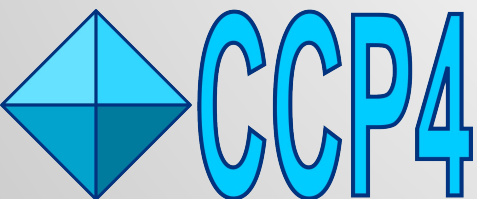




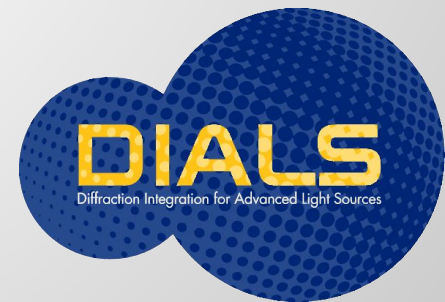
# DIALS for ED

Data analysis and structure determination using DIALS and CCP4

David Waterman  
eBIC November 2019



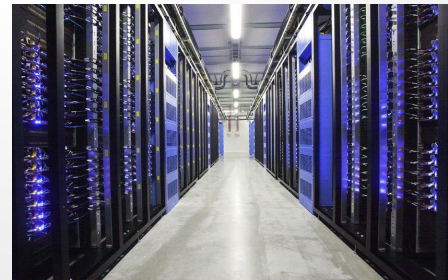
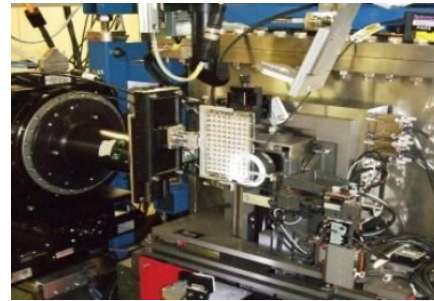
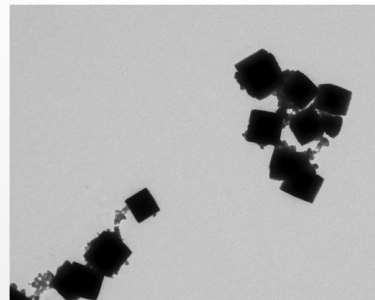
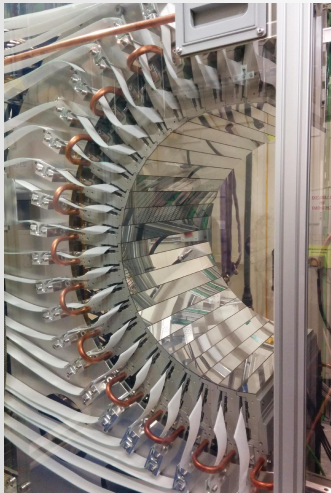
# What is DIALS?



# What is DIALS?

## Diffraction Integration for Advanced Light Sources

- Project began in late 2011 at Diamond Light Source and CCP4
- Additional funding by BioStruct-X and now Wellcome Trust
- Aim to develop new data processing software to meet modern challenges
- Now an international collaborative development



# Legacy

Built upon the strengths of older projects

## research papers

Acta Crystallographica Section D

**Biological  
Crystallography**

ISSN 0907-4449

**Wolfgang Kabsch**

Max-Planck-Institut für Medizinische Forschung,  
Abteilung Biophysik, Jahnstrasse 29,  
69120 Heidelberg, Germany

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wolfgang.kabsch@mpimf-heidelberg.mpg.de

### XDS

The usage and control of the program package *XDS* for X-ray diffraction data collection is described in the context of the program. It includes automatic data reduction, range and recognition of reflections. Moreover, the limited number of correction steps and the completeness of the data have been restructured for better measurement.

#### 1. Functional specification

The program package was developed for the recording of a planar monochromatic X-ray diffraction pattern. *XDS* accepts a wide range of rotation images from single and multiwire area detectors and produces a list of the reflections on a given way. The program is able to process a positive amount of data from an incident beam and does not impose any limitations on the directions of the rotation or the oscillation range covered.

## research papers

Acta Crystallographica Section D

**Biological  
Crystallography**

ISSN 0907-4449

**J. W. Pflugrath**

Molecular Structure Corporation, 9009 New  
Trails Drive, The Woodlands, TX 77381, USA

Correspondence e-mail: jwp@msc.com

### The finer things in X-ray diffraction data collection

X-ray diffraction images from sensitive detectors can be characterized depending on whether the rotation is greater than or less than the expected. The expectations and consequences and thin images in terms of space, X-ray background and  $I/\sigma(I)$  are discussed. A software suite for processing such data is introduced, and results from data sets from another popular package are compared.

#### 1. Introduction

Two-dimensional position-sensitive detectors for many years in X-ray diffraction, data from crystals of macromolecules and their complexes (oligonucleotides and their complexes), a multi-wire system (recently commercialized charge-coupled devices), a phosphor-coated film detector, the crystal, centered in an oscillated around a single axis through  $\sim 2.0^\circ$ , while counts from diffraction are read out for a specified time. At the end of the detector is read out and the counts are stored in a two-dimensional array with each count to a distinct position on the detector.

## research papers

Acta Crystallographica Section D

**Biological  
Crystallography**

ISSN 0907-4449

**Andrew G. W. Leslie**

MRC Laboratory of Molecular Biology,  
Hills Road, Cambridge CB2 2QH, England

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andrew@mrc-lmb.cam.ac.uk

### The integration of macromolecular diffraction data

The objective of any diffraction experiment is to produce from a set of diffraction images (with their associated uncertainties), together with the crystal unit-cell parameters, a set of reliable, but should be as accurate as possible, parameters. The first three stages. The first stage is to determine the unit-cell parameters and the second stage is to determine the space group and also to determine the initial phases, which consists of reflections on each image and the intensity of each reflection. The third stage is to determine the parameters. Basic features of each of these three stages are discussed with reference to the program.

#### 1. Introduction

The collection of macromolecular diffraction data has undergone a dramatic advance with the advent of two-dimensional detectors, CCDs, crystallographic software and monochromatic and

Centre National de la Recherche Scientifique  
Université Paris-Sud

## Laboratoire pour l'Utilisation du Rayonnement Electromagnétique

Proceedings  
of the EEC Cooperative Workshop  
on Position-Sensitive Detector Software  
(Phases I & II)  
held at L.U.R.E. from May 26 to June 7, 1986.





# Present and future

Novel features such as new indexing methods, multiple experiment joint refinement, smoothly varying models, improved data for weak diffraction...



Acta Crystallographica Section D  
Biological  
Crystallography  
ISSN 1399-0047

Richard J. Gildea,<sup>a</sup> David G. Waterman,<sup>b,c</sup> James M. Parkhurst,<sup>d</sup> Danny Axford,<sup>d</sup> Geoff Sutton,<sup>d</sup> David I. Stuart,<sup>a,d</sup> Nicholas K. Sauter,<sup>e</sup> Gwyndaf Evans<sup>a</sup> and Graeme Winter<sup>a\*</sup>

<sup>a</sup>Diamond Light Source Ltd, Harwell Science and Innovation Campus, Didcot OX11 0DE, England, <sup>b</sup>STFC Rutherford Appleton Laboratory, Didcot OX11 0QX, England, <sup>c</sup>CCPA, Research Complex at Harwell, Rutherford Appleton Laboratory, Didcot OX11 0FA, England, <sup>d</sup>Division of Structural Biology, The Wellcome Trust Centre for Human Genetics, University of Oxford, Oxford OX3 7BN, England, and <sup>e</sup>Physical Biosciences Division, Lawrence Berkeley National Laboratory, Berkeley, CA 94720, USA

Correspondence e-mail: graeme.winter@diamond.ac.uk

## New methods for indexing multi-lattice diffraction data

A new indexing method is presented which is capable of indexing multiple crystal lattices from narrow wedges of diffraction data. The method takes advantage of a simplification of Fourier transform-based methods that is applicable when the unit-cell dimensions are known *a priori*. The efficacy of this method is demonstrated with both semi-synthetic multi-lattice data and real multi-lattice data recorded from crystals of ~1 µm in size, where it is shown that up to six lattices can be successfully indexed and subsequently integrated from a 1° wedge of data. Analysis is presented which shows that improvements in data-quality indicators can be obtained through accurate identification and rejection of overlapping reflections prior to scaling.

### 1. Introduction

A fundamental limitation of conventional macromolecular crystallography is the necessity of obtaining one or more crystals of sufficient size and quality to record a reasonably complete data set. The development of microfocus beamlines has allowed data to be collected from smaller crystals than ever before [see the recent reviews of the history and capabilities of microfocus beamlines by Evans *et al.* (2011) and Smith *et al.* (2012)]. Frequently, particularly in the cases of viruses and membrane proteins, only small, poor-quality crystals may be available and it may only be possible to collect a highly incomplete data set over a small oscillation range for each individual crystal before the diffraction quality is affected by radiation damage.

research papers

research papers

STRUCTURAL  
BIOLOGY

ISSN 2059-7983

Received 7 October 2015  
Accepted 4 February 2016

Edited by E. F. Garman, University of Oxford, England

**Keywords:** global refinement; *DIALS* framework; centroid refinement.

## Diffraction-geometry refinement in the *DIALS* framework

David G. Waterman,<sup>a,b\*</sup> Graeme Winter,<sup>c</sup> Richard J. G. Parkhurst,<sup>d</sup> Aaron S. Brewster,<sup>e</sup> Nicholas K. Sauter<sup>e</sup> and

<sup>a</sup>STFC Rutherford Appleton Laboratory, Didcot OX11 0QX, England, <sup>b</sup>CCPA, Rutherford Appleton Laboratory, Didcot OX11 0FA, England, <sup>c</sup>Diamond Light Source Ltd, Didcot OX11 0DE, England, <sup>d</sup>MRC Laboratory of Molecular Biology, Francis Crick Institute, London WC2A 3LY, UK, and <sup>e</sup>Lawrence Berkeley National Laboratory, Berkeley, CA 94720, USA  
david.waterman@stfc.ac.uk, gwyndaf.evans@diamond.ac.uk

Rapid data collection and modern computing resources provide a new paradigm for revisiting the task of optimizing the model of diffraction integration. A comprehensive description is given of new methods for revisiting the task of optimizing the model of diffraction integration. A comprehensive description is given of new methods for revisiting the task of optimizing the model of diffraction integration. A comprehensive description is given of new methods for revisiting the task of optimizing the model of diffraction integration. A comprehensive description is given of new methods for revisiting the task of optimizing the model of diffraction integration.

### 1. Introduction

The successful integration of single-crystal diffraction data depends on the accurate prediction of Bragg spot locations in area-detector images. An initial model for the diffraction geometry may be constructed from metadata provided by the diffraction images (Parkhurst *et al.*, 2014) or provided by the user. This starting model is completed by estimating crystal parameters, which are usually derived from data by an indexing procedure, such as that of Steller *et al.* (1997). This model is rarely sufficient for accurate prediction throughout the entire data set.

research papers



JOURNAL OF  
APPLIED  
CRYSTALLOGRAPHY

ISSN 1600-5767

Received 1 June 2016  
Accepted 24 August 2016

Edited by A. R. Pearson, Universität Hamburg, Germany

**Keywords:** integration; robust outlier rejection; generalized linear models; background modelling.

research papers

## Robust background modelling in *DIALS*

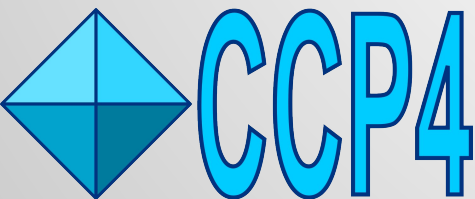
James M. Parkhurst,<sup>a,b</sup> Graeme Winter,<sup>c</sup> David G. Waterman,<sup>c,d</sup> Luis Fuentes-Montero,<sup>e</sup> Richard J. Gildea,<sup>a</sup> Garib N. Murshudov<sup>b\*</sup> and Gwyndaf Evans<sup>a\*</sup>

<sup>a</sup>Diamond Light Source Ltd, Harwell Science and Innovation Campus, Didcot OX11 0DE, UK, <sup>b</sup>Laboratory of Molecular Biology, Francis Crick Avenue, Cambridge CB2 0QH, UK, <sup>c</sup>STFC Rutherford Appleton Laboratory, Didcot OX11 0FA, UK, and <sup>d</sup>CCPA, Research Complex at Harwell, Rutherford Appleton Laboratory, Didcot OX11 0FA, UK.  
\*Correspondence e-mail: garib@mecc.lbnl.cam.ac.uk, gwyndaf.evans@diamond.ac.uk

A method for estimating the background under each reflection during integration that is robust in the presence of pixel outliers is presented. The method uses a generalized linear model approach that is more appropriate for use with Poisson distributed data than traditional approaches to pixel outlier handling in integration programs. The algorithm is most applicable to data with a very low background level where assumptions of a normal distribution are no longer valid as an approximation to the Poisson distribution. It is shown that traditional methods can result in the systematic underestimation of background values. This then results in the reflection intensities being overestimated and gives rise to a change in the overall distribution of reflection intensities in a dataset such that too few weak reflections appear to be recorded. Statistical tests performed during data reduction may mistakenly attribute this to merohedral twinning in the crystal. Application of the robust generalized linear model algorithm is shown to correct for this bias.

### 1. Introduction

In macromolecular crystallography (MX), integration programs – such as *MOSFLM* (Leslie, 1999), *XDS* (Kabsch, 2010), *d\*TREK* (Pflugrath, 1999) and *DIALS* (Waterman *et al.*, 2013) – are used to estimate the intensities of individual Bragg reflections from a set of X-ray diffraction images. Whilst details of the processing differ, these programs all follow the same basic procedure to calculate the intensity estimates. For each reflection, pixels in the neighbourhood of the predicted



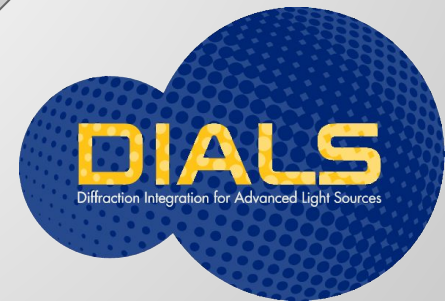
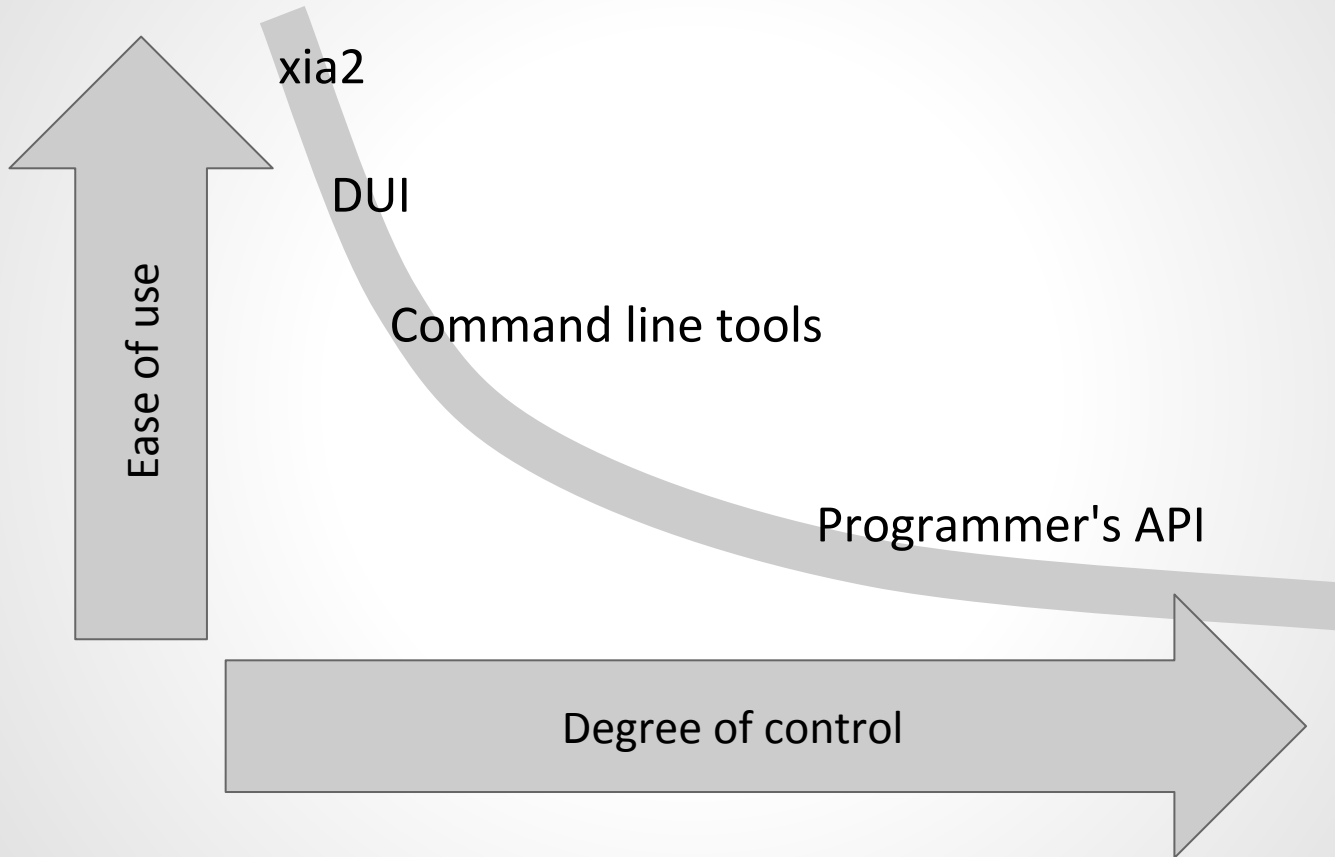


# Philosophy



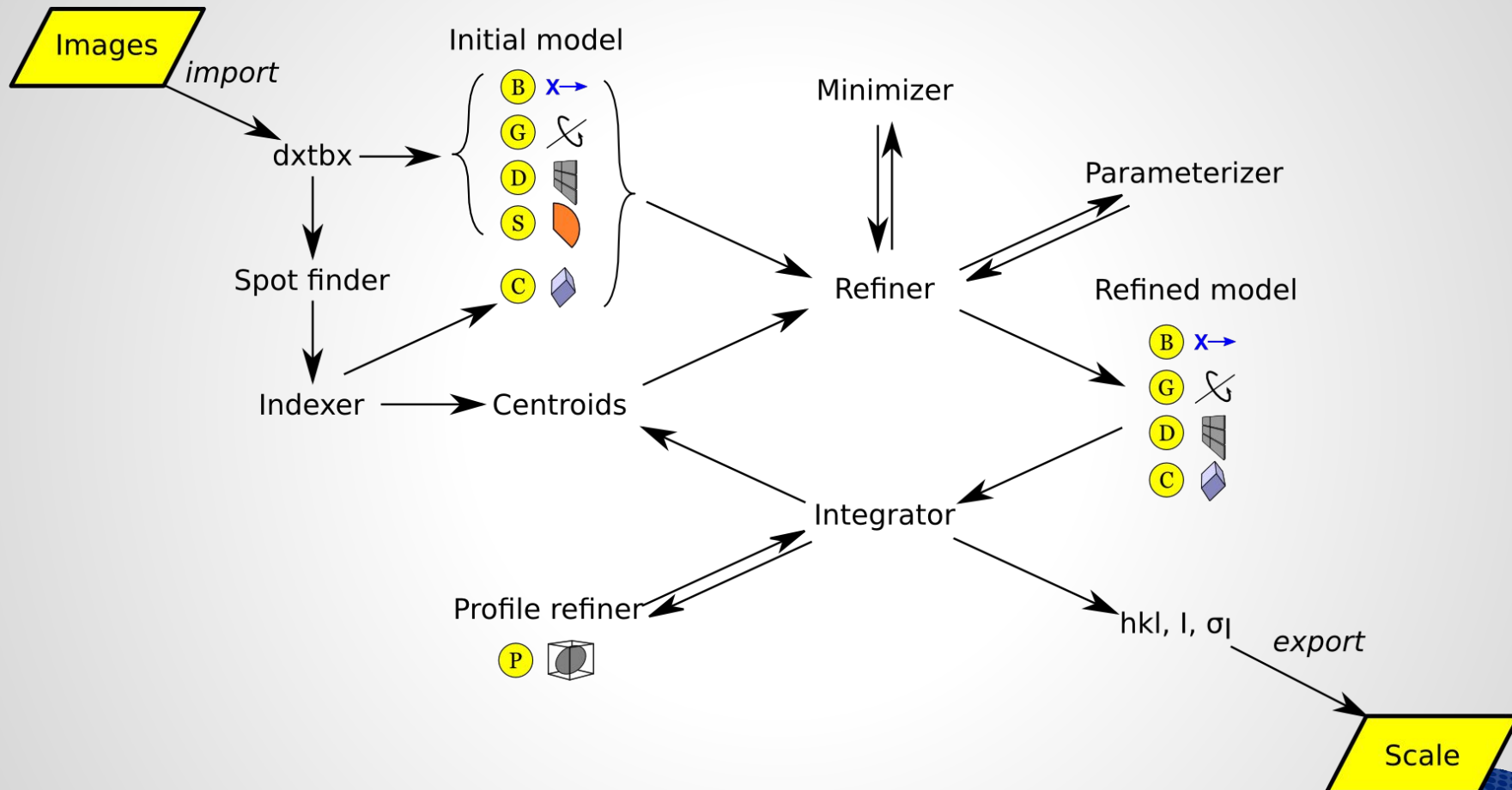
# Philosophy

Levels of interaction





# Flowchart for data processing





# DIALS files

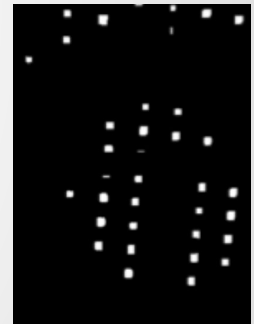
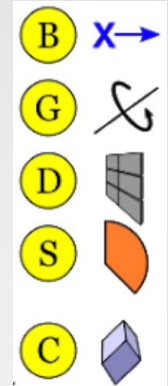
From v2.0.0 onwards:

".**expt**" file (e.g. imported.expt)

- metadata for images - file location, experimental model details (beam orientation and wavelength, detector position and orientation etc.)

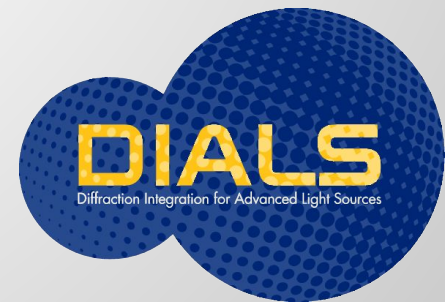
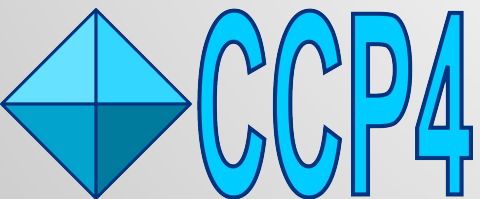
".**ref1**" file (e.g. strong.ref1)

- spot/reflection information - coordinates (centroids), intensity values, etc.





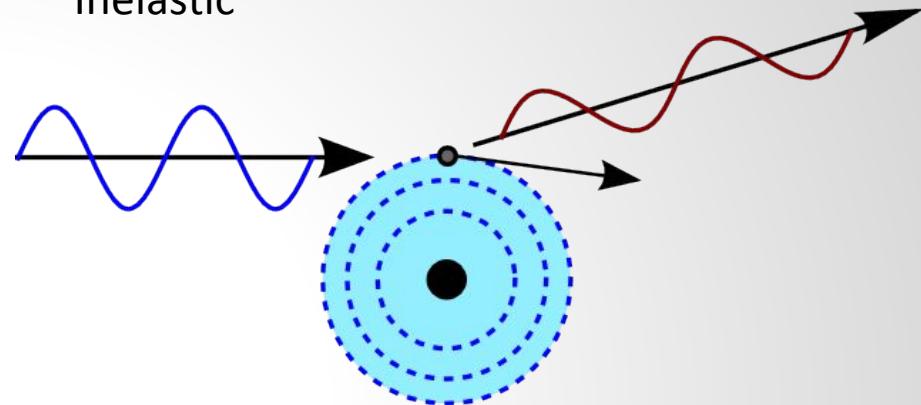
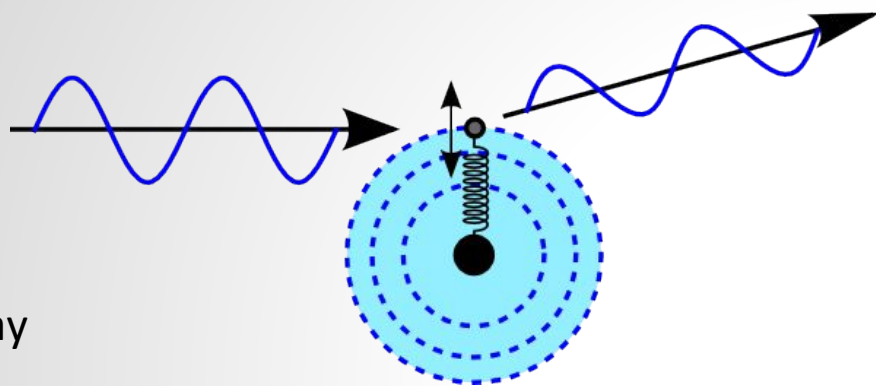
# Electron diffraction basics



# Scattering

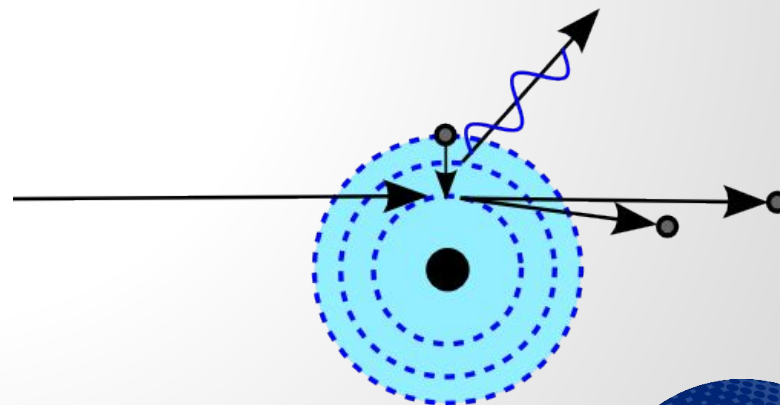
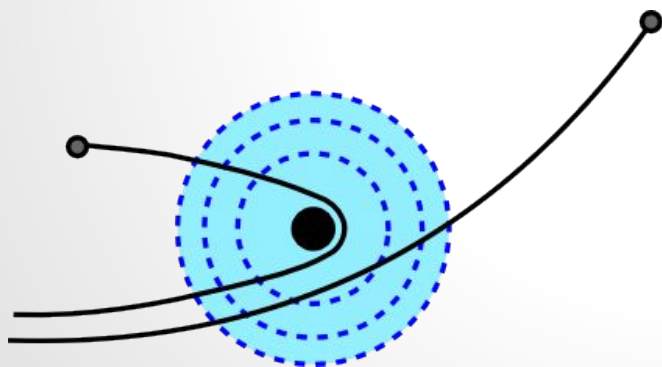
Elastic

Inelastic



X-ray

Electron





# Scattering

X-ray scattering probes electron density

Electron scattering probes electrostatic potential

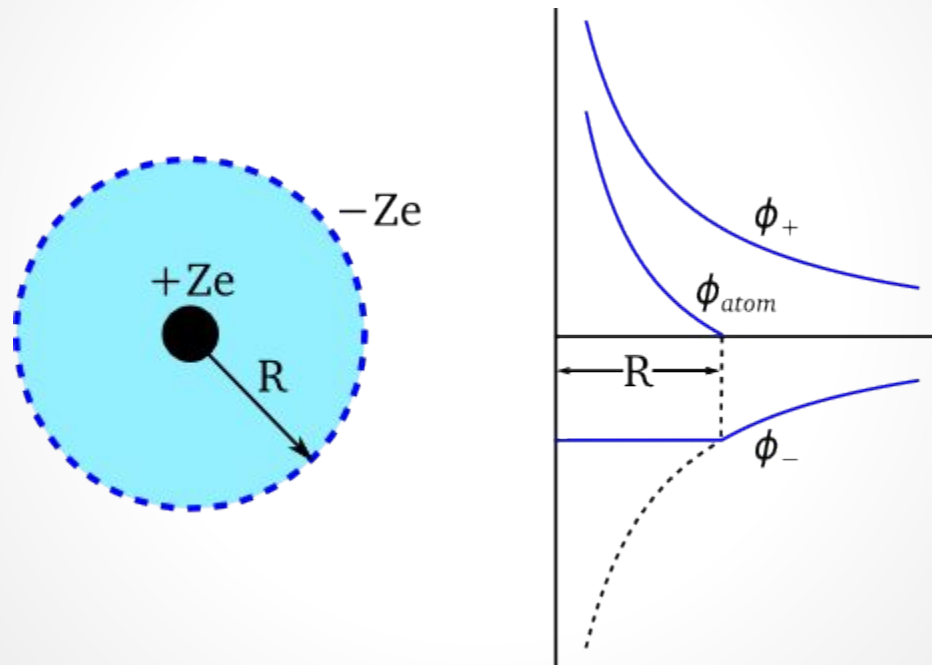
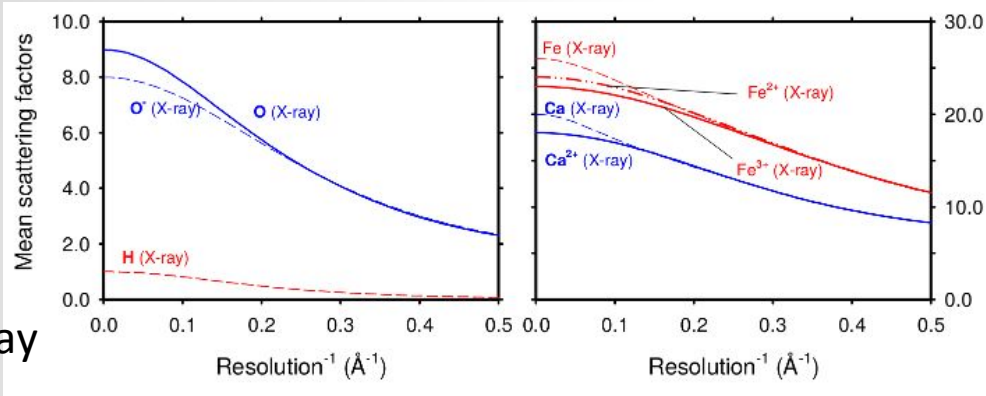


Figure adapted from Vainshtein 1964

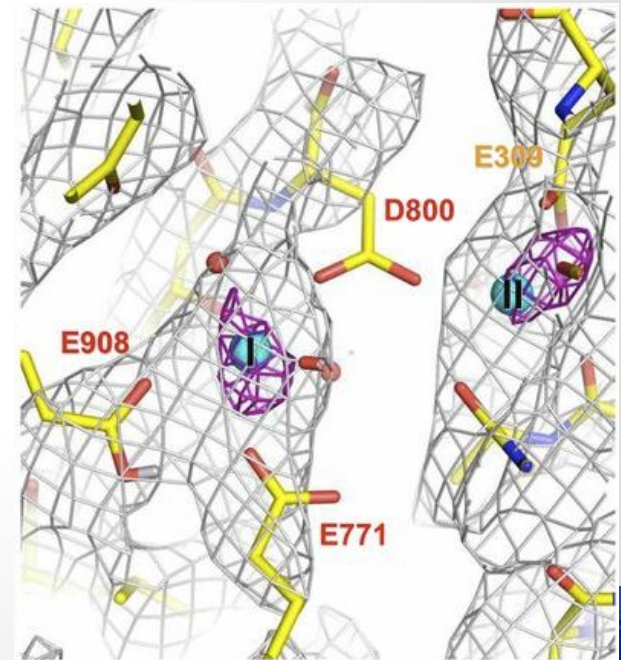
# Charged state

Coulomb potential maps can reveal information about charges  
(Yonekura *et al.* PNAS 2015)

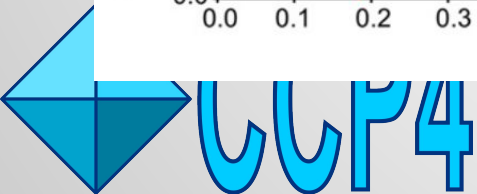
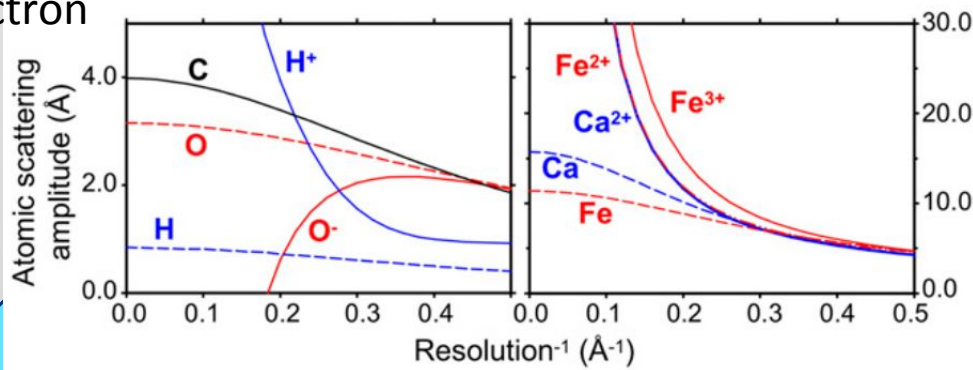


X-ray

**Ca<sup>2+</sup>-ATPase.** When neutral Ca is assumed, difference map shows large positive peaks

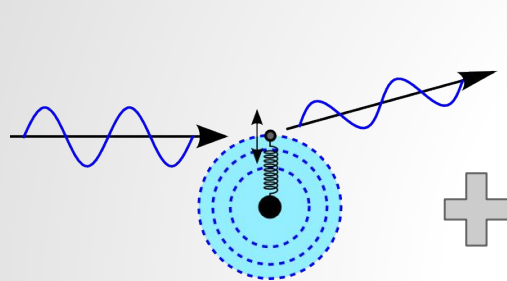


Electron

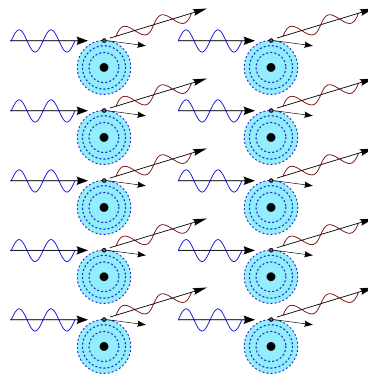


# Radiation damage

Damage accumulates alongside diffraction by the ratio of useful (elastic) to damaging (inelastic) events ([Henderson, Quart. Rev. Biophys. 1995](#))



+



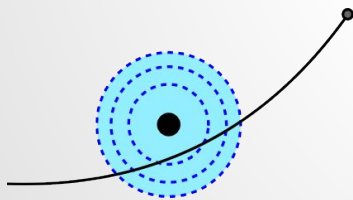
×

8000 eV = **80'000 eV**

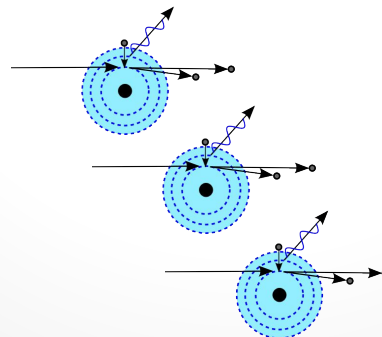
*Enough to 'kill' a unit cell*  
([Sliz et al. Structure 2003](#))

X-ray (1.5 Å)

Electron (200 keV)

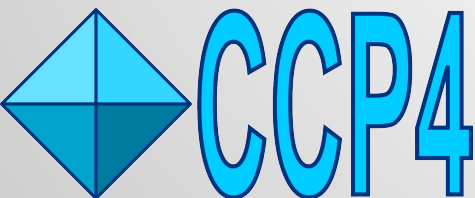


+



×

20 eV = **60 eV**



**Electrons better by >1000 times**



# Crystal size

The radiation damage argument implies that a crystal for electron diffraction can be 1000 times smaller in volume than a crystal for X-ray diffraction

Small crystals or crystal fragments may be better ordered ([de la Cruz 2017](#))

However, it is more complicated...

The strength of interaction implies multiple scattering unless the crystal thickness is much below the mean free path

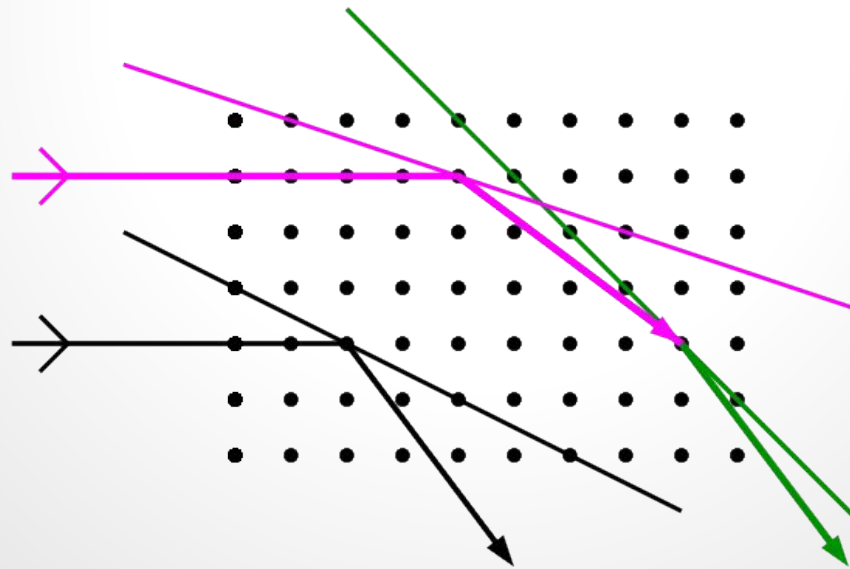


Figure credit: Tim Grüne



# Crystal size

Thin samples are *obligatory*

But not as thin as theory suggests (100 nm @ 200 keV, Subramanian 2015)

For proteins, with continuous rotation, thickness < 400 nm seems to keep dynamic effects acceptably low (Hattne 2015)

Nevertheless, *vanishingly* thin plates may still be best (Yonekura 2015)

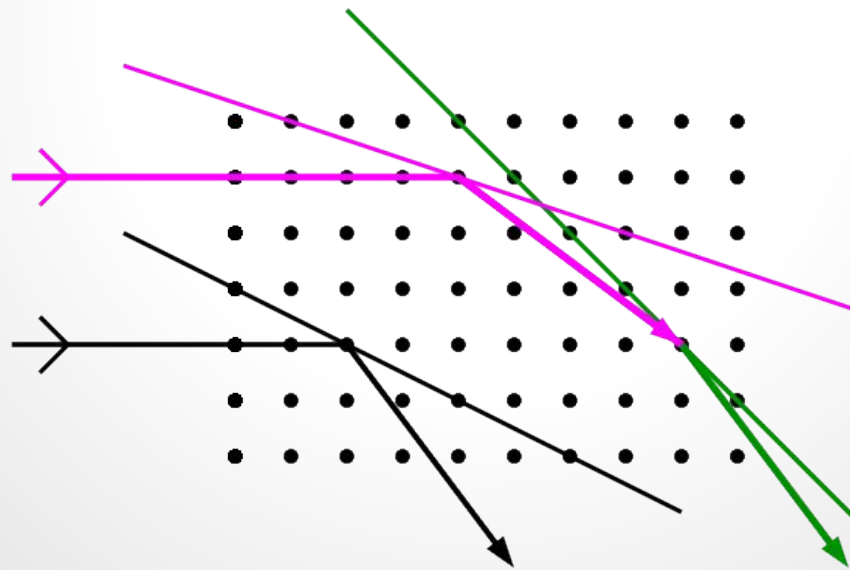
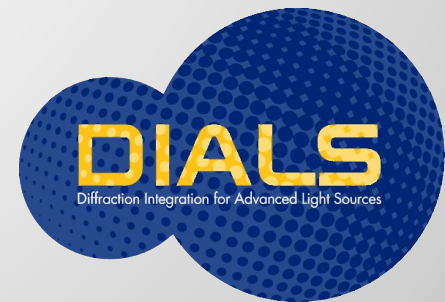
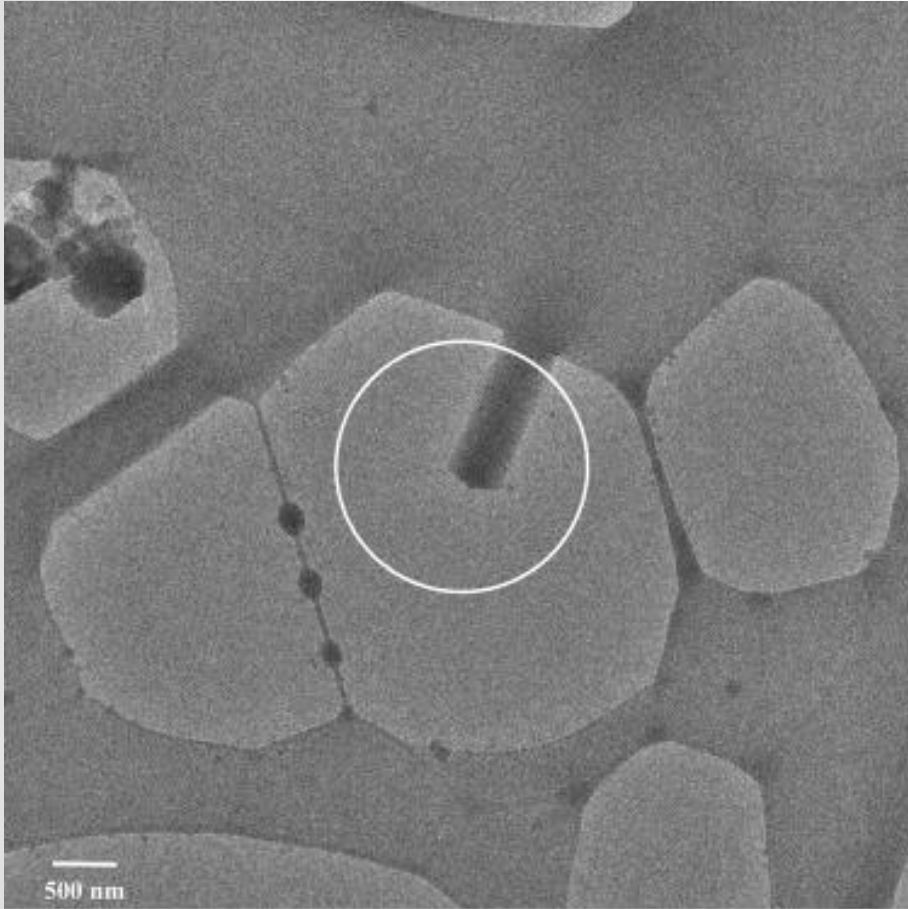


Figure credit: Tim Grüne



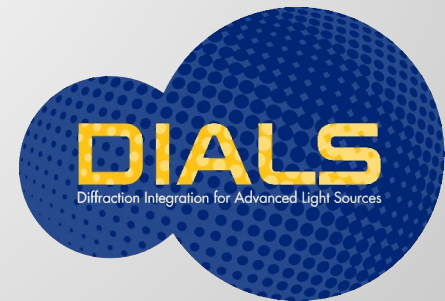
# Crystal size



## Lysozyme nanocrystal

Diffracting volume:  $0.14 \text{ mm}^3$   
( $< 6 \times 10^5$  unit cells)

*Clabbers et al. 2017*



# FIB milling as sample preparation

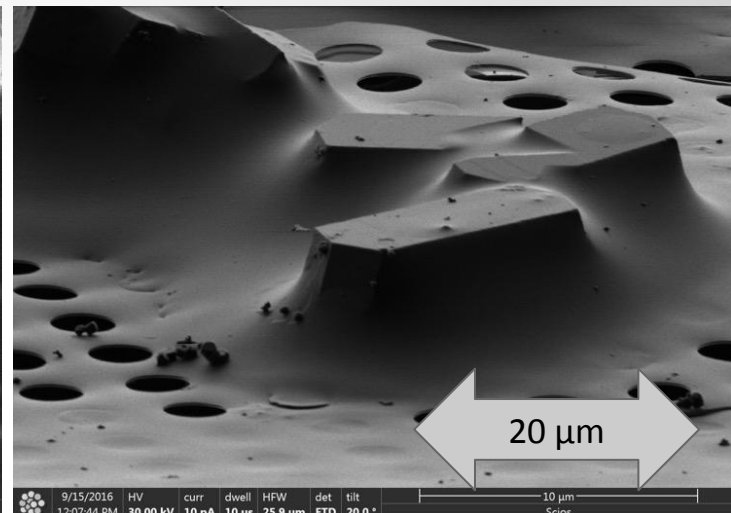
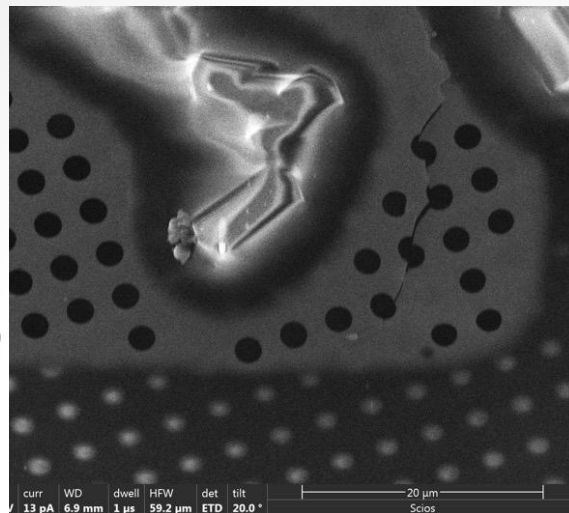
## Image credits:

Emma Beale (DLS)

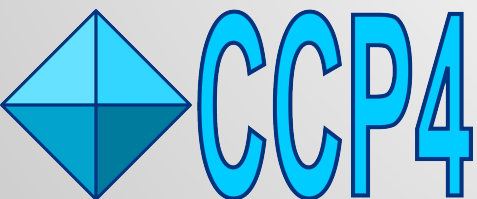
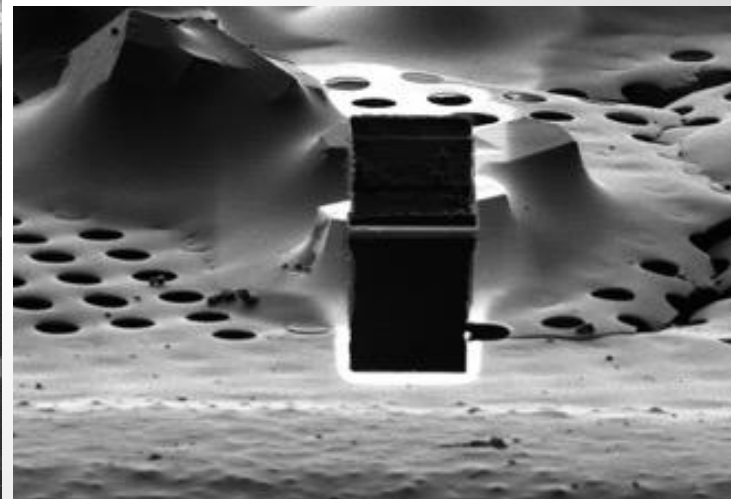
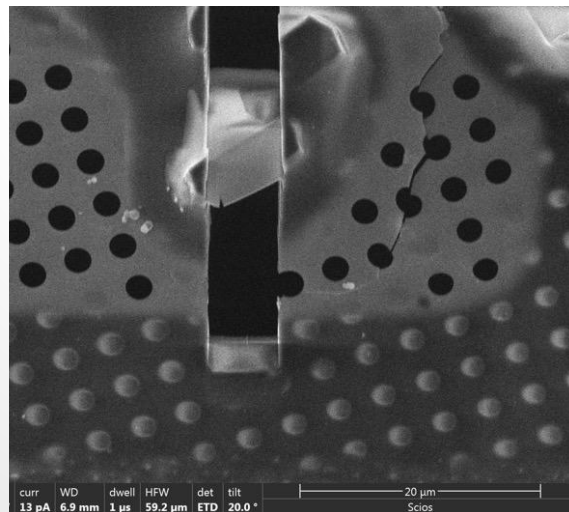
Corey Hecksel (eBIC)

Abhay Kotecha (STRUBI)

Jose Trincao (DLS)

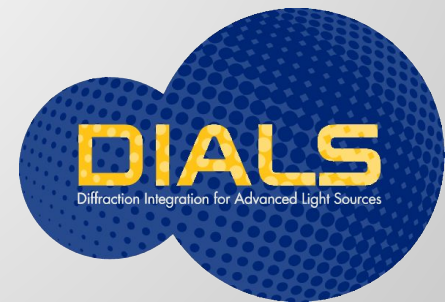


See also Duyvesteyn *et al.*  
PNAS 2018



# Image formats and metadata

*Boring but important*





# EM image formats

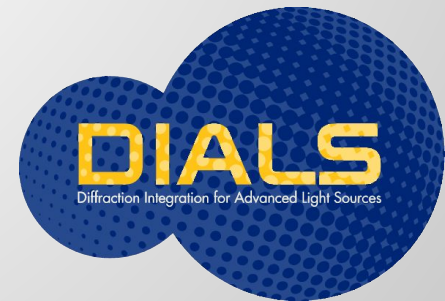
As with MX, various image formats exist, some manufacturer-specific

Independent from MX, except for generic formats (such as TIFF)

Three approaches to get the data into DIALS:

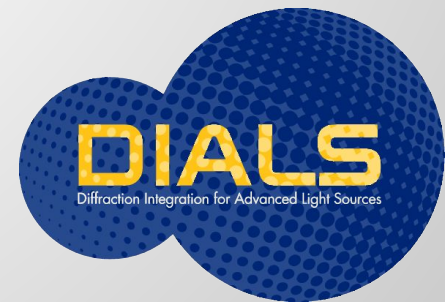
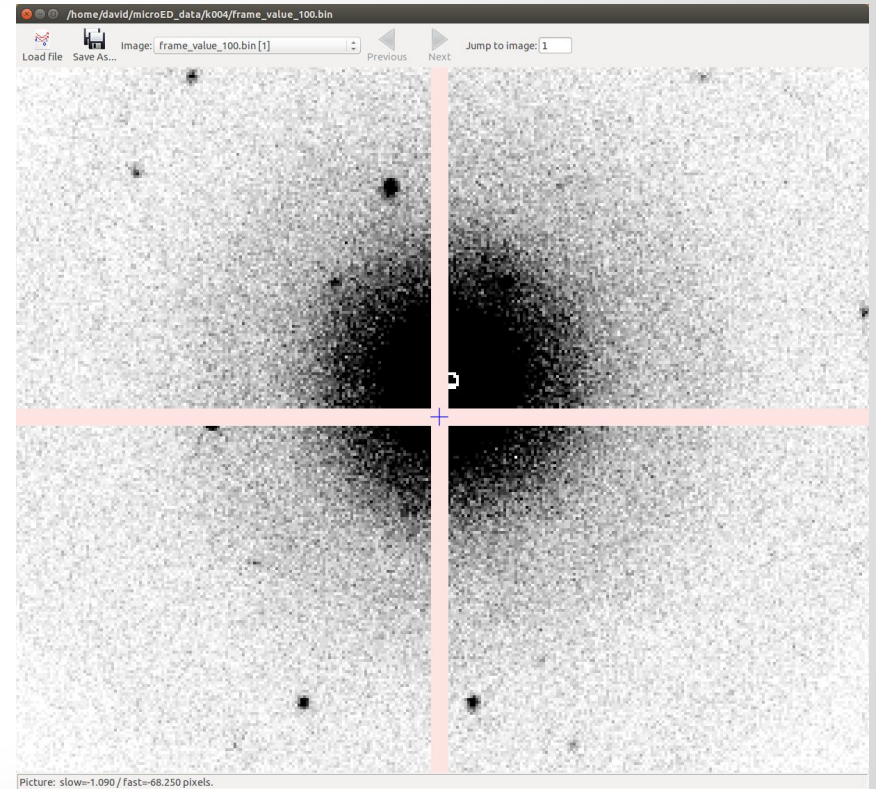
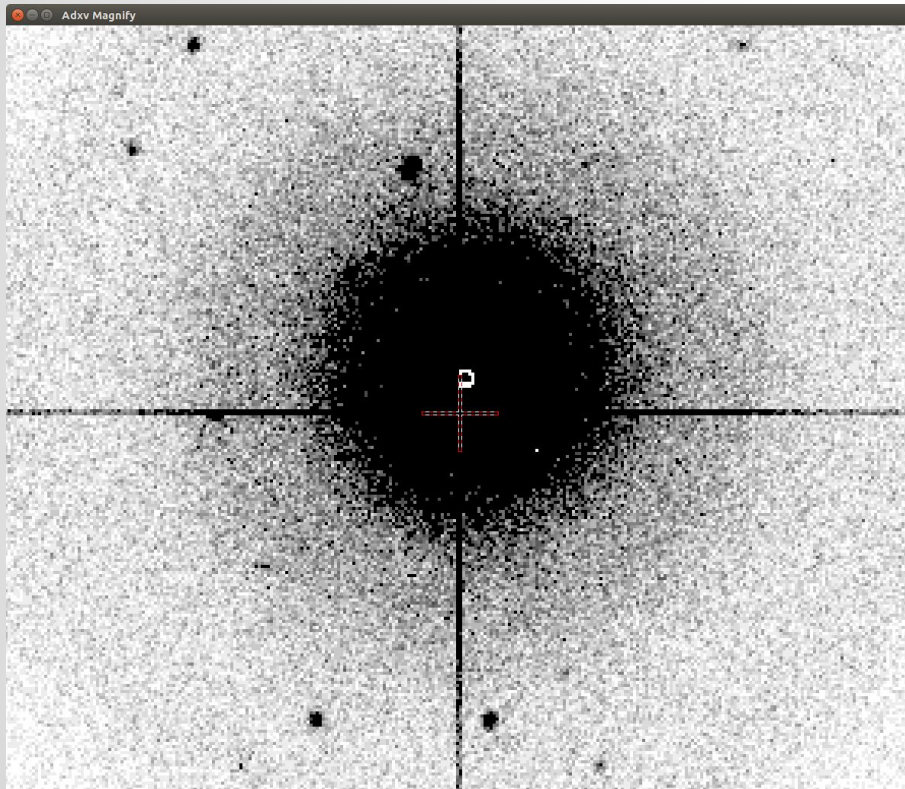
1. *External*: convert to standard MX format (SMV, CBF etc.)
2. *Internal*: write new format reading code to go into dxtbx
3. *Extension*: write new format reading code as a plug-in  
`dxtbx.install_format --user [/path/to/format/class.py] [URL]`

In any case, missing experiment geometry metadata may be a problem



# Extending dxtbx

Plug in a new Format class to recognise new image file formats



# EM image formats

Explicit support for a handful of formats (in distribution or as plug-in), e.g.:

- Timepix quad raw, miniCBF, SMV
- Timepix quad<sup>2</sup> miniCBF
- ThermoFisher Falcon II raw image
- ThermoFisher Falcon III converted to SMV
- ThermoFisher Ceta 16M image stack (.ser format, no metadata)
- ThermoFisher extended header MRC
- Gatan DM4 stack (no metadata)
- Gatan OneView converted to miniCBF
- TVIPS SMV (from tvips2smv)
- DirectElectron DE-64 converted to TIFF

[https://github.com/dials/dxtbx\\_ED\\_formats](https://github.com/dials/dxtbx_ED_formats)

*Could add others, but we don't want to be image format zookeepers*



# Experimental geometry uncertainty

Without careful calibration there may be uncertainty about various things:

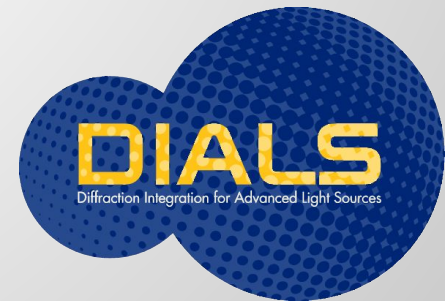
- Beam centre
- Detector (effective) distance
- Detector gain
- Multi-panel metrology
- Rotation axis handedness
- Rotation axis orientation

Relatively poor sample stages for rotation adds additional error:

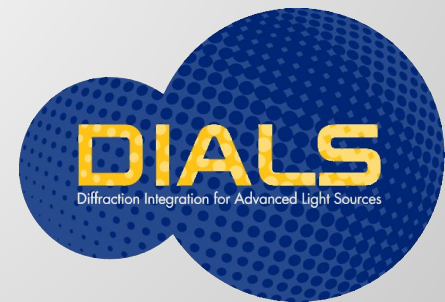
- $\Delta\phi$  / image

In addition, lenses mean questions about:

- Obliquity (parallax)
- Diffraction pattern distortion



# Diffraction geometry





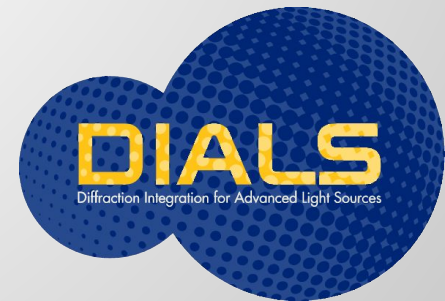
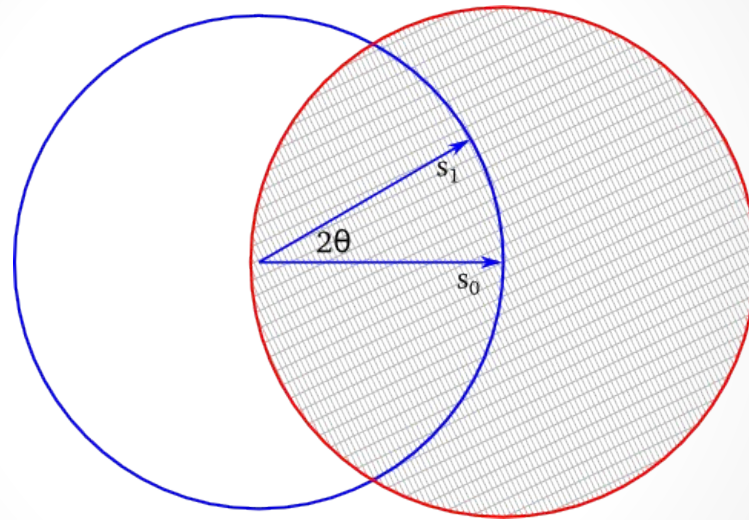
# Ewald construction

## X-ray diffraction

Photon energy 12 keV ( $\lambda = 1.03 \text{ \AA}$ )

Scattering vector at  $2 \text{ \AA}$

$2\theta = 29.9^\circ$



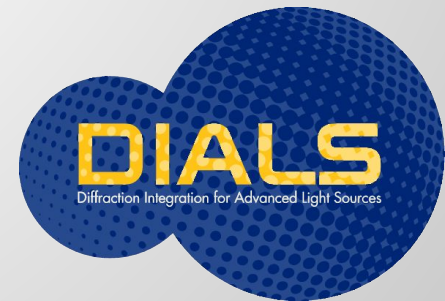
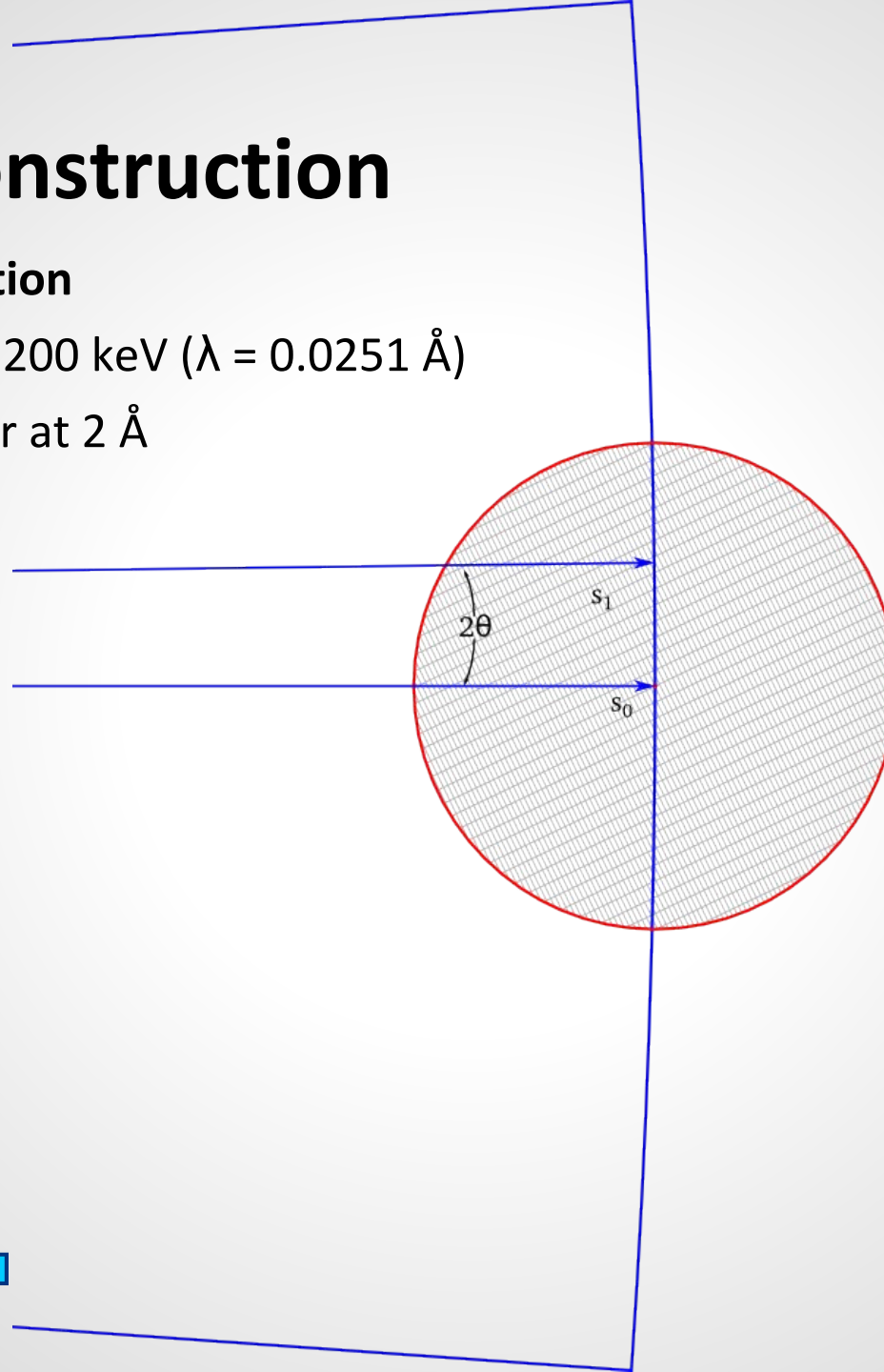
# Ewald construction

## Electron diffraction

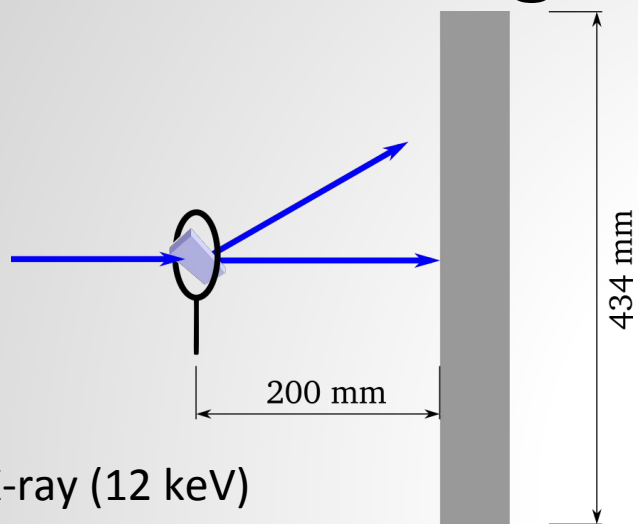
Electron energy 200 keV ( $\lambda = 0.0251 \text{ \AA}$ )

Scattering vector at  $2 \text{ \AA}$

$$2\theta = 0.72^\circ$$



# Diffraction geometry

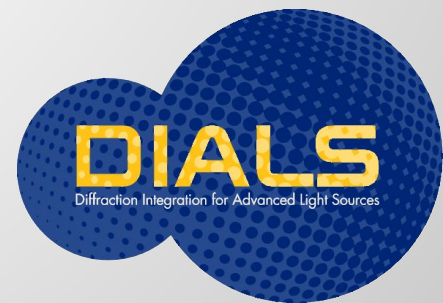
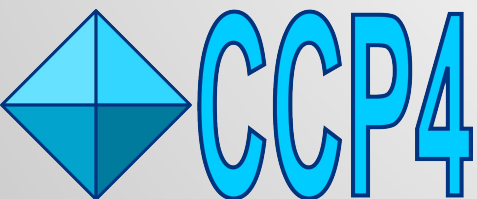
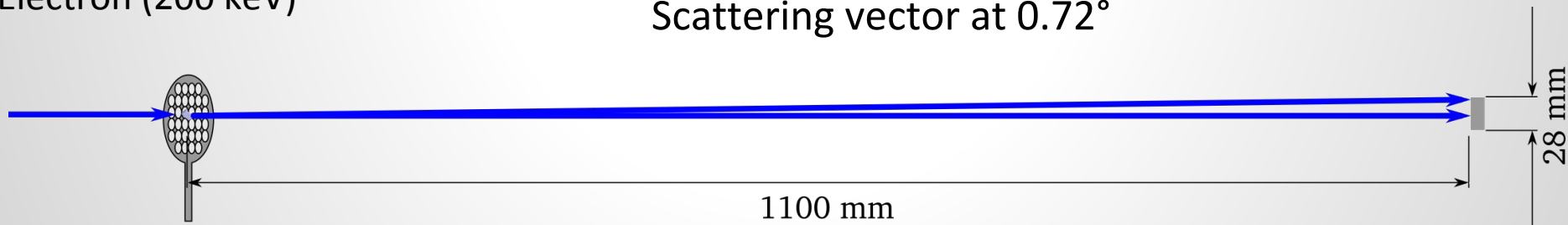


Typical MX geometry, Pilatus 6M detector  
Scattering vector at  $29.9^\circ$

X-ray (12 keV)

Real ED example, Timepix quad  
Scattering vector at  $0.72^\circ$

Electron (200 keV)



# Diffraction geometry

Real detector distance actually fixed

Beam paths are complex, through lens system

We ignore this and use the *effective* detector distance

Might also ignore parallax? Depends on detector technology

But not image distortion, if present

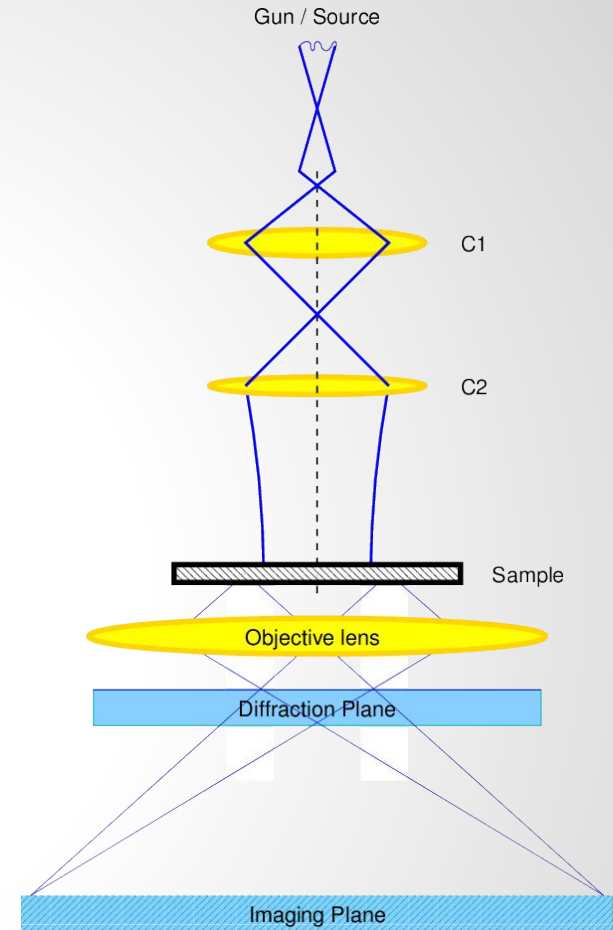
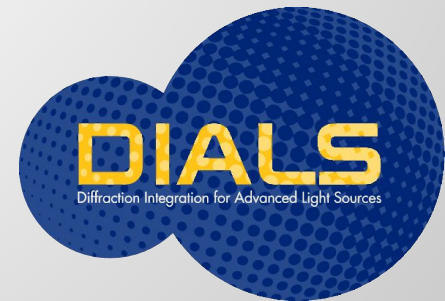
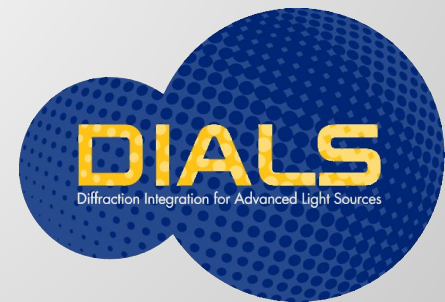


Figure credit: Tim Grüne



# Challenges

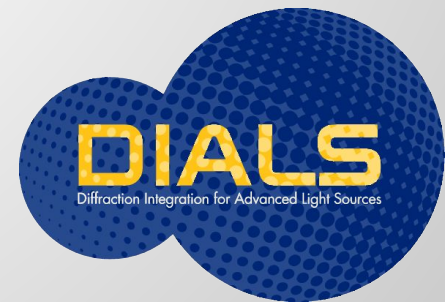




# Challenges

Almost flat Ewald sphere, high detector distance and low diffraction angle

- Lens distortions may introduce systematic error in observed positions
- Indexing from a single image is challenging
- It may even be difficult to determine the direction of rotation
- Joint refinement of detector and unit cell may not be possible
- Refined detector and unit cell parameters may be poor
- The beam centre may drift



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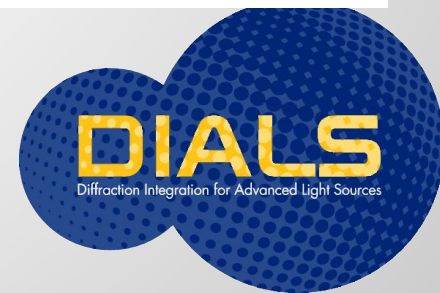
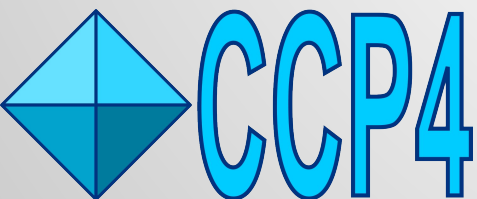
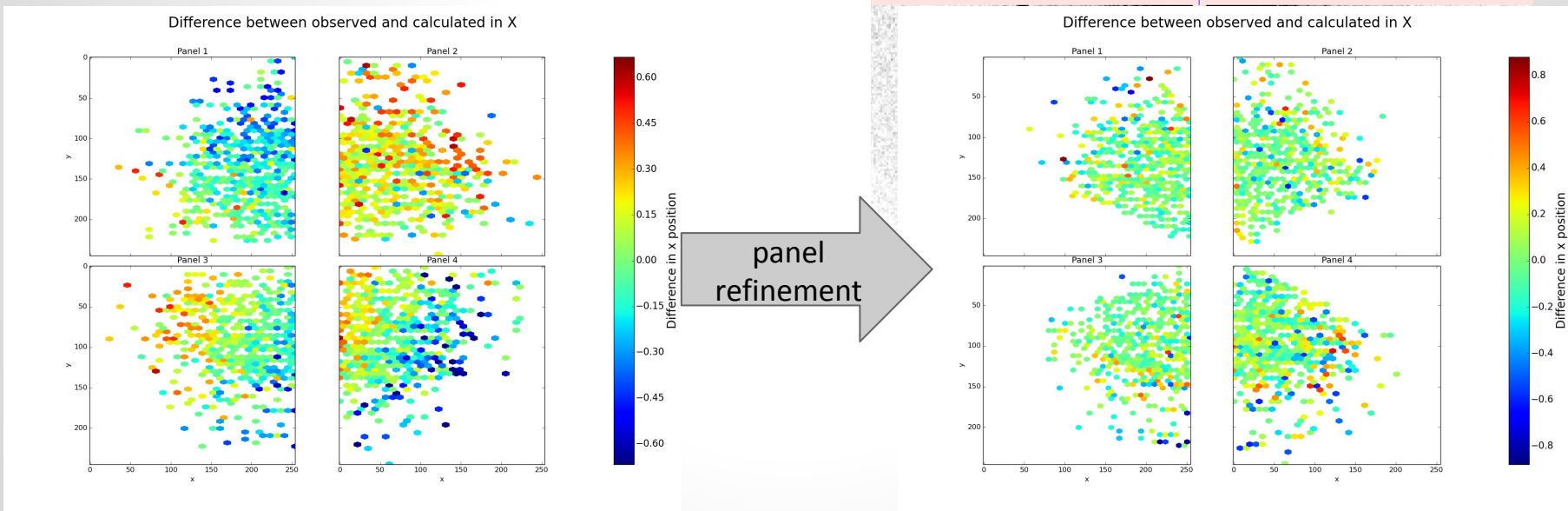
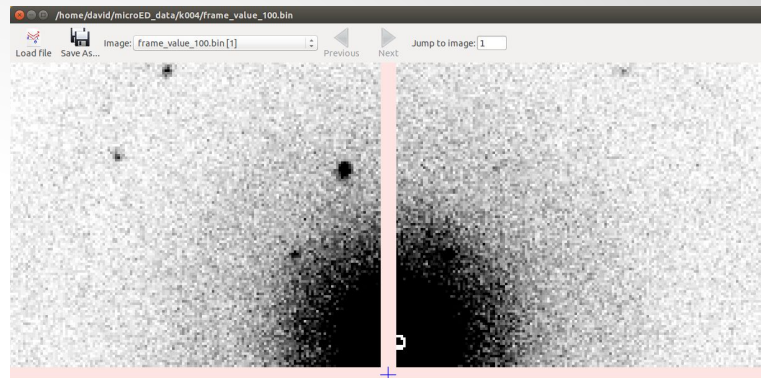


# Lens distortions

Pentasil zeolite, 64° tilt, 200 keV

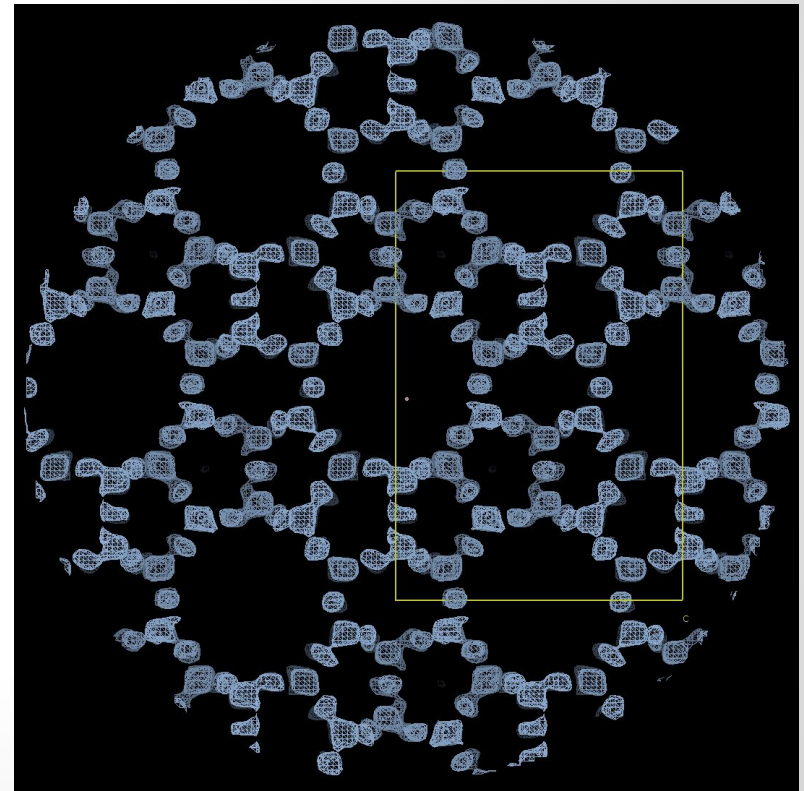
Timepix direct electron detector as a 4 panel quad

Some image distortion evident



That gross 'fix' was sufficient to integrate this dataset with DIALS  
Scaled with AIMLESS, structure solved *ab initio* by SHELXT  
Refinement with SHELXL using electron scattering factors  
Poor statistics typical for e- diffraction data, but maps are reasonable

Space group	Pnma
Cell dim (Å)	20.09, 19.96, 13.51
Resolution (Å)	14.16 - 0.70 [14.16 - 3.83] (0.71 - 0.70)
Rmerge (%)	21.9 [11.6] (53.4)
Rmeas (%)	26.0 [15.5] (64.0)
I/ $\sigma$	1.90 [4.3] (0.8)
CC $\frac{1}{2}$	0.98 [0.97] (0.92)
Completeness (%)	70.7 [60.1] (70.4)
R1 (%)	20.7
wR2 (%)	48.7





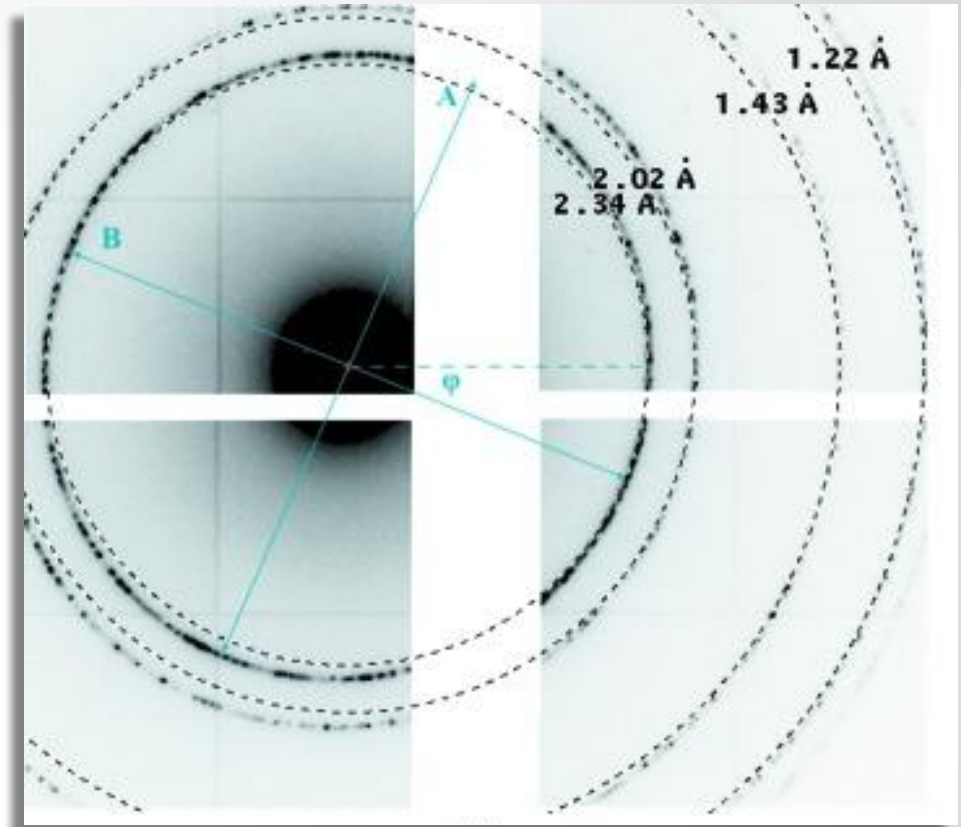
# Elliptical distortion

A more general solution is to use pixel-wise distortion tables

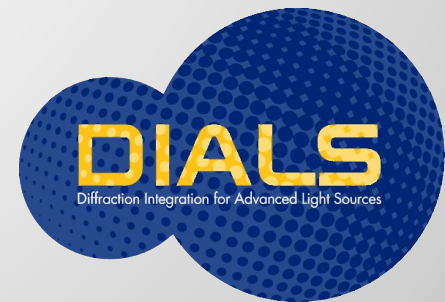
Determine parameters from e.g. Al powder diffraction standard

Potentially refine parameters from diffraction data?

***Best approach:*** avoid distortion in the first place



Clabbers *et al.* 2017

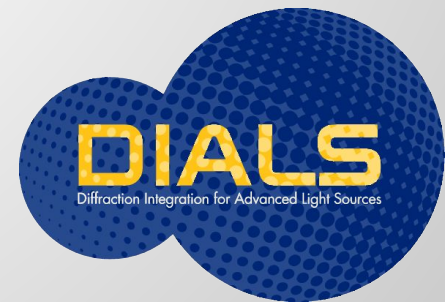




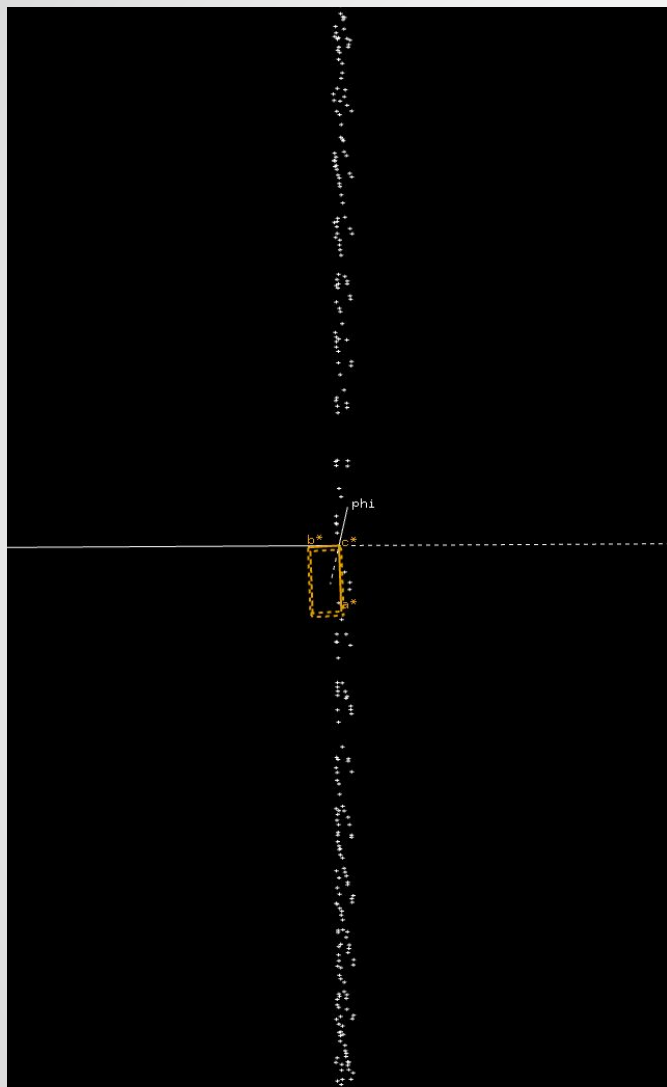
# Challenges

Almost flat Ewald sphere, high detector distance and low diffraction angle

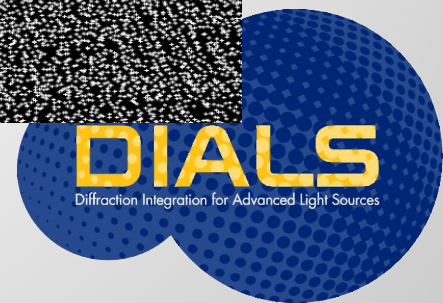
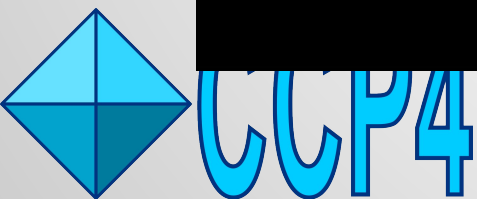
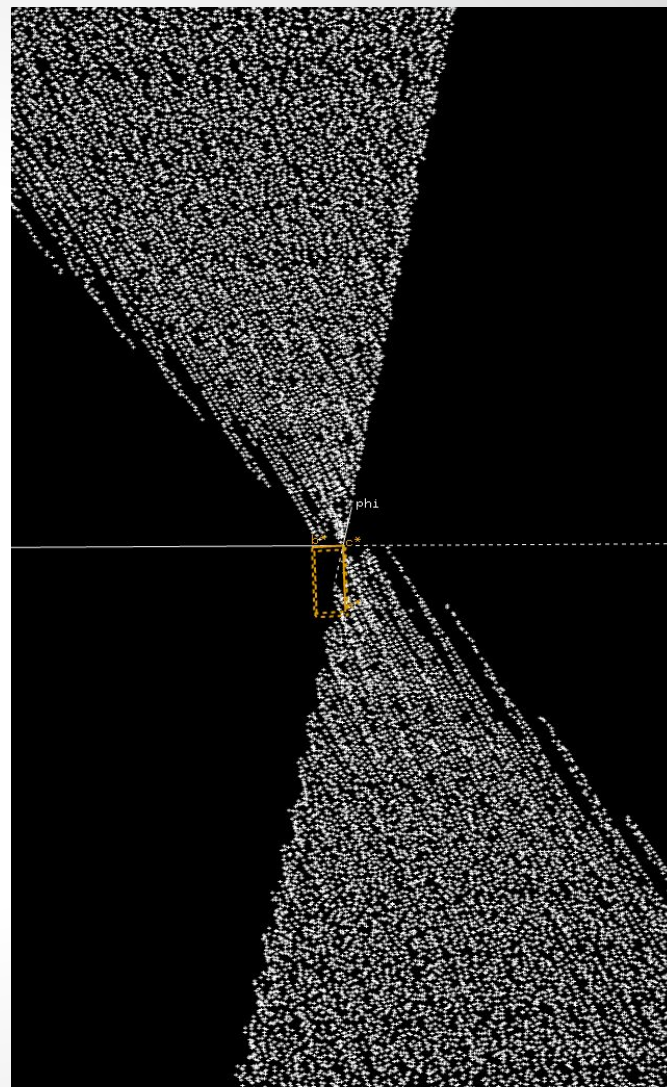
- Lens distortions may introduce systematic error in observed positions
- Indexing from a single image is challenging
- It may even be difficult to determine the direction of rotation
- Joint refinement of detector and unit cell may not be possible
- Refined detector and unit cell parameters may be poor
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single image



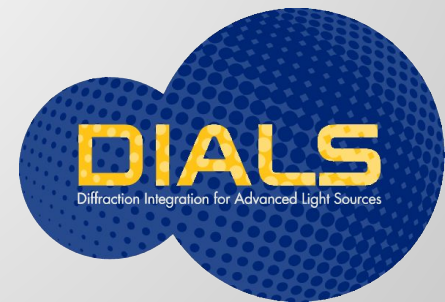
56° wedge



# Challenges

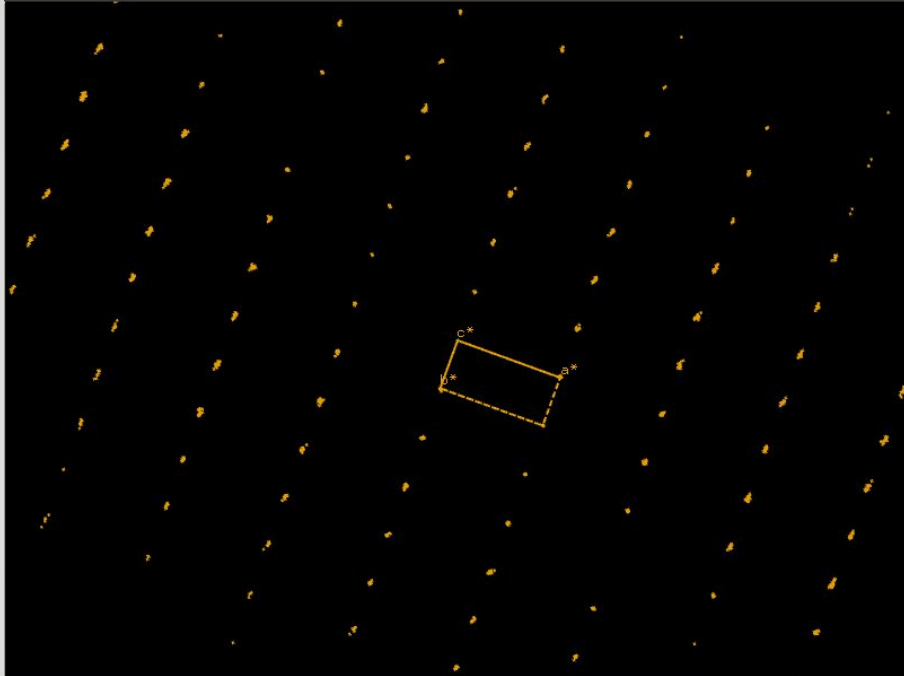
Almost flat Ewald sphere, high detector distance and low diffraction angle

- Lens distortions may introduce systematic error in observed positions
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- **It may even be difficult to determine the direction of rotation**
- Joint refinement of detector and unit cell may not be possible
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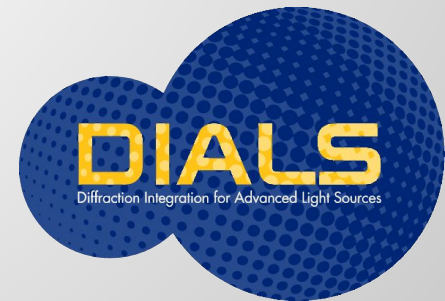


# MX geometry

right rotation axis



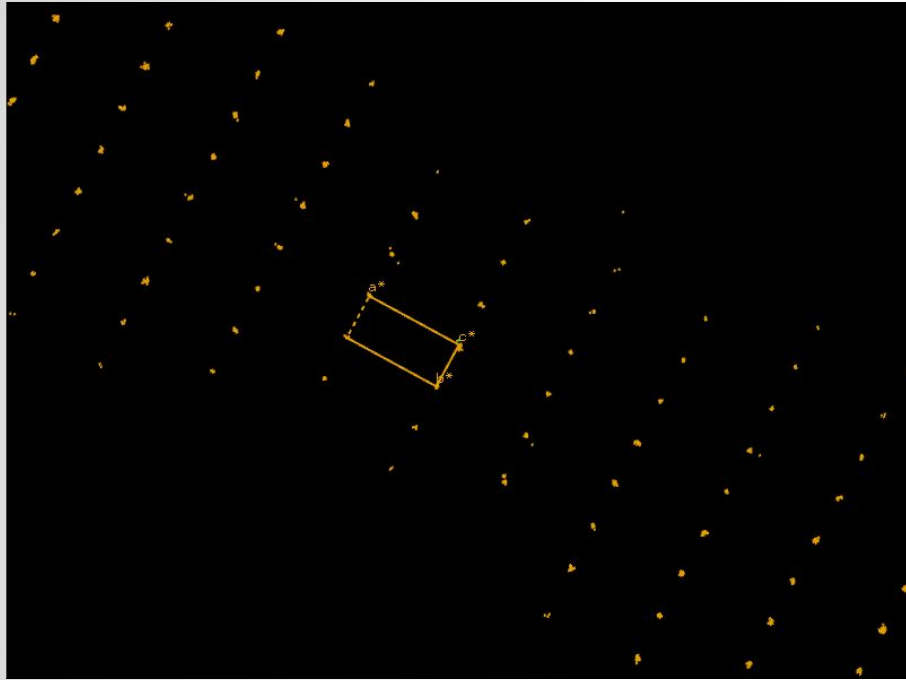
inverted rotation axis



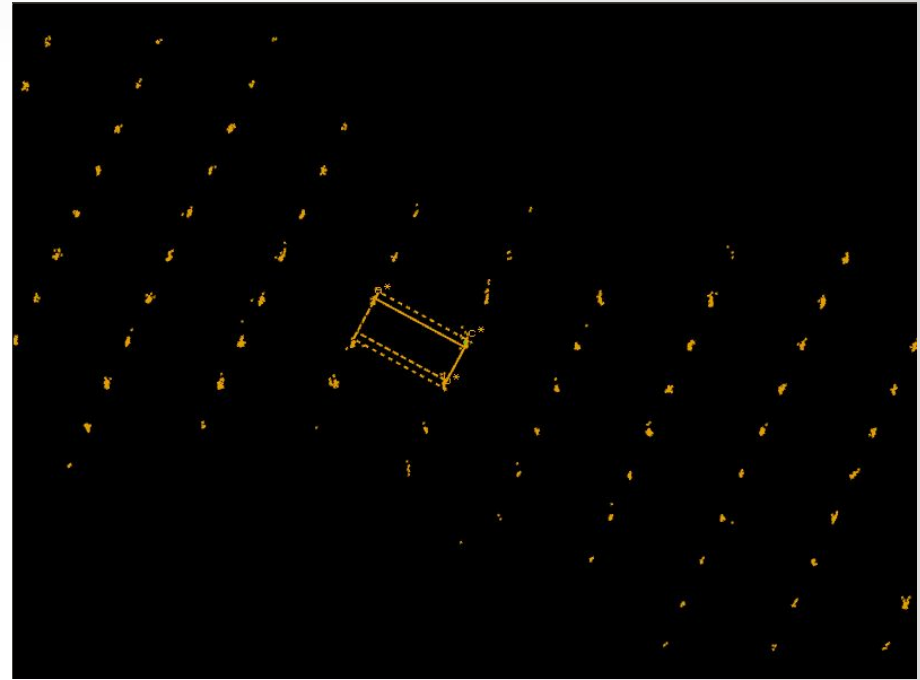


# ED geometry

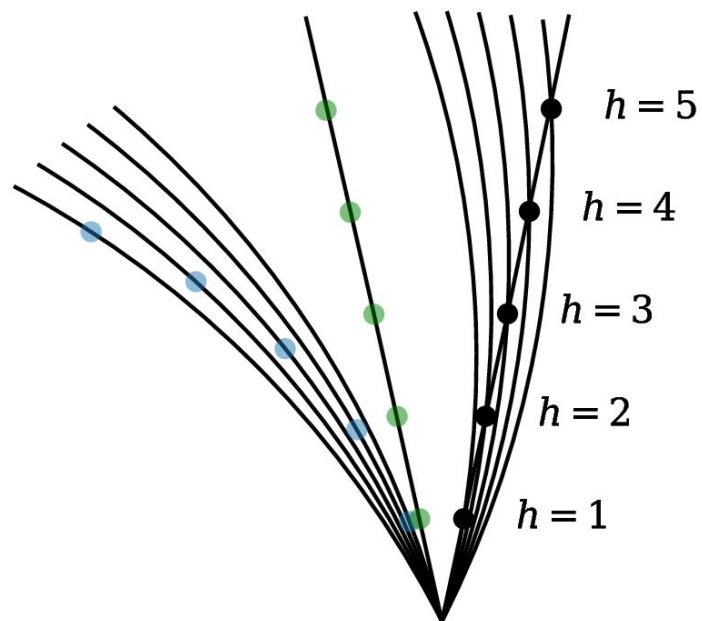
right rotation axis



inverted rotation axis



- correct rotation
- inverse rotation, ED
- inverse rotation, MX

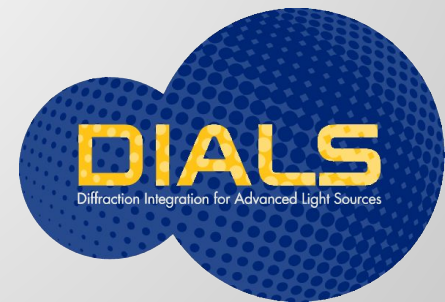


Clabbers *et al.* 2018

# Challenges

Almost flat Ewald sphere, high detector distance and low diffraction angle

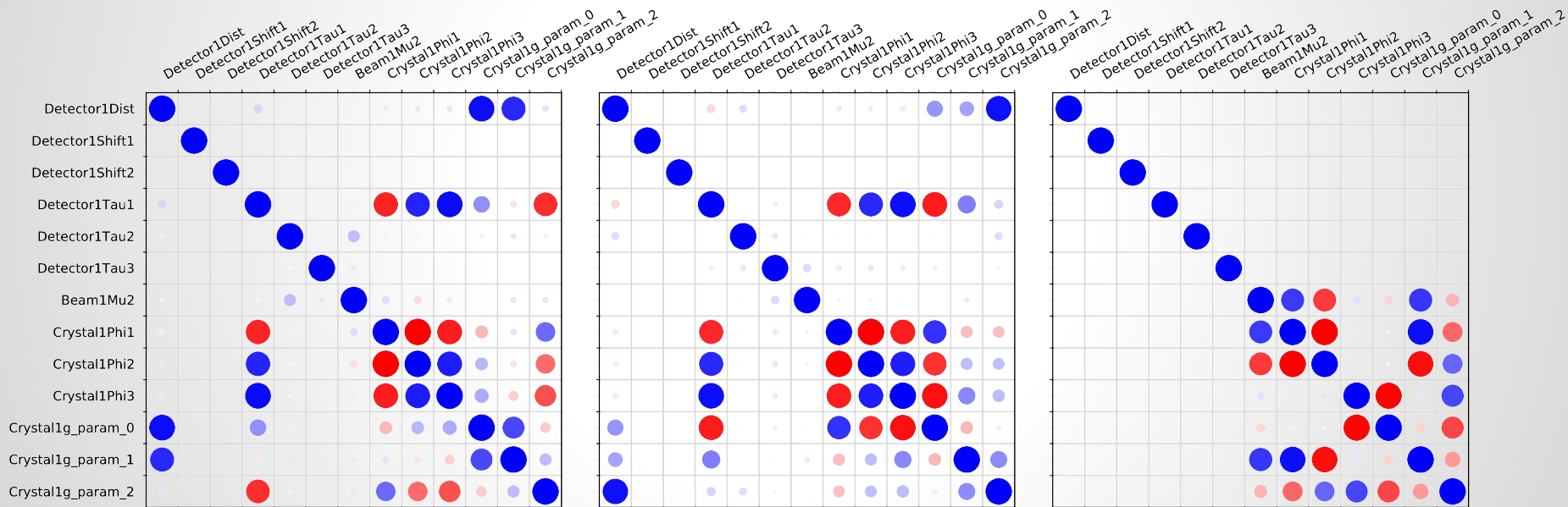
- Lens distortions may introduce systematic error in observed positions
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# Diagnostics for problematic refinement

DIALS provides diagnostics using the Jacobian from non-linear least squares refinement of the diffraction geometry

## 1. corrgrams Simulated data, MX geometry (12 keV, 200 mm distance)



X residuals

Y residuals

$\phi$  residuals

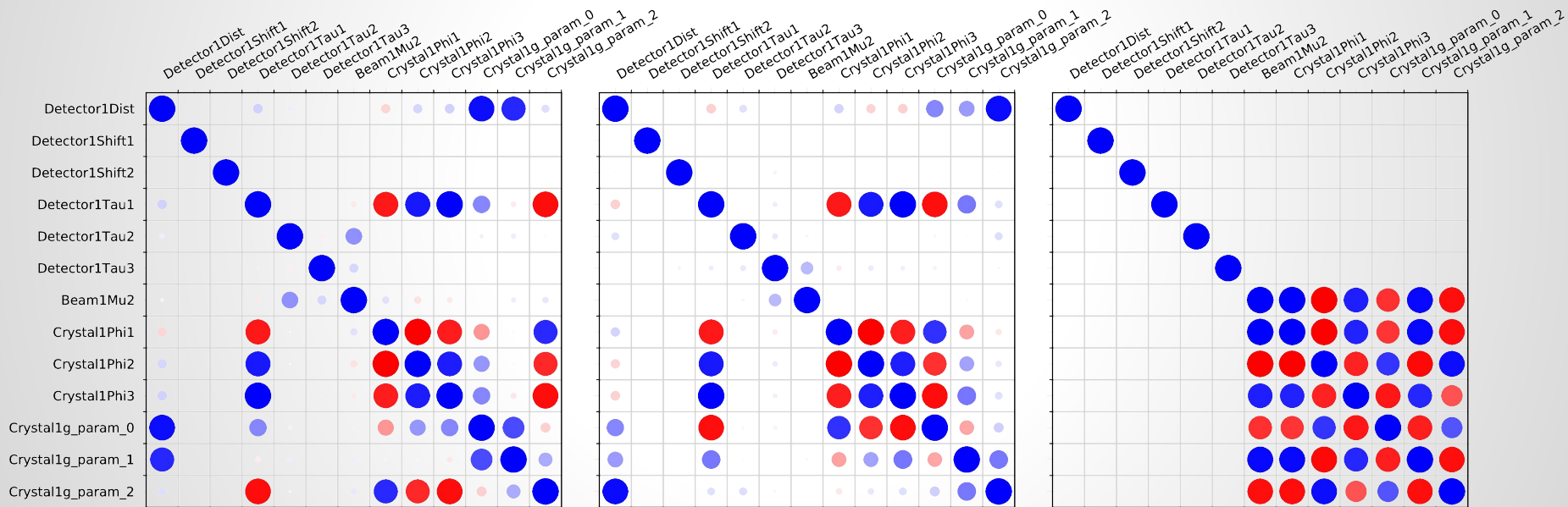




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DIALS provides diagnostics using the Jacobian from non-linear least squares refinement of the diffraction geometry

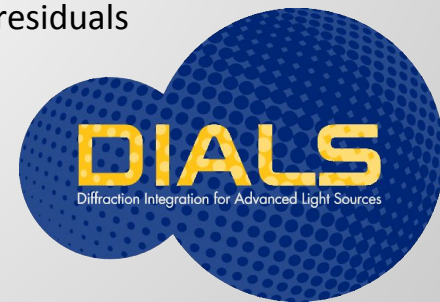
## 1. corrgrams Simulated data, ED geometry (200 keV, 1570 mm distance)



X residuals

Y residuals

$\phi$  residuals



# Diagnostics for problematic refinement

DIALS provides diagnostics using the Jacobian from non-linear least squares refinement of the diffraction geometry

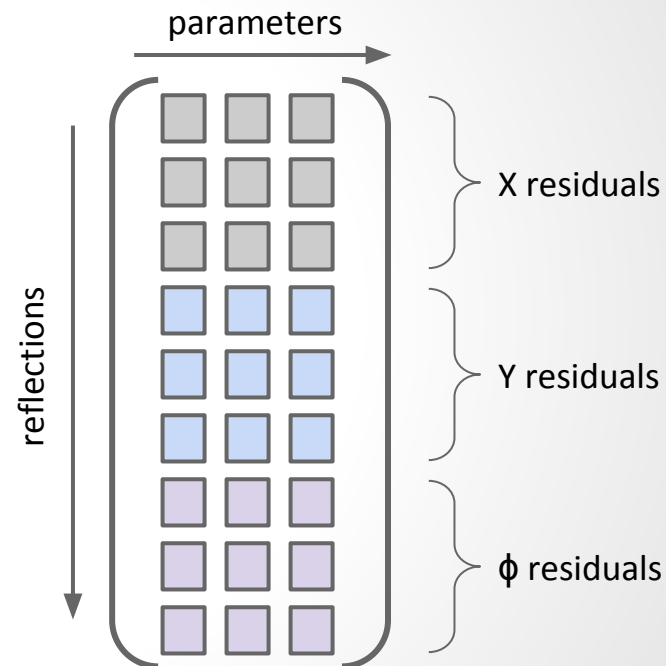
## 2. condition number

Linearised step:  $\mathbf{J} \Delta \mathbf{p} = \Delta \mathbf{r}$

For the simulated examples shown:

$$\text{cond}(\mathbf{J}_{MX}) \approx 2 \times 10^3$$

$$\text{cond}(\mathbf{J}_{ED}) \approx 5 \times 10^5$$



# Stabilising refinement

General rule: stabilise refinement by constraints (fix) or restraints

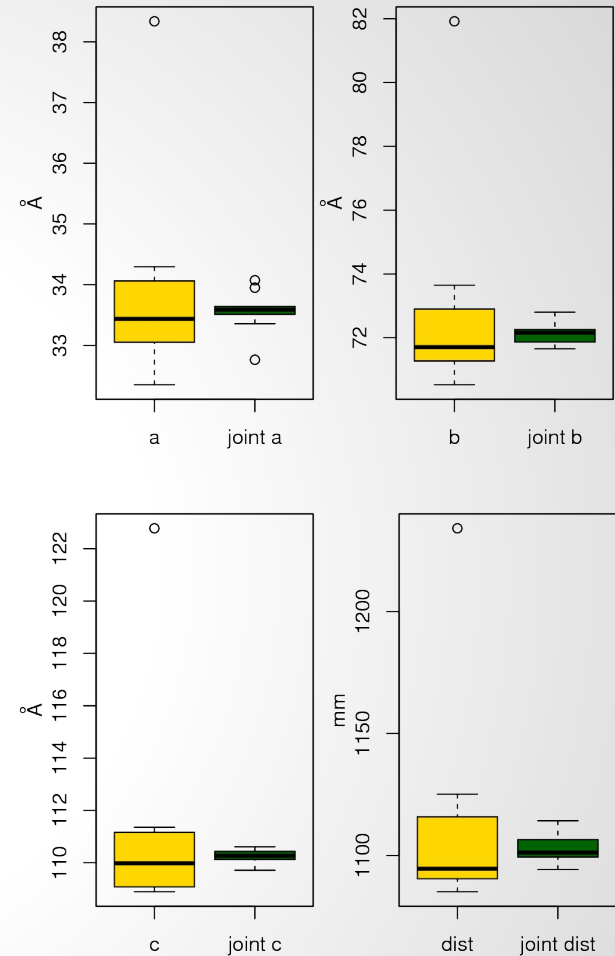
Diagnostics help to identify problematic parameters

Flat Ewald sphere → extremely high correlation between cell and detector distance

**Best case scenario:** effective distance is well-calibrated, so fix it

Other unstable parameters: detector 'tilt' and 'twist' rotations, and beam orientation

Restrain unit cell to a target, or group average in joint refinement



# Challenges

Almost flat Ewald sphere, high detector distance and low diffraction angle

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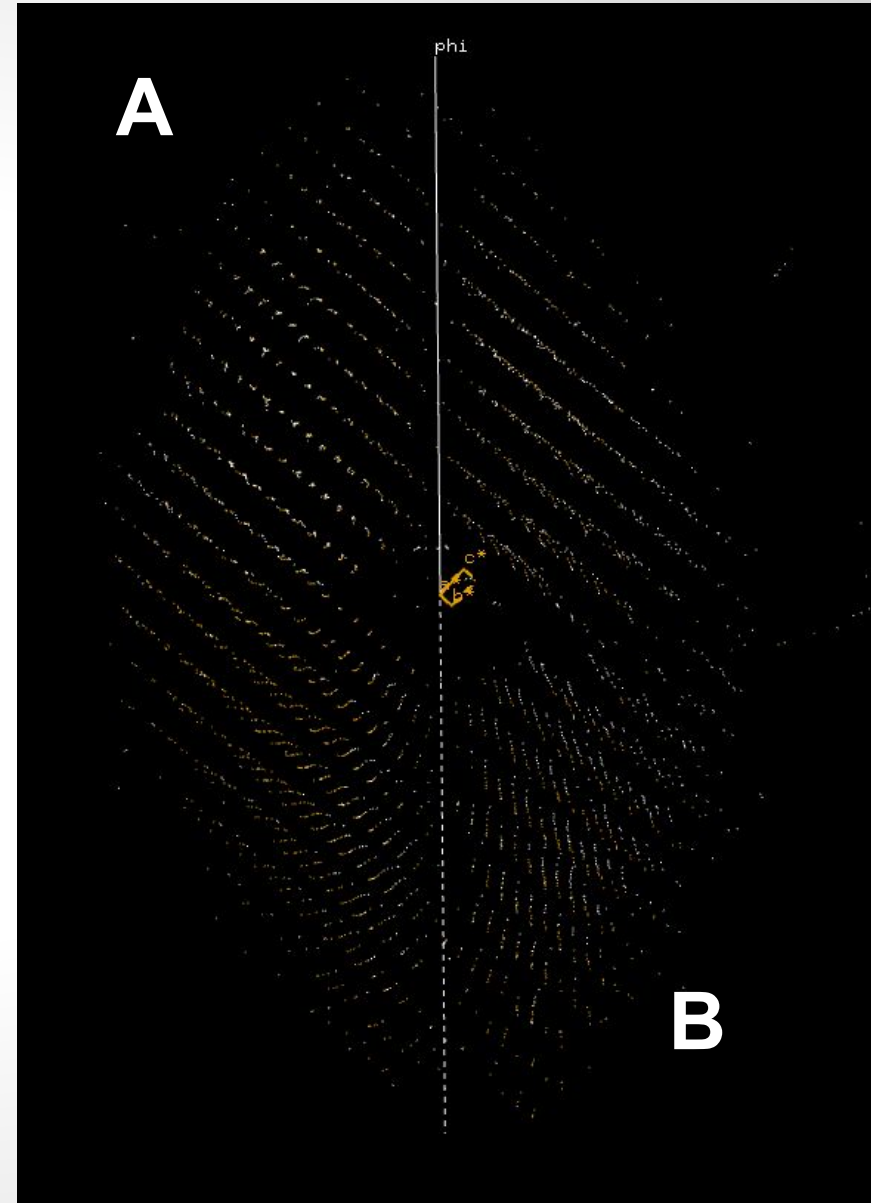
# Beam drift

Example: FIB-milled lysozyme still tilt series from eBIC

Beam direction drift during the data collection causes severe distortion

Nevertheless, spots can be indexed by `dev.dials.creep_index`

The reciprocal lattice view is aligned along planes in the region marked **A**, however in other regions, such as **B**, the observations do not map to parallel planes.

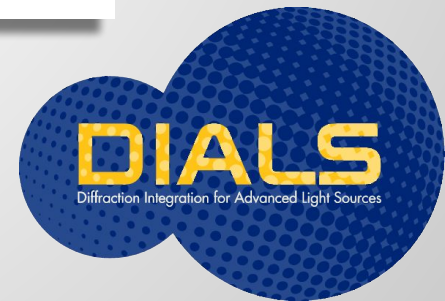
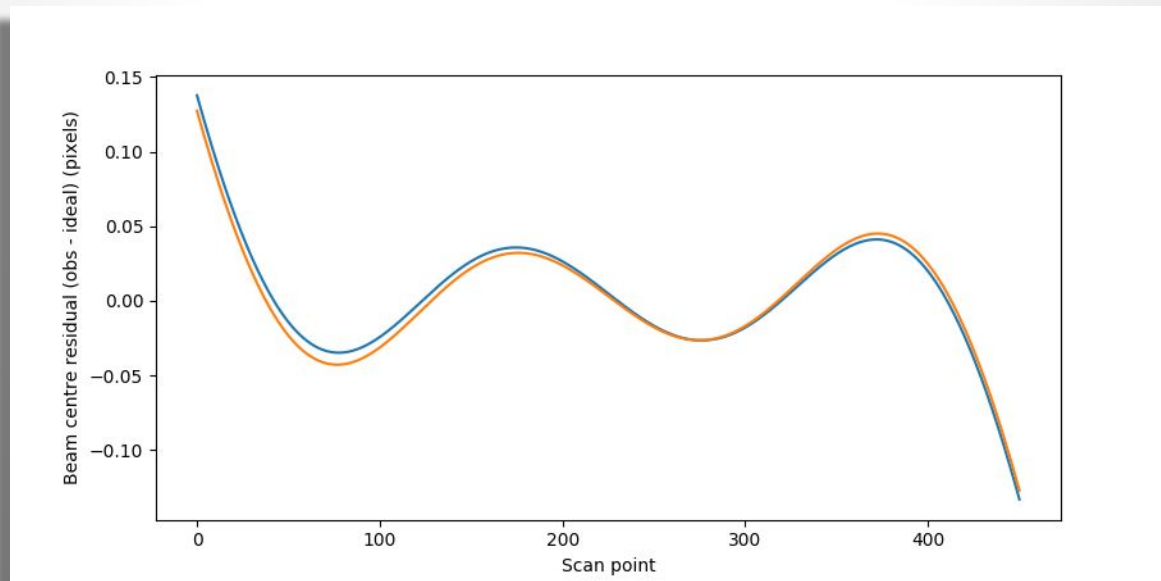


# Beam drift

Less severe beam drift seems common even with continuous rotation

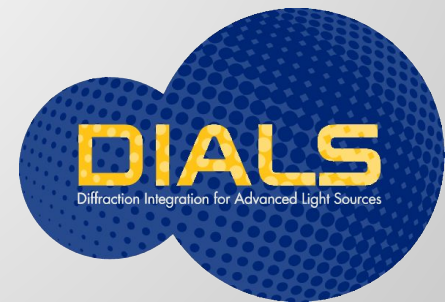
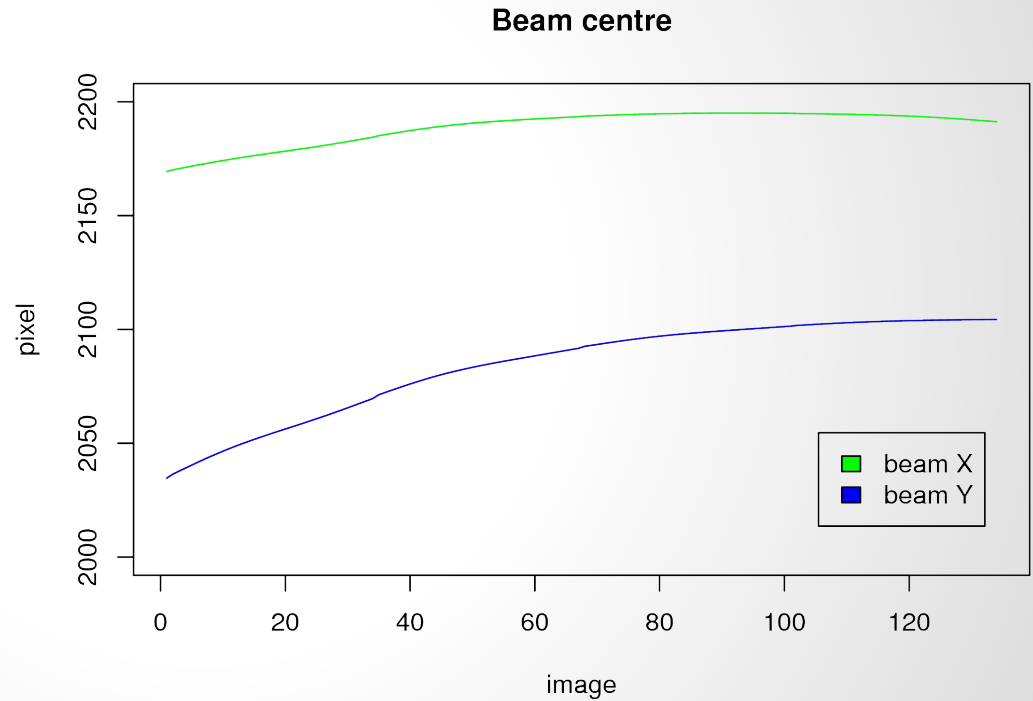
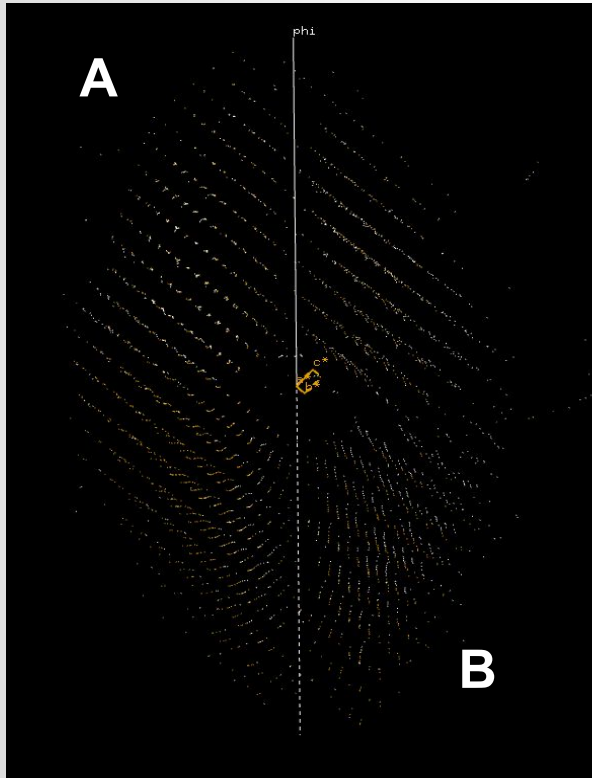
In order to process Max Clabbers' lysozyme nanocrystal data we added Gaussian-smoother scan-varying beam refinement to DIALS

Tested using simulated images created with simTBX



# Beam drift

Can track the beam drift of the lamella tilt series: about 70 pixels in Y!



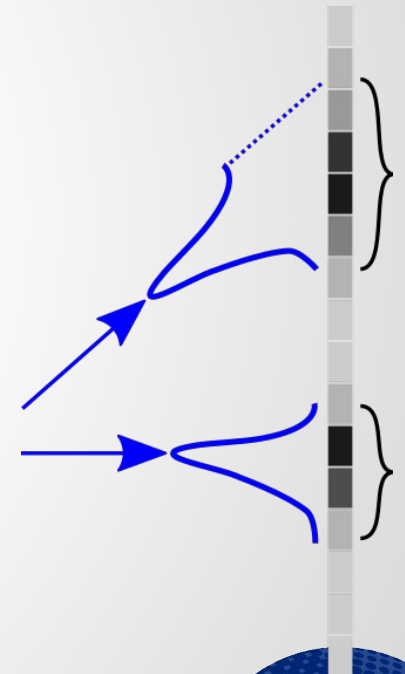
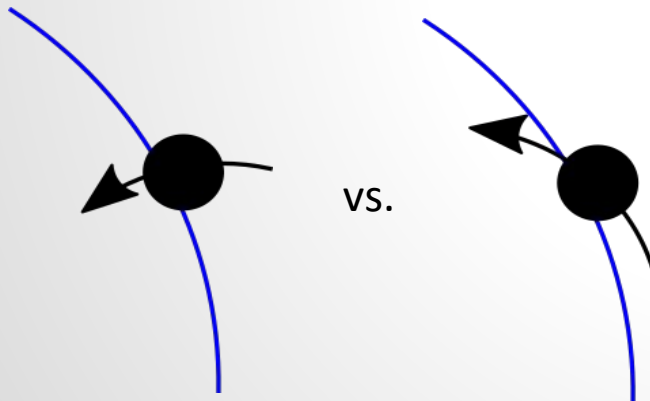
# Integration

Most programs perform empirical profile modelling using local strong spots.

**DIALS** makes 3D profile models, like **XDS**.

The 3D method takes advantage of the Kabsch transform.

- **geometry**
- crystal mosaicity
- crystal shape
- crystal size
- beam size
- beam divergence
- beam spectral dispersion
- **obliquity**
- detector point spread





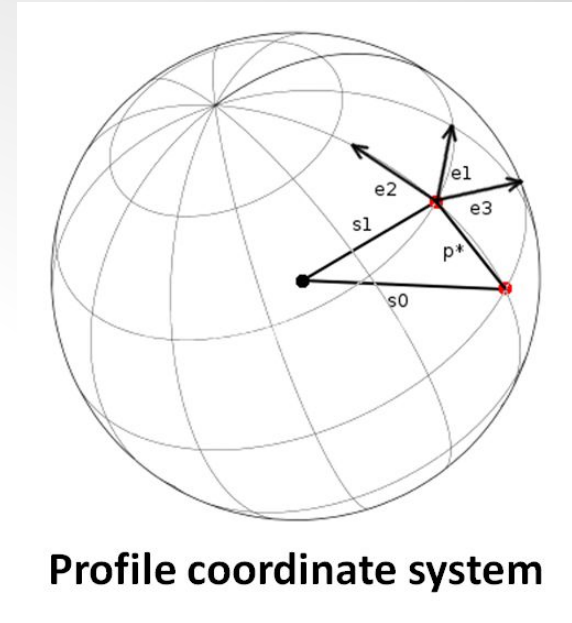
# Integration

## Kabsch's transform:

Spot shape is distorted by:

1. obliquity of rays on the detector
2. obliquity of the relp's passage through the Ewald sphere

1. is handled by mapping pixel values onto the Ewald sphere.
2. is handled by choosing a non-orthogonal third dimension along the relp's actual direction of travel.



**Profile coordinate system**

Use the Kabsch model of a normal distribution on the surface of the Ewald sphere

2 parameters:

$\sigma_D$  - roughly "beam divergence"

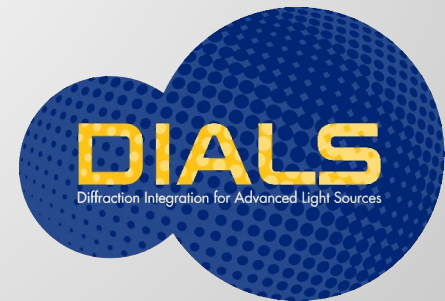
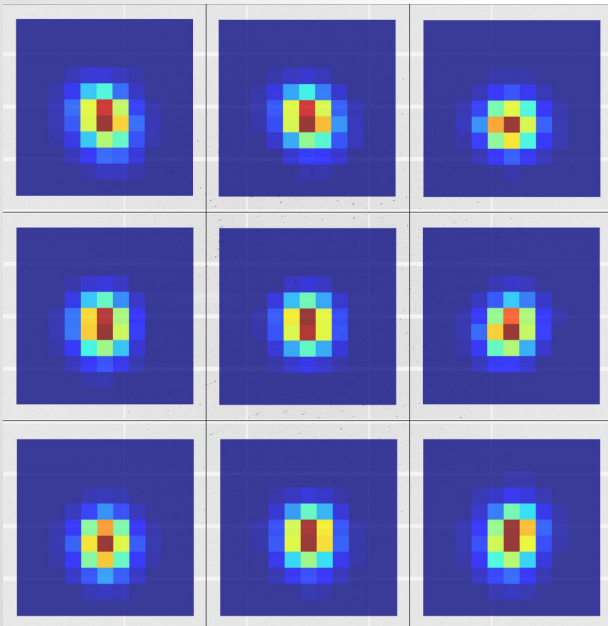
$\sigma_M$  - roughly "mosaicity"



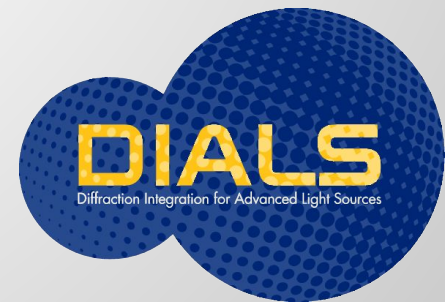
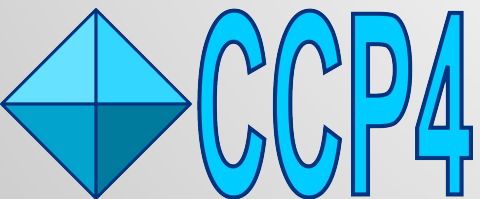
# Integration

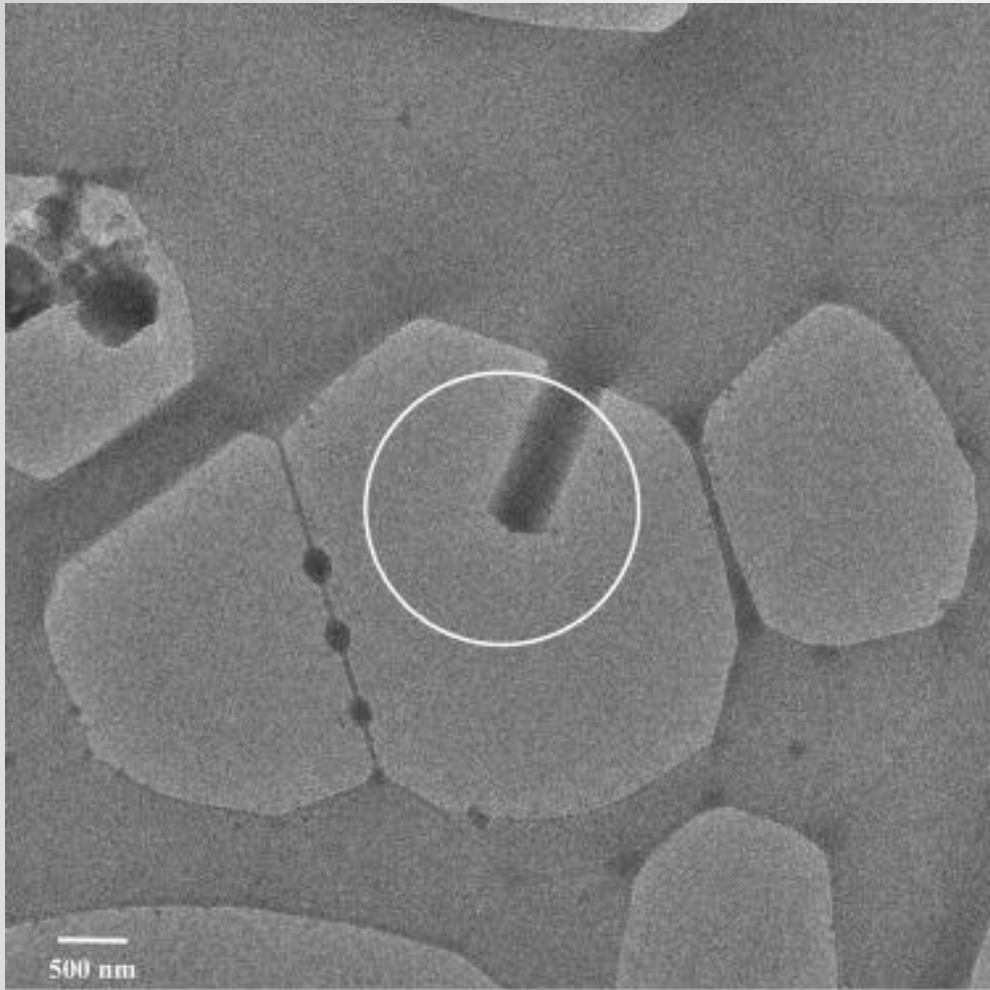
3D profiles are formed for different regions of the detector and different blocks of the  $\phi$ -scan.

**DIALS** uses a rectangular grid on the detector, and overlapping blocks in  $\phi$ , with size chosen so that each reflection is integrated fully in one block



# Example processing

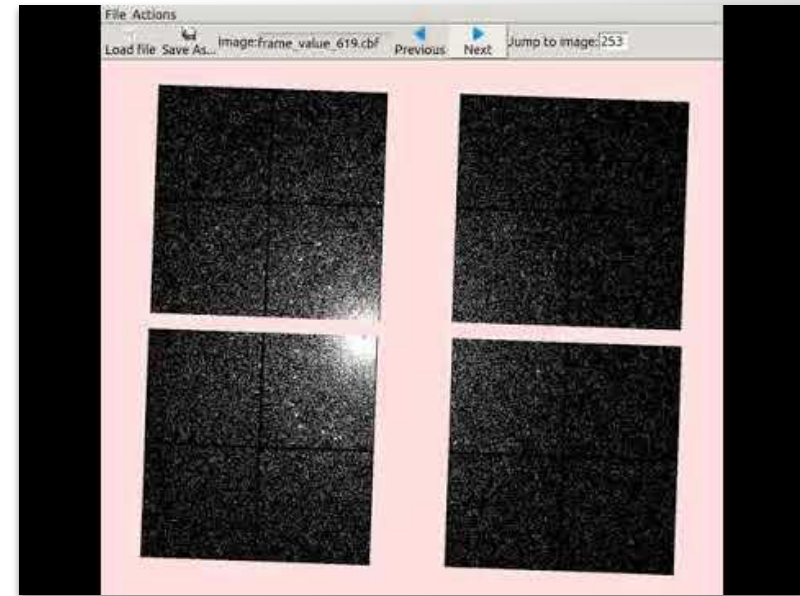




## Lysozyme nanocrystal

Diffracting volume:  $0.14 \mu\text{m}^3$   
( $< 6 \times 10^5$  unit cells)

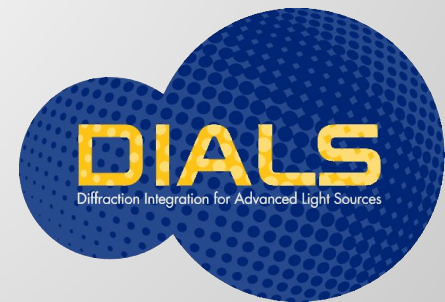
Clabbers *et al.* *Acta Cryst D*  
2017; 2018



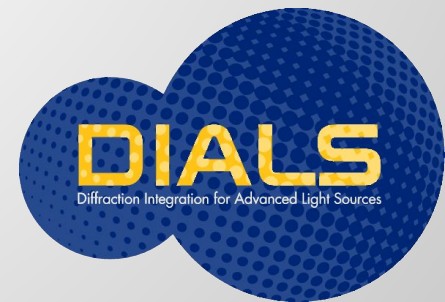
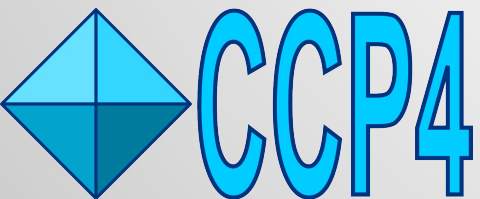
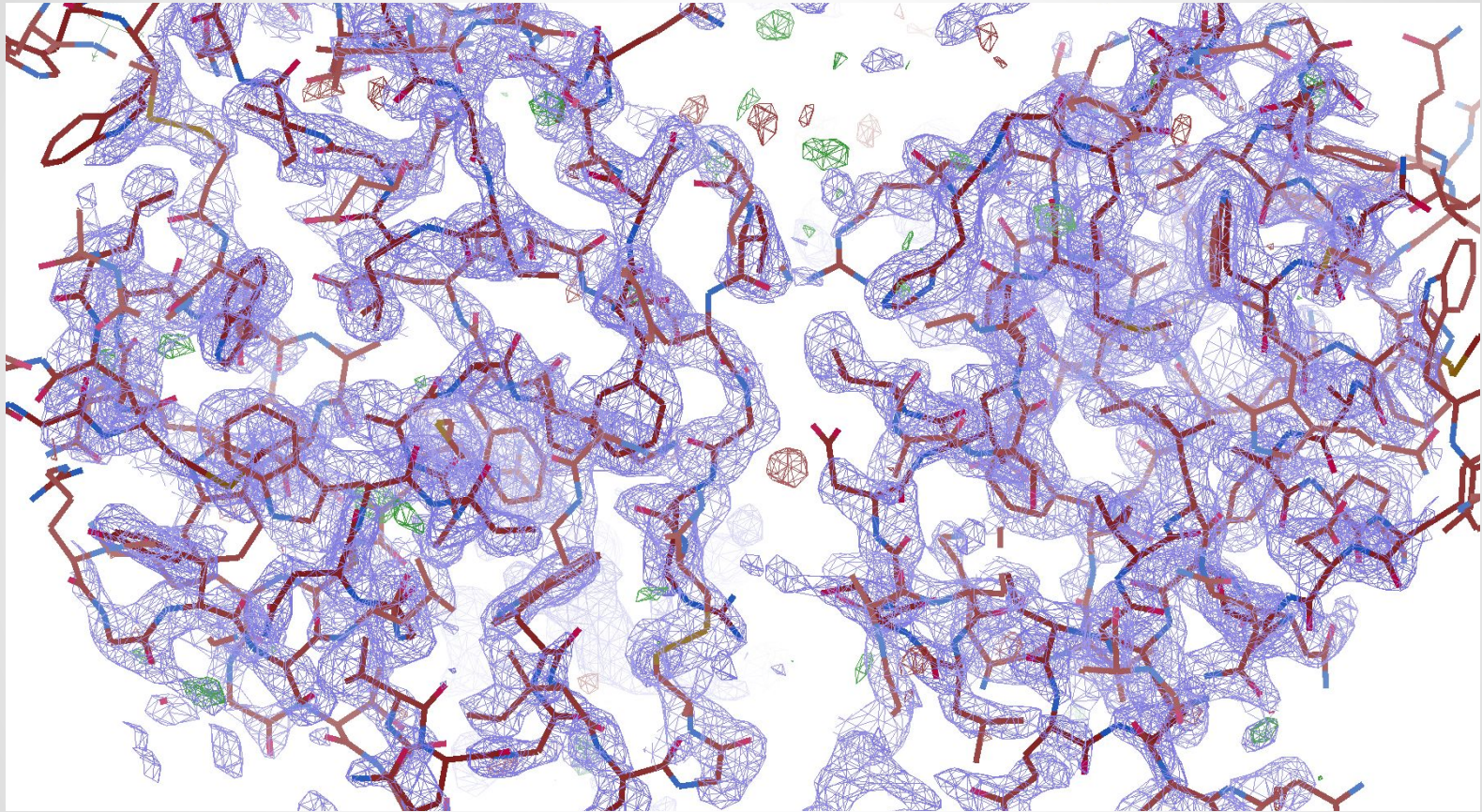


# ED structure solution with CCP4

- 7 datasets integrated with **DIALS**, including elliptical distortion and beam drift corrections as described  
[https://dials.github.io/documentation/tutorials/dials\\_for\\_ed.html](https://dials.github.io/documentation/tutorials/dials_for_ed.html)
- Combined and scaled with **pointless** and **aimless** (~60% complete to 2.1 Å)
- Phased by MR with **phaser** using FORMFACTORS ELECTRON
- Model building by **buccaneer**
- Unit cell refinement performed by **Refmac5**
- Final model refinement by **Refmac5** and **PDB\_REDO**, using SOURCE ELECTRON MB; MAPC FREE EXCLUDE
- Robust validation for incomplete data using *Rcomplete* rather than *Rfree*
- ***Rwork*=25.2%; *Rcomplete*=29.2%**
- Demonstrated equivalent data quality to that obtained by XDS  
(Clabbers et al., Acta Cryst D 2018)



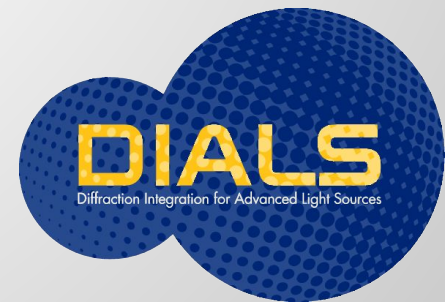
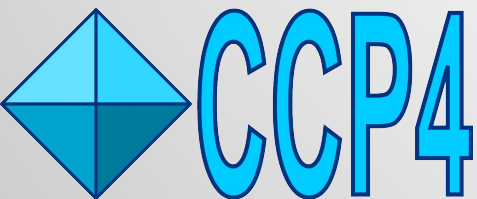
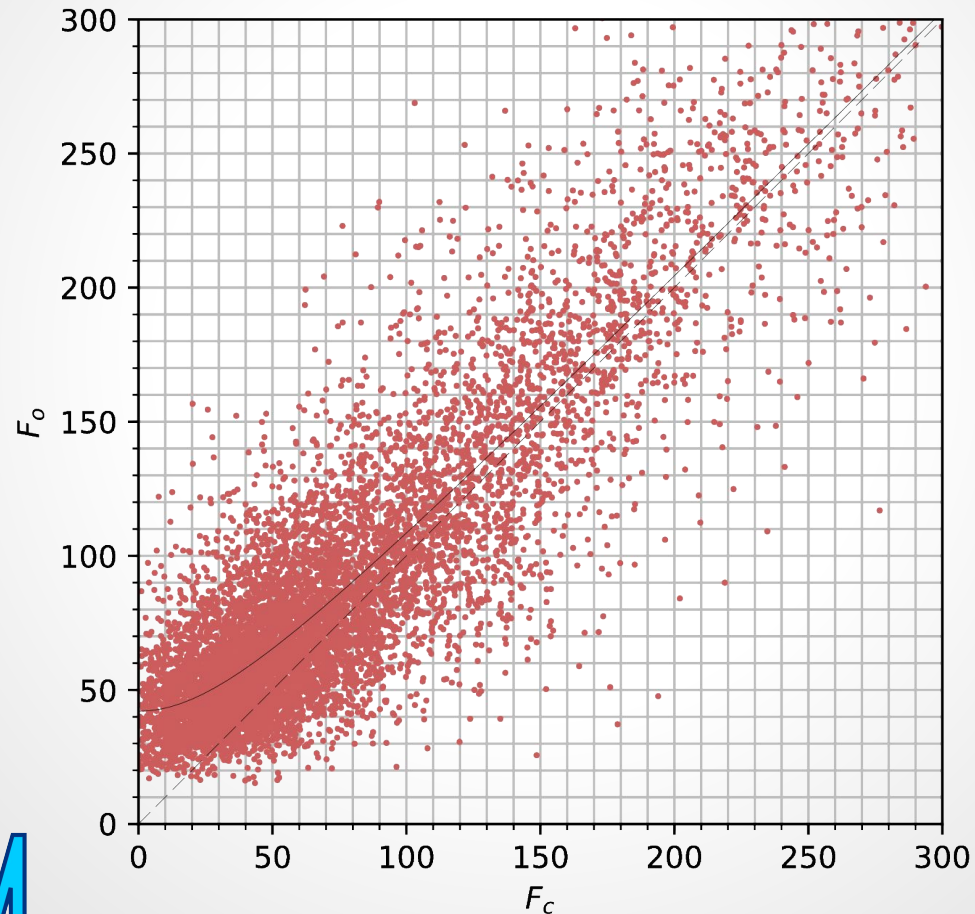
# ED structure solution with CCP4





# Breakdown of the kinematic assumption

dials.plot\_Fo\_vs\_Fc hklin=refined.mtz



DIALS for Electron Diffraction

[https://dials.github.io/documentation/tutorials/dials\\_for\\_ed.html](https://dials.github.io/documentation/tutorials/dials_for_ed.html)

# DIALS

Diffraction Integration for Advanced Light Sources

- [Home](#)
- [About](#)
- [Installation](#)
- [Documentation](#)
- [Tutorials](#)
- [How-to](#)
- [Workshops](#)
- [Publications](#)
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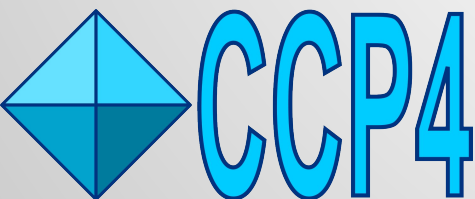
## DIALS for Electron Diffraction

### Introduction

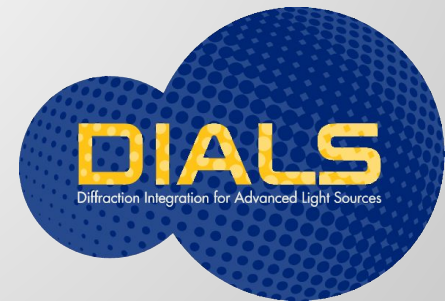
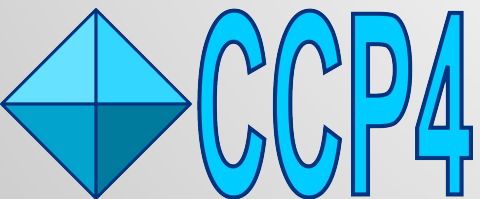
DIALS has been successfully adapted for processing electron diffraction data from protein nanocrystals. Extensions to the software and protocols for dealing with the peculiarities of electron diffraction data are described in a publication:

[Electron diffraction data processing with DIALS](#)  
Clabbers MTB, Gruene T, Parkhurst JM, Abrahams JP, Waterman DG.  
*Acta Crystallogr D Struct Biol* **74**, 506-518 (01 Jun 2018). [PMID:29872002] [PMC reprint: PMC6096487]

This tutorial reproduces the data processing results described in that paper, which were produced by DIALS version `1.dev.2084-g06727c3` and CCP4 version `7.0.051`. Results may differ with other versions of the software. The commands listed here assume the use of a Bash shell on a POSIX-compliant system, so would have to be adjusted appropriately for use on other systems such as Windows.



# Conclusions





# Conclusions

Adapting DIALS for ED required some new features: e.g. image format readers, elliptical distortion correction and smoothly varying beam

If initial experiment metadata is good enough, indexing is usually okay

Modelling accurate diffraction geometry may be challenging

Refinement diagnostics plus trial and error to find the right protocol

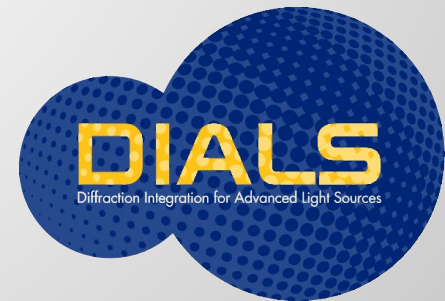
No special requirements for integration (found so far)

Phasing (MR) & refinement works, though room for optimisation

More appropriate models for electron scattering will help

Current hardware is sufficient but not ideal

**Experience with (a limited number) of examples → immediate and largest gains likely to be in hardware and experiment rather than software**



# Acknowledgements

## Development

James Parkhurst

## Simulation

James Holton

## Discussion

Andrew Leslie

Johan Hattne

## Example datasets

Tim Grüne (PSI)

Ronan Keegan (CCP4)

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(Basel/PSI)

Jan Pieter Abrahams  
(Basel/PSI)

Taimin Yang (MMK)

Hongyi Xu (MMK)

Hugo Lebrette (DDB)

Martin Högbom (DDB)

Xiaodong Zou (MMK)

## Lysozyme lamella

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Helen Ginn (STRUBI)

Felix de Haas (FEI)

Corey Hecksel (eBIC)

Abhay Kotecha (STRUBI)

Jason van Rooyen (DLS)

Jose Trincao (DLS)

Gwyndaf Evans (DLS)

Peijun Zhang (eBIC)

Dave Stuart (DLS/STRUBI)

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diamond



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Technology  
Facilities Council

