Chemical Crystallography and Structural Chemistry

VO 270063-1

Lecture № 4 — 30th March 2023

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Course Schedule

2rd	March	Lecture № 1	9th	March	Lecture № 2
16th	March	Lecture № 3	23th	March	Exercise № 1
30st	March	Lecture № 4	20th	April	Lecture № 5
27th	April	Exercise № 2	4th	May	Lecture № 6
11th	May	Exercise № 3	25th	May	Lecture № 7
1st	June	**no lecture**	15th	June	Lecture № 8
22nd	June	Exercise № 4	29th	June	Lecture № 9

Previous Lecture

- Crystallographic symmetry oparations
- Crystallographic point groups and space groups
- Unit cell conventions
- Crystal systems and Bravais lattices

Contents

1 Crystal Systems [1]

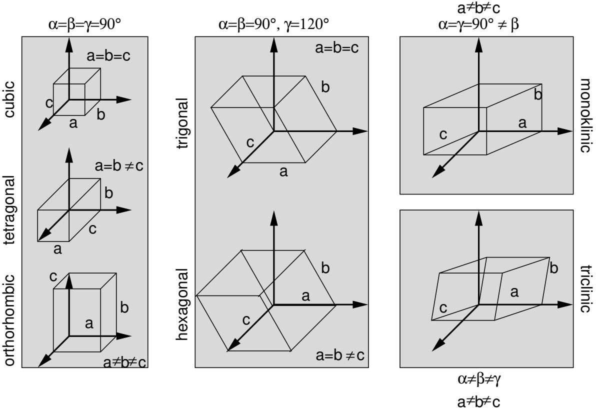
The 7 crystal systems [1]

Indepently from the content of the unit cell, the unit cell parameters $a, b, c, \alpha, \beta, \gamma$, can be classified according to regularity. These classifications result in the **seven crystal systems**

System		Conditions lengths	Conditions angles
triclinic	a	none	none
monoclinic	m	none	$\alpha = \gamma = 90^\circ$
trigonal	h	$a = b = c$	$\alpha = \beta = 90^\circ$ $\gamma = 120^\circ$
hexagonal	h	$a = b$	$\alpha = \beta = 90^\circ$ $\gamma = 120^\circ$
orthorhombic	o	none	$\alpha = \beta = \gamma = 90^\circ$
tetragonal	t	$a = b$	$\alpha = \beta = \gamma = 90^\circ$
cubic	c	$a = b = c$	$\alpha = \beta = \gamma = 90^\circ$

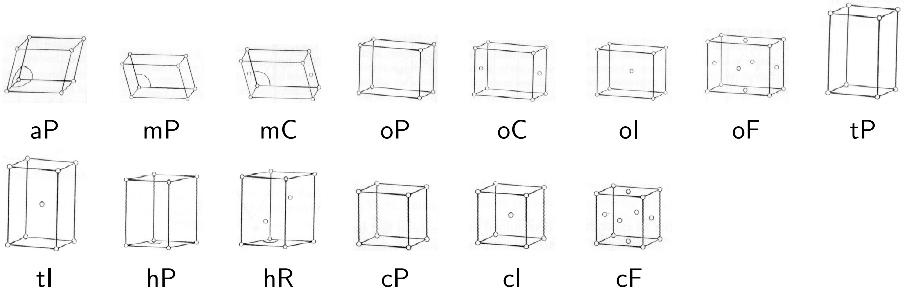
The 7 crystal systems [1]

Indepently from the content of the unit cell, the unit cell parameters $a, b, c, \alpha, \beta, \gamma$, can be classified according to regularity. These classifications result in the **seven crystal systems**



14 Bravais lattices [1]

7 crystal systems plus the requirement that the unit cell reflects the symmetry results in **14 Bravais lattices**:



Dots: Positions of symmetry elements

14 Bravais lattice — naming conventions

- lower case letters (a, m, h, o, t, c): crystal system (shape of cell).
- upper case letters (P, C, F, I, R): Symmetry. They present positions of symmetry elements within the unit cell in addition to the unit cell corners.

  P **p**rimitiv, symmetry elements only at corners

  C **C**-centred: Symmetry element at centre of C-faces (spanned by $\vec{a}$ and $\vec{b}$); (correspondingly: A- and B)

  F **f**ace centred (centred at each face)

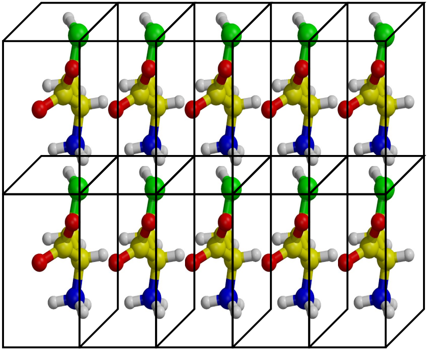
  I body centred: at the centre of the cell (German: **i**nnenzentriert)

  R **r**hombohedral

- the (P, C, F, I, R) are the same as in the Hermann-Mauguin names for space groups ($P2_12_12$, $C2/c$, ...)

Crystal system $\neq$ Space group

Do not draw conclusions on the space group from the shape of the unit cell: the space group **also** depends on the cell content.



orthorhombic box, non-symmetric space group

Positions and naming of unit cell axes: Conventions

- The origin $(0, 0, 0)$ is placed at a position of high symmetry. If present, it is placed at a centre of inversion
- There are $6 \times 4 \times 2 = 48$ possibilities to name the axes as $\vec{a}$, $\vec{b}$, und $\vec{c}$
- Conventions:
    1. right-handed coordinate system
    2. highest possible symmetry
    3. small as possible volume of unit cell
    4. $a \leq b \leq c$

2 Axis settings and Re-indexing

Axis settings and Re-indexing

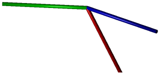
- Despite these conventions, *some* space groups still have several possible axis settings
- For a single data set, the choice is arbitrary
- when two data sets or more are collected, care must be taken to index both consistently
- Modern programs automatically take care of consistent indexing.

Axis settings and Re-indexing

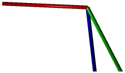
Example: trigonal space group P3

```
!!! WARNING !!! SOLUTION MAY NOT BE UNIQUE.

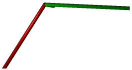
UNIT_CELL_A-AXIS=  -140.027  -180.486   -28.163
UNIT_CELL_B-AXIS=   188.097    21.258  -130.933
UNIT_CELL_C-AXIS=   123.664  -120.609   158.073
```



```
UNIT_CELL_A-AXIS=   188.097    21.258  -130.933
UNIT_CELL_B-AXIS=  -140.027  -180.486   -28.163
UNIT_CELL_C-AXIS=  -123.664   120.609  -158.073
```



```
UNIT_CELL_A-AXIS=    48.070  -159.228  -159.096
UNIT_CELL_B-AXIS=  -188.097   -21.258   130.933
UNIT_CELL_C-AXIS=  -123.664   120.609  -158.073
```



Axis settings and Re-indexing

- Single data set: choice of axis settings is irrelevant, each one is equally good
- Several data sets: with “wrong” settings, intensities do not match weil unterschiedlich indiziert
- either from the same crystal or different crystal
- re-indexing of second data set required in order to match intensities of the first one → **Reindexing of the coordinate system required**
- Worst case: testing of all possibilities
- automated in modern software

3 Symmetry and X-ray data

Symmetry and X-ray data

Overview

- Effect of symmetry on X-ray data
- Friedel's law
- Laue groups: point groups in reciprocal space

Note: Calculation of reflex intensities

Once the chemical composition *i.e. atom types and their positions*, of the asymmetric unit is know, one can calculate the electron density $\rho(x,y,z)$.

The intensity of every reflection can be calculated from the electron density $\rho(x,y,z)$[1]

$$I(hkl) = \left| \int_{V\,(\text{u.c.})} \rho(x,y,z) e^{2\pi i(hx+ky+lz)} d^3x \right|^2$$

---

[1] *International Tables* Volume B, Ch. 1.2

Symmetry in reciprocal space

Reminder: A symmetry operation $(R, \vec{t})$ leaves the entire crystal, and in particular the unit cell, unchanged, *i.e.* for every point in the unit cell:

$$\rho(R\vec{x} + \vec{t}) = \rho(\vec{x})\text{“u.c.”} = R \cdot \text{“u.c.”} + \vec{t}$$

This translates towards the intensities:

$$\begin{aligned}
\Rightarrow I(hkl) &= \left| \int_{V(\text{u.c.})} \rho(x, y, z) e^{2\pi i(hx+ky+lz)} d^3x \right|^2 \\
&= \left| \int_{V(\text{u.c.})} \rho(R\vec{x} + \vec{t}) e^{2\pi i(\vec{h}^T(R\vec{x}+\vec{t}))} d^3(R\vec{x} + \vec{t}) \right|^2 \\
&= I(R^T\vec{h})
\end{aligned}$$

(The last step include quite some calculations)

This means: The intensities of the two reflections (h, k, l) and $R(h, k, l)$ are identical.

Symmetry in reciprocal space

For every symmetry operation $(R, \vec{t})$ of the space group of a crystal:

$$I(\vec{h}) = I(R^T\vec{h}) = I(R^TR^T\vec{h}) = \dots$$

- Crystal symmetry also means symmetry for the reflections
- Translational symmetry is “dropped” in reciprocal space
- Translational symmetry results in a phase shift, that cannot be measured.

Friedel's Law

Even without any symmetry, *i.e.* in all space groups including $P1$:

$$I(h,k,l) = I(\bar{h},\bar{k},\bar{l})$$

Reciprocal space **always** has a centre of inversion. This is called Friedel's law[2]

---

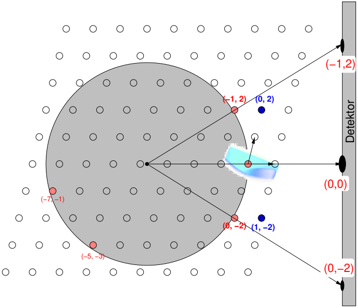
[2] Georges Friedel, 1865–1933

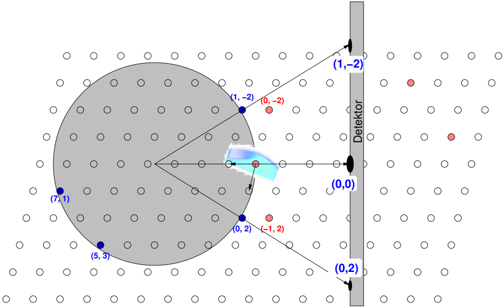
Excursus: Mathematics for Friedel's Law

$$
\begin{aligned}
I(\bar{h}\bar{k}\bar{l}) &= \left|\int_{V(\text{E.Z.})} \rho(x,y,z) e^{2\pi i(\bar{h}x+\bar{k}y+\bar{l}z)} d^3x\right|^2 \\
&= \left|\int_{V(\text{E.Z.})} \rho(x,y,z) e^{-2\pi i(hx+ky+lz)} d^3x\right|^2 \\
&= \int_{V(\text{E.Z.})} \rho(x,y,z) e^{-2\pi i(hx+ky+lz)} d^3x * \left(\int_{V(\text{E.Z.})} \rho(x,y,z) e^{-2\pi i(hx+ky+lz)} d^3x\right)^* \\
&= \int_{V(\text{E.Z.})} \rho(x,y,z) e^{-2\pi i(hx+ky+lz)} d^3x * \int_{V(\text{E.Z.})} \rho(x,y,z) e^{2\pi i(hx+ky+lz)} d^3x \\
&= \left|\int_{V(\text{E.Z.})} \rho(x,y,z) e^{2\pi i(hx+ky+lz)} d^3x\right|^2 \\
&= I(hkl)
\end{aligned}
$$

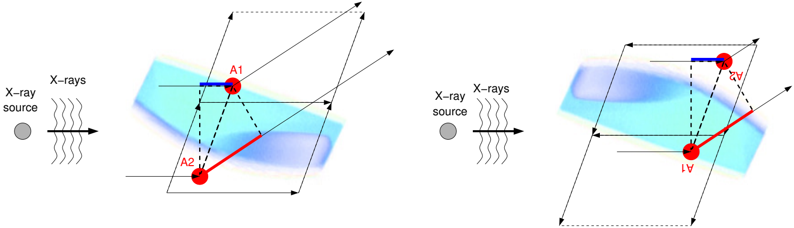
Measurement of Friedel pairs

Two reflections $I(hkl)$ and $I(\bar{h}\bar{k}\bar{l})$ form a **Friedel pair**. They can be measured *e.g.* by rotation the crystal by $180°$





Phase difference of Friedel pairs



$$\Delta_{\text{left}} = -\Delta_{\text{right}}$$

$$\Rightarrow \delta_{\text{left}} = -\delta_{\text{right}} \qquad (\delta = 2\pi\Delta/\lambda)$$

negative phase, same path difference:
$I(hkl) = I(\bar{h}\bar{k}\bar{l})$ and $\Phi(hkl) = -\Phi(\bar{h}\bar{k}\bar{l})$

Laue groups

- Crystals belong to one of 230 space groups
- The diffraction pattern contains the symmetry of the space group, but:
    1. no translational component
    2. always centre of inversion (Friedel's law)
- This results in a subset of groups: the 11 **Laue groups**.

11 Laue groups

Crystal system	**Laue group**	**point group**
Triclinic	$\bar{1}$	1, $\bar{1}$
Monoclinic	$2/m$	2, m, 2/m
Orthorhombic	mmm	222, mm2, mmm
Tetragonal	$4/m$	4, $\bar{4}$, 4/m
	$4/mmm$	422, 4mm, $\bar{4}2m$, 4/mmm
Trigonal	$\bar{3}$	3, $\bar{3}$
	$\bar{3}m$	32, 3m, $\bar{3}m$
Hexagonal	$6/m$	6, $\bar{6}$, 6/m
	$6/mmm$	622, 6mm, $\bar{6}m2$, 6/mmm
Cubic	$m\bar{3}$	23, $m\bar{3}$
	$m\bar{3}m$	432, $\bar{4}3m$, $m\bar{3}m$

http://de.wikipedia.org/wiki/Lauegruppe

Extinctions

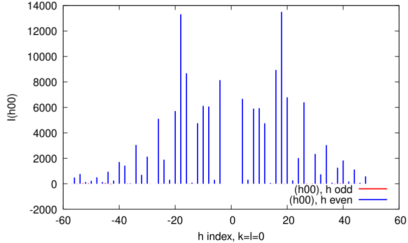
- Extinctions are reflections with systematically zero intensity.
- Extinctions occur in non-primitive Bravais lattices or in the presence of symmetry elements with translational part, *i.e.* glide planes and screw axes.
- Extinctions are important for space group determination, *e.g.* to differentiate between $P4$ and $P4_3$.
- The "Int. Tabl. Vol. A" list the "general reflection conditions", *i.e.* those reflections with non-zero intensity:

  $P3_1$ **(No. #144)** $00l : l = 3n$

  - only if $(hkl) = \ldots (00-6)$, $(00-3)$, (003), ...: Intensities $\neq 0$;
  - reflections (001), (002), (004), (005), ..., should have zero intensity

Example: Extinctions in $P4_32_12$

- Reflection condition: $h00 : h = 2n$ and $00l : l = 4n$
- Only reflections with $k = 0, l = 0$ and h even should have non-zero intensity
- All reflections with $k = 0, l = 0$ and h odd should have zero intensity
- Example: Lysozyme data set



Example: Extinctions in $P4_32_12$

Output from the program `xprep` for Lysozyme data:

```
Systematic absence exceptions:
41/43  42    n--    -b-    -c-    -n-  -21-    --c
N         5     3  3490  2365  2359  2358    89  1549
N I>3s    0     0  2188  1256  1361  1275     0   931
<I>     0.9   0.9  97.0  64.6  80.7  65.4   0.8  85.0
<I/s>   0.2   0.2   8.2   6.7   7.3   6.6   0.4   7.5
Option  Space Group  No.  Type  Axes  CSD  R(sym) N(eq)  Syst.
Abs.   CFOM
[A] P4(1)2(1)2     # 92  chiral   1   245  0.067 140065  0.4 /
6.6   1.99
[B] P4(3)2(1)2     # 96  chiral   1   245  0.067 140065  0.4 /
6.6   1.99
```

Based on the data alone, we cannot distinguish between $P4_12_12$ and $P4_32_12$ (due to Friedel's law). One has to solve the structure and see which one makes sense. For protein structures: the right space group will consist of L-amino acids, the wrong one of D-amino acids.

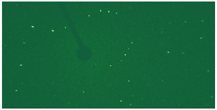
Summary: Space group determination

- Crystal symmetry is present in reflection data intensities
- No translational symmetry in reciprocal space
- Only one of the 11 Laue groups can be determined from symmetry in intensities
- Systematic absences are important to distinguish between space groups within a Laue group

4 Experimental procedure: from data collection to structure

From Data Collection to Structure

Data collection →



several GB

Data integration →

```
0 0 -1      2.7   0.9
0 0  1      4.0   1.0
0 0 -2 1'257.0  35.5
0 0 -2 1'600.0  42.7
```

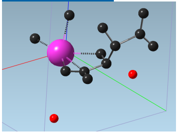
several files, 100’s MB

Data Scaling

```
0 0 -1      2.8  0.55
0 0  1      3.8  0.63
0 0 -2 1'432.0  95.7
0 0 -2 1'282.0  85.9
```

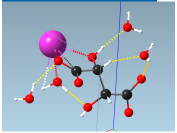
1 “hkl”-file, 50MB

→ **Phasing**



Starting model

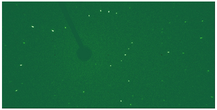
→ **Refinement**



Chemically sensible model

Data Collection

Data collection → Data integration → Data Scaling



several GB

```
0 0 -1      2.7   0.9
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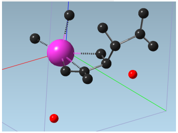
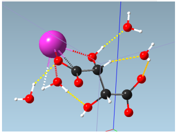
1 “hkl”-file, 50MB

→ Phasing → Refinement



Starting model



Chemically sensible model

How to collect good data

Data resolution

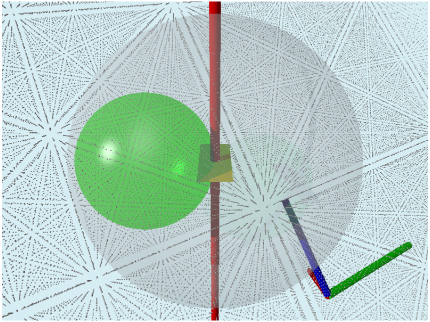
Data completeness

Data multiplicity

Data quality

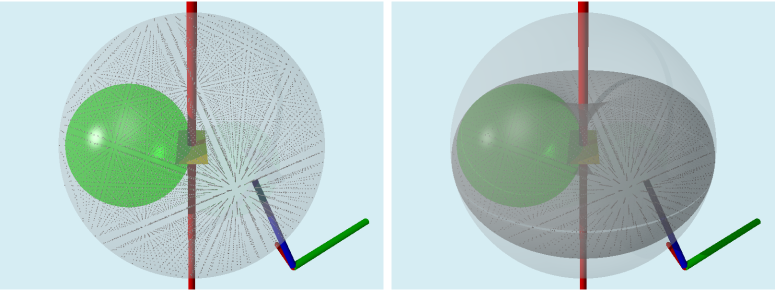
Data resolution

- highest possible resolution: $d_{\text{min}} > \lambda/2$
- good crystals diffract better than this limit (instrumentation limited resolution)
- bad crystals may not reach this resolution (sample limited resolution)
- NB: low resolution are also important



Data completeness

- Only reflections with resolution sphere can be collected (radius in reciprocal space: $r = 2./\lambda$)
- Laue equations permit to compute their location, and how to rotate the crystal into an appropriate position.
- Single rotation axis: torus shape of reflections.

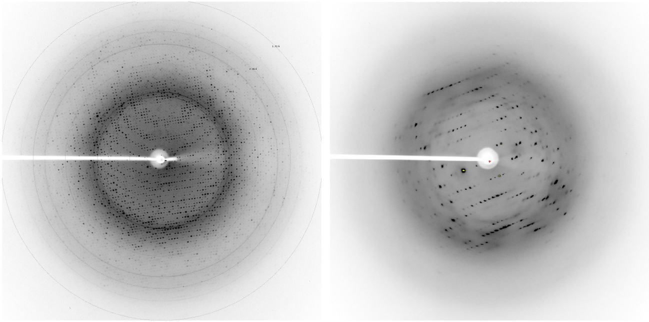


Data multiplicity

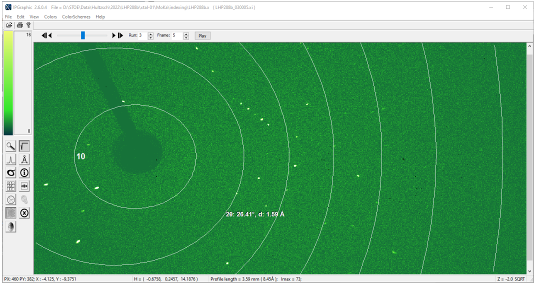
- Intensity $(I(hkl)$ of the identical reflection (hkl) can be measured multiple times
- Intensities $I(hkl)$ and $I'(R(hkl))$ symmetry equivalent reflections increase multiplicity
- Measuring on different positions on detector: reduction of systematic errors
- increasing multiplicity reduces uncertaintig $\sigma(I)$

Data quality

- “Diffraction data acquisition is the final experimental stage of the crystal structure analysis.” (Z. Dauter, [2])
- Ensure proper data collection strategy (desired resolution, multiplicity; adjust detector distance to unit cell parameters, etc.)
- Crystal quality can be the limiting factor



Steps of data integration: initial diffraction images



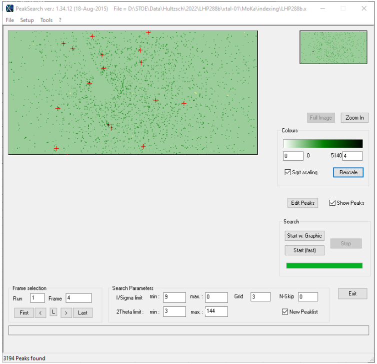
IPGraphic 2.6.0.4 File = D:\STOE\Data\Hultzsch\2022\LHP288b\xtal-01\MoKa\indexing\LHP288b.x (LHP288b_030005.xi)

Run: 3 Frame: 5

PX: 460 PY: 382; X : -4.125, Y : -9.3751 H = (-0.6758, 0.2457, 14.1876) Profile length = 3.59 mm (8.45Å); Imax = 73; Z = -2.0 SQRT

- typically four short runs:
- 2×10°–15°: 0°–10° and 90°–100°
- two detector settings each (low to mid resolution and mid to high resolution)

Steps of data integration: peak finding


PeakSearch ver.: 1.34.12 (18-Aug-2015) File = D:\STOE\Data\Hultzsch\2022\LHP288b\xtal-01\MoKa\indexing\LHP288b.x

Colours
0 0 5140 4
☑ Sqrt scaling

☑ Show Peaks

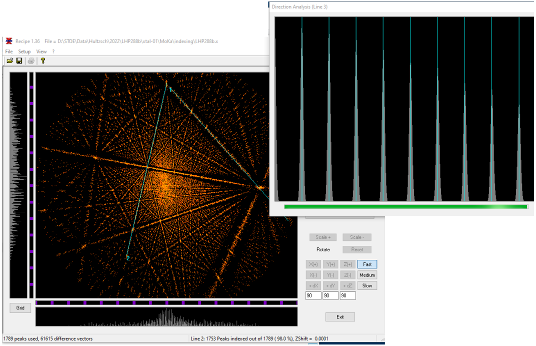
Frame selection
Run 1 Frame 4

Search Parameters
I/Sigma limit min: 9 max.: 0 Grid 3 N-Skip 0
2Theta limit: min: 3 max.: 144
☑ New Peaklist

3194 Peaks found

- simple (non-crystallographic) pattern recognition algorithm: peak above background
- main parameter: desired peak strength (I/sigma)

Steps of data integration: finding unit cell



Recipe 1.36 File = D:\STOE\Data\Hultzsch\2022\LHP288b\xtal-01\MoKa\indexing\LHP288b.x

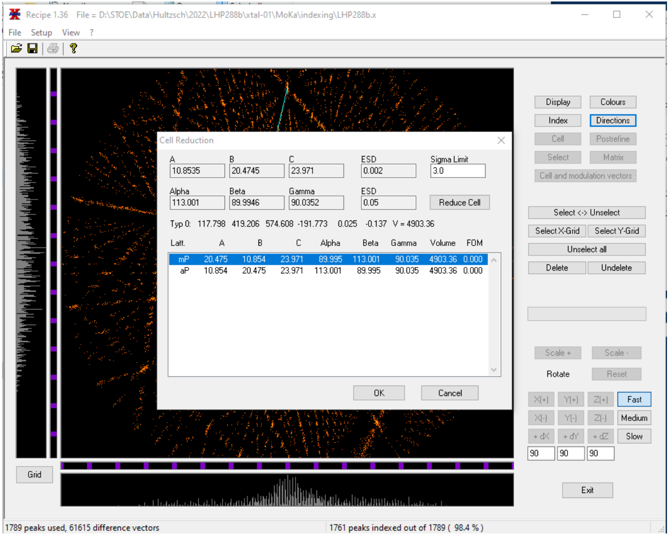
Direction Analysis (Line 3)

1789 peaks used, 61615 difference vectors

Line 2: 1753 Peaks indexed out of 1789 (98.0 %), ZShift = 0.0001

- known instrument geometry: project peaks into reciprocal space
- find a lattice basis

Steps of data integration: finding unit cell



File = D:\STOE\Data\Hultzsch\2022\LHP288b\xtal-01\MoKa\indexing\LHP288b.x

A: 10.8535
B: 20.4745
C: 23.971
ESD: 0.002
Sigma Limit: 3.0

Alpha: 113.001
Beta: 89.9946
Gamma: 90.0352
ESD: 0.05

Typ 0: 117.798 419.206 574.608 -191.773 0.025 -0.137 V = 4903.36

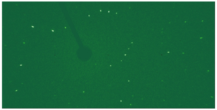
Latt.	A	B	C	Alpha	Beta	Gamma	Volume	FOM
mP	20.475	10.854	23.971	89.995	113.001	90.035	4903.36	0.000
aP	10.854	20.475	23.971	113.001	89.995	90.035	4903.36	0.000

1789 peaks used, 61615 difference vectors

1761 peaks indexed out of 1789 (98.4 %)

Data Integration

Data collection →



several GB

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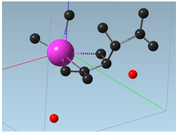
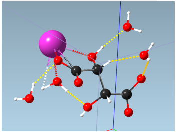
1 "hkl"-file, 50MB

→ **Phasing**



Starting model

→ **Refinement**



Chemically sensible model

Data Integration

Data integration comprises

1. Indexing: Determination of unit cell dimensions, orientation of the crystal, point group
2. Extraction of spot intensities from detector images.
3. Optimisation of experimental parameters

Programs for data integration (incomplete)

Saint Licensed by Bruker AXS. Specific to Bruker programs. Good for data from twinned crystals. Derived from XDS.

X-Area Software suite distributed with Stoe X-ray diffractometers. Free to use. Very good interactive indexing routine, good for twinned data.

XDS Free for non-commercial users (`http://xds.mpimf-heidelberg.mpg.de`). Supports nearly all detector formats, very well documented. Very fast.

DIALS Free for non-commercial users. Very active development. (`https://dials.diamond.ac.uk/`)

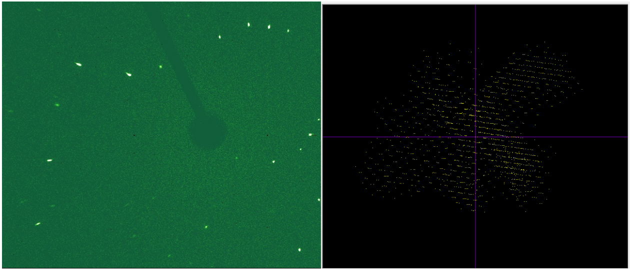
EVAL Suite Free for non-commercial users (`http://www.crystal.chem.uu.nl/distr/eval`). Can integrate *e.g.* incommensurate crystals

Crysalis Pro Licensed by Rigaku (`https://www.rigaku.com/products/smc/crysalis`)

iMosflm Free for non-commercial users, distributed with CCP4 (`http://www.ccp4.ac.uk`)

HKL3000 Very good visualisation GUI for fine-tuning of parameters. very popular in the US (`https://hkl-xray.com/`)

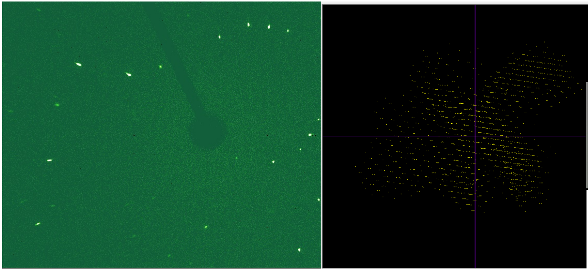
Indexing

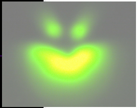


“Ewald sphere backwards:”

- find 200–1000 **strong** spots
- backtransform into reciprocal space (Laue equations)
- find a lattice and a suitable basis
- basis for reciprocal lattice corresponds to reduced unit cell constants

Indexing





Unfocused synchrotron beam, courtesy N. Sanishvili, APS, Chicago, USA

Possible reasons for indexing problems:

- Incorrect parameters: detector distance, direction of rotation, wavelength, especially at synchrotrons
- Too few reflections
- Distorted spots (lattice defects, unfocused beam)
- Alien spots (ice, metal, contaminant)
- multiple lattices *twins*

References

[1] W. Massa. *Crystal Structure Determination*. Springer Verlag Berlin, Heidelberg, 2002.

[2] Zbigniew Dauter. 'Collection of X-Ray Diffraction Data from Macromolecular Crystals'. In: *Protein Crystallography: Methods and Protocols*. Ed. by Alexander Wlodawer, Zbigniew Dauter and Mariusz Jaskolski. New York, NY: Springer New York, 2017, pp. 165–184. DOI: `10.1007/978-1-4939-7000-1_7`.