

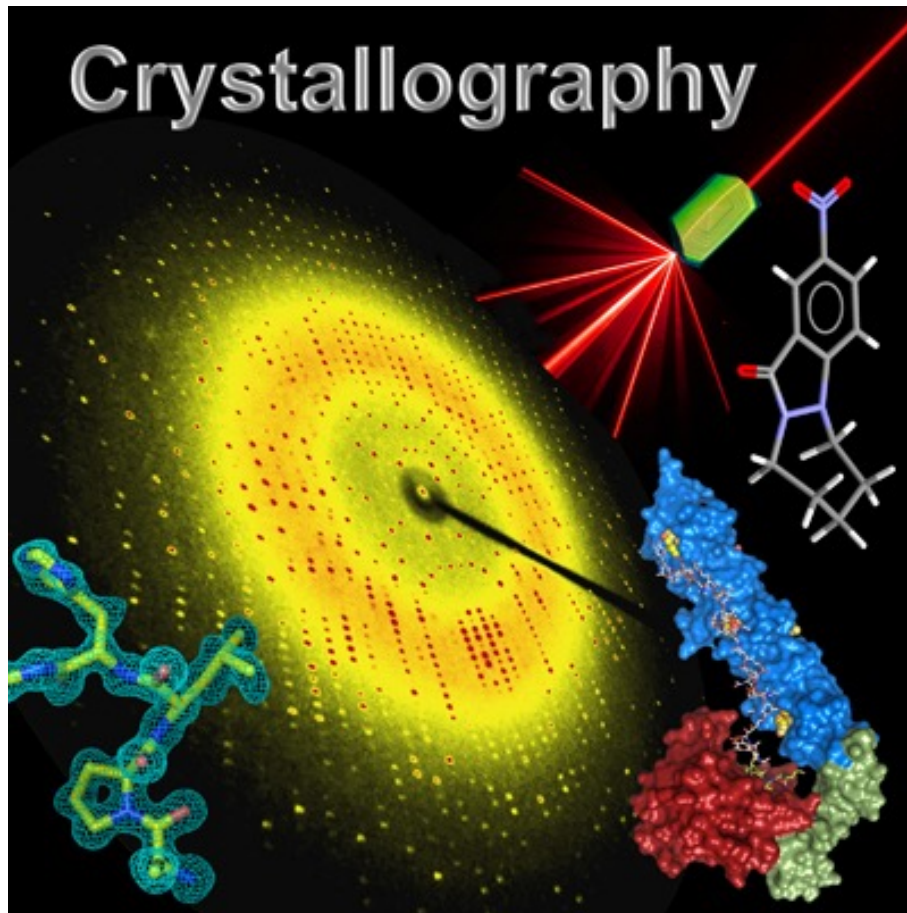
C7270

Biological X-Ray Crystallography and
Cryo-Electron Microscopy

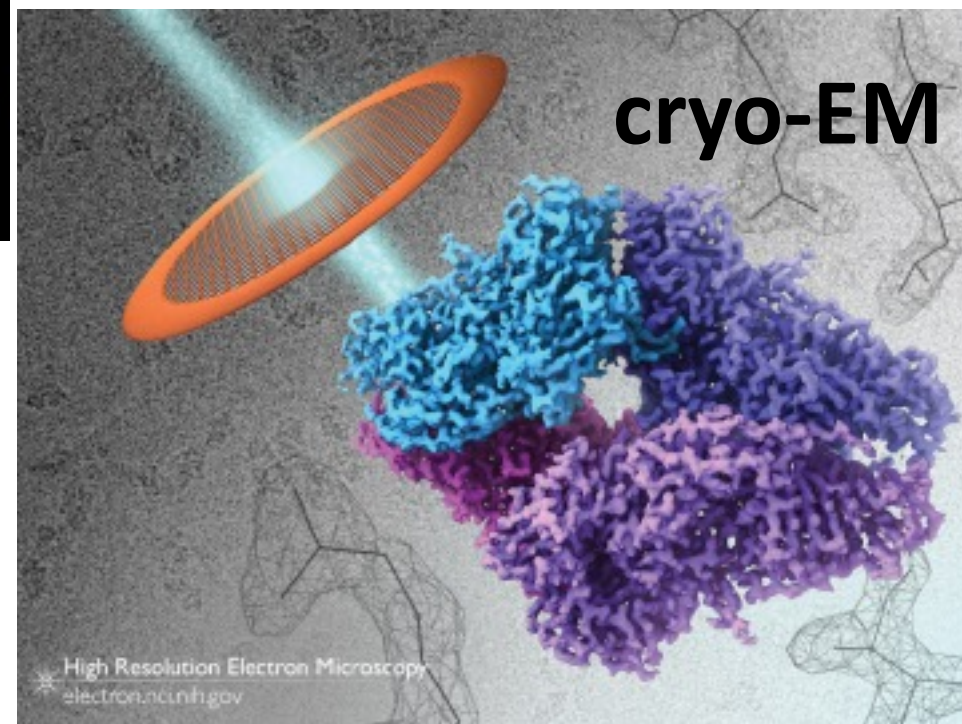
Fall 2024

Pavel Plevka, Tibor Füzik, Jiří Nováček

Crystallography



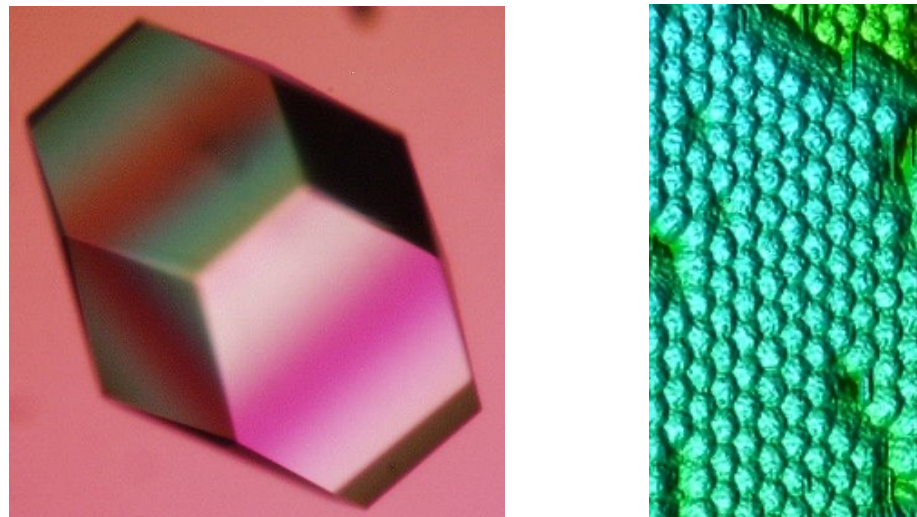
cryo-EM



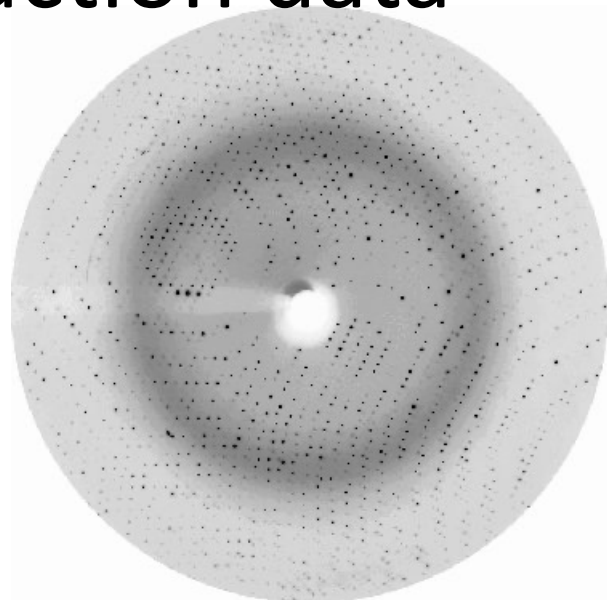
1. Expression & purification



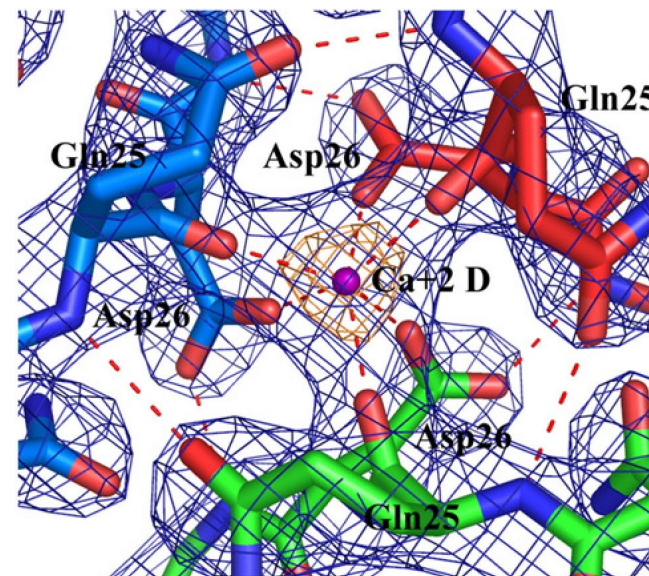
2. Crystallization



3. Diffraction data



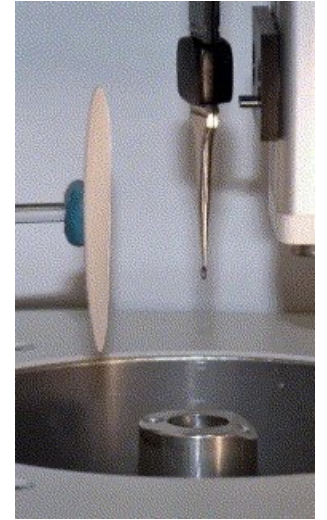
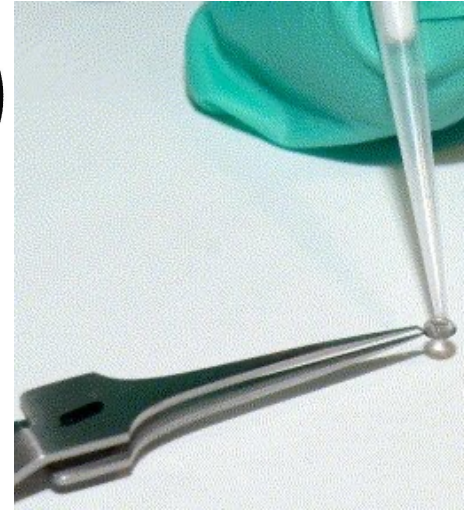
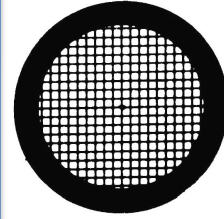
4. Solve structure



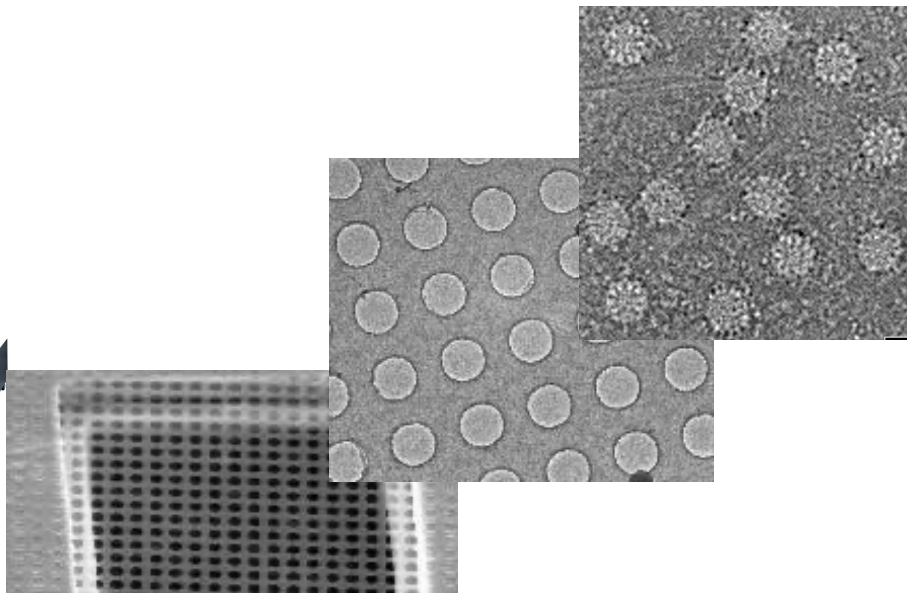
1. Expression & purification



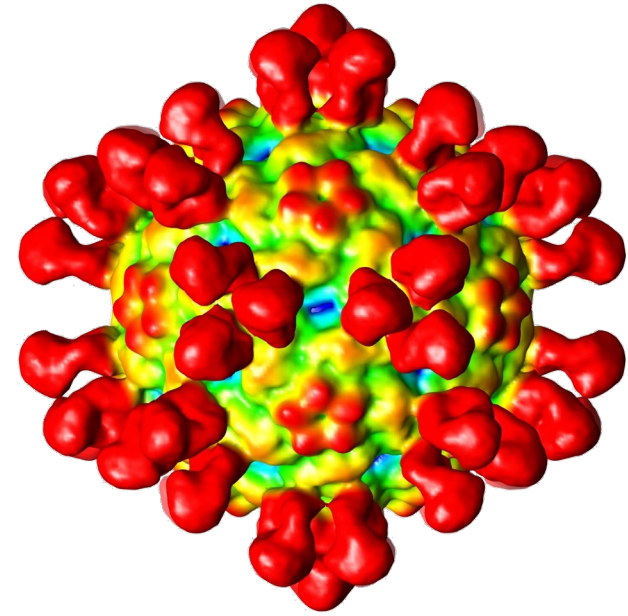
2. Grid preparation



3. cryo-EM data



4. Reconstruction



Aims of the course

- Diffraction of light
- Approaches to resolve phase problem in crystallography
- Use of electrons to display objects with high magnification and fine detail
- Calculation of three-dimensional reconstruction from two-dimensional projections

What is asked of you:

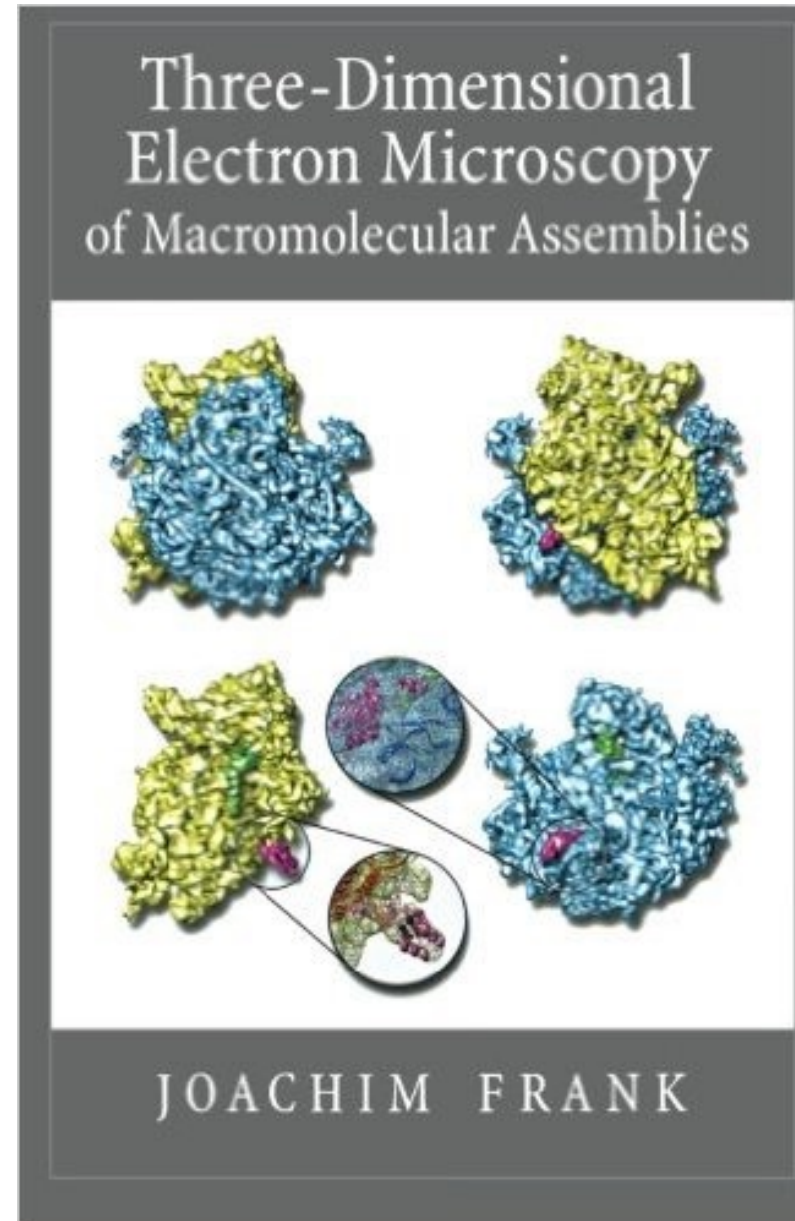
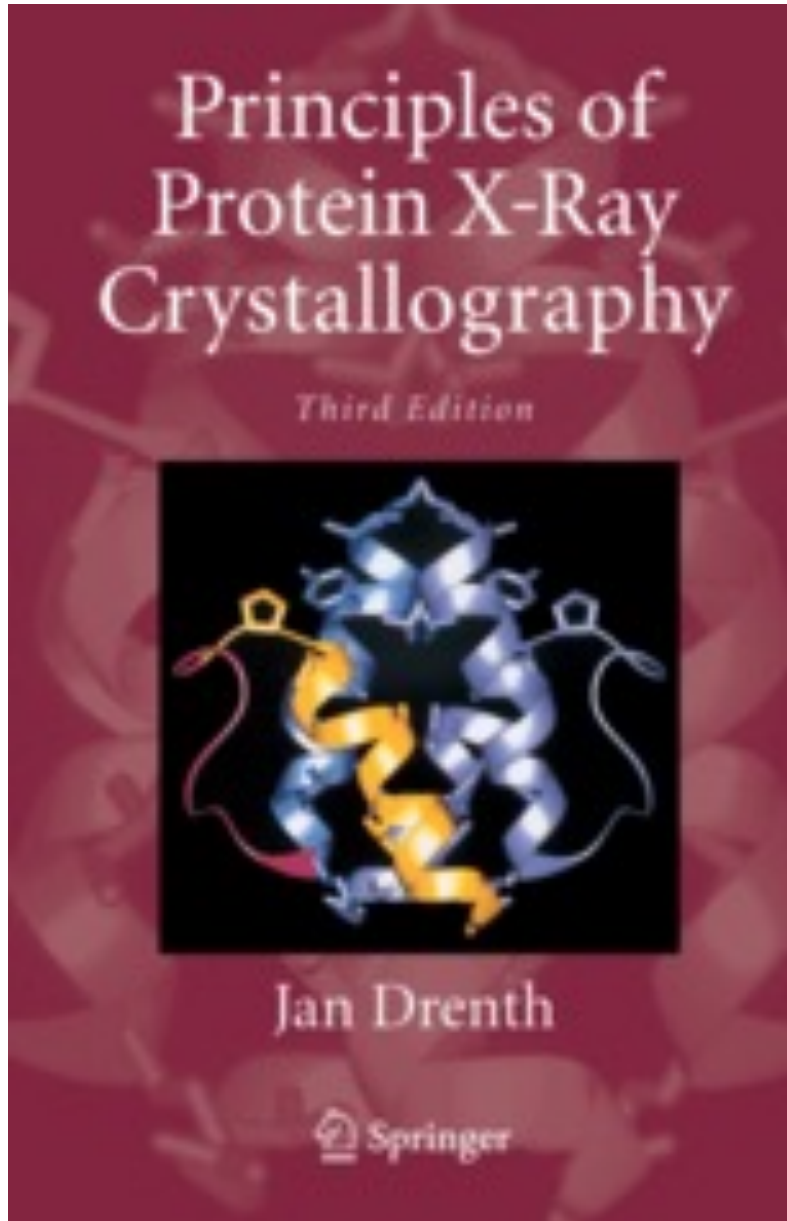
- Be present and awake
- Participate in discussions
- I am here to help, learning is up to you!

- Ask questions - it will help to clarify the issue not only for you but for your peers as well!
- In class discussions, be respectful of other students' opinions.

Not part of this course:

- Basic math – mental overload by dealing with simple equations.
(Observed before.)
- Reserve time for thinking.

Course textbooks:

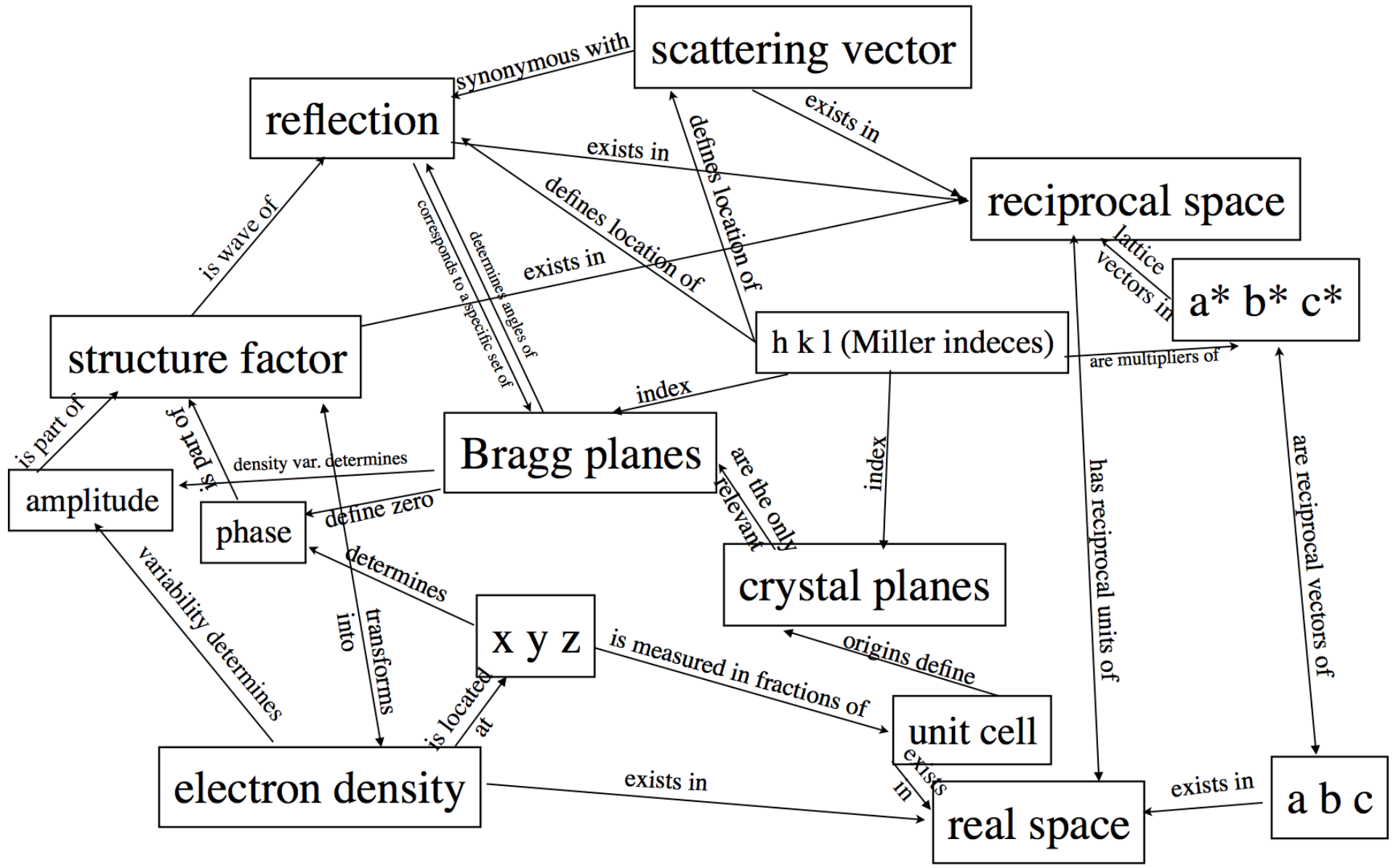


L#	Date	Time	Lecturer	Topic	Chapter reading
1	13.9.	12:00-13:25	Pavel Plevka	Development of X-ray crystallography, crystallization of macromolecules, phase diagram, Crystal symmetry, symmetry operators, point groups, space groups.	Drenth: 1, 2, 3
2	20.9.	12:00-14:30	Pavel Plevka	Diffraction of light by electrons, atoms, unit cell, crystal. Bragg's law. Diffraction images and indexing.	Drenth: 4
	27.9.			No lecture	
3	4.10.		Pavel Plevka	Fourier transform, structure factor, intensity of diffraction spots.	Drenth: 4, 5
4	11.10.		Pavel Plevka	Solutions to phase problem in X-ray crystallography. Isomorphous replacement, SAD, MAD, Molecular replacement. Rotation and translation function. Model building and refinement.	Drenth: 7, 10
5	18.10.		Tibor Füzik	Electron microscope. Interaction of electrons with matter, electron imaging. Amplitude and phase contrast. Contrast transfer function.	Frank: 1, 2
6	25.10.		Tibor Füzik	Fourier transform and its properties, convolution, point spread function.	Frank: 2
7	1.11.		Jiří Nováček	Analysis of electron micrographs. 2D classification. Principal component analysis.	Frank: 3, 4
8	8.11.		Jiří Nováček	Three dimensional reconstruction - single particle reconstruction and tomogram calculation. 3D classification.	Frank: 5
9	15.11		Jiří Nováček	Improving cryo-EM reconstruction, particle polishing, Ewalds, sphere correction, per particle CTF, ... Model building and refinement. Detection of errors, validation and detection of mistakes.	Frank: 6
10	TBD	TBD	Holger Stark	State-of-the-art cryo-EM of macromolecular complexes.	
11	TBD	TBD	Holger Stark	State-of-the-art cryo-EM of macromolecular complexes.	

Course plan

No lecture
next week!

Biological X-Ray Crystallography





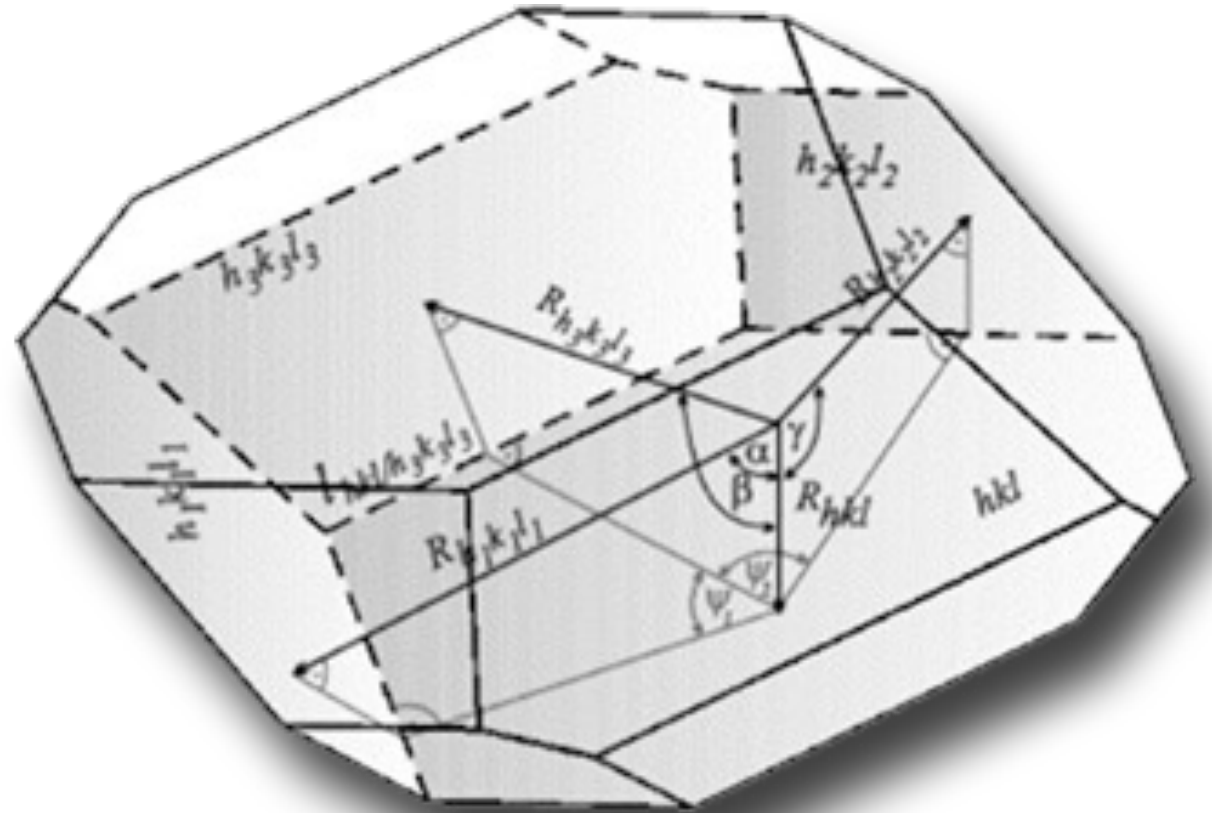
Why do single snowflakes, before they become entangled with other snowflakes, always fall with six corners? Why do snowflakes not fall with five corners or with seven?



Johannes Kepler (1571-1630)

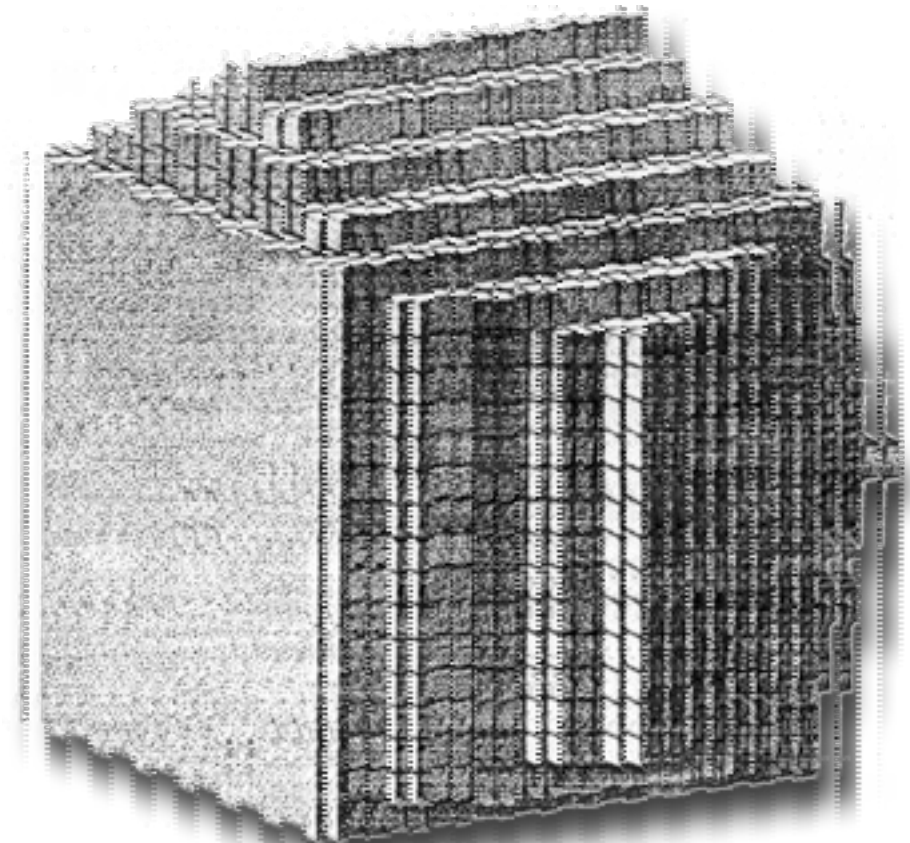


Although crystals of quartz and hematite appear in a great variety of shapes and sizes, the same interfacial angles persisted in every specimen. “*Law of Constancy of Angles*”



Niels Stensen (1638-1686)

“Law of Constancy of Angles”

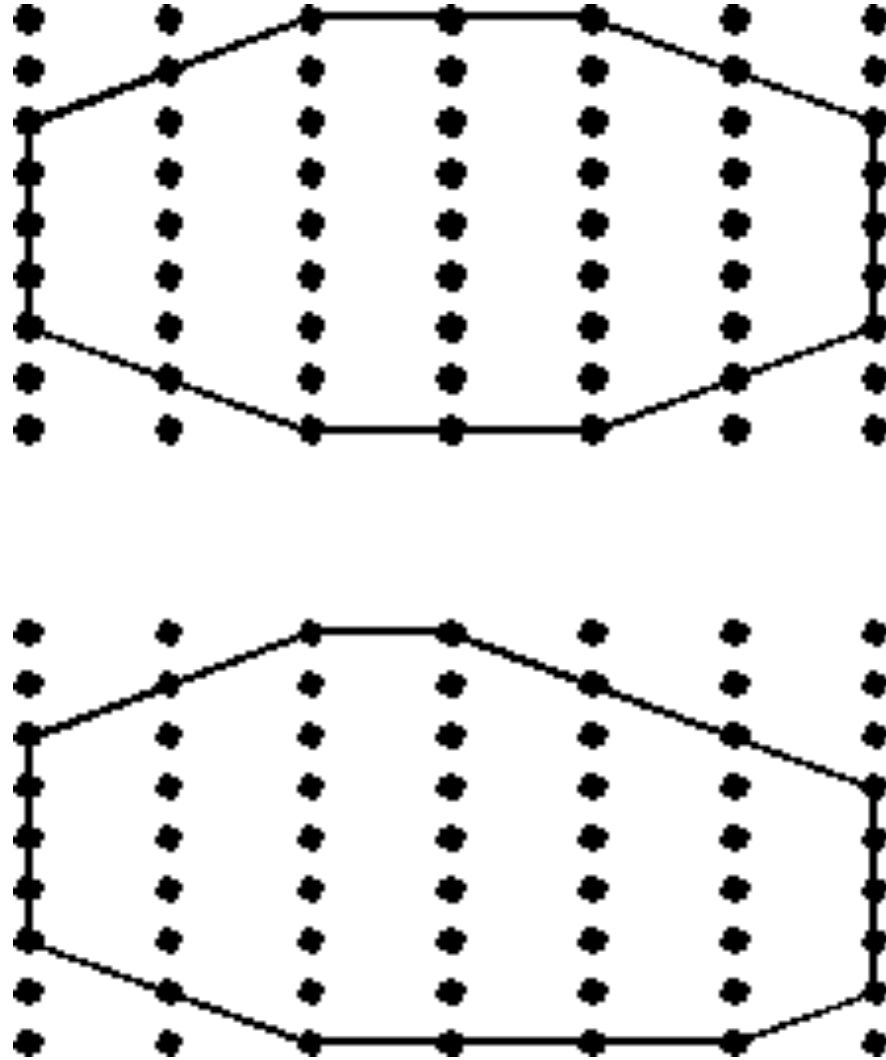


René Just Haüy (1743-1822)

“Law of Constancy of Angles”



René Just Haüy (1743-1822)

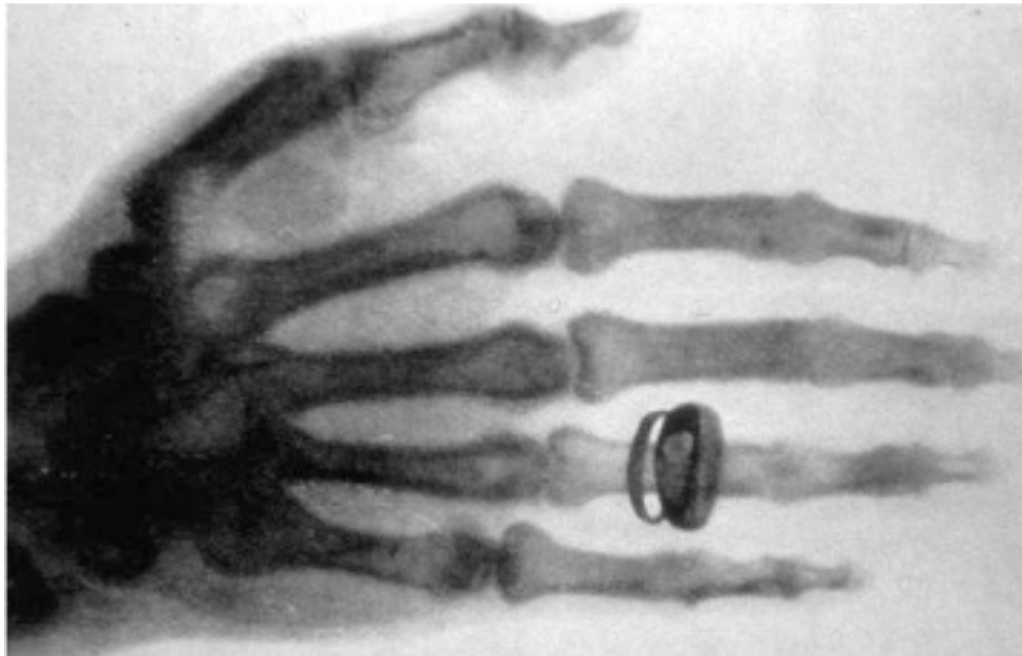


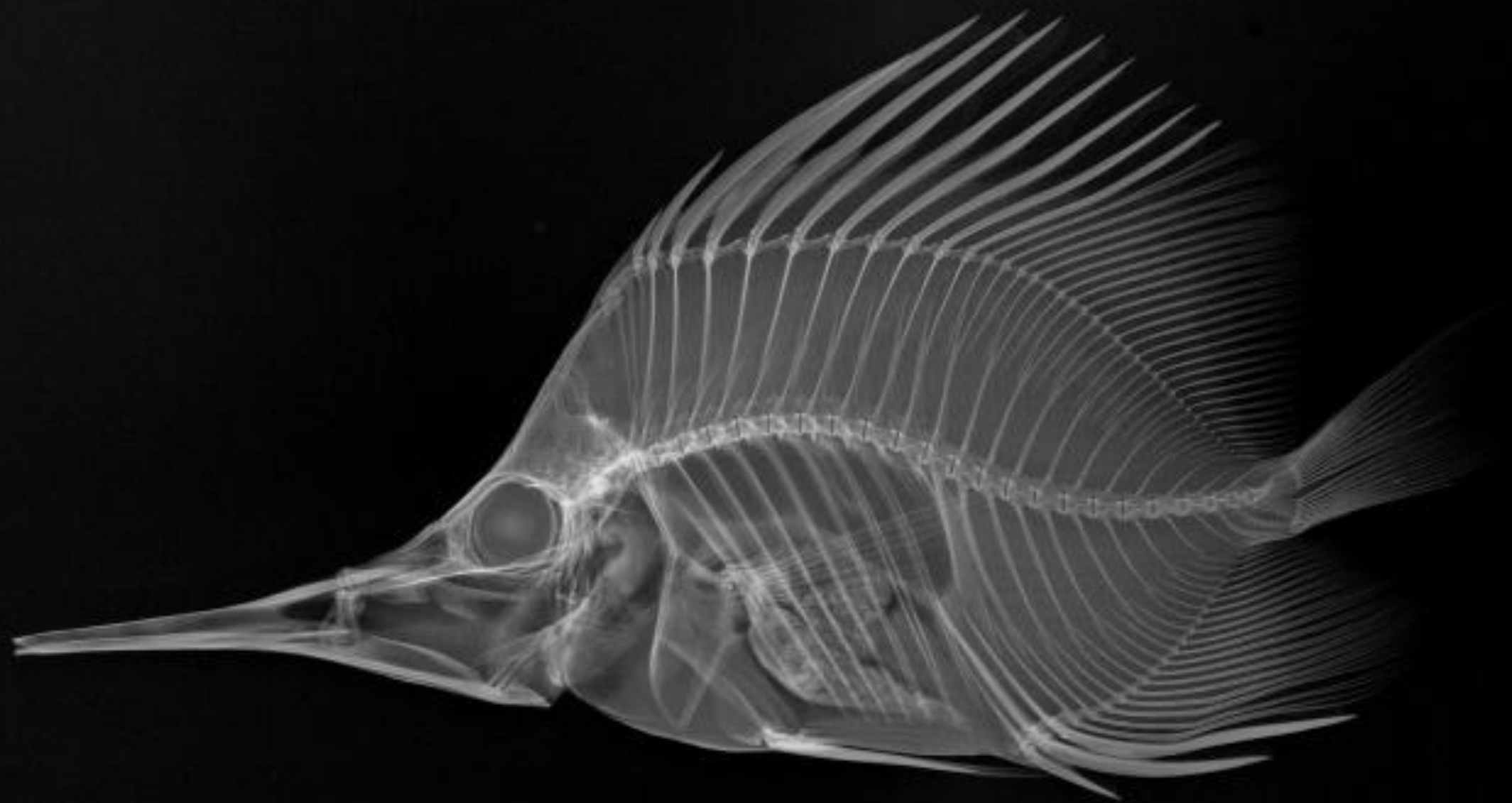
History of fundamental discoveries

WILHELM CONRAD RÖNTGEN (1845-1923)

- **1901 Nobel Laureate in Physics**

discovery of the remarkable rays subsequently named after him

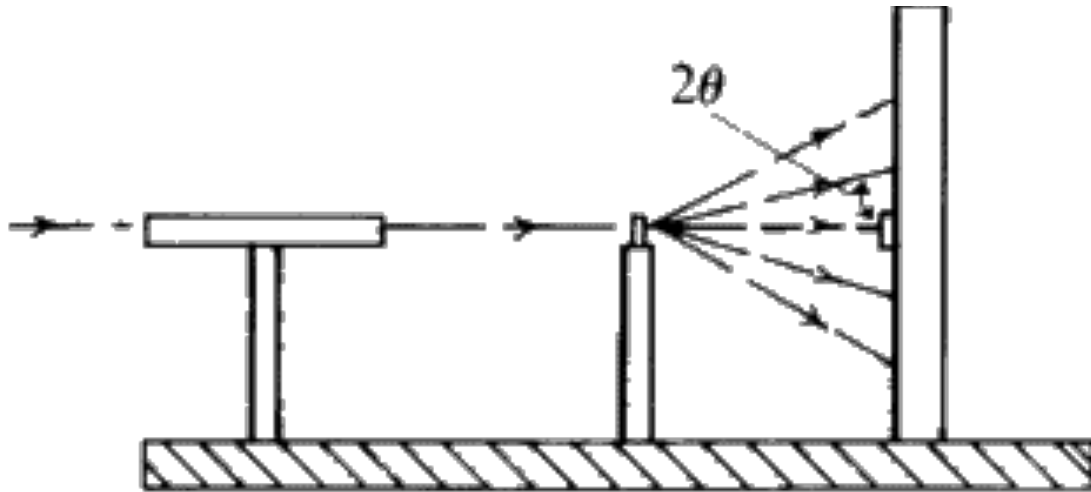




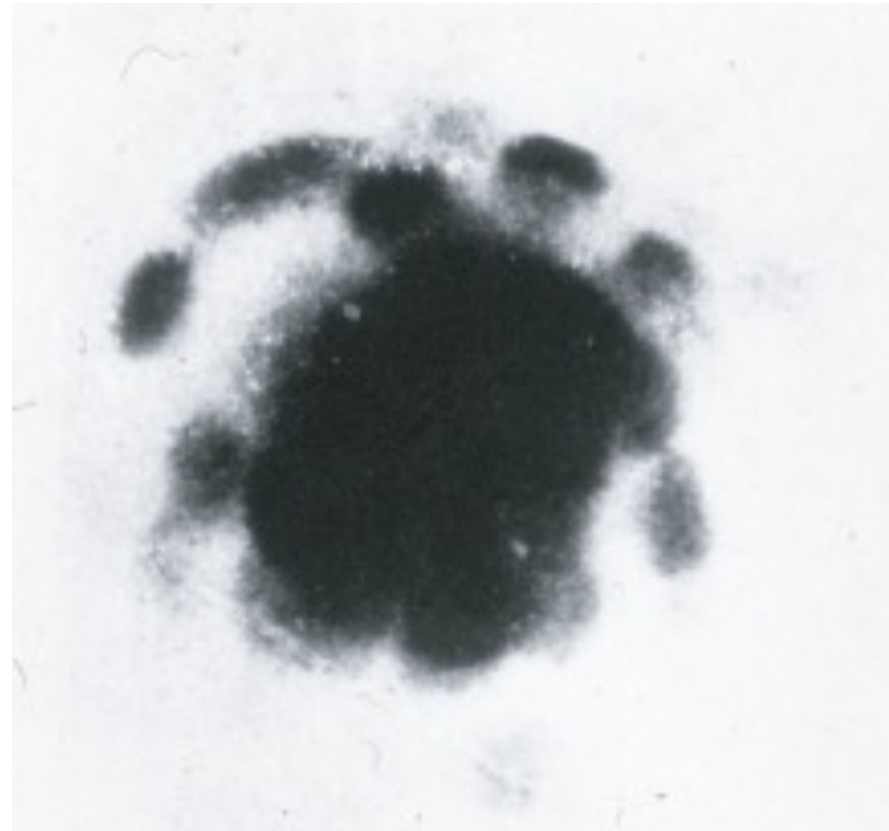
MAX VON LAUE (1879-1960)

- **1914 Nobel Laureate in Physics**

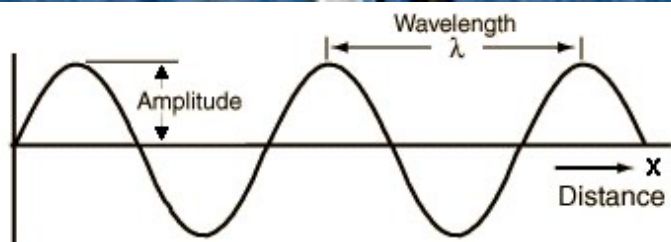
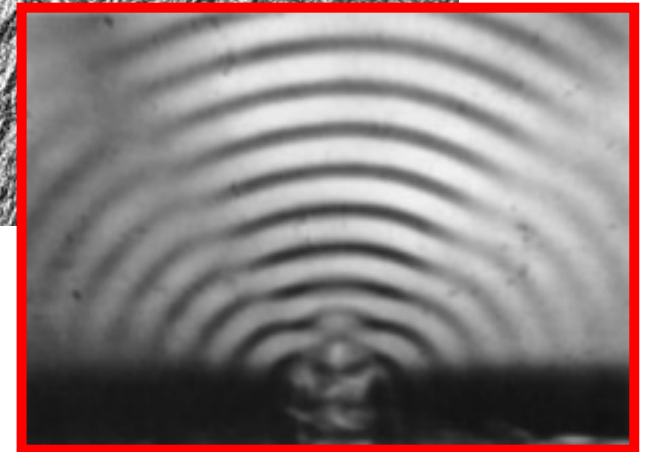
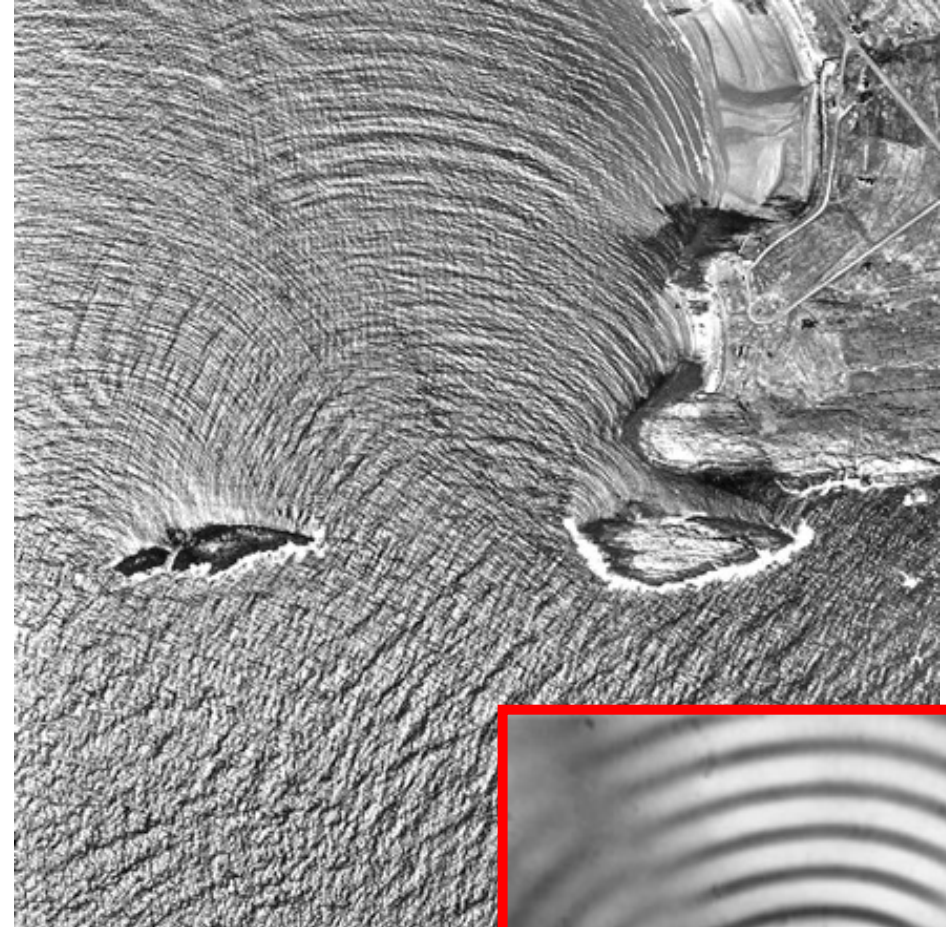
for his discovery of the diffraction of X-rays by crystals



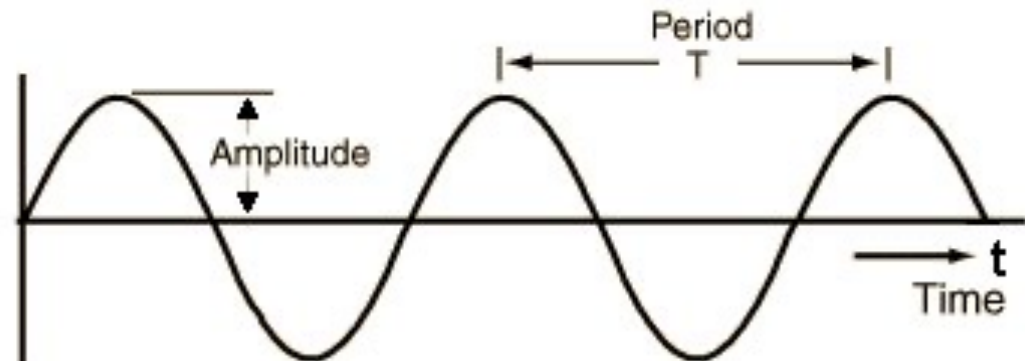
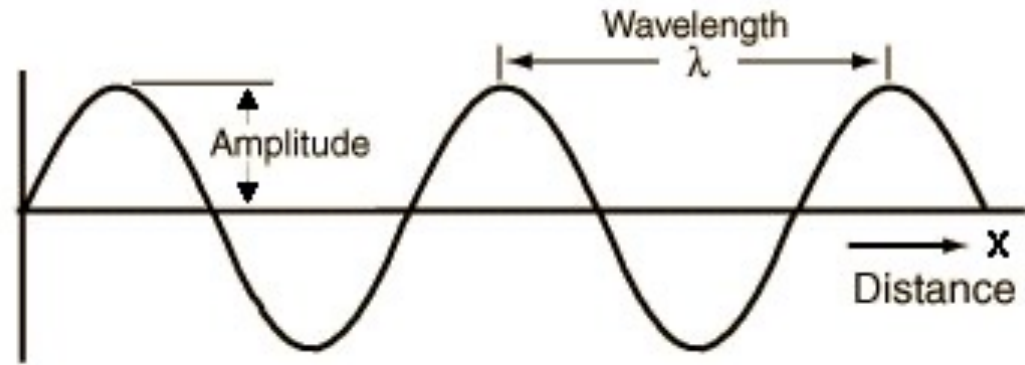
Friedrich and Knipping



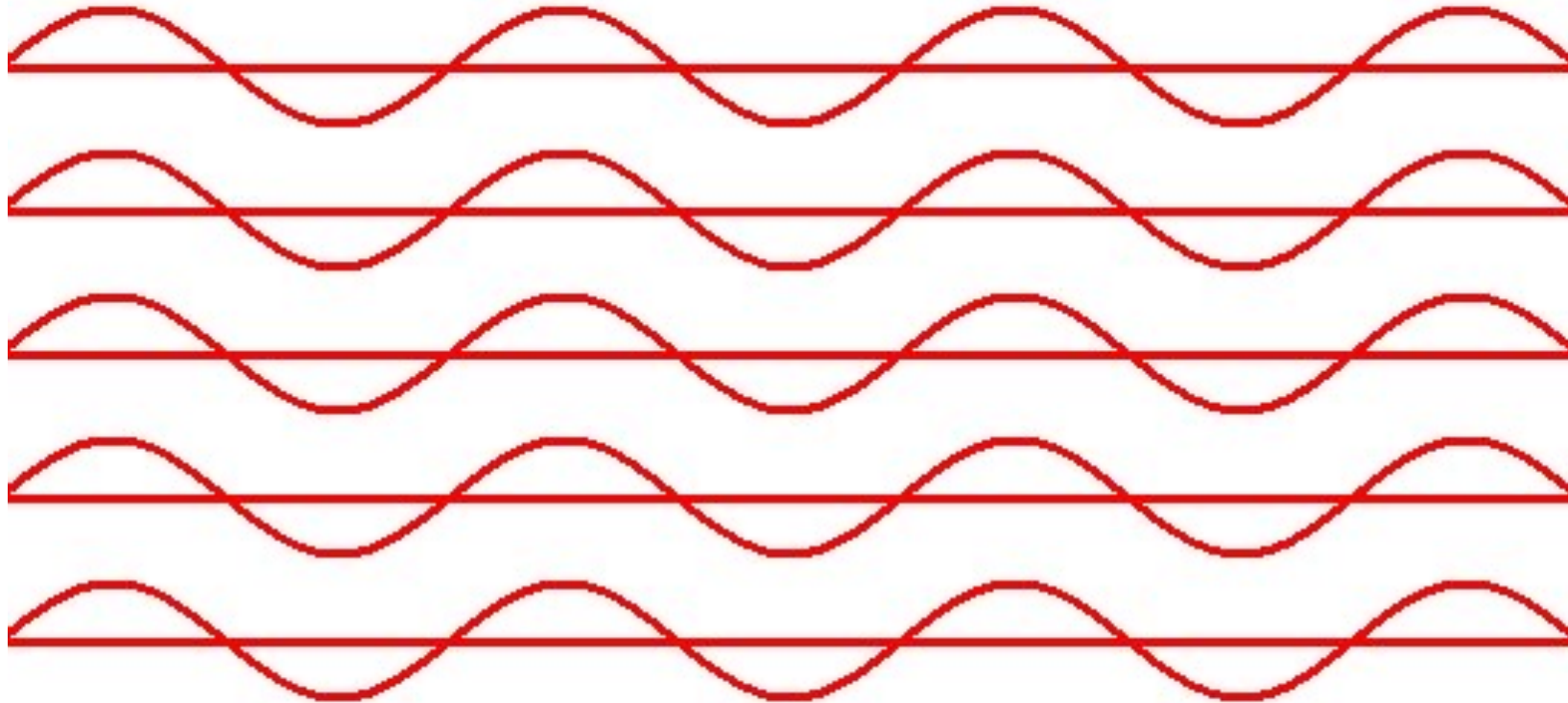
Wavelength and diffraction



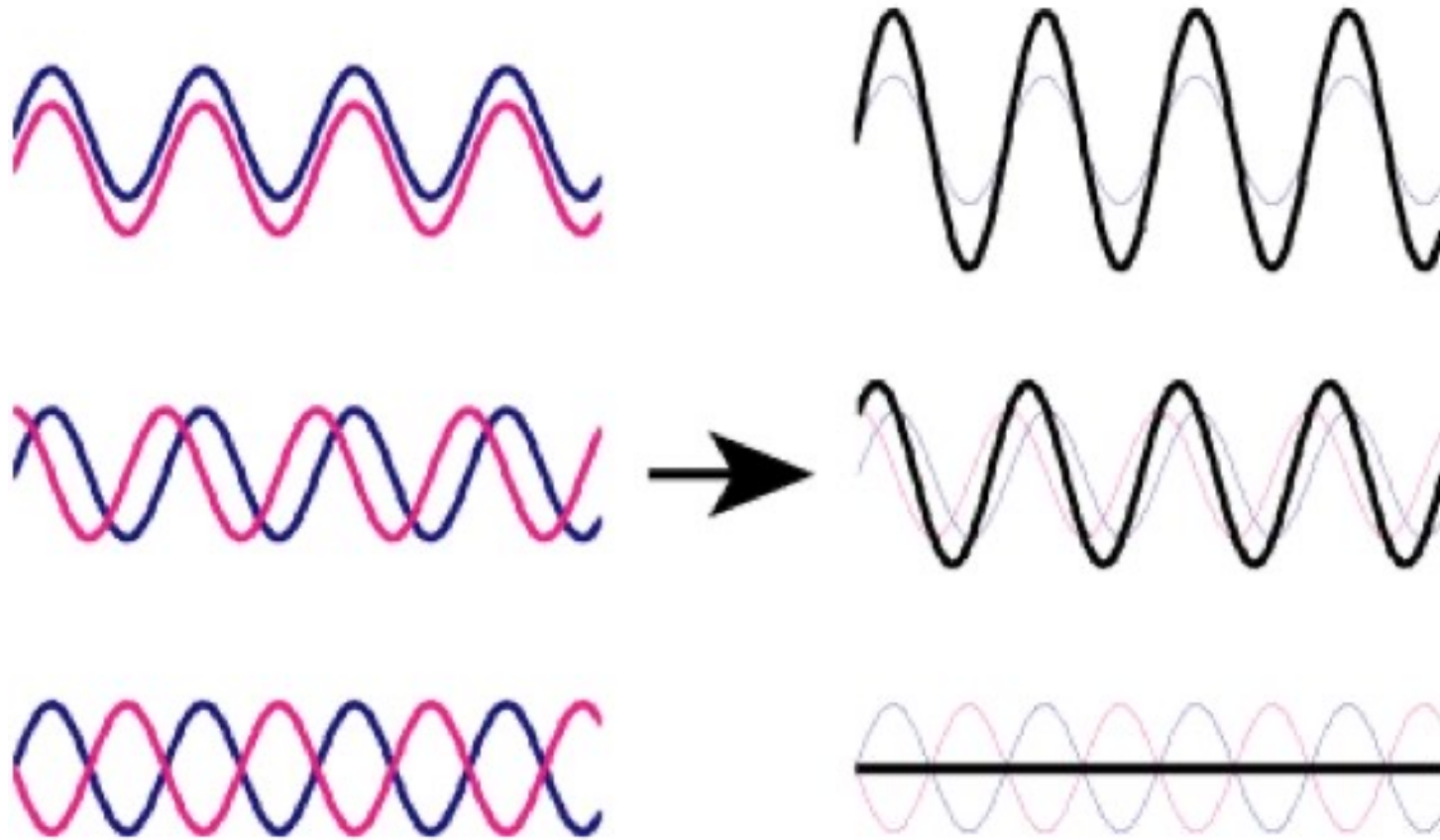
Waves



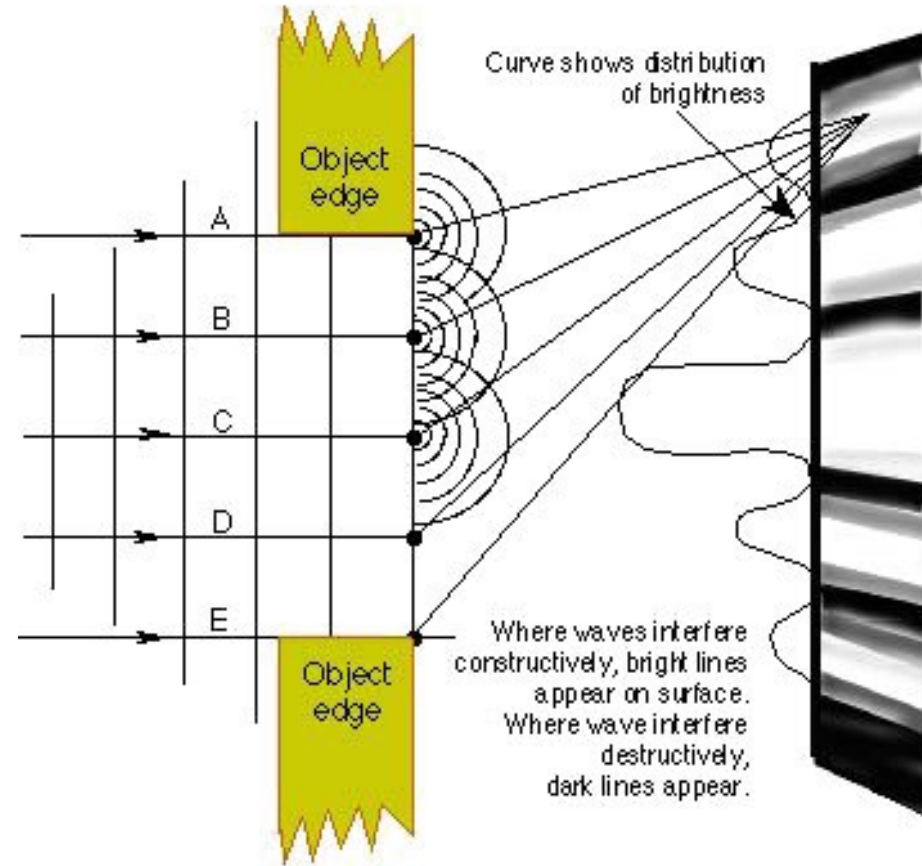
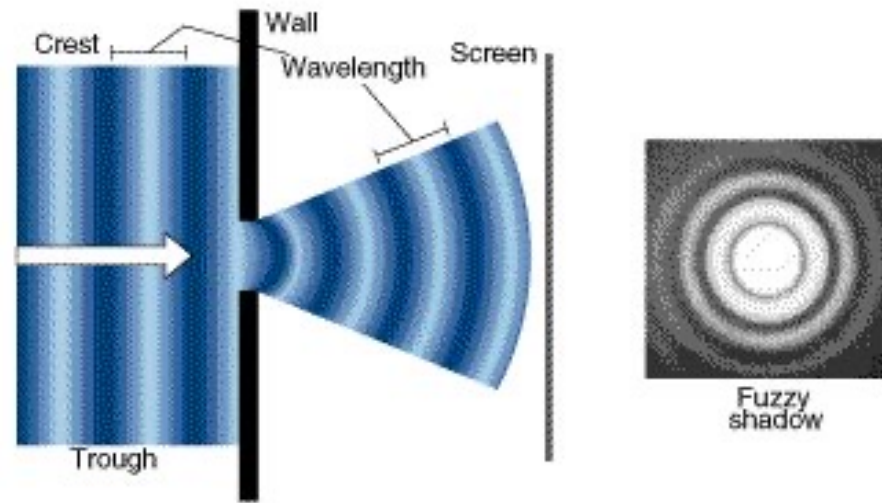
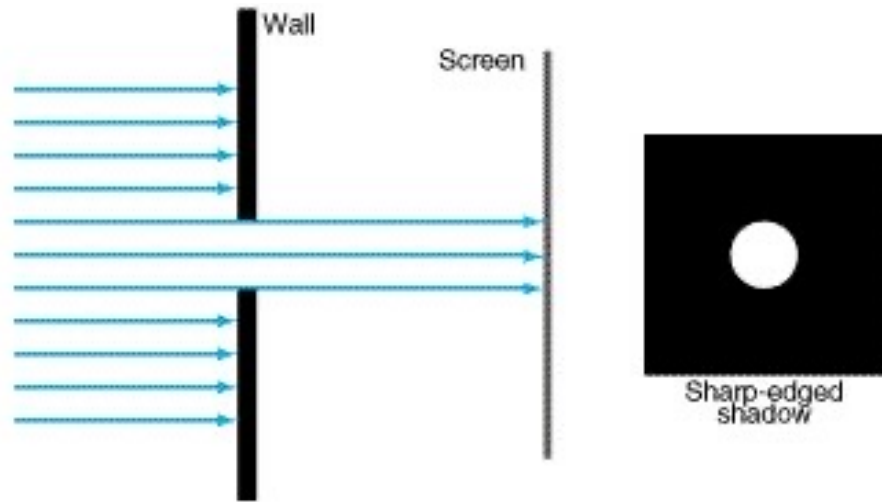
Coherent beam



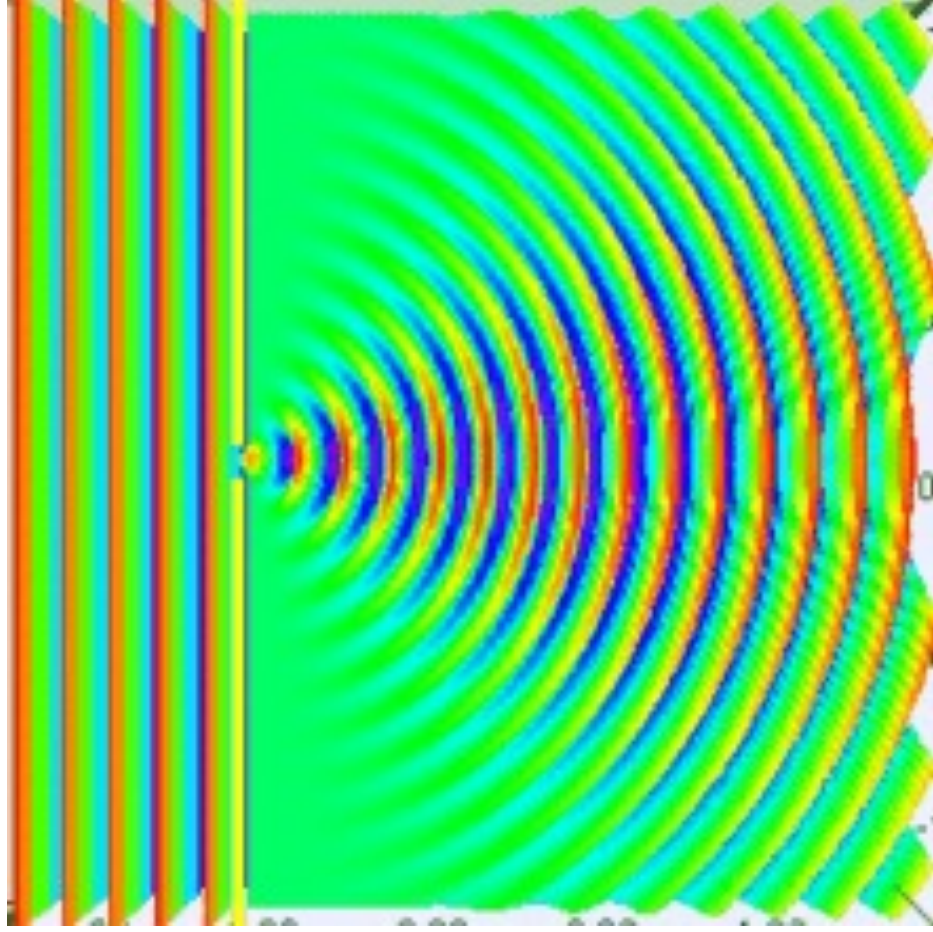
Addition of waves



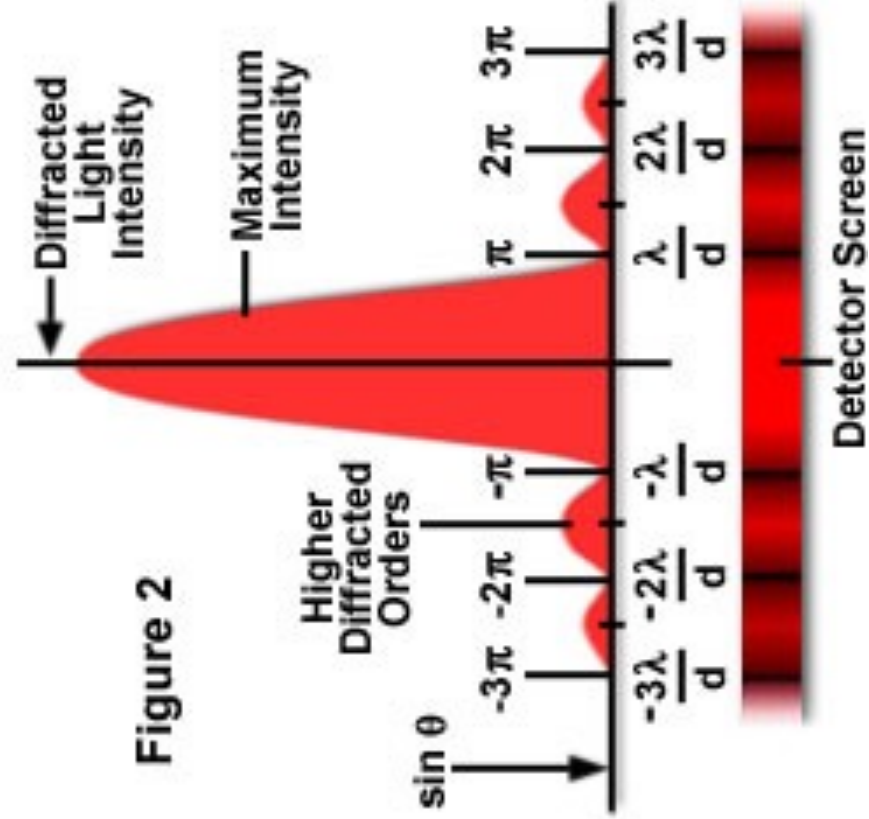
Particles & waves



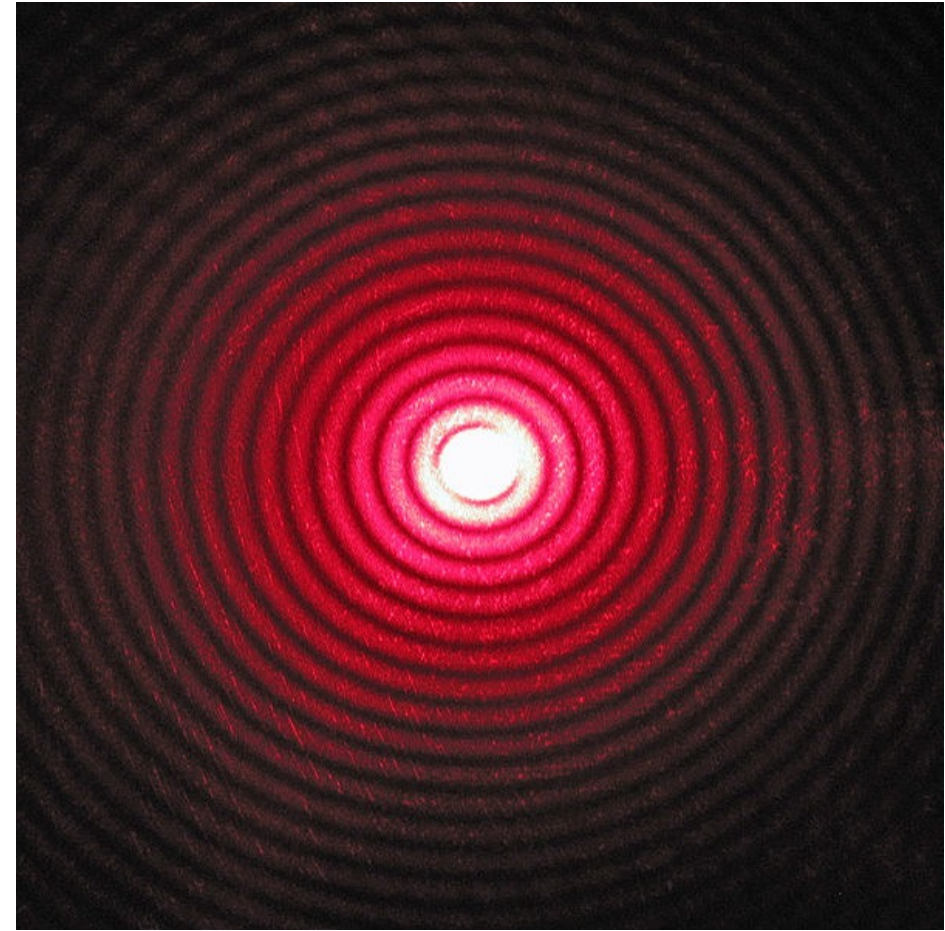
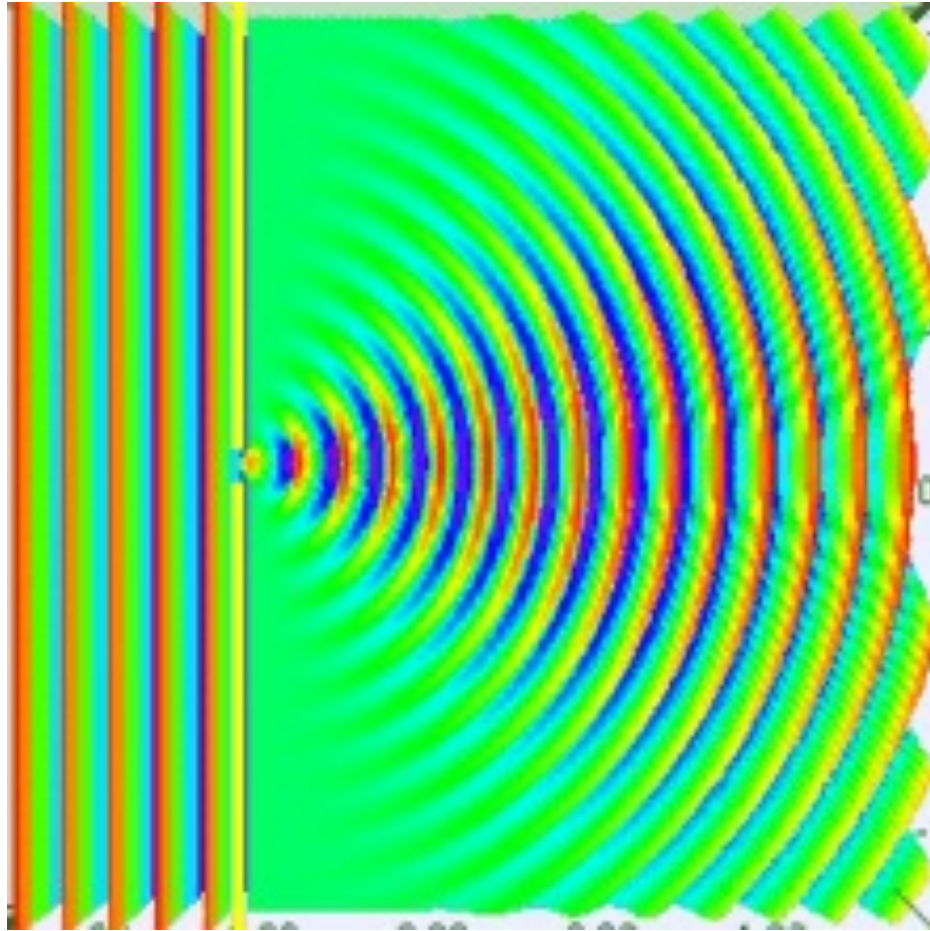
Diffraction of light



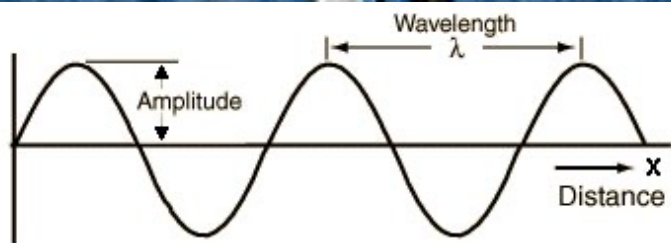
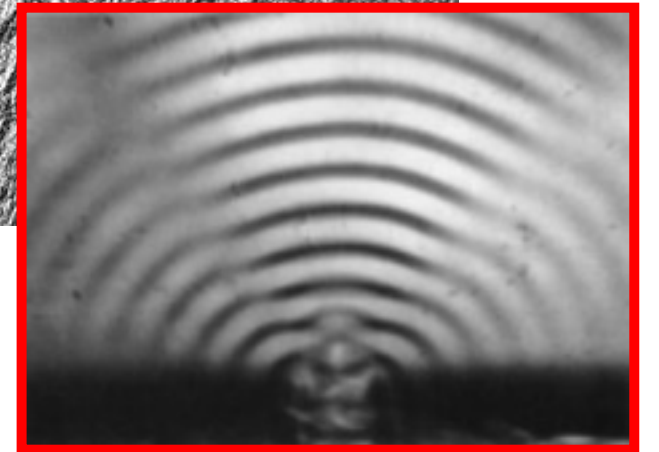
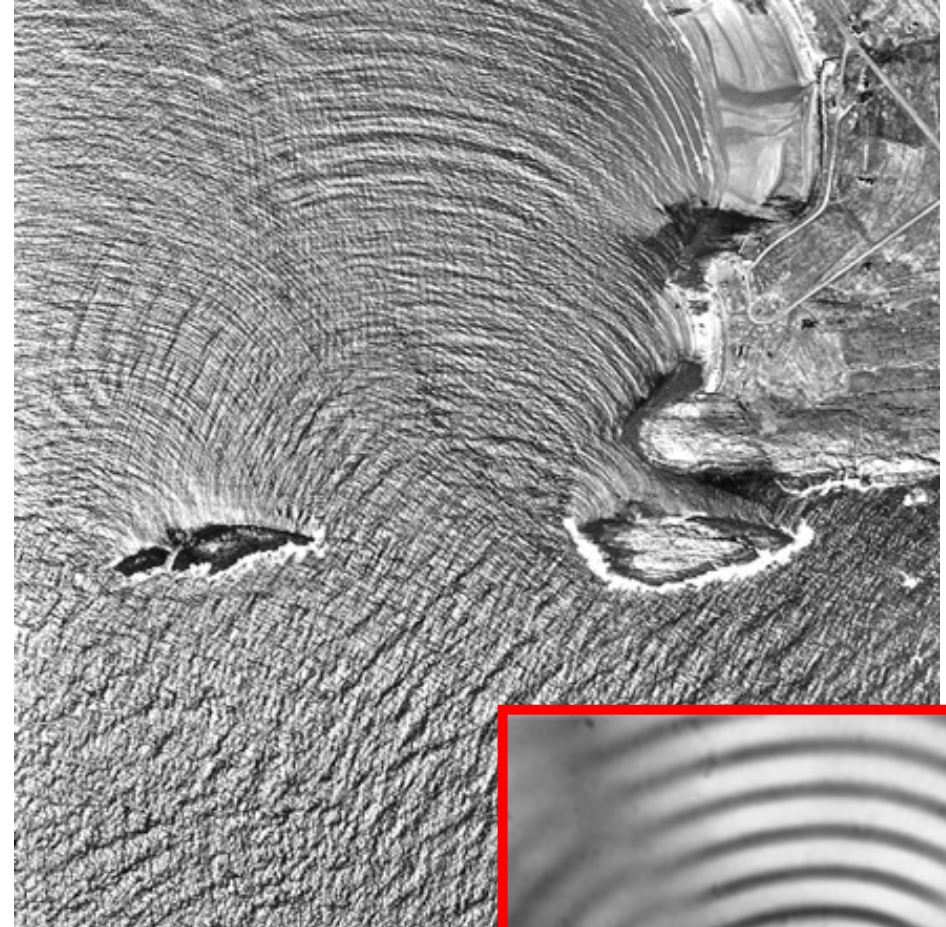
Intensity Distribution of Diffracted Light



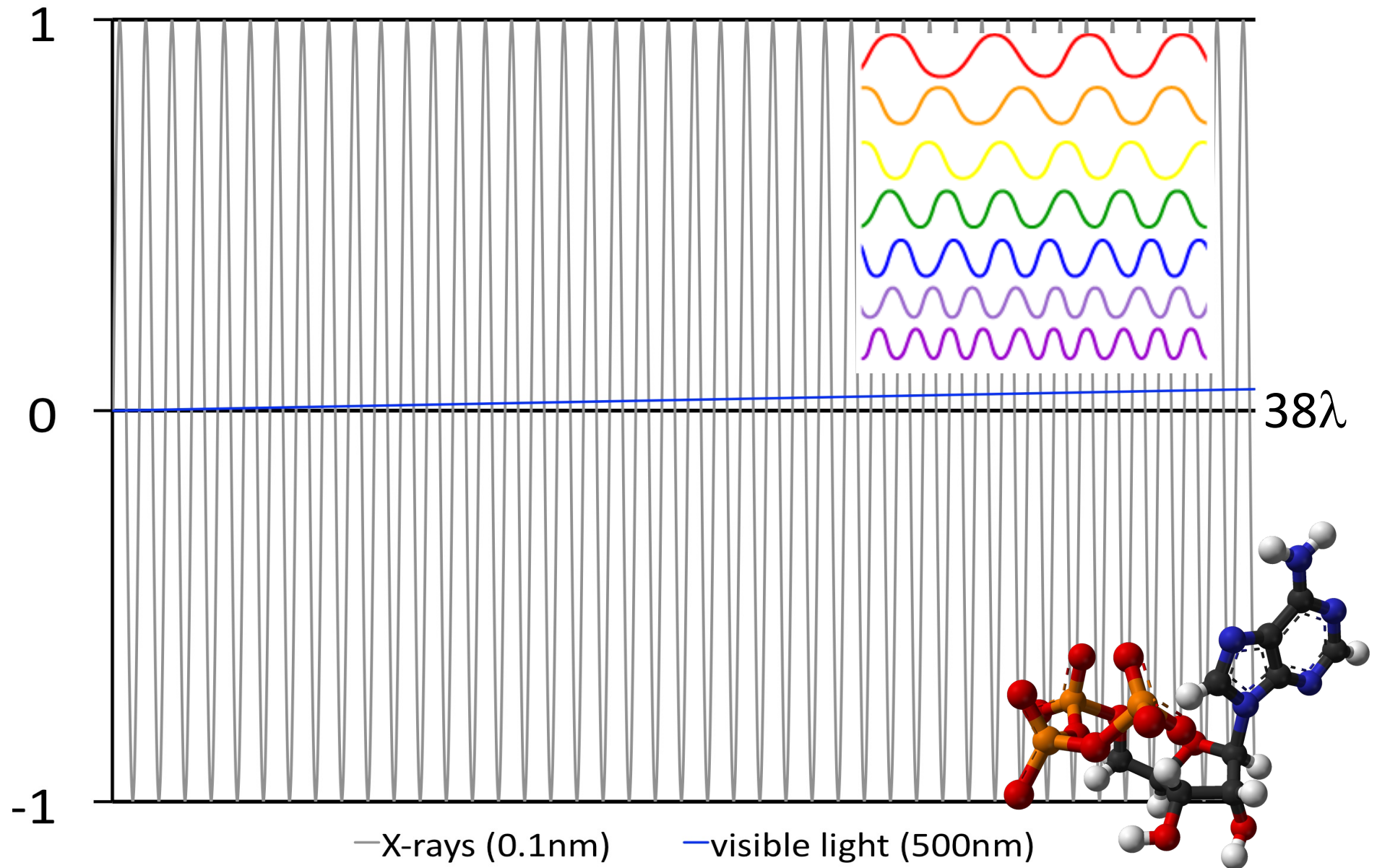
Diffraction of light



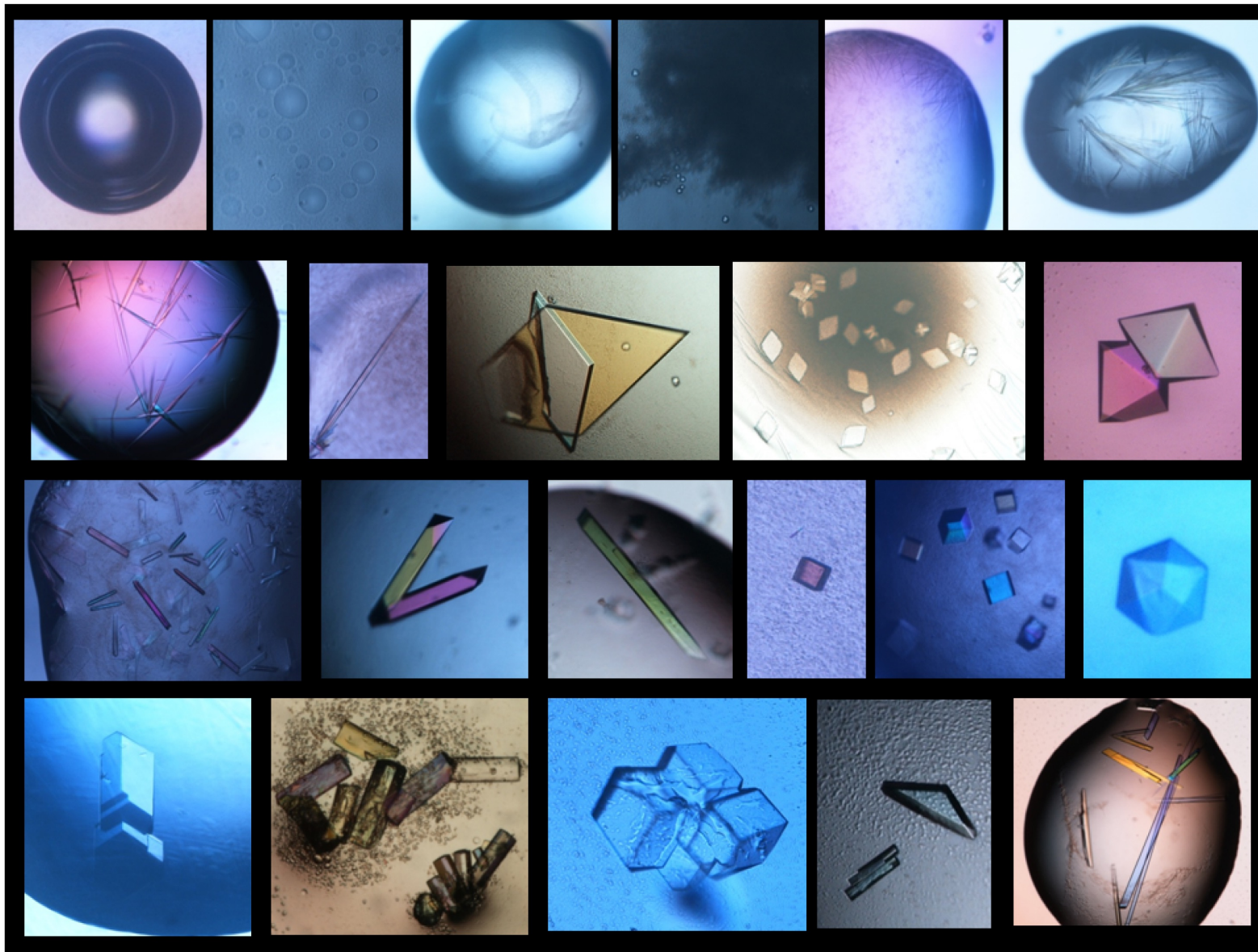
Wavelength and diffraction



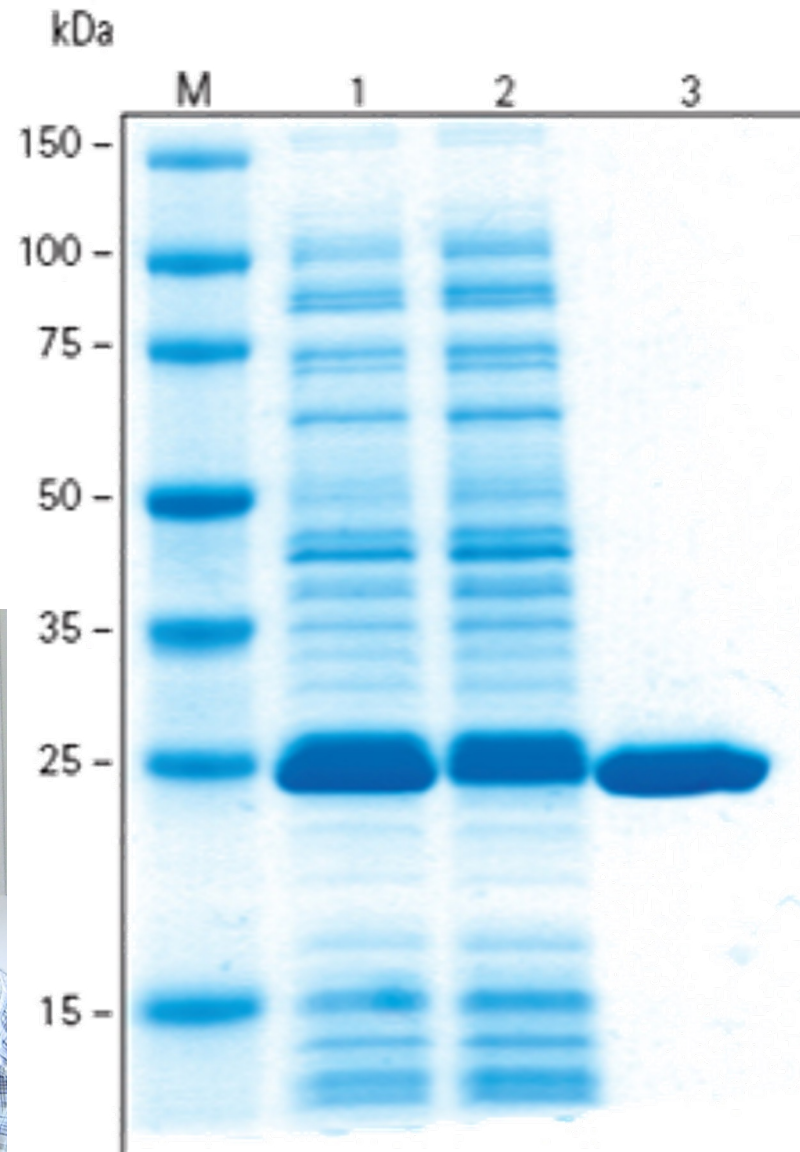
Wavelength comparison of X-rays and visible light



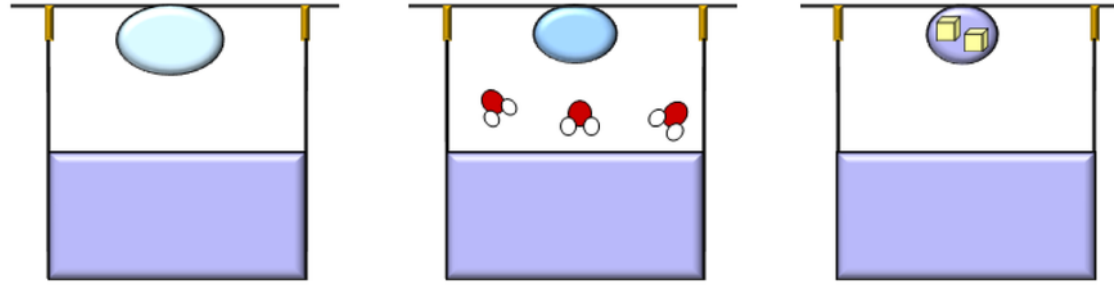
Crystallizing a Protein



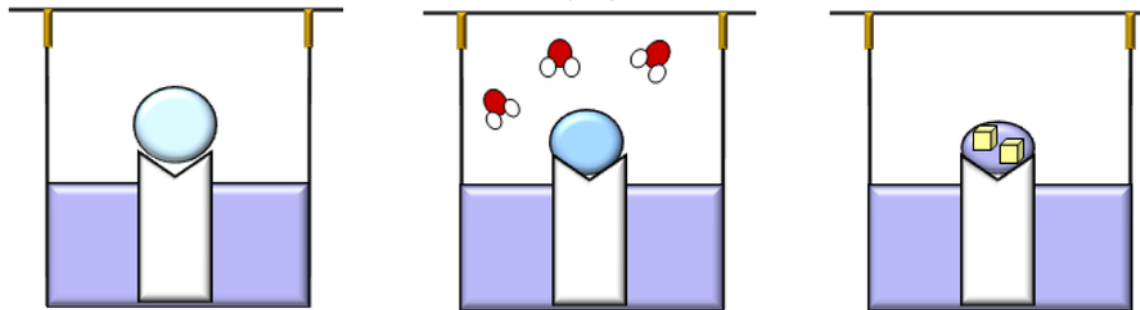
Protein expression and purification



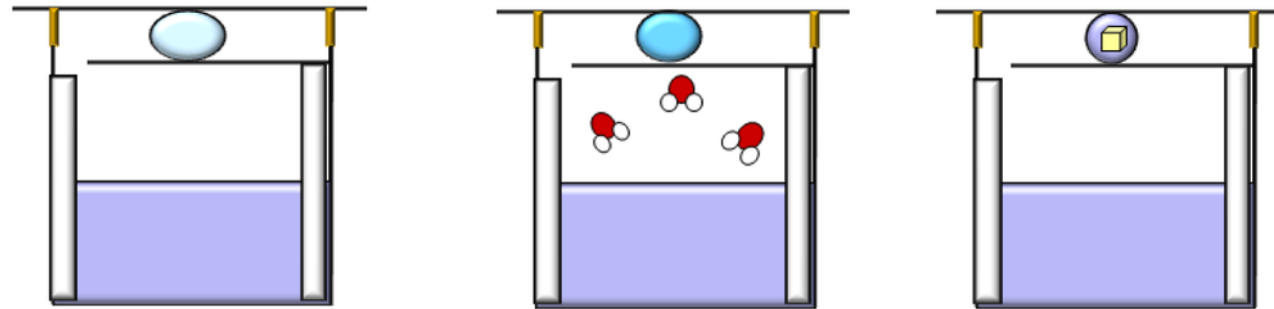
Vapor-diffusion



(A)

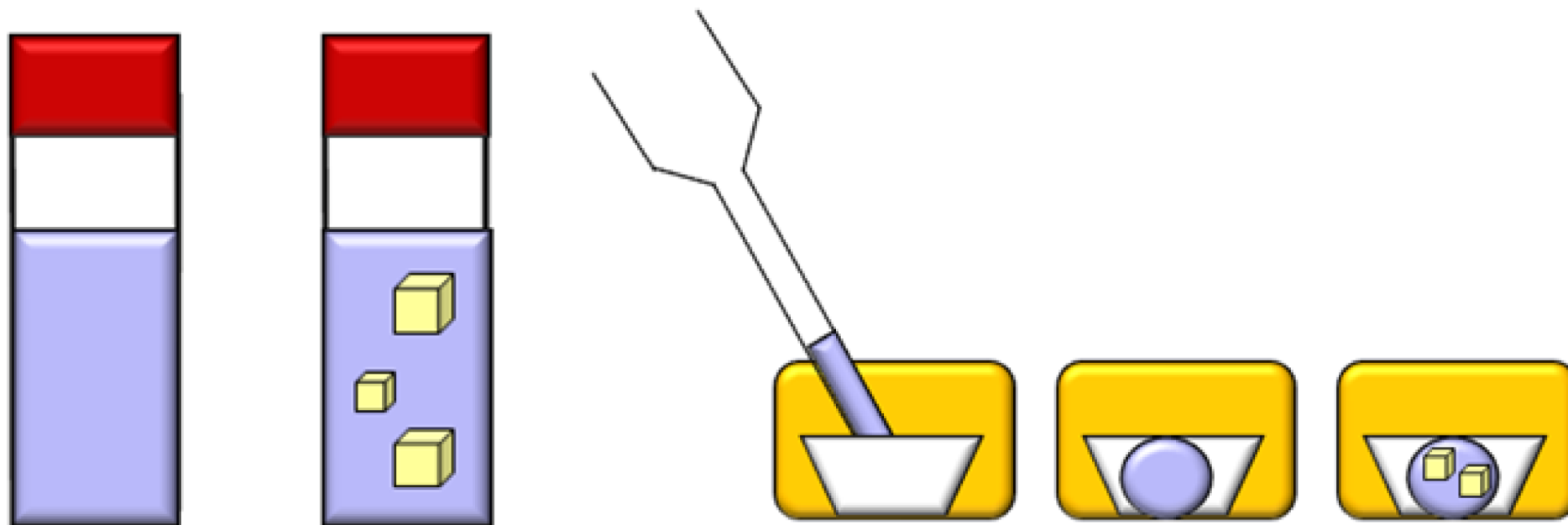


(B)

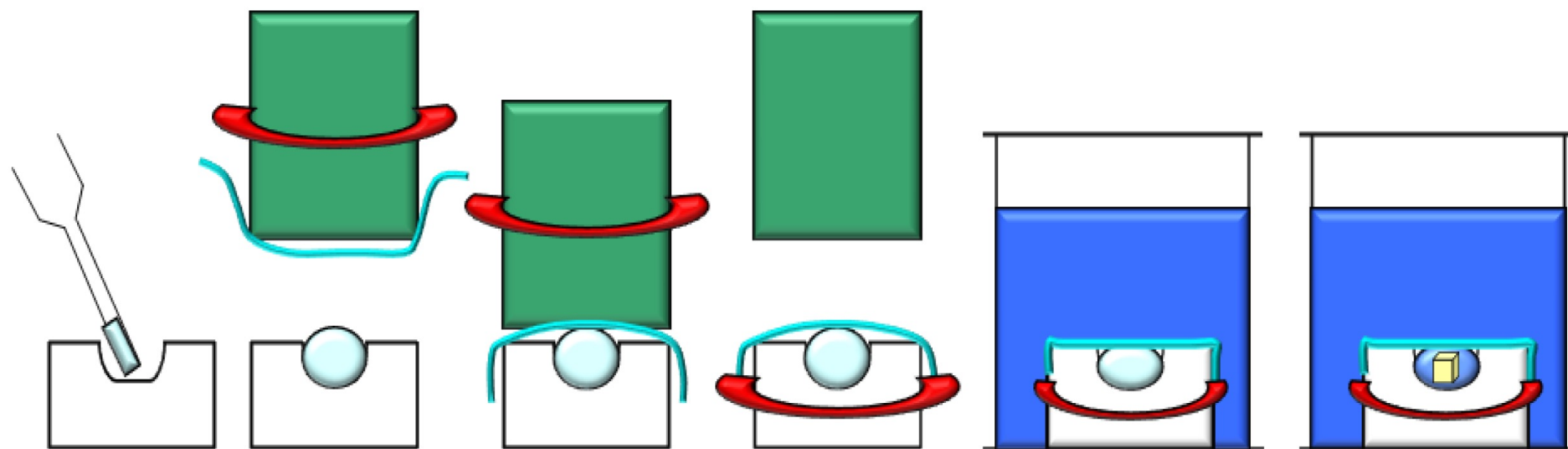


(C)

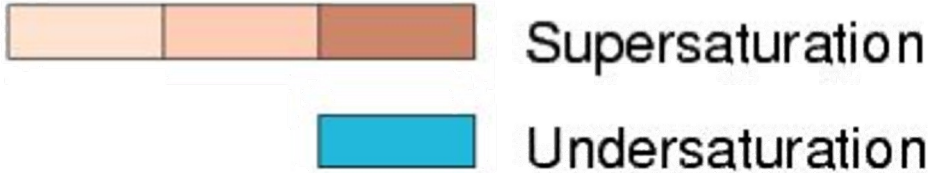
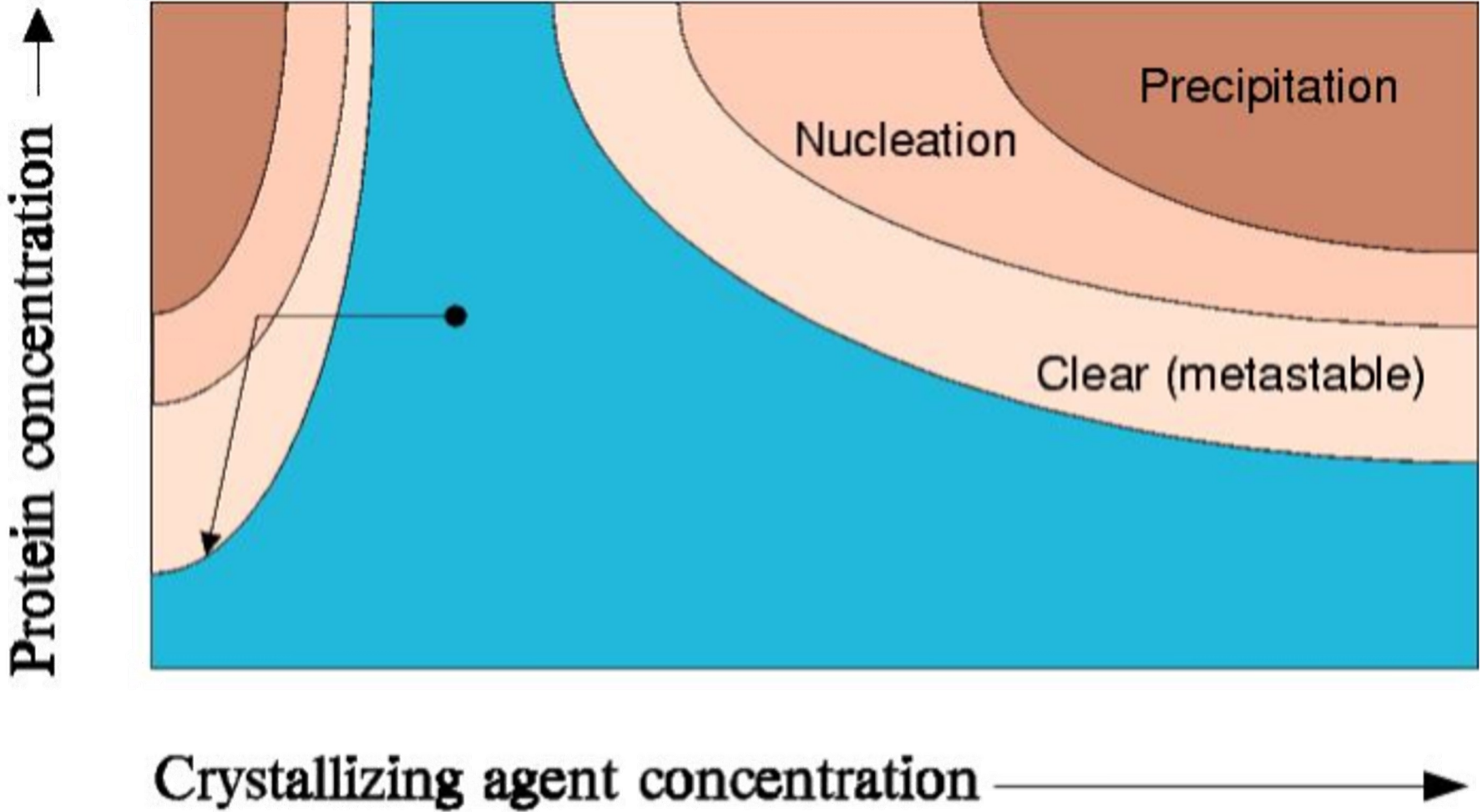
Batch and microbatch

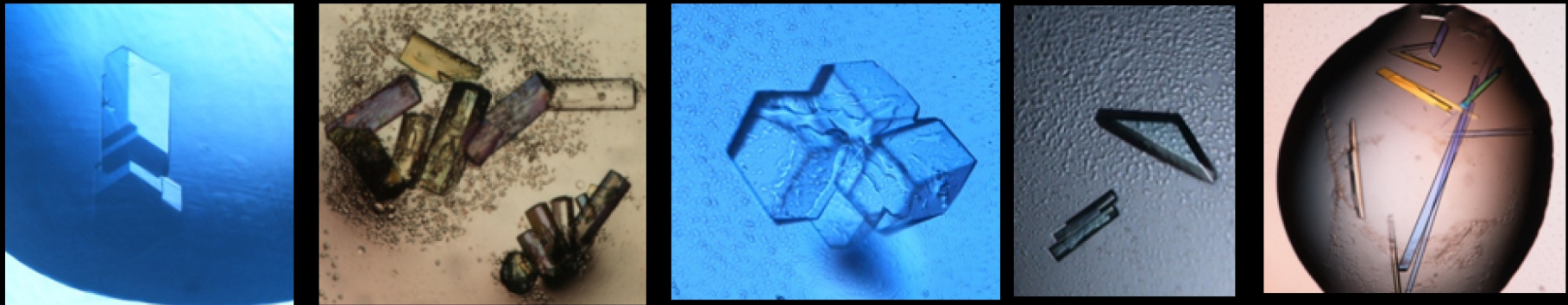
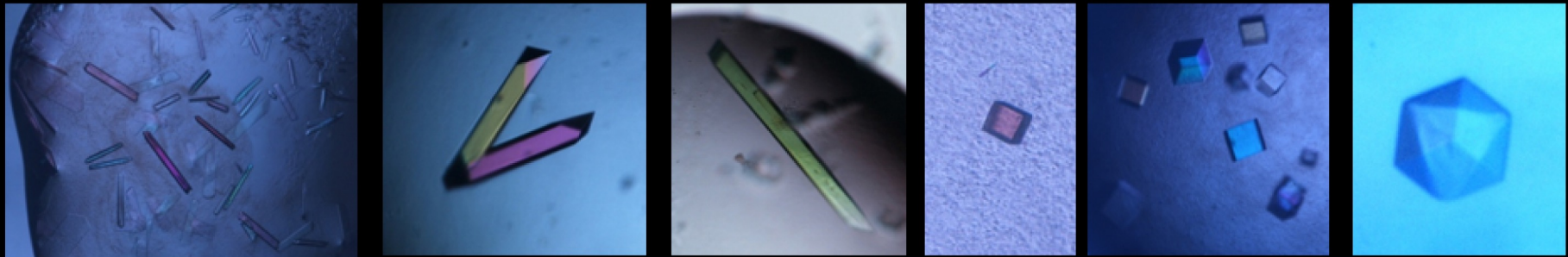
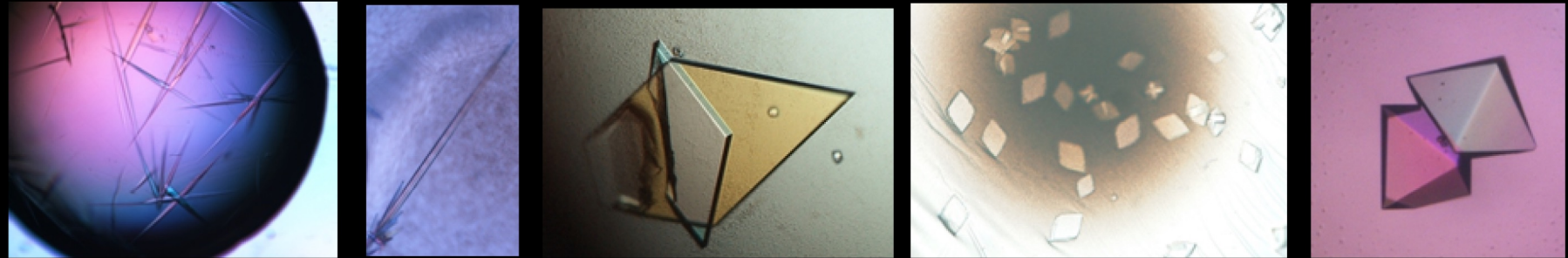
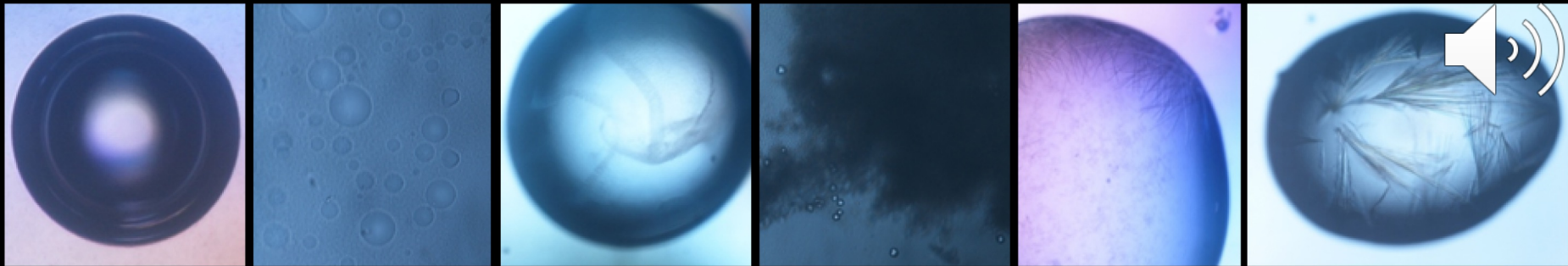


Microdialysis



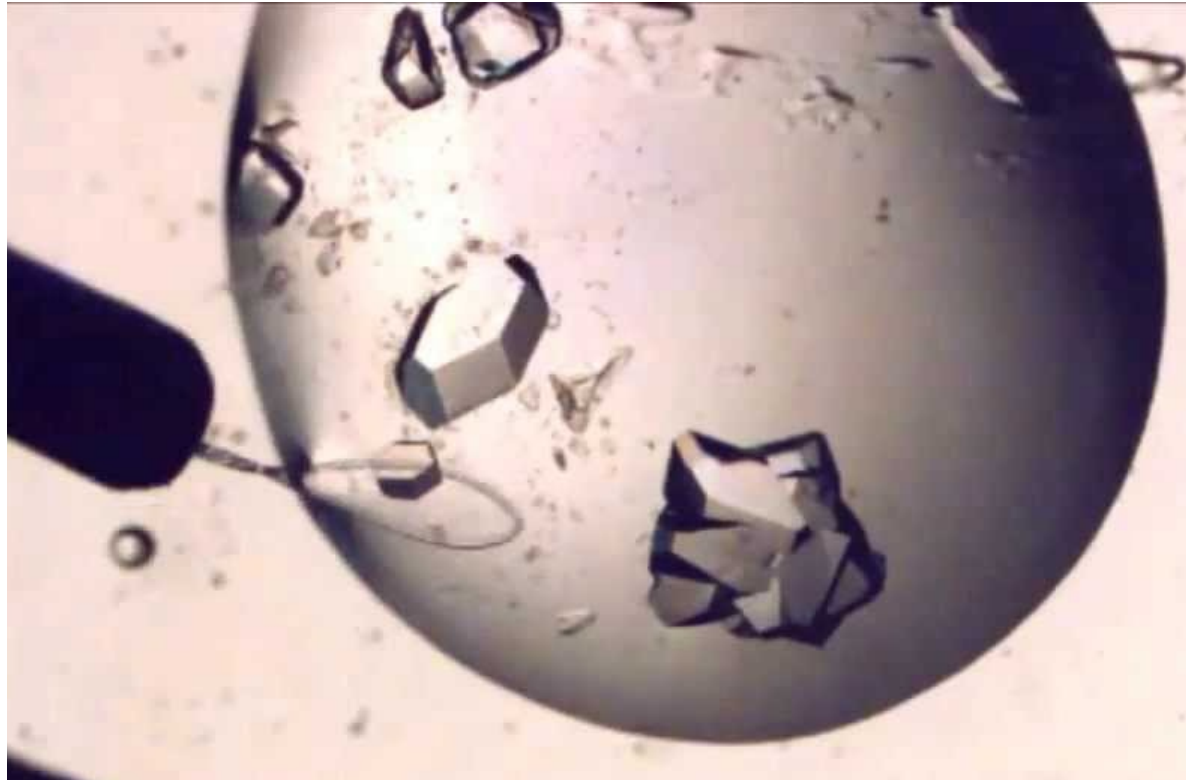
Protein crystallization phase diagram



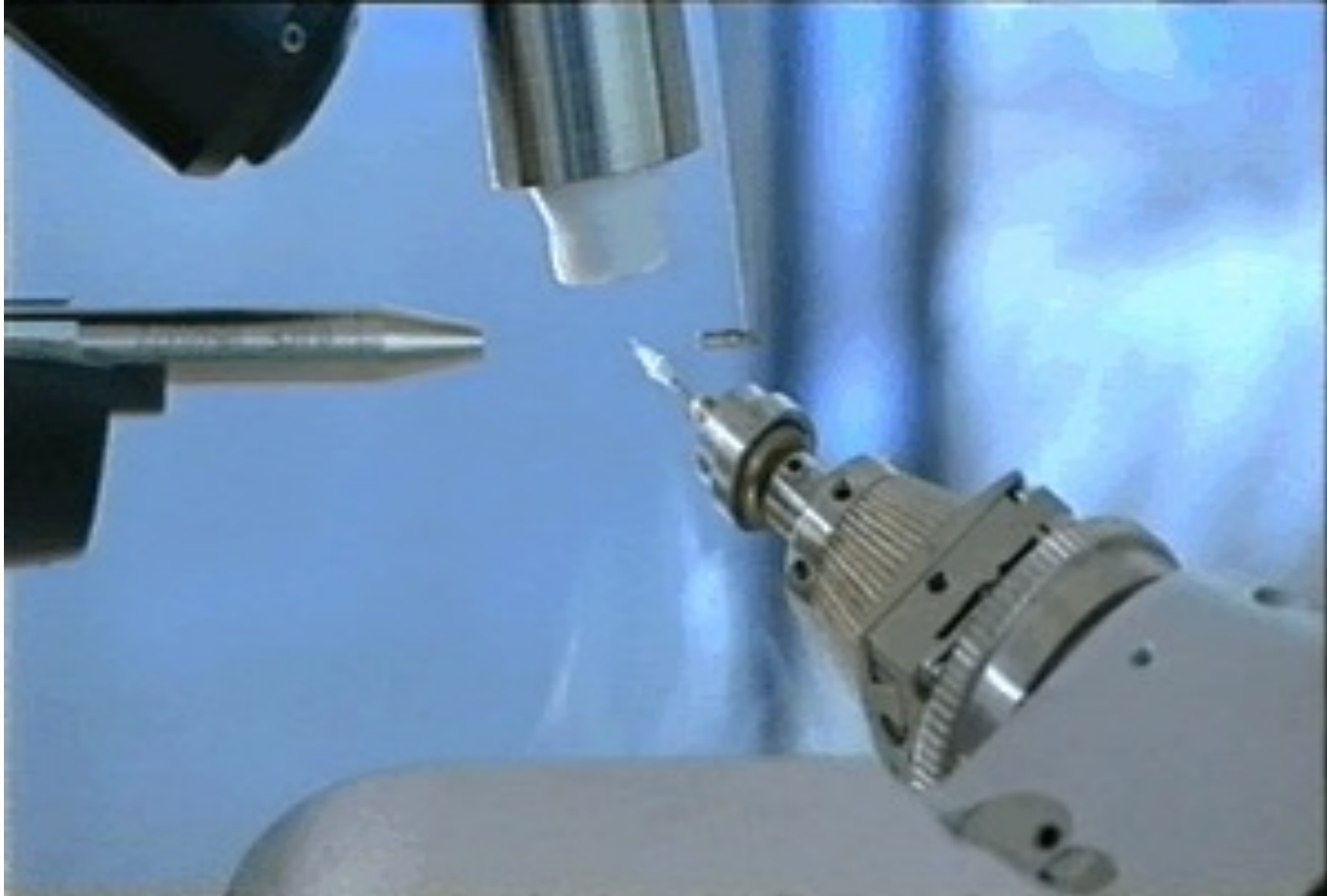


Preparing crystals for diffraction experiment

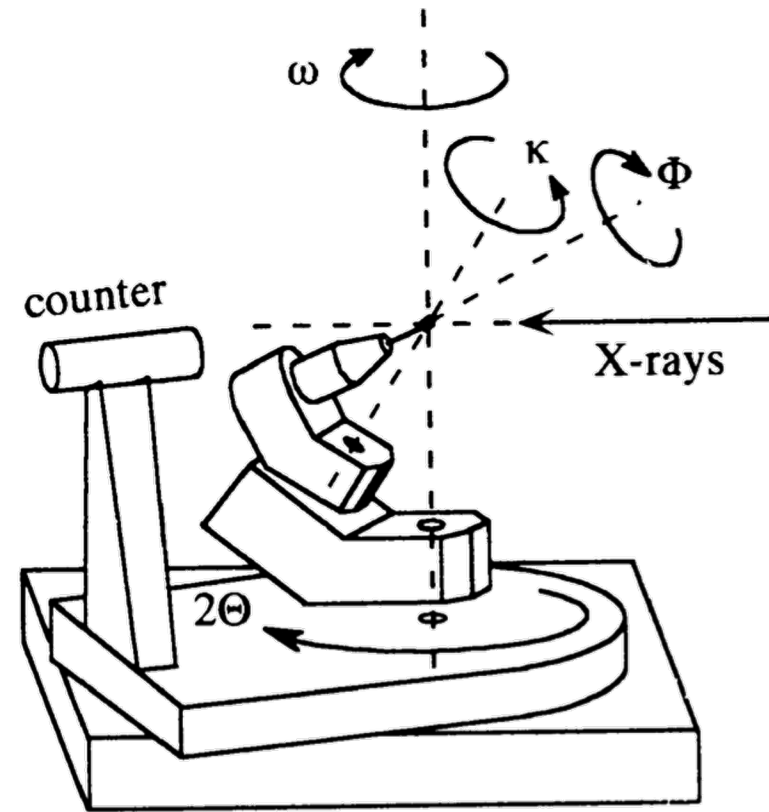
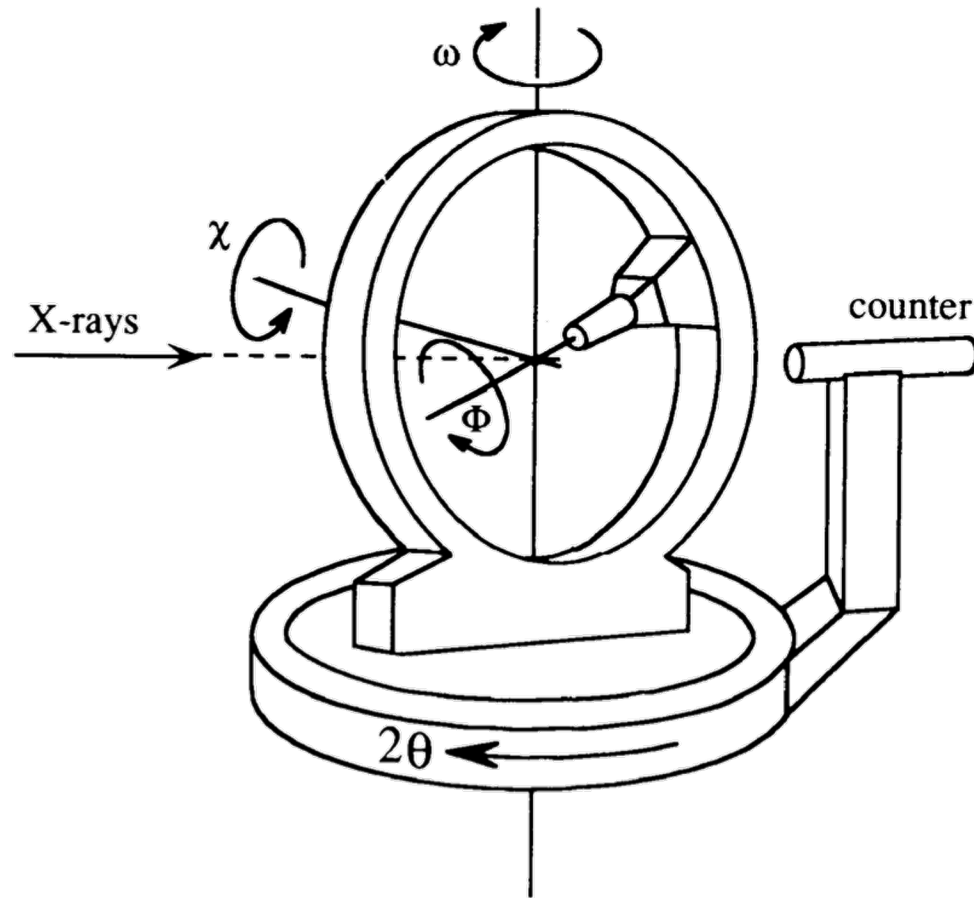




Diffractionmeter with goniometer

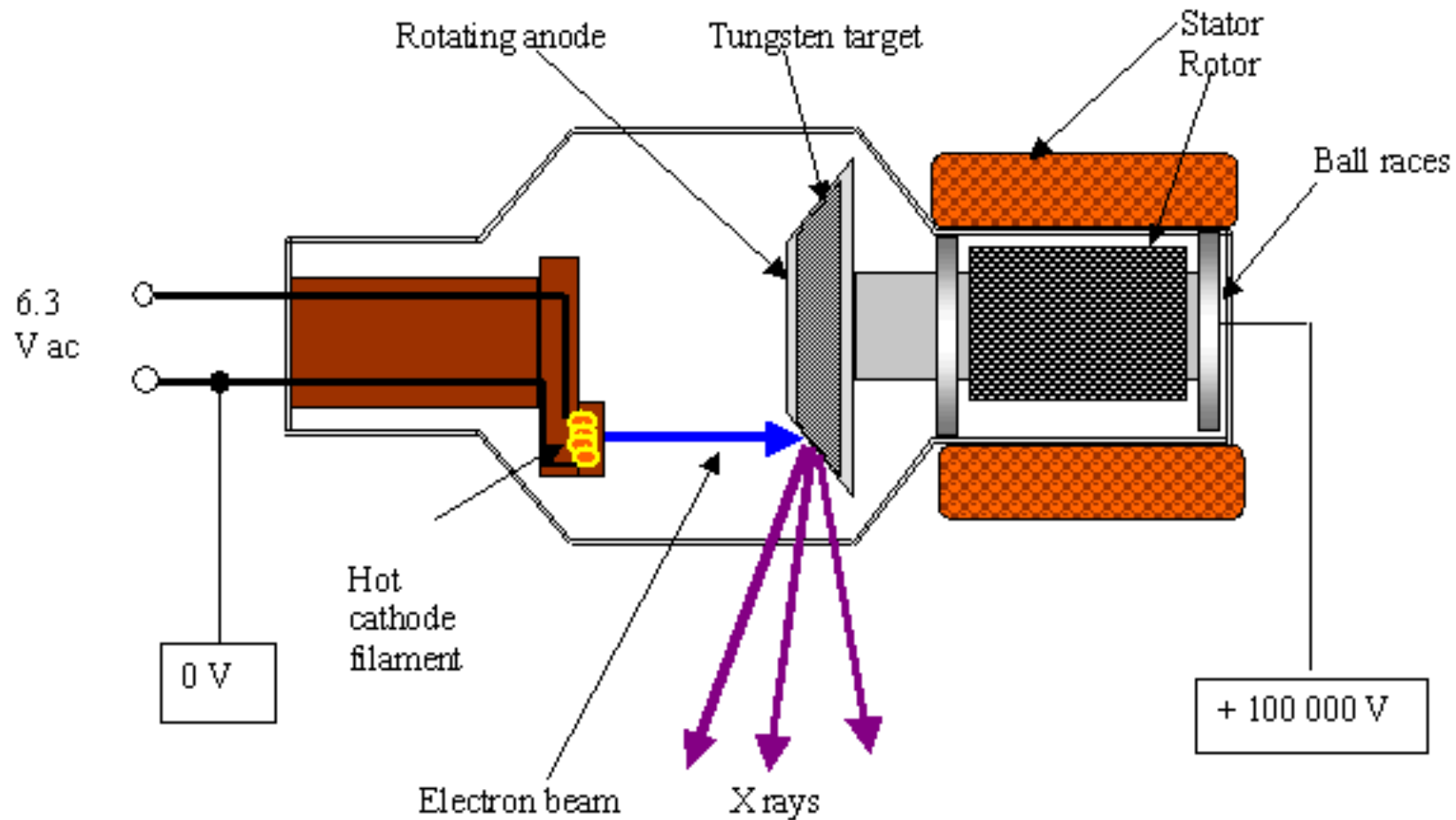


Diffractometer with goniometer

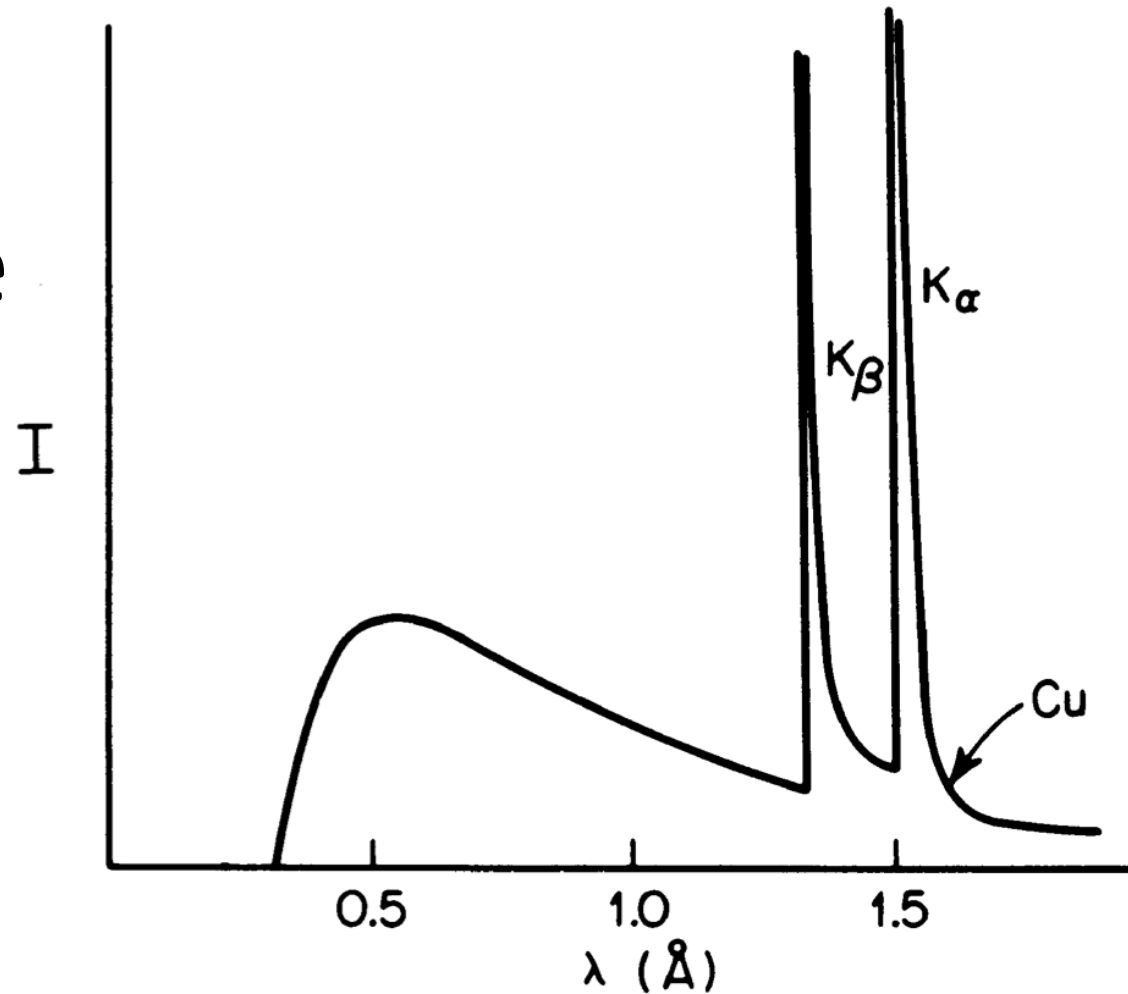


X-ray sources

- sealed X-ray tube



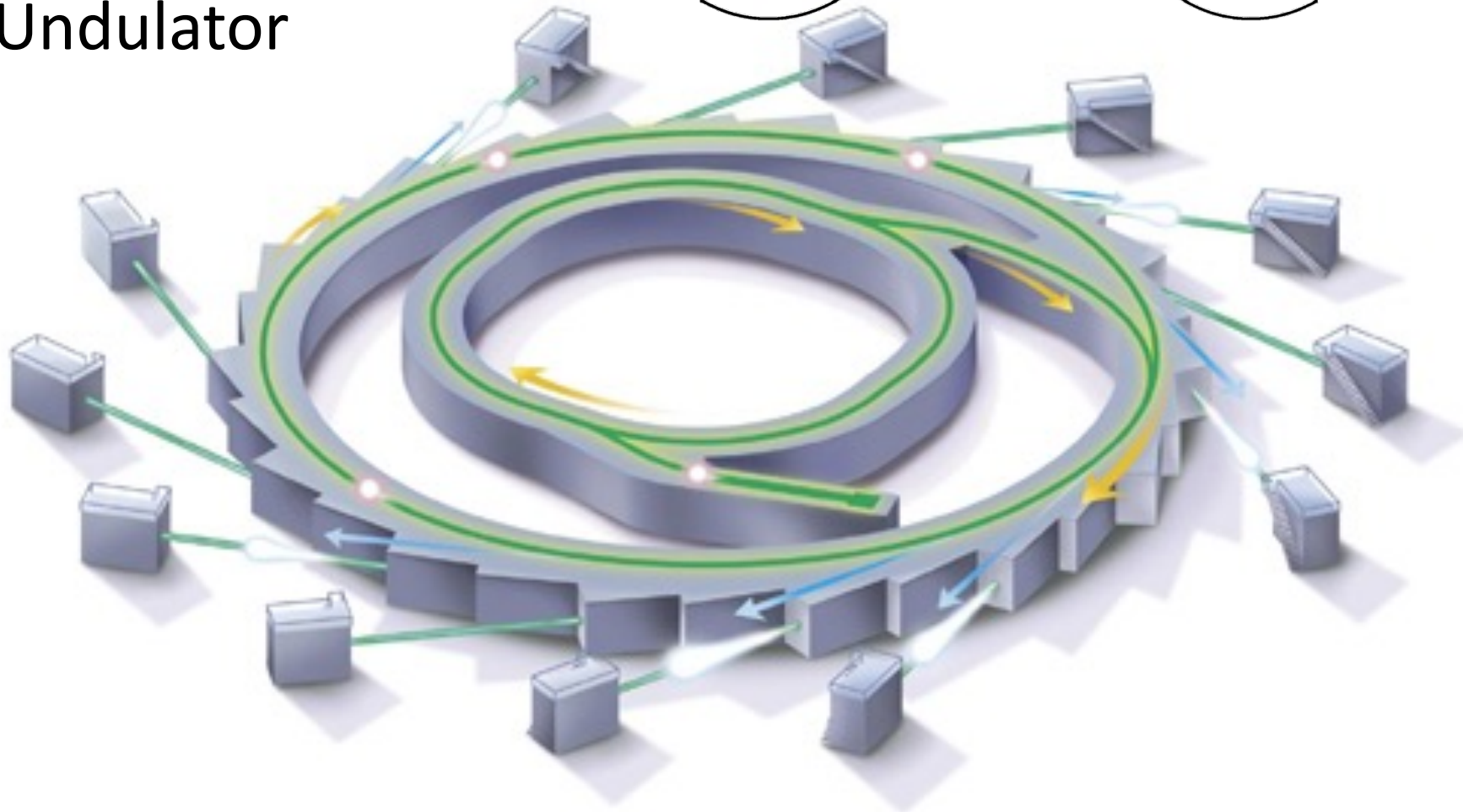
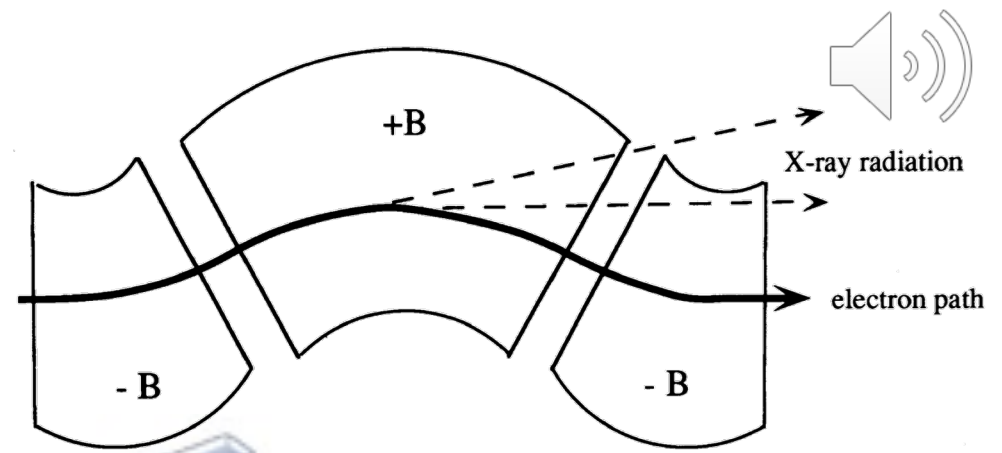
Spectrum of copper anode



	λ (Å)	
$K_{\alpha}(1)$	1.54051	The weight average value for $K_{\alpha}(1)$ and $K_{\alpha}(2)$ is taken as 1.54178 Å because the intensity of $K_{\alpha}(1)$ is twice that of $K_{\alpha}(2)$
$K_{\alpha}(2)$	1.54433	
K_{β}	1.39217	

Synchrotron

- Bending magnet
- Wavelength shifter
- Wiggler
- Undulator



X-ray detectors

Single photon counter

Film

Image plates

Area detectors:

- CCDs

- Direct X-rays detectors - Pilatus



Crystals

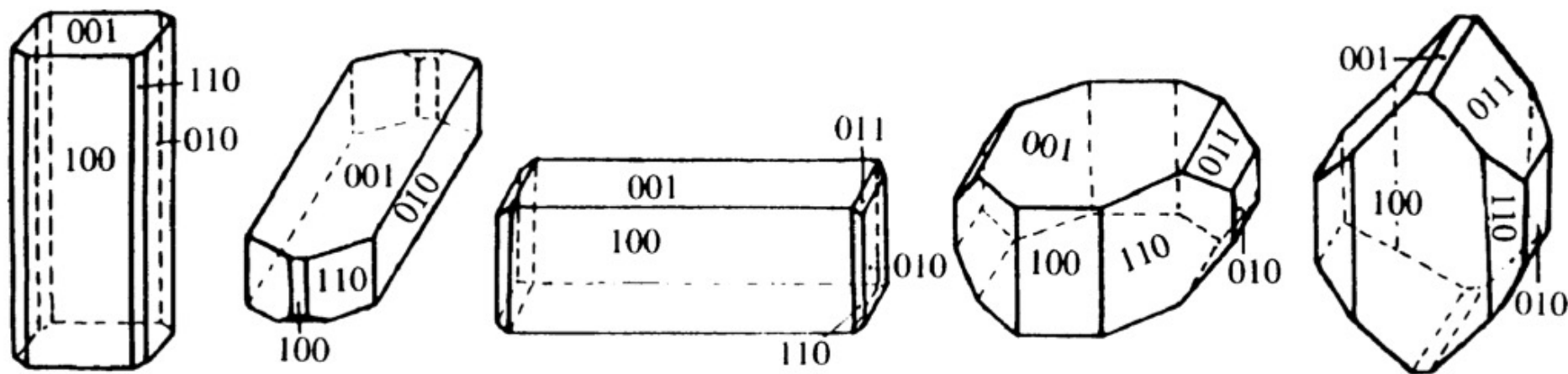
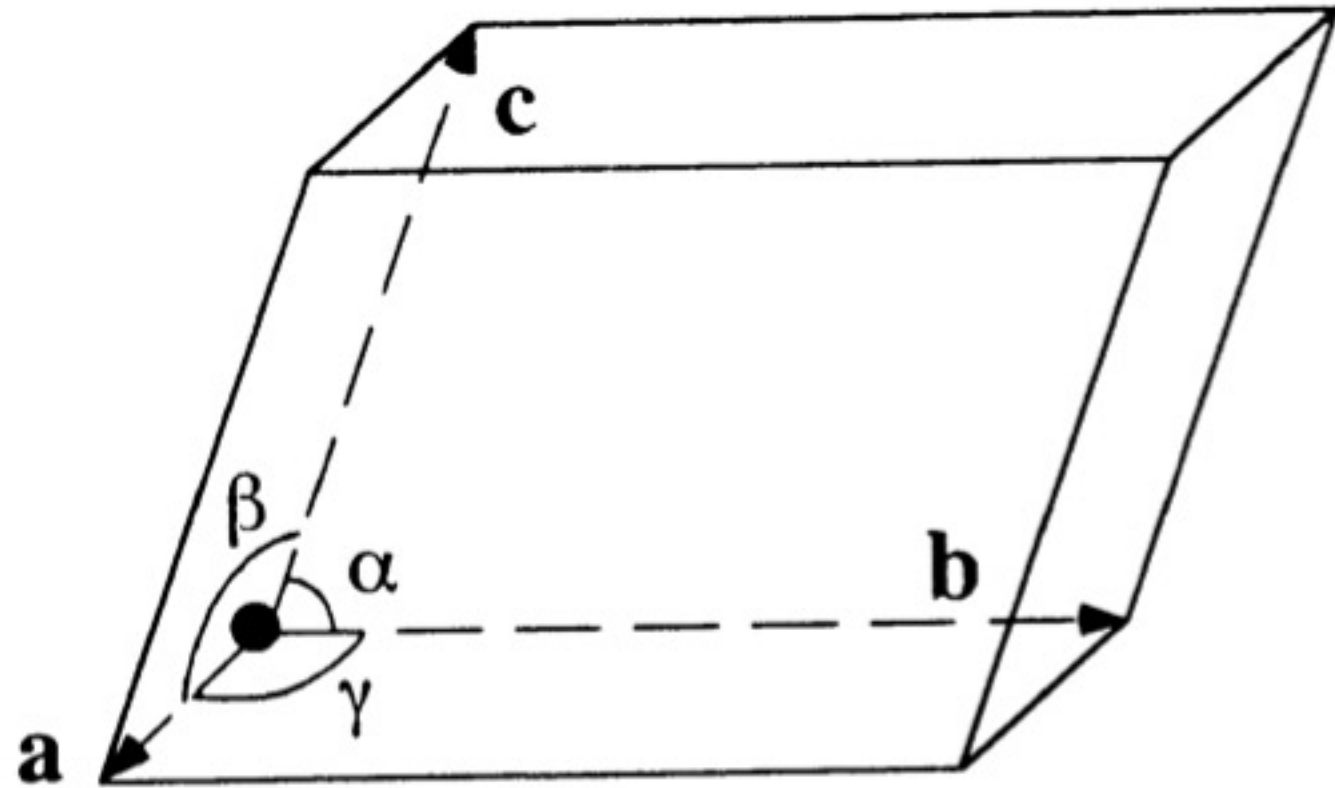


Figure 3.1. Crystals of trimethylammonium bromide belonging to the same crystal form but exhibiting a range of morphologies.



● Origin

Figure 3.3. One unit cell in the crystal lattice.

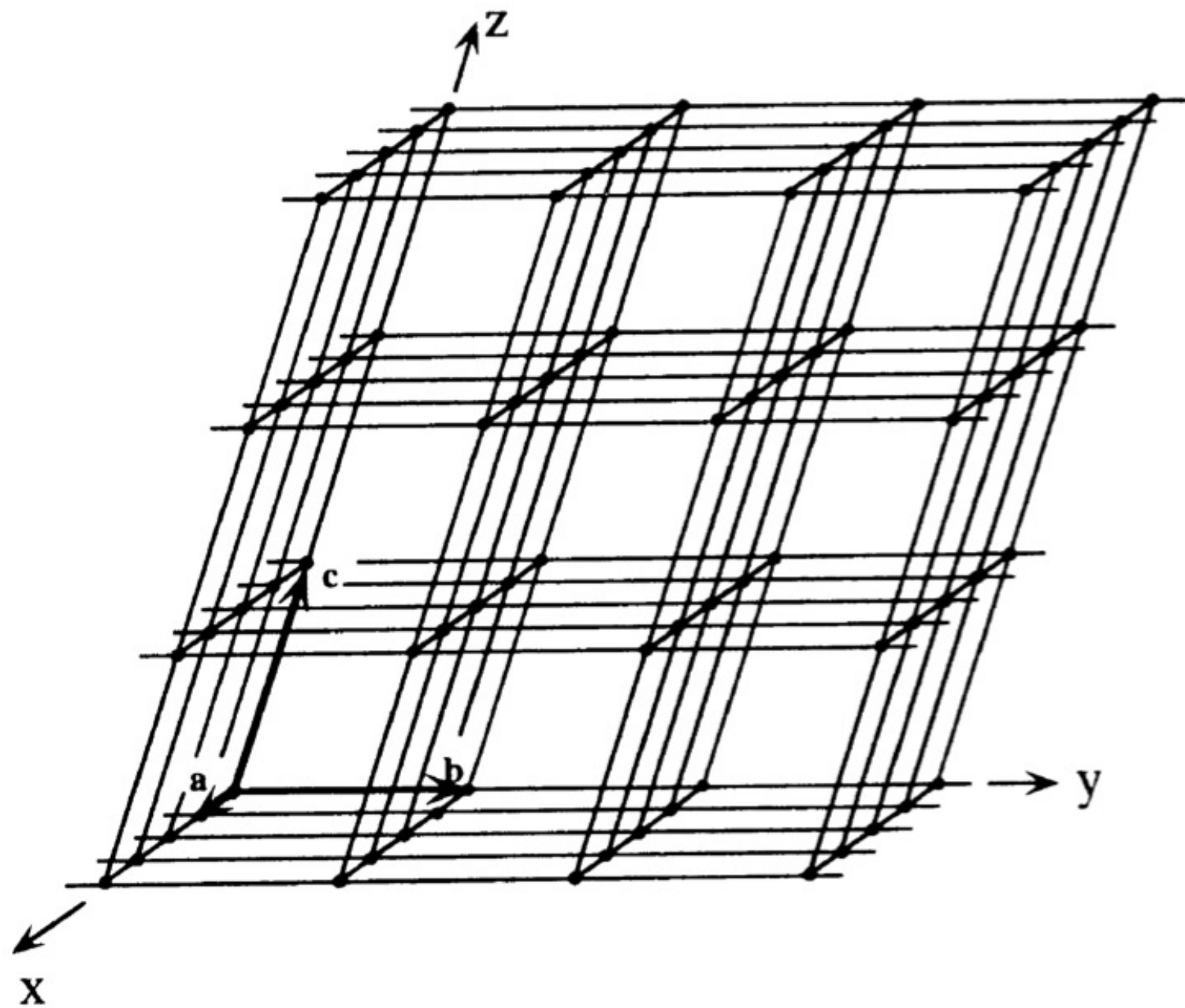
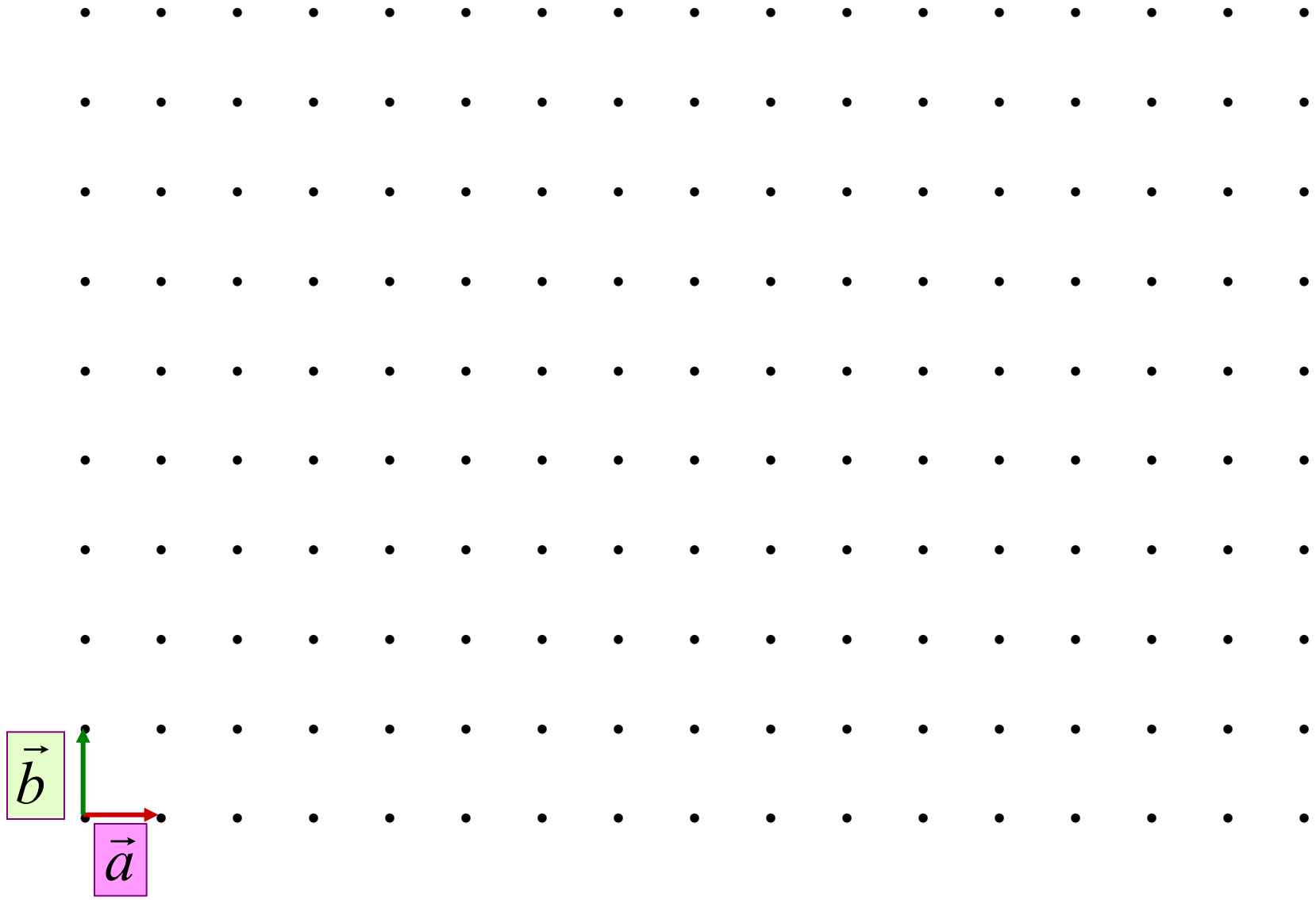


Figure 3.4. A crystal lattice is a three-dimensional stack of unit cells.

A 2D lattice



Lattice

Translationally periodic arrangement of **points**

Crystal

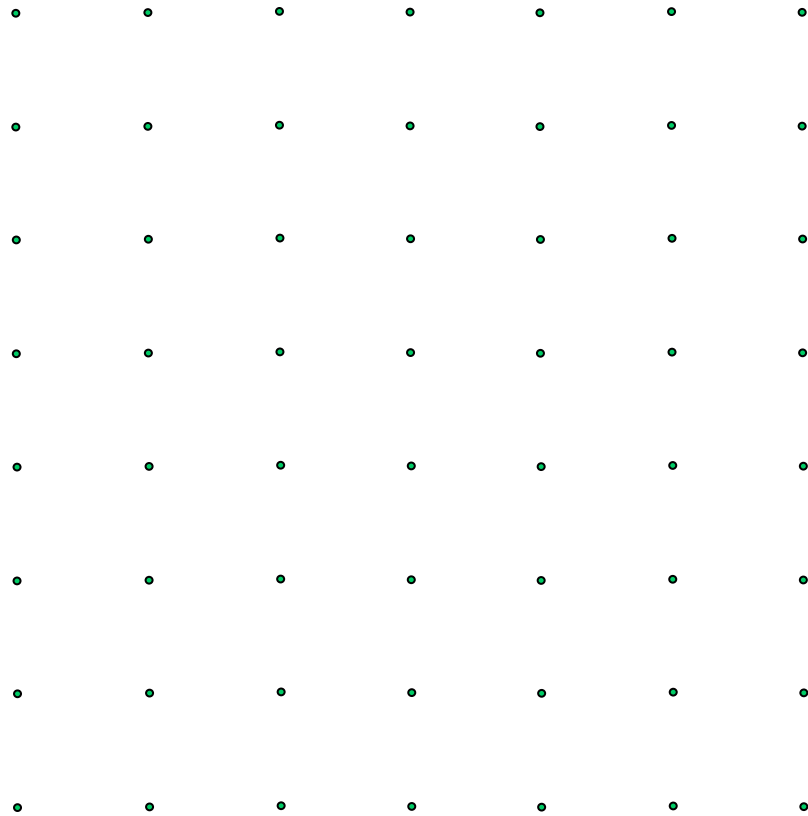
Translationally periodic arrangement of **motifs**

Crystal = Lattice + Motif

Lattice ➤ the underlying periodicity of the crystal

Motif ➤ atom or group of atoms associated with each lattice point

Lattice



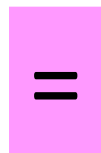
+

Motif





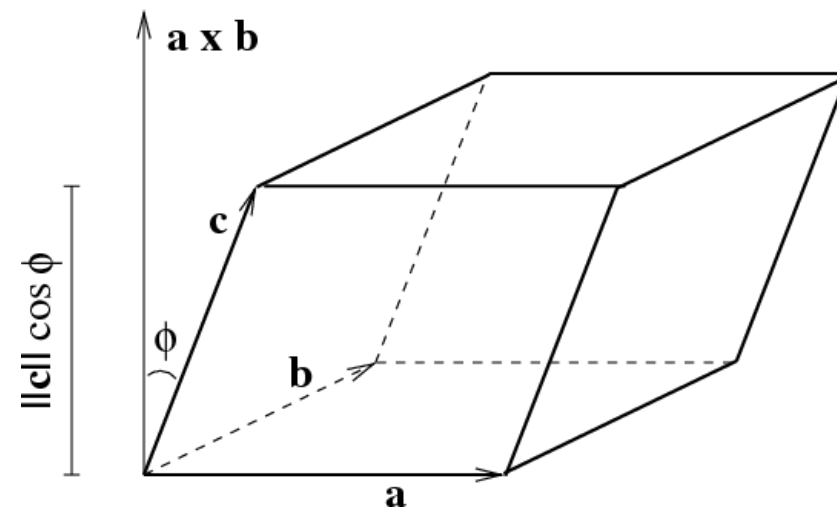
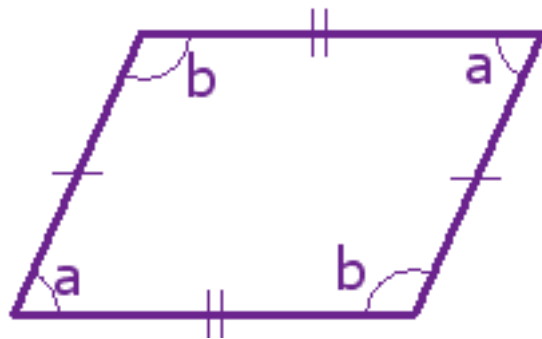
Crystal

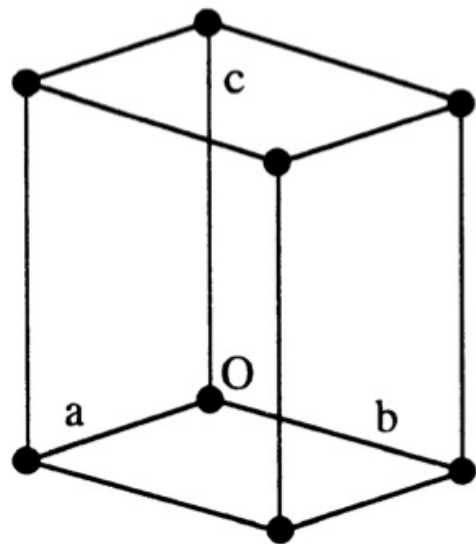


Unit cells

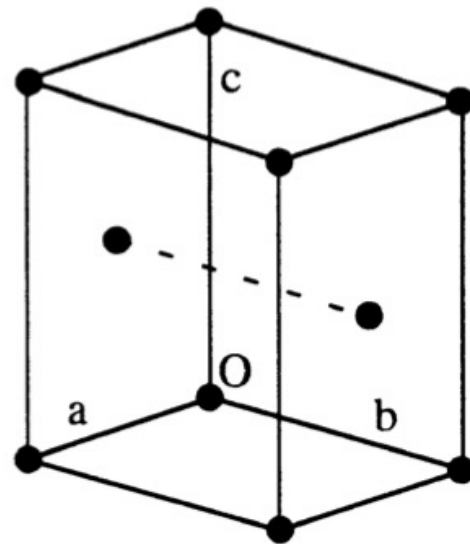
Instead of drawing the whole structure I can draw a representative part and specify the repetition pattern

- A cell is a finite representation of the infinite lattice
- A cell is a parallelogram (2D) or a parallelepiped (3D) with lattice points at their corners.
- If the lattice points are only at the corners, the cell is primitive.
- If there are lattice points in the cell other than the corners, the cell is nonprimitive.

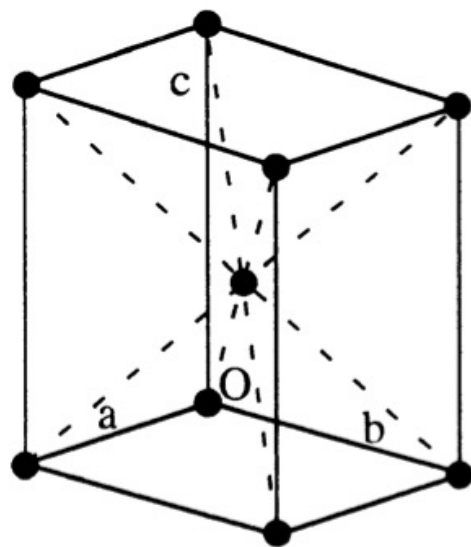




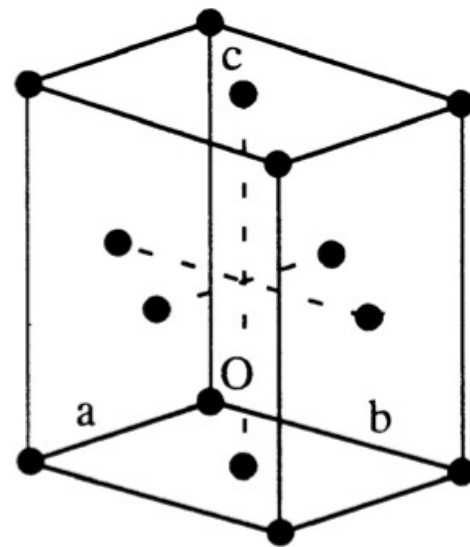
a primitive unit cell (P)



a unit cell centered in the (010) planes (B)



a body-centered unit cell (I)



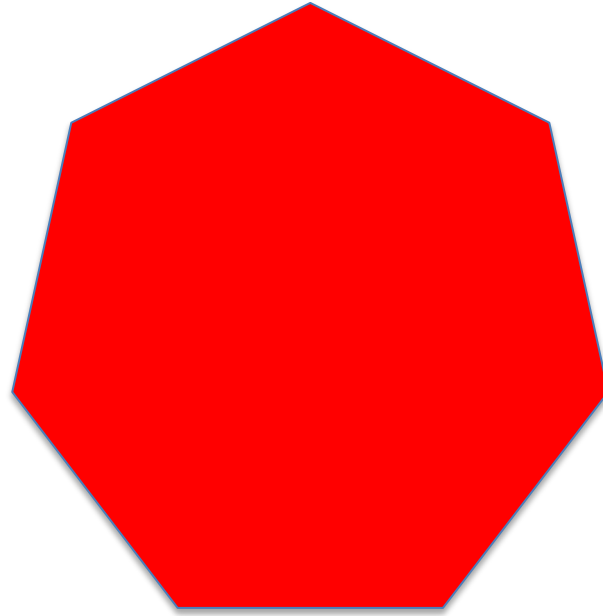
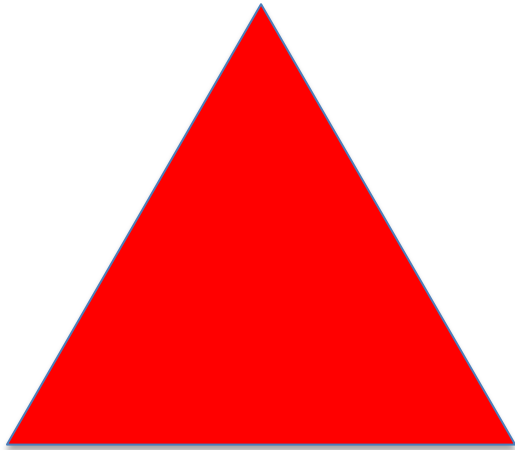
a face-centered unit cell (F)

Arrangement of lattice points in the unit cell

No. of Lattice points / cell

		Position of lattice points	Effective number of Lattice points / cell
1	P	8 Corners	$= 8 \times (1/8) = 1$
2	I	8 Corners + 1 body centre	$= 1$ (for corners) + 1 (BC)
3	F	8 Corners + 6 face centres	$= 1$ (for corners) + 6 x (1/2) $= 4$
4	A/ B/ C	8 corners + 2 centres of opposite faces	$= 1$ (for corners) + 2x(1/2) $= 2$

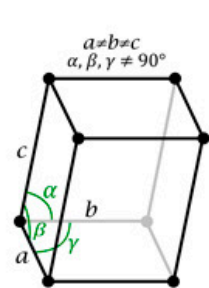
SYMMETRY



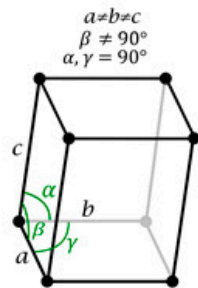
If an object is brought into self-coincidence after some operation it said to possess symmetry with respect to that operation.

Bravais Lattice

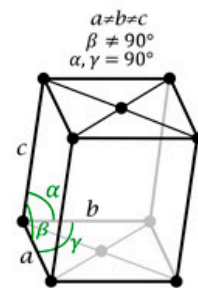
A **lattice** is a set of points constructed by translating a single point in discrete steps by a set of *basis vectors*. In three dimensions, there are 14 unique **Bravais** lattices (*distinct from one another in that they have different space groups*) in three dimensions. All crystalline materials recognized till now fit in one of these arrangements.



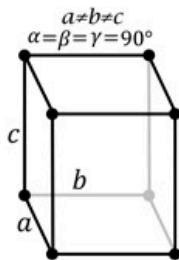
Triclinic



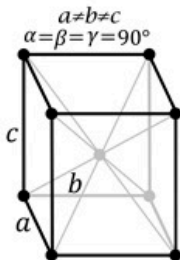
P Monoclinic



C

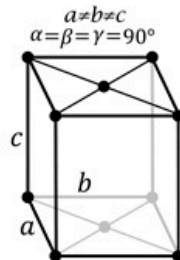


P

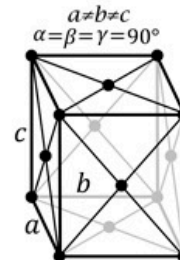


I

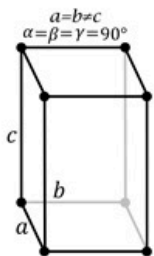
Orthorhombic C



C

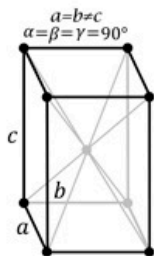


F

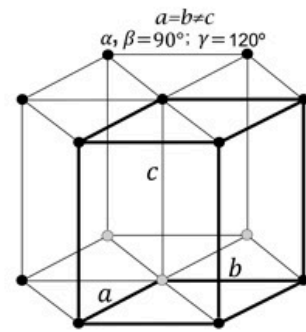


P

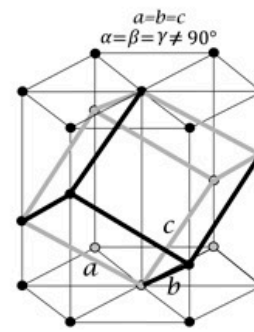
Tetragonal



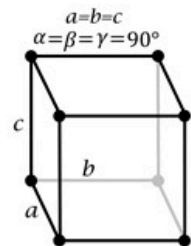
I



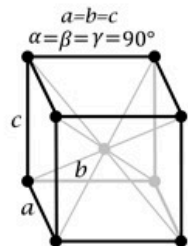
Trigonal / Hexagonal P



Trigonal R

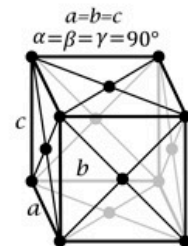


P



I

Cubic



F



Table 3.2. The Seven Crystal Systems

Crystal system	Conditions imposed on cell geometry	Minimum point group symmetry
Triclinic	None	1
Monoclinic	$\alpha = \gamma = 90^\circ$ (b is the unique axis; for proteins this is a 2-fold axis or screw axis) or: $\alpha = \beta = 90^\circ$ (c is unique axis; for proteins this is a 2-fold axis or screw axis)	2
Orthorhombic	$\alpha = \beta = \gamma = 90^\circ$	222
Tetragonal	$a = b; \alpha = \beta = \gamma = 90^\circ$	4
Trigonal	$a = b; \alpha = \beta = 90^\circ; \gamma = 120^\circ$ (hexagonal axes) or: $a = b = c; \alpha = \beta = \gamma$ (rhombohedral axes)	3
Hexagonal	$a = b; \alpha = \beta = 90^\circ; \gamma = 120^\circ$	6
Cubic	$a = b = c; \alpha = \beta = \gamma = 90^\circ$	23

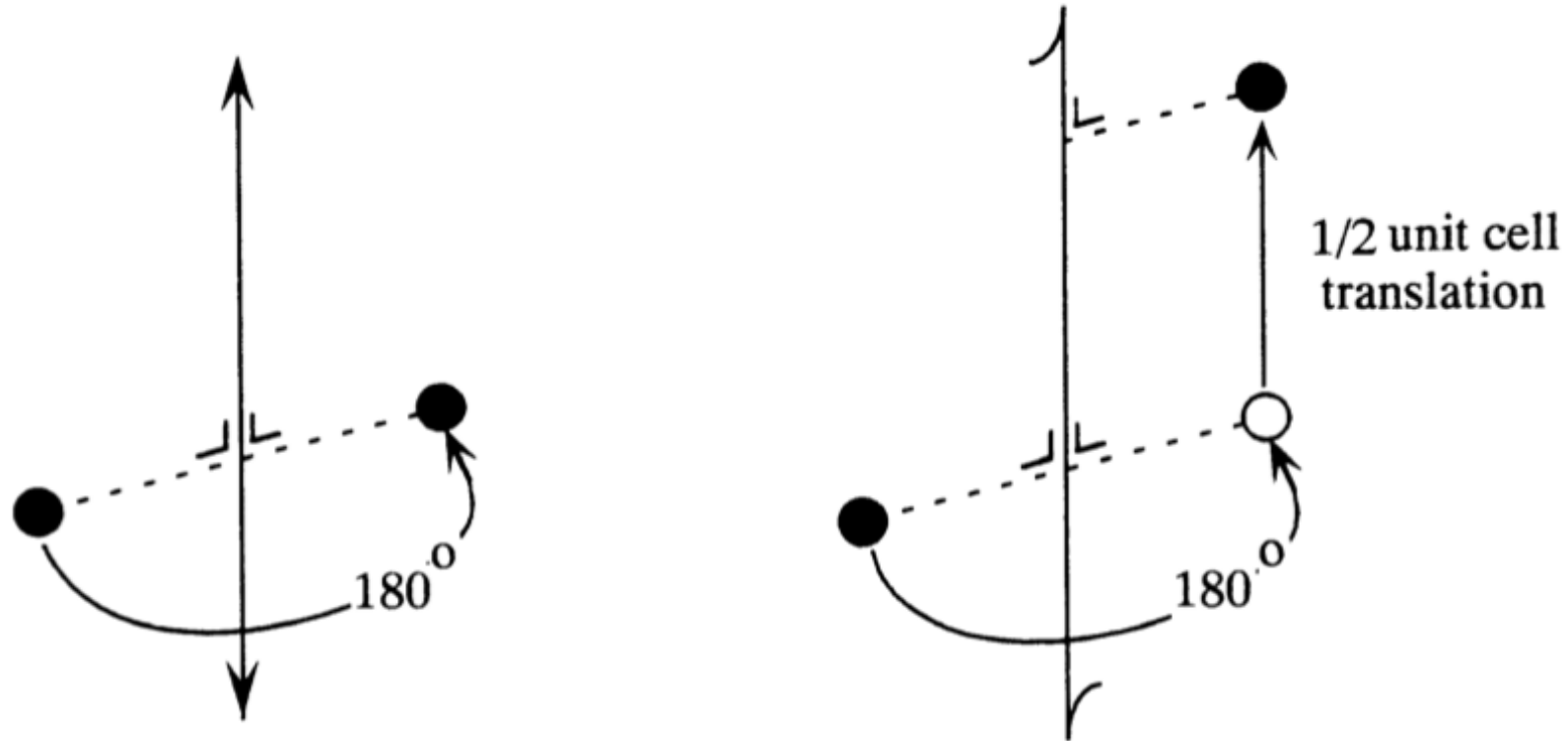
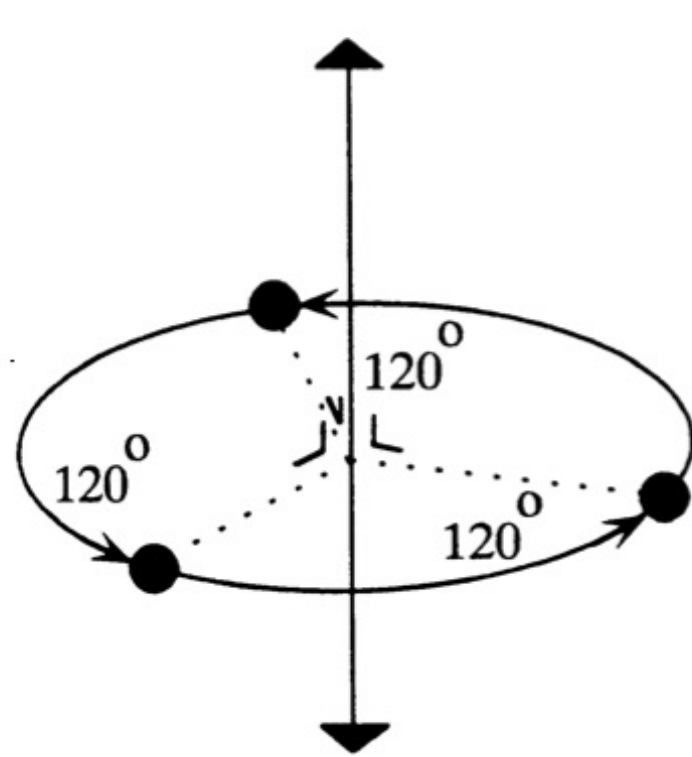
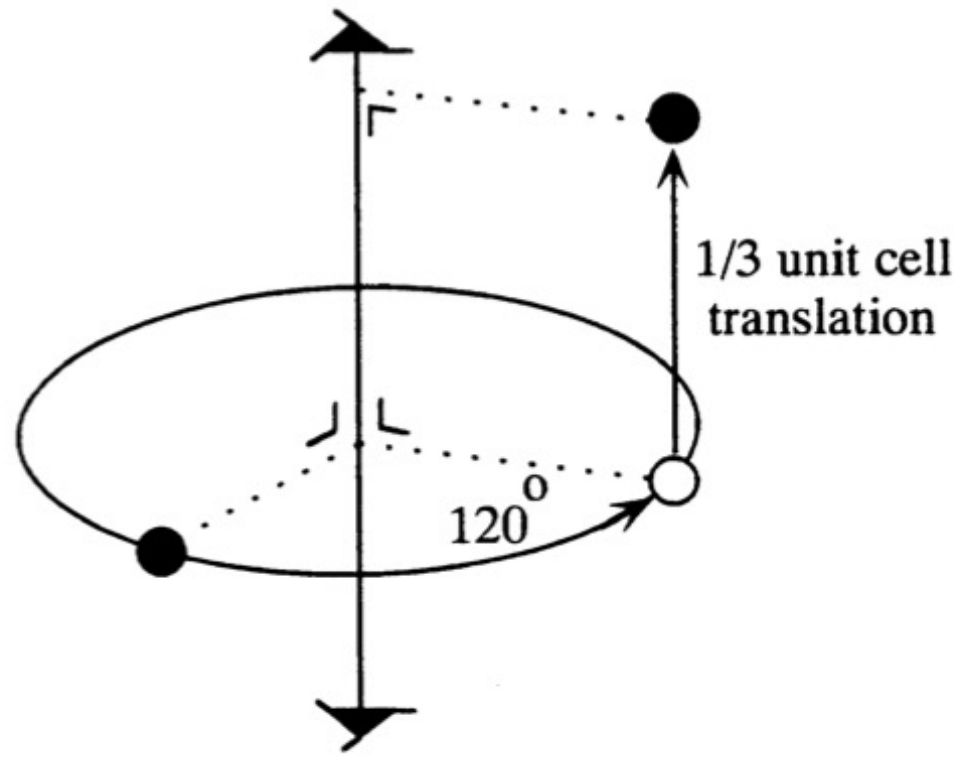


Figure 3.12. A 2-fold axis (left) and a 2-fold screw axis (right); the latter relates one molecule to another by a 180° rotation plus a translation over half of the unit cell.

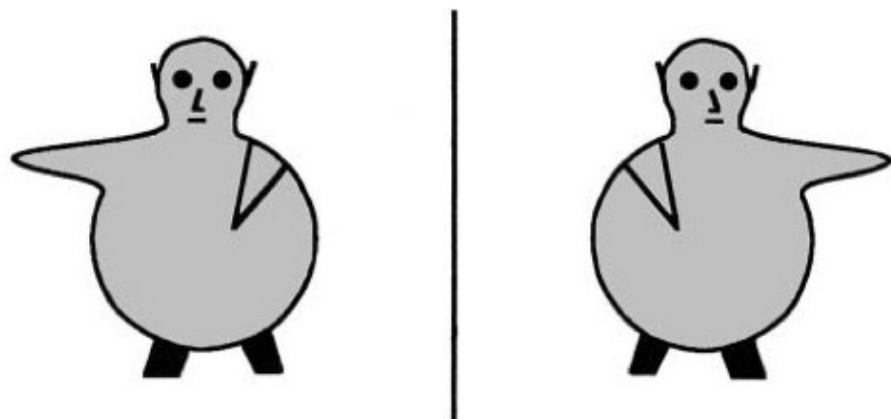


a three-fold rotation axis

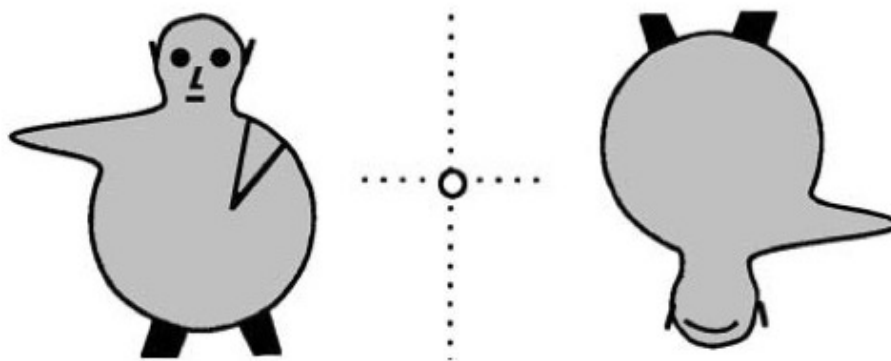


a three-fold screw axis

Figure 3.13. A 3-fold axis (left) and a 3-fold screw axis (right); the latter relates one molecule to another by a 120° rotation and a translation over one-third of the unit cell.



mirror plane



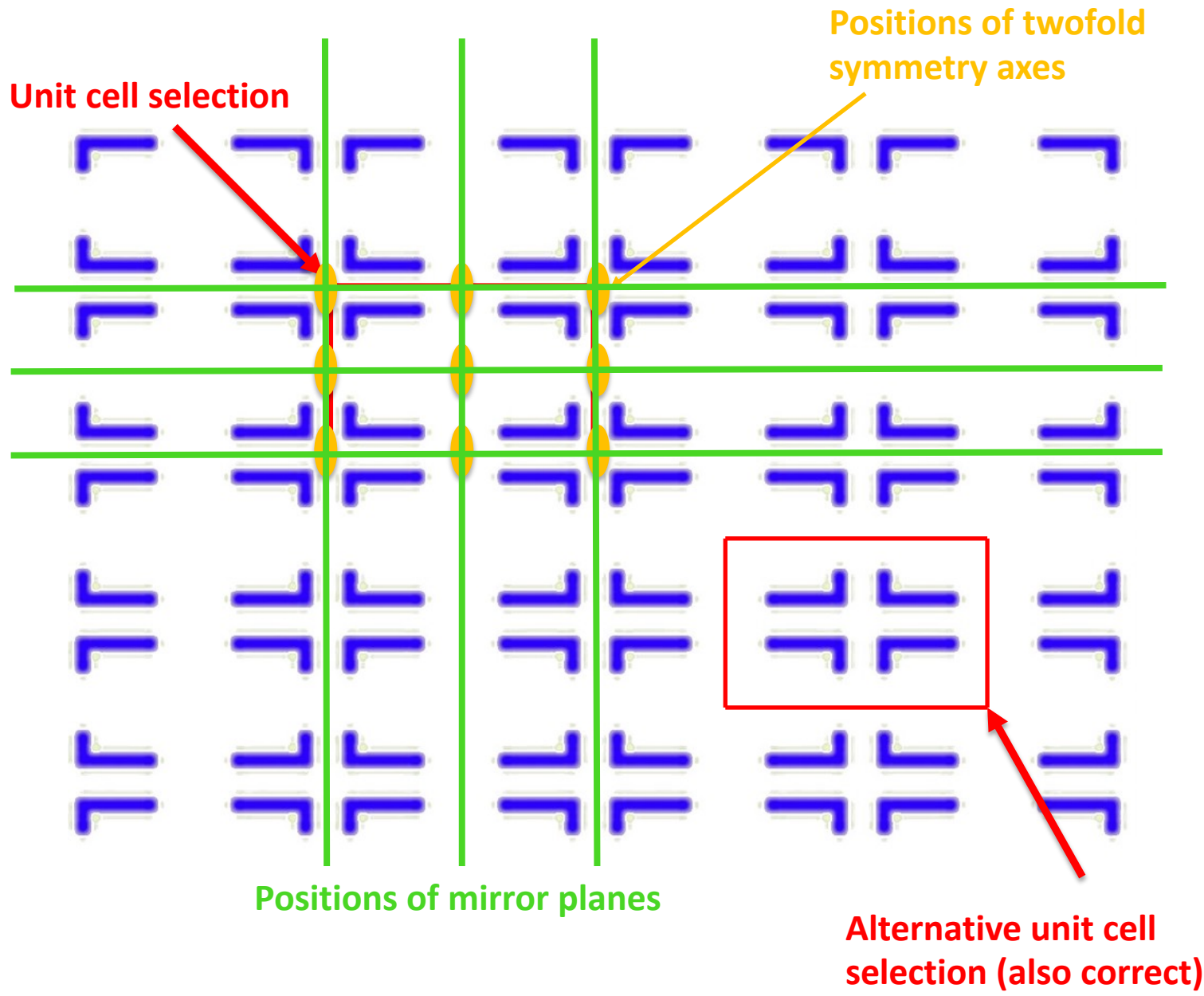
center of symmetry
or inversion center

Figure 3.14. The effect of a mirror and of an inversion center.

Guide to the recognising of wallpaper groups

1. Identify the smallest unit cell that represents all the symmetry included in the pattern. (Be particularly careful in the case of centered symmetry. Use rhomb shaped cells for patterns with 3 and 6-fold rotation axes.)
2. Search for mirror and glide planes, mark rotation axes if any.
3. Use the following table to identify the wallpaper group:
 - i. Find the least rotation.
 - ii. Are there mirror planes in the pattern?
 - iii. Answer the subsequent question(s) if there are any.

Least rotation	Has the pattern mirror plane(s)?	
	Yes	No
60°	p6m	p6
90°	Do the 4-fold axes lie on mirrors? yes - p4mm no - p4g	p4
120°	Is there at least one rotation centre not lying on mirrors? yes - p31m no - p3m1	p3
180°	Are the mirrors perpendicular? Yes No Is there at least one rotation centre not lying on mirrors? Yes - c2mm No - p2mm	p2mg Has the pattern glide plane? Yes - p2gg No - p2
360°	Has a glide plane not identical with mirror plane? Yes - cm No - pm	Has the pattern glide plane? Yes - pg No - p1



Unit cell selection

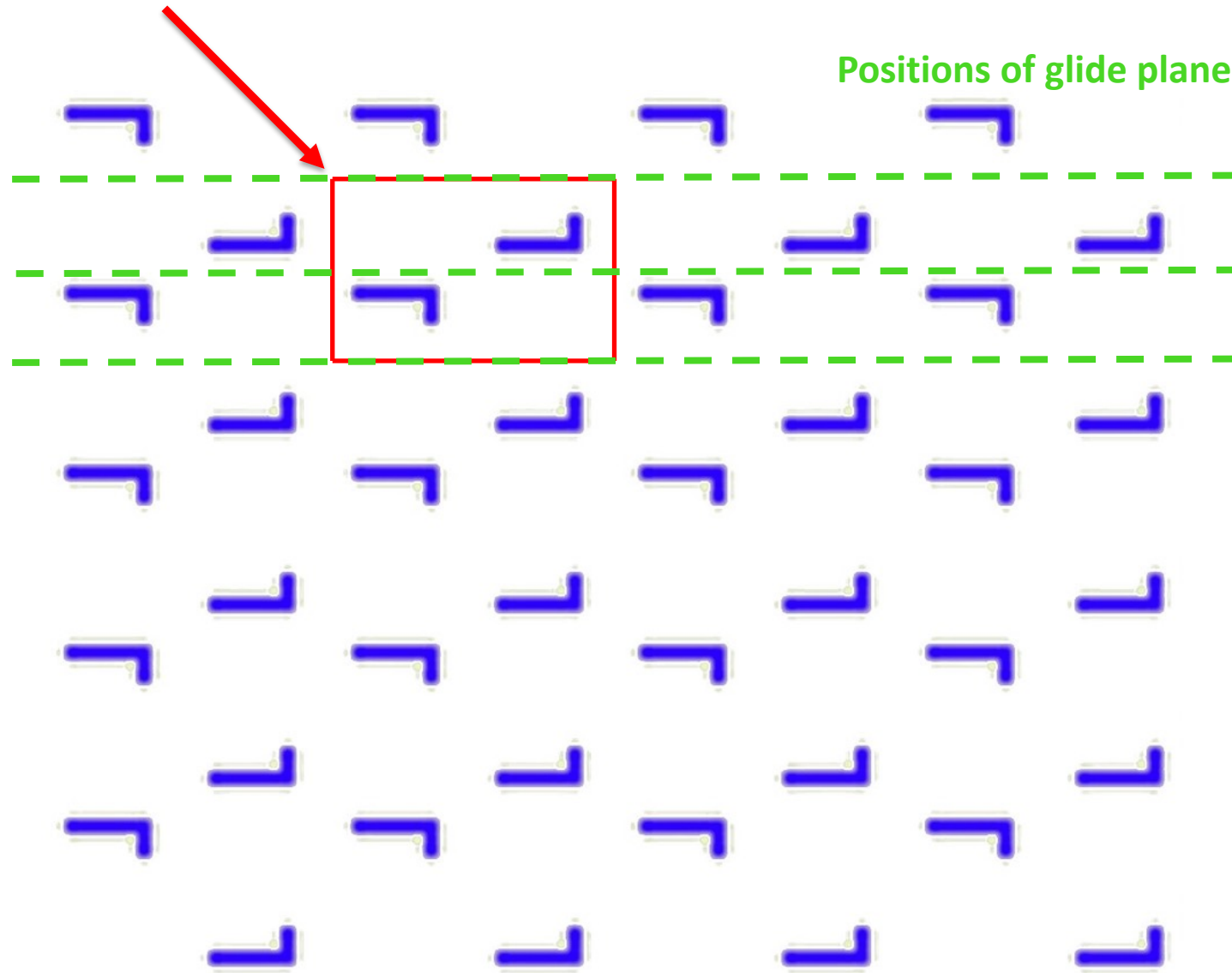
Positions of twofold symmetry axes

Positions of mirror planes

Alternative unit cell selection (also correct)

Unit cell selection

Positions of glide planes



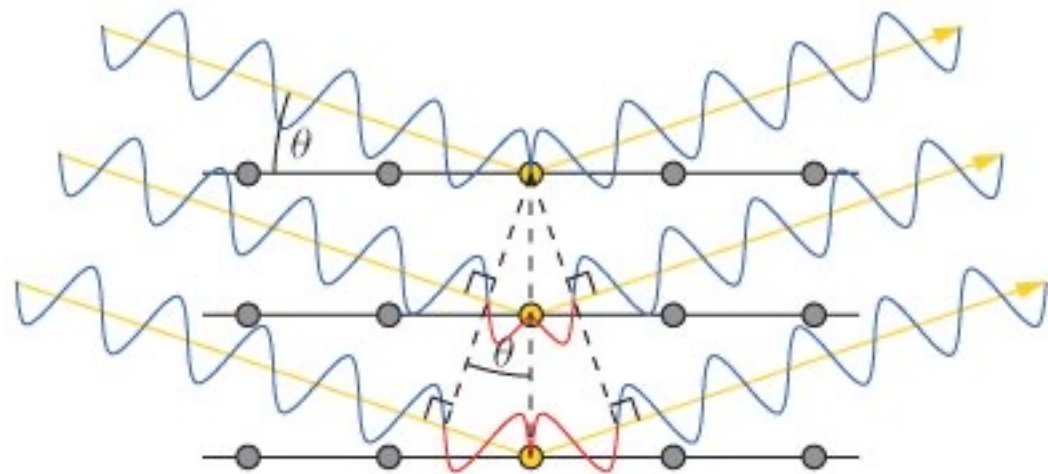
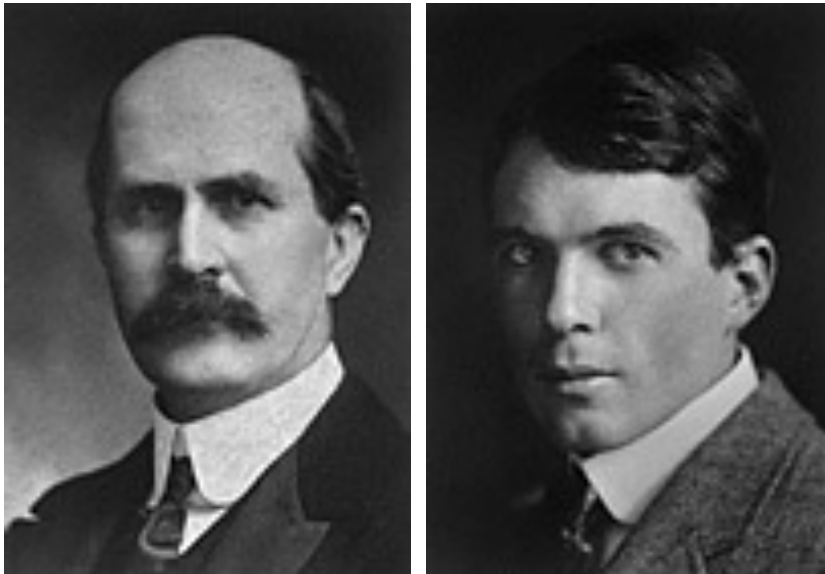
End of lecture #1 in 2022

SIR WILLIAM HENRY BRAGG (1862-1942)
SIR WILLIAM LAWRENCE BRAGG (1890-1971)

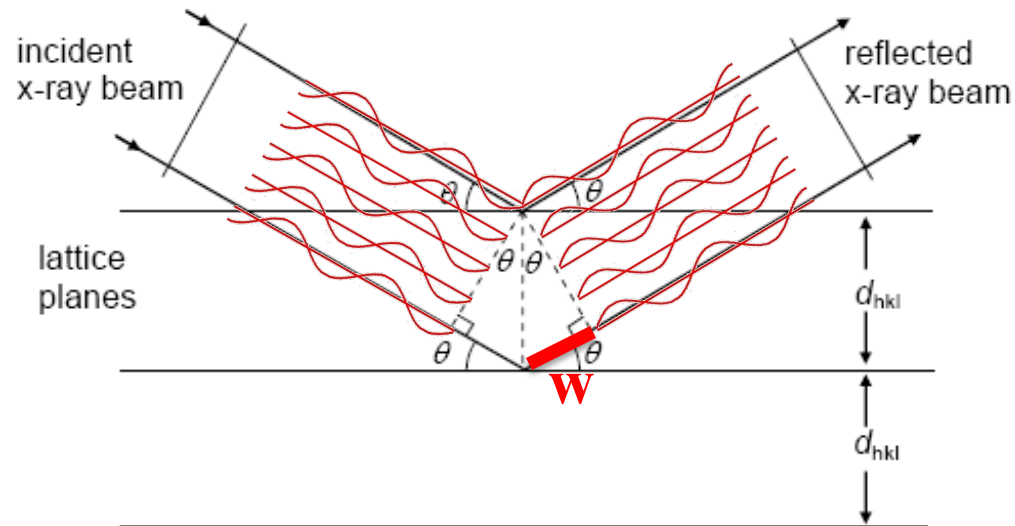
- **1915 Nobel Laureates in Physics**

*for the analysis of crystal structure by means
of X-rays*

$$n\lambda = 2d \sin\theta$$



There is NO PHASE DIFFERENCE if the path differences are equal to whole number multiplies of wavelength (λ)

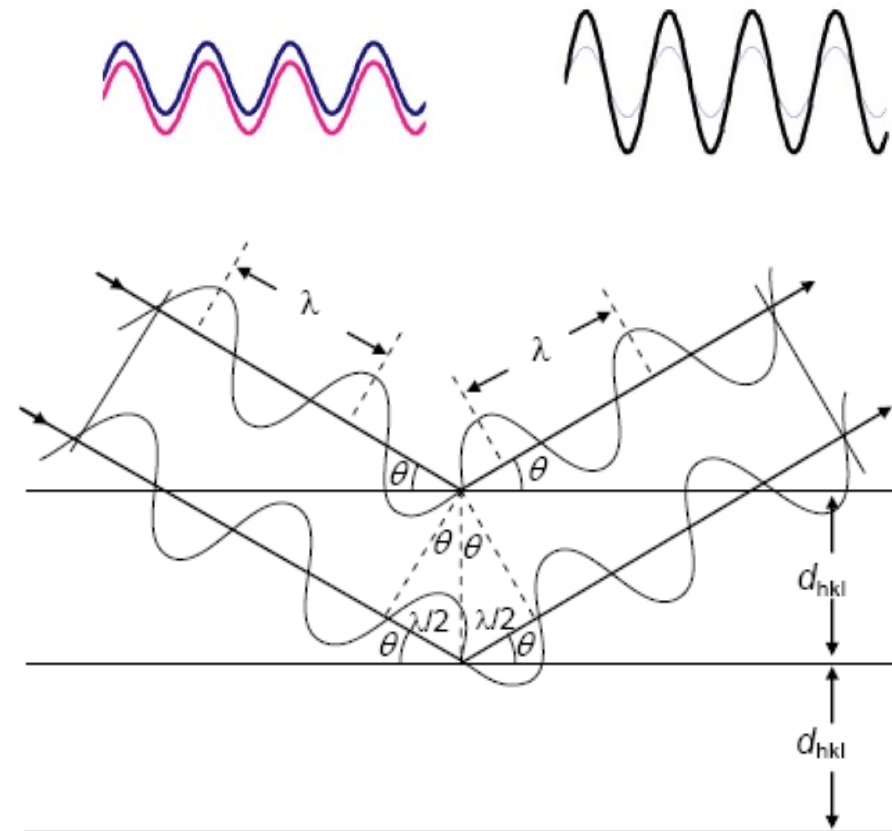


$$\sin\theta = w/d$$

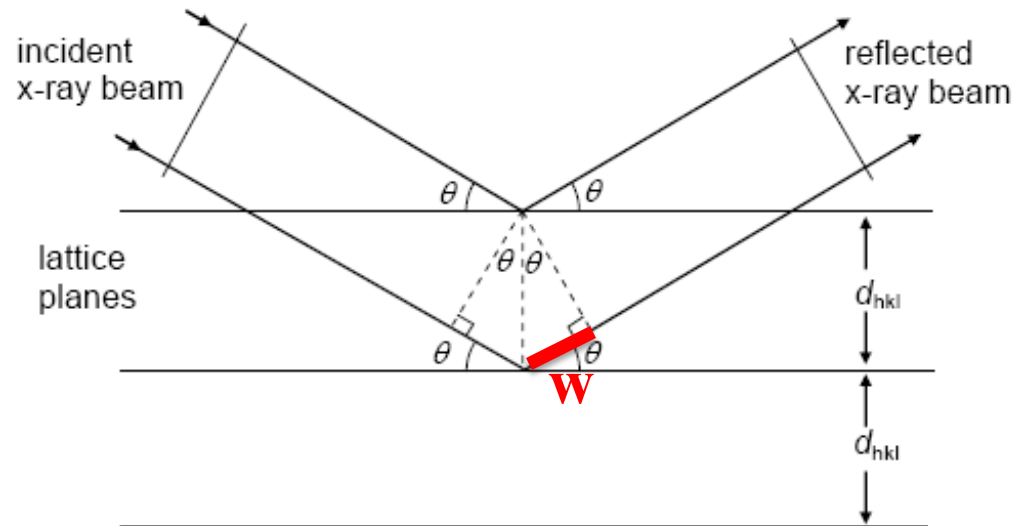
$$2w = n\lambda$$

Bragg's law:

$$n\lambda = 2d \sin\theta$$



There is NO PHASE DIFFERENCE if the path differences are equal to prime number multiplies of wavelength (λ)

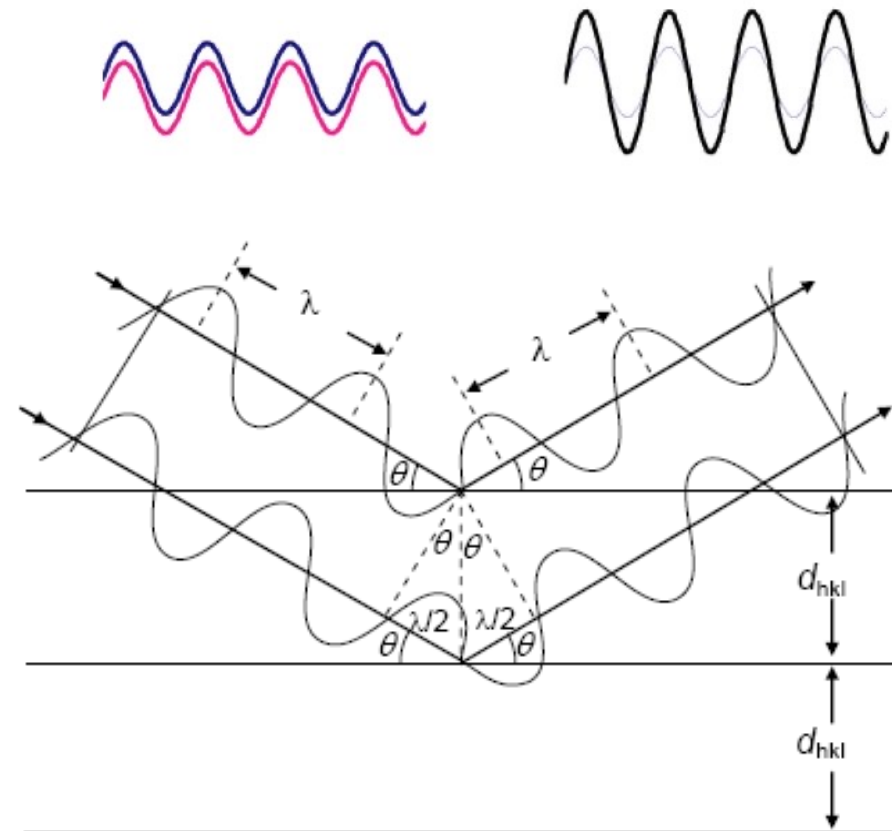


$$\sin\theta = w/d$$

$$2w = n\lambda$$

Bragg's law:

$$n\lambda = 2d \sin\theta$$



$$n\lambda = 2d \sin \theta$$

