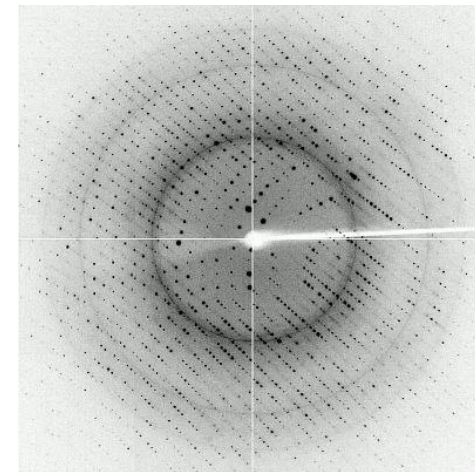
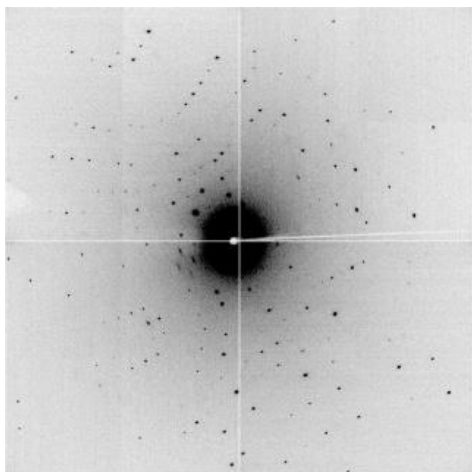




Crystallography



Dr Rosemary Young

Beamline Scientist – MX1/2

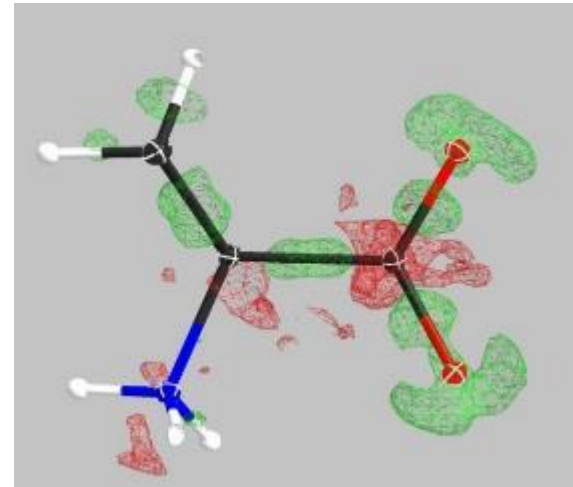
Australian Synchrotron

Science. Ingenuity. Sustainability.

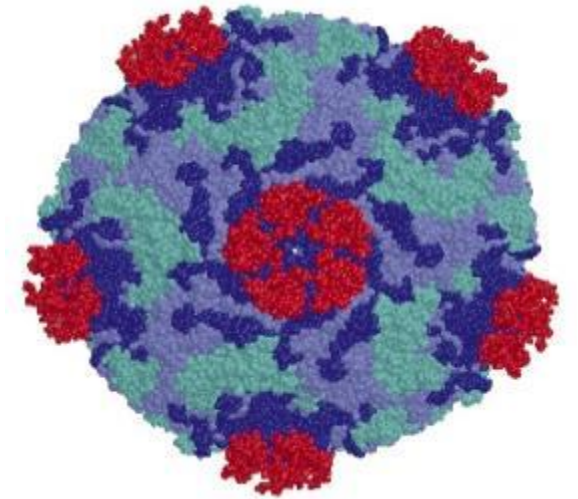
What is crystallography?

"To determine the atomic or molecular structure of a crystal by X-ray diffraction"

1. Have a (single) crystal
2. Perform an X-ray diffraction experiment
3. Determine the structure



~3 Å



~300 Å

Results:

Structure, connectivity, chirality, bonding, packing, porosity, supramolecular interactions ...

Why do crystallography?

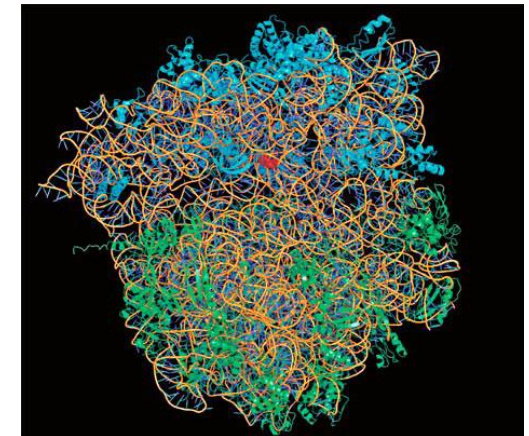
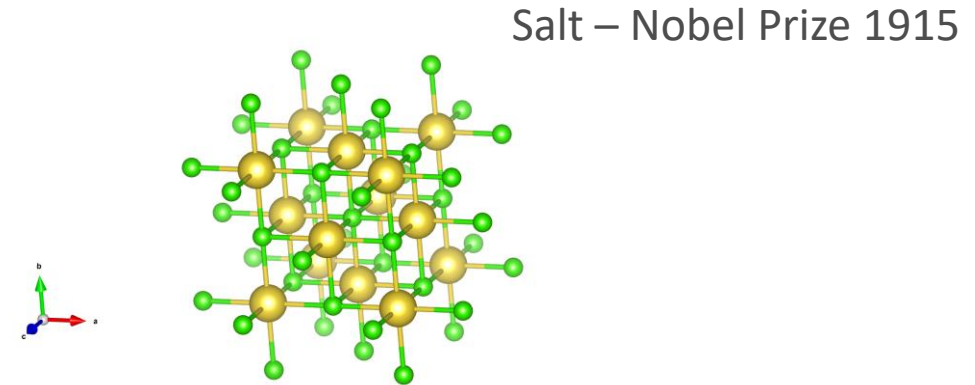
*'Why water boils at 100°C and methane at -161 ° C;
why blood is red and grass is green; why diamond is
hard and wax is soft;*

*why graphite writes on paper and silk is strong;
why glaciers flow and iron gets hard when you
hammer it;*

*how muscles contract; how sunlight makes plants
grow and how living organisms have been able to
evolve into ever more complex forms...?*

*The answers to all these problems have come from
structural analysis'*

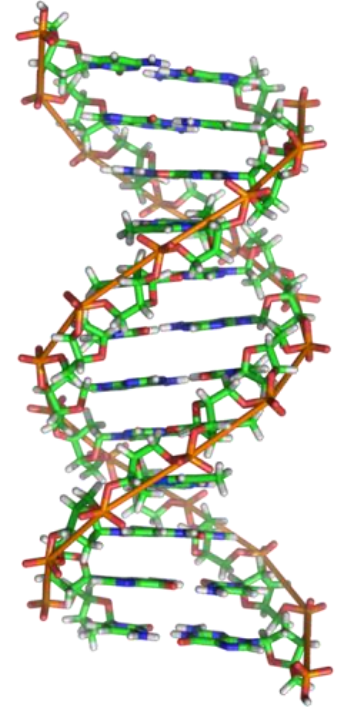
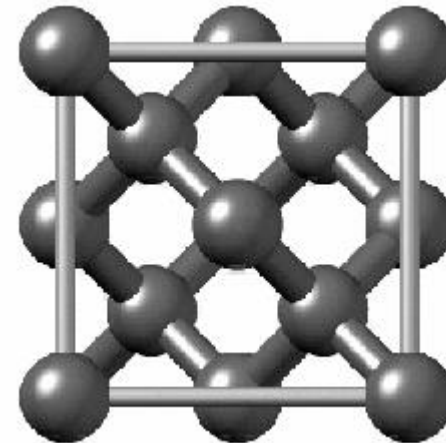
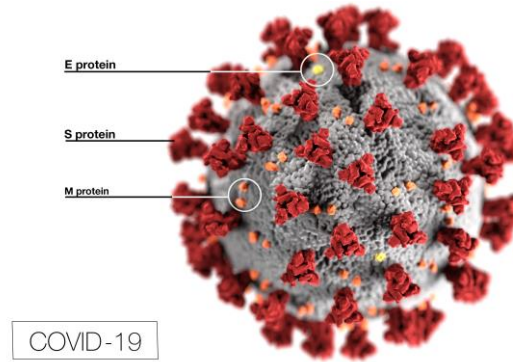
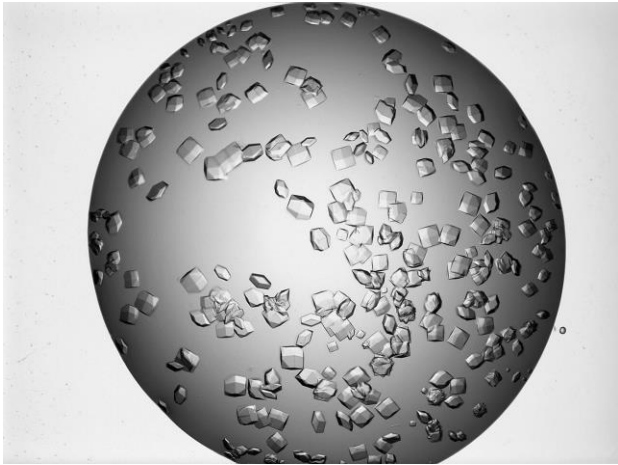
Max Perutz (Nobel Prize 1962)



Ribosome –
Nobel Prize 2009

What is a crystal?

- A solid with highly ordered components

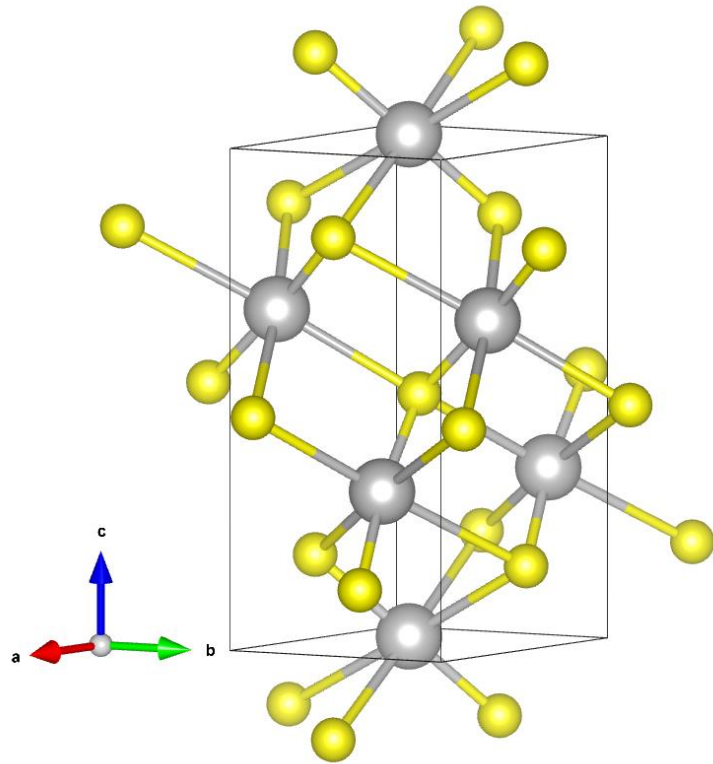


How do we find the crystal structure?

Crystals and Symmetry

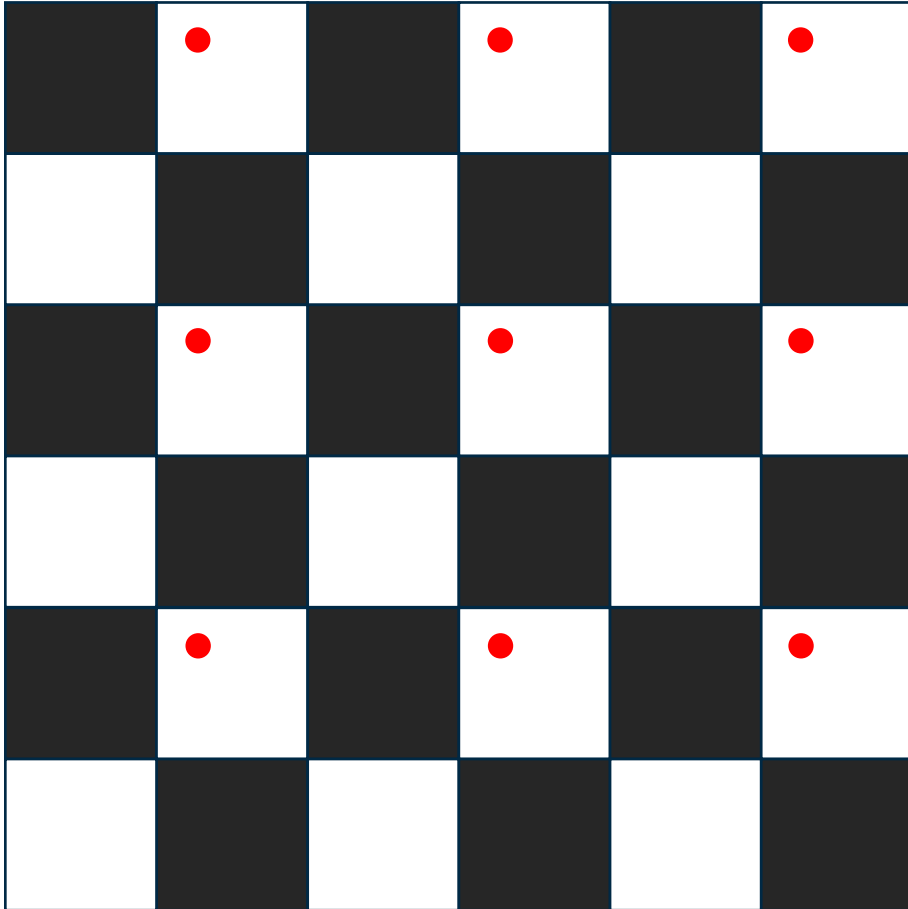
- 1 mg of matter will contain around 10^{19} atoms.
- Symmetry provides a systematic way of describing where all those atoms are

Crystallographic Definitions



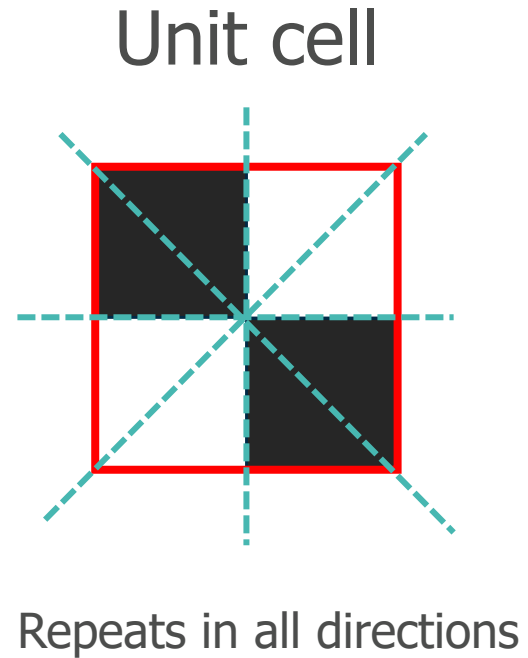
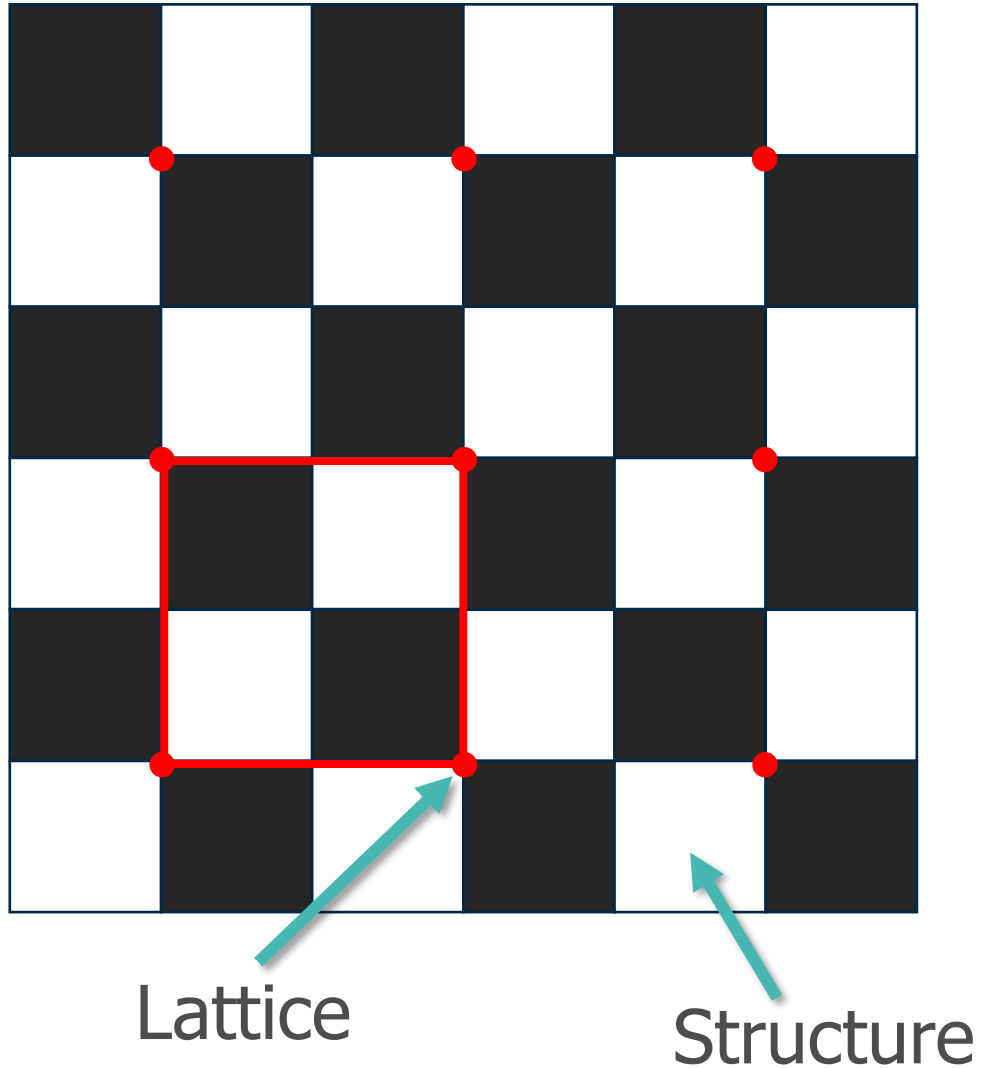
- **Lattice** – an infinite array of points in space where each point has identical surroundings
- **Crystal structure** – the periodic arrangement of atoms in a solid
- **Unit Cell** – the smallest component from which the entire crystal can be built up, with purely translational displacements

Lattice and structure



- Identical points in the pattern define a lattice.
- Lattice points can be chosen anywhere (but we tend to choose high-symmetry points).

Crystallographic Definitions

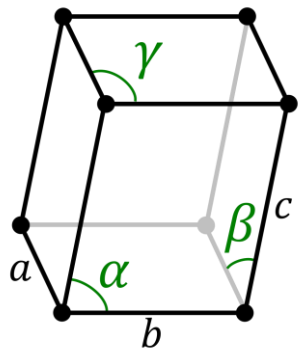


Asymmetric unit

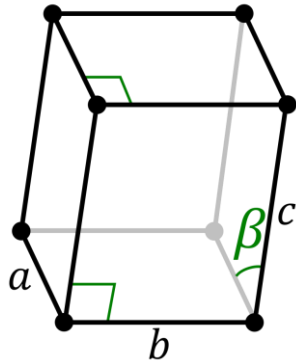


Smallest unit taking into account symmetry

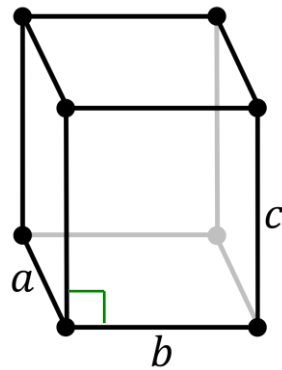
Unit cell in three-dimensions



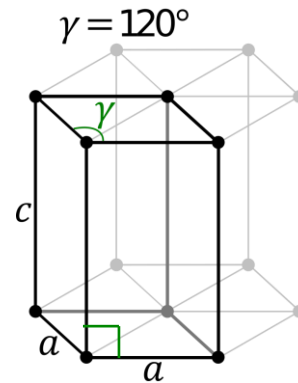
Triclinic
 $a \neq b \neq c$
 $\alpha \neq \beta \neq \gamma$



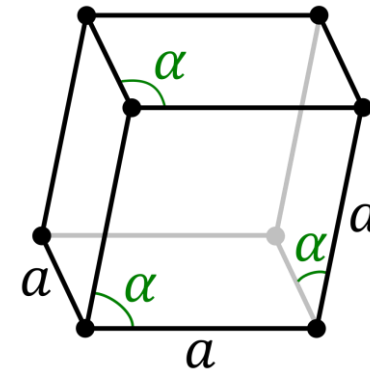
Monoclinic
 $a \neq b \neq c$
 $\alpha = \gamma = 90^\circ, \beta \neq 90^\circ$



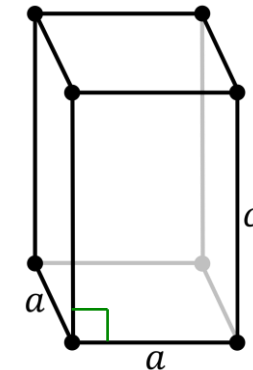
Orthorhombic
 $a \neq b \neq c$
 $\alpha = \beta = \gamma = 90^\circ$



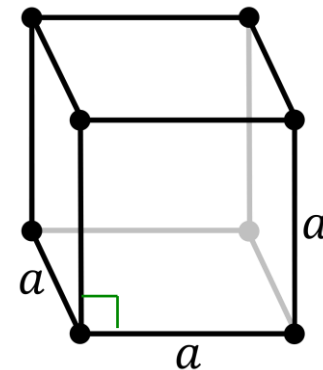
Hexagonal
 $a = b \neq c$
 $\alpha = \beta = 90^\circ, \gamma = 120^\circ$



Rhombohedral
 $a = b = c$
 $\alpha = \beta = \gamma \neq 90^\circ$



Tetragonal
 $a = b \neq c$
 $\alpha = \beta = \gamma = 90^\circ$



Cubic
 $a = b = c$
 $\alpha = \beta = \gamma = 90^\circ$

- 14 Bravais lattices (unit cells)
- 7 Crystal Systems

Symmetry in solids

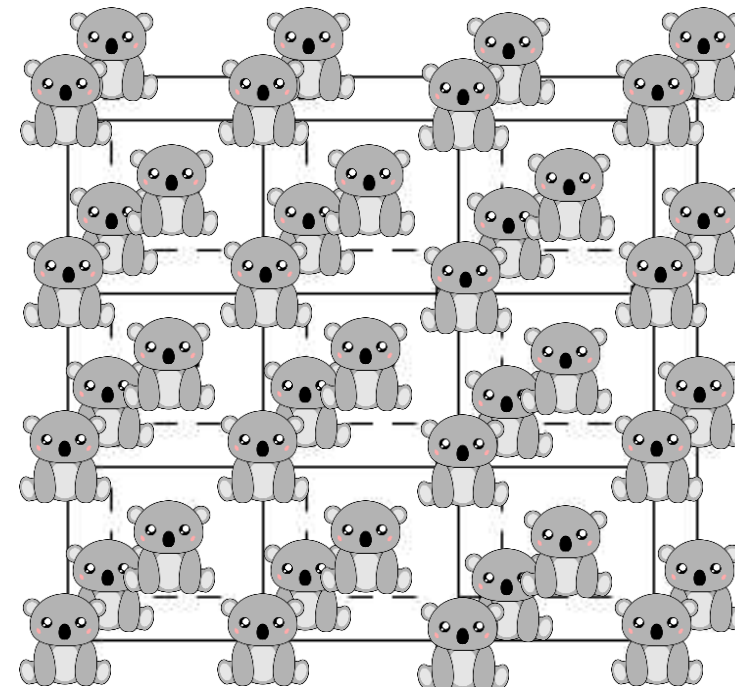
- **Molecular symmetry**

- Symmetry of isolated objects
- Point group symmetry
- 32 point groups



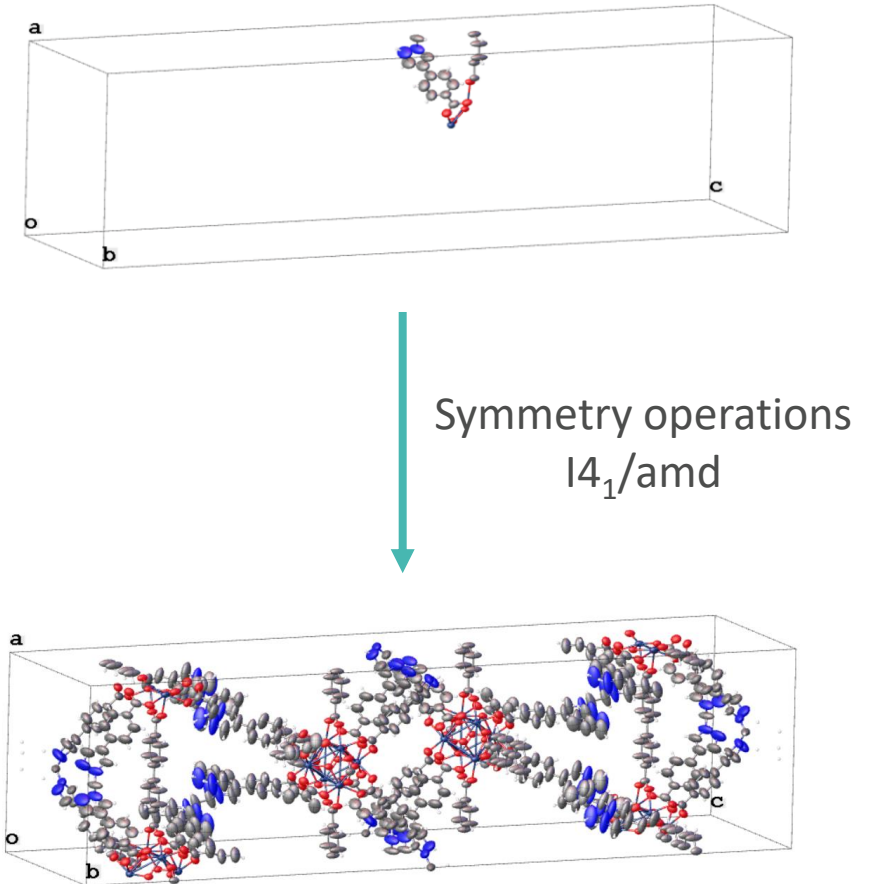
- **Crystallographic Symmetry**

- Symmetry of periodic arrays
- Space group symmetry
- 230 space groups



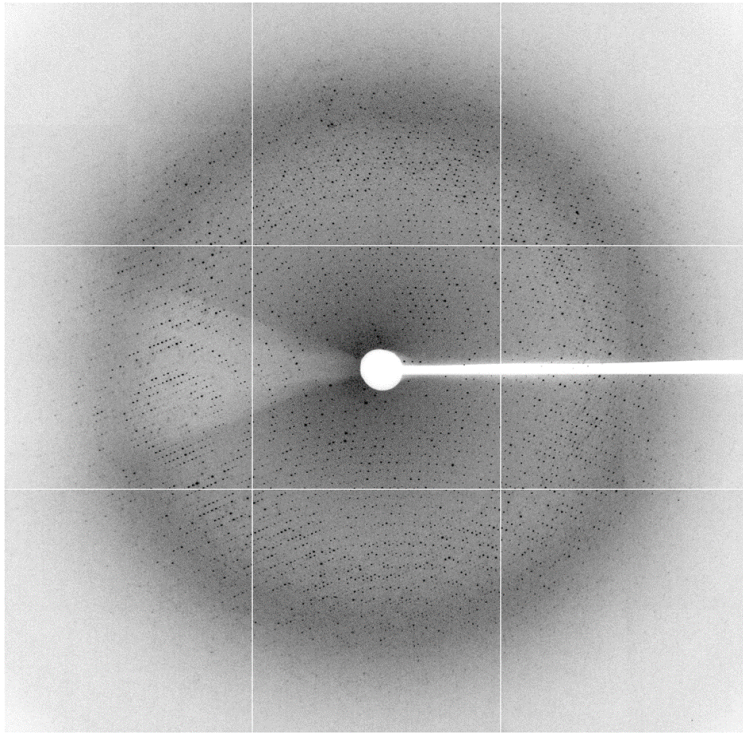
Asymmetric unit

- Smallest portion of the structure that must be specified before space group symmetry defines the entire structure
- Crystallographically unique (independent) atoms
- Can be equal to/more/less than one molecule (molecular solids)
- Can be equal to/more/less than the formula unit (extended solid)



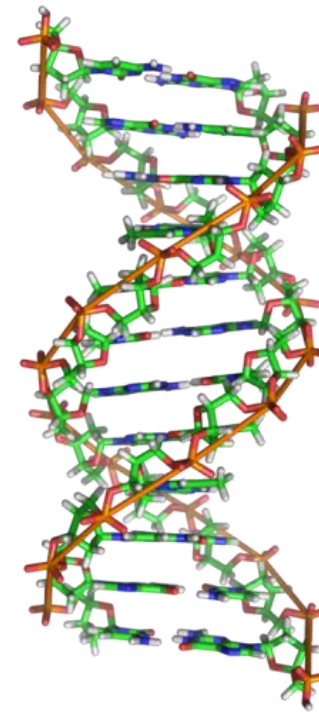
Diffraction

How to go from this (or this):

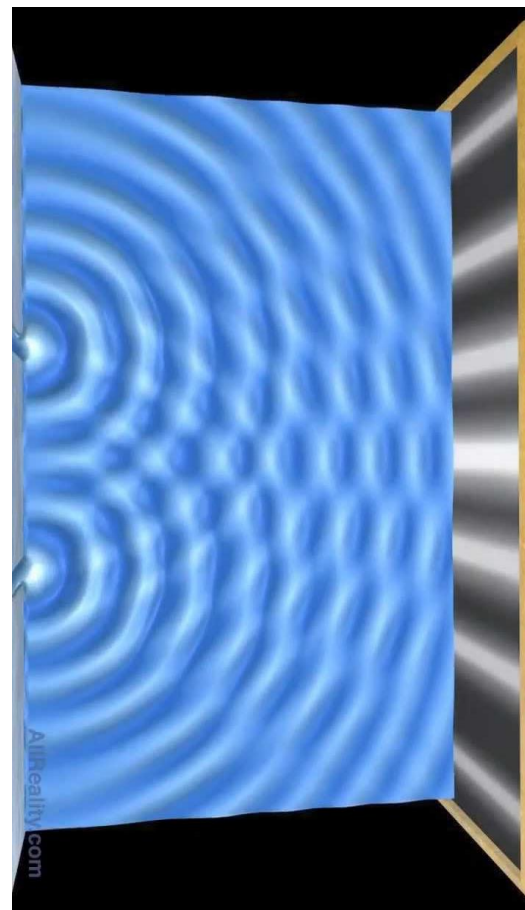
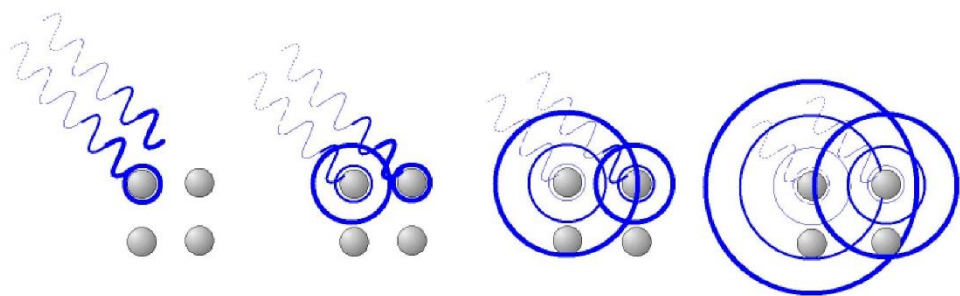


Forwood, 2015ish

To this:

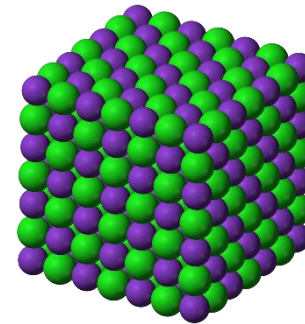
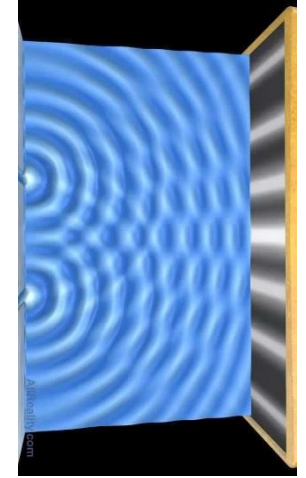
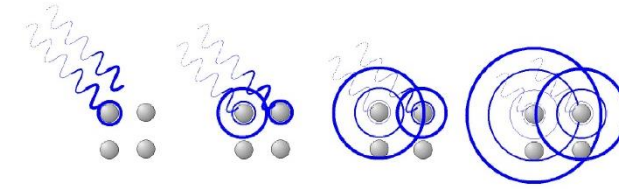
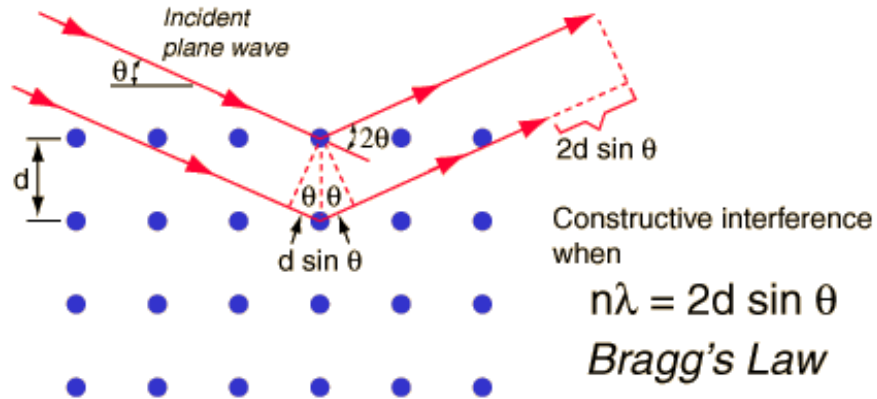


Diffraction theory



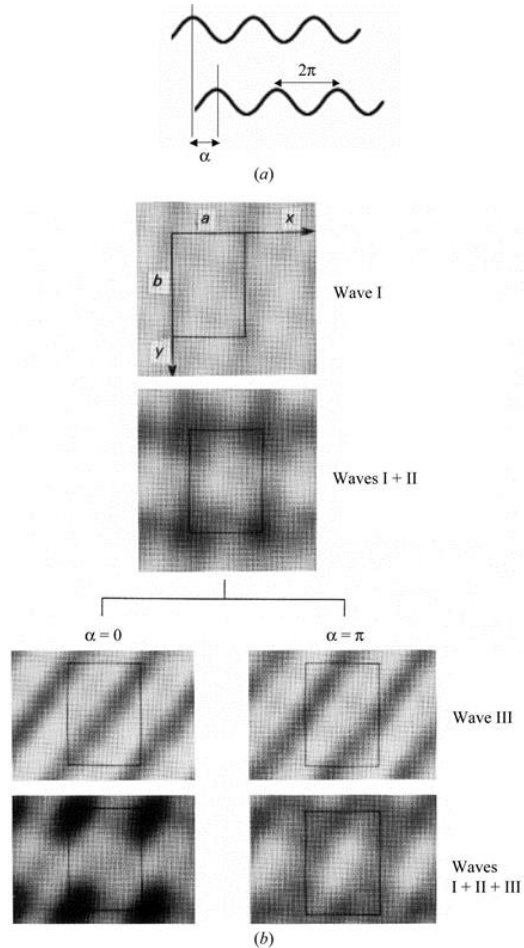
Diffraction theory

- Crystal lattices have regularly-spaced planes of atoms
- We only observe diffracted X-rays when Bragg's law is satisfied -> constructive interference
- In phase in a few selected directions



n is an integer
 λ is the X-ray wavelength
 d is the inter-planar spacing
 2θ is the diffraction angle

Phase problem



Diffraction
intensity

$$\sim F(hkl) = \sum_j b_j e^{2\pi i(hx_j + ky_j + lz_j)}$$

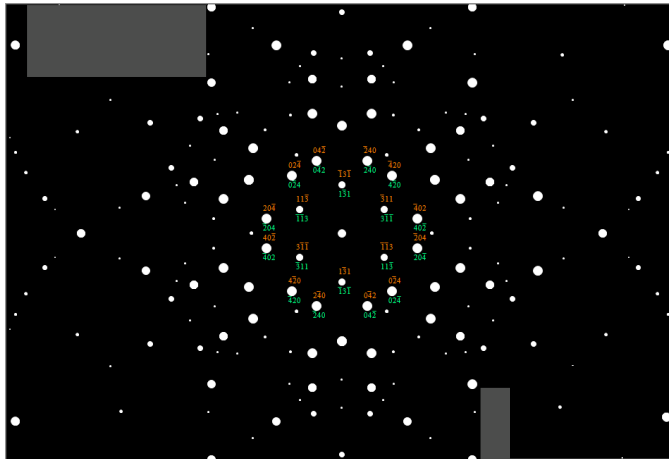
- Needs to be noted that we actually measure $I_{(hkl)}$
- We have information on the **amplitude** of the structure factor not its phase
- Hence direct Fourier transforms to obtain crystal structures is not possible – need to fit models

Powder vs Single Crystal

- Indexing is harder with powder diffraction.
- Anisotropic atomic displacement parameters also more challenging to determine
- Whole powder pattern analysis methods such as Rietveld analysis allow quite detailed information to be extracted

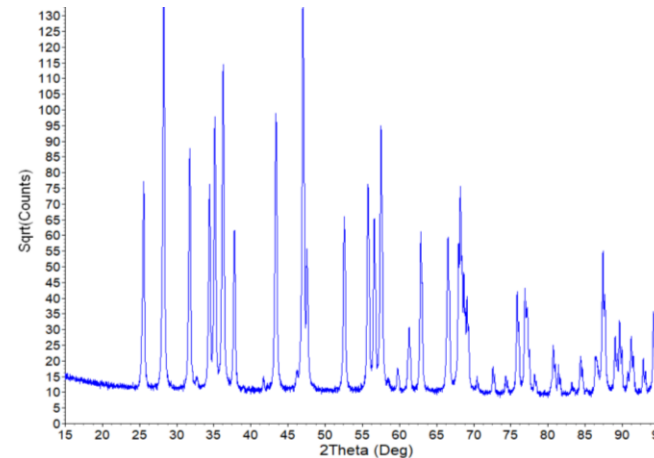
Single crystal: 3D diffraction data

→ 3D unit cell

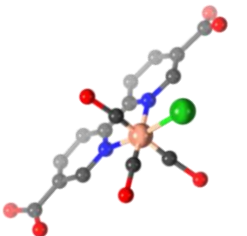
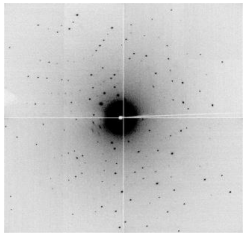
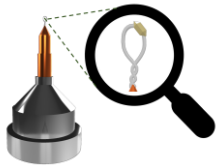
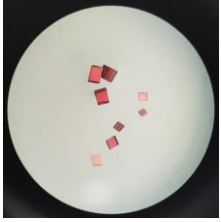


Powder diffraction: 1D diffraction data

→ Unit cell size & shape can be ambiguous



Timeline of an X-ray crystallography experiment



1. Grow a crystal (minutes - months...)

2. Mount it on a loop (seconds - minutes)

3. Collect a dataset (seconds)

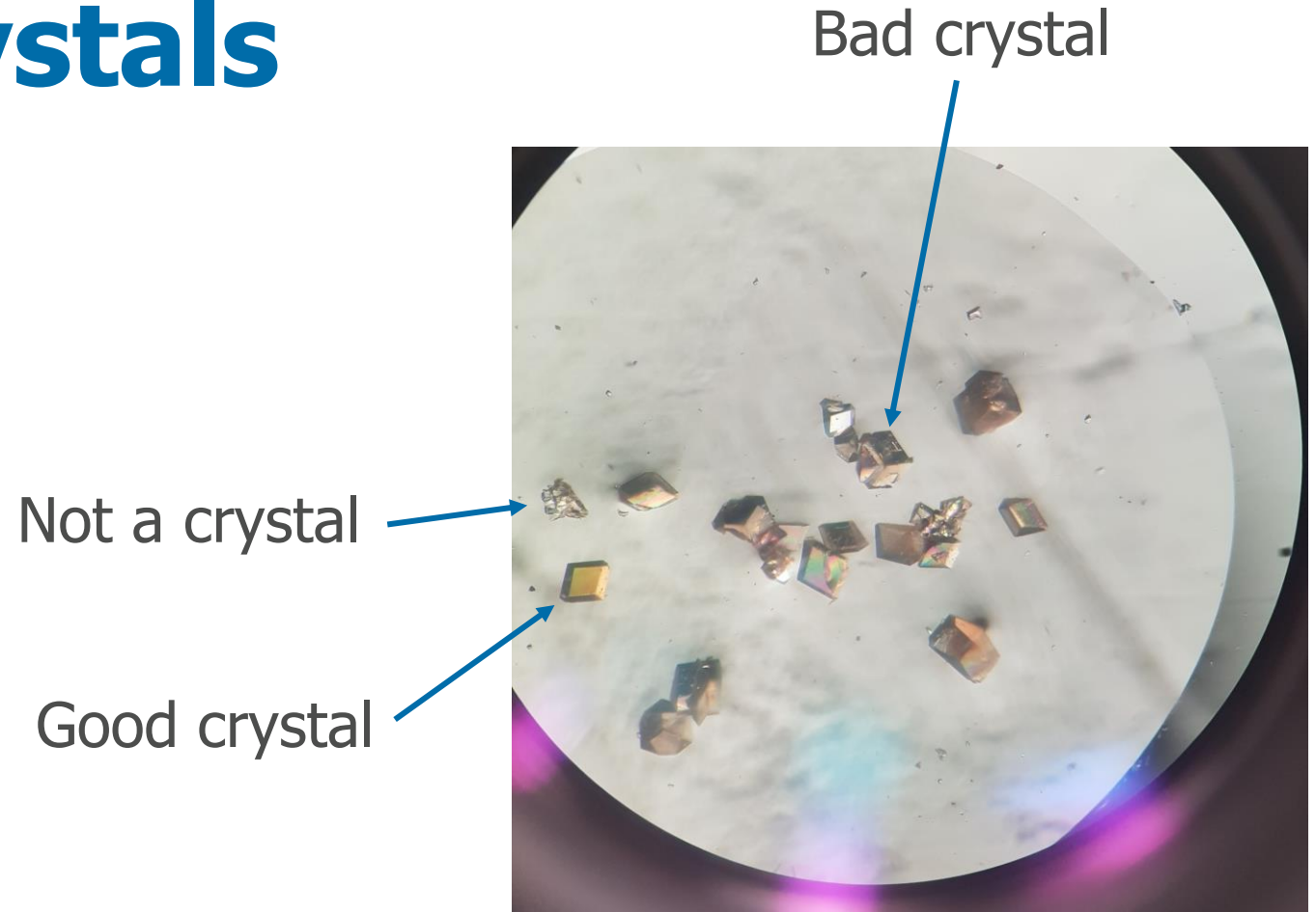
4. Data processing (minutes)

5. Solving and refining the crystal structure (hours - days)

Synchrotron

Growing good crystals

- Sharp edges
- Regular faces
- Clear
- Extinguish under cross polarized light



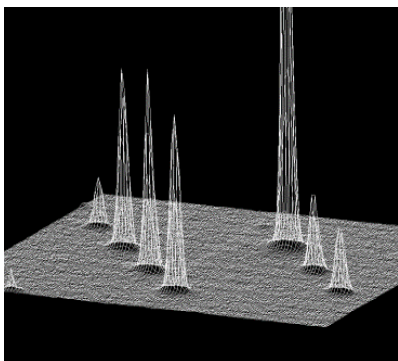
Methods – slow evaporation, vapour diffusion, liquid/liquid diffusion, gel diffusion, solvothermal, slow cooling, sublimation

<https://www2.chemistry.msu.edu/Facilities/Crystallography/downloads/xtalgrow.pdf>

Why use a synchrotron?

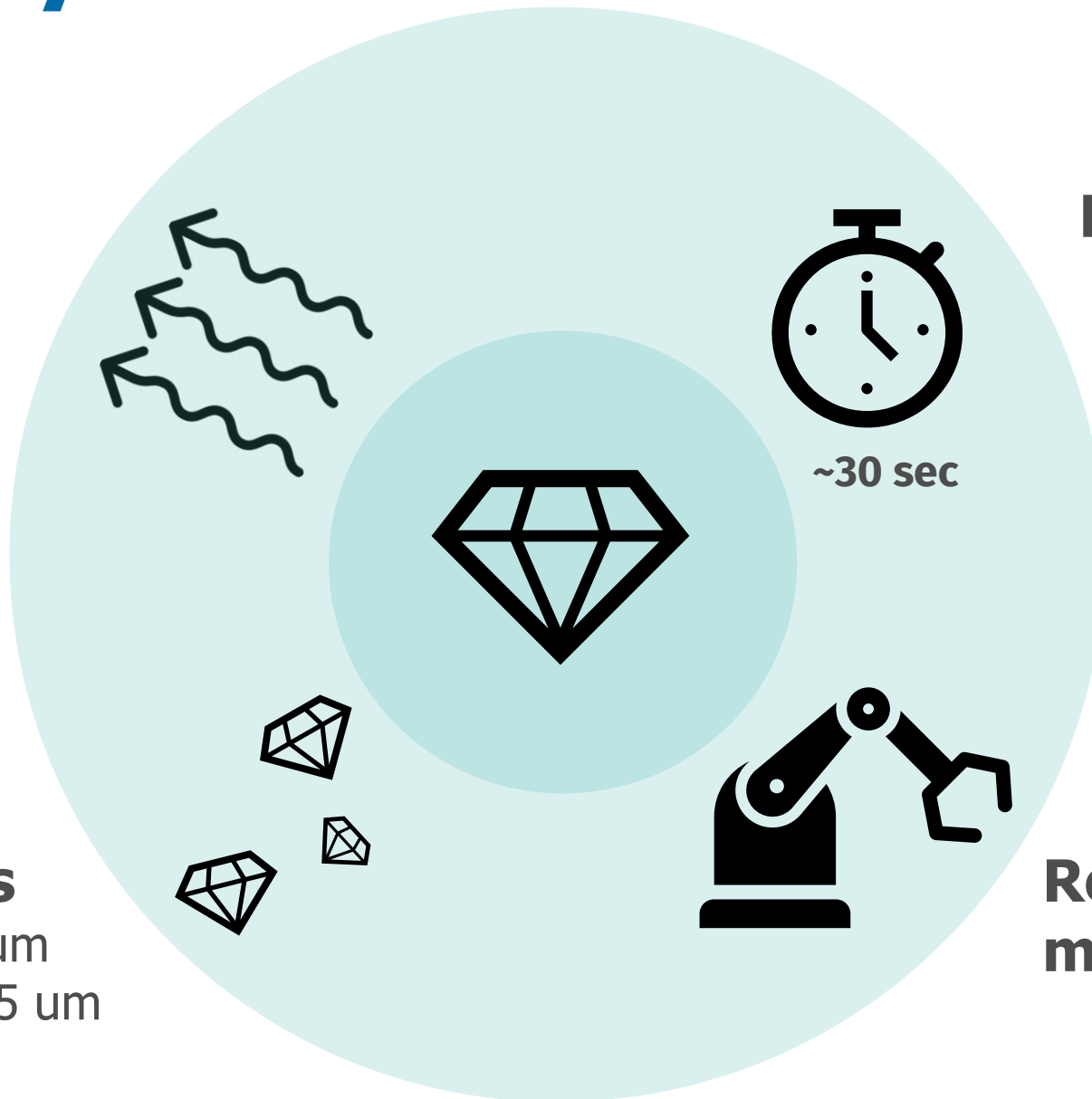
X-ray beam

High flux
Small beam
High signal/noise
Tunable wavelength



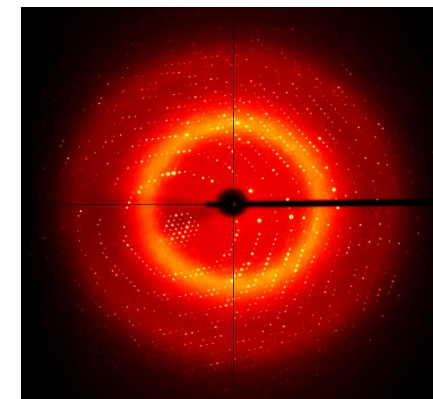
Small crystals

Chemical $<1\text{ }\mu\text{m}$
Biological $>3\text{-}5\text{ }\mu\text{m}$



Rapid data collection

Serial collections



Robotic sample mounting

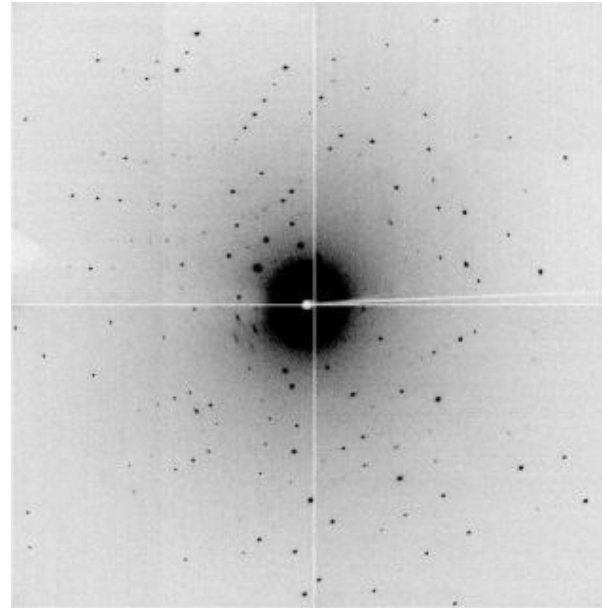
Remote access

Chemical or “small molecule” crystallography

What's the difference between anyway?

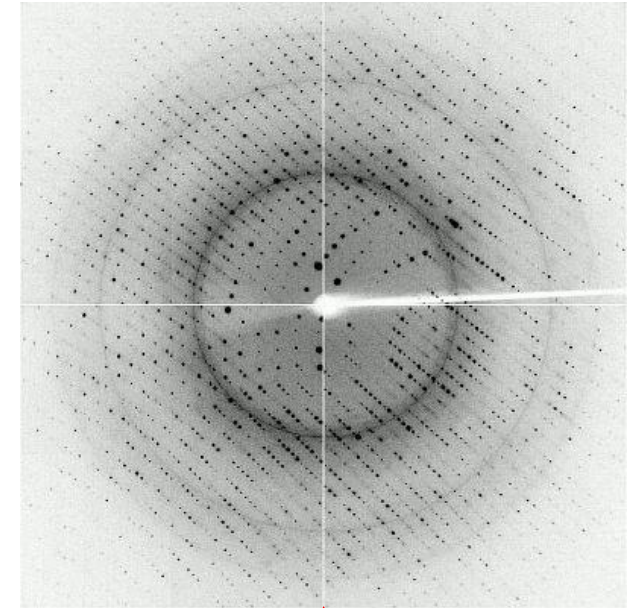
- Size of molecule
- Size of unit cell
- Size of asymmetric unit
- Use of direct methods
- Publication resolution limits
- Software

Chemical



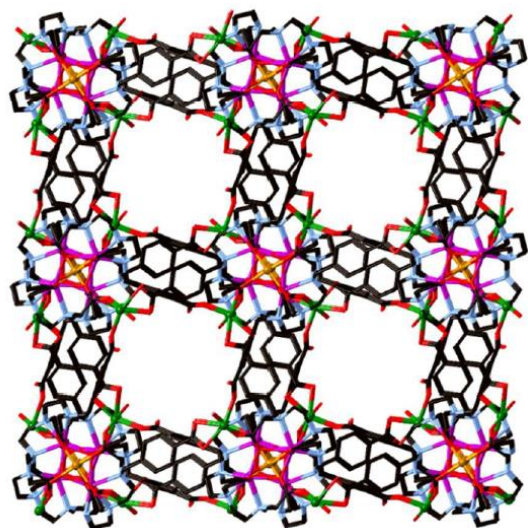
0.76 Å
(17.444 keV, 0.71 Å)

Protein

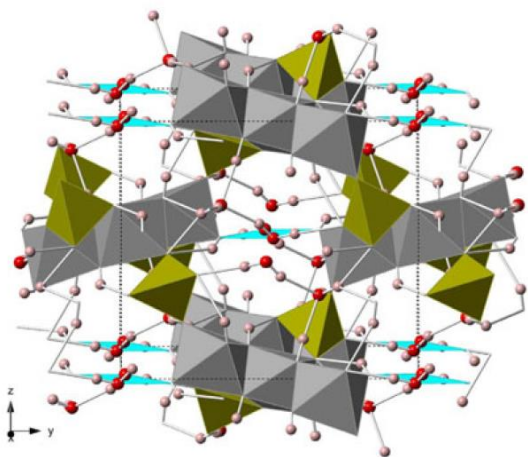


1.76 Å resolution
(13.0 keV, 0.95 Å)

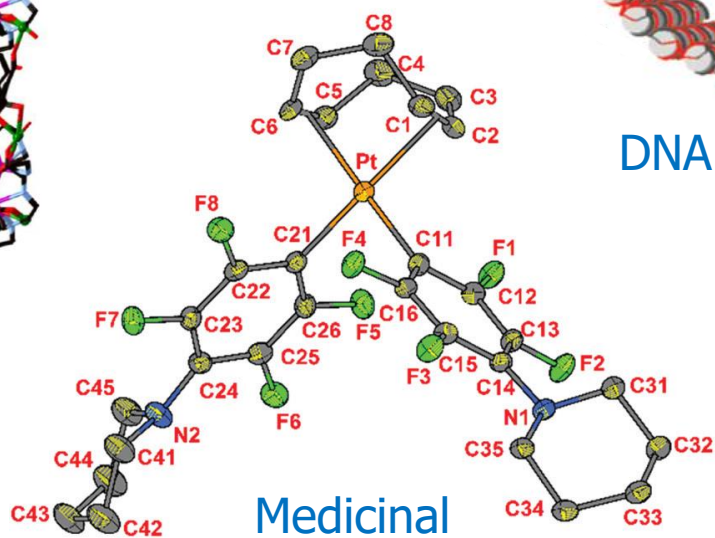
Chemical Crystallography & Advanced Materials



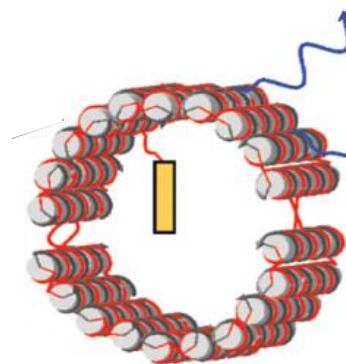
Gas Separation & Storage



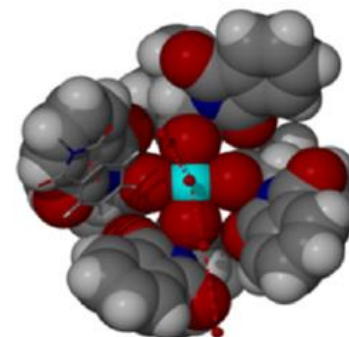
Mineralogy



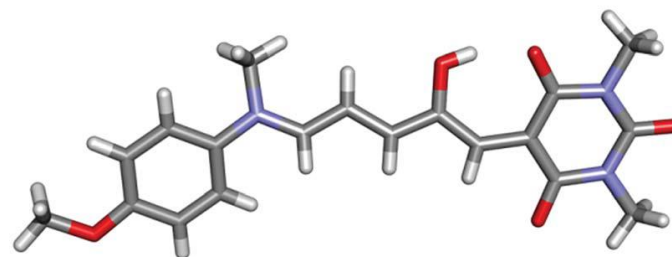
Medicinal Chemistry



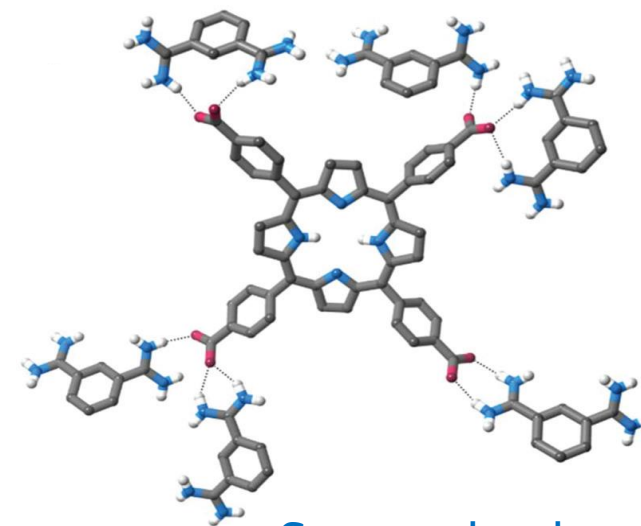
DNA Origami



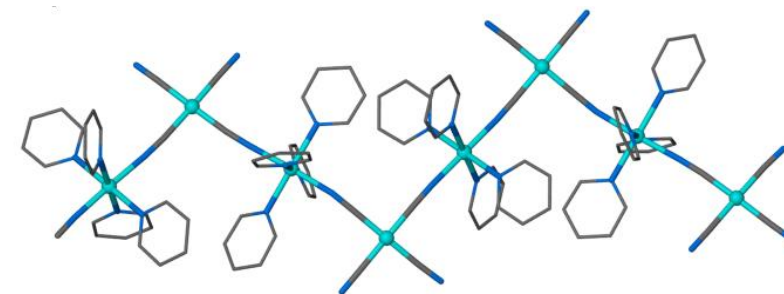
Catalysts



Photochromic Switches



Supramolecular Frameworks



Coordination Polymers

Different requirements for different users

Heavy-atom phasing
(SAD/MAD)

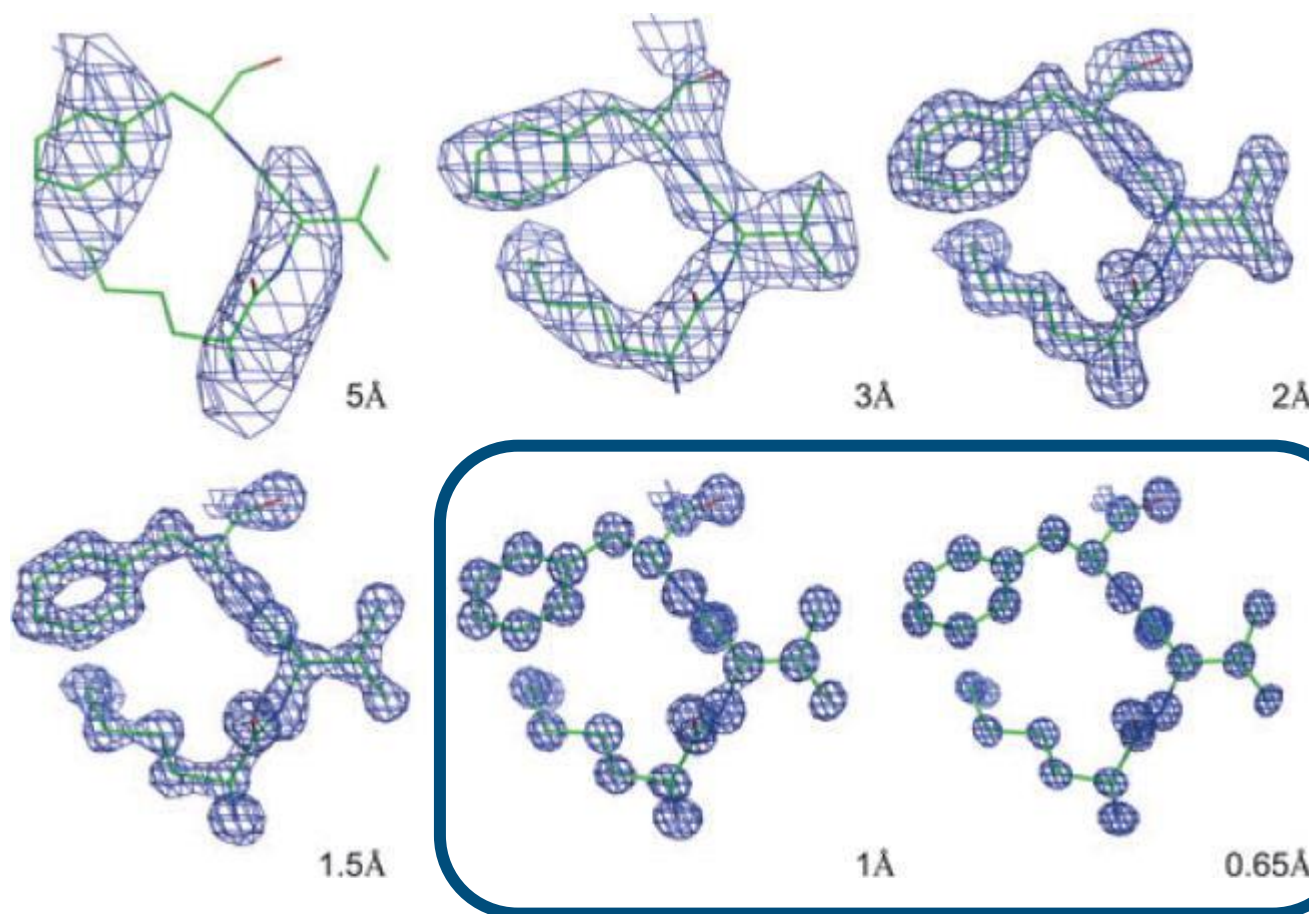
Elemental composition

Temperature

Radiation sensitivity

Space groups

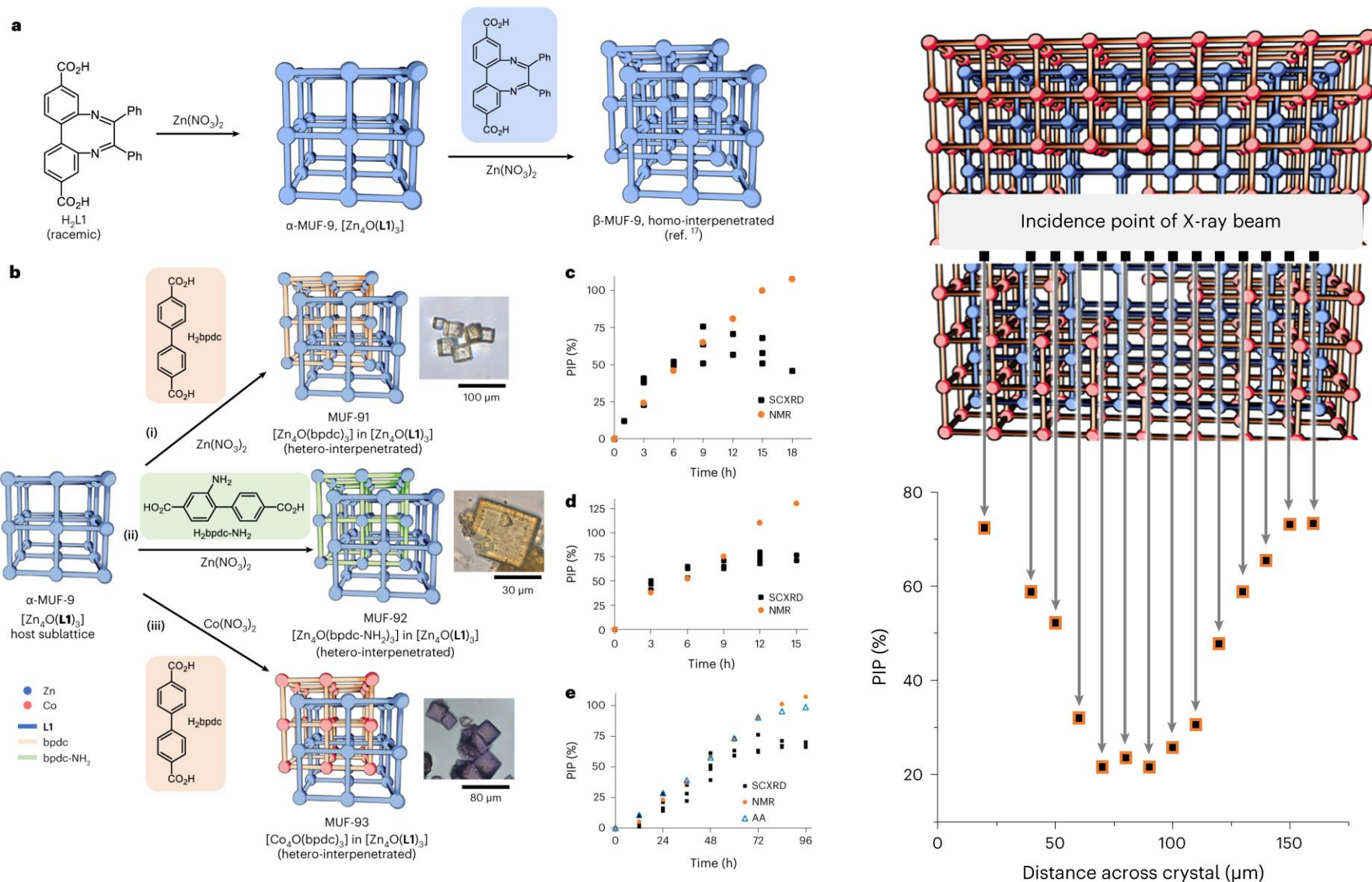
Cryoprotectants



Chemical Crystallography at MX1/MX2

- X-ray energy set at 17.444 keV = 0.71Å (Mo K alpha)
- Detector at closest approach – highest resolution
- Different processing pipeline for data indexing and reduction

Framework catalysts for chiral synthesis



In-crystallo experiments

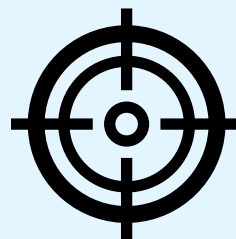


Variable temperature

90-400 K

Automated ramping and data collection

Phase changes, spin-crossover



Micro-focus beam

7.5, 10 and 20 μm beams

Automated rastering for spatial analysis

Bendy crystals, multiple domains



High pressure

Up to 5 GPa (50,000 atm)

Micro custom diamond anvil cells

Spin-crossover, molecular rotors



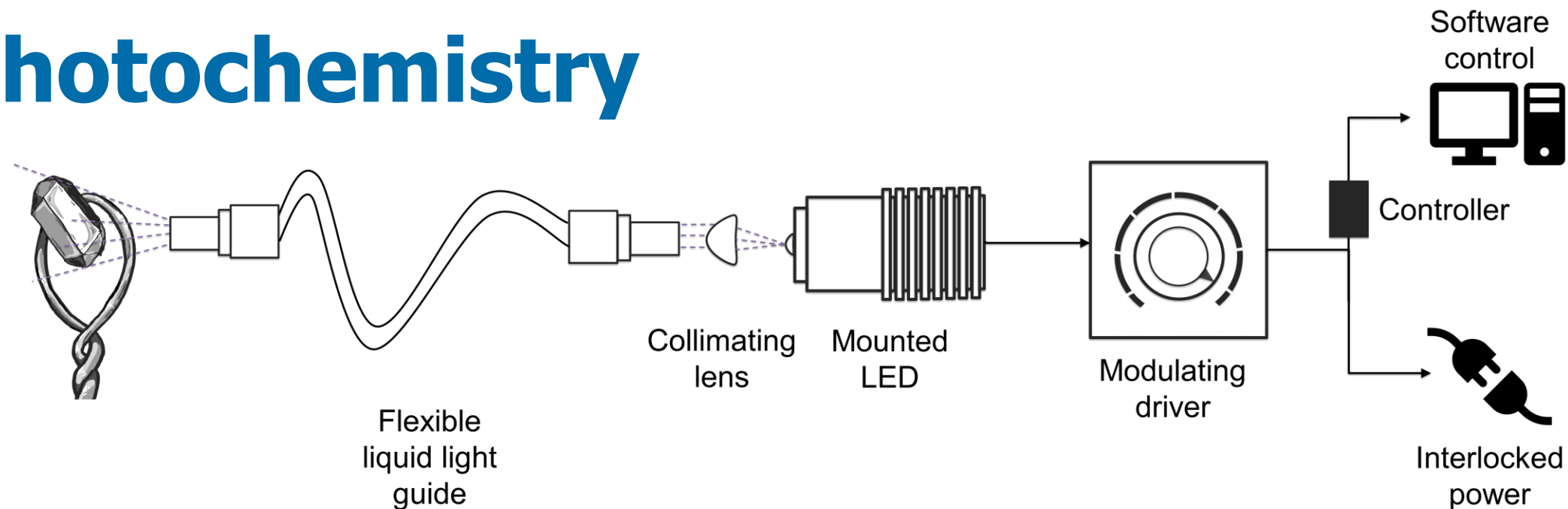
Photochemistry

25 narrow-bandwidth LEDs

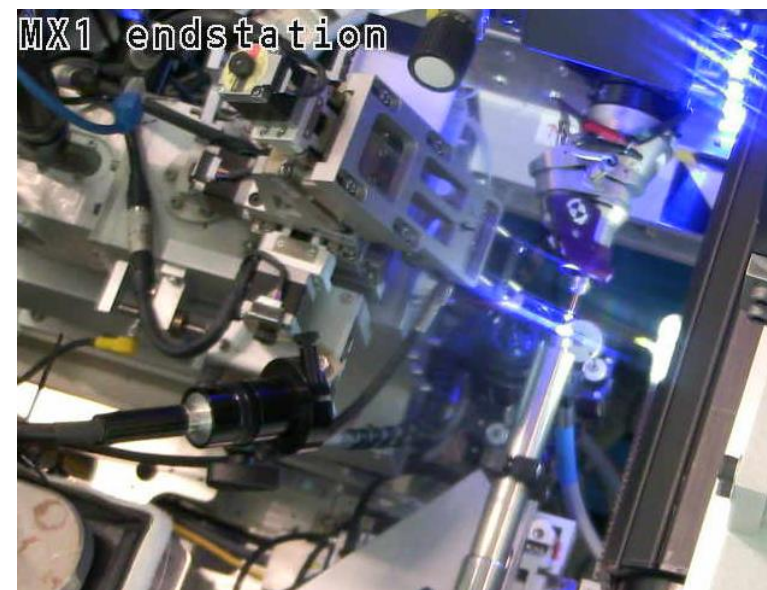
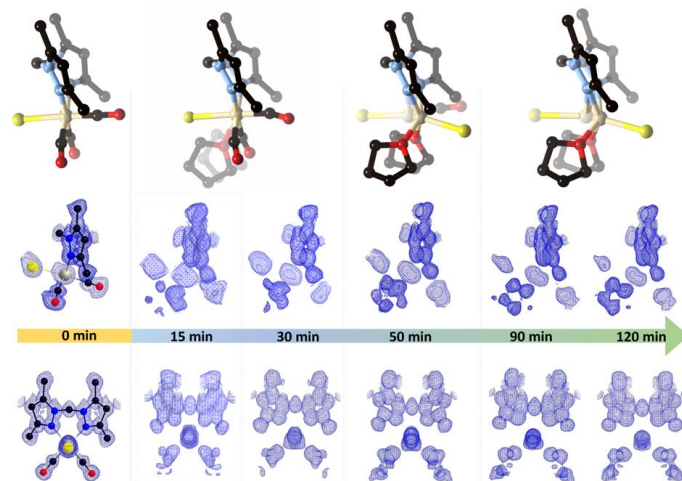
265-1050 nm

Redox activity, bond cleavage

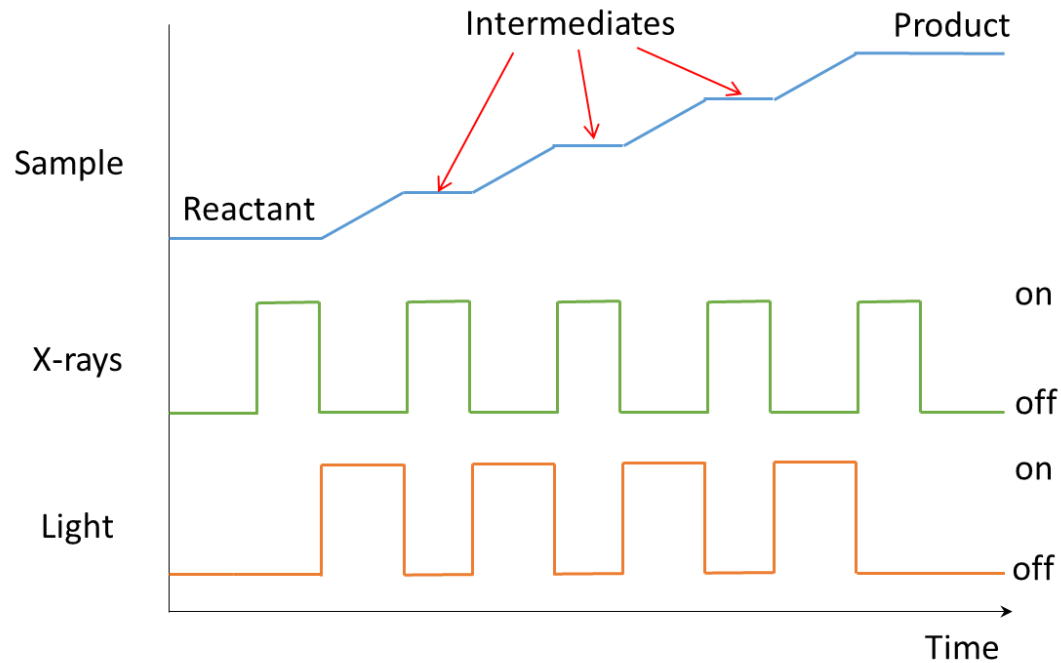
Photochemistry



Studying
irreversible
photo-chemical
reactions



Photochemistry



MX1 User Controls Mini-Kappa Cryo Temperature Distance selector Light and attenuation DAC centering **LEDs** Variable Position

LED control for photochemistry

Manual LED control

Check table of LEDs in user wiki for required driver current

LED table...

Driver current: 1000mA

Power (%): 0

LED on LED off

Read back: 0 %

Automated data collection

Under development - ask staff to use

Wavelength (nm): 365.00

Power (%): 100

Total irradiation time (min): 3.00

Collection interval (min): 1.00

Collect To stop automated collection input Ctrl C into pop-up terminal

1. Set the cryo to the temperature you require
2. Center and screen your crystal
3. Fill in collection details in the collection tab* and the LED and experiment details above
4. Press *Collect*
5. Set the cryo back to 100K and check that the LED is turned off

For more information see the user wiki

*Make sure that your experiment prefix is unique to ensure that "prefix"_ASPhoto.cif is not overwritten

LED

Data collection

Green - running

Red - off

25 narrow-bandwidth LEDs 265-1050nm

High Pressure

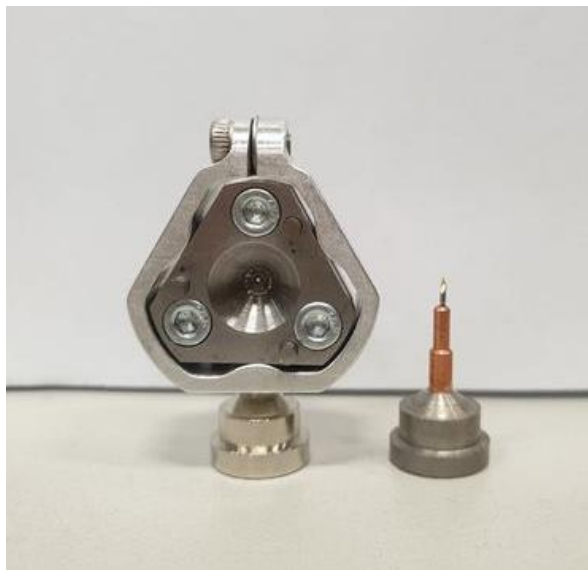
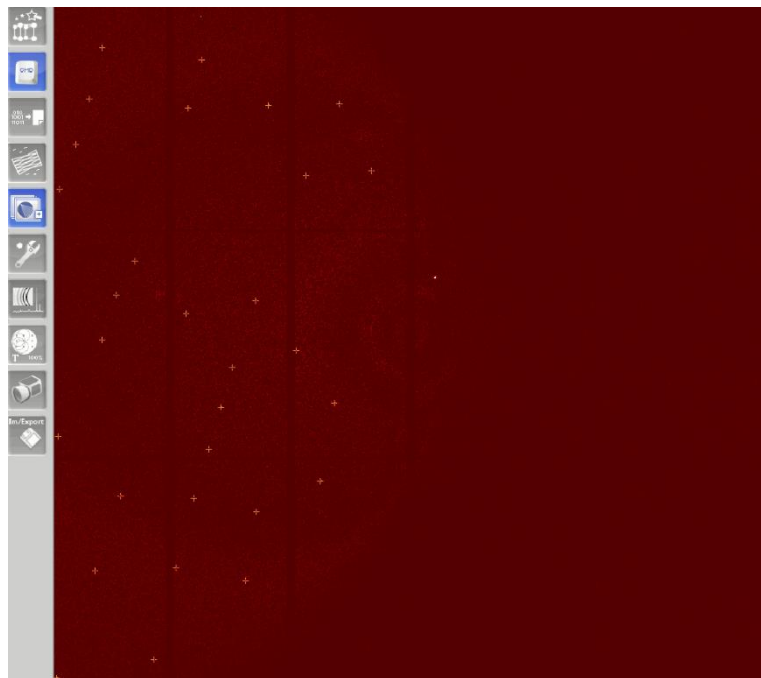
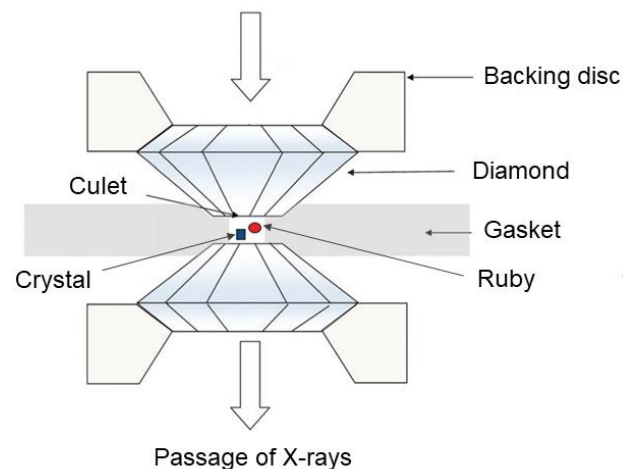
Mini Diamond Anvil Cell can be mounted as a normal pin

Data collection at room temperature

Up to $\approx 5 \text{ GPa}$
 $\approx 50,000 \text{ atm}$



Steph Boer

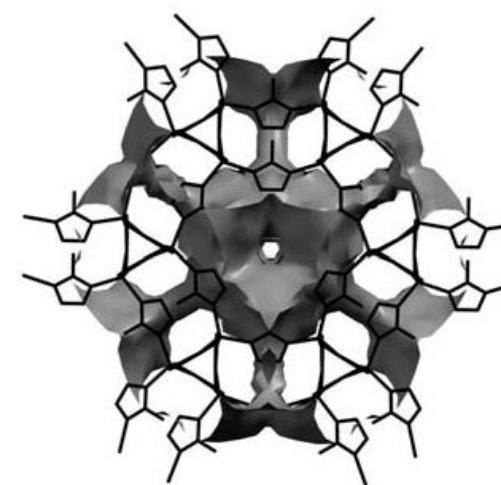
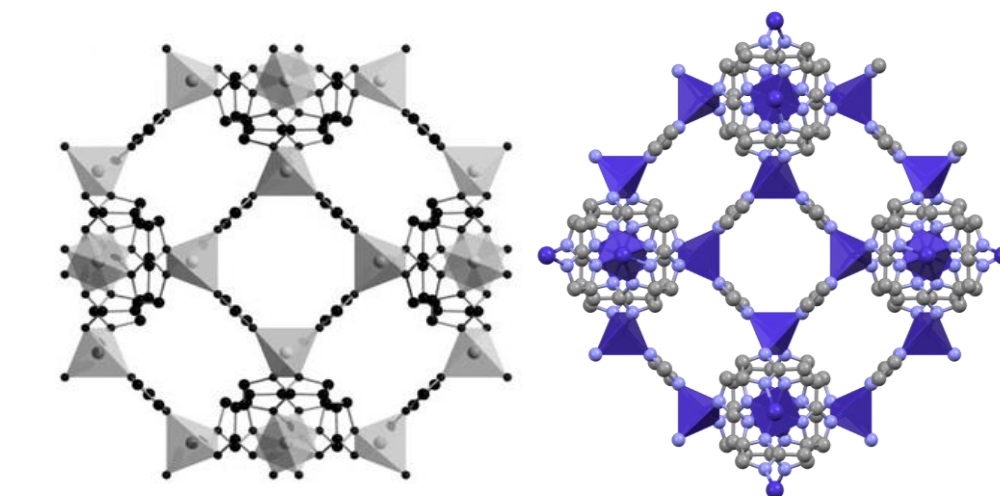


MOFs under pressure

	ZIF-8	ZIF-67
Diffractometer	Bruker Smart Apex diffractometer	MX1
Radiation	Mo _{Kα} ($\lambda = 0.71073 \text{ \AA}$)	Synchrotron ($\lambda = 0.71076 \text{ \AA}$)
Detector	Apex 2 CCD	Eiger2 9M
Collection time	24 hours†	70 seconds
R_1^*	0.0512	0.1290
R_{int}	0.073	0.0456
Completeness	0.996	0.925
Resolution	0.80 $\text{\AA}$	0.80 $\text{\AA}$
Reflections collected	14248	2784
Independent Reflections	956	875
GooF	0.964	1.808
Data/parameter	21.9	25.7

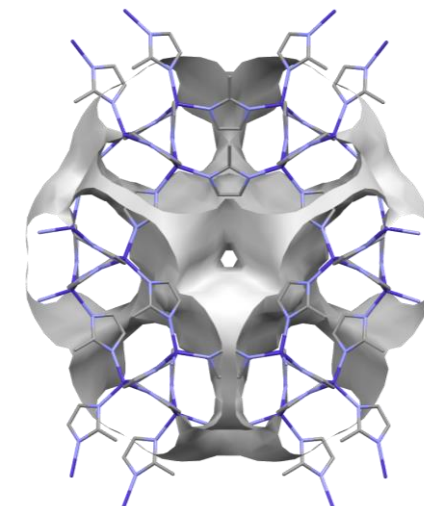
* $[I] \geq 2\sigma(I)$

† Could be collect in ~1 hour with more modern instruments



1.47 GPa

ZIF-8
(Zn)

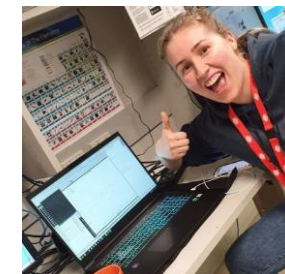


1.57 GPa

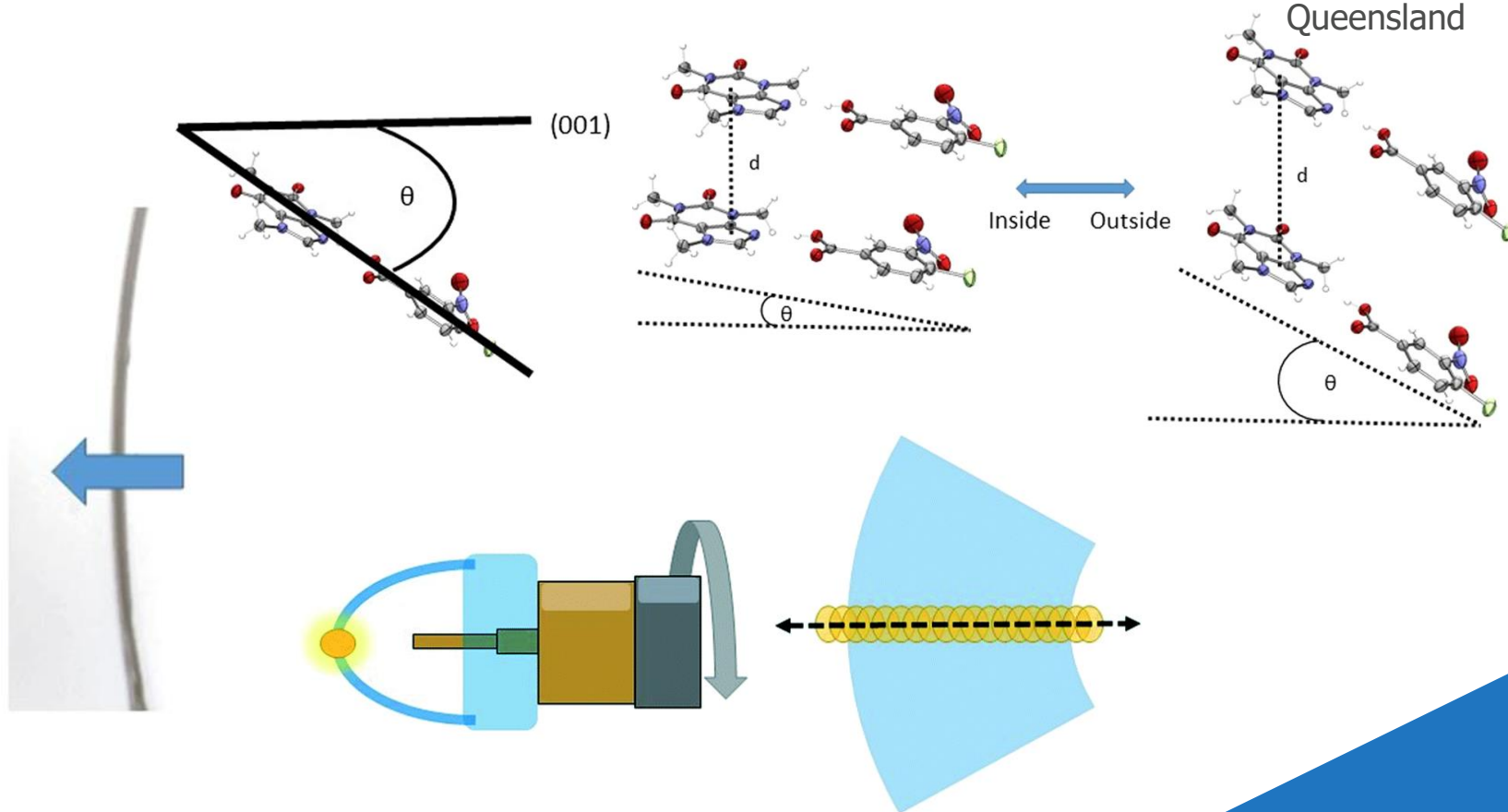
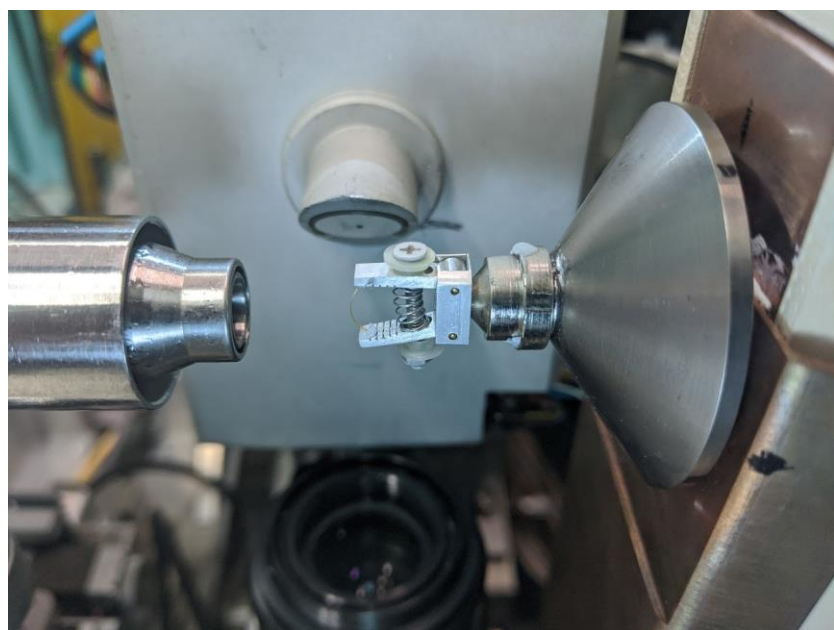
ZIF-67
(Co)

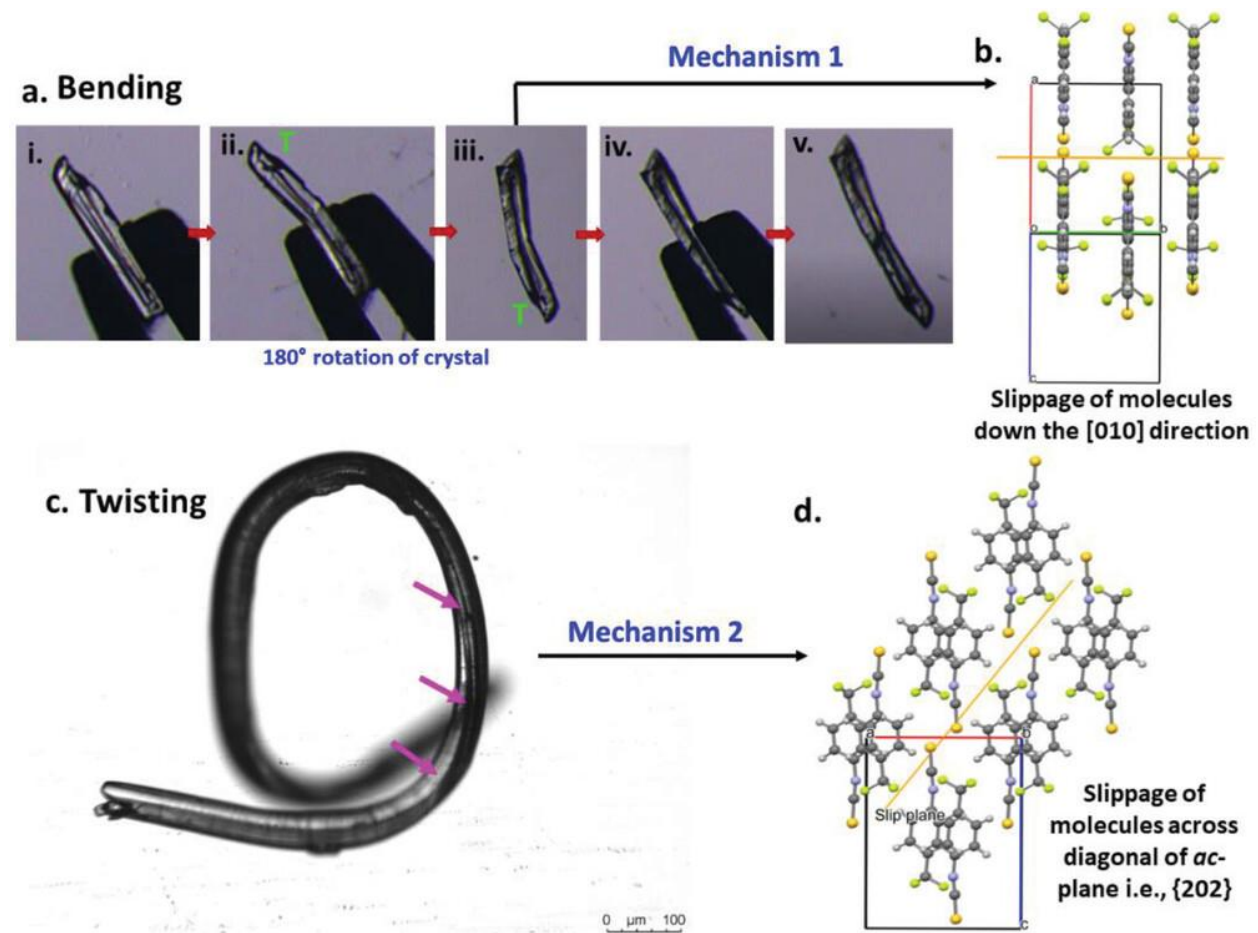
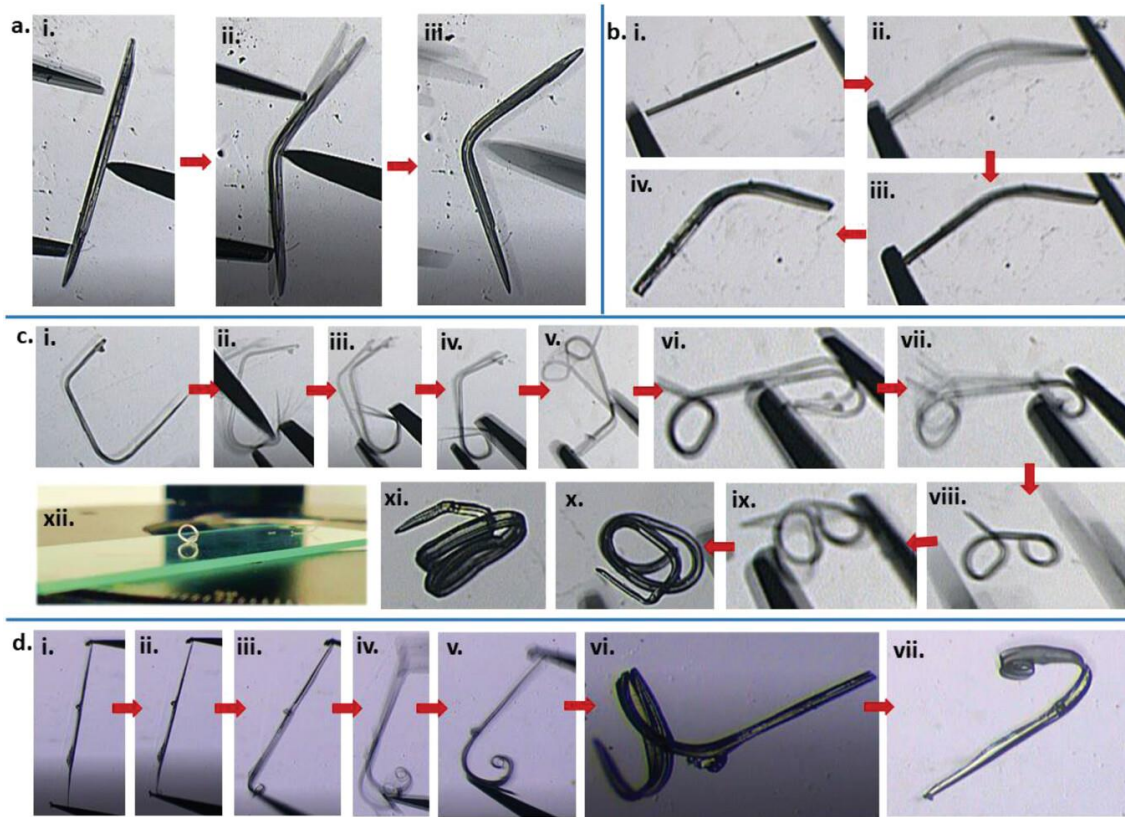
Position analysis

Mapping studies on MX2 using the 7.5 micron microcollimator

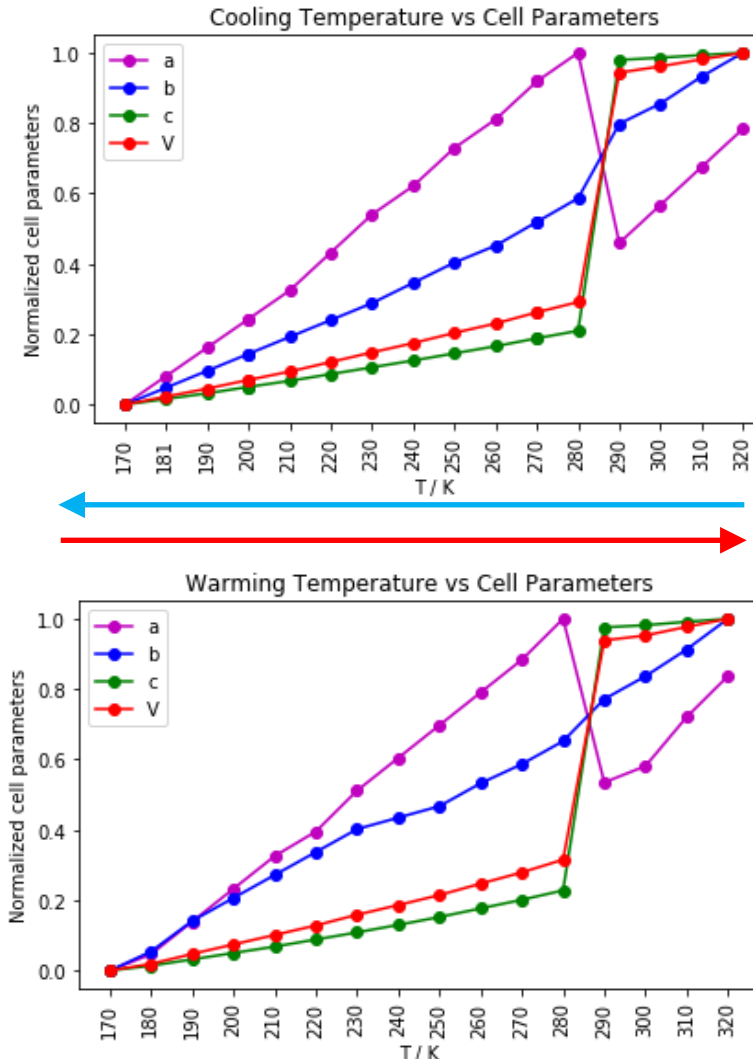
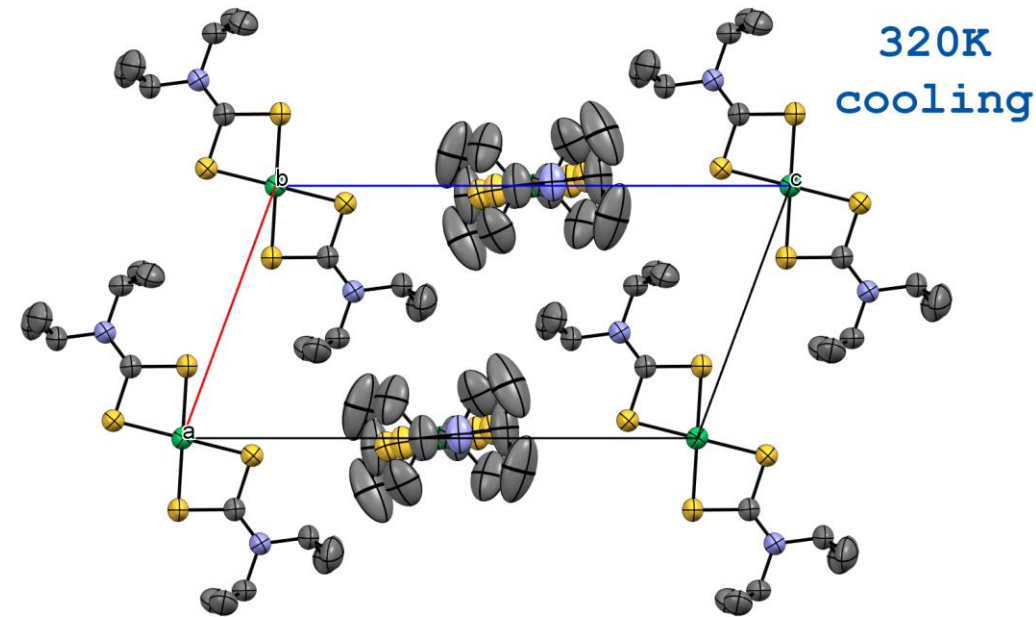


Amy Thompson,
University of
Queensland



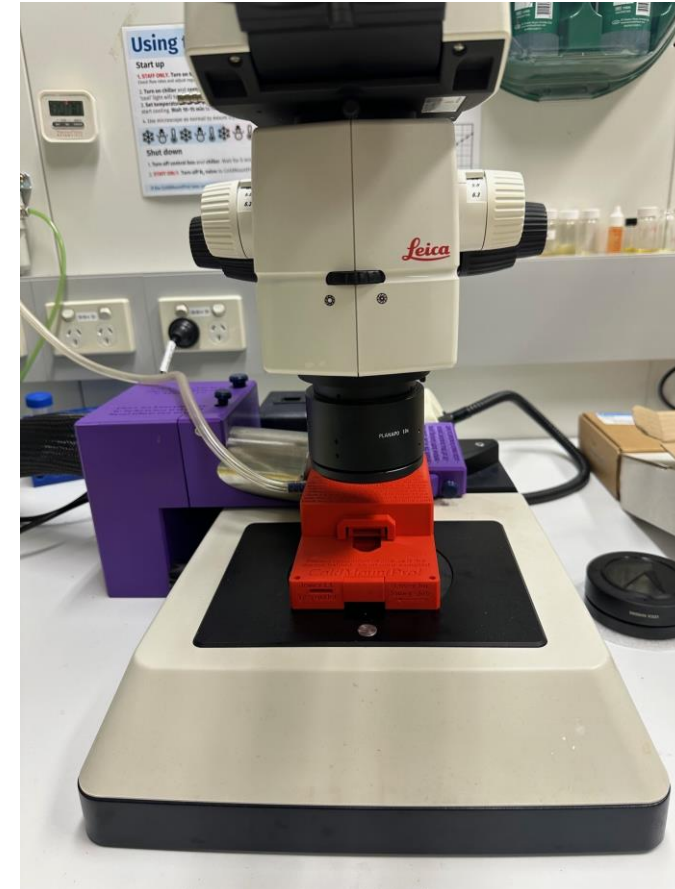
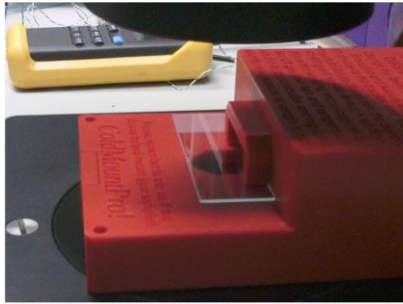
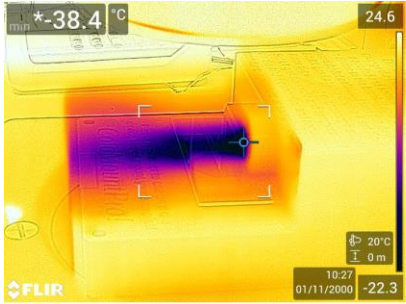


Variable temperature: phase transition



- Temperature ramp
 - Ramp temperature and trigger data collection at temperature.
- Heat 5K every minute
- Collect every 2 mins (10K),
- 32 full data collections in 60 minutes
- 240° sweep, 12 s, 200Hz

Handling Sensitive Crystals (ColdMountPro)



Australian
National
University

Designed and built by Dr
Michael Gardiner



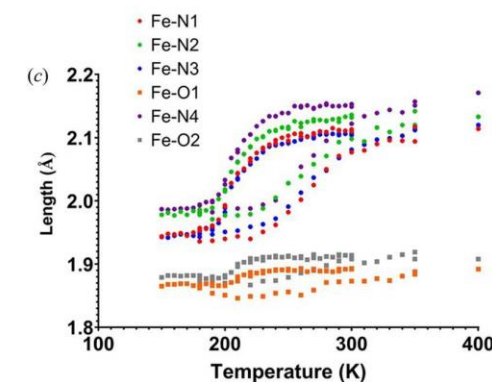
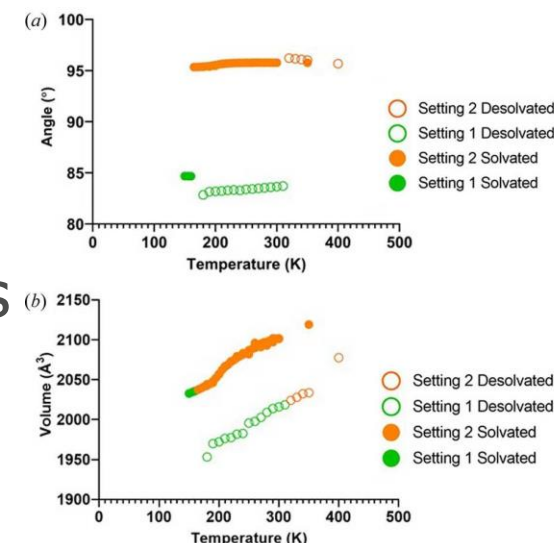
-80 to $+40^{\circ}\text{C}$

Excellent for reactive or fragile crystals
Easy to use (stays cold and doesn't ice up
for hours!)

CX-ASAP

Chemical *X*tallography – Australian *S*ynchrotron *A*uto-*P*rocessing

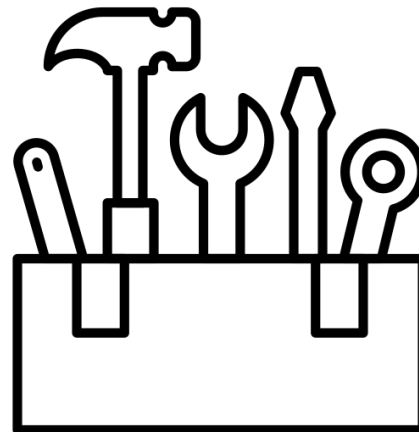
- Open-source data processing and refinement software
- Modular architecture to allow for job-specific pipelines
- Perfect for dynamic crystallographic experiments
 - Variable temperature
 - High pressure
 - Photocrystallography
 - Application of force on crystals (bendy crystals)



Multi-purpose beamlines

Disadvantages

- Changing between collection modes takes time and staff intervention
- Not as optimised as specialised beamlines for the intended experiment



Advantages

- Access a wide range of techniques, software and equipment
- More varied expertise
- Mixing of user communities
- 'Outside-the-box' experiments

Thank you!

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