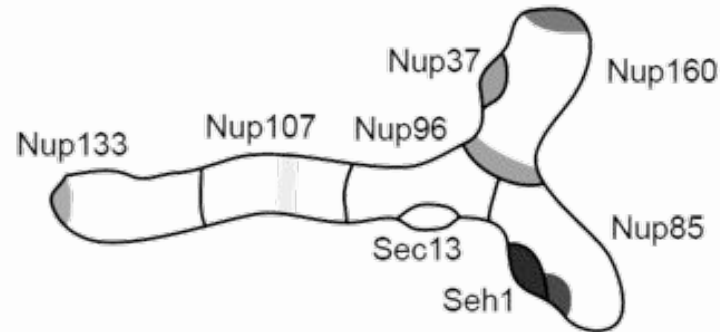
Reconstructing the NPC by Super Resolution Microscopy



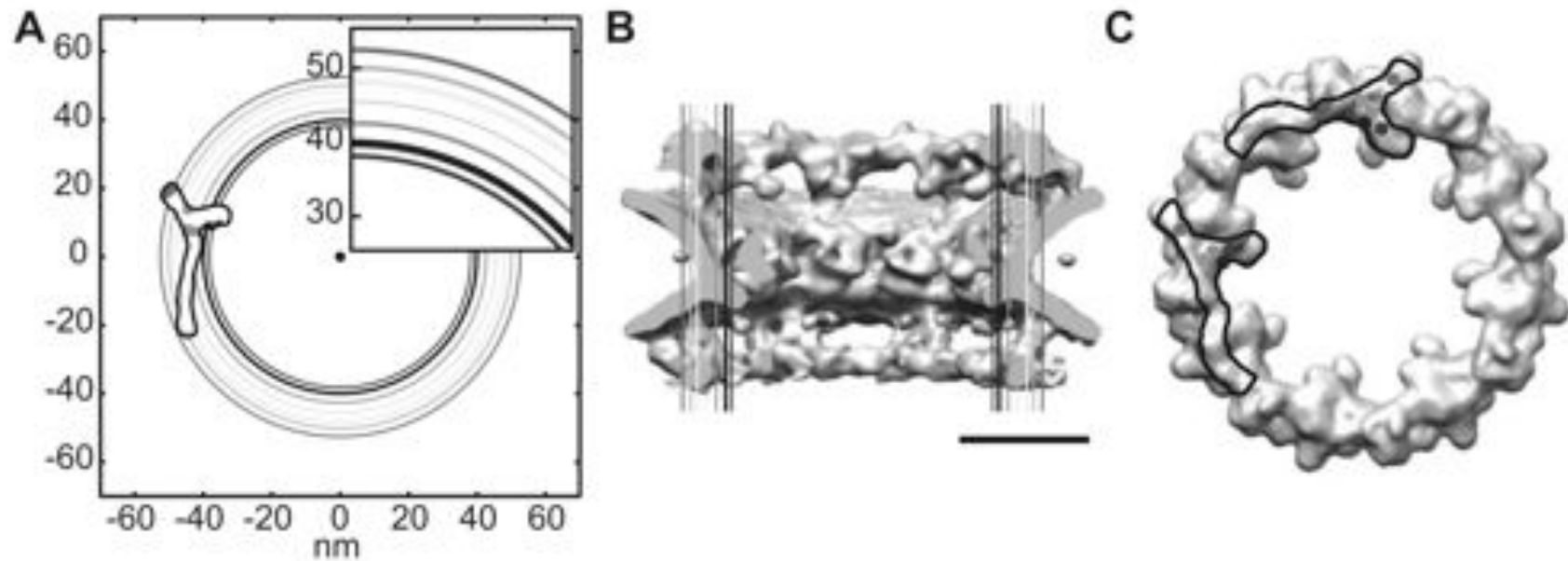
Szymborska et al., 2013, Science 341:655

GSDIM = ground state depletion microscopy followed by individual molecule return

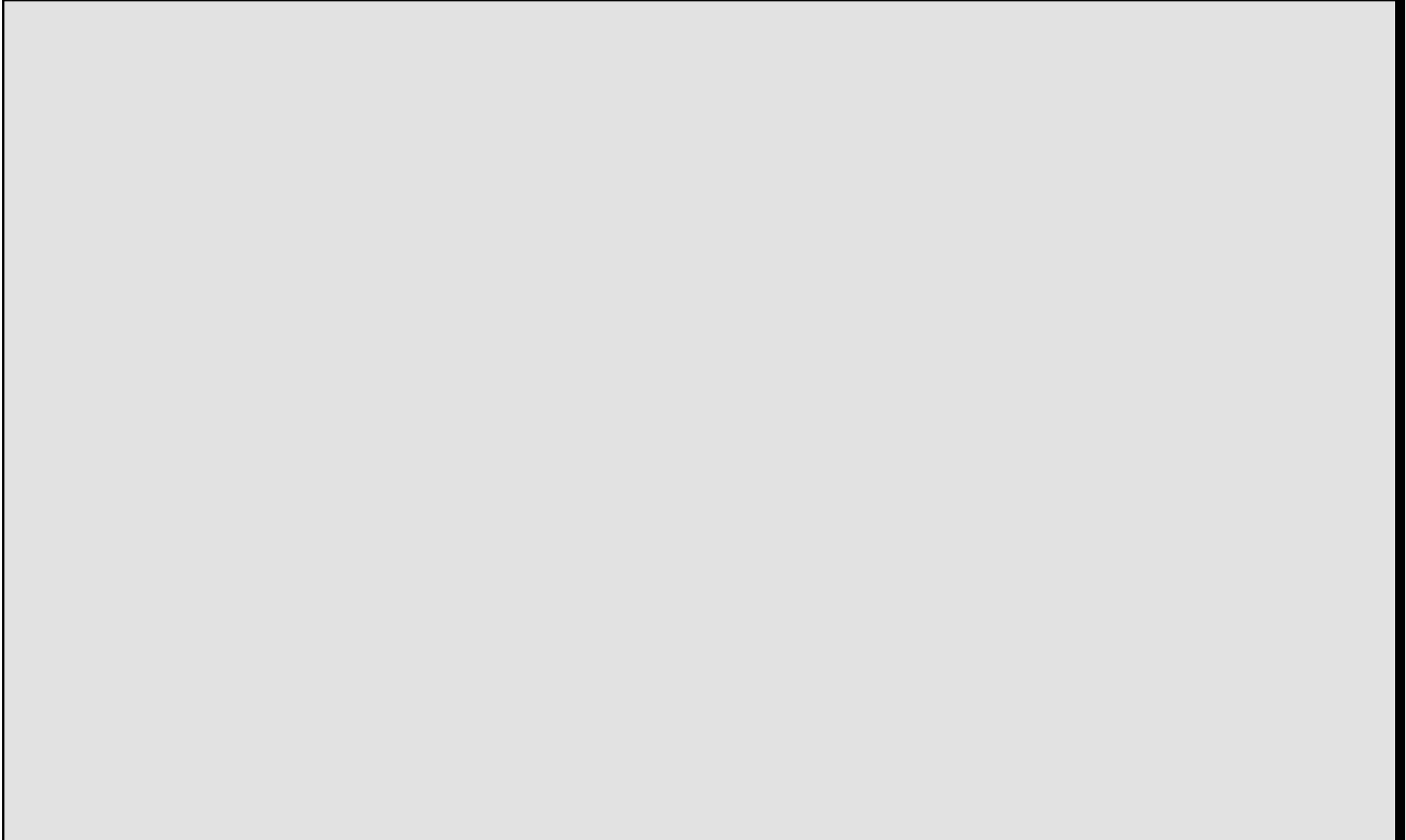
Mapping the radial orientation of the Y-shaped complex inside the NPC



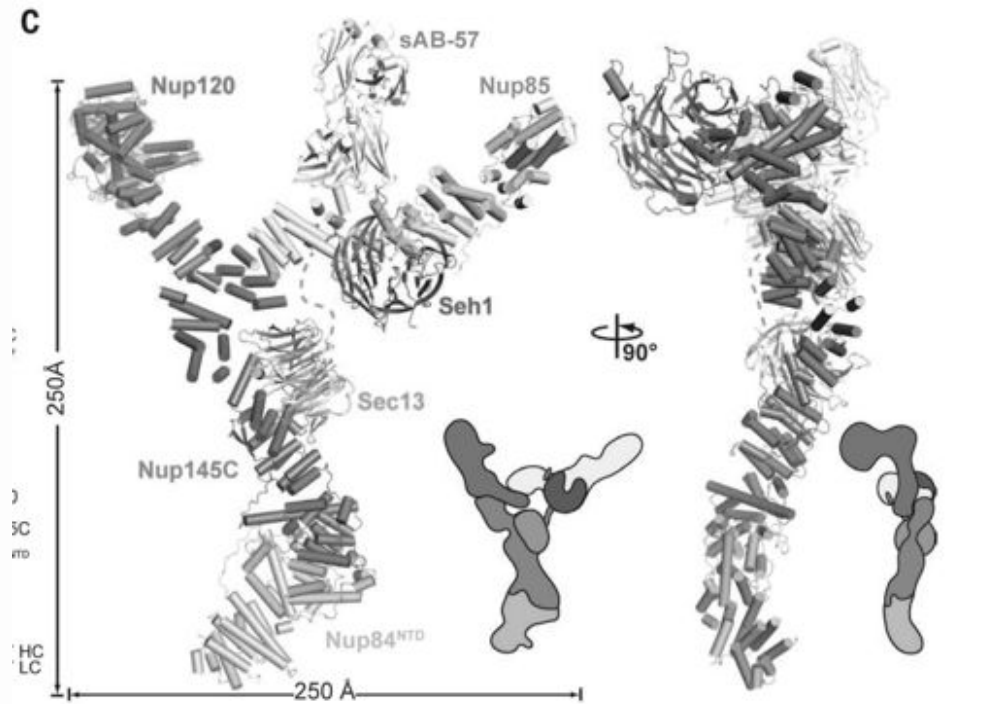
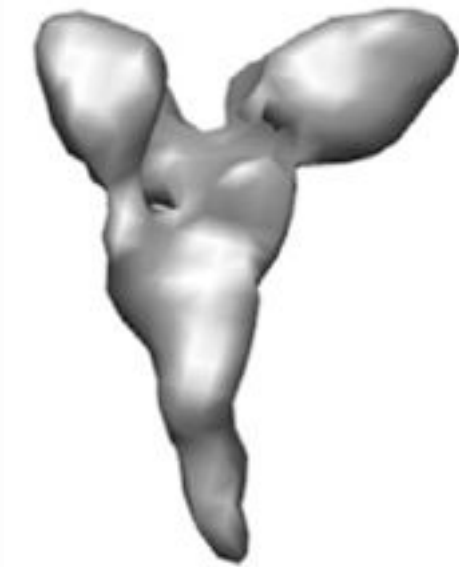
Putting the Y-shaped complex



Szymborska et al., 2013, Science 341:655



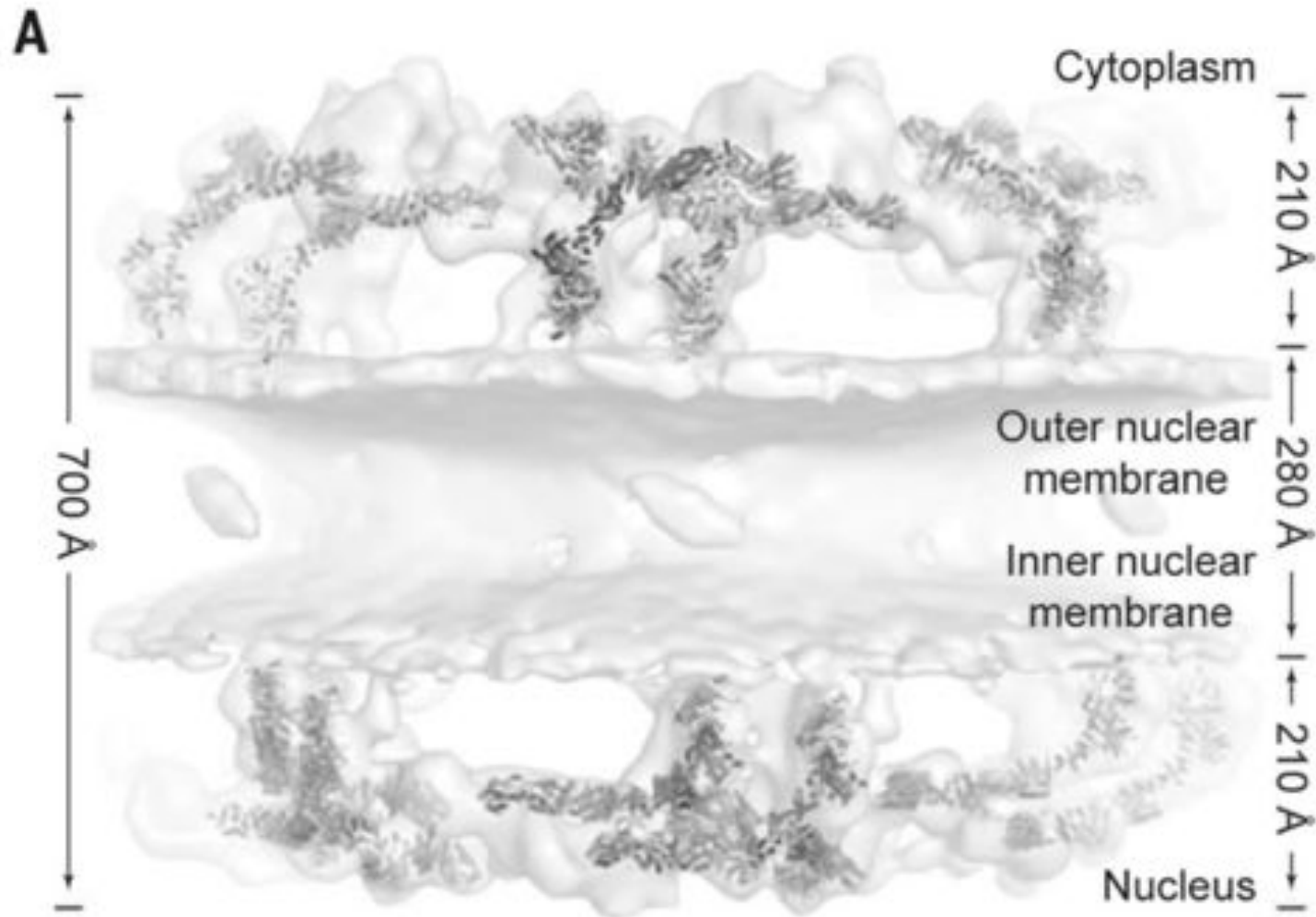
Crystallographic structure of the Y-shaped complex



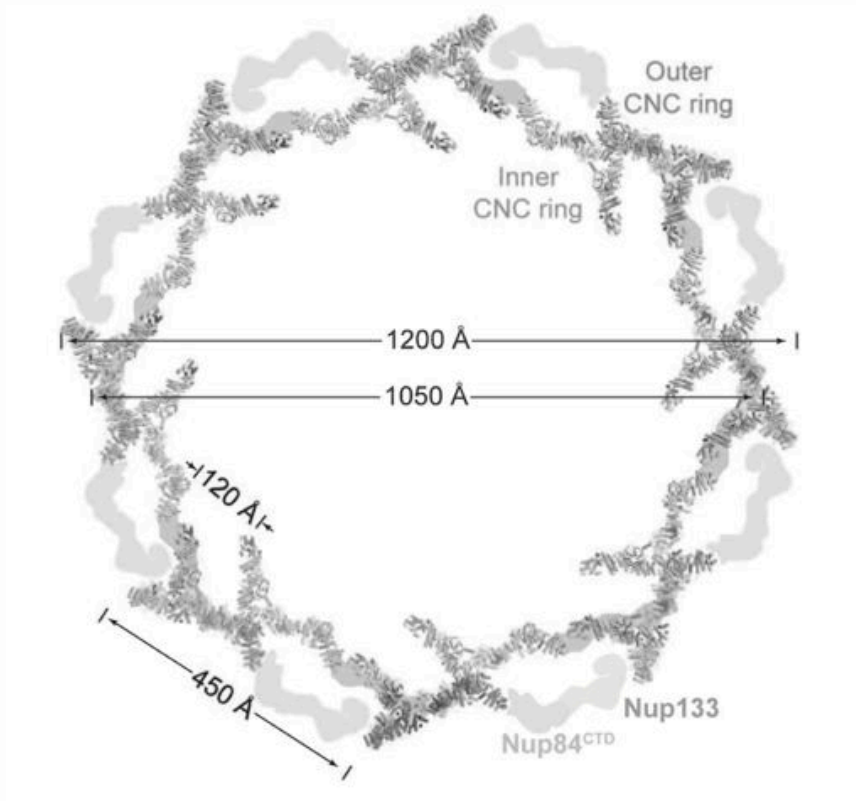
CNC (Nup107) by X-ray Crystallography: 7.4 Å

Stuwe et al. (2015) Architecture of the nuclear pore complex coat. Science 347:1148

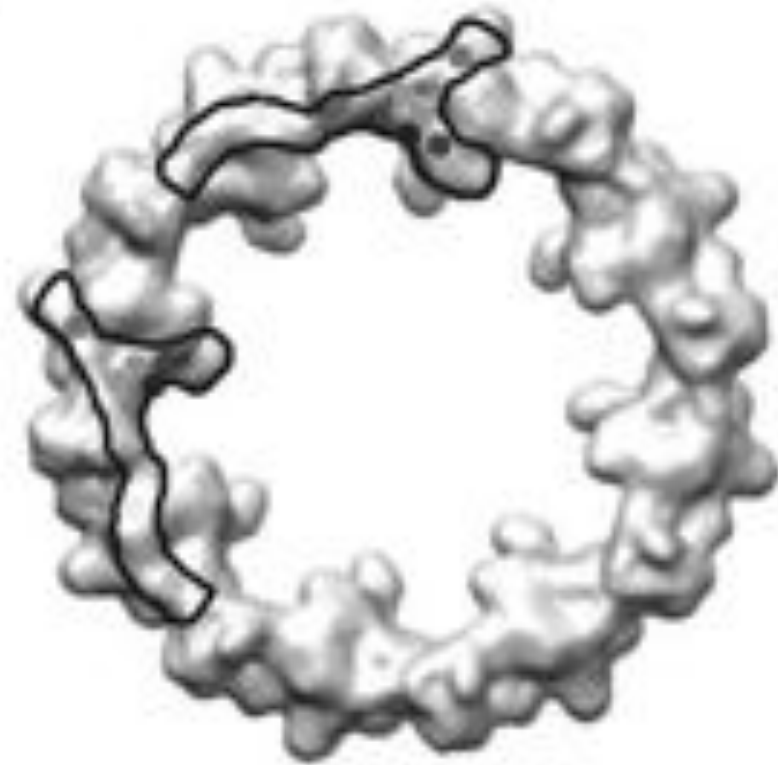
Putting things back together



Consistency?



Stuwe et al. (2015)
Science 347:1148

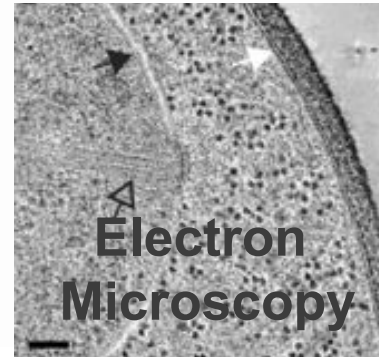
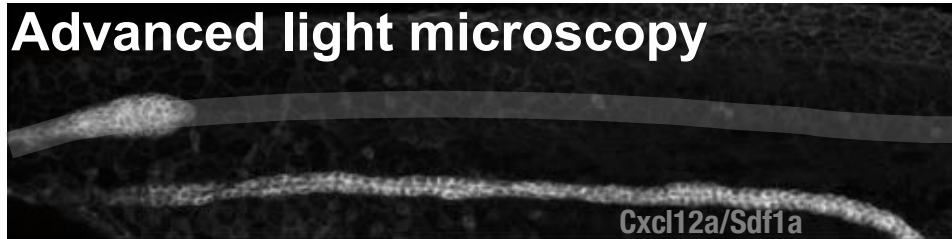


Szymborska et al., (2013)
Science 341:655

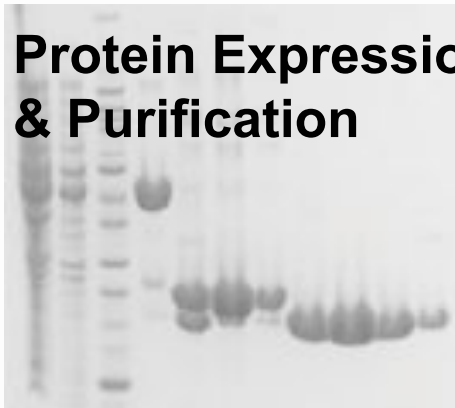
Core Facilities

EMBL Scientific Core Facilities

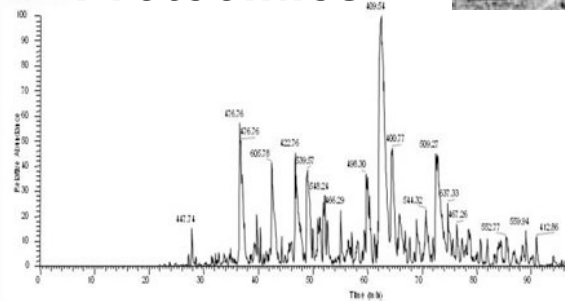
Advanced light microscopy



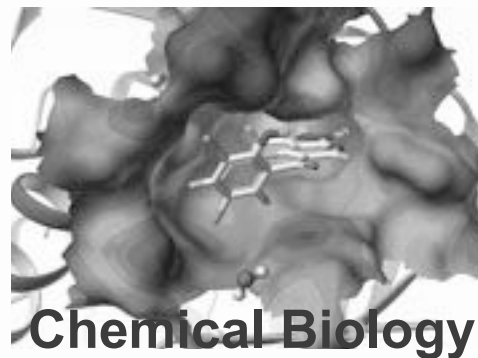
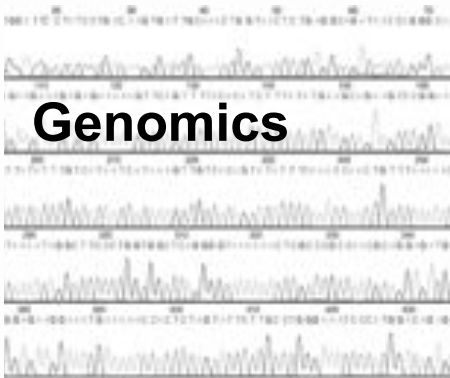
Protein Expression & Purification



Proteomics

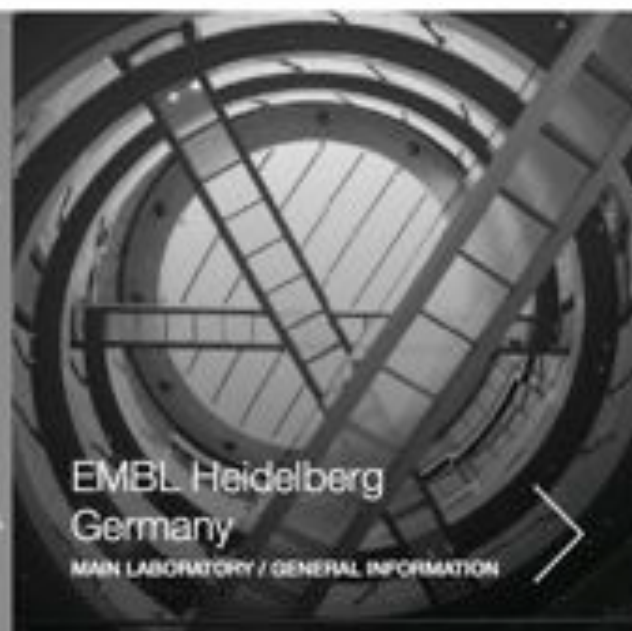


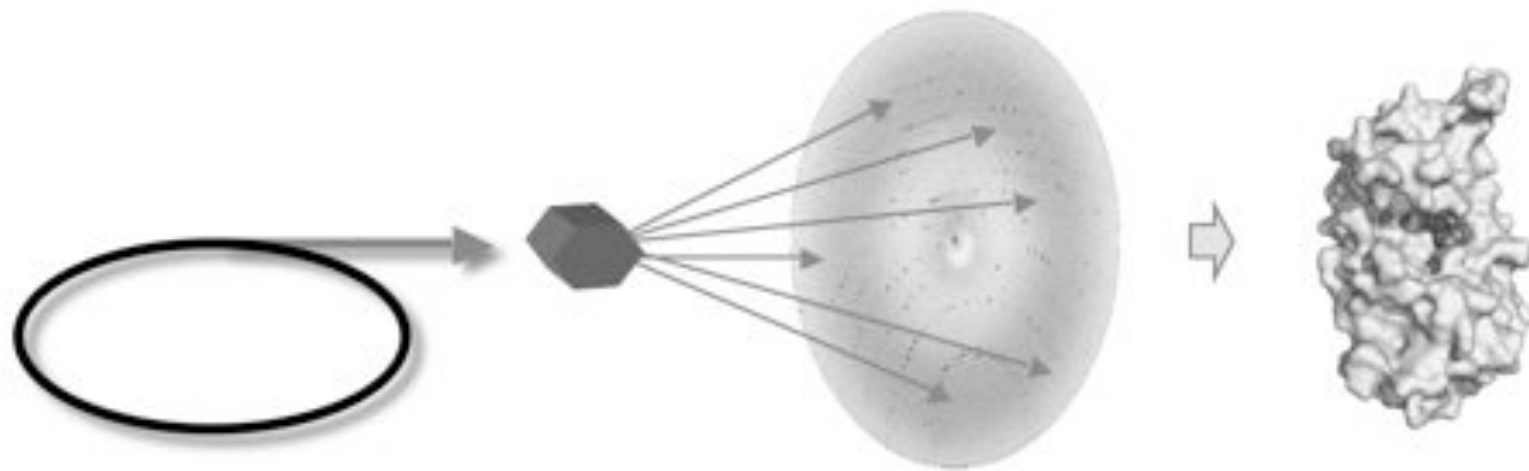
Genomics



Current Industrial Partners of the ALMF







Macromolecular Crystals

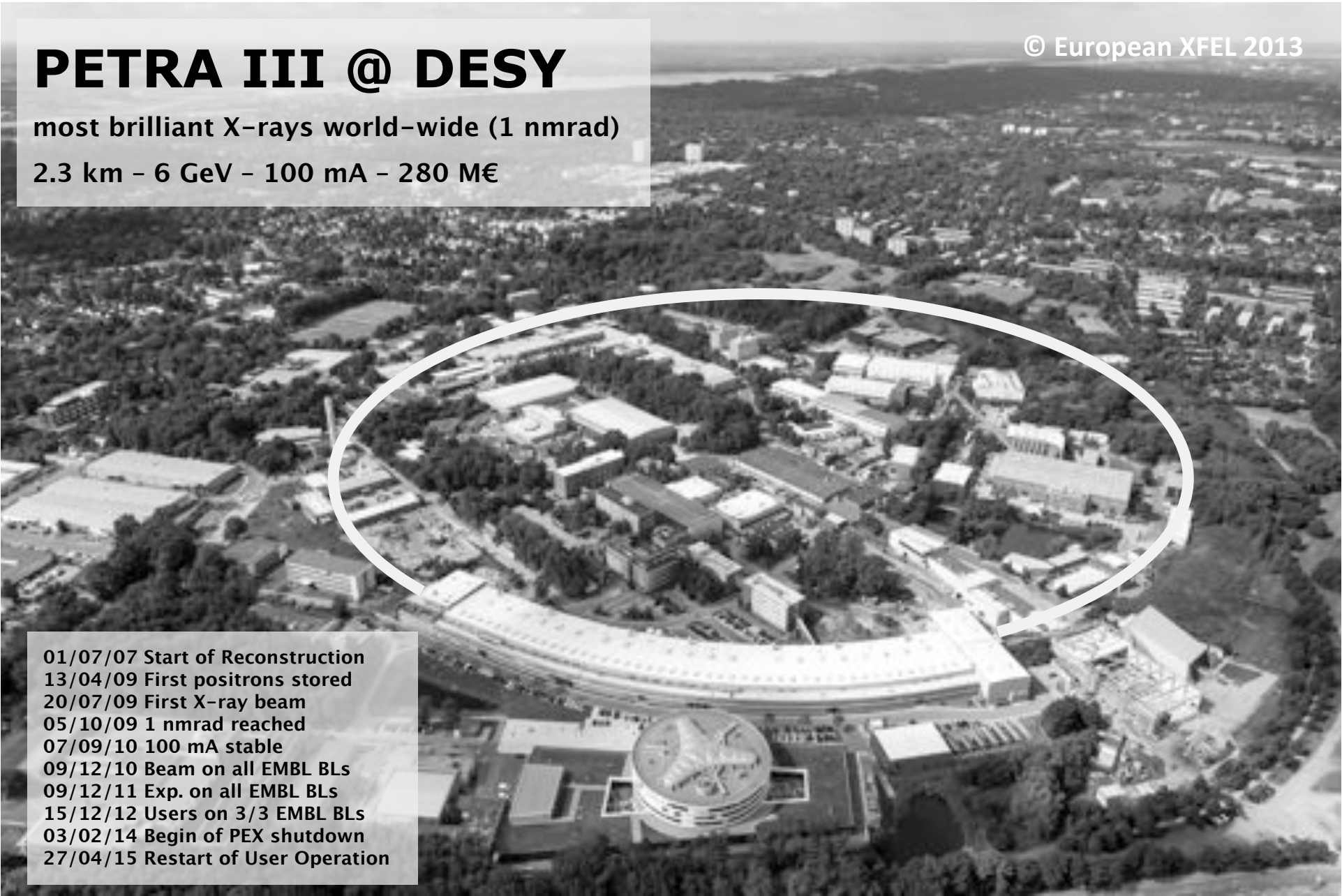
- Are made of very precious material
- Are difficult to grow
- Are often very small (microns)
- Are containing large unit cells
- Are often inhomogeneous
- Are mechanically fragile
- Are radiation sensitive
- Are difficult to reproduce
- Are well-ordered, big, sturdy

PETRA III @ DESY

most brilliant X-rays world-wide (1 nmrad)

2.3 km – 6 GeV – 100 mA – 280 M€

© European XFEL 2013



01/07/07 Start of Reconstruction
13/04/09 First positrons stored
20/07/09 First X-ray beam
05/10/09 1 nmrad reached
07/09/10 100 mA stable
09/12/10 Beam on all EMBL BLs
09/12/11 Exp. on all EMBL BLs
15/12/12 Users on 3/3 EMBL BLs
03/02/14 Begin of PEX shutdown
27/04/15 Restart of User Operation



P13

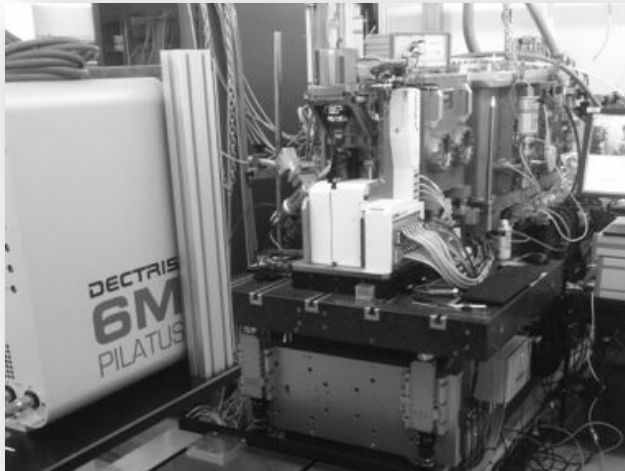
4-15 keV, 30 μ m focus
160 SPINE pins, < 30 s cycle time

P14

7-15 [35] keV, 4 x 6 [1x5] μm focus

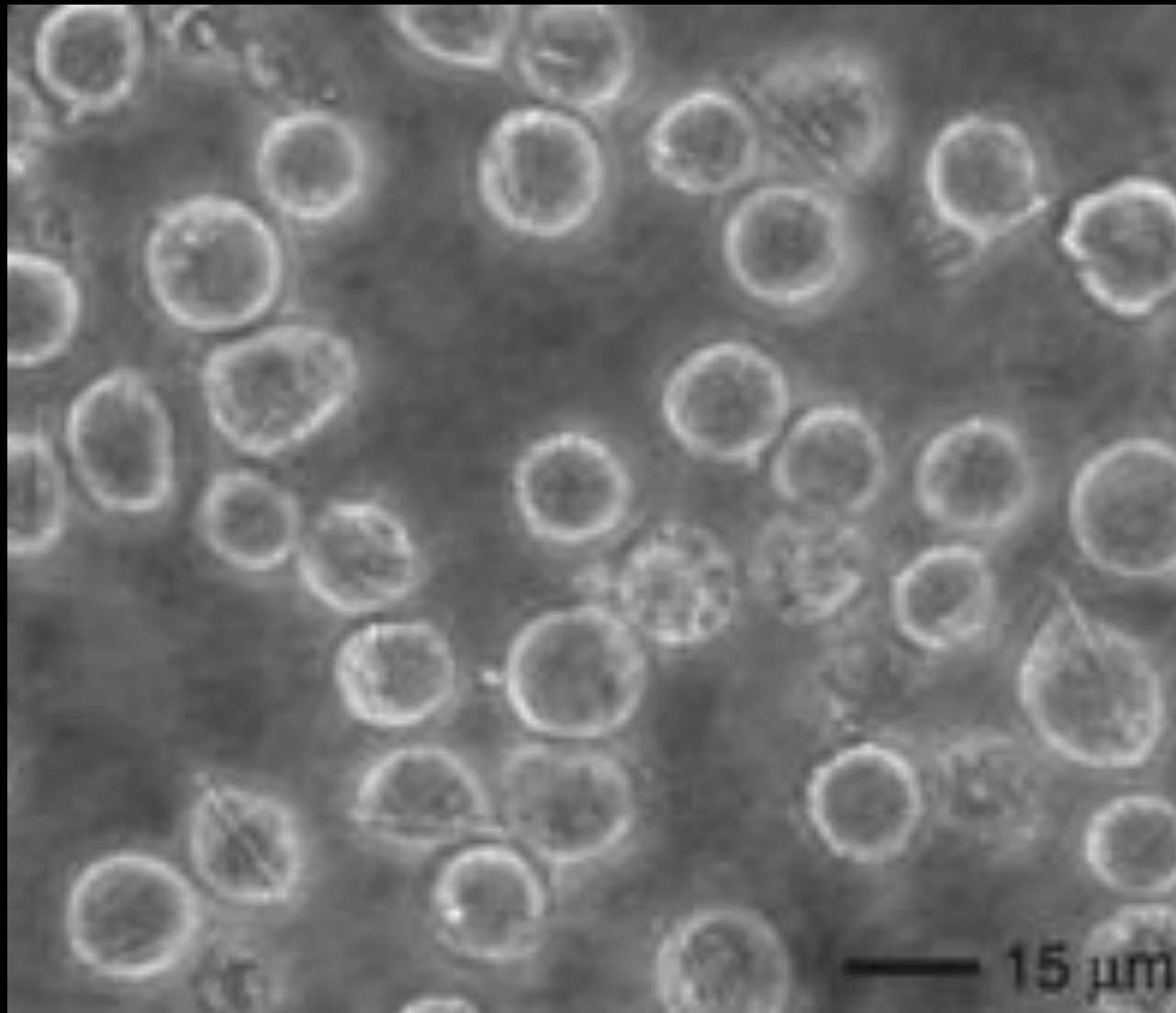
DECTRIS
6M
PILATUS

100 MGy/s



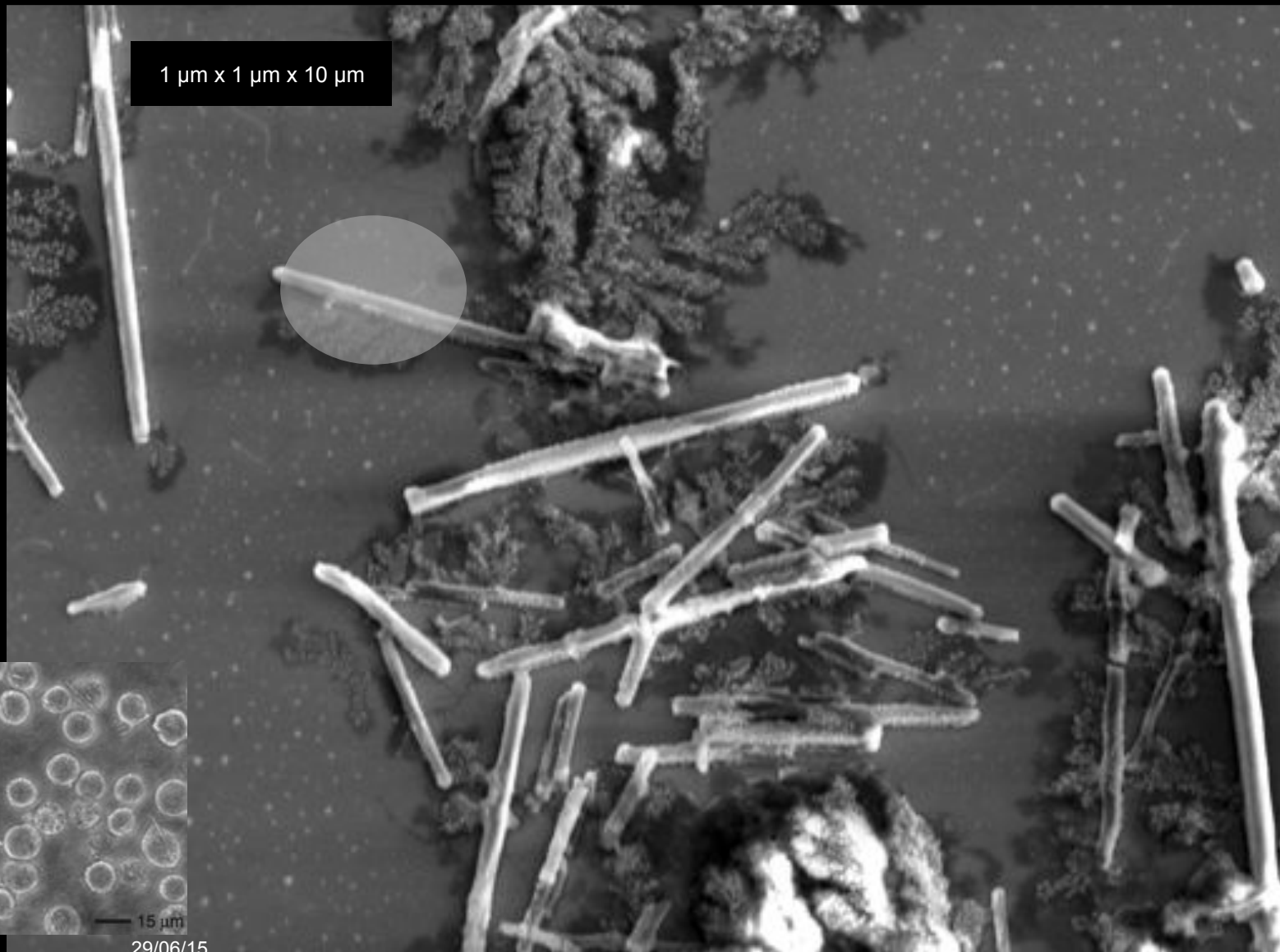
- 5×10^{12} ph/s into $5 \times 5 \mu\text{m}^2$
- 500 ms at 100 K
- 10 ms at 300 K

Cathepsin B

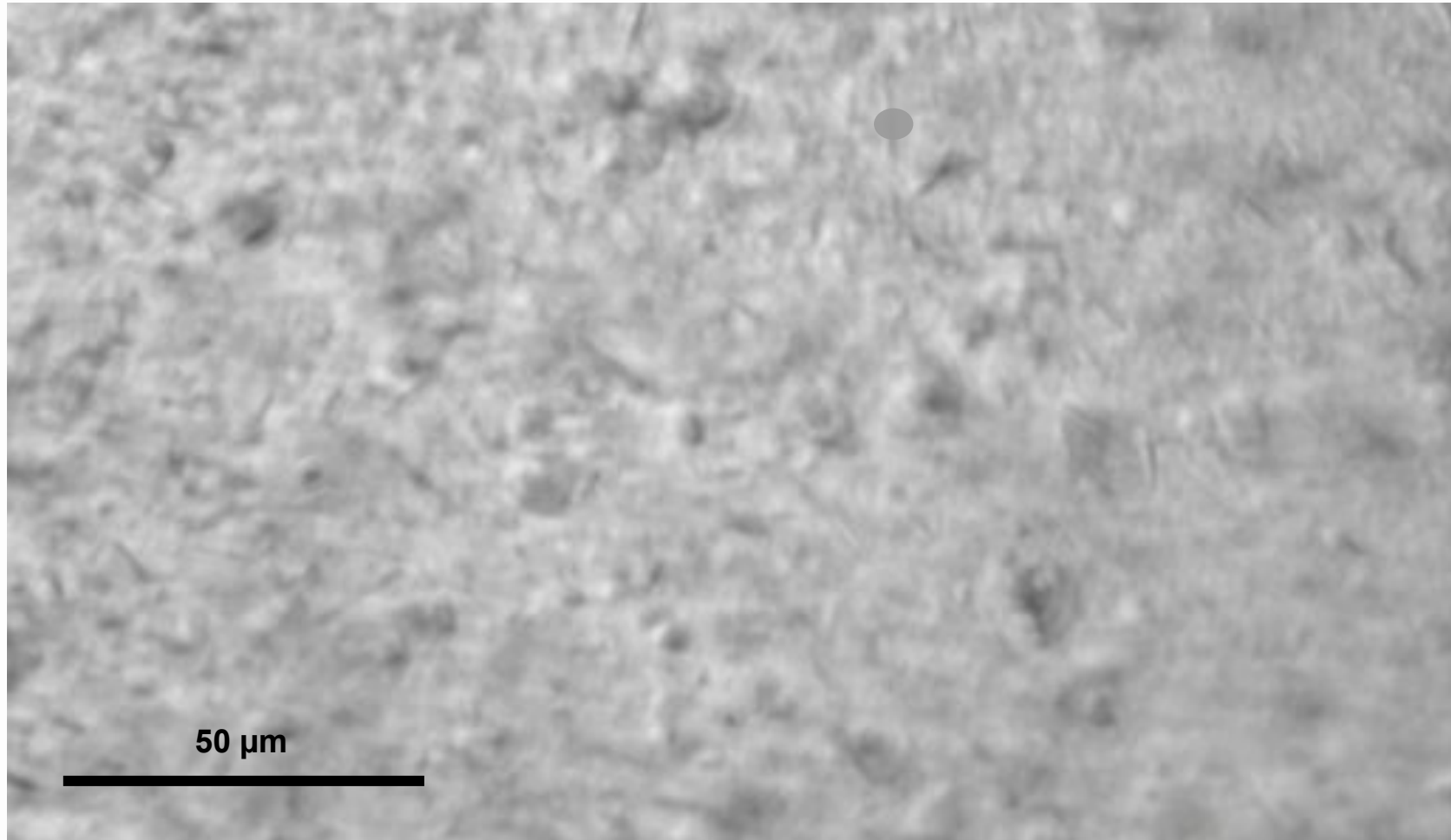


Cathepsin B

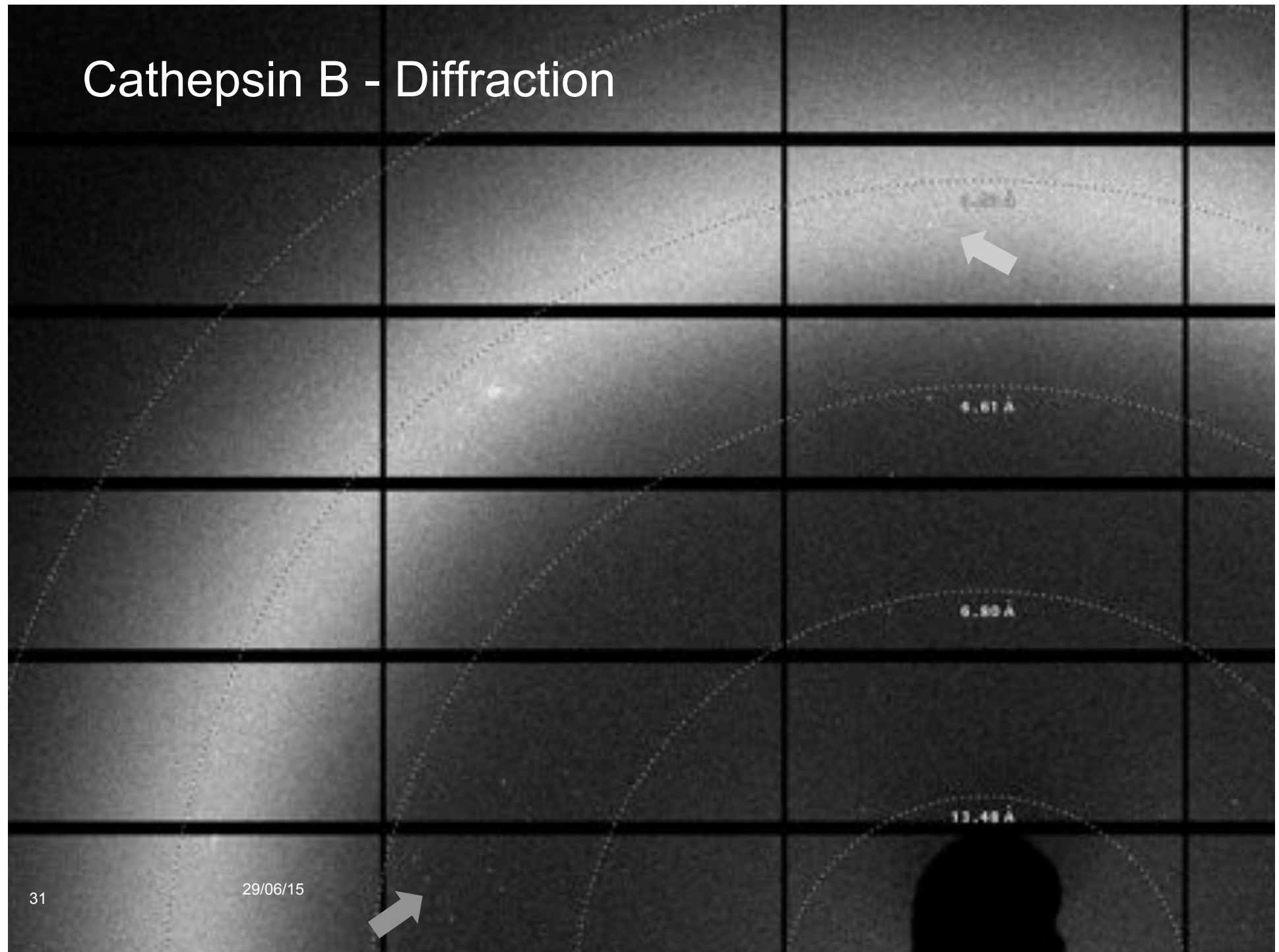
Redecke, L., ... Chapman, H. (2012): Natively Inhibited Trypanosoma brucei Cathepsin B Structure Determined by Using an X-ray Laser. Science 339:227 [4HWY:2.1 Å]



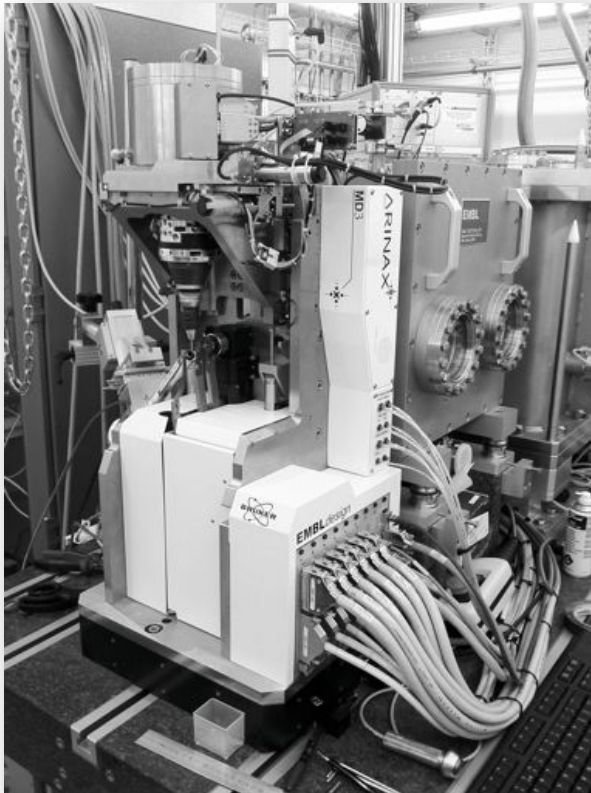
Cathepsin B – Suspension in a loop



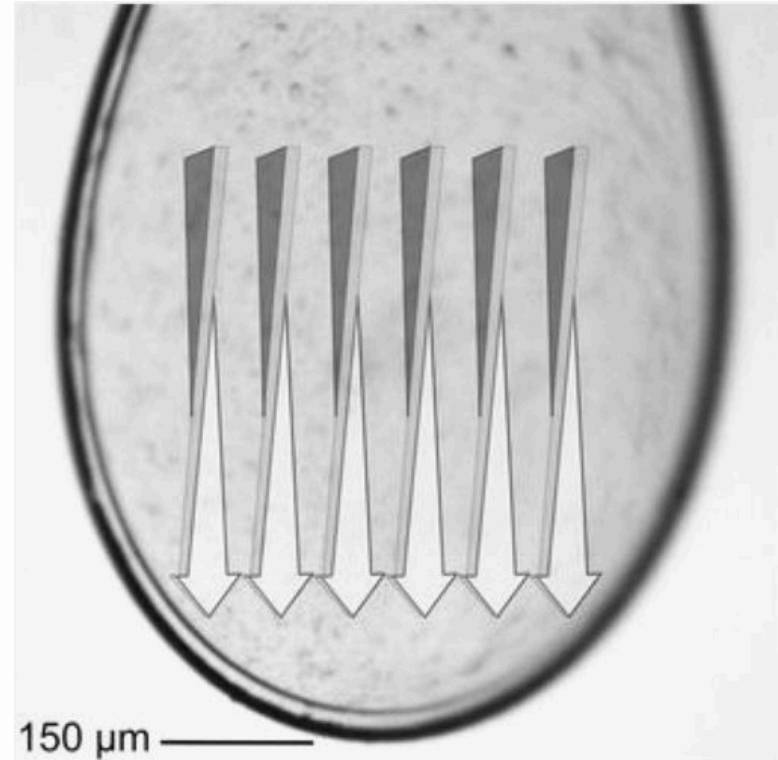
Cathepsin B - Diffraction



Serial Synchrotron Crystallography (2013)



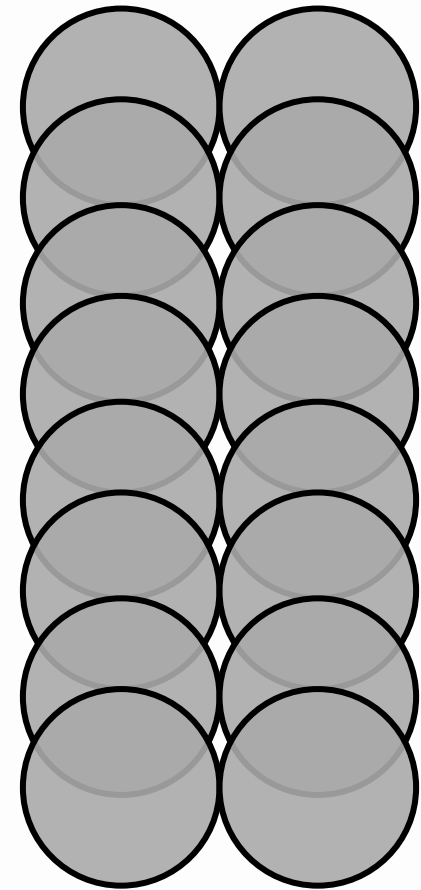
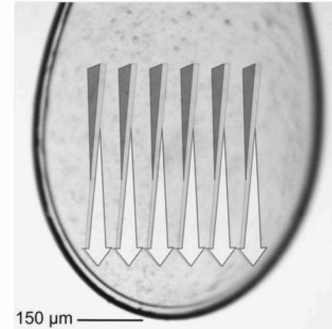
Presentation of frozen suspension of micro-crystals to a micro-beam using an MD3 (EMBL-GR+HH)



Data collection using **continuous** highly-precise 'serial helical scans' as implemented on MD3.

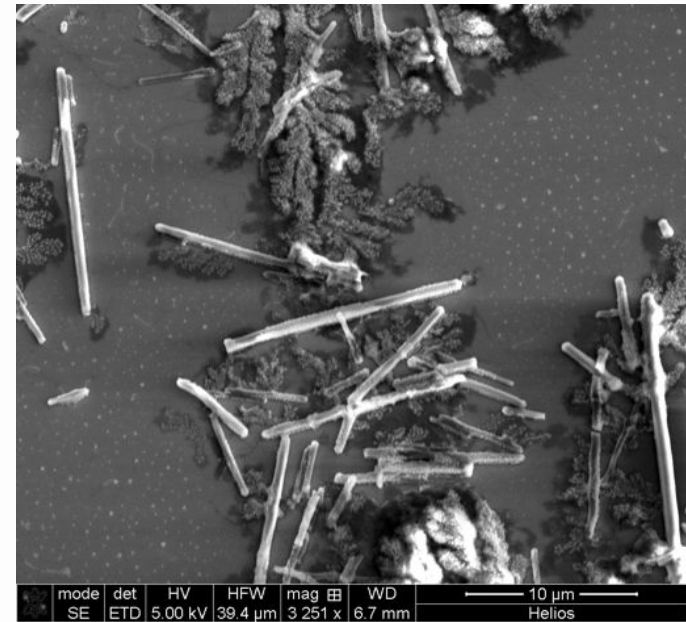
Exposure conditions (in 2013)

- 1.2×10^{12} ph/sec into $4 \times 5 \mu\text{m}^2$
 - < 1 s crystal lifetime
- $600 \times 600 \mu\text{m}^2$ ROI
 - 120 parallel scans $5 \mu\text{m}$ apart
 - Each scan $600 \mu\text{m}$ from -45° to $+45^\circ$ with 240 images
 - $2.5 \mu\text{m}$ per image, 0.375° per image
 - 50 – 60 MGy for each volume / crystal
- 28800 frames in 8 hours.
- Flux limited! (1 Hz)



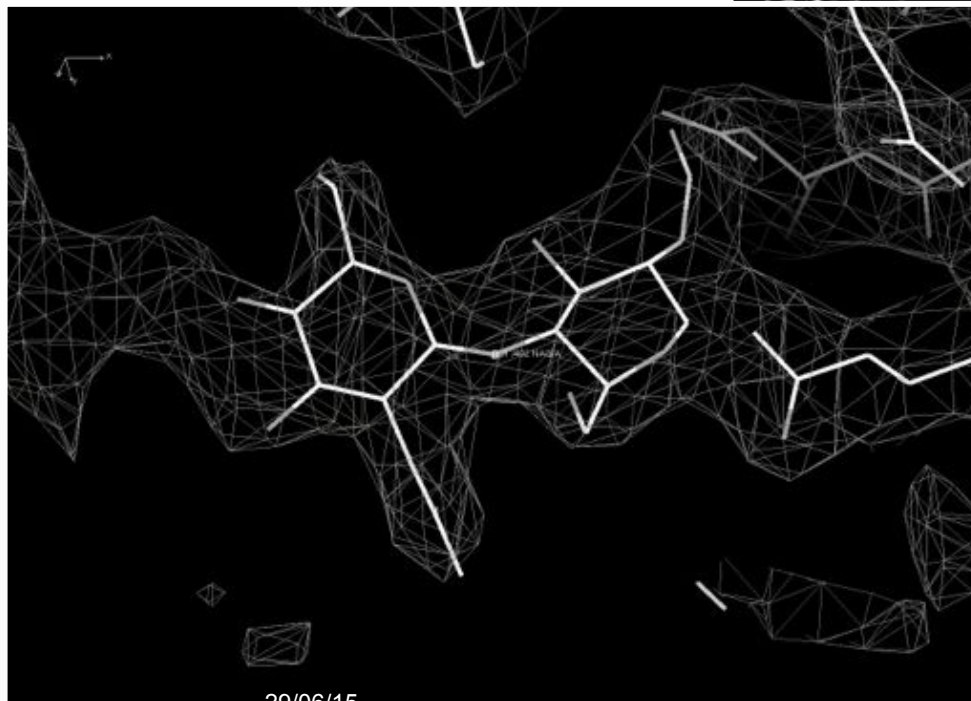
Extraction of data

- $120 * 240 = 28800$ frames = 172 GB
- ~2000 crystal hits identified by CrystFEL [White et al.]
- 500 clusters of adjacent hits along scan direction (i.e. the same crystal hit more than once).
- 150 series of frames integrated with XDS
- 97 partial data sets were merged with XSCALE
- ~ 3 weeks for processing

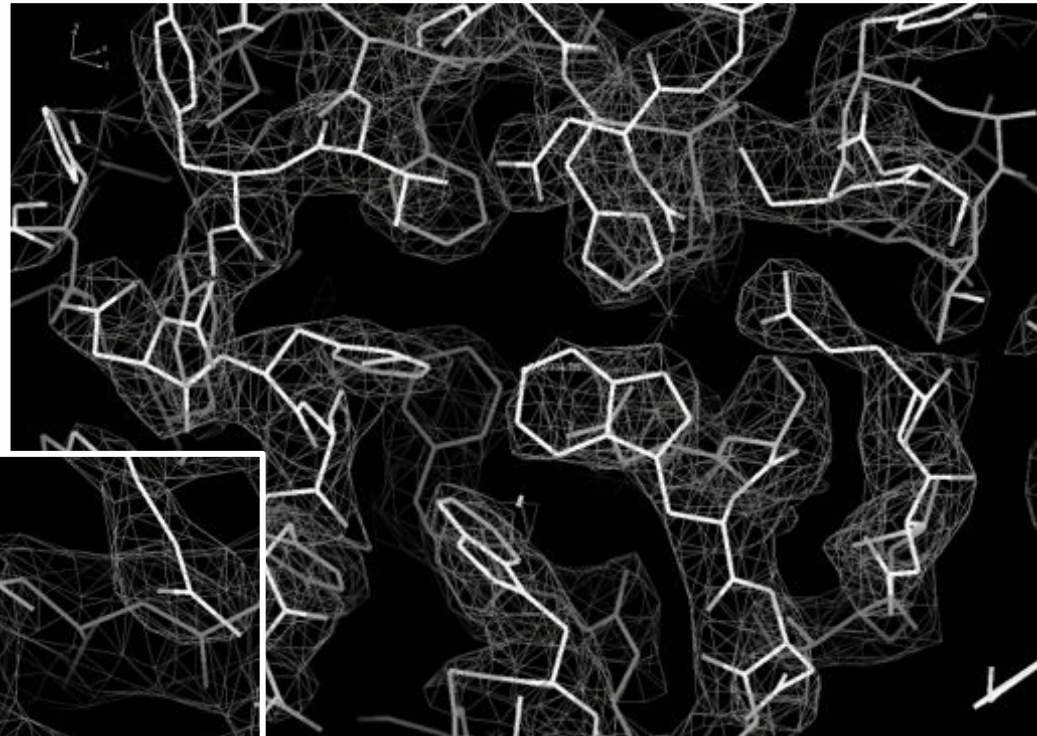


Cathepsin B – Refinement

- REFMAC5. 2442 atoms (jelly body) against 8394 reflections [87.4, 3.0] Å.
- $R_{\text{work,free}} = 22.9, 26.1$



20/06/15



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USA

Serial crystallography on *in vivo* grown
microcrystals using synchrotron radiation

Cornelius Gati,^{a,*} Gleb Bourenkov,^{b,*} Marco Klinge,^c Dirk Rehders,^c Francesco Stellato,^a Dominik Oberthür,^{a,d} Oleksandr Yefanov,^a Benjamin P. Sommer,^{d,e} Stefan Mogk,^c Michael Duszynski,^c Christian Betzel,^f Thomas R. Schneider,^{b,g} Henry N. Chapman^{h,i} and Lars Redecke^{a,*}

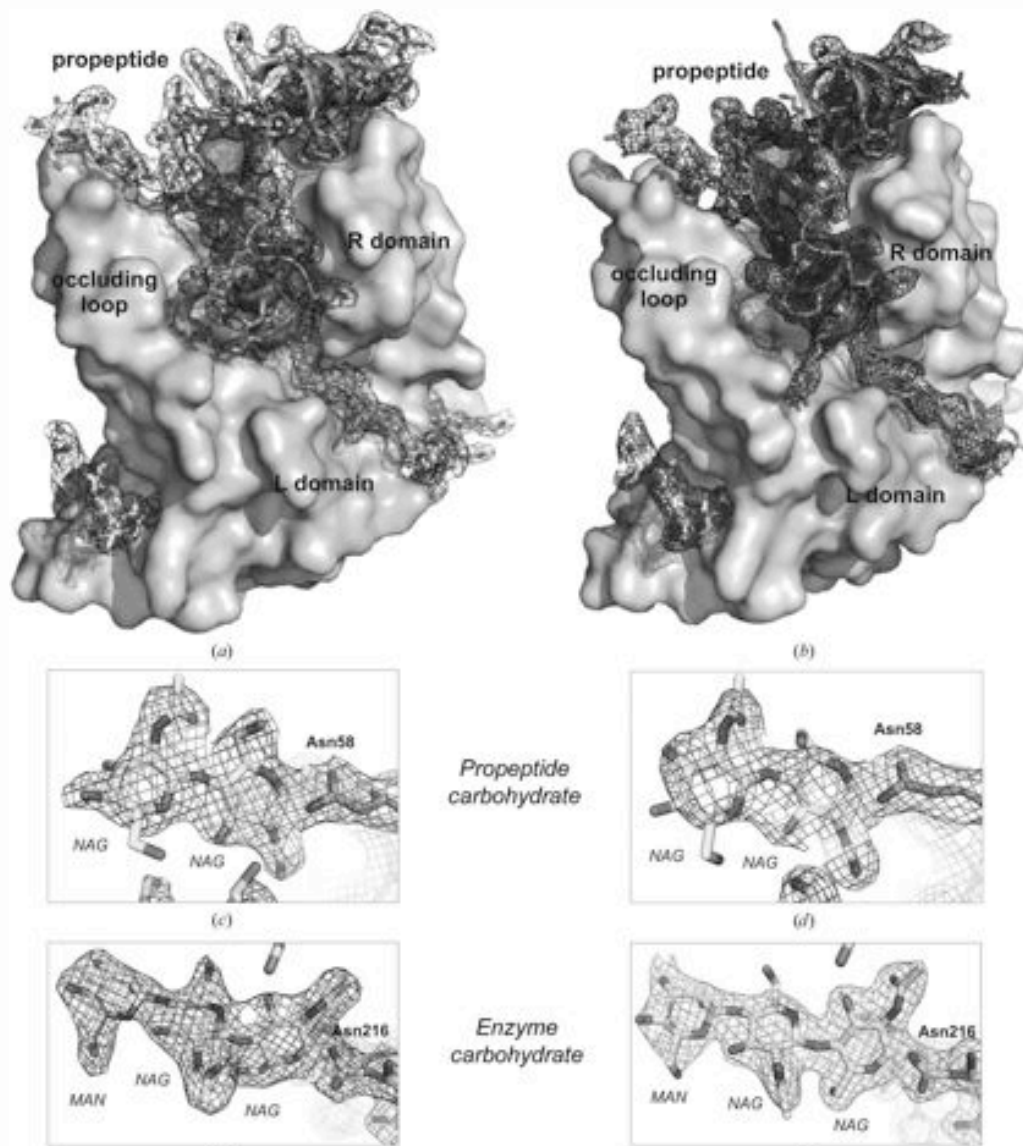
^aCenter for Free-Electron Laser Science (CFEL), Deutsches Elektronensynchrotron (DESY), Notkestrasse 85, 22607 Hamburg, Germany, ^bEuropean Molecular Biology Laboratory (EMBL), Hamburg Outstation, Notkestrasse 85, 22607 Hamburg, Germany, ^cJoint Laboratory for Structural Biology of Infection and Inflammation, Institute of Biochemistry and Molecular Biology, University of Hamburg, and Institute of Biochemistry, University of Lübeck, Notkestrasse 85, 22607 Hamburg, Germany, ^dInstitute of Biochemistry and Molecular Biology, University of Hamburg, Notkestrasse 85, 22607 Hamburg, Germany, ^eInterfaculty Institute of Biochemistry, University of Tübingen, Hoppe-Seyler-Strasse 4, 72076 Tübingen, Germany, and ^fInstitute of Experimental Physics, University of Hamburg, Luruper Chaussee 149, 22761 Hamburg, Germany. *Correspondence e-mail: thomas.schneider@embl-hamburg.de, henry.chapman@desy.de, redecke@biochem.uni-luebeck.de

IUCrJ (2014) 1 87-94

EMBL

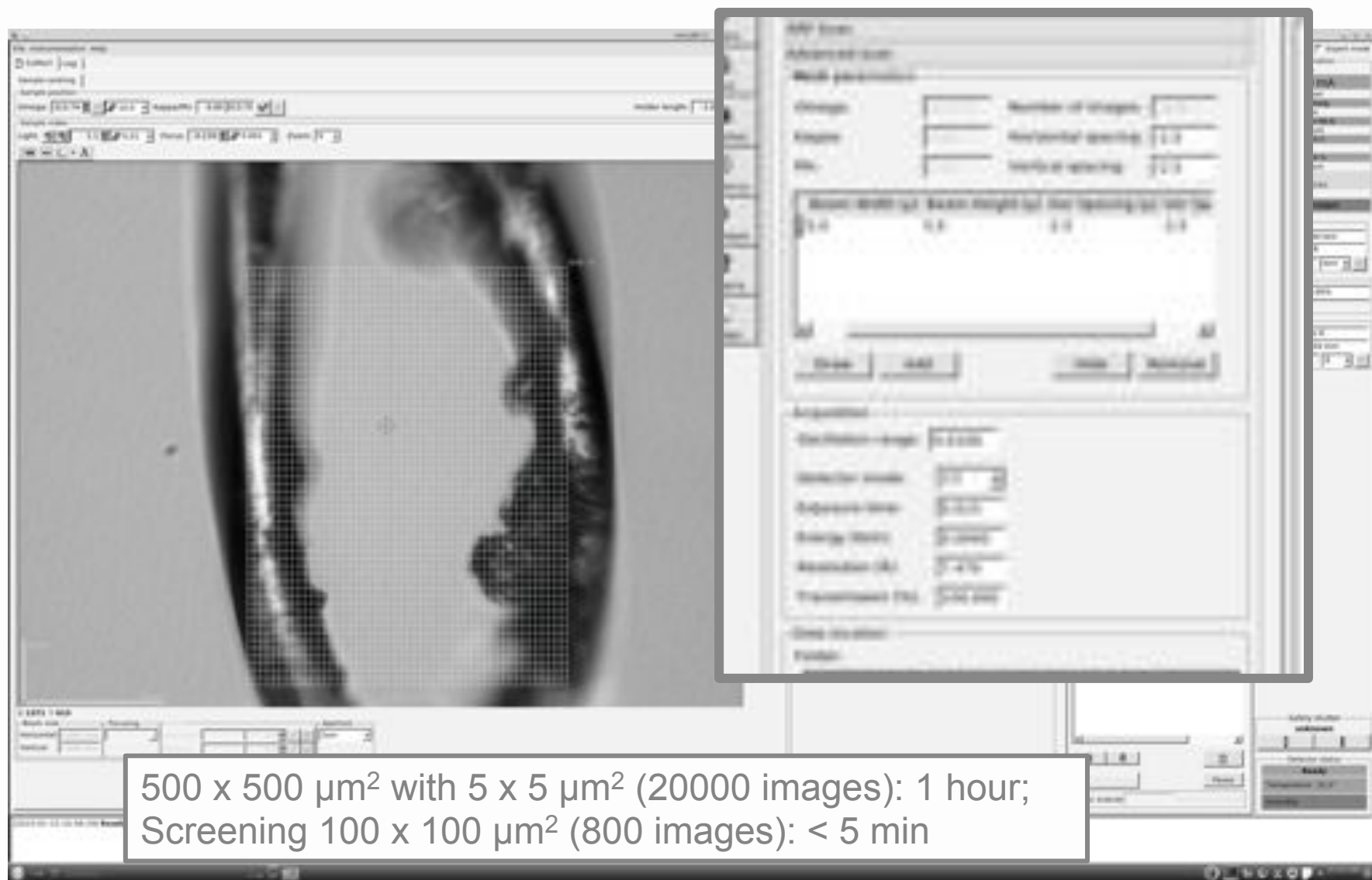
PETRA III

XFEL



PETRA III	XFEL
Crystal Size	
10 ⁷ unit cells [10 x less than smallest crystals used at synchrotrons before]	
Resolution	
3 Å	2.1 Å
Material used	
15 nl	10 ml
Result	
Models are identical within error	

Implementation

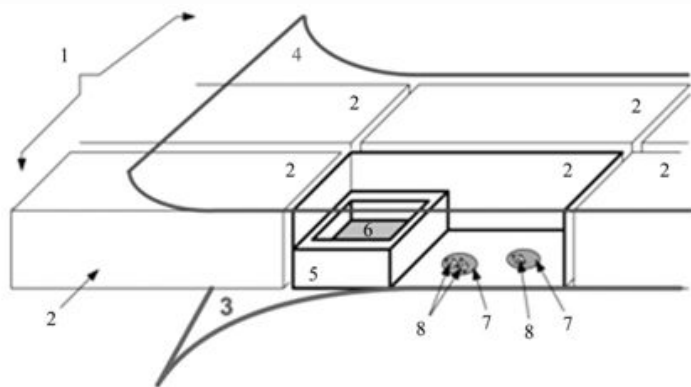


500 x 500 μm^2 with 5 x 5 μm^2 (20000 images): 1 hour;
Screening 100 x 100 μm^2 (800 images): < 5 min

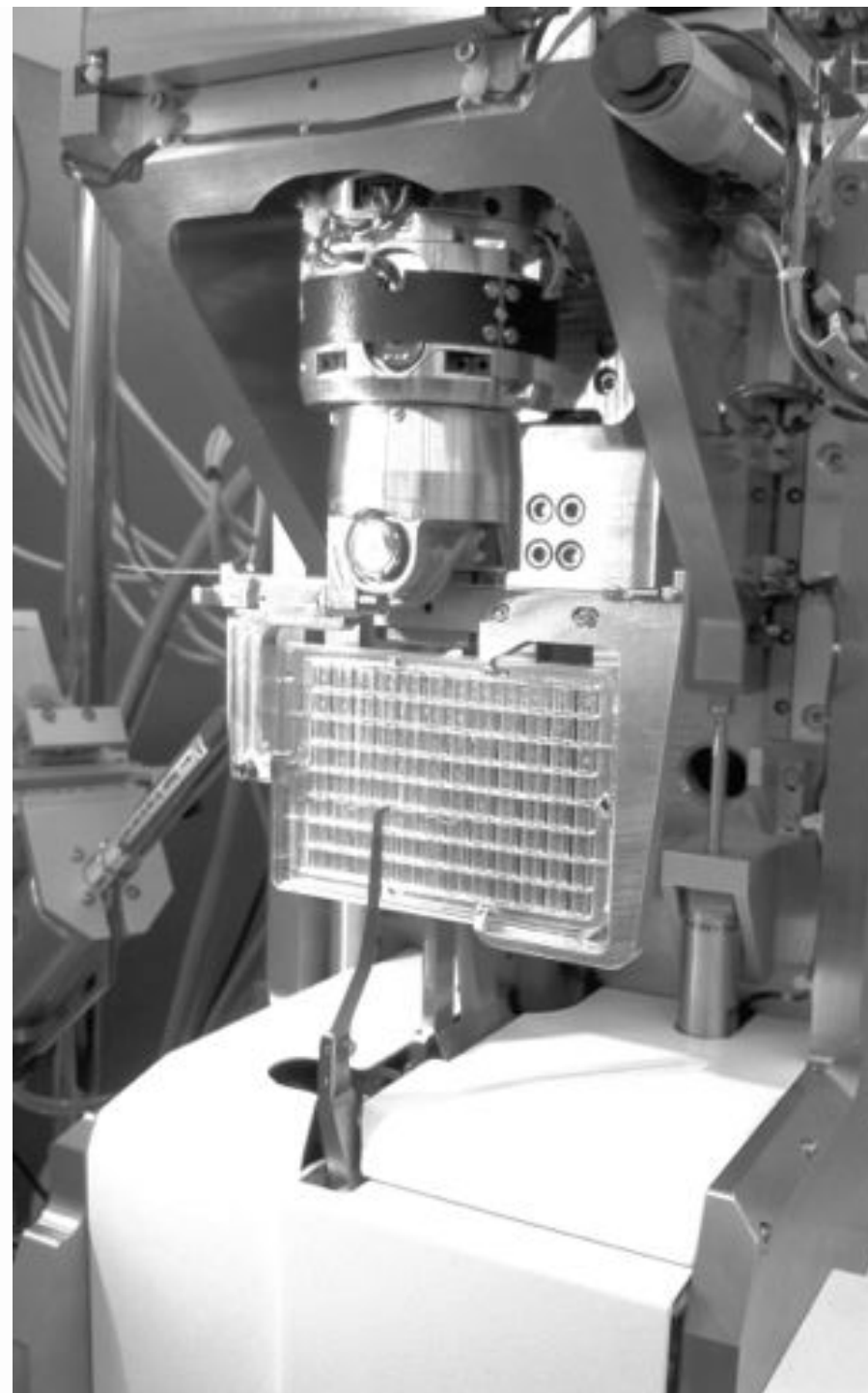
'MxCuBE- collaboration with ESRF

In Situ Experiments with CrystalDirect

- Mechanics and software are in place for data collection from CrystalDirect™ plates.
- Crystals grow on a thin polymer foil with negligible X-ray scatter
- Cryst. life-time in focused beam < 10 ms

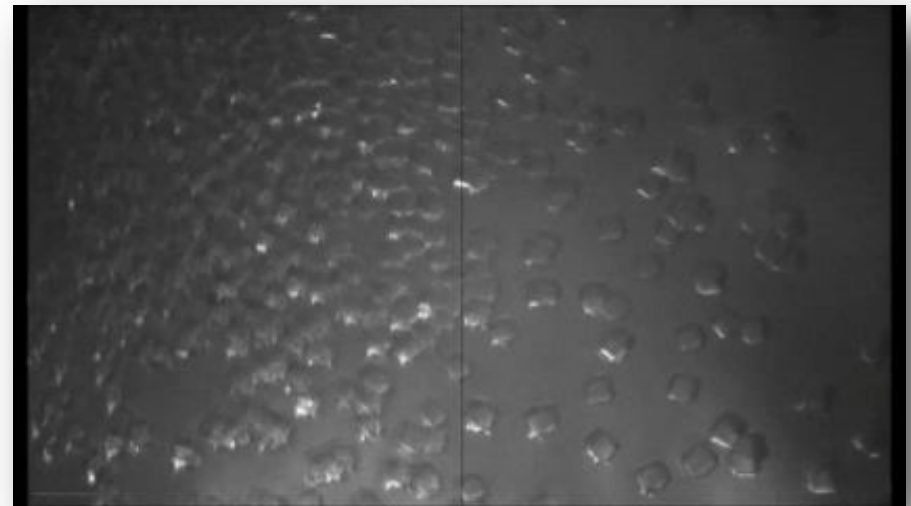
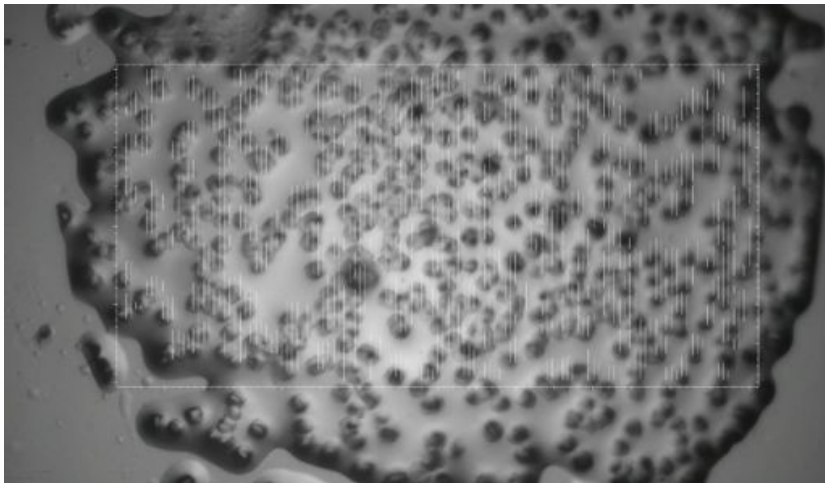
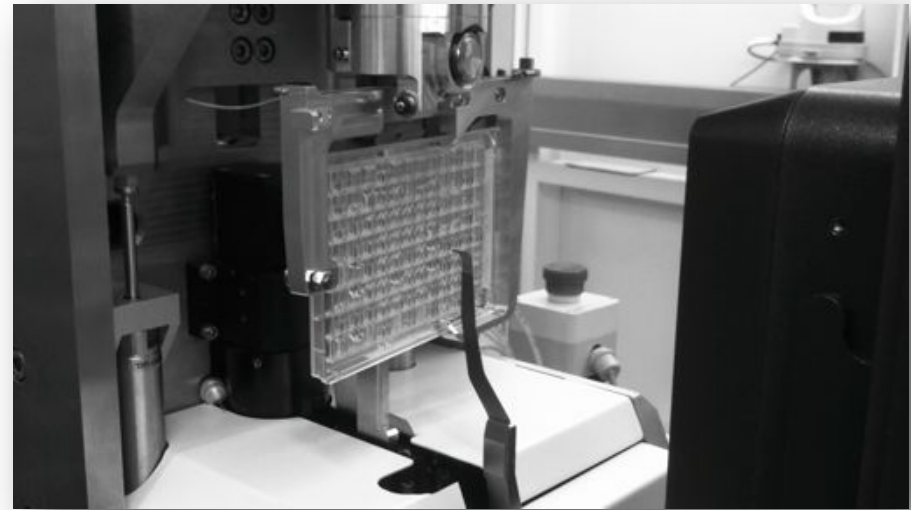


Cipriani, Marquez et al. (2012) 'CrystalDirect: a new method for automated crystal harvesting based on laser-induced photoablation of thin films.' Acta Cryst D68:1393.

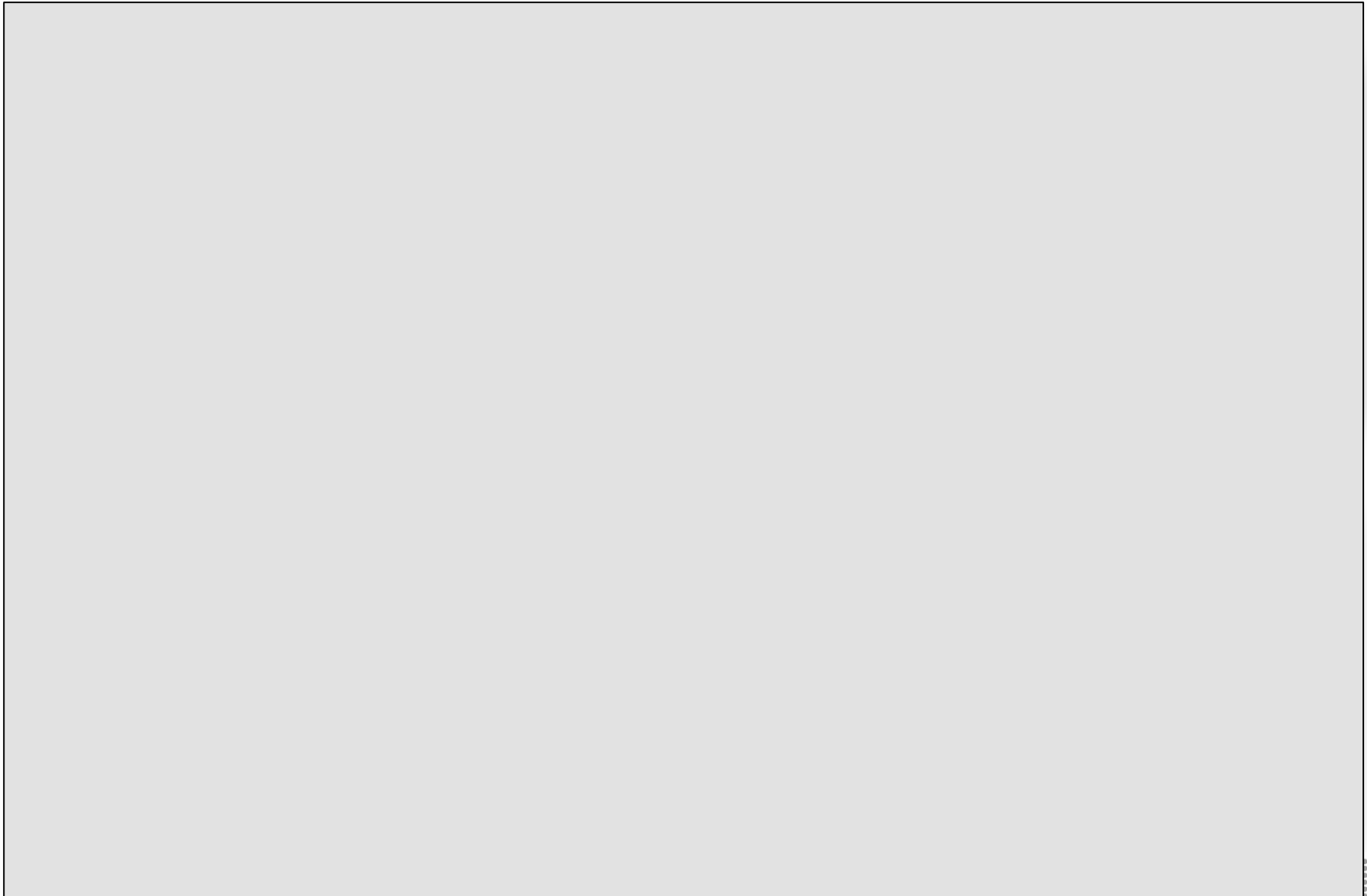


In situ data collection

- Continuous serial helical scans with a micro-beam on CrystalDirect plates

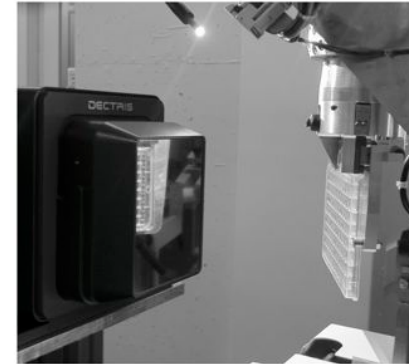


In situ serial data collection at room temperature

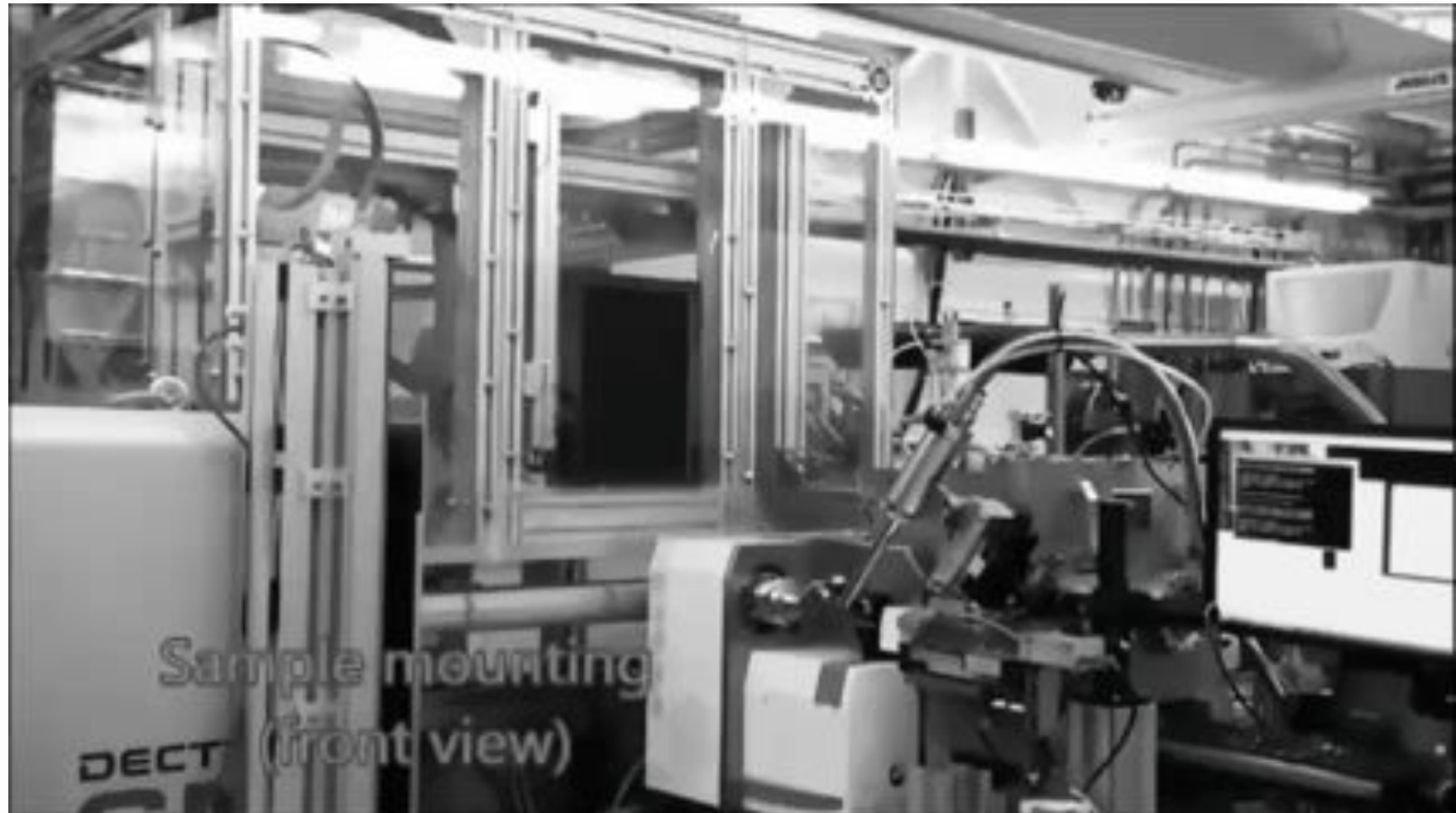


Detectors?

- PILATUS3 can run at 500 Hz.
 - Time required for read-out is ca. 1 ms
 - In continuous scan mode, the detector is 'blind' for 50% of the time
-
- EIGER 4M can run at 750 Hz
 - Time required for read-out is ca. 3 μ sec
 - 'blind' for < 1% of the time



Robotics ...



No operator error / remote operation / no hot bodies

Business ...



The goals of EMBLEM's technology transfer activities are to:

- promote the commercial use of research results and innovations;
- foster exchange between EMBL research and industry;
- return value to stakeholders including society at large;
- support EMBL spin-off companies working in the life sciences;
- increase the attractiveness of EMBL for top researchers by providing professional technology transfer service;
- create high-tech jobs.

Software downloads

- Licensing for different scenarios
 - Academic
 - For profit



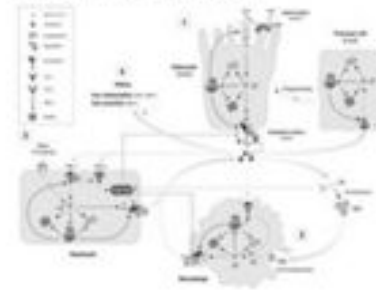
PROTEIN-FUNCTION ANALYSIS



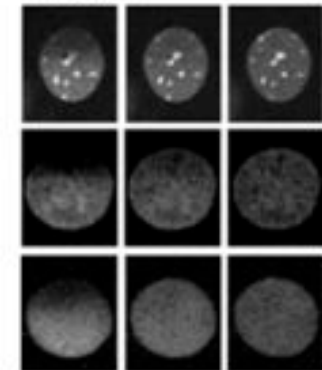
STRUCTURAL ANALYSIS



SYSTEMS BIOLOGY



IMAGING



CHEMOINFORMATICS



INSTRUMENT CONTROL



EMBL-EM: Portfolio companies

www.embl-em.de



**BIOBYTE
SOLUTIONS**



Summary

- Cutting edge instrumentation is crucial for pushing the boundaries of Structural Biology (object size and imaging resolution).
- Whatever probe is useful will be used (light, e-, n, ...).
- Technology development, technology provision (as service), technology dissemination (commercial) for research in the member states.
- Biologists, biochemists, chemists, physicists, computer scientists, engineers, lawyers, and others working together makes the difference.
- Transition from *experiment* to *measurement* needs to be made.
- Software becomes ever more important (download, web-services).
- Centralized user facilities / 'infrastructures' are a (the only possible?) way to deal with technical complexity and cost.