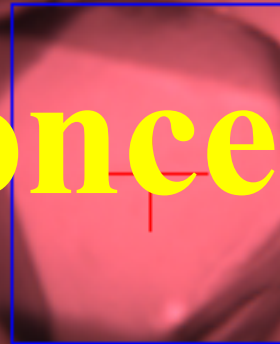




Diffraction by crystalline materials

Part II

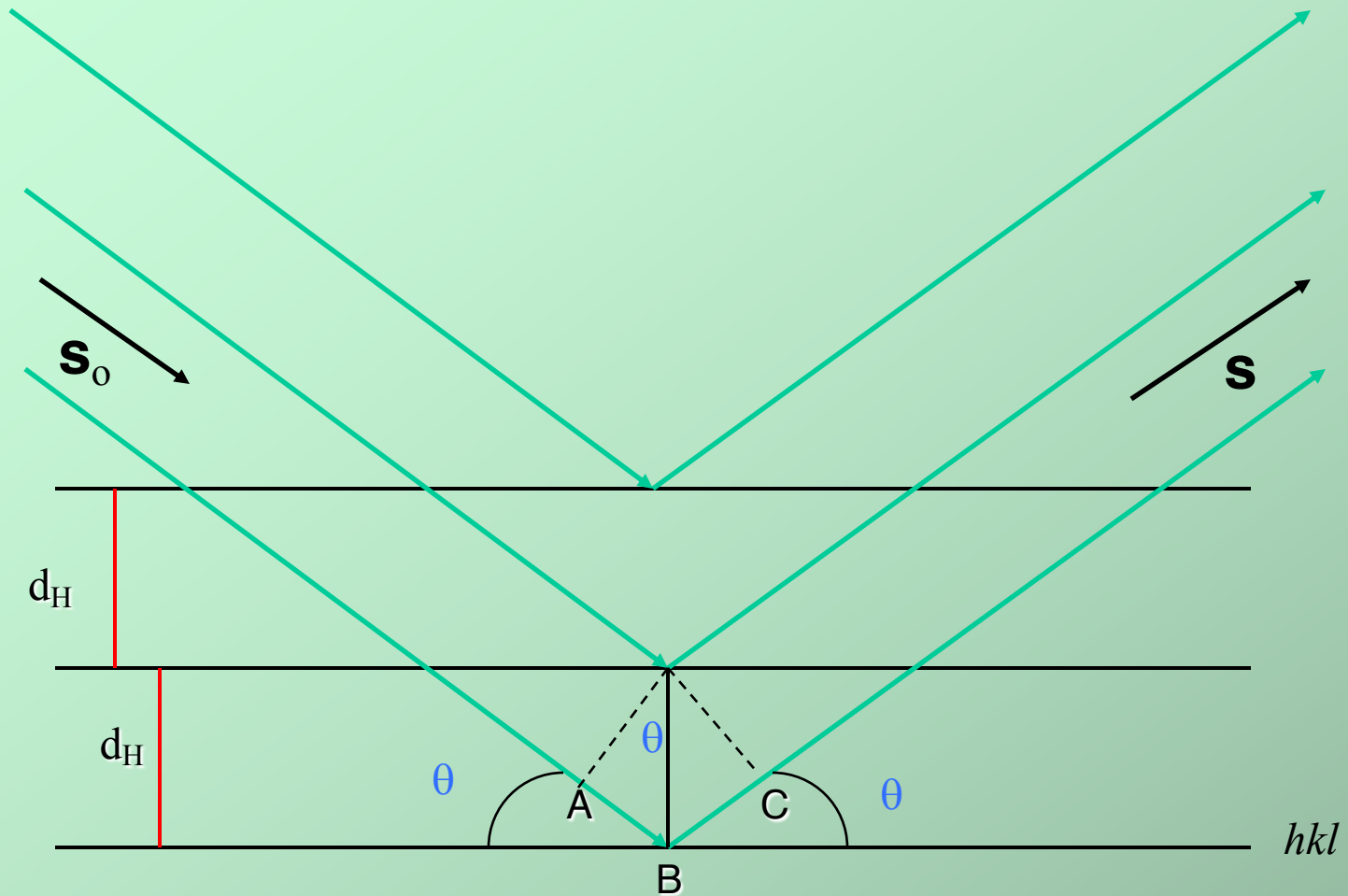
Other useful concepts



100 μm

100 μm

$$2 \sin \theta / \lambda = 1 / d_H = |S_H|$$

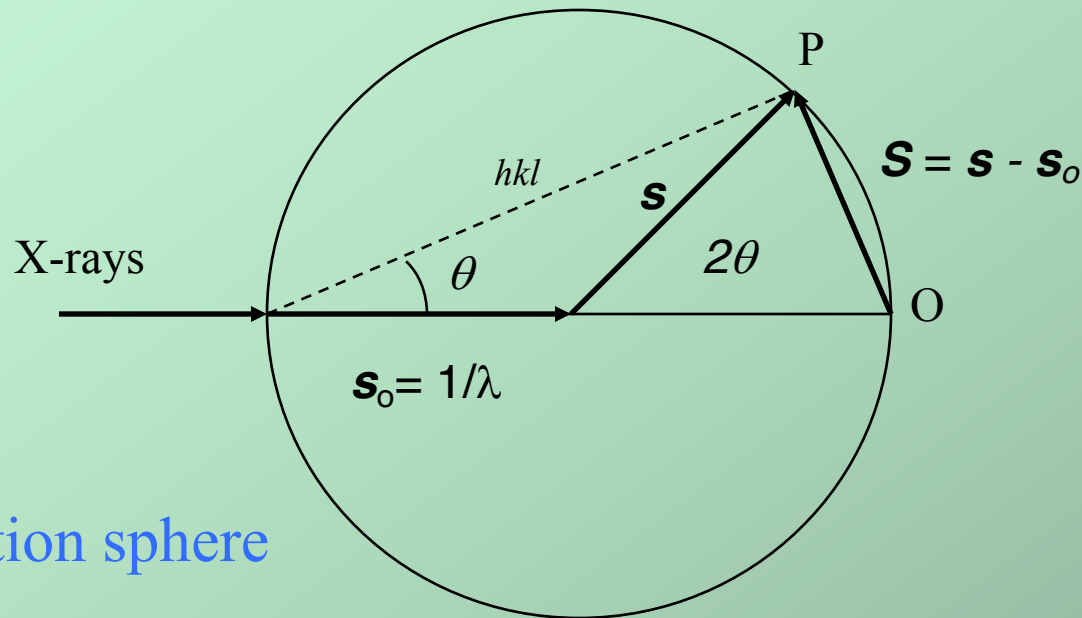


$$AB + BC = 2d_H \sin \theta = n\lambda$$

The Bragg's Law

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

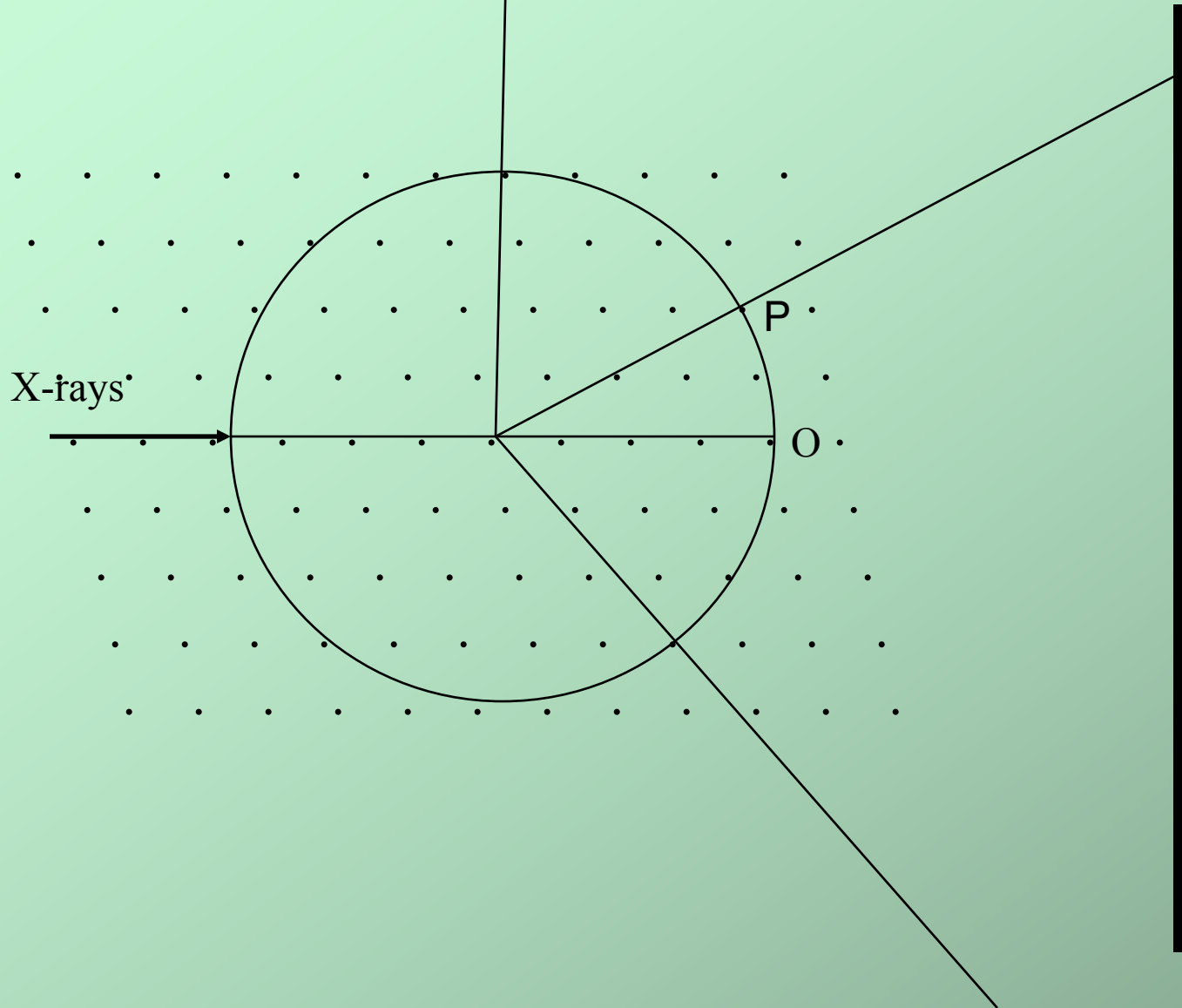
The Bragg's Law relates a distance d in the real space with the modulus of vector \mathbf{S} in the reciprocal space and with indexes (hkl) . The smallest distance d in the real space is related to resolution.



The reflection sphere

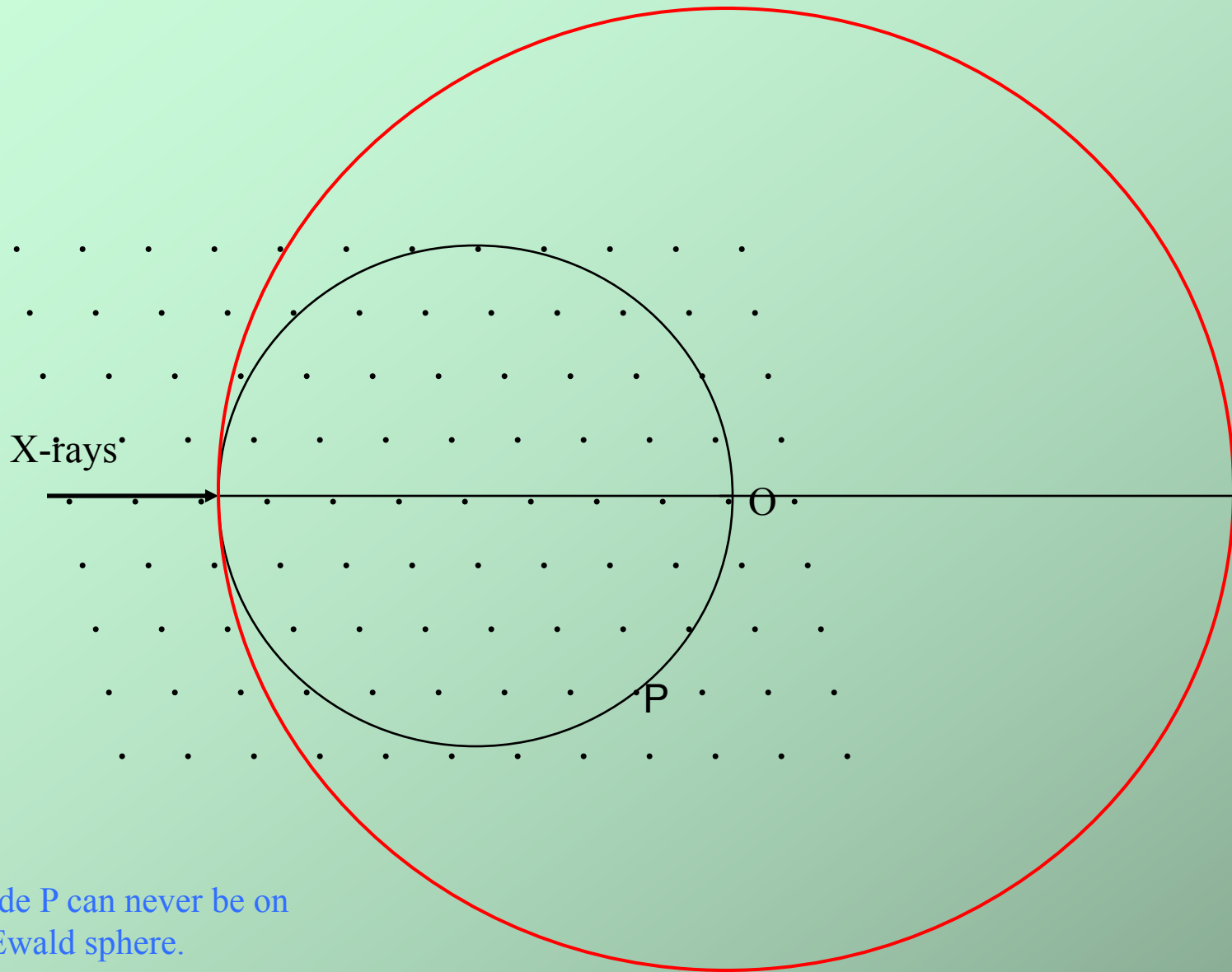
The reflection (Ewald) sphere

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



The limiting sphere

radius = 2λ



If $OP > 2/\lambda$, the node P can never be on the surface of the Ewald sphere.

Resolution: the minimum d spacing corresponding to the maximum useful value of $\sin\theta/\lambda$

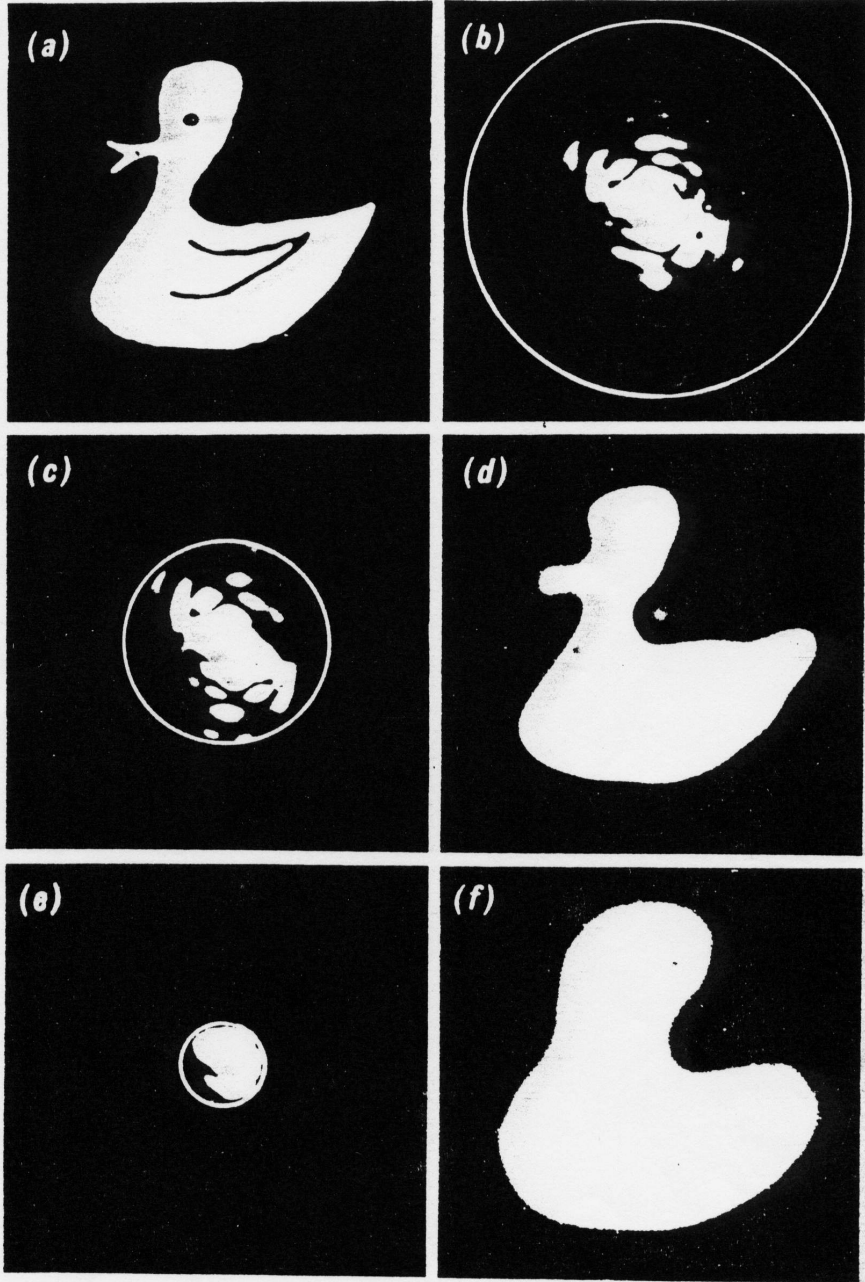
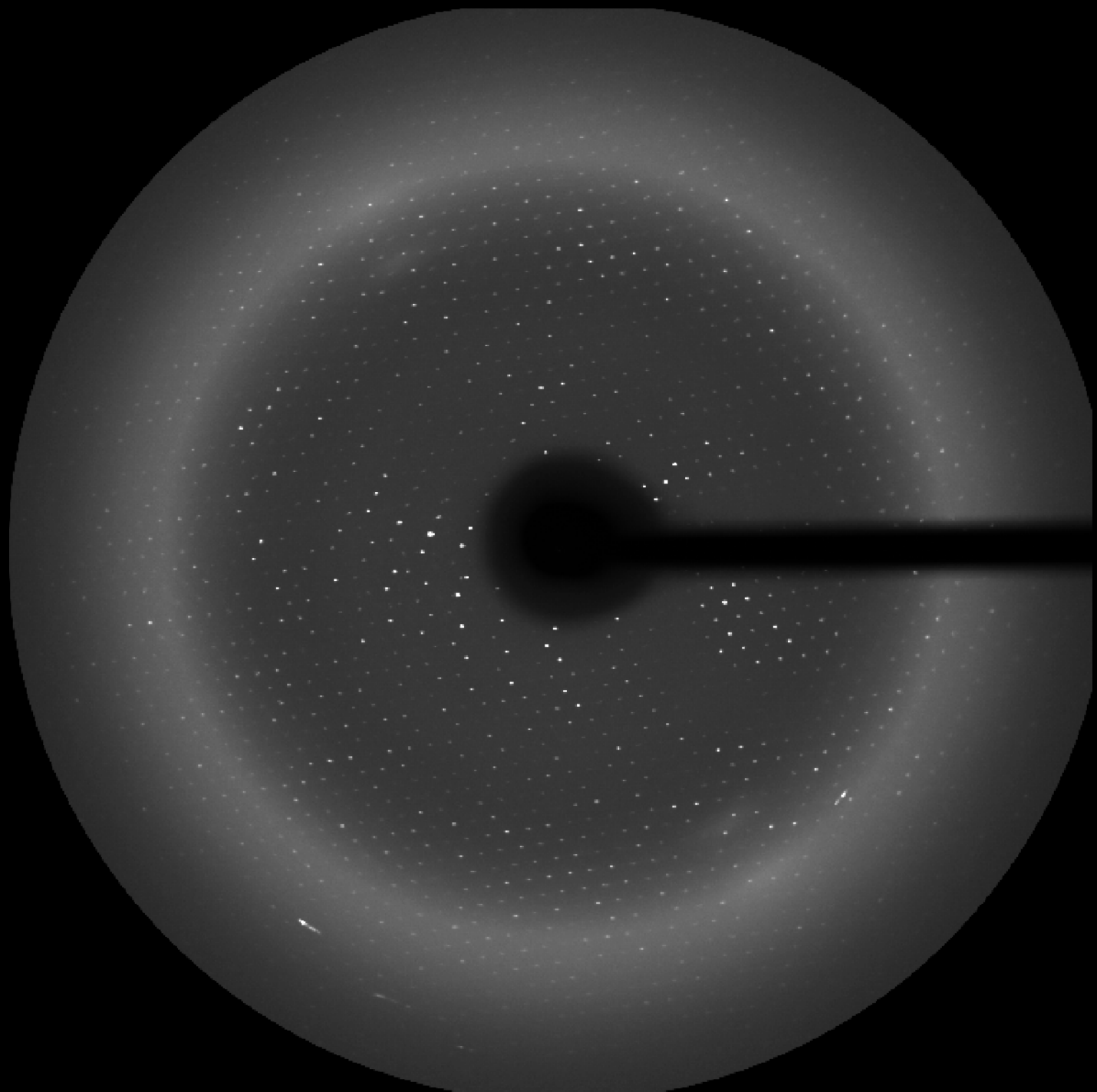


PLATE 44. (a) is an irregular object and (b) is its optical transform. (d) and (f) are the recombined images of the portions of the transform shown at (c) and (e) respectively. See 9.7



Polarization and Lorentz factors

The coherent part of the elastic scattering of x-rays by a particle can be expressed (Thompson):

$$I_{e(Th)} = I_i [e^4/(m^2 r^2 c^4)] (1 + \cos^2 2\theta)/2$$

Where I_i is the intensity of the incident beam. P_0 is the polarization factor when the incident beam is completely unpolarized.

$$(1 + \cos^2 2\theta)/2 = P_0$$

When the radiation source is a synchrotron, the radiation is partially polarized and the polarization factor changes accordingly.

The Lorentz factor takes into account the time a single reflection is in diffracting conditions, and its form depends from the geometry of the data collection.



**Polycrystalline
samples
and others**

100 μm

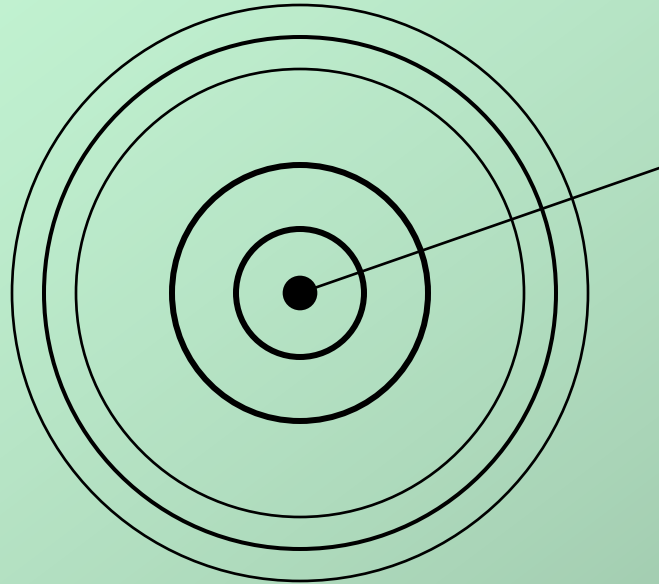
100 μm

Diffraction techniques can be used to measure the diffracted intensities, $I(\mathbf{S})$, on different types of samples:

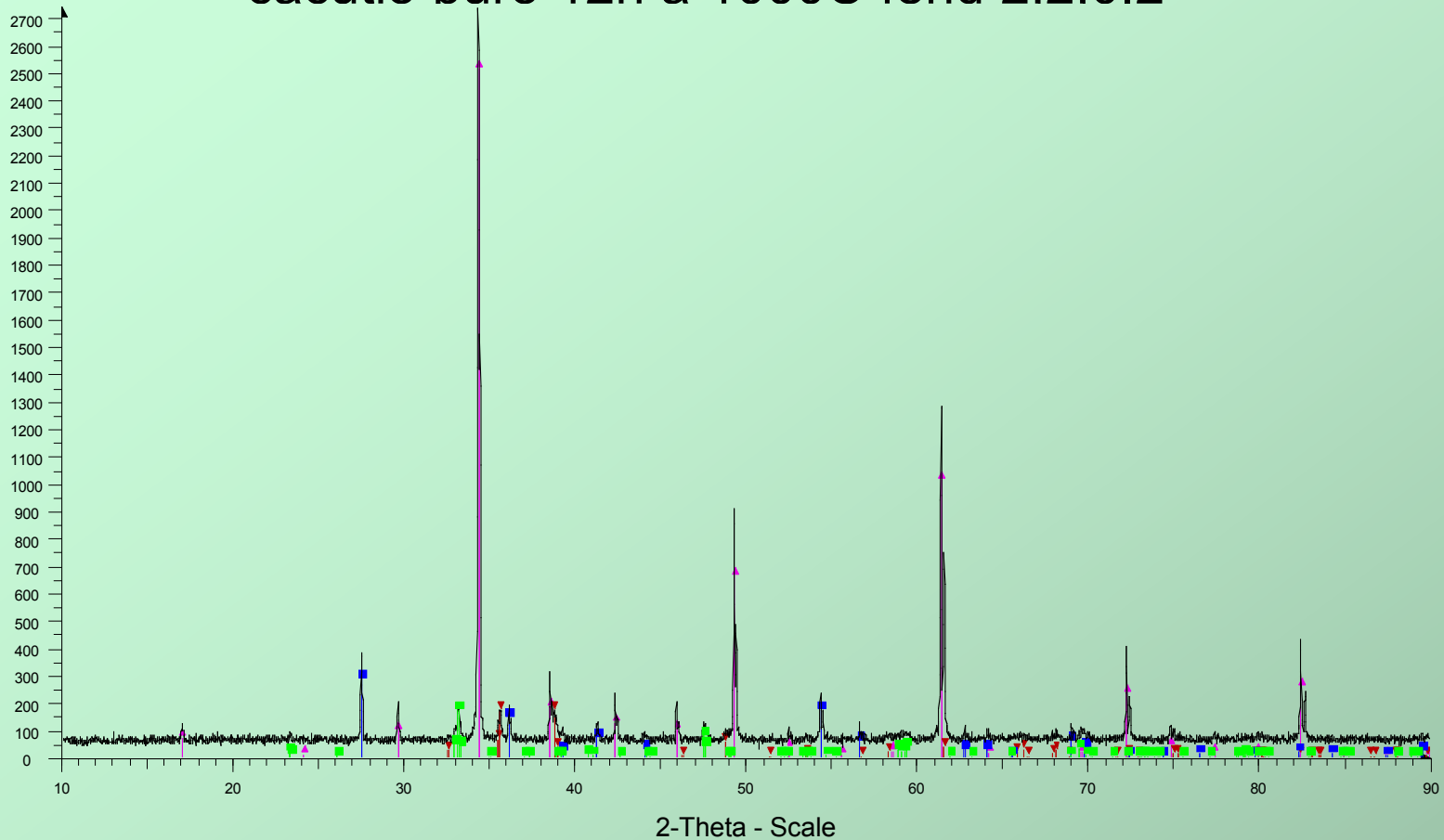
- A single crystal using a monochromatic radiation
- A single crystal with a polychromatic radiation (Laue method)
- A polycrystalline sample (powder) using a monochromatic radiation
- A sample formed by oriented polymers, i.e. with the fibers roughly oriented along one direction

A crystalline powder is formed by an infinite number of randomly oriented small crystals. Their Fourier transform will be an infinite number of randomly oriented reciprocal lattices, all with a common origin.

Each reciprocal lattice node \mathbf{S}_H will assume all the possible orientations, consequently they all will describe a sphere of radius $|\mathbf{S}_H|$.



cacutio puro 12h a 1000C fend 2.2.0.2

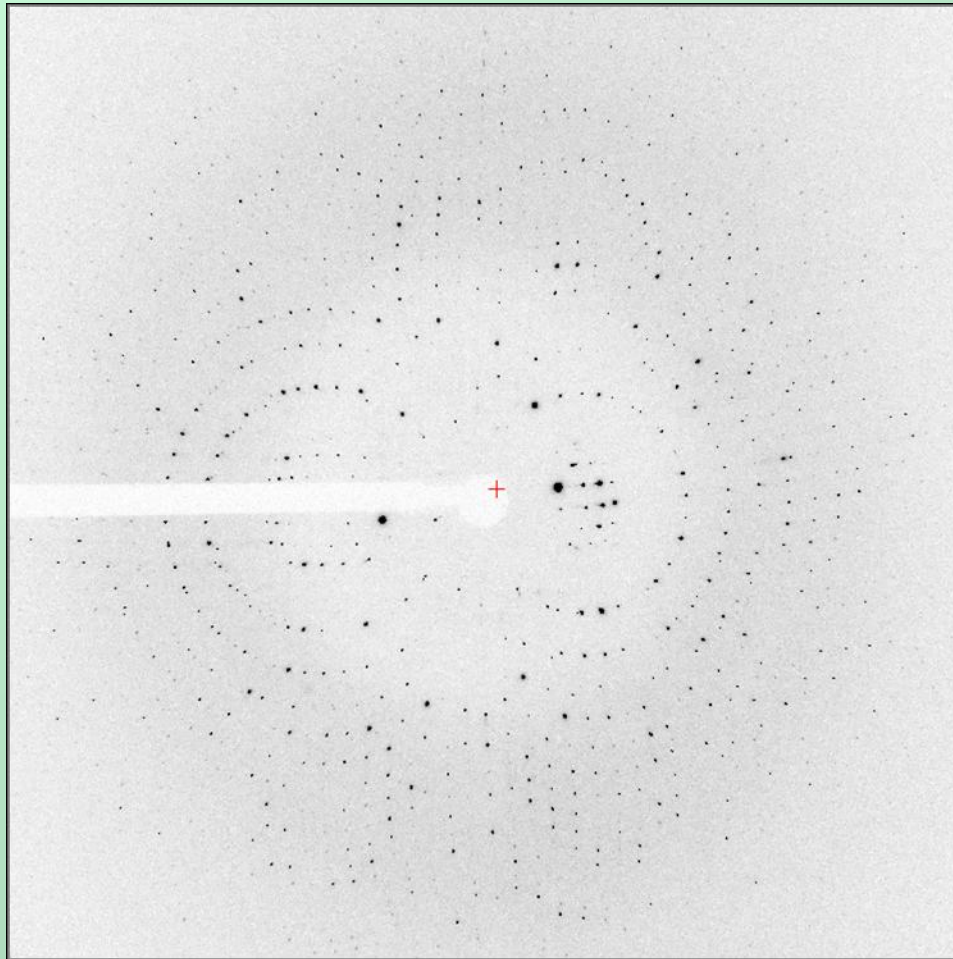


☒ cacutio puro 12h a 1000C fend 2.2.0.2 - File: 1-12h-1000.RAW - Tvoe: 2Th/Th locked - Start: 10.000 ° - End: 90.000 ° - Step: 0.020 ° - Step time: 1. s - Temp.: 25 °C (Room) - Ti
Operations: Import

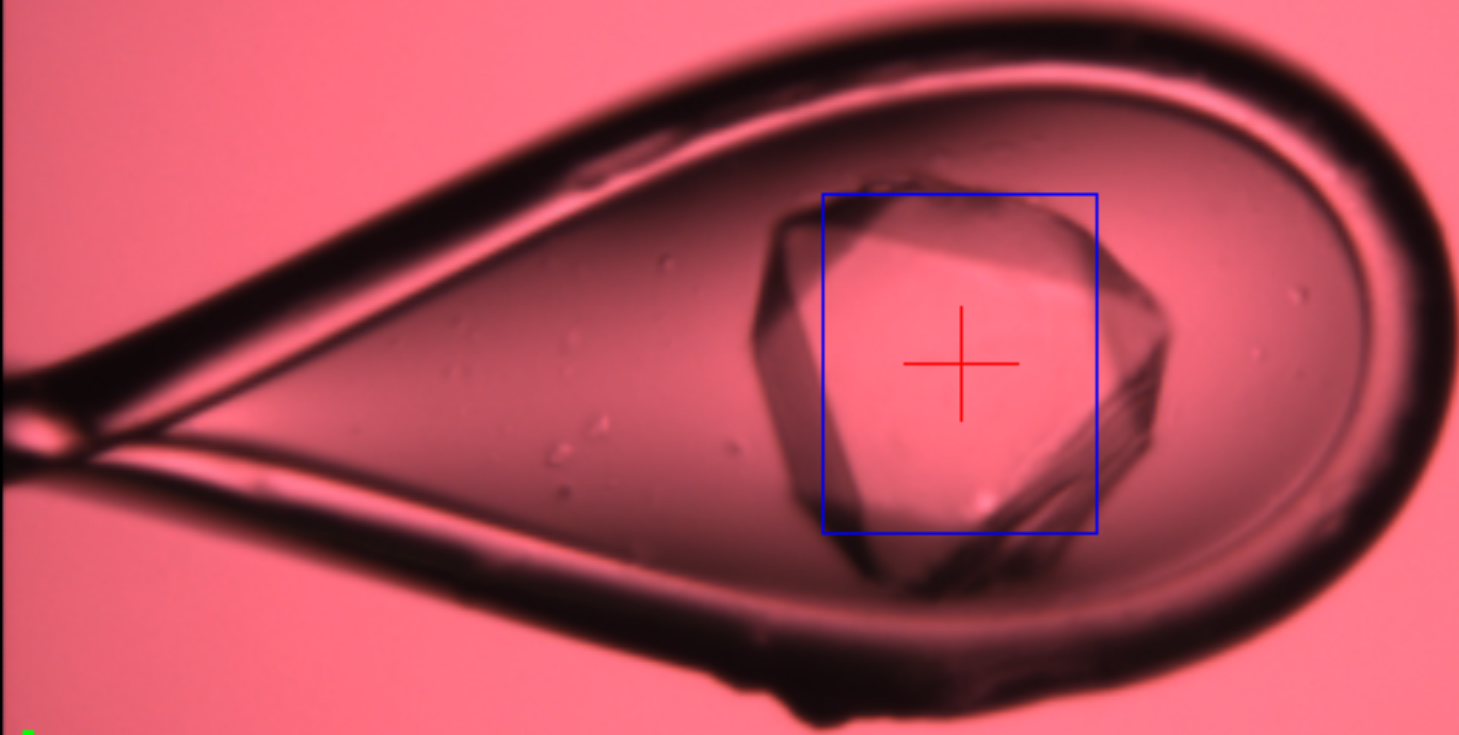
- ▲ 01-075-2188 (C) - Calcium Copper Titanium Oxide - (CaCu₃Ti₄O₁₂) - Y: 91.84 % - d x bv: 1. - WL: 1.54056 - Cubic - a 7.39100 - b 7.39100 - c 7.39100 - alpha 90.000 - beta 90.000 - gamma 90.000 - delta 90.000
- ▼ 00-048-1548 (*) - Tenorite. svn - CuO - Y: 6.25 % - d x bv: 1. - WL: 1.54056 - Monoclinic - a 4.68830 - b 3.42290 - c 5.13190 - alpha 90.000 - beta 99.506 - gamma 90.000 - delta 90.000
- 00-021-1276 (*) - Rutile. svn - TiO₂ - Y: 10.42 % - d x bv: 1. - WL: 1.54056 - Tetragonal - a 4.59330 - b 4.59330 - c 2.95920 - alpha 90.000 - beta 90.000 - gamma 90.000 - delta 90.000
- 00-042-0423 (*) - Perovskite. svn - CaTiO₃ - Y: 6.25 % - d x bv: 1. - WL: 1.54056 - Orthorhombic - a 5.44240 - b 7.64170 - c 5.38070 - alpha 90.000 - beta 90.000 - gamma 90.000 - delta 90.000

Courtesy by V. Massarotti, Pavia

Laue diffraction pattern from hemoglobin, generated with one 160ps X-ray pulse (BioCars, The University of Chicago)

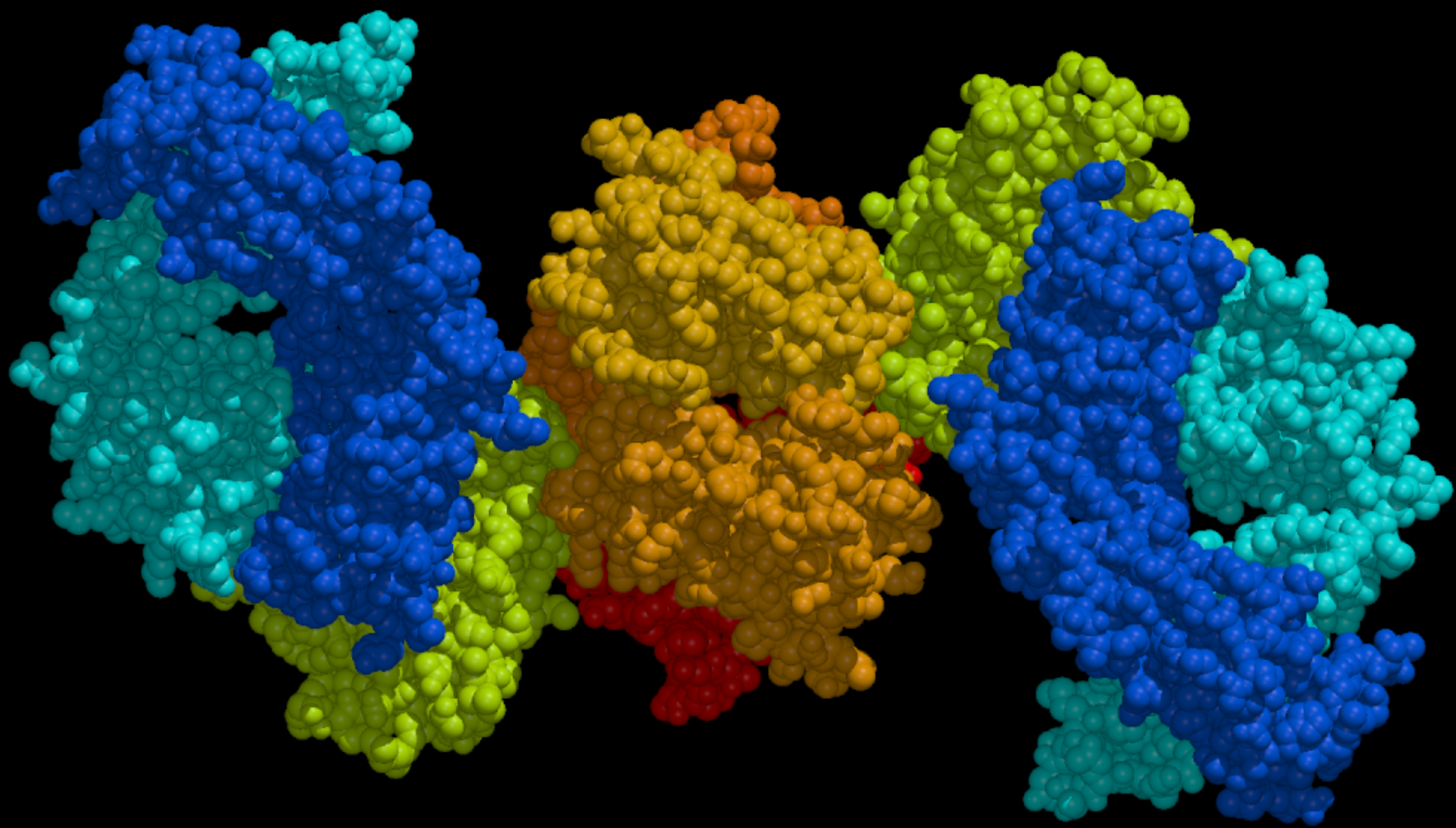


Limits



100 μm

100 μm

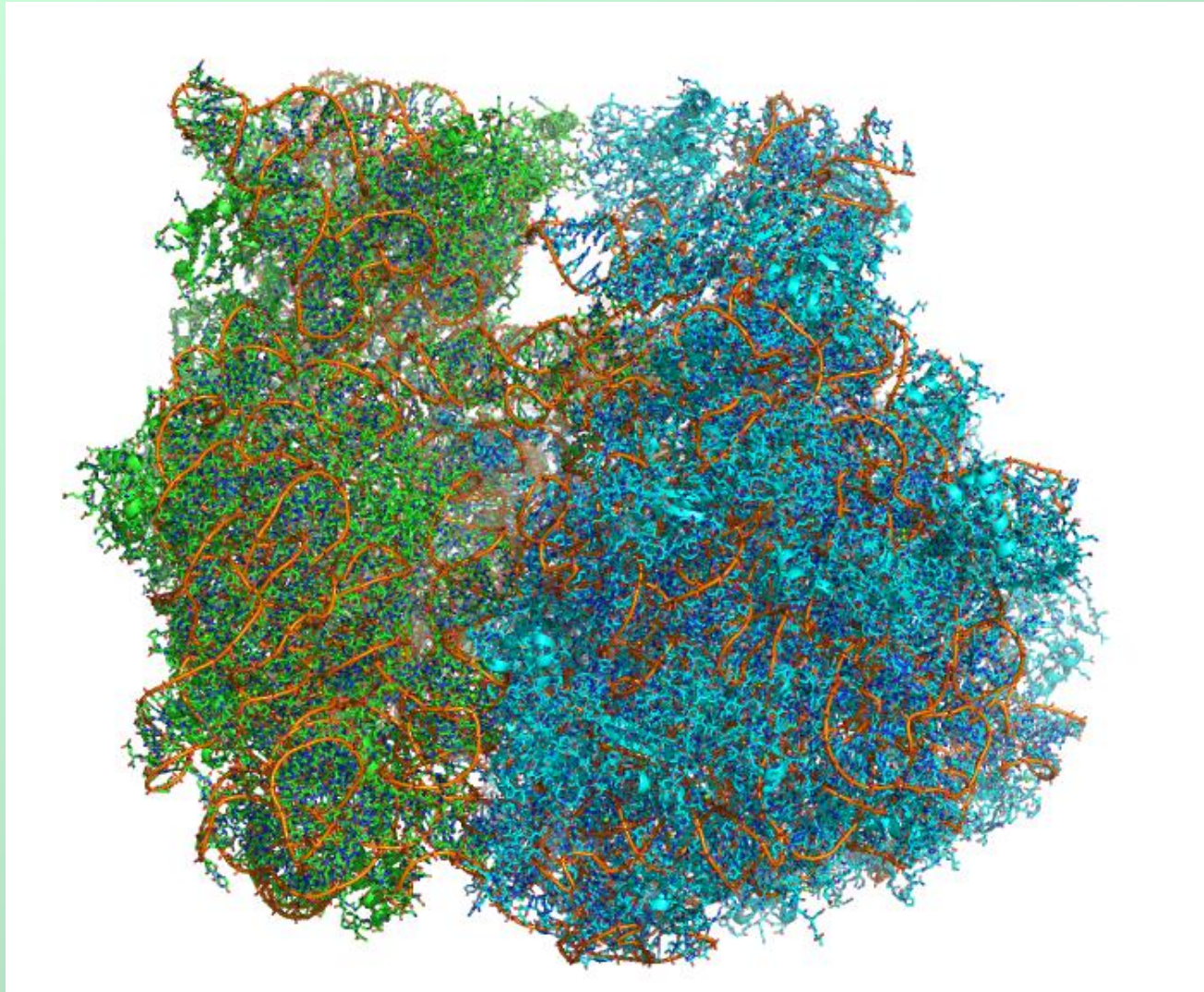


human adenovirus

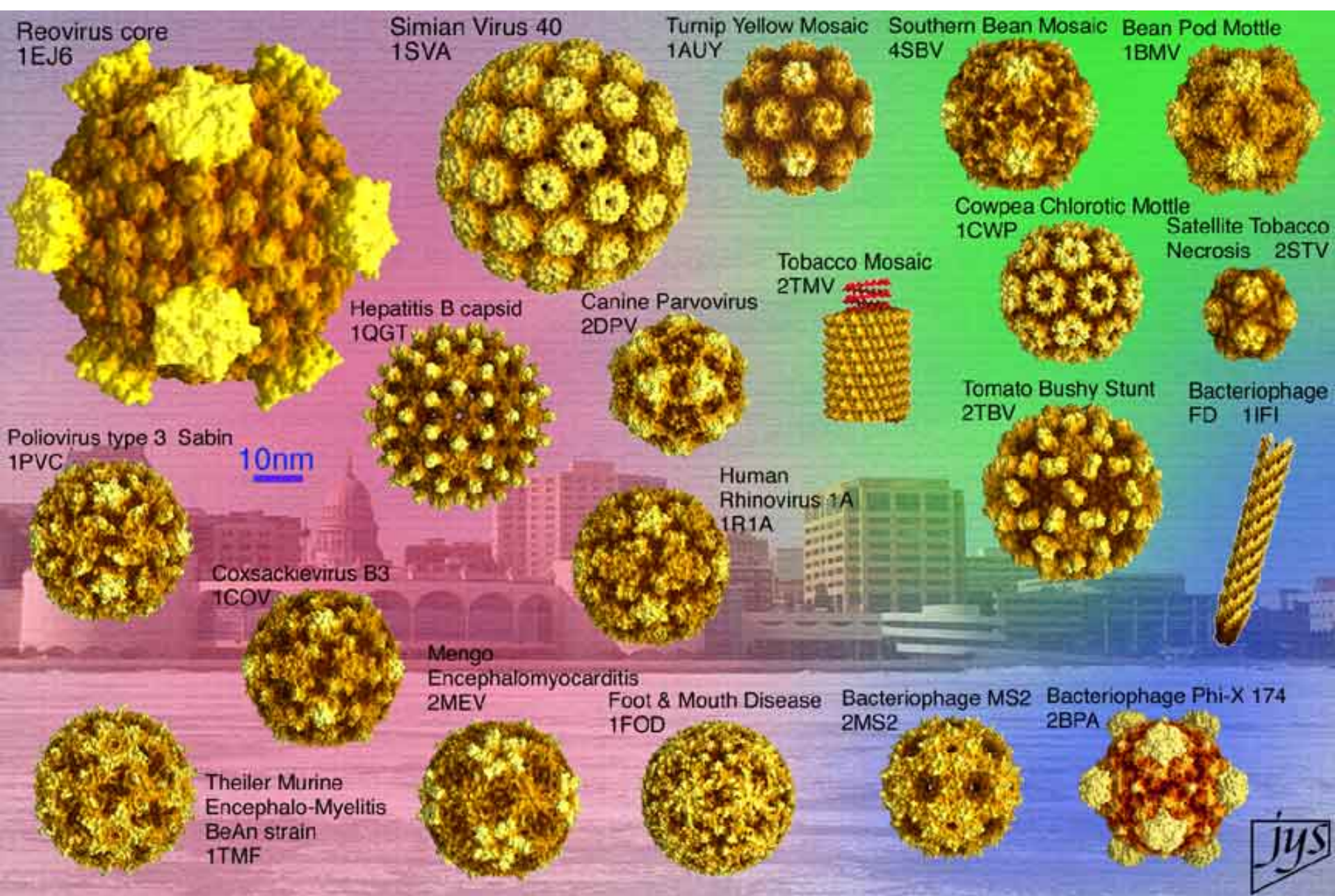


Number of atoms in a.u.: $\approx 92,000$

Ribosome



Number of atoms in a.u.: $\approx 60,000$



Animal (red area), plant (green area) and bacteriophages (blue area) are depicted to scale (see 10nm bar) as GRASP surfaces from published X-ray crystallography coordinates. Virus names are followed by their PDB entry code (see www.rcsb.org or mmtsb.scripps.edu/viper). For downloadable images see also www.bocklabs.wisc.edu. Background: Madison landscape seen from Monona lake. All Images by Dr. Jean-Yves Sgro, Institute for Molecular Virology, UW-Madison.



Cambridge Structural Database (www.ccdc.ac.uk)

1.037.850 crystal structures

Protein data bank. (www.rcsb.org)

181.969 macromolecular structures

End of part II

Which is the minimum crystal size for useful measurement of diffraction data?

$$E(hkl) \propto |F(hkl)|^2 V_{\text{cryst}}/V_{\text{cell}}$$

Inorganic crystal

$V_{\text{cell}} = 1000 \text{ \AA}^3$
edges $10 \mu\text{m}$
 10^{12} cells

Protein crystal

$V_{\text{cell}} 100,000 - 1 \text{ million } \text{ \AA}^3$
edges $10 \mu\text{m}$
 $10^{10} - 10^9$ cells

