PAUL SCHERRER INSTITUT

SLS Detector Group

# PILATUS:
# A Pixel Detector for Diffraction Experiments at the Swiss Light Source

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SLS at PSI

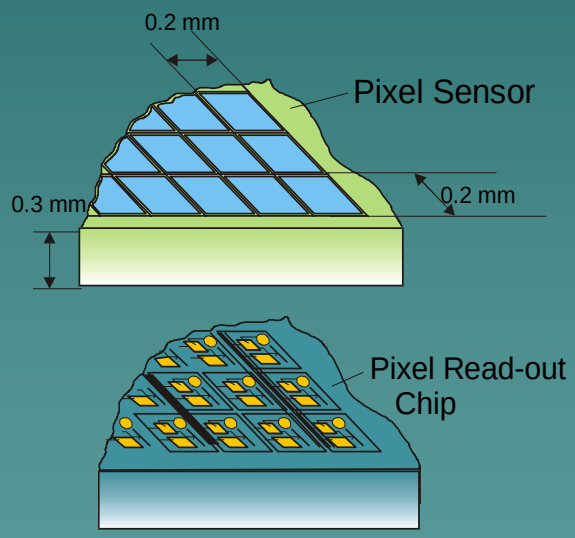
Mount Pilatus

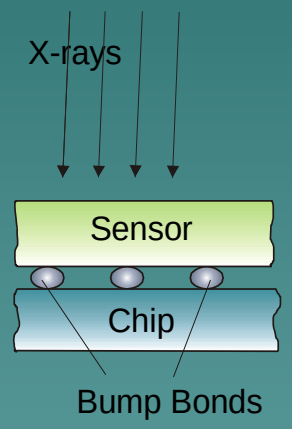
PIxeL ApparaTUs for the SLS

# PILATUS:
# A Pixel Detector for Diffraction Experiments at the Swiss Light Source

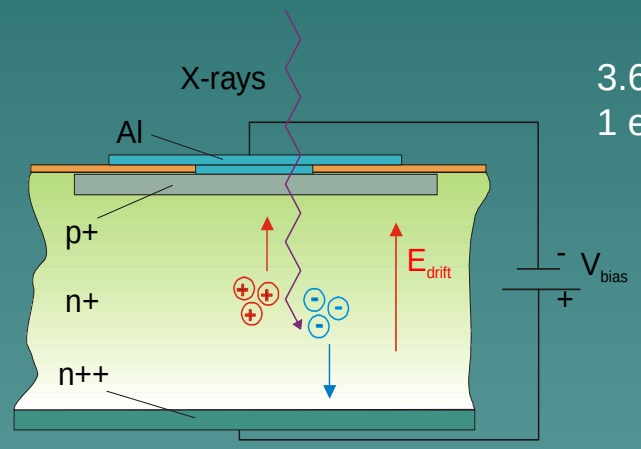
- The Principle of the PILATUS Detector
- The 1kx1k PILATUS Detector and Single Module Detector
- Performed Experiments:
  - Protein Crystallography at Beamline X06SA (SLS)
  - Protein Crystallography at Beamline BL38B1 (SPring-8)
  - Surface Diffraction at Beamline X04SA (SLS)
  - Radiography and Tomography at Beamline X04SA (SLS)

# The PILATUS Detector




Sensor: Si pn-junction



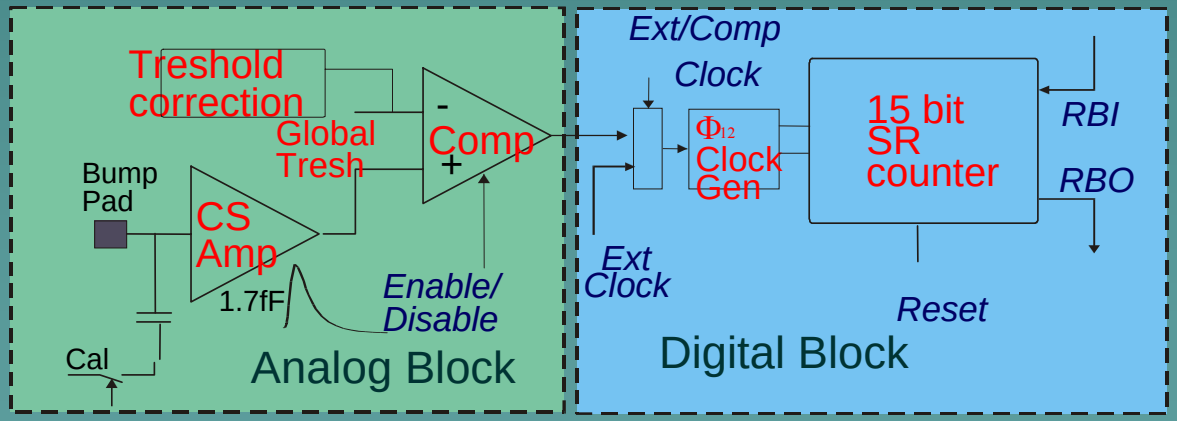

3.6 eV to create
1 eh-pair

# Single Photon Counting Electronics

- Radiation tolerant DMILL technology
- 44 x 78 pixels, 217 x 217 $\mu m^2$
- pixels are XY-addressable
- The analog output can be monitored
- Read-out time of the whole chip:
  6.7 ms (at 10 MHz)
- 3 % defective pixels

Each Pixel contains:

- Low noise analog block (ENC tot = 70 e-)
- Shaping time $t_{sh}$ ~ 1 $\mu$s
- 15 bit pseudo random counter
- Individual threshold adjustment
- ➢ Low overall threshold variation (s<100 e-)



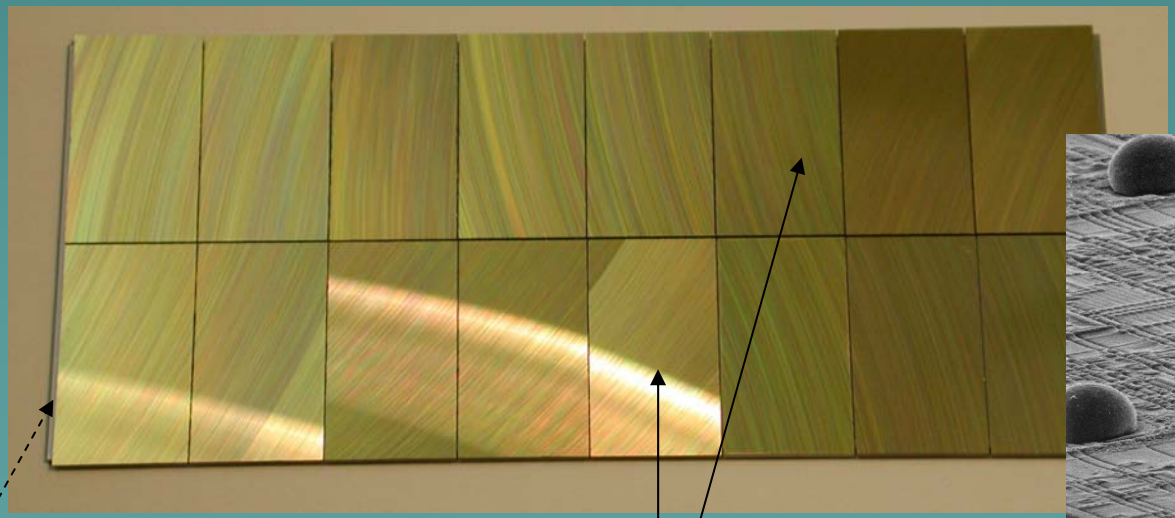

- ➢ No background from dark current
- ➢ No readout noise

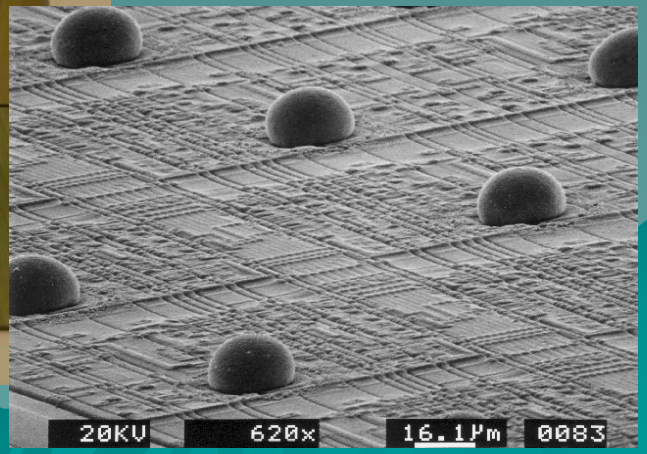
# A 2D interconnection: Micro-Bump-Bonding

**Sensor:**
- Wafers with Indium
- Dicing
- Reflow

**Readout Chips:**
- Wafers with UBM+Indium
- Dicing
- Testing of the chips

- Bump pressing (~5 kg)
- Reflow of the assembly
- Good chips hold > 300 g (~0.1 g / bump)

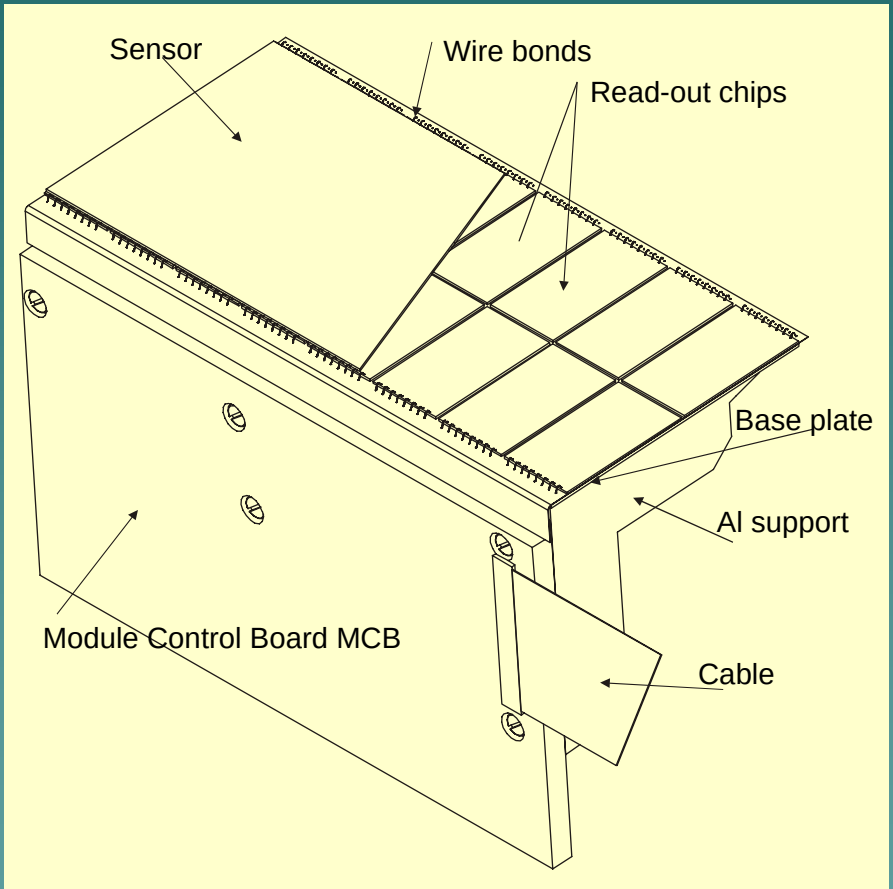


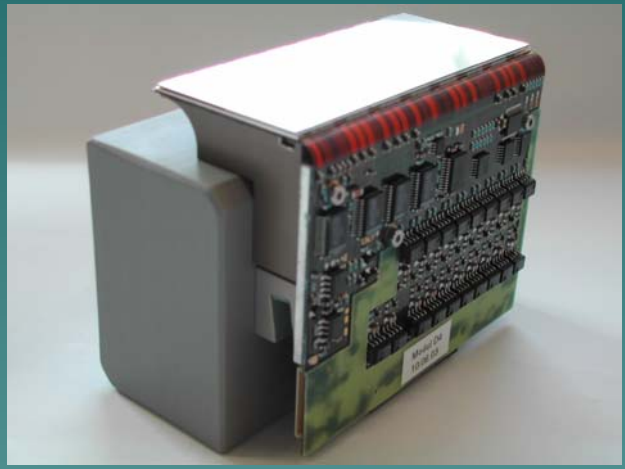



Sensor (not visible)

Readout Chips (back side)

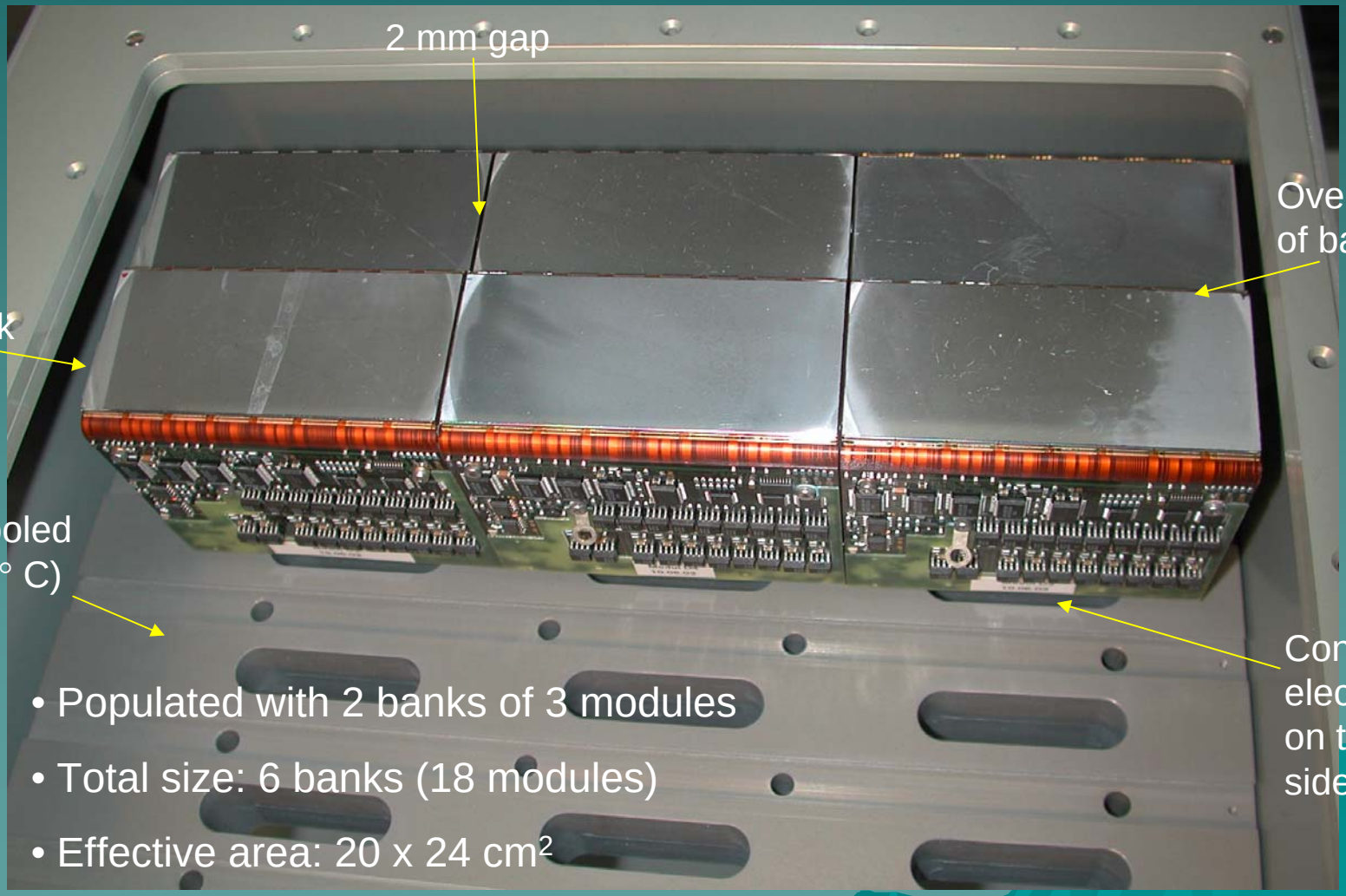
# The PILATUS Module



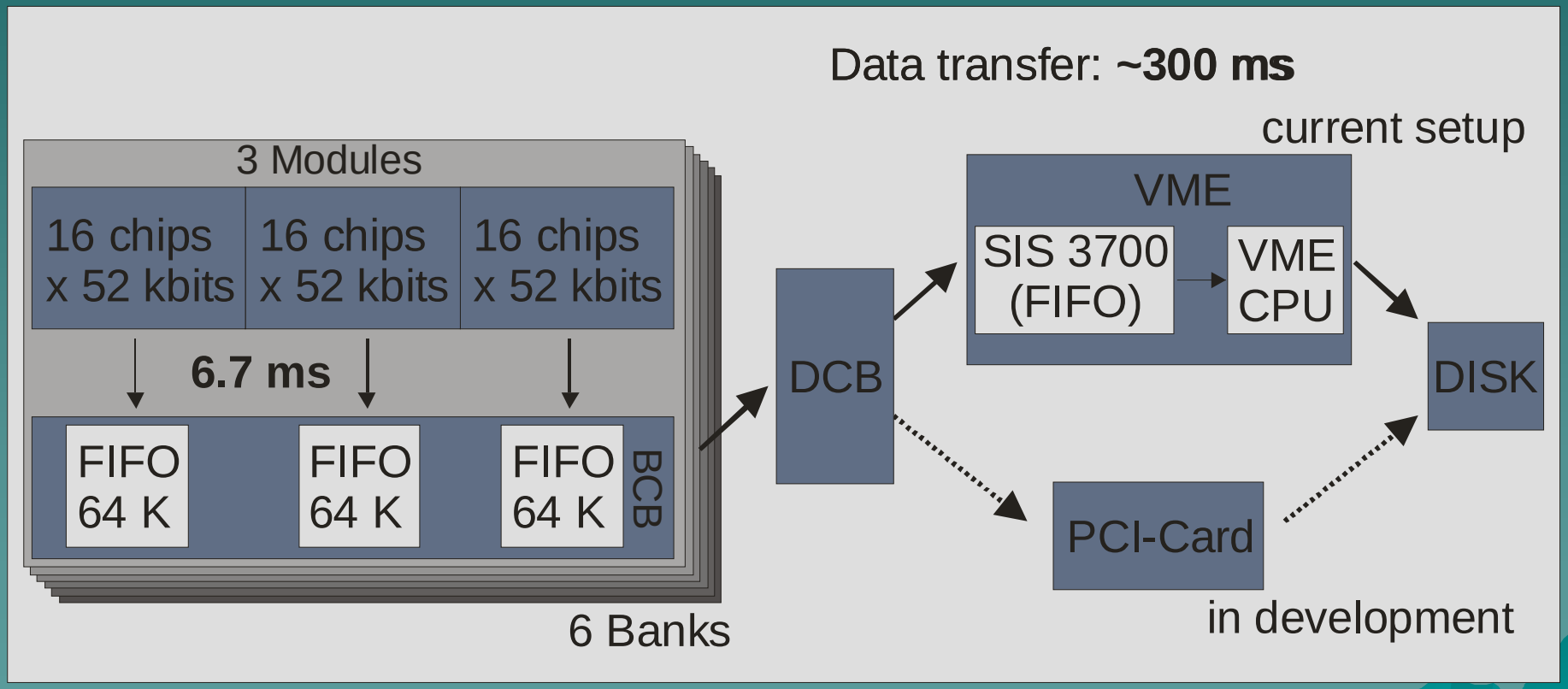
- 80 x 35 mm$^2$ continuous sensitive area
- 2 x 8 readout chips
- 57462 pixels
- Pixel size: 217x217 $\mu$m$^2$

# The 1k x 1k PILATUS Detector




- Populated with 2 banks of 3 modules
- Total size: 6 banks (18 modules)
- Effective area: 20 x 24 $cm^2$
- One million individual pixels

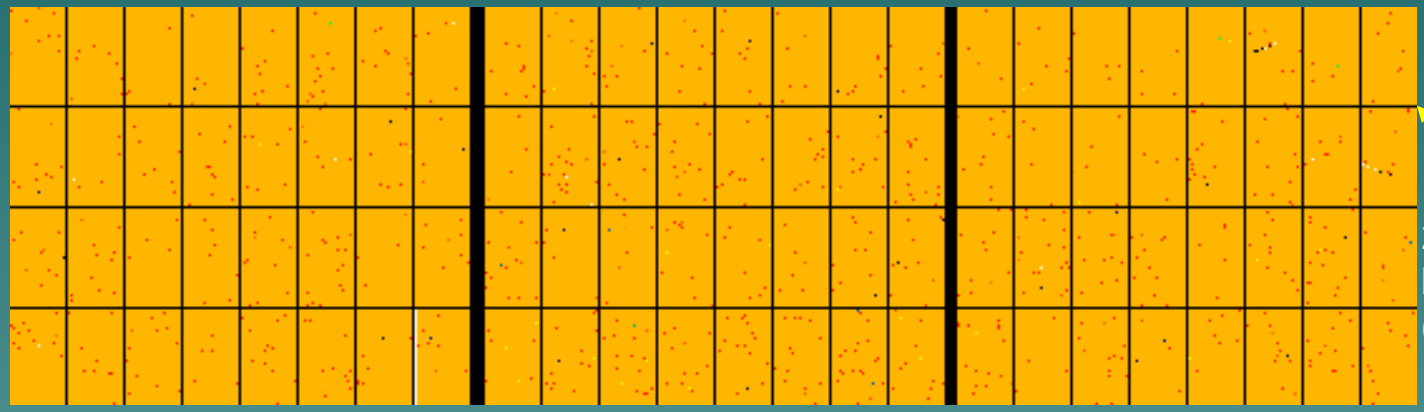
# The PILATUS readout architecture




- Readout time: 6.7 ms
- Framing time: 10 Hz (2 Mbyte/image)

# The PILATUS Readout Results of 2 Banks

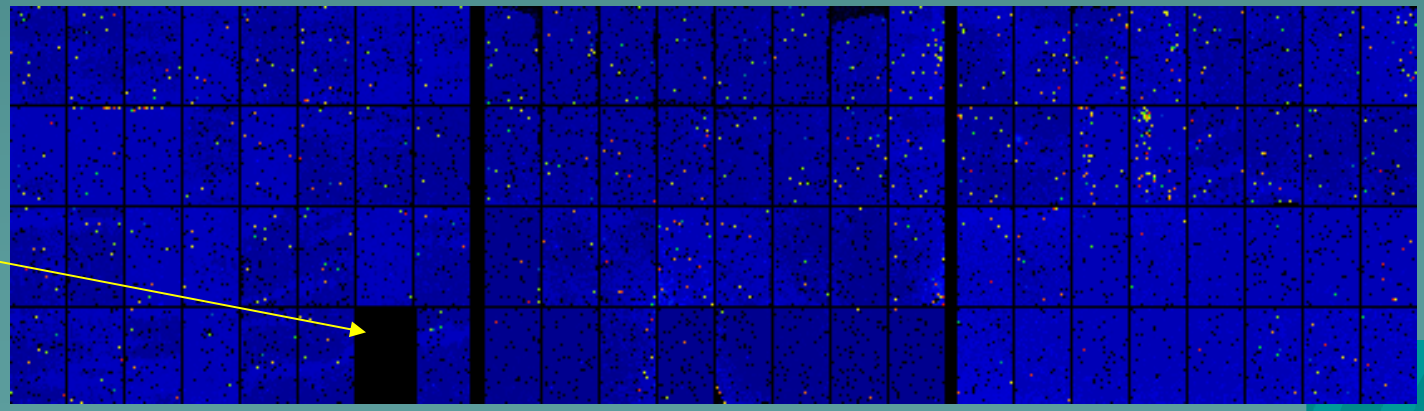
2 mm gap between modules



2 pixels gap between chips (double pixels)

Digital readback

Defective chip



Readout after 100 calibrate pulses to each pixel

- 3% defective pixels

# The Single Module Detector (SMD)

Properties:

- Active area: 80 x 35 $mm^2$
- Exposure time: >100 $\mu$s
- Readout-time: 6.7ms
- Current framing time: ~300 ms
- Cooling with Peltier elements (18° C)

Currently installed at:

- SLS X04SA (Material Science BL)
- SPring-8 (Japan)
- SINQ (Sensor with Gd $\Rightarrow$ neutron imaging)

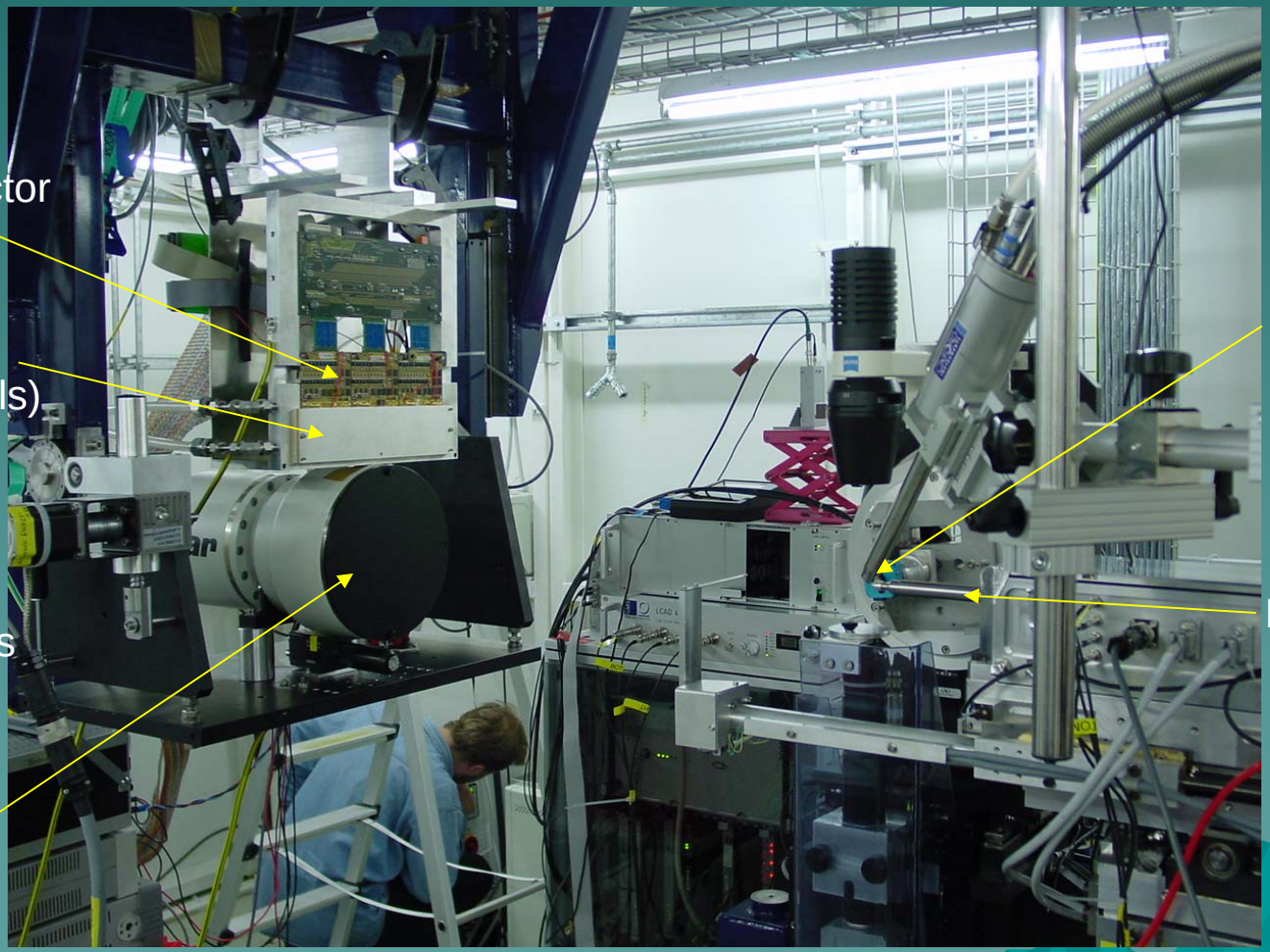
# Measurements at Beamline X06SA

one-bank-detector

Sensitive area:
24.3 x 3.4 $cm^2$
(1120x157 pixels)

Vertical translation in 7 positions
→ 1k x 1k pixels

MAR-CCD



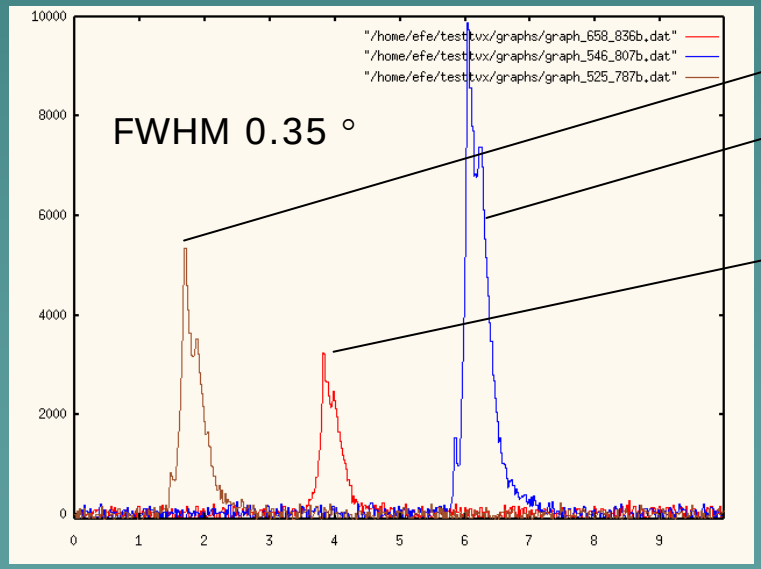
Specimen (cryo-cooled)

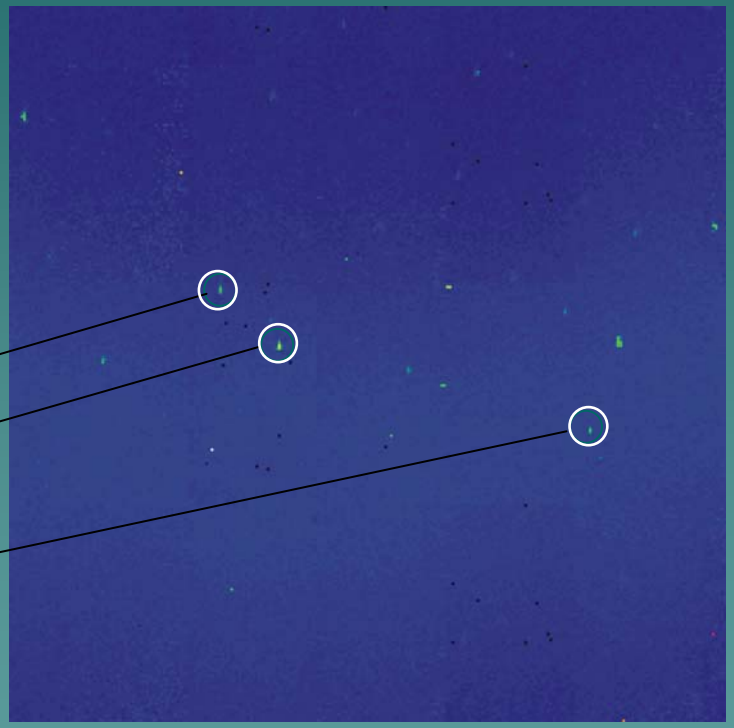
Beam

# Fine ϕ-sliced Crystallography with Continuous Sample Rotation

Lysozyme crystal

- continuous rotation with 0.02 °/ image
- 500 ms exposure time
- 6.7 ms readout time
- no mechanical shutter
- 12 keV X-rays



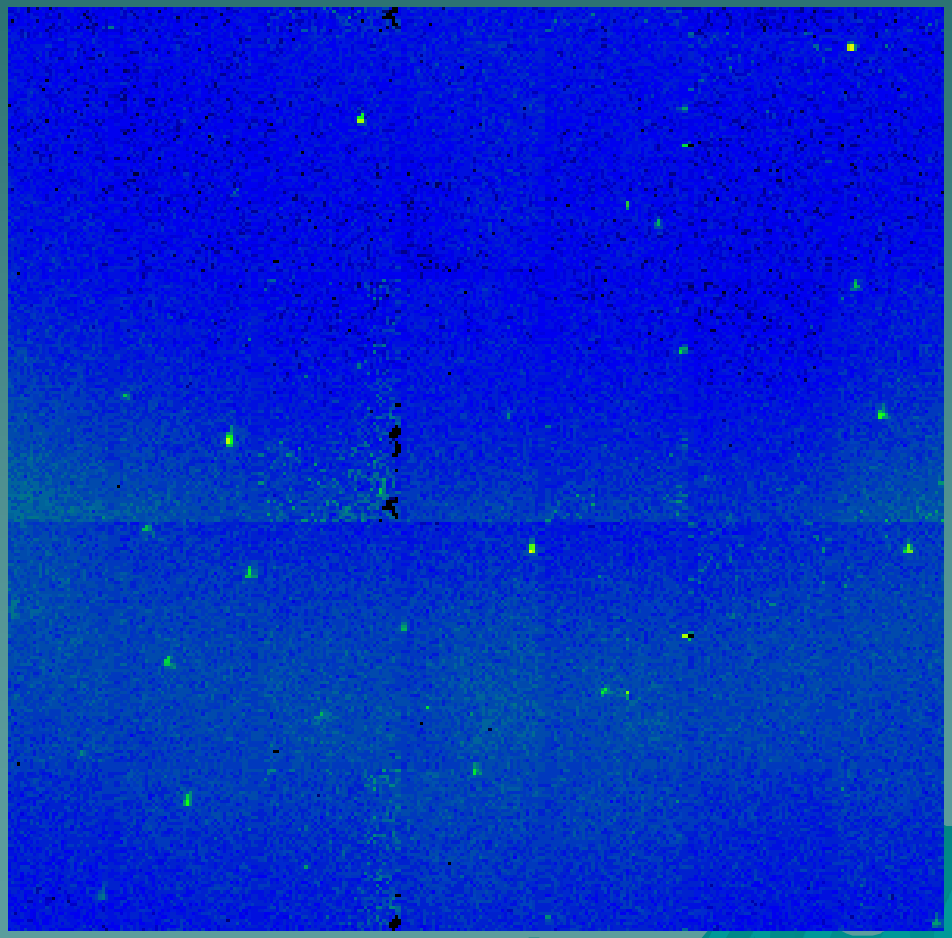
Sum of 3 fine-slice images

# Fine ϕ-sliced Crystallography with Continuous Sample Rotation

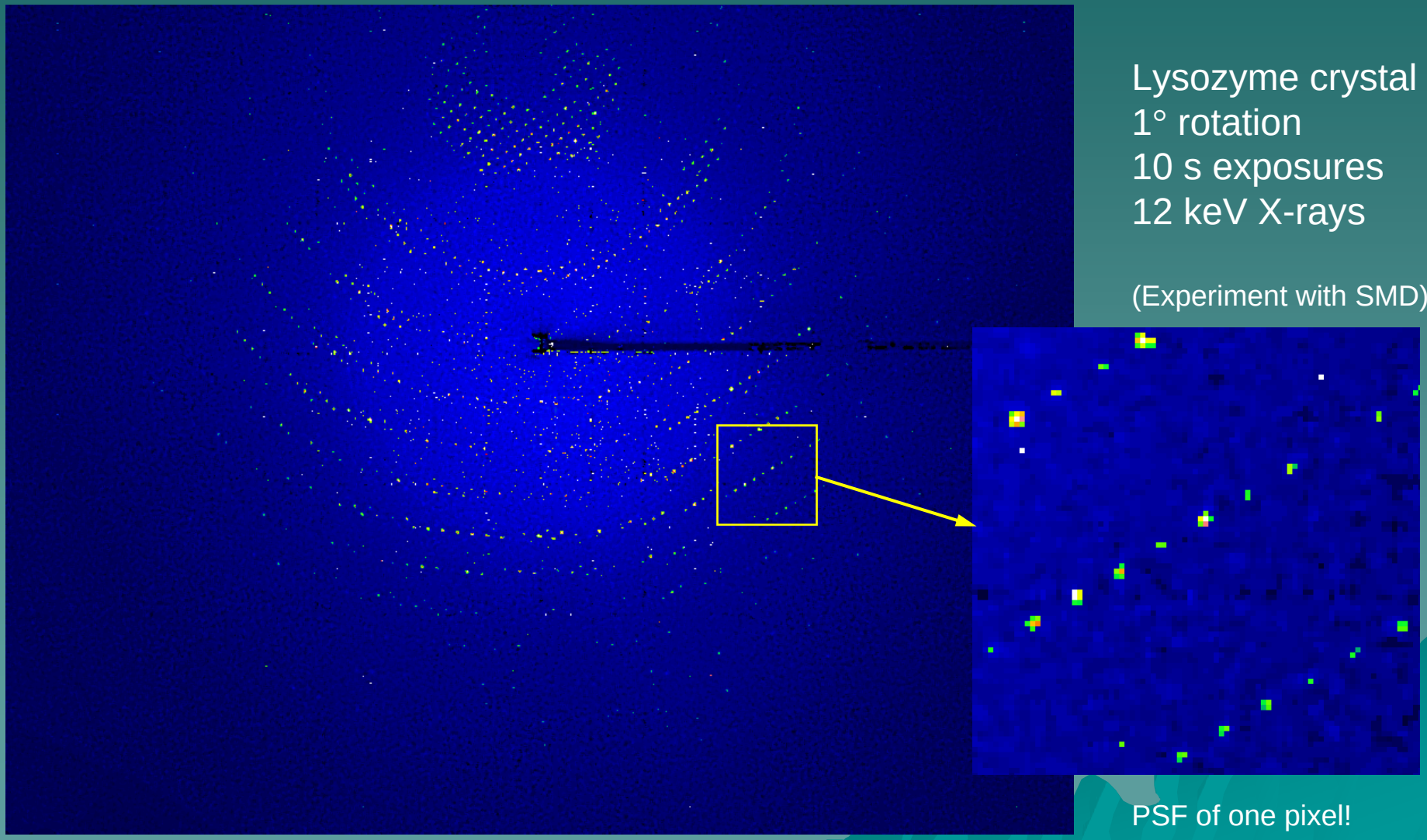
Lysozyme:
- 500 images
- 10 deg
- Total time: 4 min

Electronic shutter:
- Precise timing
- Stable background

Top-up operation



# Crystallography at BL38B1 – SPring-8



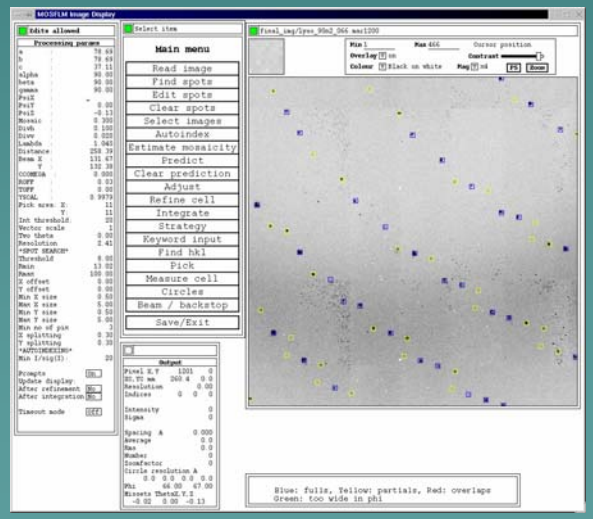
Lysozyme crystal
1° rotation
10 s exposures
12 keV X-rays

(Experiment with SMD)

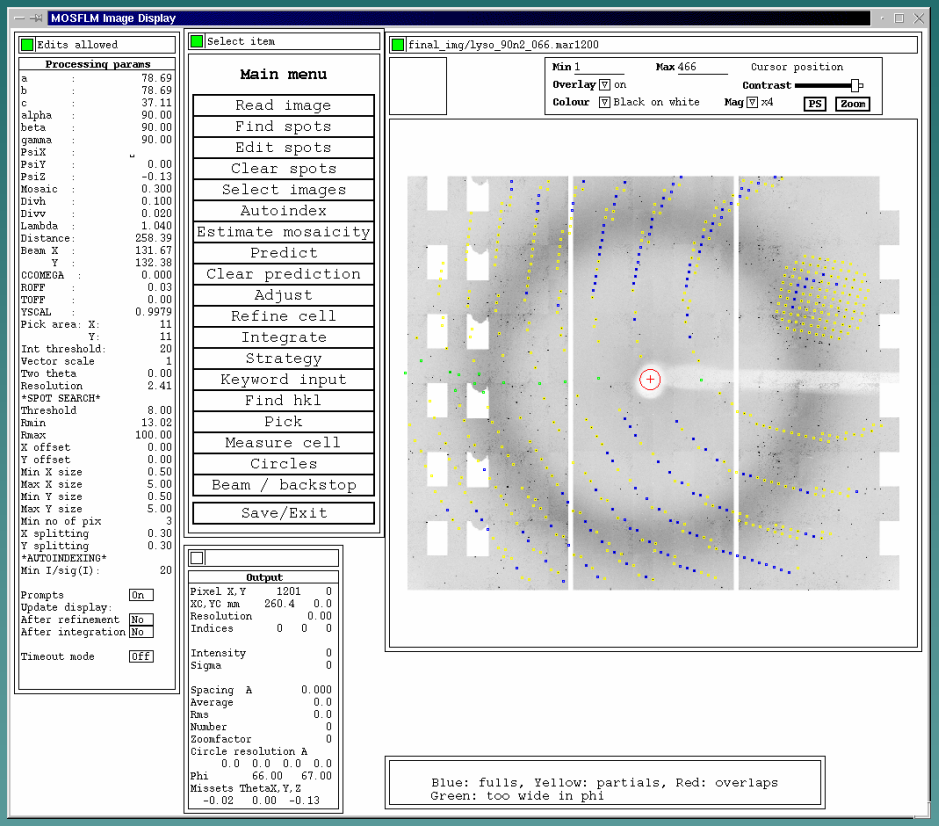
PSF of one pixel!

# Data analysis

Analysis of the data
with
MOSFLM

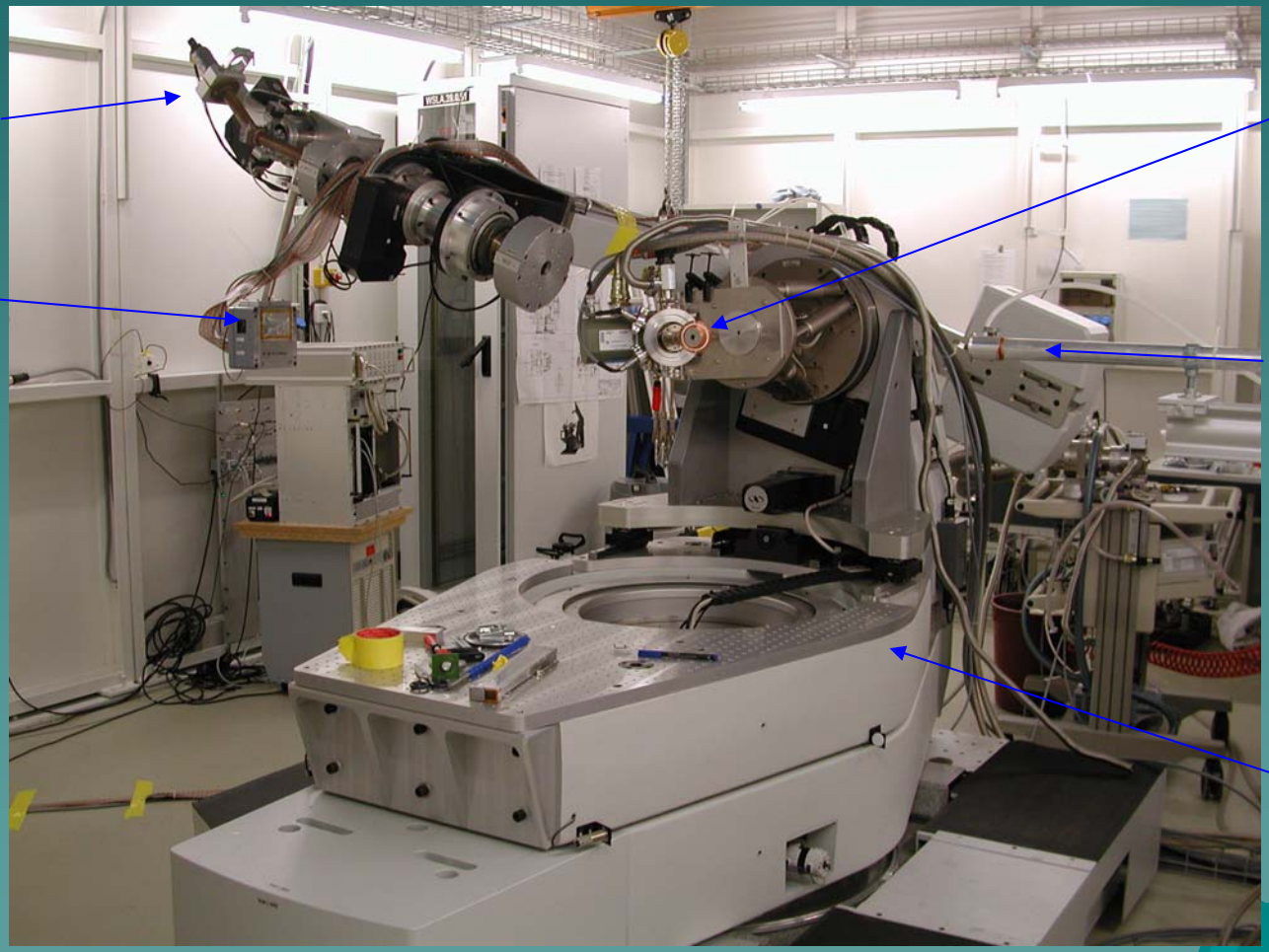


Lysozyme: MOSFLM - Refined Cell

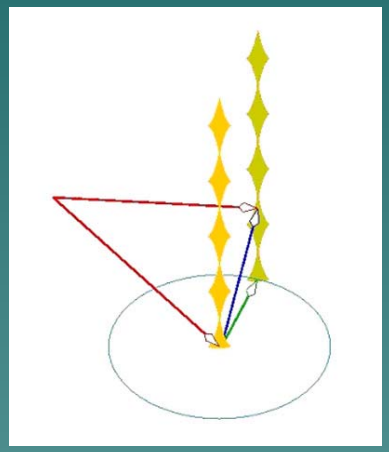



Lysozyme: MOSFLM – “Autoindex” and “Predict”

# The Surface Diffraction Station at X04SA



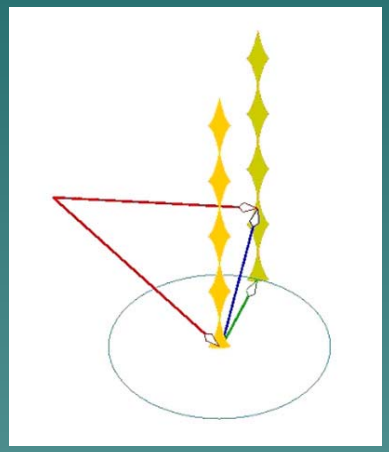
# Measurements of a crystal truncation rod (CTR)



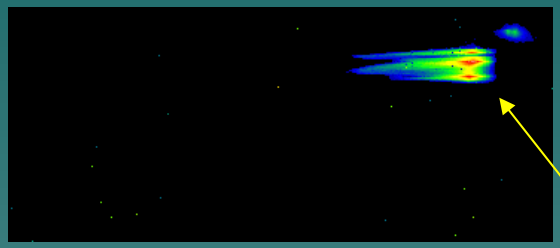
surface-sensitive structural information

CTR:
Extended distribution in reciprocal space
of scattered intensity
due to the abrupt termination of the crystal lattice
at the surface

# Measurements of a crystal truncation rod (CTR)



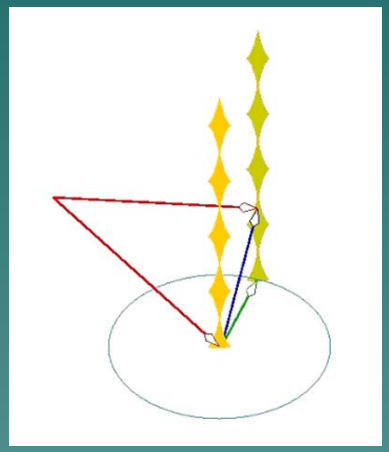
surface-sensitive structural information



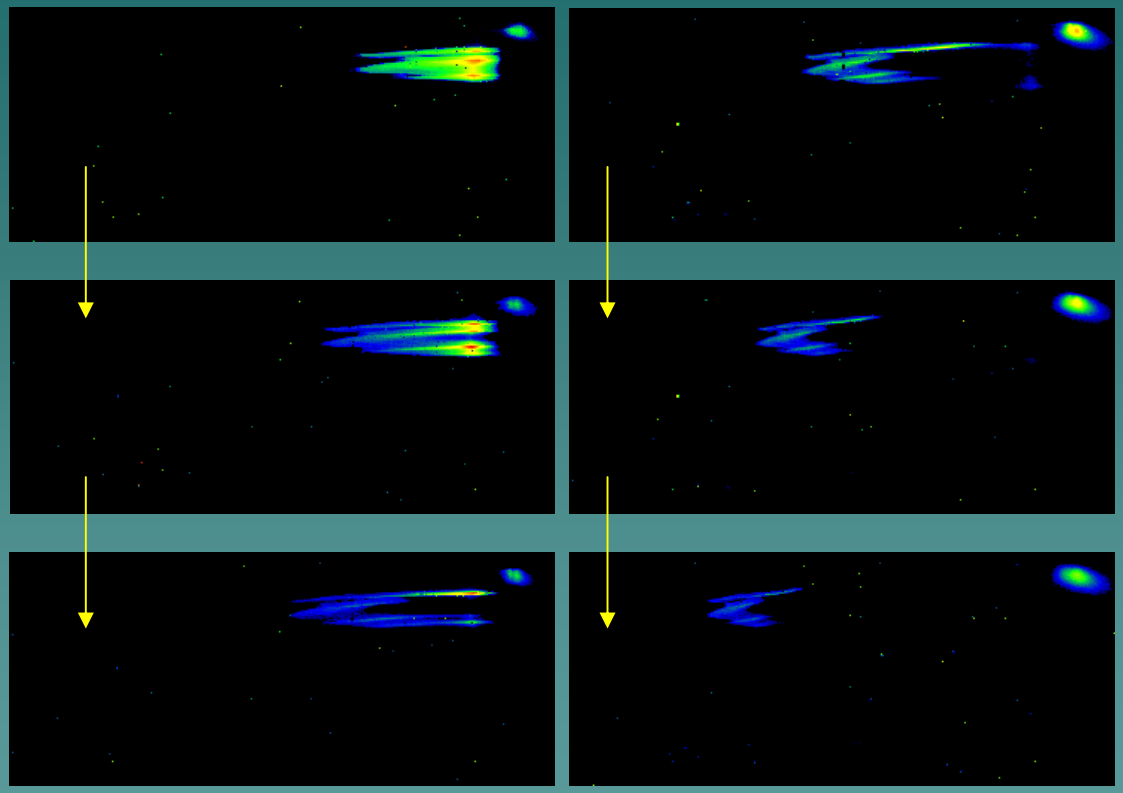
Reflection belonging to a CTR of $SrTiO_3$ - surface

Classic:
Time-consuming scans with a point detector at points along the CTR

# Measurements of a crystal truncation rod (CTR)



surface-sensitive structural information

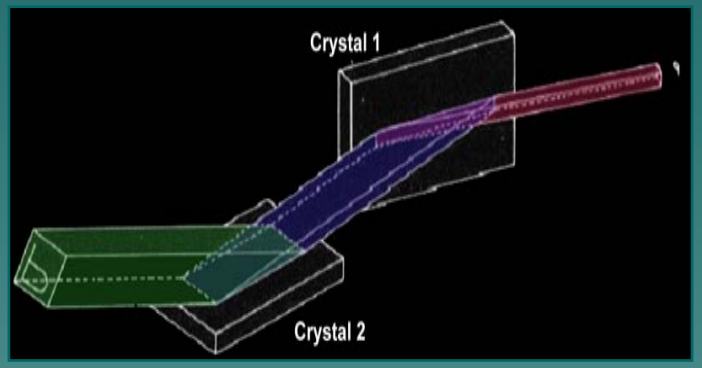


- 90 “snapshots” at points along the CTR
- X-ray energy:15 keV
- Exposure time was adjusted (intensity varies over 8 orders of magnitude)

- **Time significant reduced**
- **Background signals can be identified and rejected**

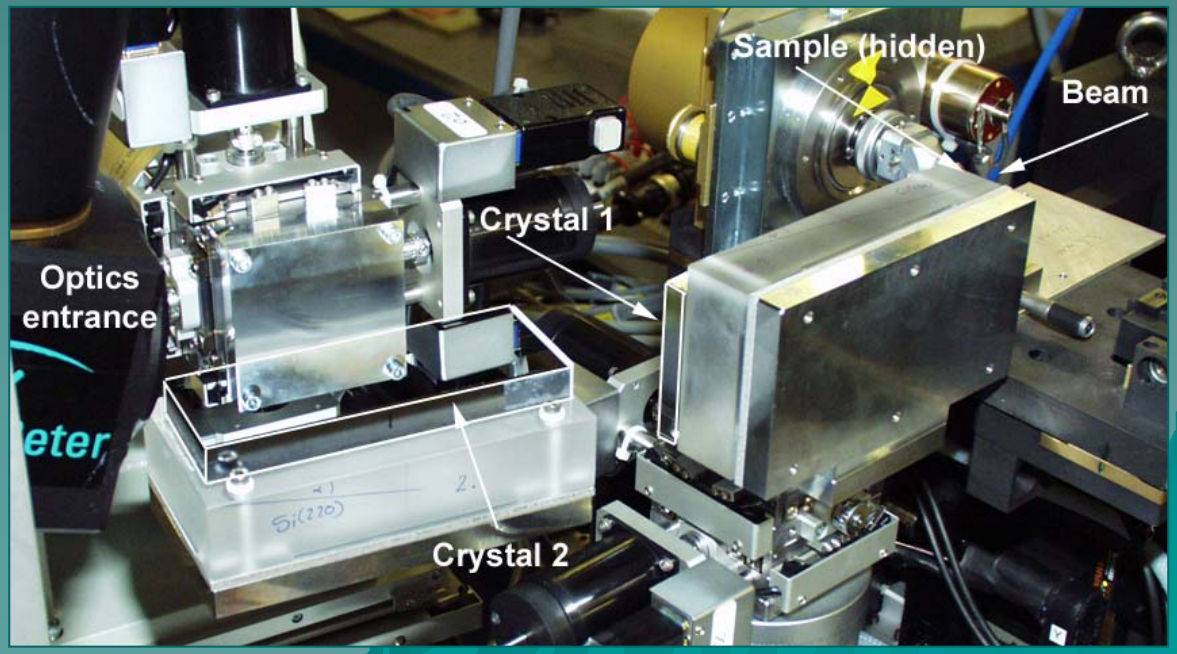
P. Willmott and B. Patterson

# The Bragg Magnifier at the Radiography and Tomography Station

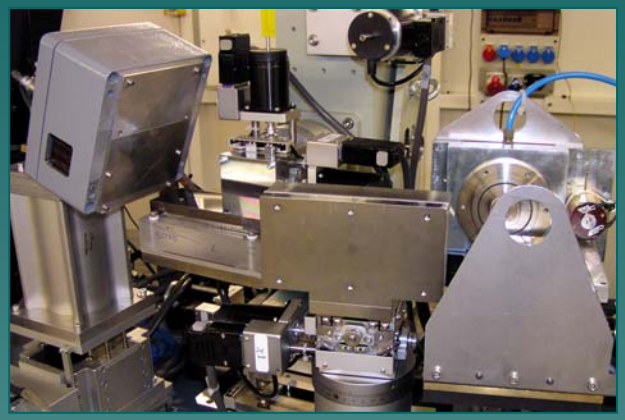



- Asymmetrical diffraction from Crystal 1 produces one-dimensional magnification
- A successive diffraction from Crystal 2, with the same magnification factor but perpendicular diffraction planes, produces uniform two-dimensional magnification

Magnification Factor of 100x100 could be achieved with the optical coupled CCD



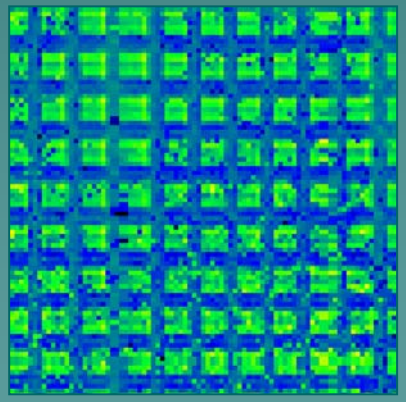
# Radiography with the SMD



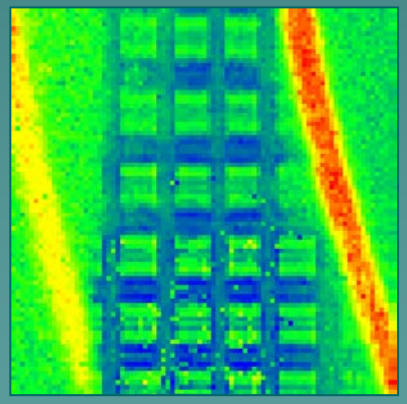
Setup with the SMD

X-ray energy 21.1 keV

Sample: Gold mesh
- Pattern repeat 16 μm
- Hole size 9 μm

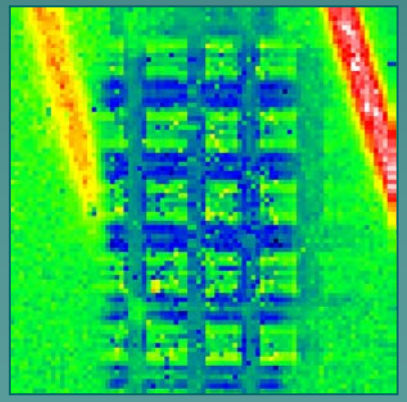


100x100
(limit so far)



200x200

3.7 mm (17 pixel)



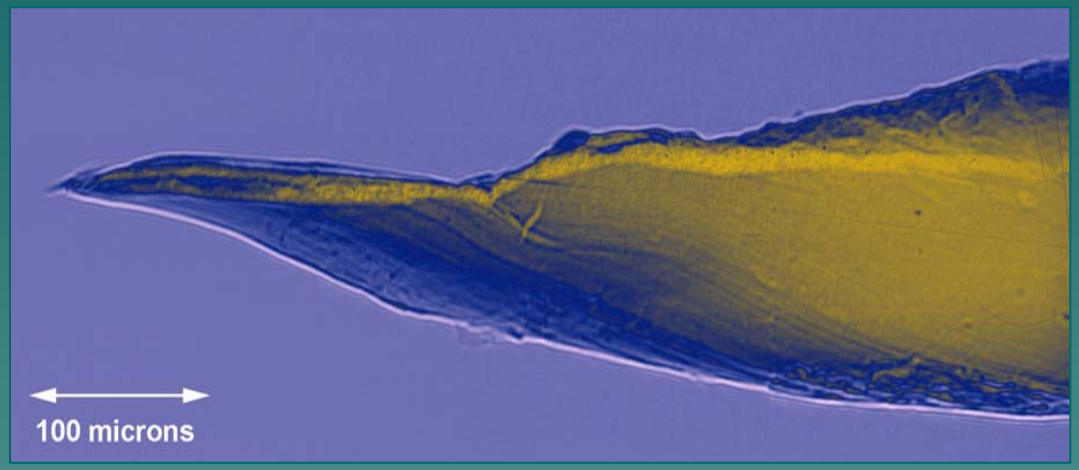
250x250

➢ Improvement of the performance of the Bragg Magnifier

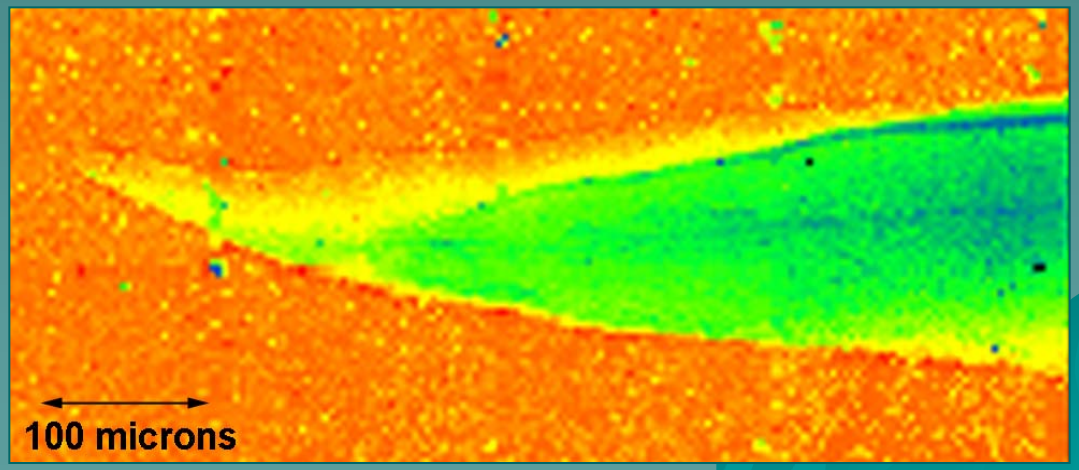
# Tomography with the SMD

Tomogram:
- Fragment from a turbine blade
- Magnification of 40 x 40
- Continuous sample rotation 0.5 °/s
- 21.1 keV X-rays

➢ 900 projections recorded in 6 minutes!




Bragg Magnifier with optics: 5 s/image, TPS=0.35x0.35 $\mu m^2$




Bragg Magnifier with PILATUS: 0.1 s/image, TPS=5x5 $\mu m^2$

# Conclusion

- A single photon counting detector for protein crystallography is currently under construction:

  - 1k x 1k pixels
  - High efficiency around 12 keV
  - No background from dark current, no readout noise
  - Fast readout of 6.7 ms

  ➔ Fine $\phi$-sliced experiments with continuous sample rotation

- Single module detectors have been extensively tested:

  - Both diffraction and radiography applications
  - Experiments show the advantages of this technology

# Outlook

- A new readout chip is being designed in 0.25 μm technology:
  - Radiation tolerant
  - Faster amplifier - higher count rate
  - Larger dynamic range - 20 bit counter
  - Smaller pixels - 170 x 170 $\mu m^2$
  - Faster readout
  - Prototypes currently under test

**Technology enables the production of many different detector types through redesigning the readout chip.**

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