

# Determination of crystal structure by single crystal X-ray diffraction

Mestrado em Química e Mestrado em Química Tecnológica  
2020/2021

**Fátima Piedade**

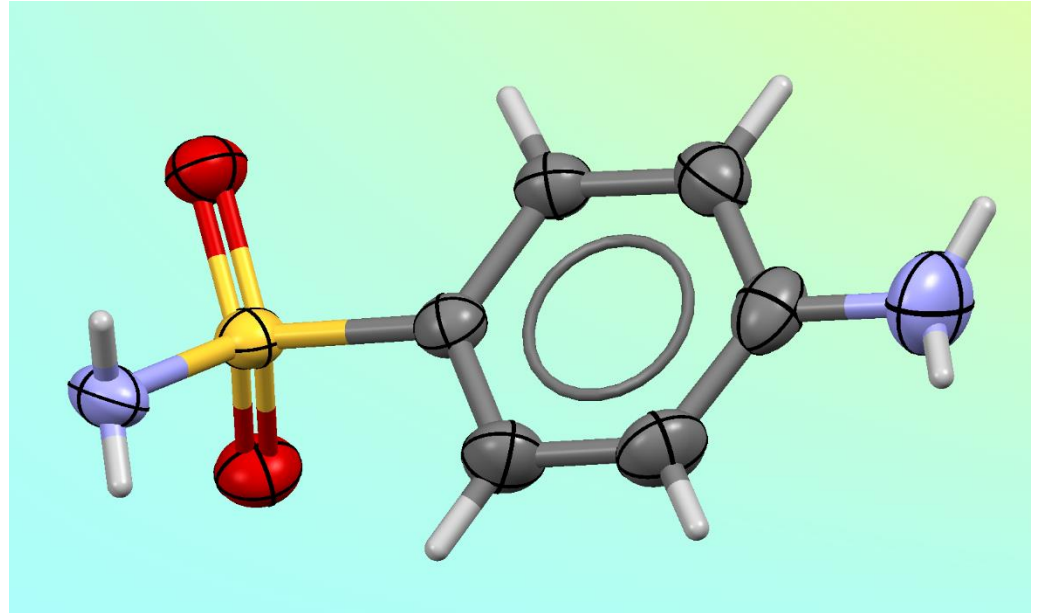
**[mdpiedade@fc.ul.pt](mailto:mdpiedade@fc.ul.pt)**

## **Why this class on structural analysis of single crystal**

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- **One of the most common and more accurate methods for determining the three-dimensional structure of crystalline compounds**

# SULFONAMIDE



## **Why this class on structural analysis of single crystal**

---

- **One of the most common and more accurate methods for determining the three-dimensional structure of crystalline compounds**
- **There is virtually no scientific publication of a new compound, without its crystalline structure.**

**Toward Controlled Nucleation: Balancing Monolayer Chemistry with Monolayer Fluidity** Abstract | Supporting Info  
 Conrad Lendrum and Kathryn M. McGrath  
 pp 4463-4470  
 Publication Date (Web): September 13, 2010 (Article)  
 DOI: 10.1021/cg100675d  
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**Environmentally Friendly Growth of Well-Developed LiCoO<sub>2</sub> Crystals for Lithium-Ion Rechargeable Batteries Using a NaCl Flux** Abstract | Supporting Info  
 Katsuya Tachima, Sunghyng Lee, Yusuke Mizuno, Hihara Inagaki, Masato Hozumi, Keiichi Kohama, Kunio Yubuta, Toetsu Shishido, and Shuji Oishi  
 pp 4471-4475  
 Publication Date (Web): August 27, 2010 (Article)  
 DOI: 10.1021/cg100705d  
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**Supramolecular Architectures in 5,5'-Substituted Hydantoins: Crystal Structures and Hirshfeld Surface Analyses** Abstract | Supporting Info  
 Basab Chattopadhyay, Alok K. Mukherjee, N. Narendra, H. P. Hemantha, Vommina V. Sureshbabu, Madeline Mellinell, and Monika Mukherjee  
 pp 4476-4484  
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 DOI: 10.1021/cg100706n  
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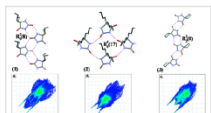


Figure 1 of 8

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Crystal Growth & Design: Volume 10, Issue 10 (ACS Publications)

**Crystal Growth & Design: Volume 10, Issue 10 (ACS Publications)**

**Polyoxometalate Supported Transition Metal Complexes: Synthesis, Crystal Structures, and Supramolecular Chemistry** Abstract | Supporting Info  
 T. Arumuganathan, A. Srinivasa Rao, and Samar K. Das  
 pp 4272-4284  
 Publication Date (Web): September 21, 2010 (Article)  
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**Formation and Self-Assembly of Cadmium Hydroxide Nanoplates in Molten Composite-Hydroxide Solution** Abstract  
 Jing Zhang, Yonghao Wang, Zhang Lin, and Feng Huang  
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 Publication Date (Web): September 15, 2010 (Article)  
 DOI: 10.1021/cg101509z  
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**First Principles Simulations of the Structural and Dynamical Properties of Hydrated Metal Ions Me<sup>2+</sup> and Solvated Metal Carbonates (Me = Ca, Mg, and Sr)** Abstract | Supporting Info  
 Devii Di Tommaso and Nora H. de Leeuw  
 pp 4292-4302  
 Publication Date (Web): September 1, 2010 (Article)  
 DOI: 10.1021/cg100055p  
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**Crystal Polymorphs and Transformations of 2-Iodo-4-nitroaniline** Abstract | Supporting Info  
 Dawn M. Kelly, Kevin S. Eccles, Curtis J. Elcoate, and Humphrey A. Moynihan  
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 DOI: 10.1021/cg1001418  
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**Lanthanide Contraction and Temperature-Dependent Structures of Lanthanide Coordination Polymers with Imidazole-4,5-Dicarboxylate and Oxalate** Abstract | Supporting Info  
 Wen-Guan Liu, Long Jiang, and Tong-Bu Lu  
 pp 4310-4318  
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**Relationship between the Crystal Structure and Morphology of Carboxylic Acid Polymers. Predicted and Experimental Morphologies** Abstract | Supporting Info  
 Evelyn Moreno-Calvo, Teresa Calvet, Miguel Angel Cuevas-Diarte, and Dino Aquilano  
 pp 4322-4371  
 Publication Date (Web): September 10, 2010 (Article)  
 DOI: 10.1021/cg101436p  
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Crystal Growth & Design: Volume 10, Issue 10 (ACS Publications)

ACS Publications  
 Crystal Growth & Design  
 Table of Contents  
 October 6, 2010  
 Volume 10, Issue 10  
 Pages 4203-4670  
 About the Cover:  
 The first systematic crystallographic study of the whole family of nonplanar polyaromatic hydrocarbons having a stepwise increase in surface area, curvature, and strain is presented (*Cryst. Growth Des.* 2010, 10, 4607-4621). The effect of controlled extension of *m*-aromatic surfaces on the solid state structures of the resulting crystalline solids and their implications for molecular electronics are discussed. Cover art image produced by Alexander Filatov. View the article.  
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 Fiona C. Meldrum, Radjibab I. Ristic  
 pp 4203-4205  
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**Fluorobenzonitriles: Influence of the Substitution Pattern on Melting and Crystallization Properties** Abstract | Supporting Info  
 Vera Vasylyeva and Klaus Merz  
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 Publication Date (Web): September 15, 2010 (Article)  
 DOI: 10.1021/cg100794c  
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**Creation of Nanoscale Two-Dimensional Patterns of ZnO Nanorods using Laser Interference Lithography Followed by Hydrothermal Synthesis at 80 °C** Abstract  
 Tae-Uh Kim, Jin-A Kim, S. M. Pawar, Jong-Ho Moon, and Jin Hyock Kim  
 pp 4256-4261  
 Publication Date (Web): August 30, 2010 (Article)  
 DOI: 10.1021/cg100723c  
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**Use of Silver(I) and Copper(II) Ions to Assist the Self-Assembly of Polyrotaxanes Incorporating Symmetrical  $\alpha,\alpha',\beta,\beta'$ -Tetramethylcarbamoyl-R[5]uril** Abstract | Supporting Info  
 Jin-Ping Zeng, Shi-Min Zhang, Yun-Qian Zhang, Zhu Tao, Qian-Jiang Zhu, Sai-Feng Xue, and Gang Wei  
 pp 4509-4515  
 Publication Date (Web): September 9, 2010 (Article)  
 DOI: 10.1021/cg100779c  
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**A Racemic Conglomerate Nipped in the Bud: A Molecular View of Enantiomer Cross-Inhibition of Conglomerate Nucleation at a Surface** Abstract | Supporting Info  
 Abel Robin, Patrizia Iavicoli, Klaus Wurst, Matthew S. Dyer, Sam Haq, David B. Amabilino, and Susanna Ravaioli  
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 DOI: 10.1021/cg100809v  
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**Morphology Control of Fluorapatite Crystallites by Citrate Ions** Abstract | Supporting Info  
 Yu-Ju Wu, Yao-Hung Tseng, and Jerry C. C. Chan  
 pp 4240-4242  
 Publication Date (Web): August 23, 2010 (Communication)  
 DOI: 10.1021/cg100899m  
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 Hi-Res PDF [2659K]  
 PDF w/ Links [821K]

**Sulfioxides: Potent Co-Crystal Formers** Abstract | Supporting Info  
 Kevin S. Eccles, Curtis J. Elcoate, Stephen P. Stokes, Anita R. Maguire, and Simon E. Lawrence  
 pp 4243-4245  
 Publication Date (Web): August 23, 2010 (Communication)  
 DOI: 10.1021/cg101019z  
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Figure 1 of 6

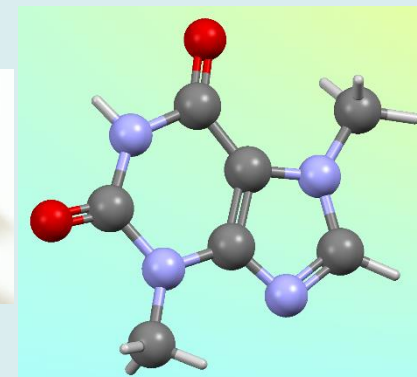
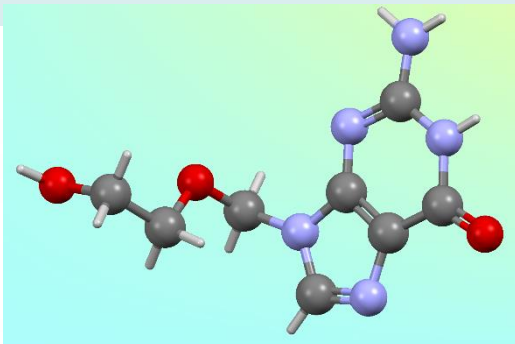
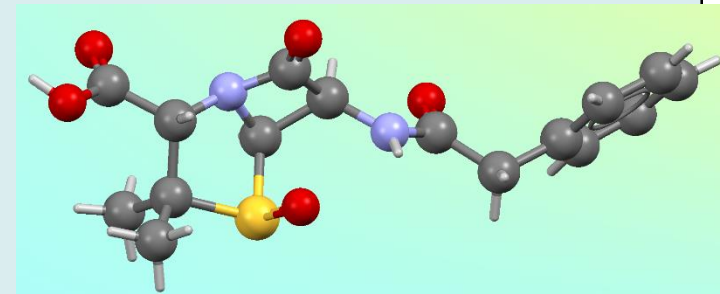
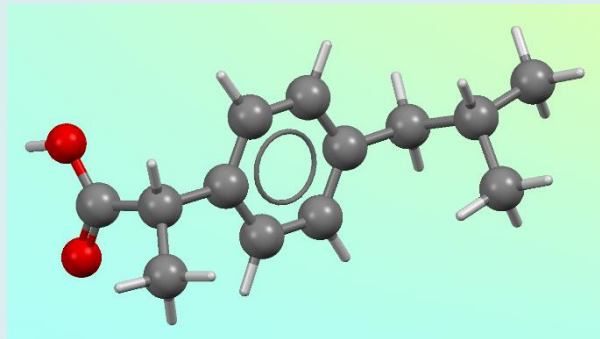
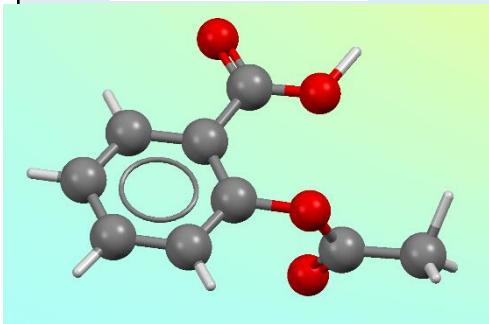


## **Why this class on structural analysis of single crystal**

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- **One of the most common and more accurate methods for determining the three-dimensional structure of crystalline compounds**
- **There is virtually no scientific publication of a new compound, without its crystalline structure.**
- **Much information about molecular and non-molecular crystals.**
- **Most of the students come in contact with this method during their degree, or postgraduate courses.**

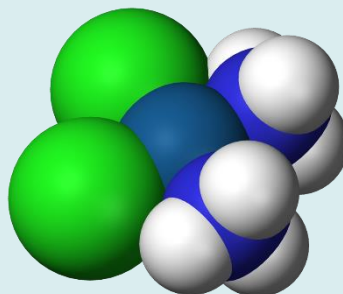
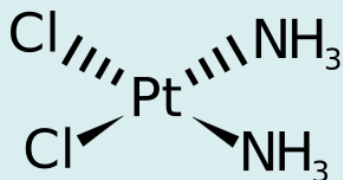
# Examples of organic compounds



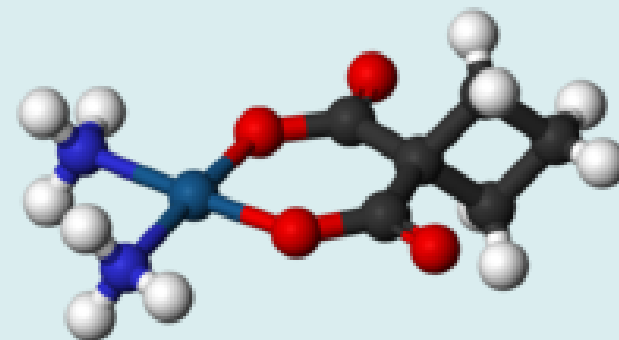
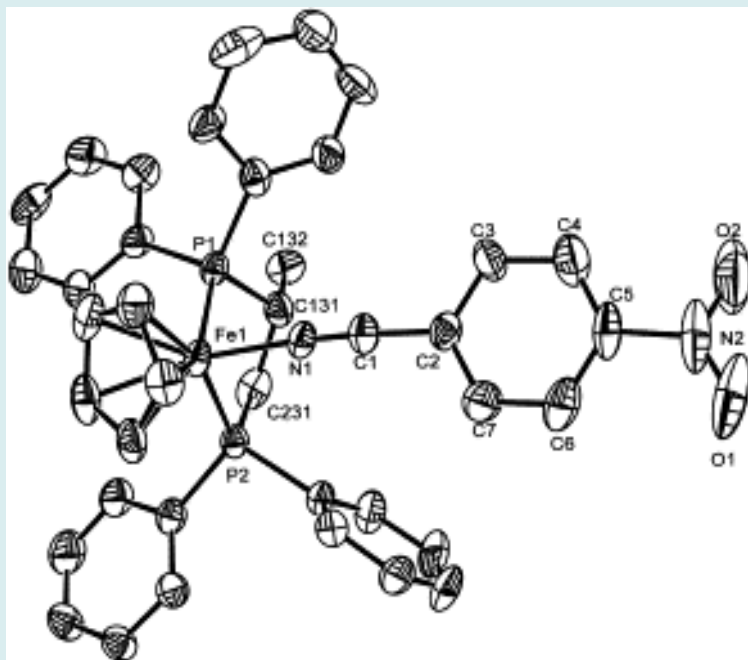
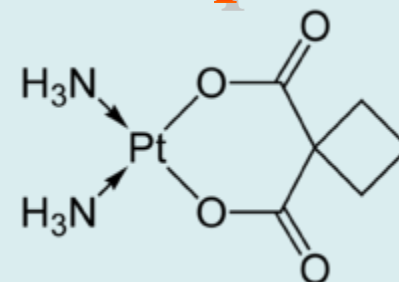


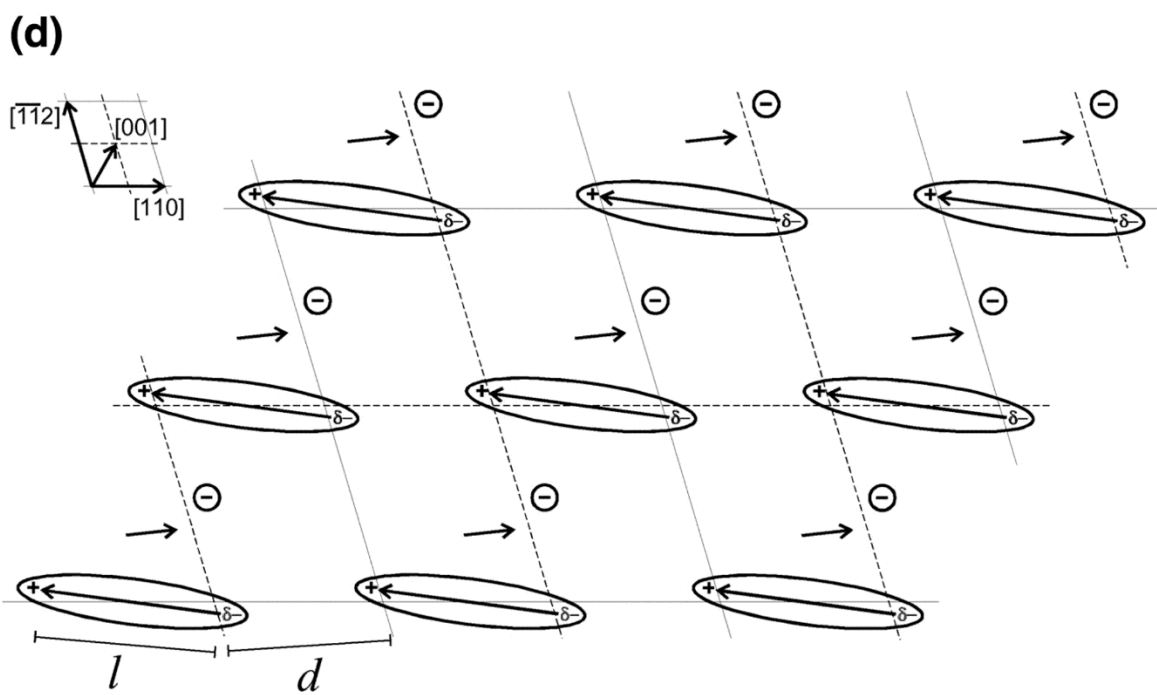
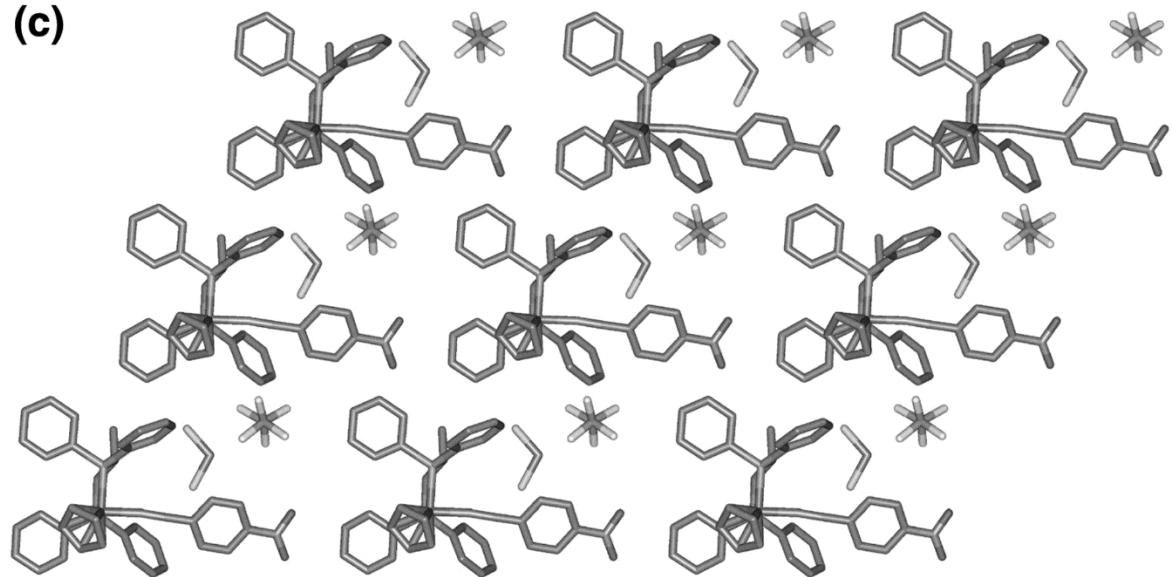
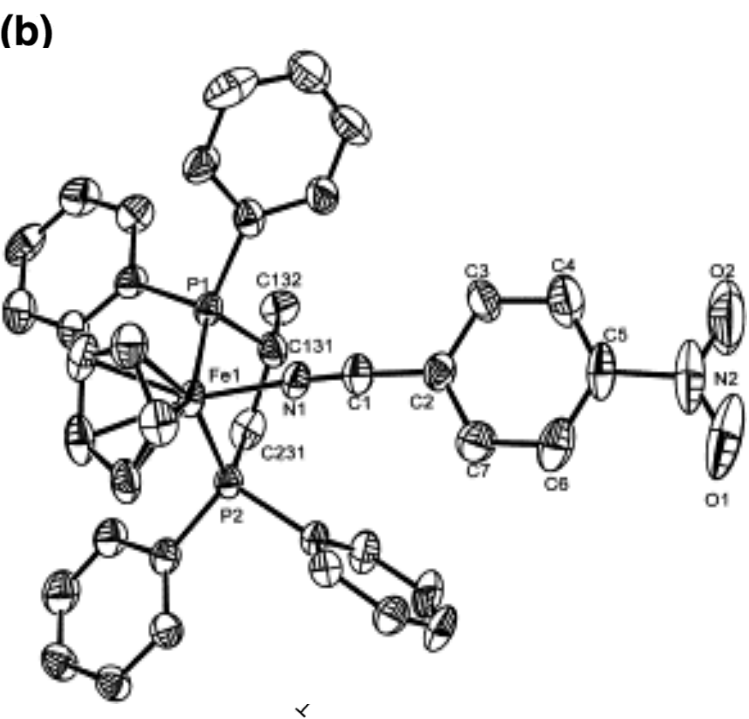
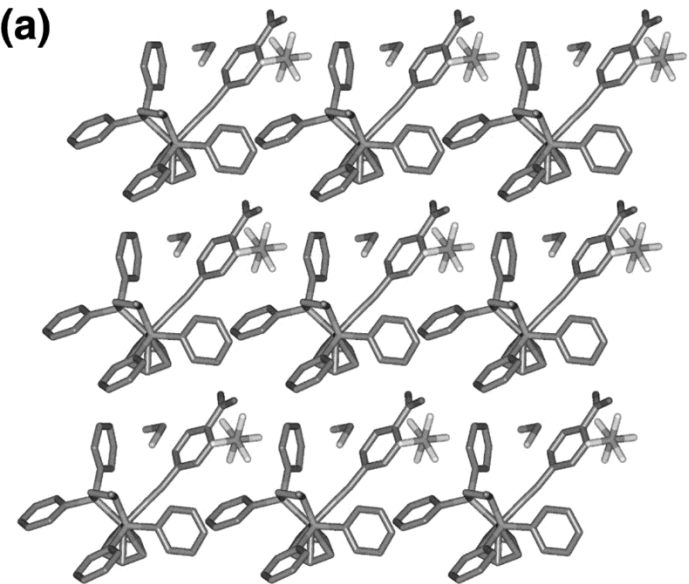
# Examples of inorganic compounds

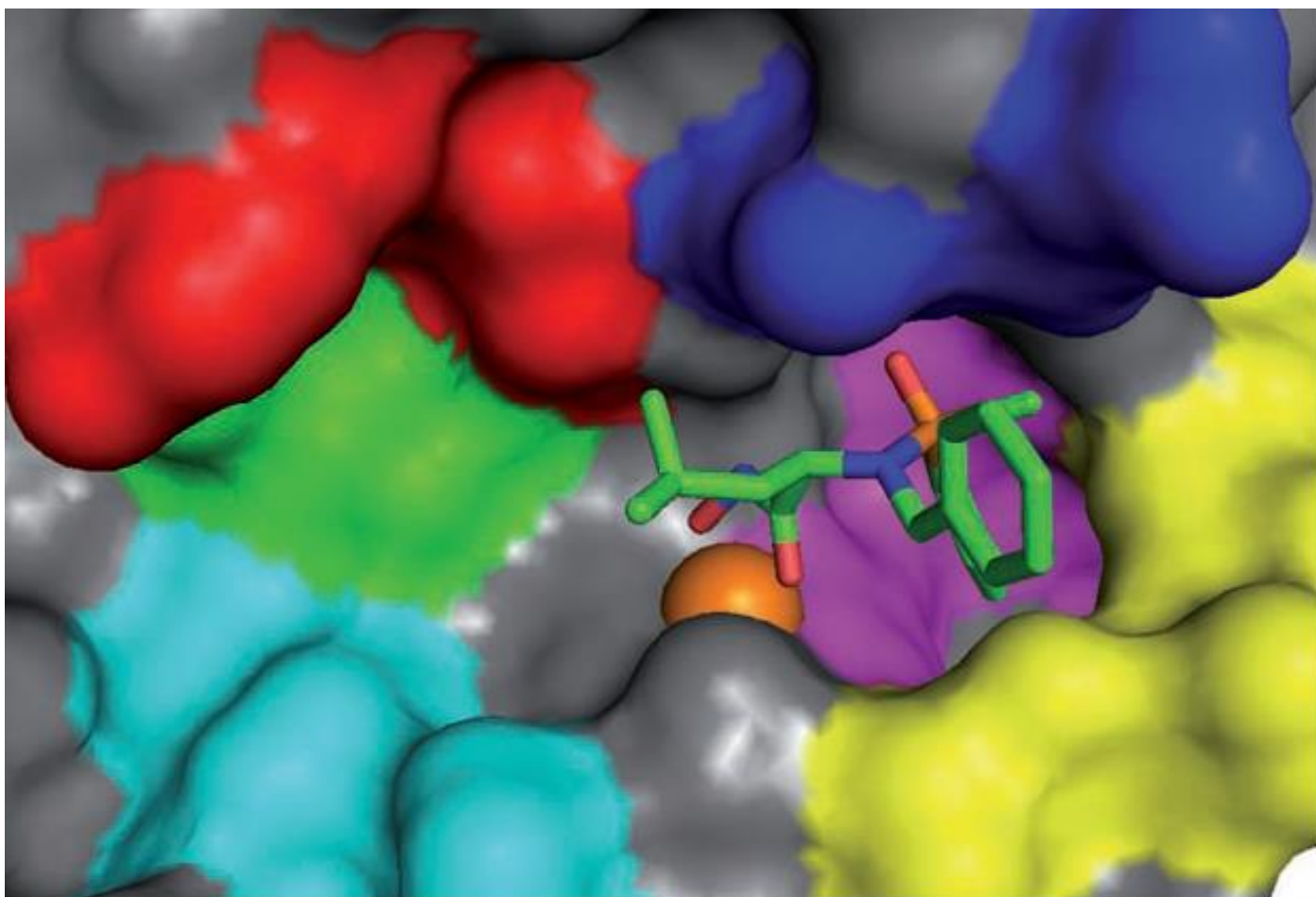
## cisplatin



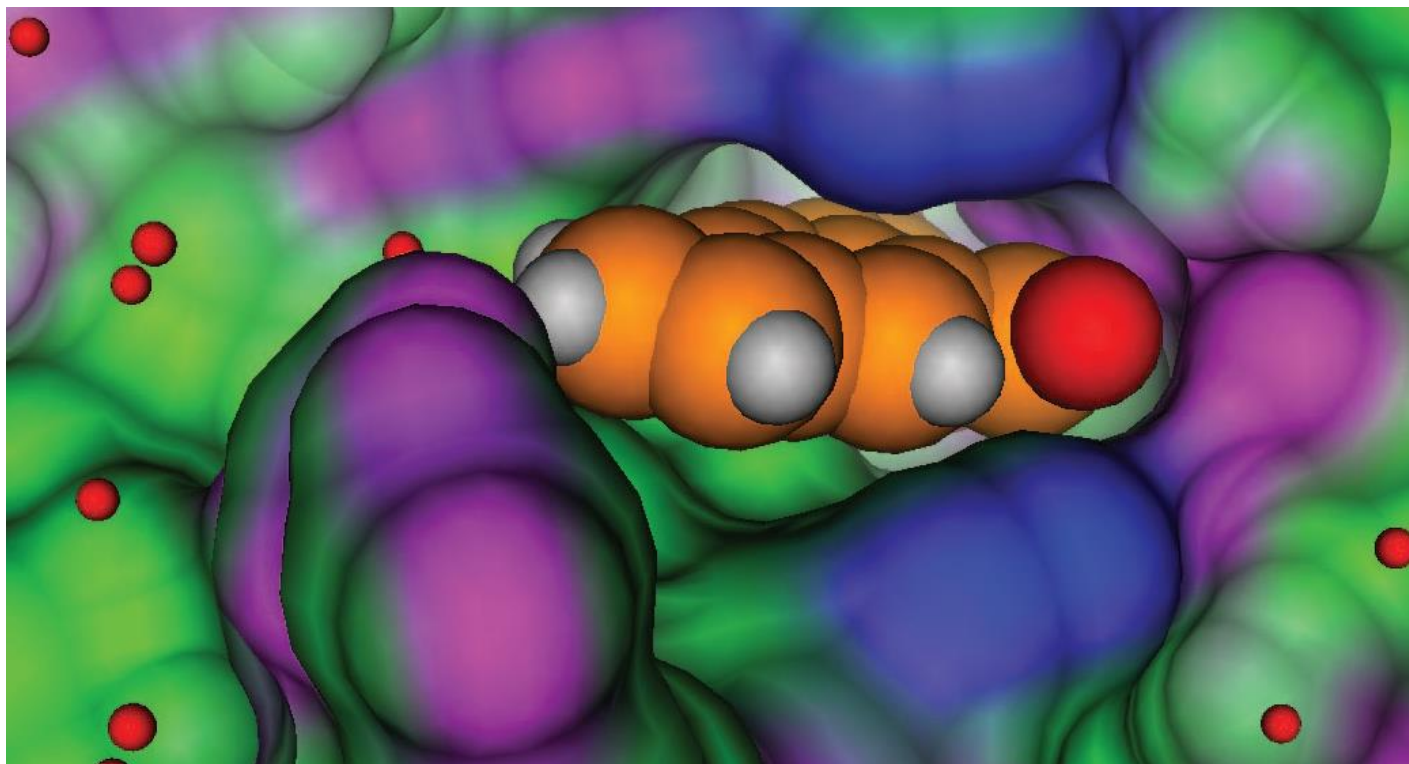
## carboplatin







**In the design of a new molecule in chemistry the crystalline structure is very important because one can visualize the way it binds to the receptor.**



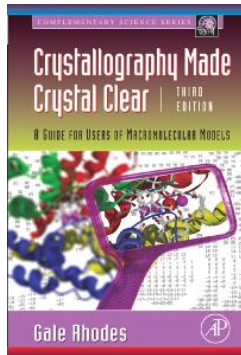
**Using this information the chemist can synthesize analogous compounds, making changes to increase the interaction with the receptor molecule and / or alter the properties of the drug without decreasing the affinity of the parent compound to the target compound.**

## **Why this class on structural analysis of single crystal**

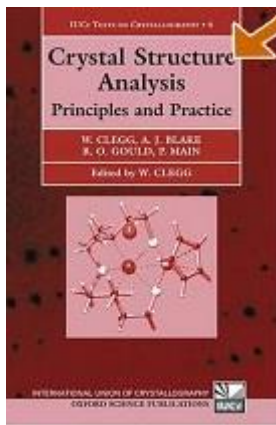
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- **One of the most common and more accurate methods for determining the three-dimensional structure of crystalline compounds**
- **There is virtually no scientific publication of a new compound, without its crystalline structure.**
- **Much information about molecular and non-molecular crystals.**
- **Most of the students come in contact with this method during their degree, or postgraduate courses.**
- **Knowledge of the crystal structure of a compound is absolutely necessary for a deeper understanding of their physical properties.**

# BIBLIOGRAFIA



**Crystallography Made Crystal Clear**  
**A Guide for Users of Macromolecular Models**  
Gale Rhodes  
Elsevier



***Crystal Structure Analysis: Principles and Practice***  
**William Clegg, A. J. Blake, R. O. Gould and P. Main**  
Oxford University Press

**Website**

<http://www.iucr.org/>

## **Objectives that must learn in this lesson on structural analysis of single crystal**

---

- **Theoretical basis of this method**
- **How to make the structural determination?**
- **Possibilities: What can be learned in a single crystal structure?**
- **Limitations: How precise and accurate is this method? What can be determined?**
- **Critical view of the results in a structural determination?**
- **How can analyze the result and the quality of a structural determination?**
- **How can detect possible errors in structural analysis?**

# What is X-ray diffraction useful for?

- Gives information about the molecule: relative position of the atoms, bond lengths and angles, torsion angles, conformation and flexibility of the molecule.
- Allows the understanding of the non-bonded interactions and therefore the 3D structure – supramolecular arrangement

**Is a non-destructive method**

Is an **essential** tool for the design of new compounds.

**STRUCTURE** → **FUNCTION**



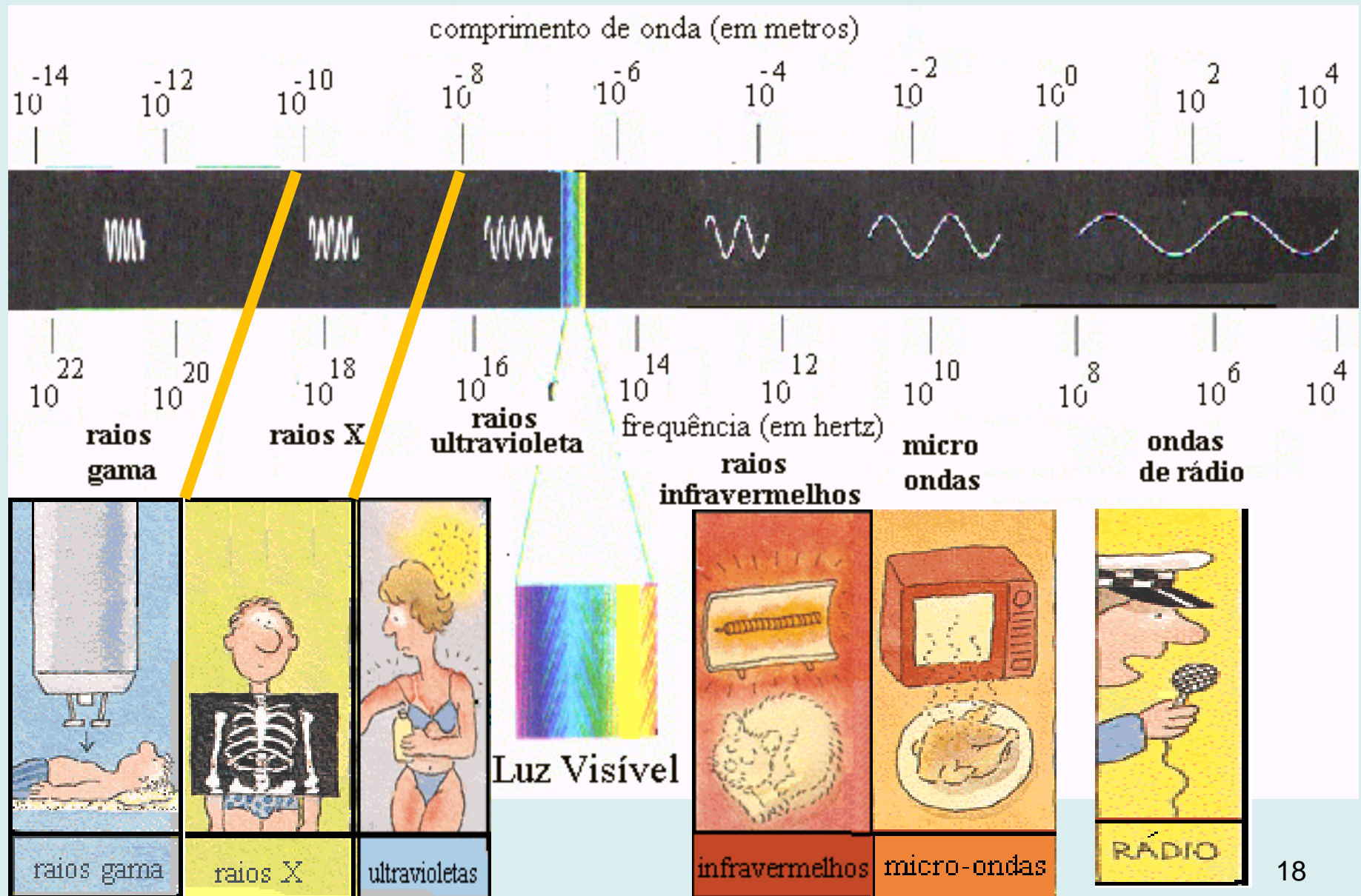
# X-ray diffraction analysis

- **Crystals!** How to obtain them? **Crystallization techniques**
- What are **X-rays**? How are they generated? **X-ray tubes and synchrotron radiation**
- **Diffraction** **X-rays interact with electrons (van Laue equations; Bragg's law)**
- **Real /reciprocal spaces**  
(electronic density, atomic positions / structure factors, Miller indices)
- **Real space versus reciprocal space** **FOURIER Transform**
- **Phase: Model >> fitting >> refinement**  
(model - experimental electronic density)

• **Structural Information**

**Design**

# Electromagnetic spectrum



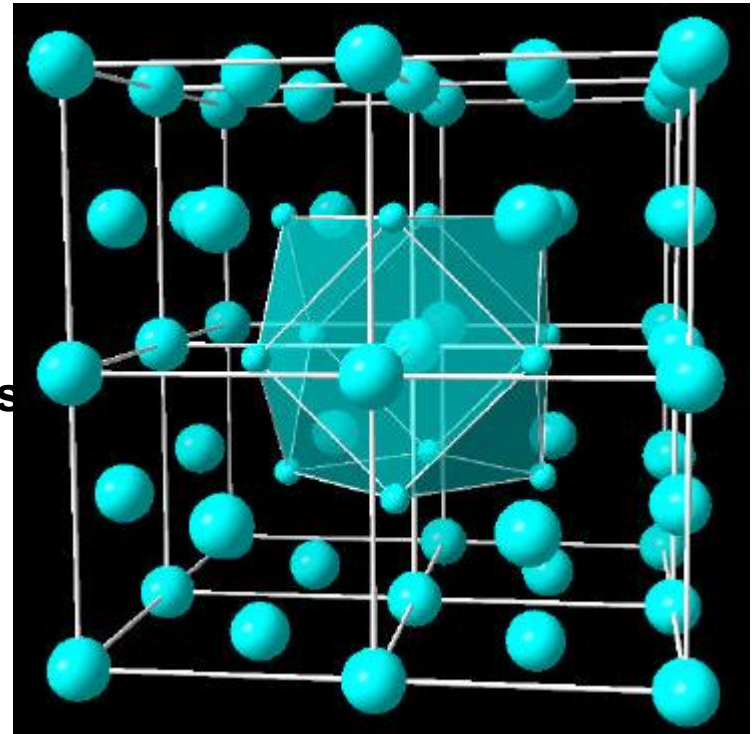
# Definition of single crystal structure made by X-ray diffraction

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Determination of the exact three-dimensional arrangement of blocks (atoms, ions, molecules) using a compound of X-ray radiation.  
Analysis of a single crystal structure by X-ray diffraction

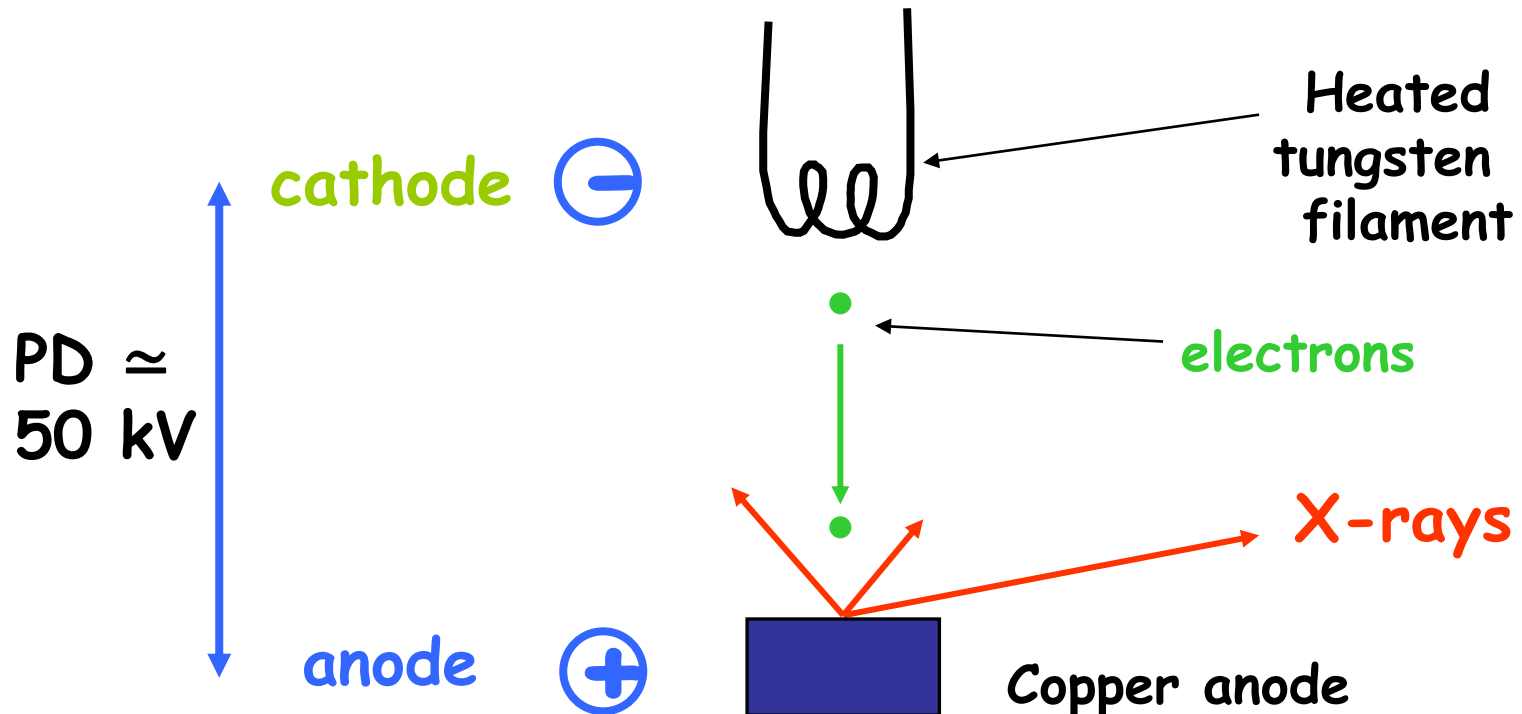


**Wilhelm Conrad  
Röntgen  
1845-1923  
Physics teacher  
Discovered the X-rays  
on 08/11/1895  
1st Physics Nobel  
Prize in 1901**



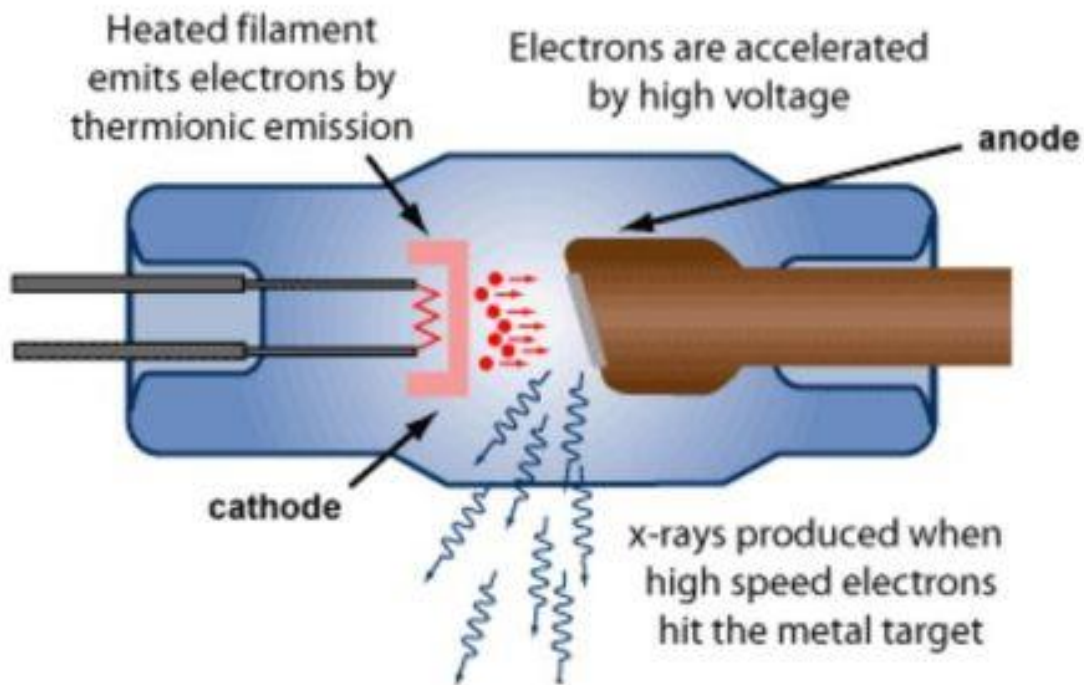
# X-Rays

- Radiation obtained when electrons produced by termoionic emission from a W filament are accelerated by potential difference towards the anode.
- High energy electrons ( $\approx 50$  keV) hit the metallic target (e.g. Cu ou Mo)
- X-rays are generated by the interaction between the electrons and the target



# HOW ARE X-RAYS PRODUCED ?

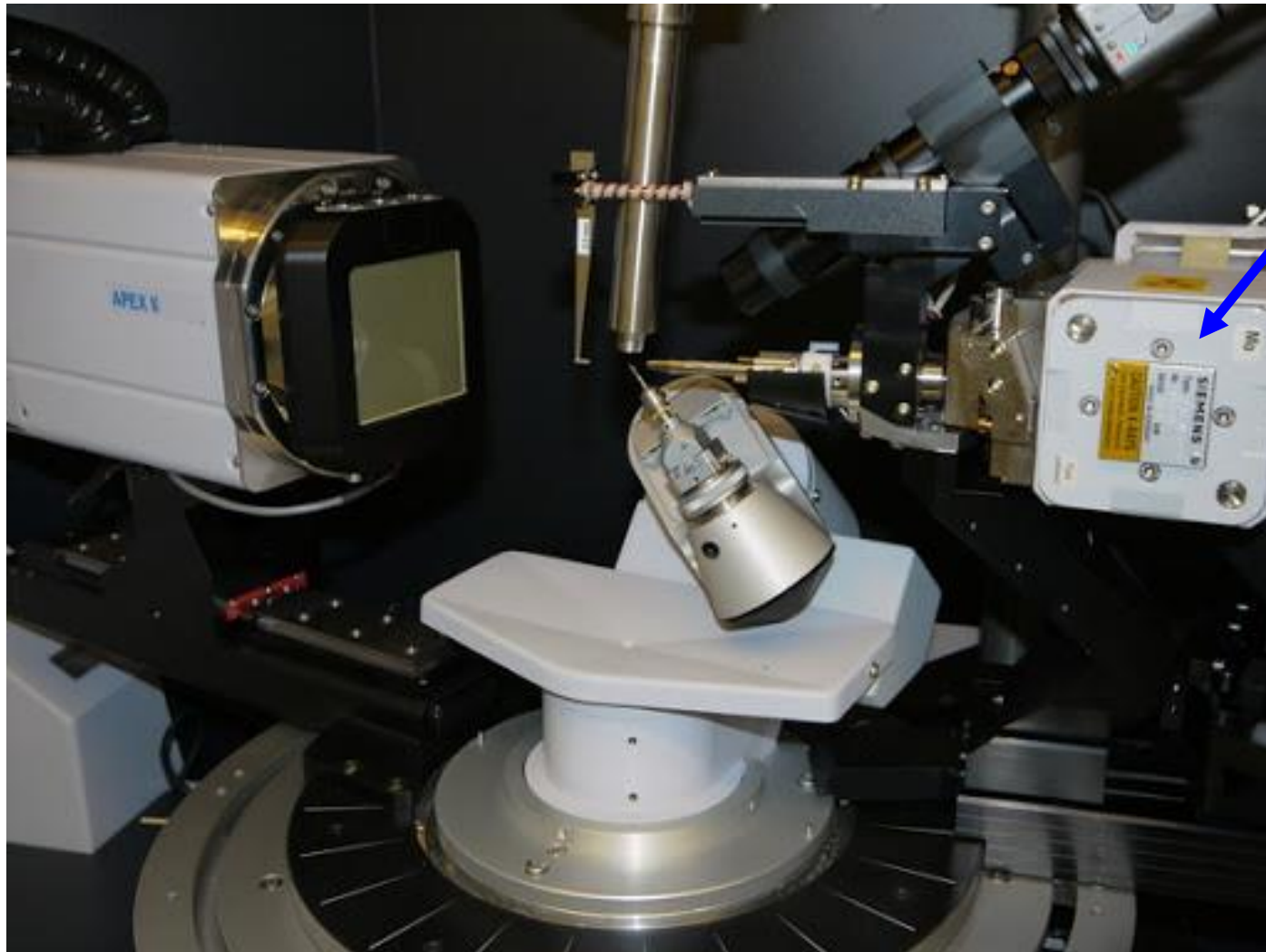
## Typical X-ray tube operation



**X- RAY  
TUBE**



**CAUTION  
HIGH INTENSITY  
X-RAY BEAM**



X-ray tube

# How a Synchrotron Works

## 4. Storage Ring

The booster ring feeds electrons into the storage ring, a many-sided donut-shaped tube. The tube is maintained under vacuum, as free as possible of air or other stray atoms that could deflect the electron beam. Computer-controlled magnets keep the beam absolutely true.

Synchrotron light is produced when the bending magnets deflect the electron beam; each set of bending magnets is connected to an experimental station or beamline. Machines filter, intensify, or otherwise manipulate the light at each beamline to get the right characteristics for experiments.

## 5. Focusing the Beam

Keeping the electron beam absolutely true is vital when the material you're studying is measured in billionths of a metre. This precise control is accomplished with computer-controlled quadrupole (four pole) and sextupole (six pole) magnets. Small adjustments with these magnets act to focus the electron beam.

## 3. An Energy Boost

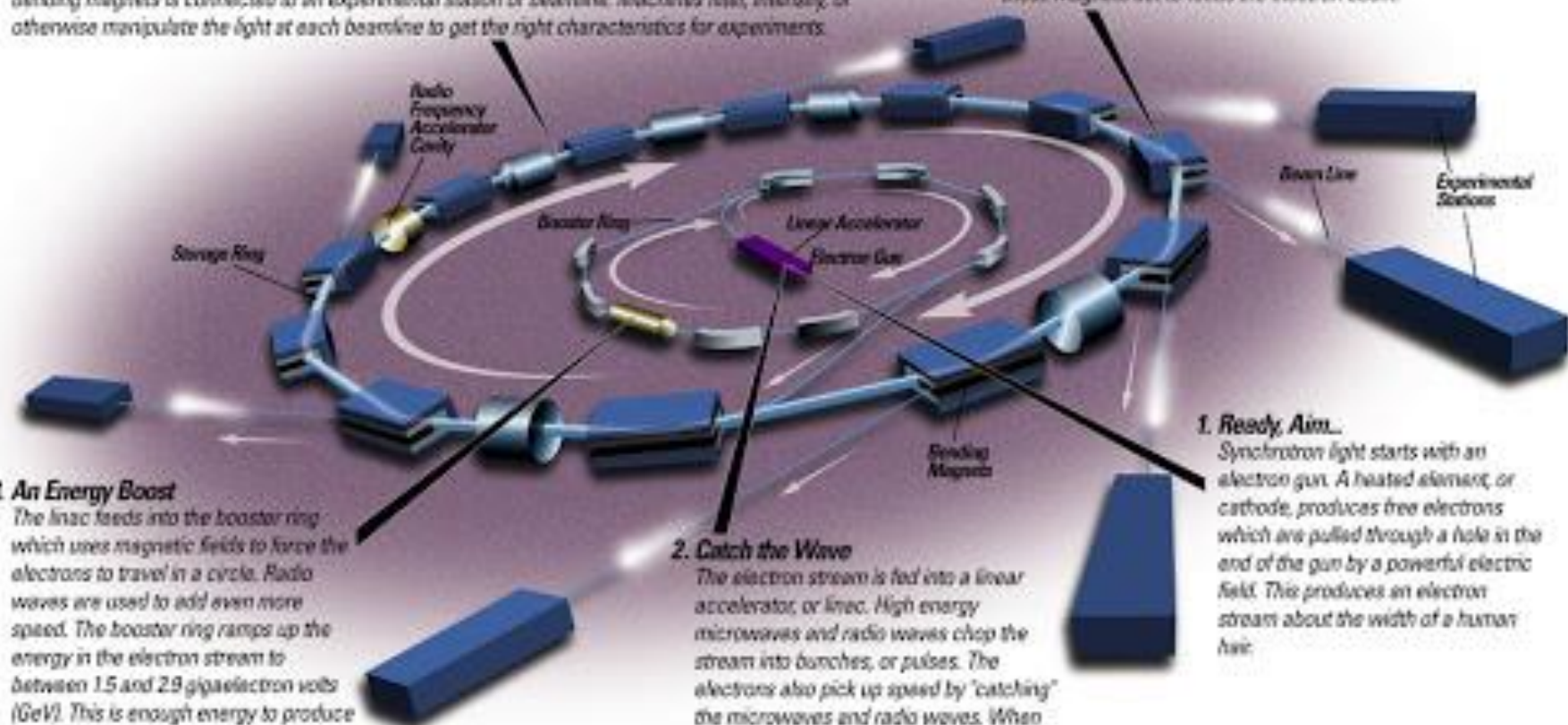
The linac feeds into the booster ring which uses magnetic fields to force the electrons to travel in a circle. Radio waves are used to add even more speed. The booster ring ramps up the energy in the electron stream to between 1.5 and 2.9 gigaelectron volts (GeV). This is enough energy to produce synchrotron light in the infrared to hard X-ray range.

## 2. Catch the Wave

The electron stream is fed into a linear accelerator, or linac. High energy microwaves and radio waves chop the stream into bunches, or pulses. The electrons also pick up speed by "catching" the microwaves and radio waves. When they exit the linac, the electrons are travelling at 99.99986 per cent of the speed of light and carry about 300 million electron

## 1. Ready, Aim...

Synchrotron light starts with an electron gun. A heated element, or cathode, produces free electrons which are pulled through a hole in the end of the gun by a powerful electric field. This produces an electron stream about the width of a human hair.



Source: University of Saskatchewan / Paradigm Media Group Inc.

# A SYNCHROTRON X-RAY SOURCE @ GRENOBLE - ESRF





# Why use the X-rays?

---

You can not view objects that are not separated by at least half the wavelength of the radiation used (resolution).

$$\lambda/2$$

In a molecule the atoms are separated by distances on the order of  $1 \text{ \AA} = 0.1 \text{ nm} = 1 \times 10^{-10} \text{ m}$ .

.

# Why do you use the X-rays?

You can not view objects that are not separated by at least half the wavelength of the radiation used (resolution).

$$\lambda/2$$

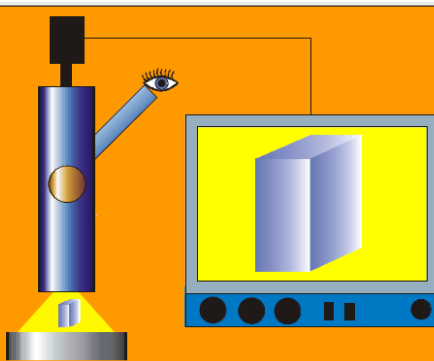
In a molecule the atoms are separated by distances on the order of  $1 \text{ \AA} = 0.1 \text{ nm} = 1 \times 10^{-10} \text{ m}$ .

$$1 \text{ \AA} = 10^{-8} \text{ cm}$$

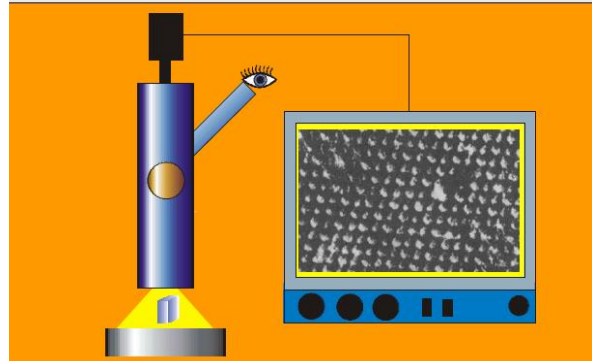
Visible light  $\lambda = 4 \text{ a } 8 \times 10^{-5} \text{ cm}$

X-ray  $\lambda = 10^{-8} \text{ cm}$

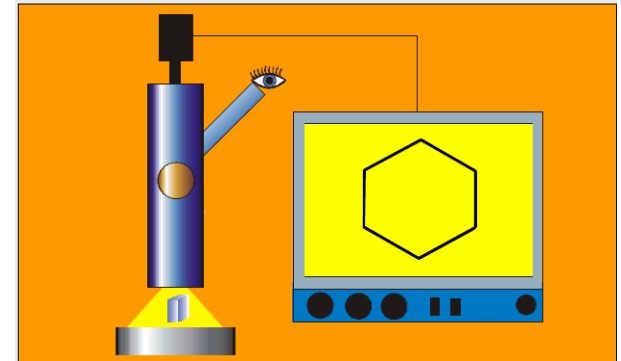
This is the range of right wavelength?



Light microscope



Electron microscope



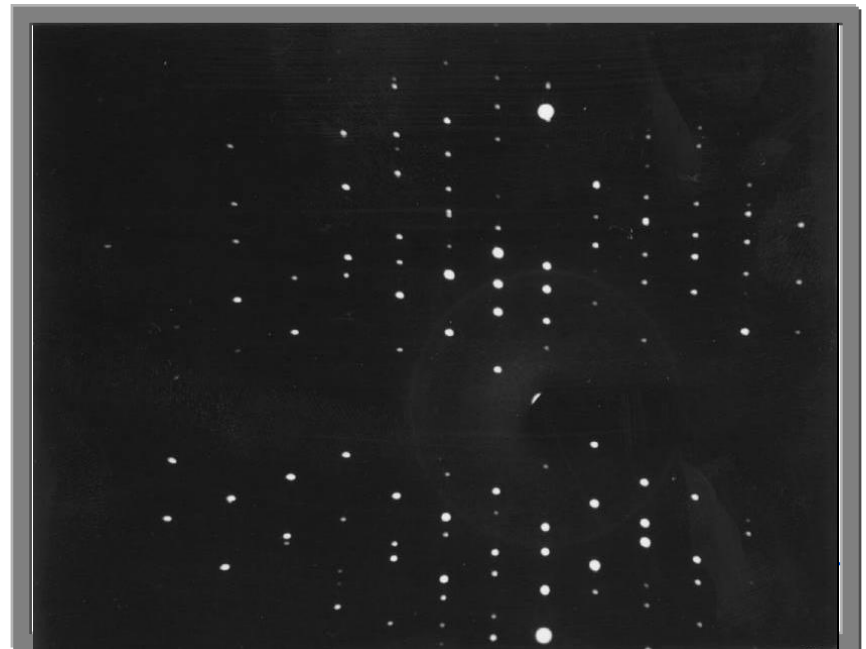
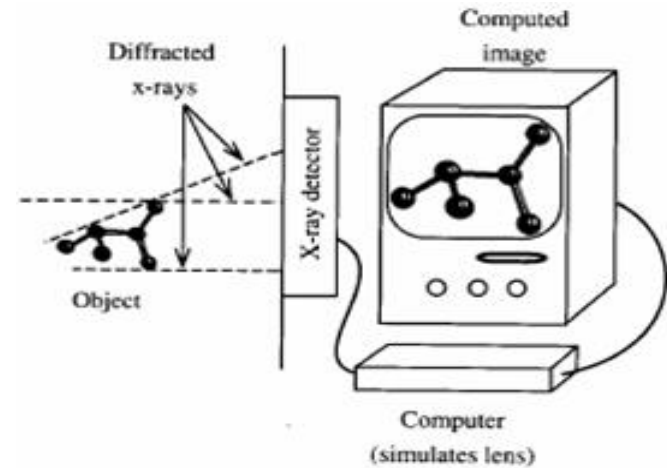
X-ray microscope

# However . . .

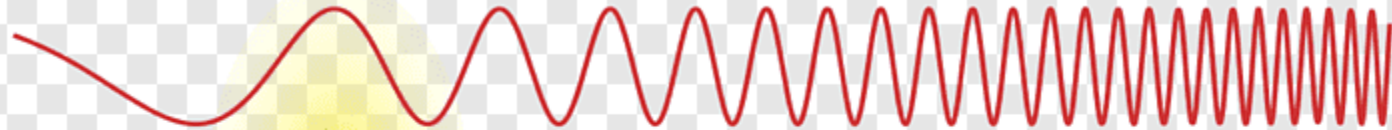
► Unlike to what happens in microscope, there is no way to focus X-rays diffracted.

► Alternatively collect the diffraction pattern (spots) or a list of intensities of the diffracted reflections.

**Determination of the crystal structure**



Penetrates Earth's Atmosphere?



Radiation Type  
Wavelength (m)

**Radio**  $10^3$  **Microwave**  $10^{-2}$  **Infrared**  $10^{-5}$  **Visible**  $0.5 \times 10^{-6}$  **Ultraviolet**  $10^{-8}$  **X-ray**  $10^{-10}$  **Gamma ray**  $10^{-12}$

Approximate Scale  
of Wavelength



Frequency (Hz)

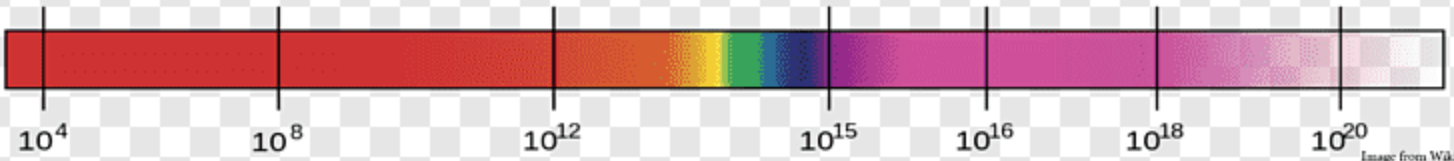


Image from Wikipedia

**IMPOSSIBLE TO SEE THE MOLECULES USING A MICROSCOPE - NO LENS CAN BE USED**

# Discover of X-ray diffraction by a crystal

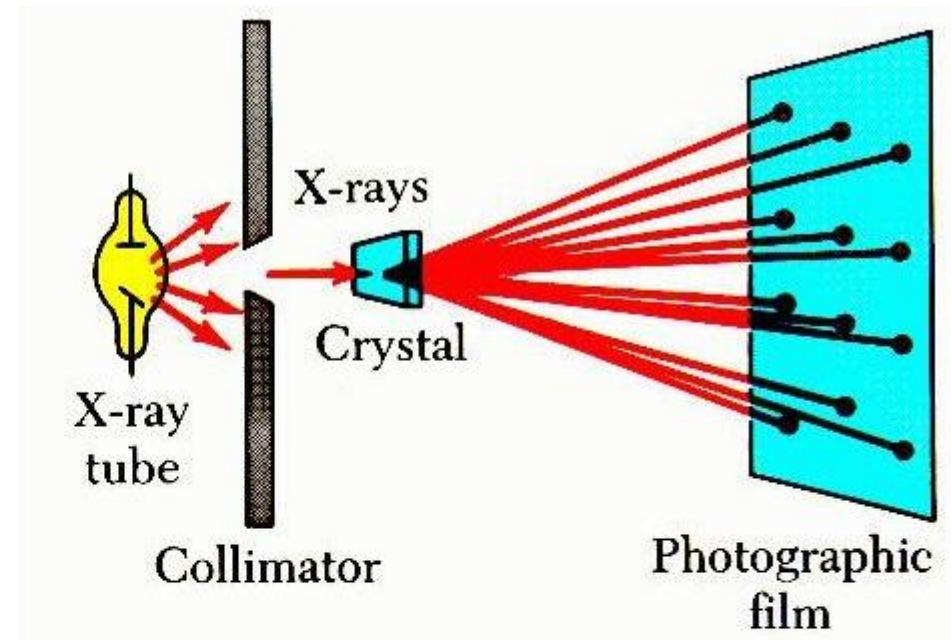
Max Felix Theodor von Laue

1879-1960

Professor for physics



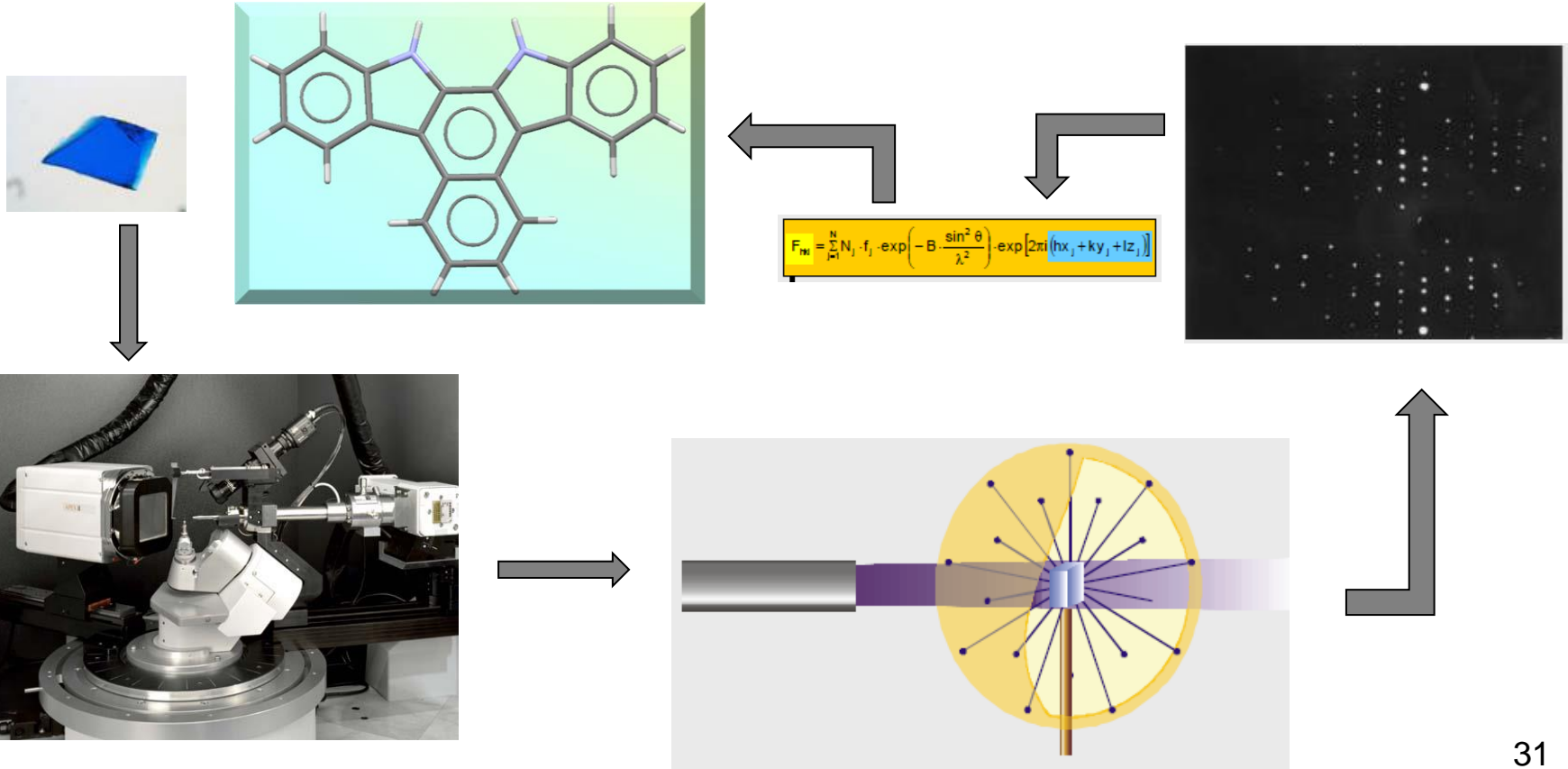
Von Laue discovered X-ray interference at crystal lattices and proved the wave nature of X-rays in 1912 together with Walther Friedrich and Paul Knipping. For this he became a Nobel prize winner in physics in 1914.



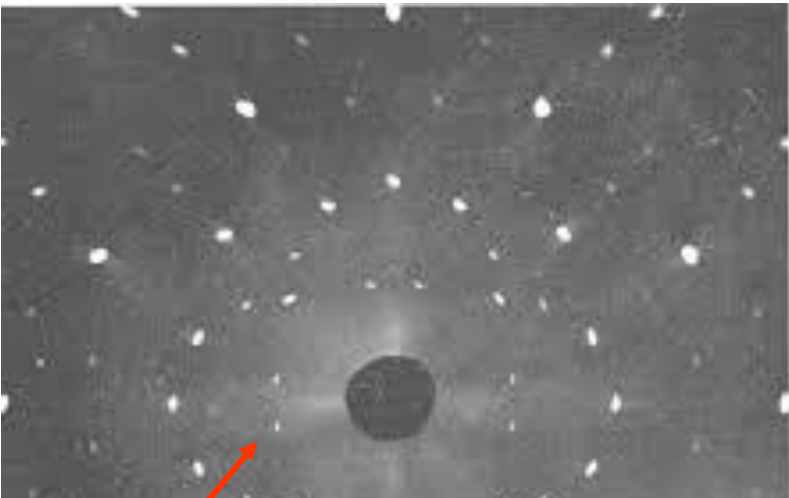
# What is X-Ray Crystallography?

It's a process of:

- Measure the diffraction produced by a X - ray beam passing through a single crystal.
- Calculate the electron density corresponding to each reflected X - ray.
- Determine the molecular model that best fits the experimental data.



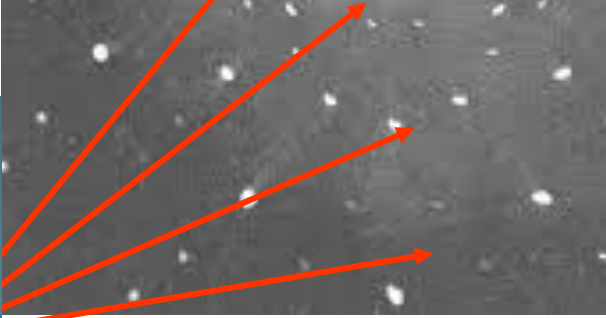
**Diffraction pattern**  
Reciprocal space



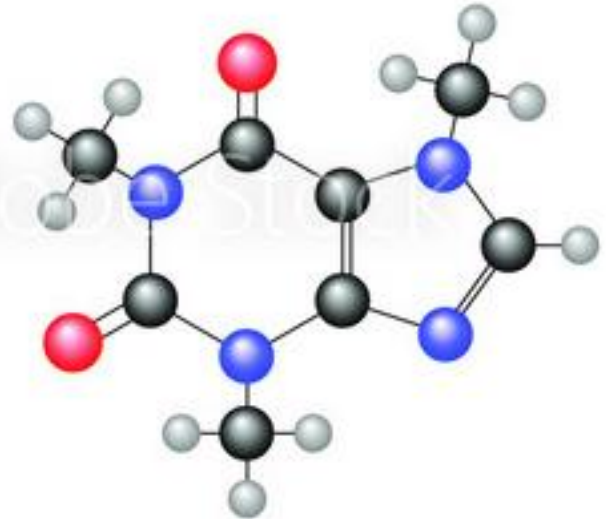
**Fourier Transform**



**Crystal**  
Real space



**Diffracted beam**



**Structure**  
Real space

X- Rays

# BASIC CONCEPTS

**CRYSTALS** - CRYSTALLINE SYMMETRY

SYMMETRY OPERATION

UNIT CELL

CRYSTALLINE CLASSE

SPACE GROUP

ASSYMETRIC UNIT

**X-RAY DIFFRACTION** - BRAGG'S LAW  
RECIPROCAL SPACE  
Fourier Transforms

**INTENSITY of REFLECTION** - Electronic density ( $\rho(xyz)$ )  
STRUCTURE FACTOR

What is  $F(hkl)$  and how is it obtained??

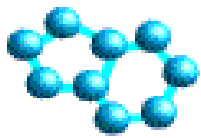


# Crystals

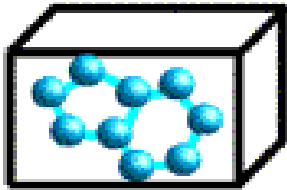
**What is a crystal?**

It is a homogeneous solid that exhibits a high degree of internal order

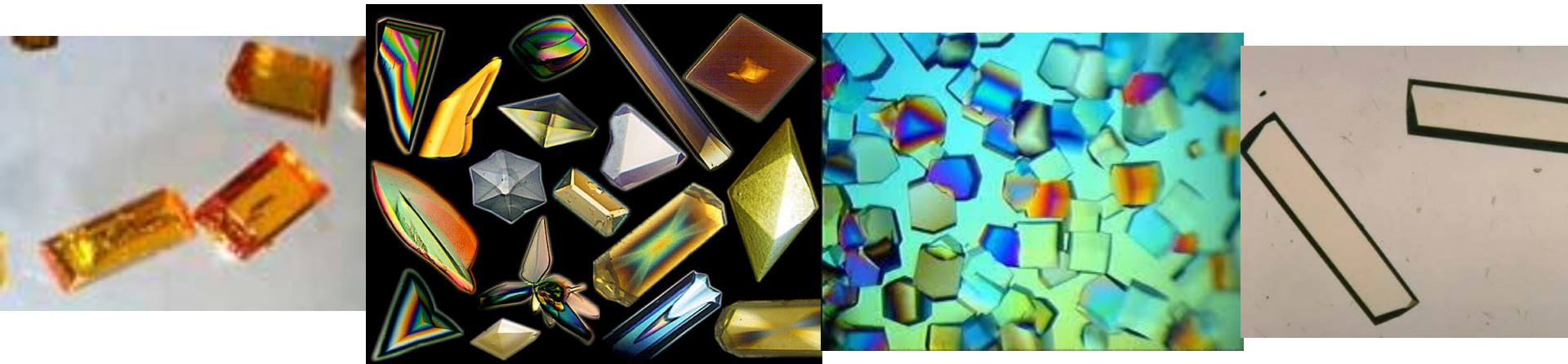
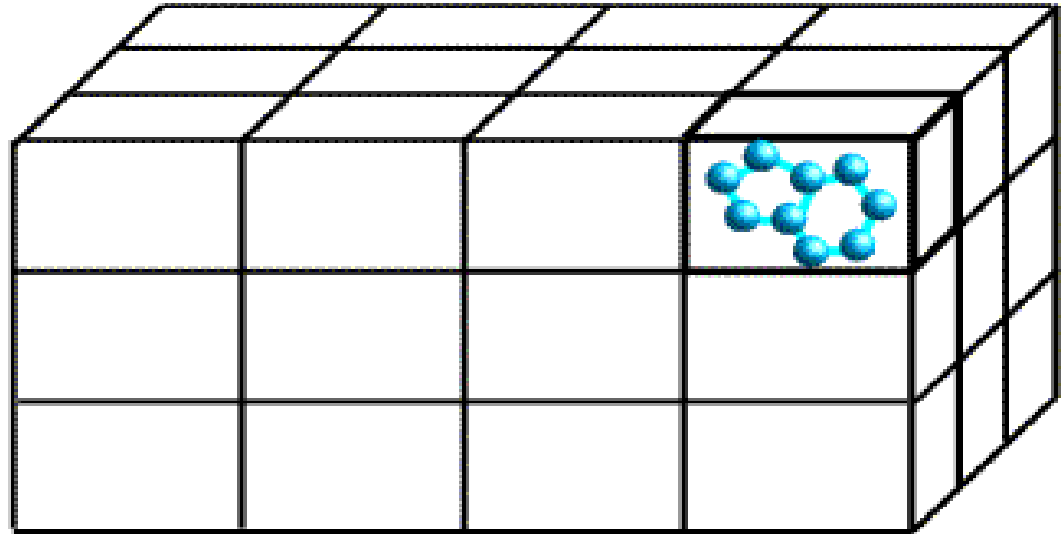
molecule



Repetitive motif



crystal

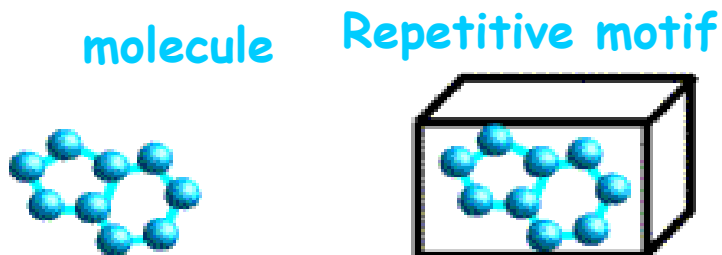




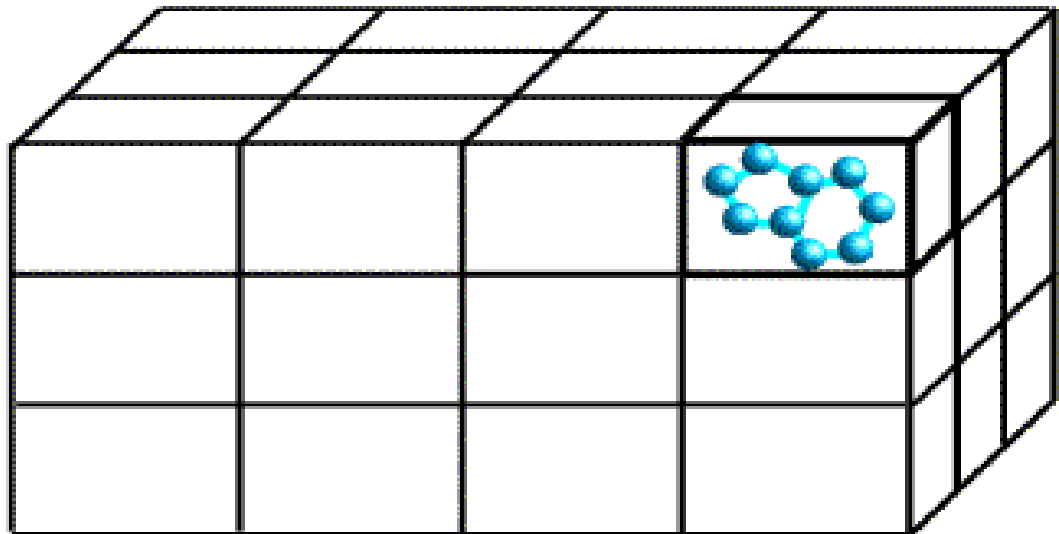
# Crystals

## What is a crystal?

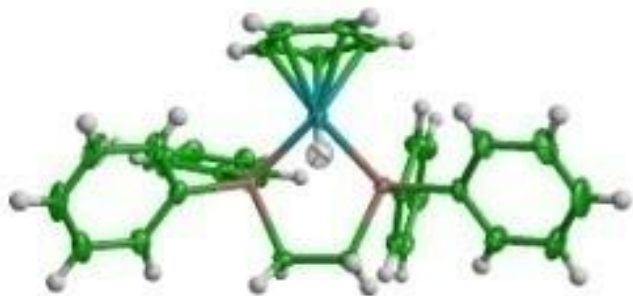
It is a homogeneous solid that exhibits a high degree of internal order



crystal



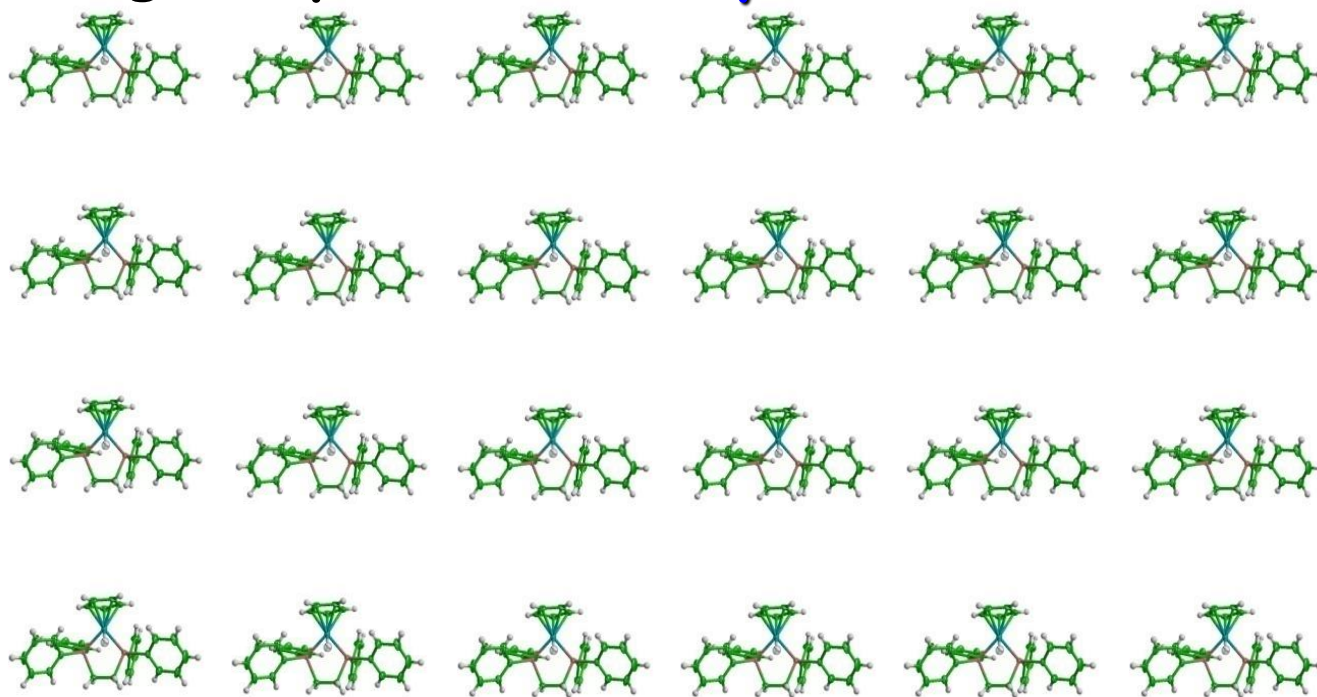
- ❖ In the crystalline state, the molecules adopt one or more orientations producing a repetitive three-dimensional structure of molecules
- ❖ The unit cell is the smallest possible volume that, when repeated, represents the entire crystal.
- ❖ The unit cell therefore contains multiple copies of the same molecule whose positions are governed by rules of symmetry.



One molecule is not enough to obtain a X-ray diffraction pattern

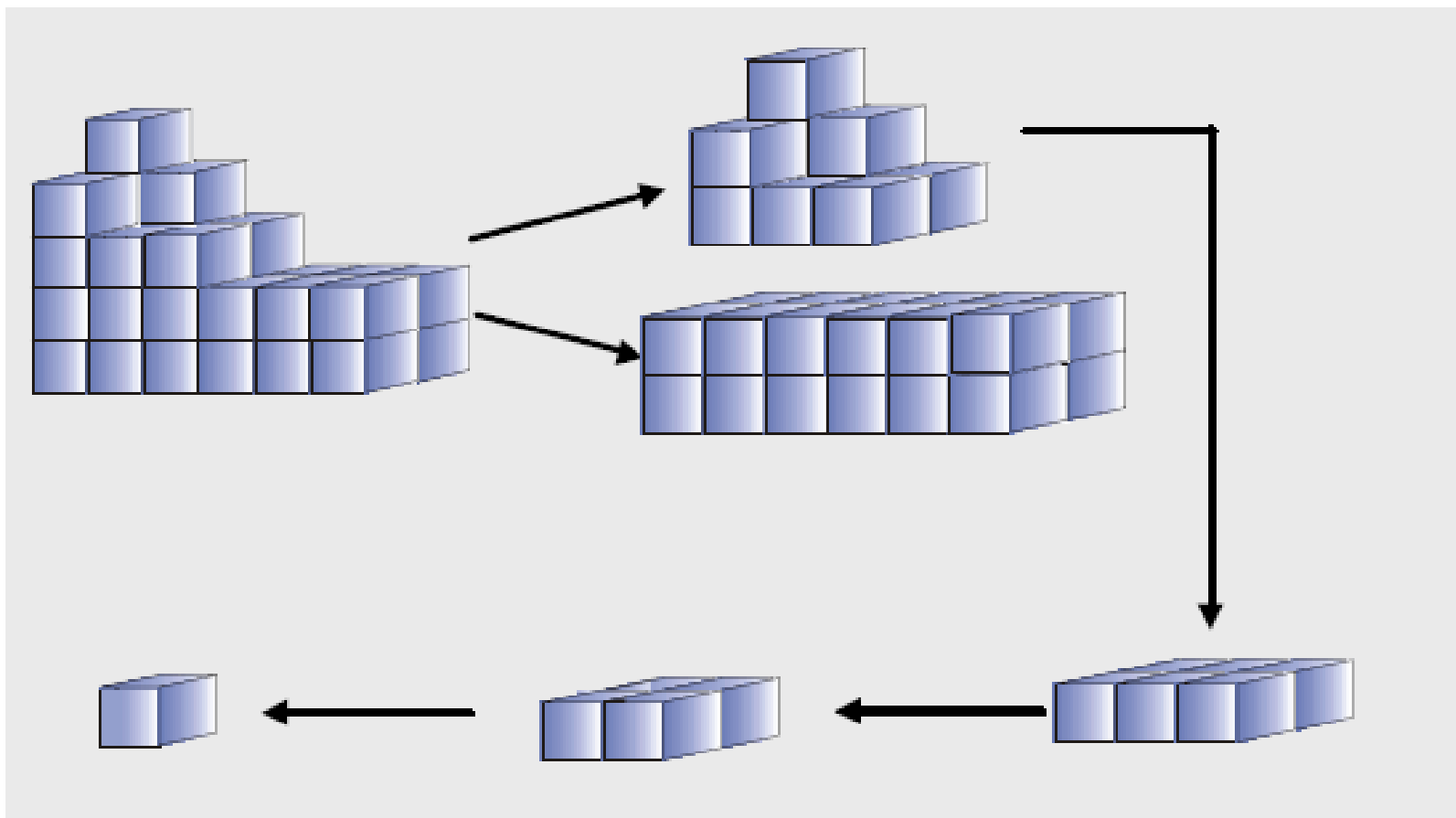
The X-rays are diffracted by the electronic density

The solution for this problem is to use many molecules arranged in a **3D** regular pattern: **A crystal**



The crystal acts as an amplifier

# THE UNIT CELL CONCEPT



Numbers of unit cells in a crystal of  $1 \text{ mm}^3$  ( $10^6 \text{ \AA}^3$ ):

NaCl	$10^{19}$ unit cells
D-xylose-isomerase	$10^{15}$ unit cells

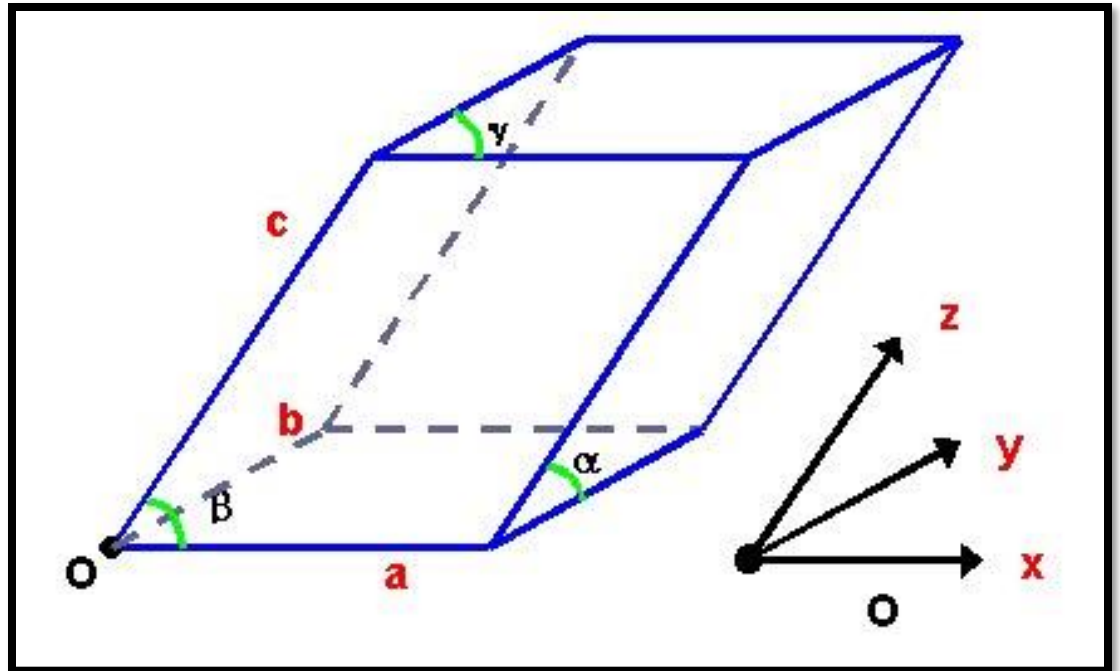
# DEFINITIONS

## UNIT CELL

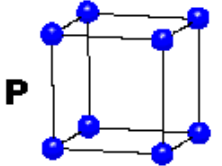
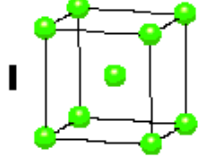
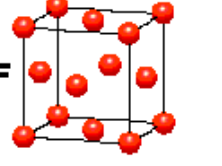
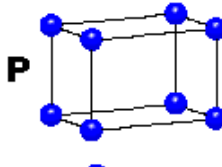
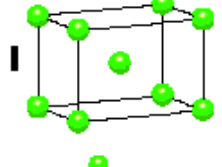
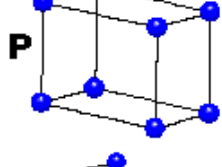
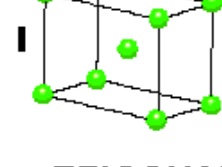
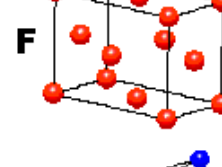
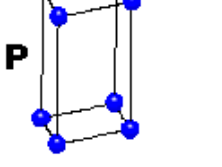
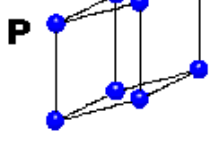
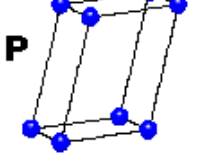
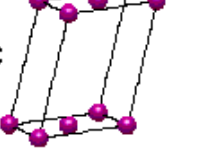
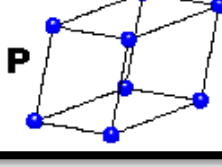
“The smallest repeat unit of a crystal structure, in 3D, which shows the full symmetry of the structure”

Unit cell is defined by:

- 3 axis -  $a$ ,  $b$ ,  $c$
- 3 angles -  $\alpha$ ,  $\beta$ ,  $\gamma$



# BRAVAIS LATTICES AND SPACE GROUPS

<b>CUBIC</b> $a = b = c$ $\alpha = \beta = \gamma = 90^\circ$			
<b>TETRAGONAL</b> $a = b \neq c$ $\alpha = \beta = \gamma = 90^\circ$			
<b>ORTHORHOMBIC</b> $a \neq b \neq c$ $\alpha = \beta = \gamma = 90^\circ$			
<b>HEXAGONAL</b> $a = b \neq c$ $\alpha = \beta = 90^\circ$ $\gamma = 120^\circ$		<b>TRIGONAL</b> $a = b = c$ $\alpha = \beta = \gamma \neq 90^\circ$	
<b>MONOCLINIC</b> $a \neq b \neq c$ $\alpha = \gamma = 90^\circ$ $\beta \neq 120^\circ$			
<b>TRICLINIC</b> $a \neq b \neq c$ $\alpha \neq \beta \neq \gamma \neq 90^\circ$			

4 Types of Unit Cell  
 P = Primitive  
 I = Body-Centred  
 F = Face-Centred  
 C = Side-Centred  
 +  
 7 Crystal Classes  
 → 14 Bravais Lattices

32 point groups, 14 Bravais lattices, each of the latter belonging to one of the 7 lattice systems

230 space

# Unit Cell, the Atomic Planes and the Lattice



Large number of identical molecules arranged in a regular



Repeated in all directions to give a highly ordered tri-dimensional structure

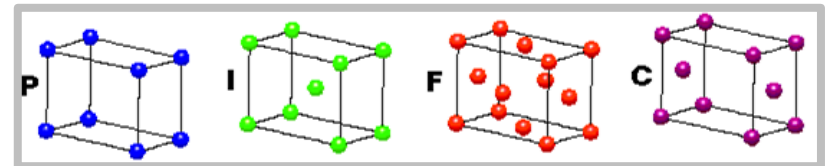
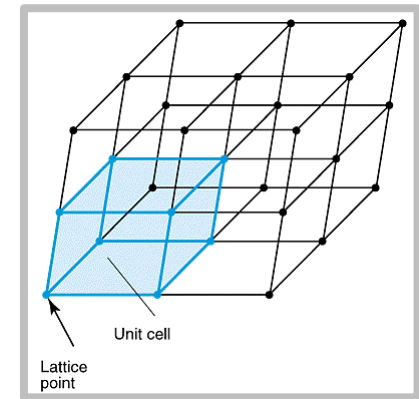
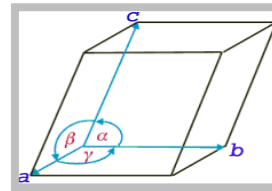
Way Symmetry in the Unit Cell

7 Lattice Systems

14 Bravais Lattices

32 Point Groups

230 Space Groups



Primitive unit cell

Centred unit cells

- Non-translational:      Translational:
- ✓ Most commons:
  - ✓ Rotation
  - ✓ Reflection
  - ✓ Inversion
  - ✓ Improper rotation
- ✓ Screw axes
  - ✓ Glide planes
- Triclinic system - No restrictions  
 Monoclinic system -  $\alpha = \gamma = 90^\circ$   
 Orthorhombic system -  $\alpha = \beta = \gamma = 90^\circ$

## Space groups: construction plan of crystals

The combination of all symmetry elements including the translation symmetry elements yields only 230 combinations.

These combinations are called "space groups".

The correct determination of the space group is absolutely necessary for the determination of the crystal structure.

Space groups	Symmetry elements
Centrosymmetric	Translation, rotational axis, mirror planes, center of inversion and combinations
Non-centrosymmetric	Translation, rotational axis, mirror planes and combinations
Chiral	Translation, rotational axis and combinations



## Characteristics and advantages of the unit cell concept

### Characteristics of the unit cell:

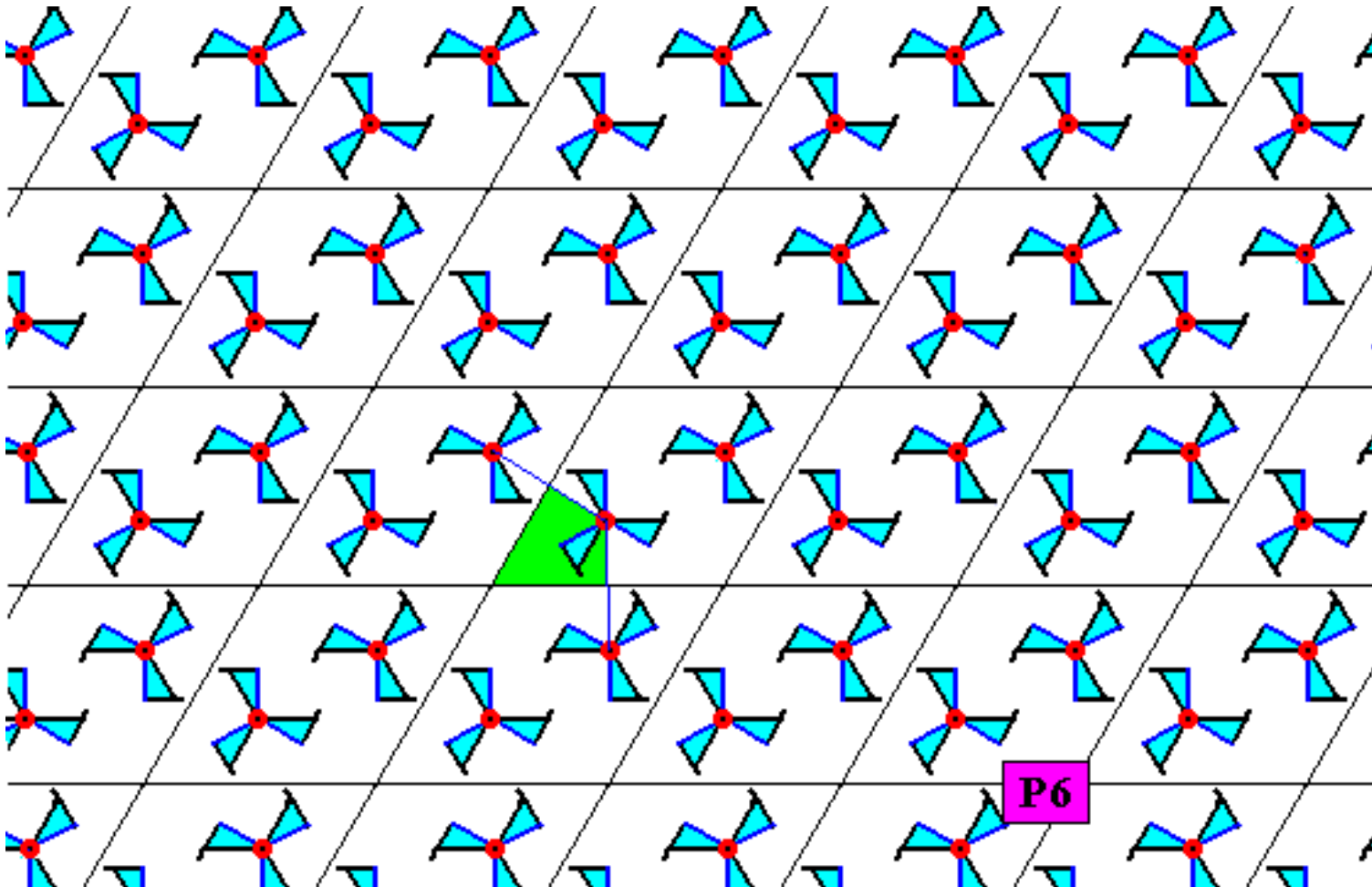
- Imaginary building block that helps to appreciate the internal periodicity of crystals (that contains atoms or molecules, not unit cells)
- is useful for an easier description of the periodicity in crystals

### Advantages of the unit cell concept:

- The crystal is divided into small identical units
- For the description of the whole structure only a few parameters are needed
- The problem of determining the structure is reduced to that of determining the structure of the content of only one unit cell; any other unit cell will be like the first.
- Only the positioning of the atoms in the unit cell must be determined.

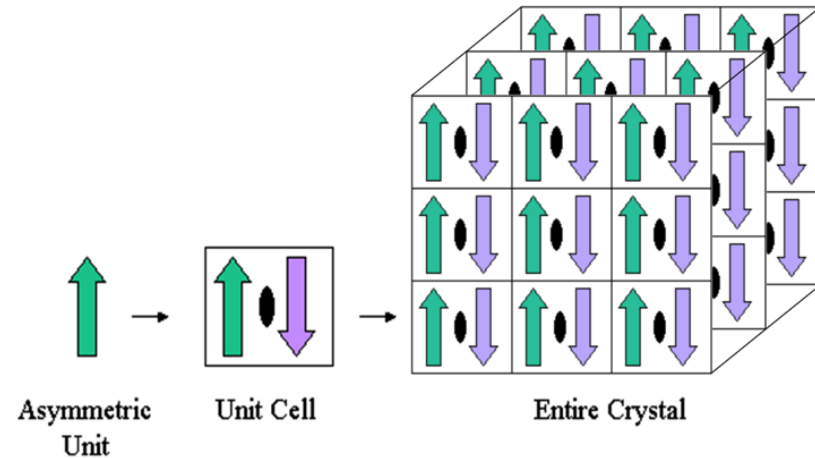
# Which atomic positions must be determined ?

The content of one unit cell or something less ?



# Asymmetric unit

- The asymmetric unit contains a number of atoms whose positions have to be determined in a crystal structure determination.
- These atoms together with the symmetry operations giving by the space group are sufficient to describe the content of the unit cell and therefore the whole crystal structure.



**In a crystal structure analysis only the positions of the atoms of the asymmetric unit have to be determined.**

# BASIC CONCEPTS

**CRYSTALS** - CRYSTALLINE SYMMETRY

SYMMETRY OPERATION

UNIT CELL

CRYSTALLINE CLASSE

SPACE GROUP

ASSYMETRIC UNIT

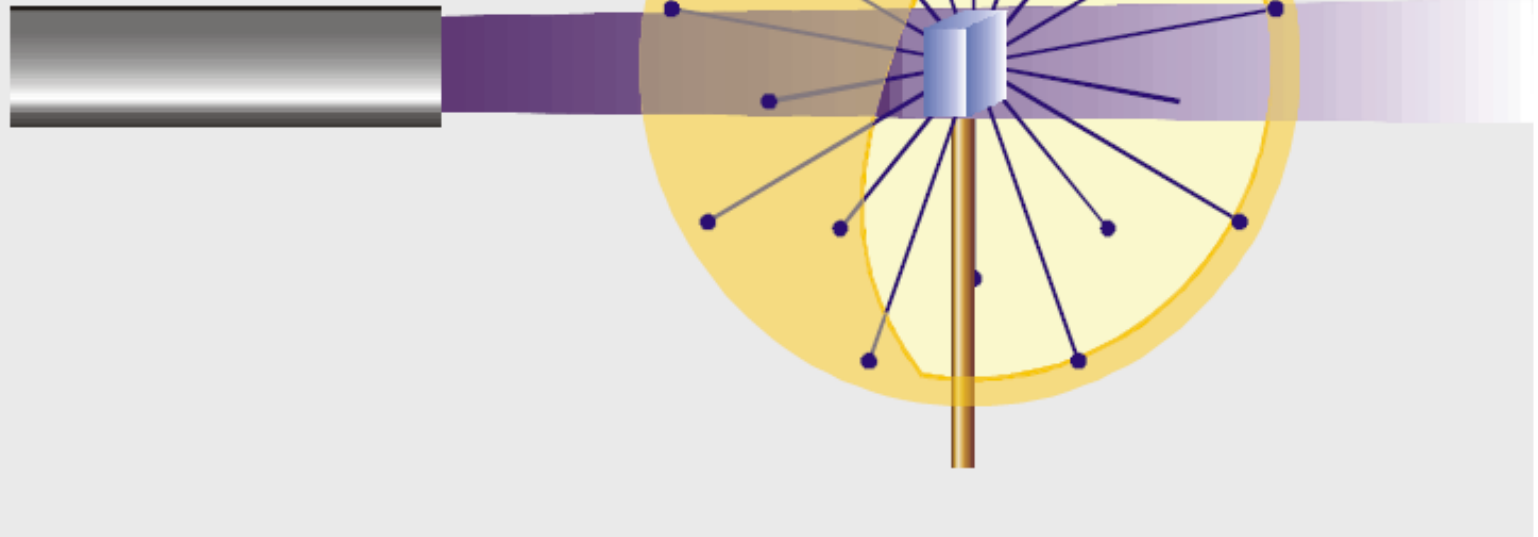
**X-RAY DIFFRACTION** - BRAGG'S LAW  
RECIPROCAL SPACE  
Fourier Transforms

**INTENSITY of REFLECTION** - Electronic density ( $\rho(xyz)$ )  
STRUCTURE FACTOR

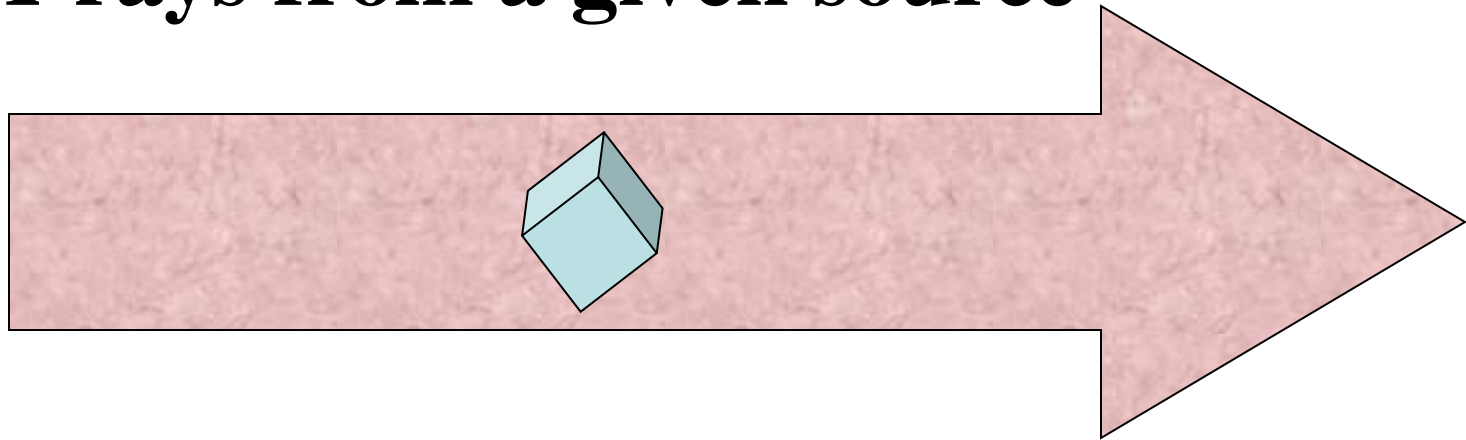
What is  $F(hkl)$  and how is it obtained??

# DIFFRACTION: What positions can be expected to diffract points?

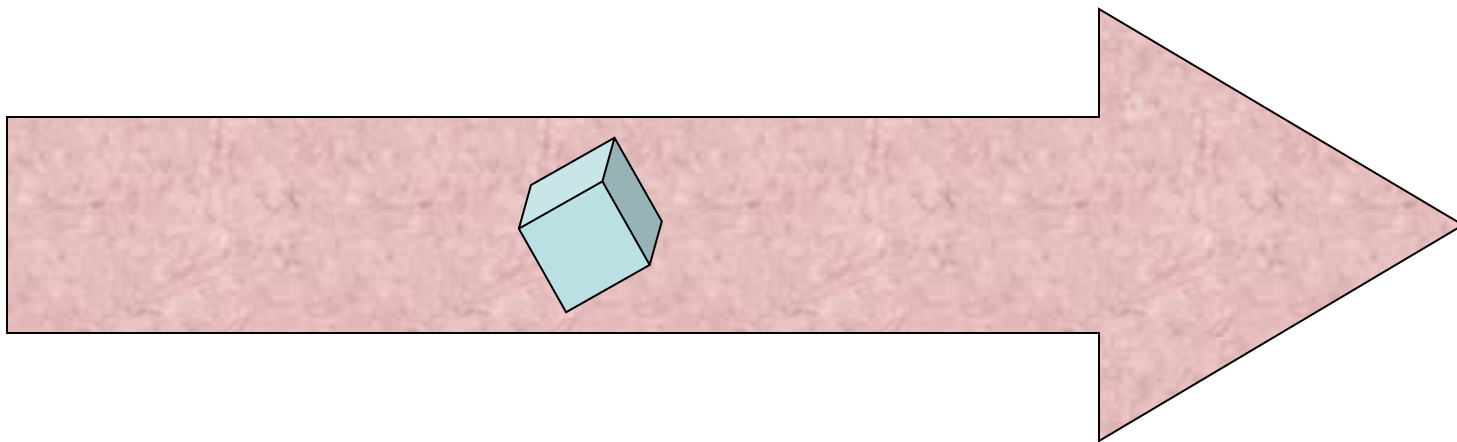
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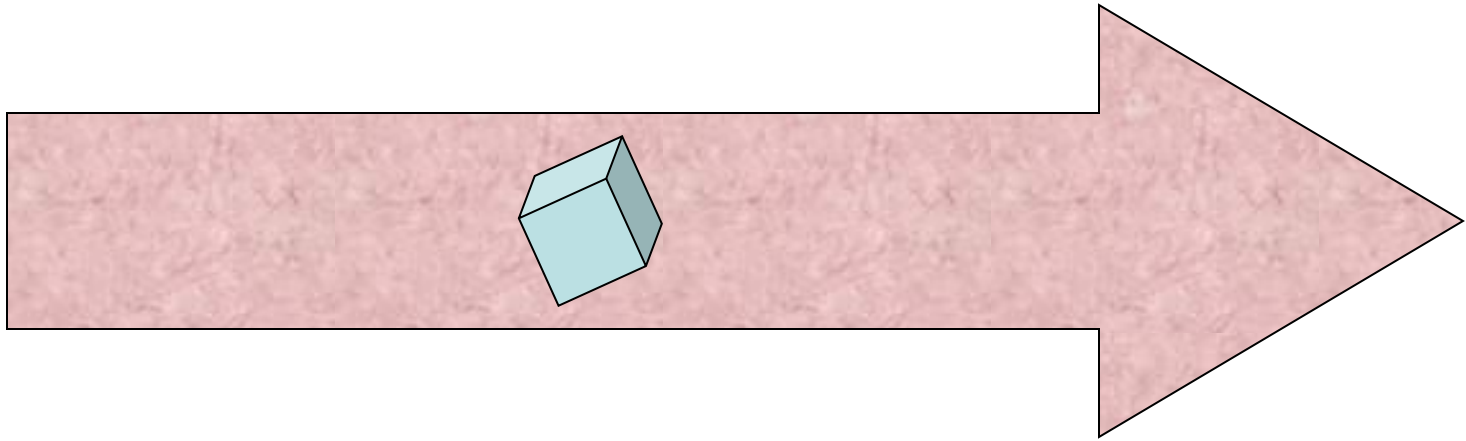


**X-rays from a given source**

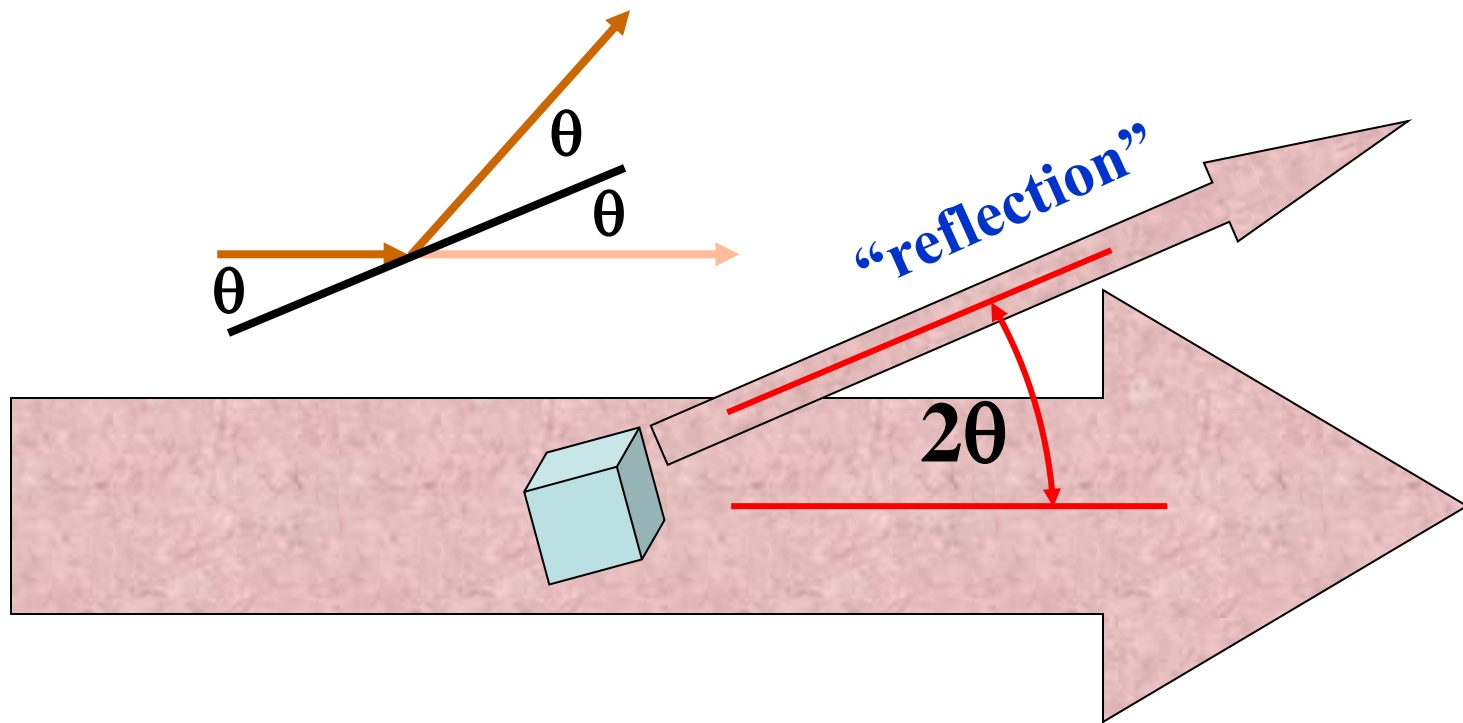


**The crystal is kept in the  
incident beam during the  
rotation**







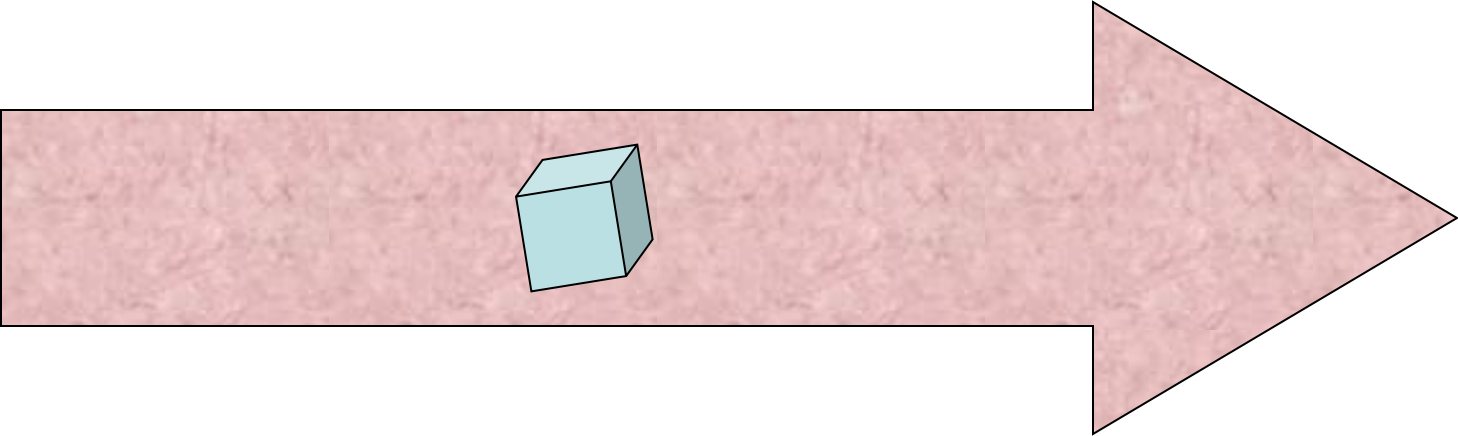


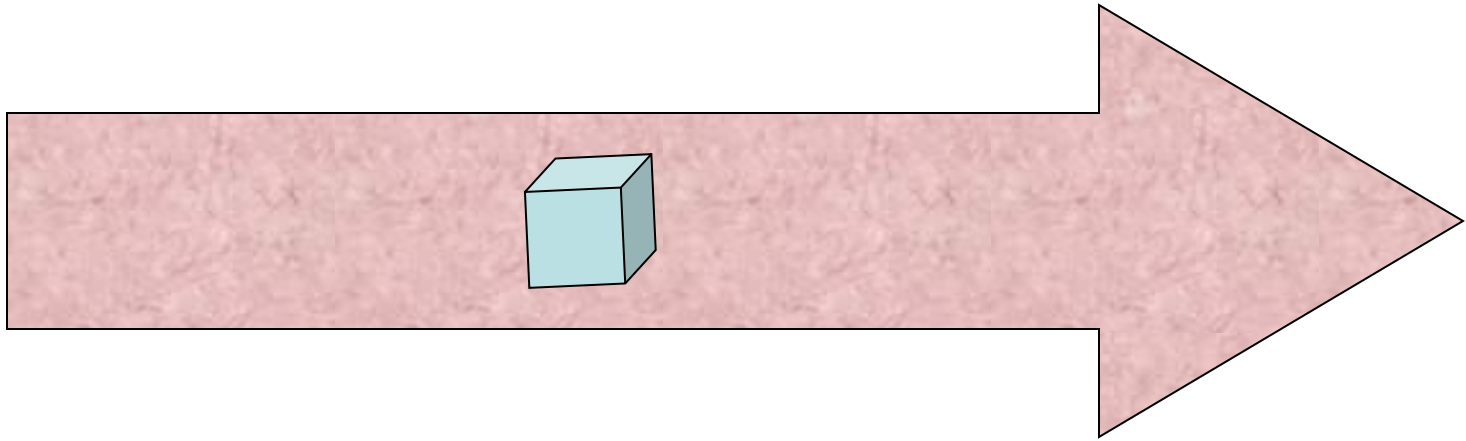
$\theta$  = Bragg angle,  $2\theta$  = scattering angle

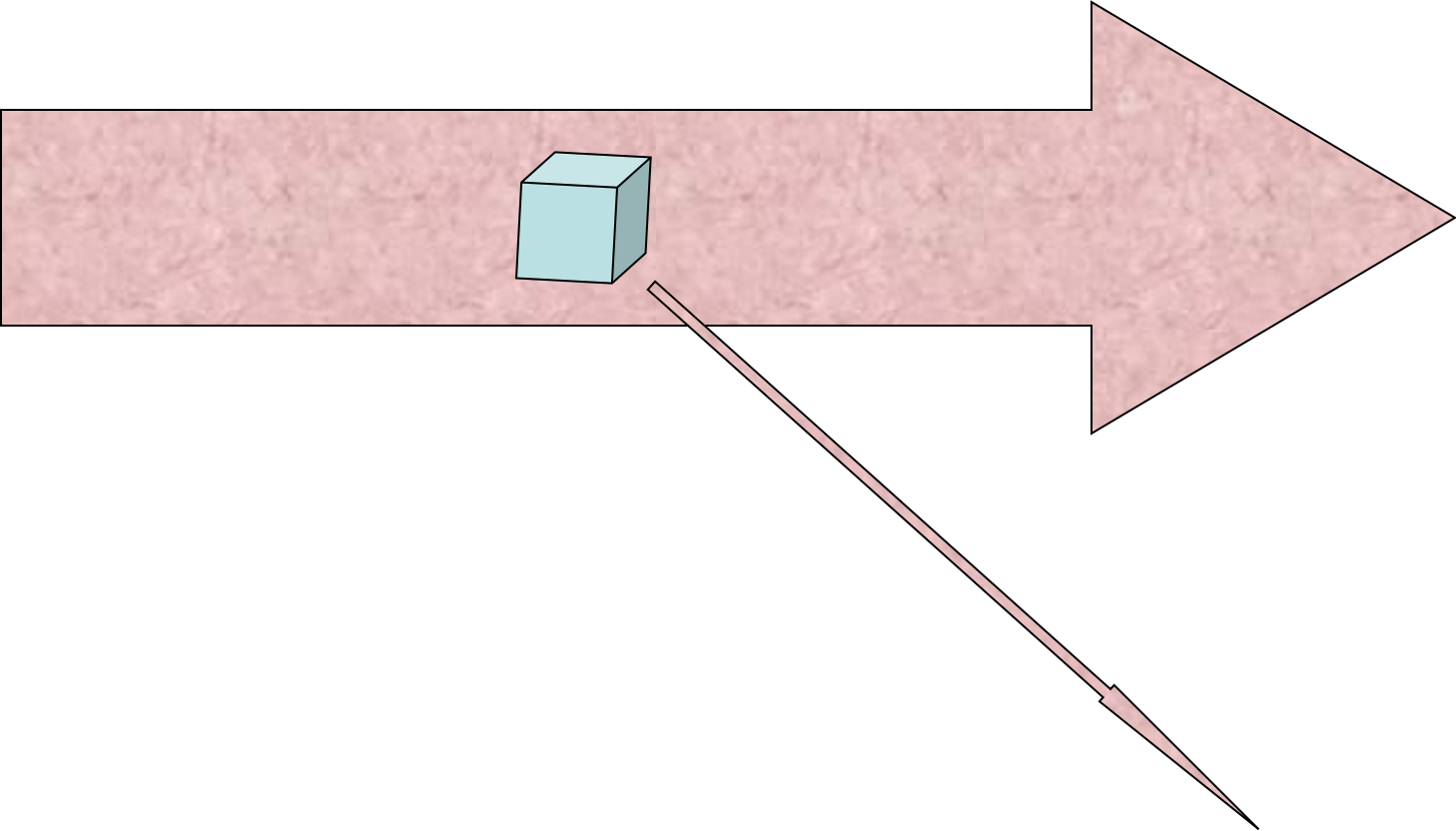
$\lambda = 2d_{hkl} \sin \theta$  (Bragg's law)

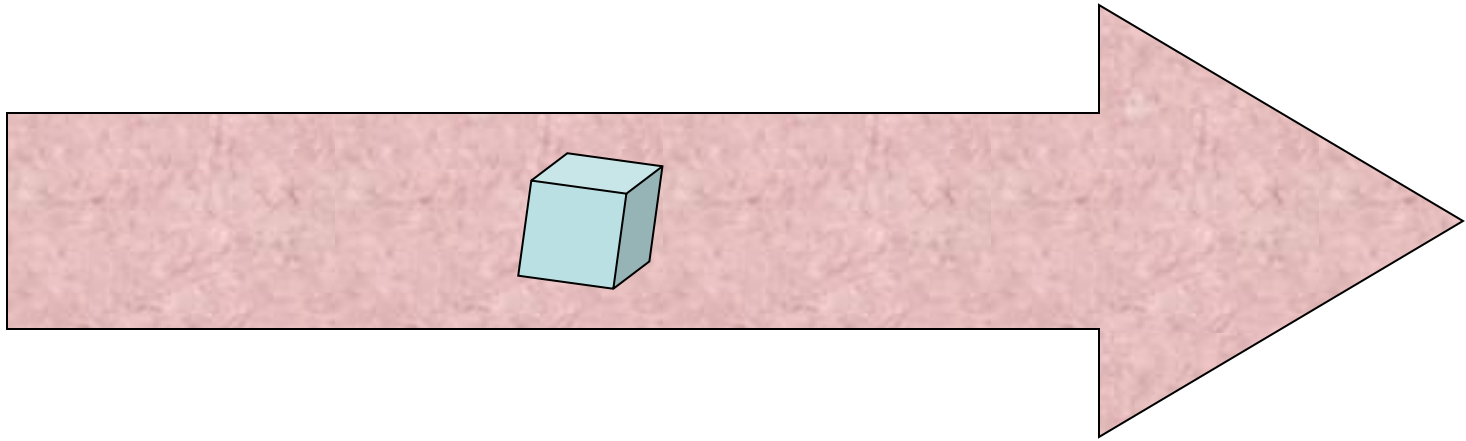
$\lambda$  = X-ray wavelength

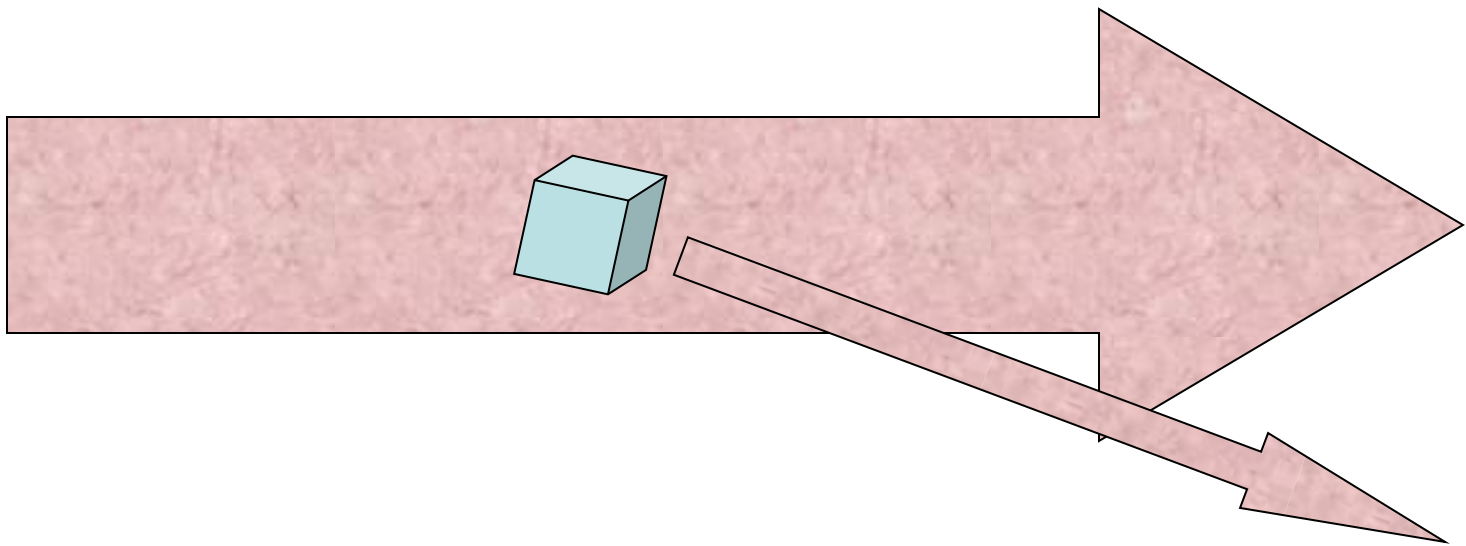
$d_{hkl}$  = interplanar spacings in the crystal

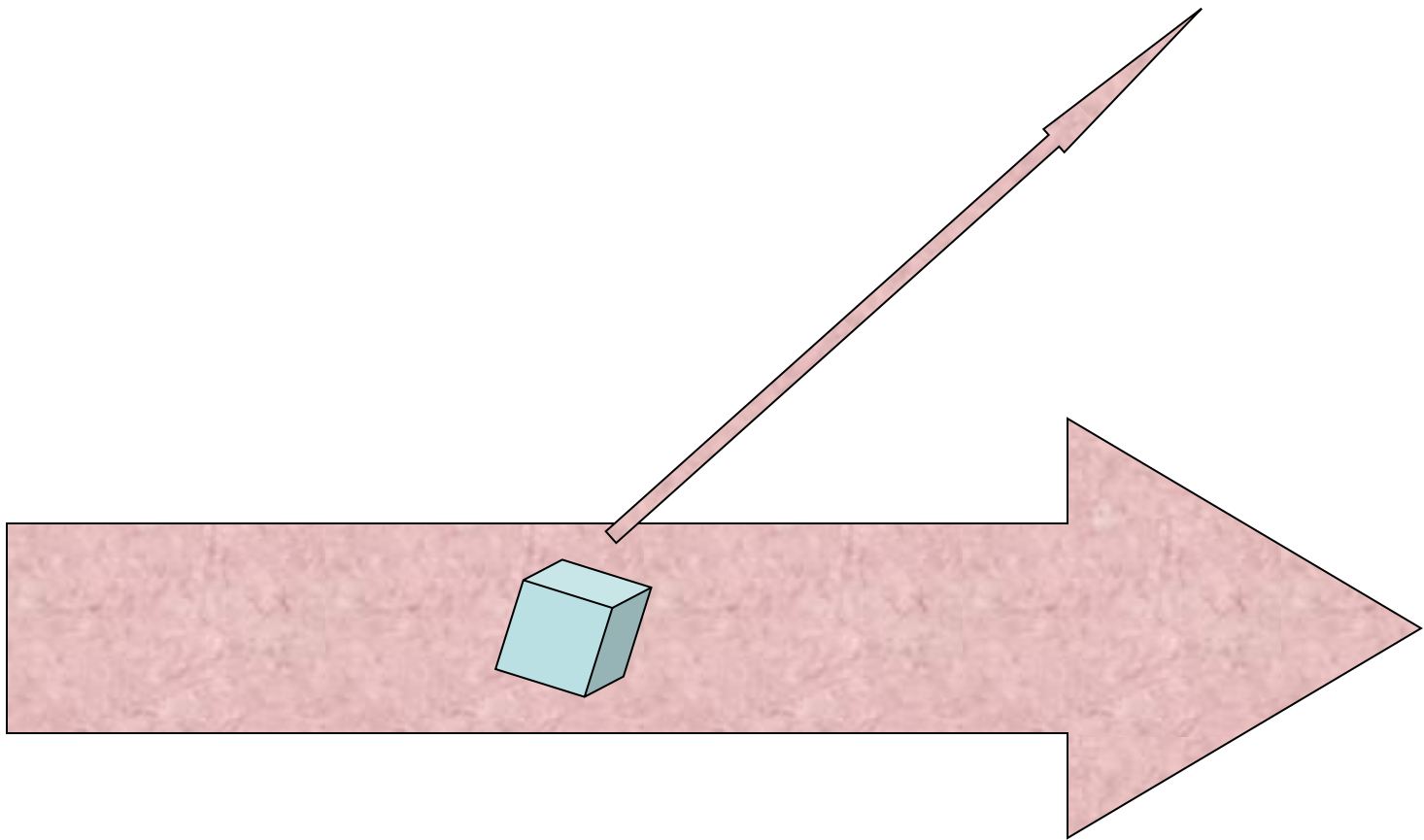


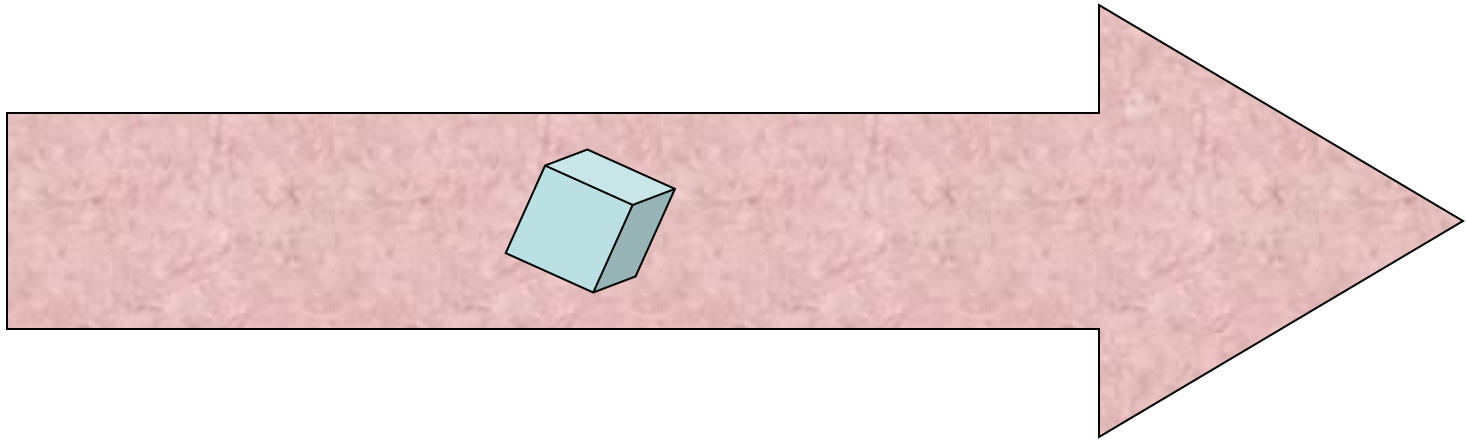




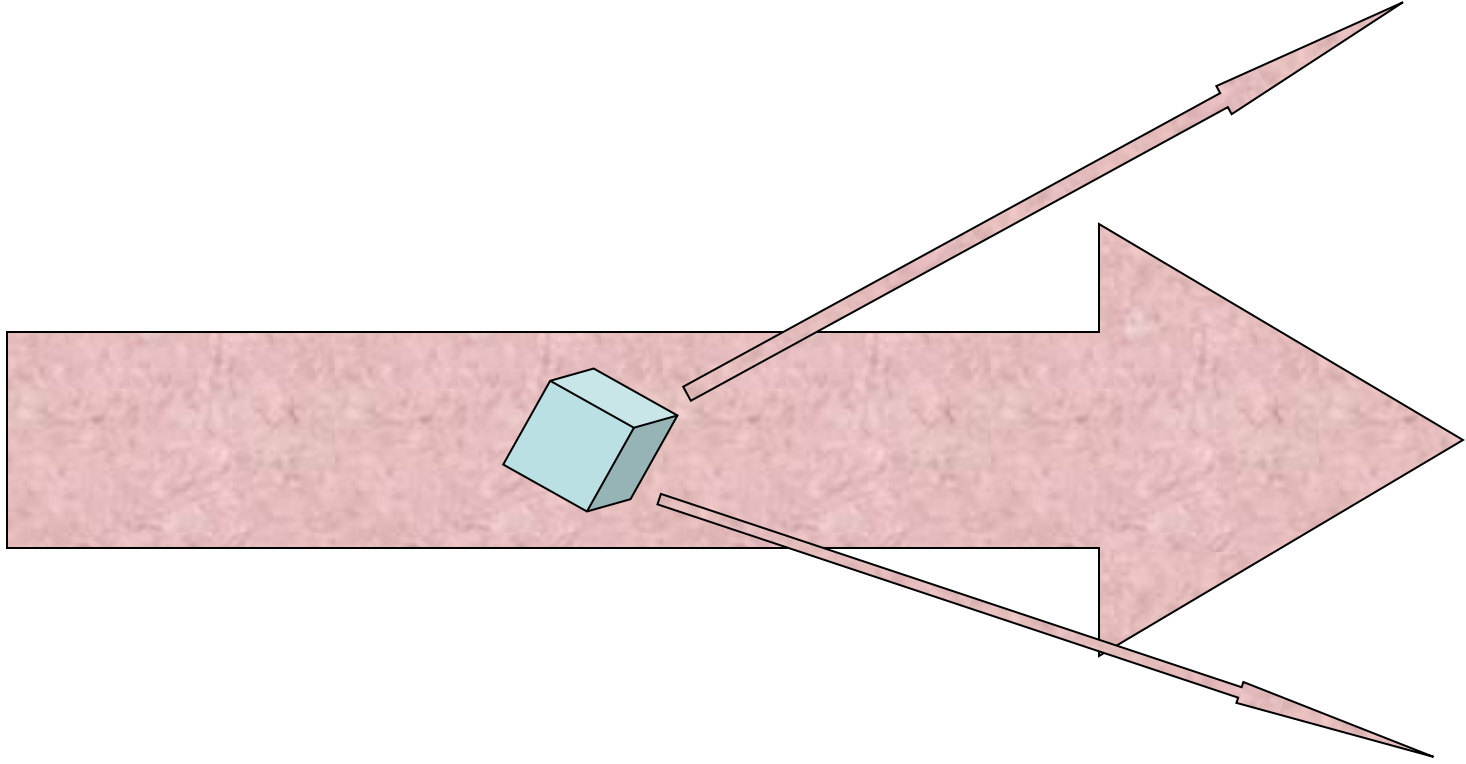




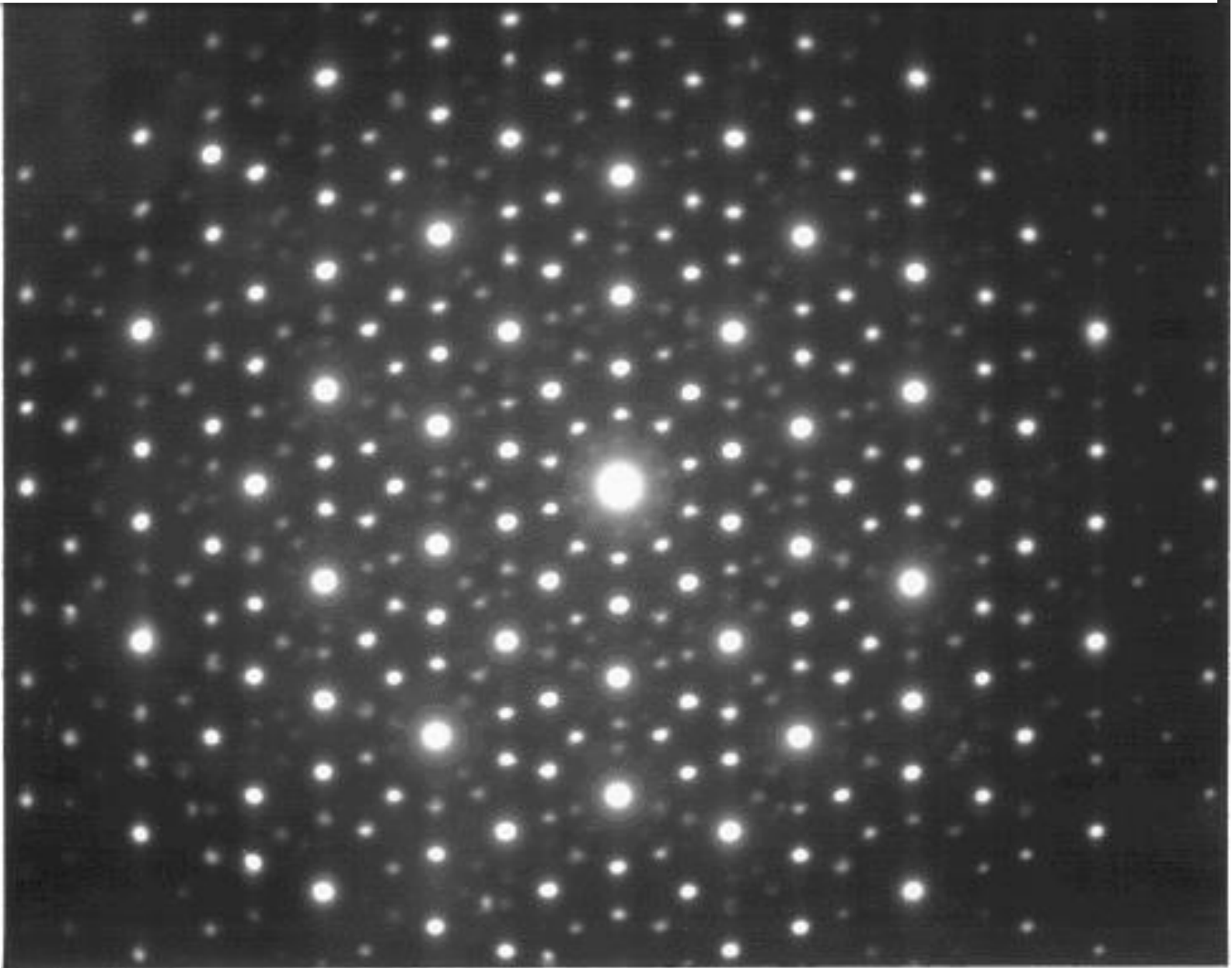


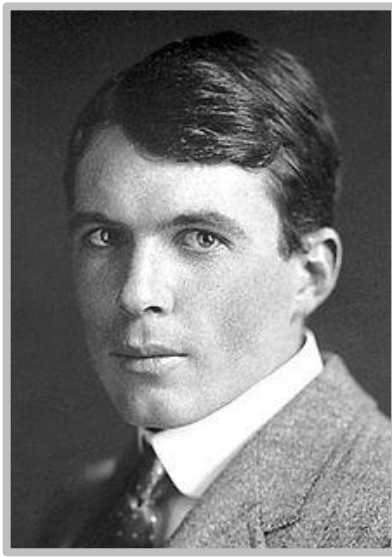
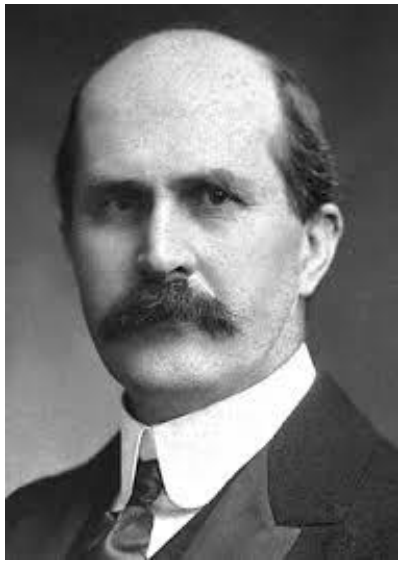






# DIFFRACTION: Examples of diffraction patterns





In 1912, Sir William Henry Bragg and William Lawrence Bragg developed the **Bragg's Law**

The Nobel Prize in Physics 1915 was awarded jointly to Sir William Henry Bragg and William Lawrence Bragg "for their services in the analysis of crystal structure by means of X-rays"

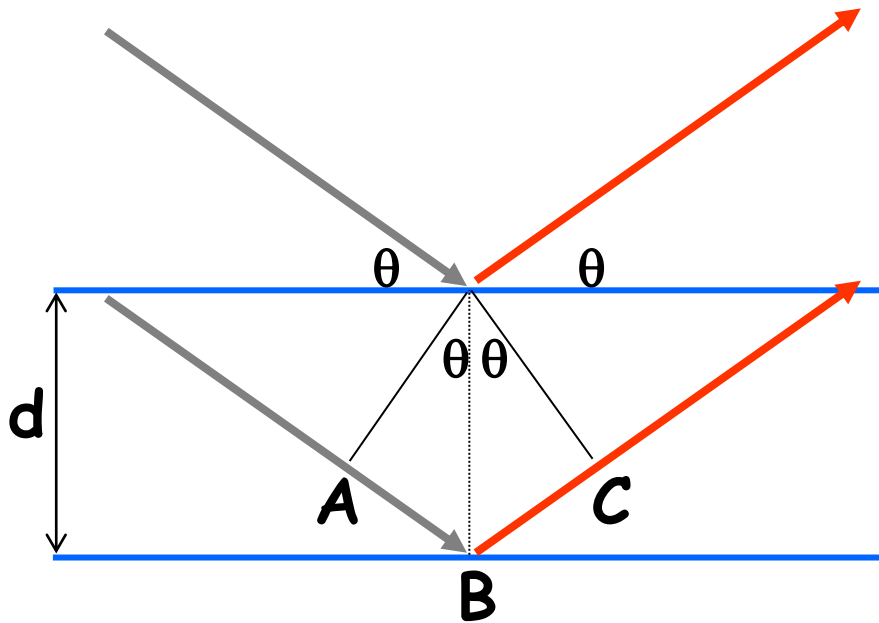
$$2d_{hkl} \sin \theta = n\lambda$$

Diffraction  $\approx$   
Reflection from planes  
in the lattice

Basis for X-ray  
diffraction  
geometry

# Diffraction: Bragg's Law

A simple way to describe the diffraction conditions established by Bragg in 1912, is to consider the diffraction as a reflection of the X radiation by adjacent planes in the crystal lattice



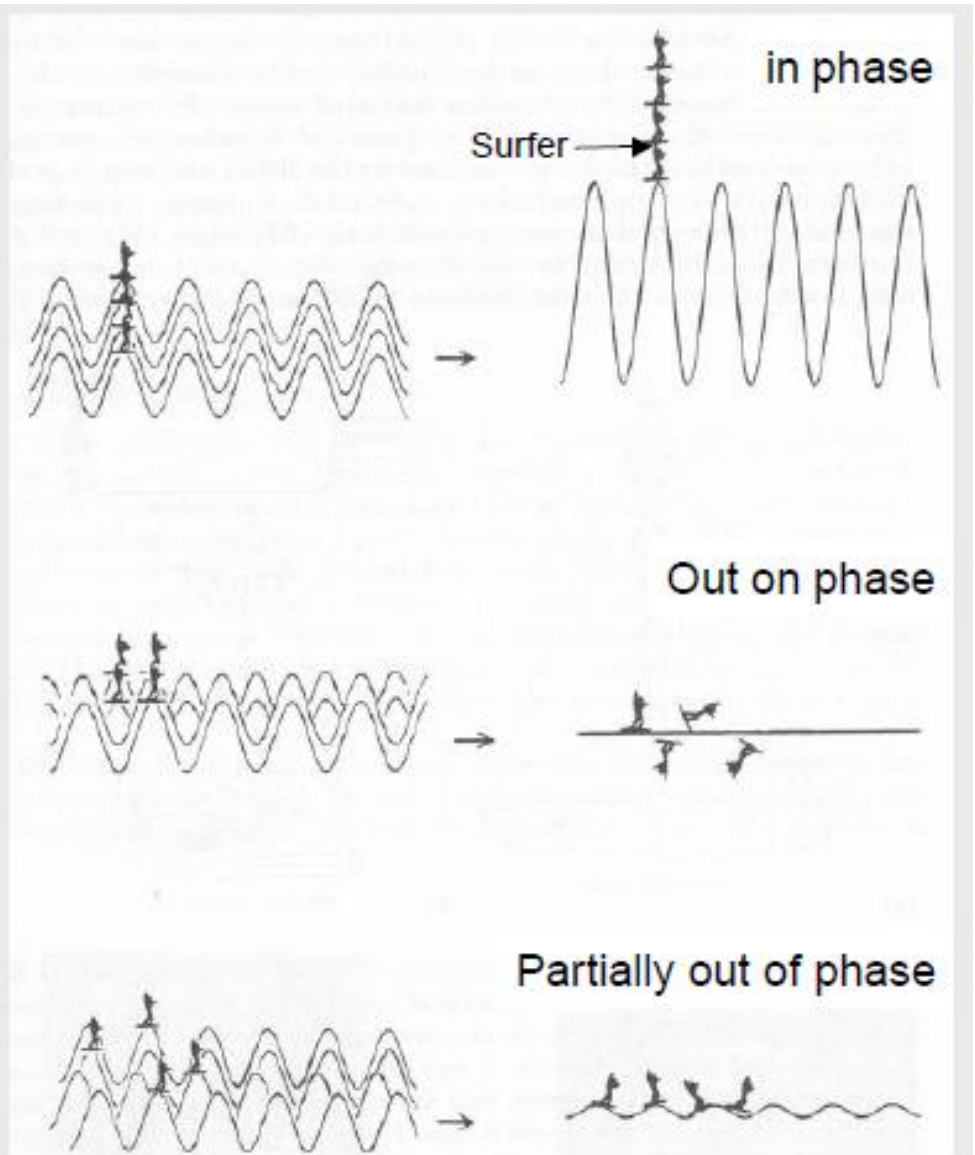
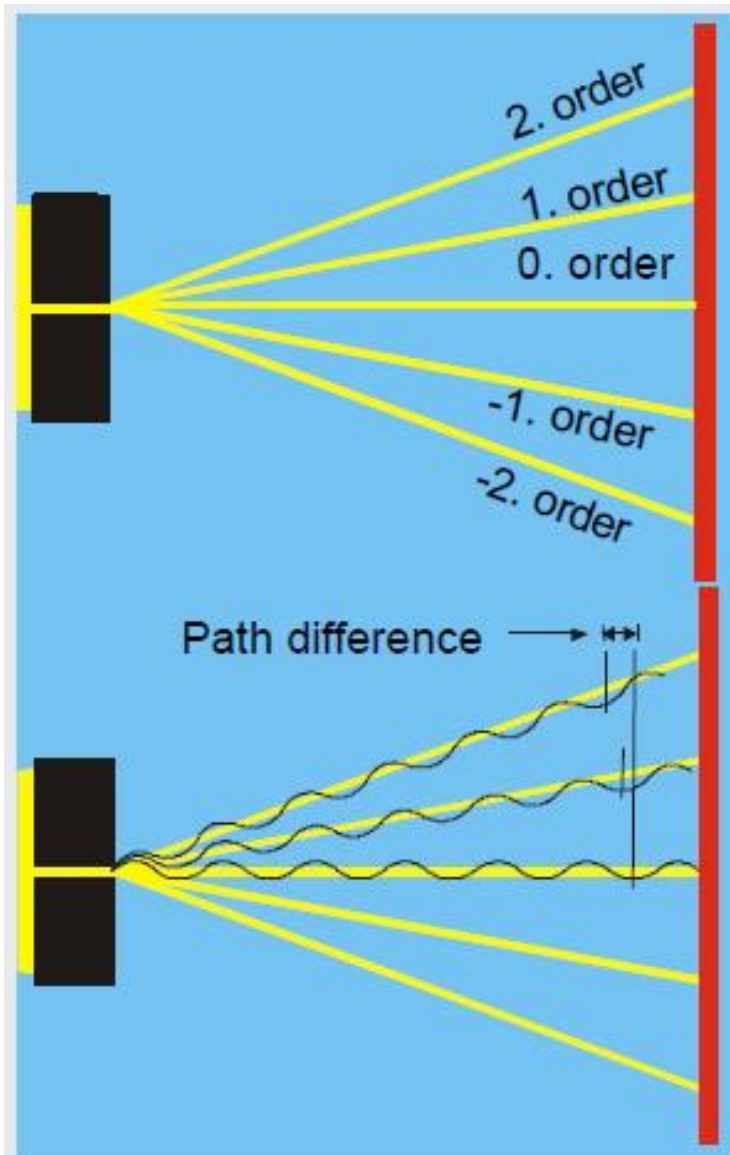
$$\begin{aligned}\text{Difference in the pathway} &= AB + BC \\ &= d\sin\theta + d\sin\theta \\ &= 2d\sin\theta\end{aligned}$$

Condition for a constructive interference:

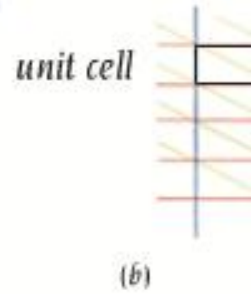
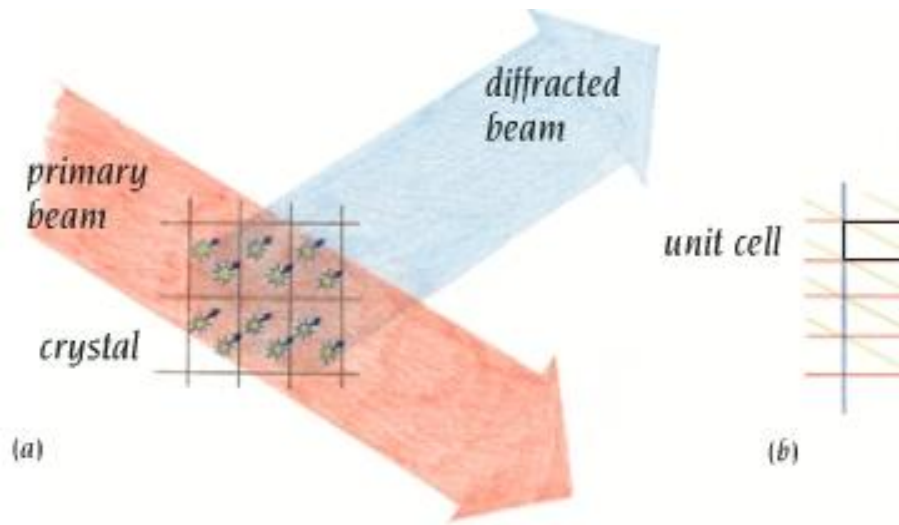
$$\text{Difference in the pathway} = n\lambda \Rightarrow n\lambda = 2d\sin\theta \quad (n = 0, 1, 2, \dots)$$

$$1/d = 2\sin\theta / \lambda = |s|$$

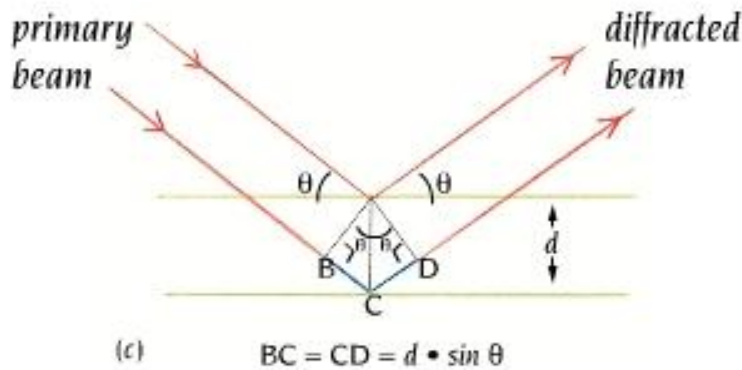
# INTERFERENCE



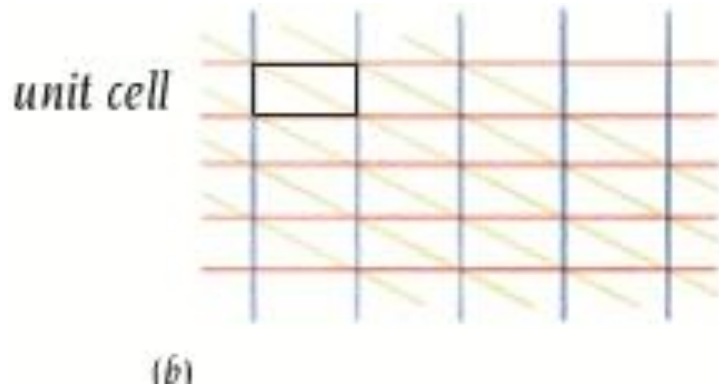
# Diffraction by a Crystal



- When the X-ray beam hits a crystal, all the atoms in the crystal disperse the radiation in all the directions. In most cases, the radiation is cancelled, but in a certain direction it is added and forms a diffracted beam.



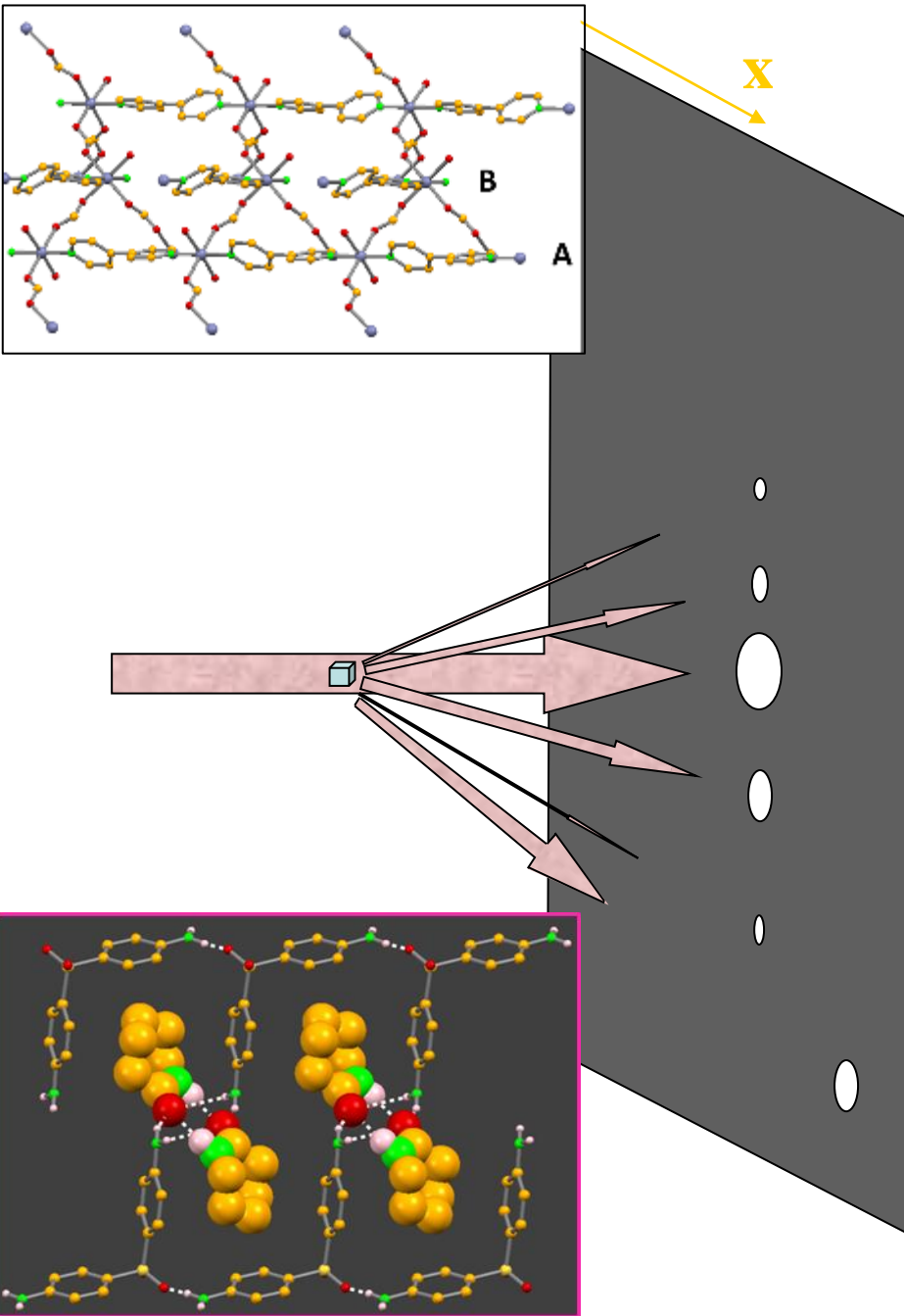
- Different planes disperse the radiation in such a way that each diffracted beam can be visualized as a reflection of the incident beam by a system of parallel planes separated by a distance  $d$ .



**Crystals produce  $10^2$ - $10^5$  reflections.**

**Each crystal produces a unique pattern of reflections, as a fingerprint.**

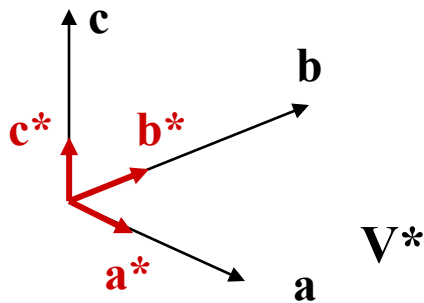
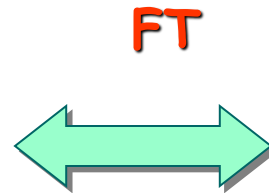
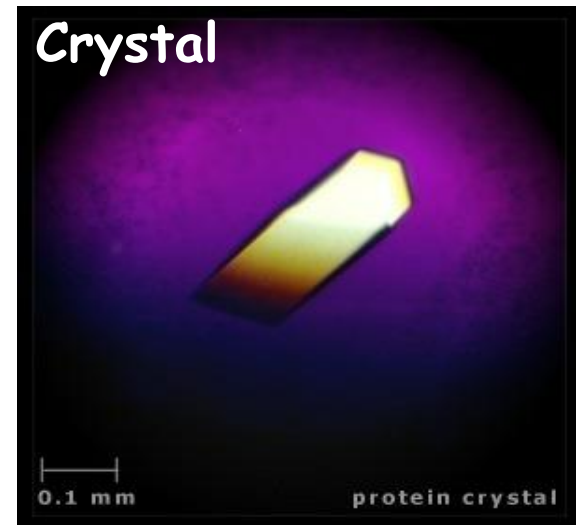
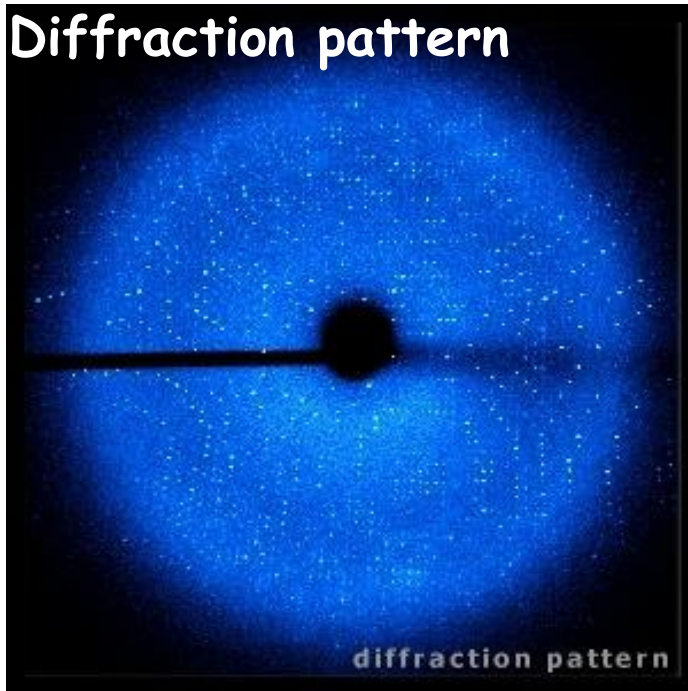
**The interpretation of the pattern leads to the crystalline and molecular structure.**



# REAL AND RECIPROCAL SPACES

Reciprocal space

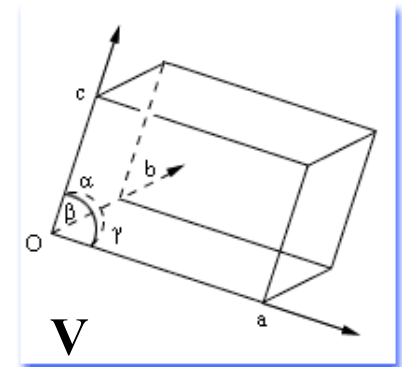
Real space



$$V^* = 1/V$$
$$a^* = 1/a; b^* = 1/b; c^* = 1/c$$

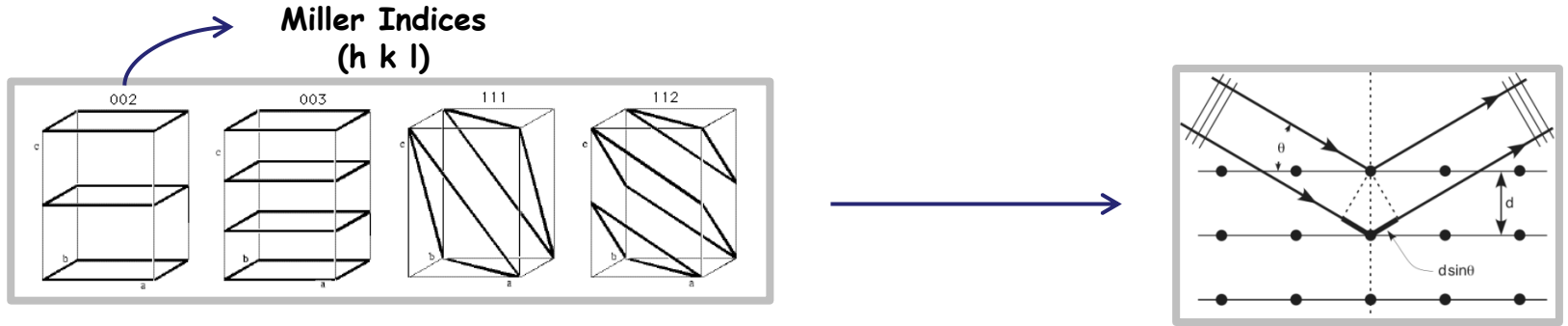
The symmetry is kept.

The dimensions are inverted.





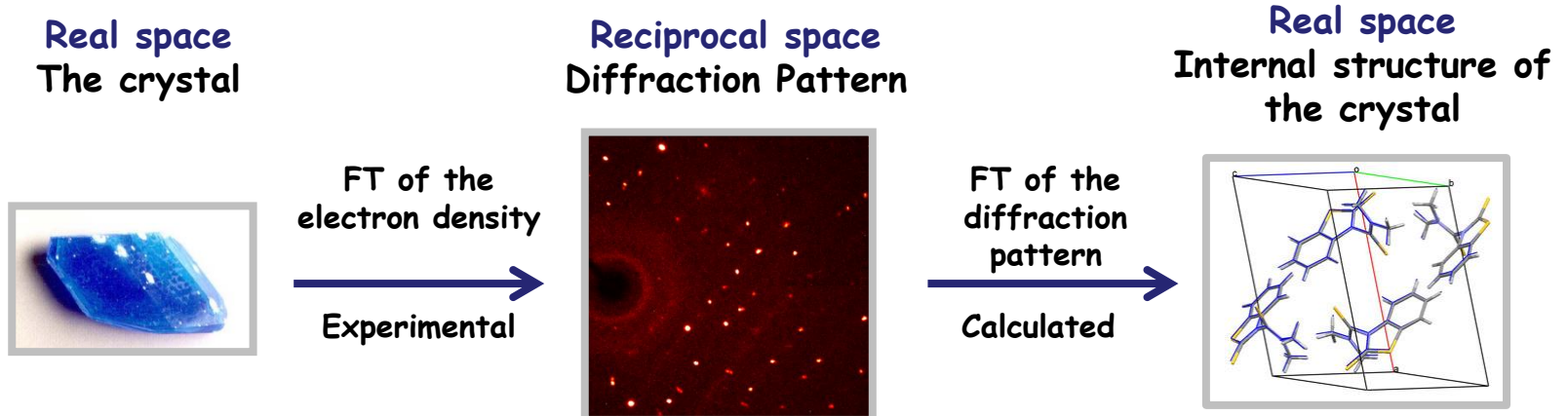
# DIFFRACTION - THE BRAGG'S LAW



⇒ Diffraction occurs when a X-ray (with  $\lambda$  wavelength) focus into the set of parallel planes (with  $d_{hkl}$  distance) with  $\theta$  angle and is reflected at the same angle

$$2d_{hkl} \sin \theta = n\lambda$$

## REAL SPACE AND RECIPROCAL SPACE



$$\rho(xyz) = \frac{1}{V} \sum_{hkl} F(hkl) e^{-2\pi i(hx+ky+lz)} \quad F(hkl) = |F(hkl)| e^{i\Phi(hkl)} \quad |F(hkl)| = \sqrt{I(hkl)}$$

Phase Problem For small molecules (<1000 non-H atoms) - Direct Methods

# BASIC CONCEPTS

**CRYSTALS** - CRYSTALLINE SYMMETRY

SYMMETRY OPERATION

UNIT CELL

CRYSTALLINE CLASSE

SPACE GROUP

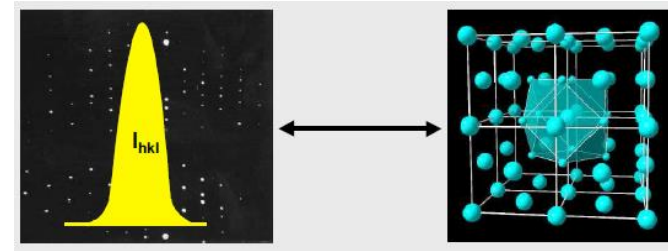
ASSYMETRIC UNIT

**X-RAY DIFFRACTION** - BRAGG'S LAW  
RECIPROCAL SPACE  
Fourier Transforms

**INTENSITY of REFLECTION** - Electronic density ( $\rho(xyz)$ )  
STRUCTURE FACTOR

What is  $F(hkl)$  and how is it obtained??

Electronic density = Fourier Transform  
FT is reversible, thus:  $\rho \leftrightarrow F$



Electronic density

Unit cell volume

phase

$$\rho(x,y,z) = 1/V \sum_{h,k,l} |F(h,k,l)| e^{i\alpha(h,k,l)} e^{-2\pi i(hx,ky,lz)}$$

$$|F(hkl)| = \sqrt{I(hkl)}$$

Structure factor  
amplitude

Average intensities

# The angle $\alpha$ is unknown... PHASE PROBLEM!!

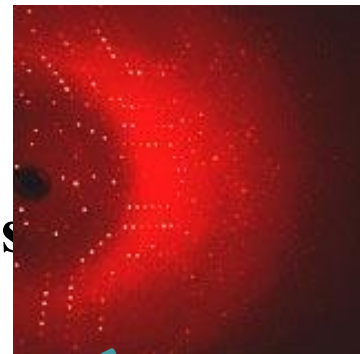
**Electronic density**      **Unit cell volume**      **phase**

$$\rho(x,y,z) = 1/V \sum_{h,k,l} |F(h,k,l)| e^{i\alpha(h,k,l)} e^{-2\pi i(hx,ky,lz)}$$

$$|F(hkl)| = \sqrt{I(hkl)}$$

**Structure factor amplitude**

**Average intensities**



**Those we have**

**So, an approximate model for the structure,  
the position parameters (x,y,z) are needed to  
determined  $|F_{\text{calc}}| e^{i\alpha_{\text{calc}}}$**

**It is assumed that each reflection can be  
described by a Fourier series:**

$$F(hkl) = \sum f(j) \exp 2 \pi i (hx_j+ky_j+lz_j)$$

**in which  $f(j)$  is the contribution of atom  $j$  for  
 $F(hkl)$**

# Methods for the phase determination

## 1- Heavy atom method (Patterson):

**Considers that the diffraction is mostly due to the heavy atoms  
(mostly used in coordination compounds)**

## 2 – Direct Methods

**Probability methods, purely based on mathematical relations  
(organic molecules)**

# Diffraction and Fourier synthesis

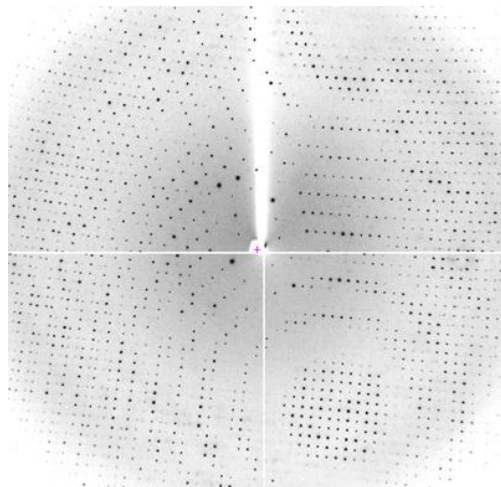
For a crystal:

$$F(s) = T [r(r)]$$

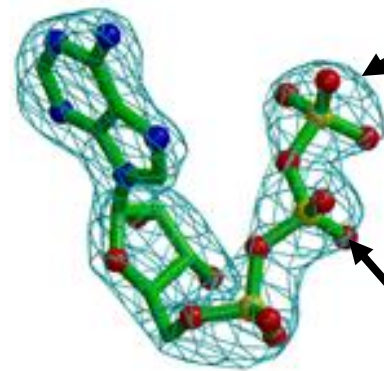
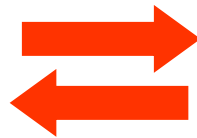
diffraction pattern = TF of electronic density

$$r(r) = T^{-1}[F(s)]$$

electronic density = TF of diffraction pattern



Diffraction pattern



Electronic density map

Atomic model

We can always go back and forth with the TF:

- from the electronic density calculate the diffraction pattern
- from the diffraction pattern calculated the electronic density

# Resolution: why is it important?

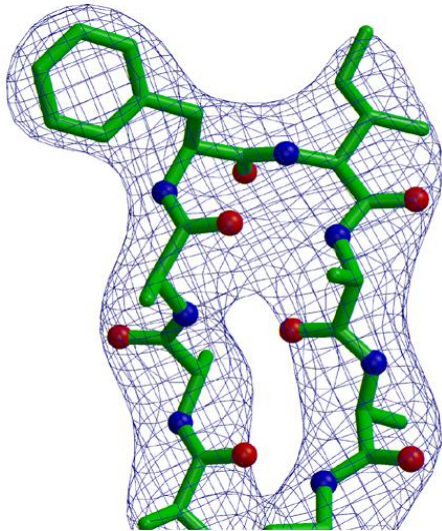
“Resolution” is related with the level of detailed that can be obtained: a high resolution map gives more detailed image of the atomic structure

$$\text{Resolution: } \sin \theta / \lambda$$

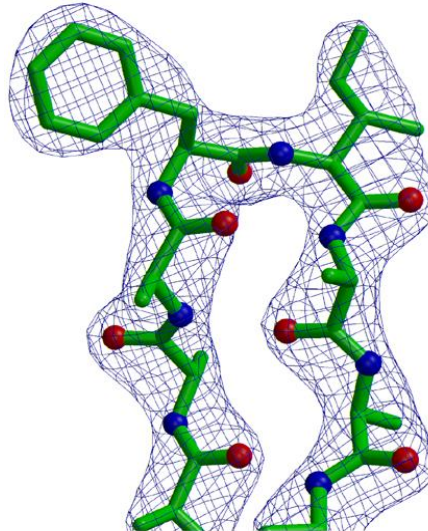
Low resolution  
low  $\theta$ , high  $d$



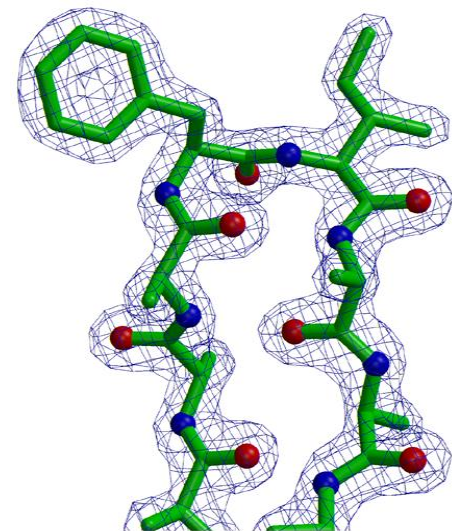
High resolution  
high  $\theta$ , low  $d$



Map at 4 Å  
Diffuse



Map at 2.9 Å



Map at 2 Å  
Almost contains the atomic detail



# Refinement & Errors

- Refinement removes the initial errors in the model by optimizing the model with experimental measures
- The difference between the model and the experimental parameters is expressed by the R factor:

$$R = \frac{\sum_{hkl} ||F_{\text{obs}}| - k|F_{\text{calc}}||}{\sum |F_{\text{obs}}|}$$

A good quality structure determination should have R-factor ~ 5 (10)% and small standard deviations

- Error sources:
  - Error in the intensity measures
  - Slight variations in conformation of the molecules

# Steps of a structure determination

- 1. Obtain crystals**
- 2. Selecting a crystal using a microscope**
- 3. Collect diffraction data**
- 4. Data collection, data reduction and absorption correction**
- 5. Solve structure**
- 6. Refinement - accurate determination of atomic coordinates and temperature factors**
- 7. Validate and check structure**
- 10. Structural analysis - Distances, angles, graphics and confidence factors**

## 1. Obtain crystals

## 2. Selecting a crystal using a microscope

- ✓ Transfer the crystals to inert oil
- ✓ Select one crystal under a microscope
- ✓ Mount in the X-ray apparatus

# Crystallization techniques

## Small molecules

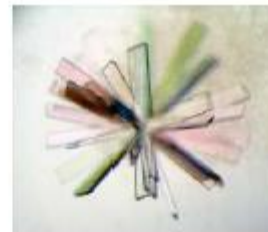
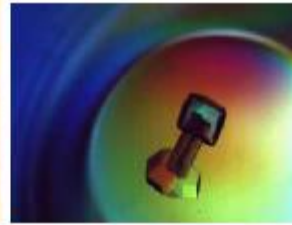
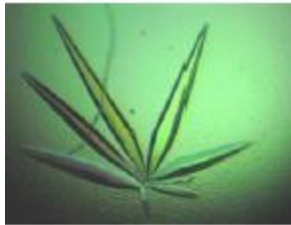
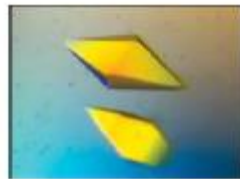
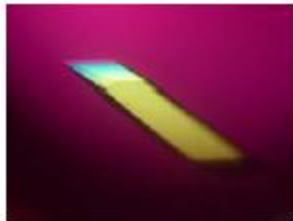
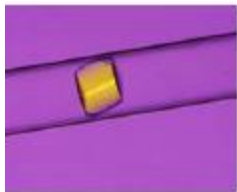
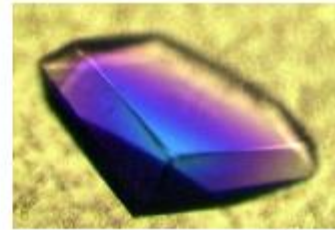
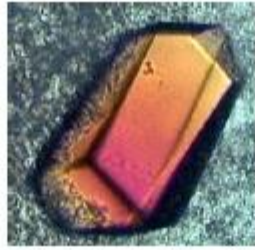
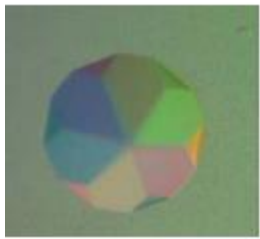
- Slow evaporation from the solvente
- Slow vapor diffusion
- Mixture of miscible and non-miscible solvents (several techniques: direct, gel permeation, evaporation...)
- Slow diffusion of solventes (porous plates, gel..)
- Slow precipitation
- Use of low temperature

**Getting good crystals is o major importance!**

**– Well organized molecules: Stronger diffraction**

**Better results!**

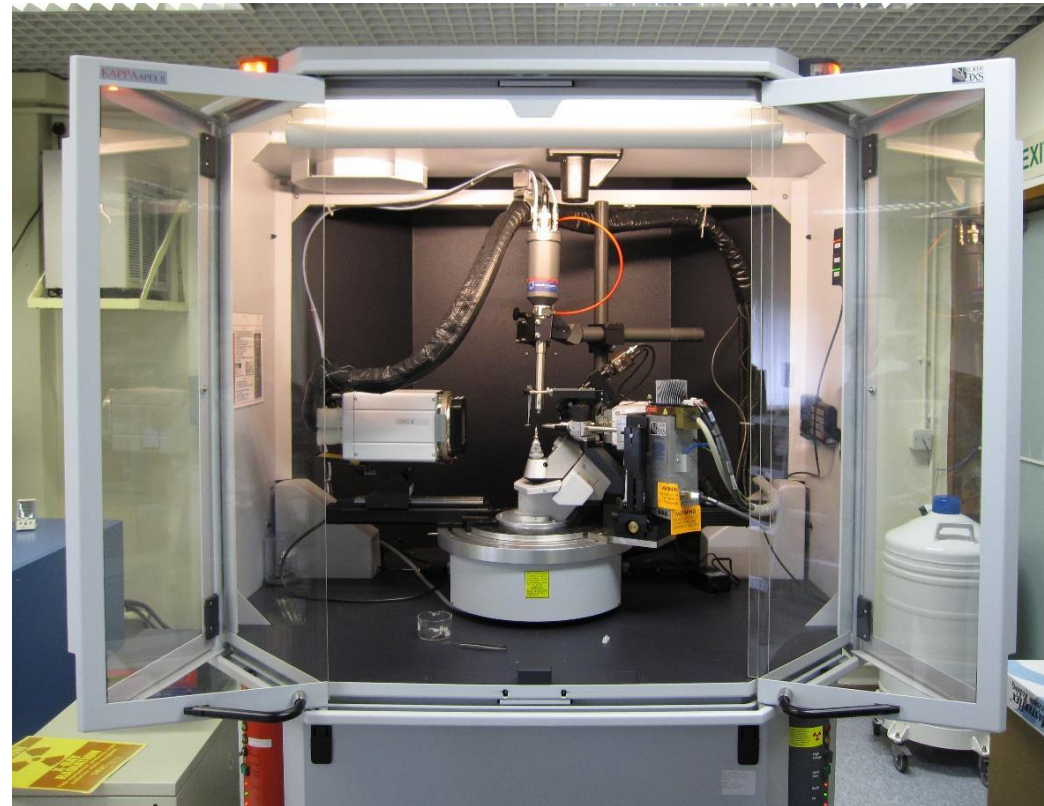
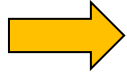
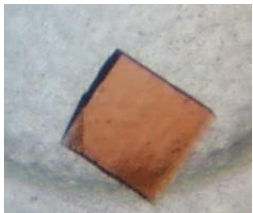
# CRYSTALS

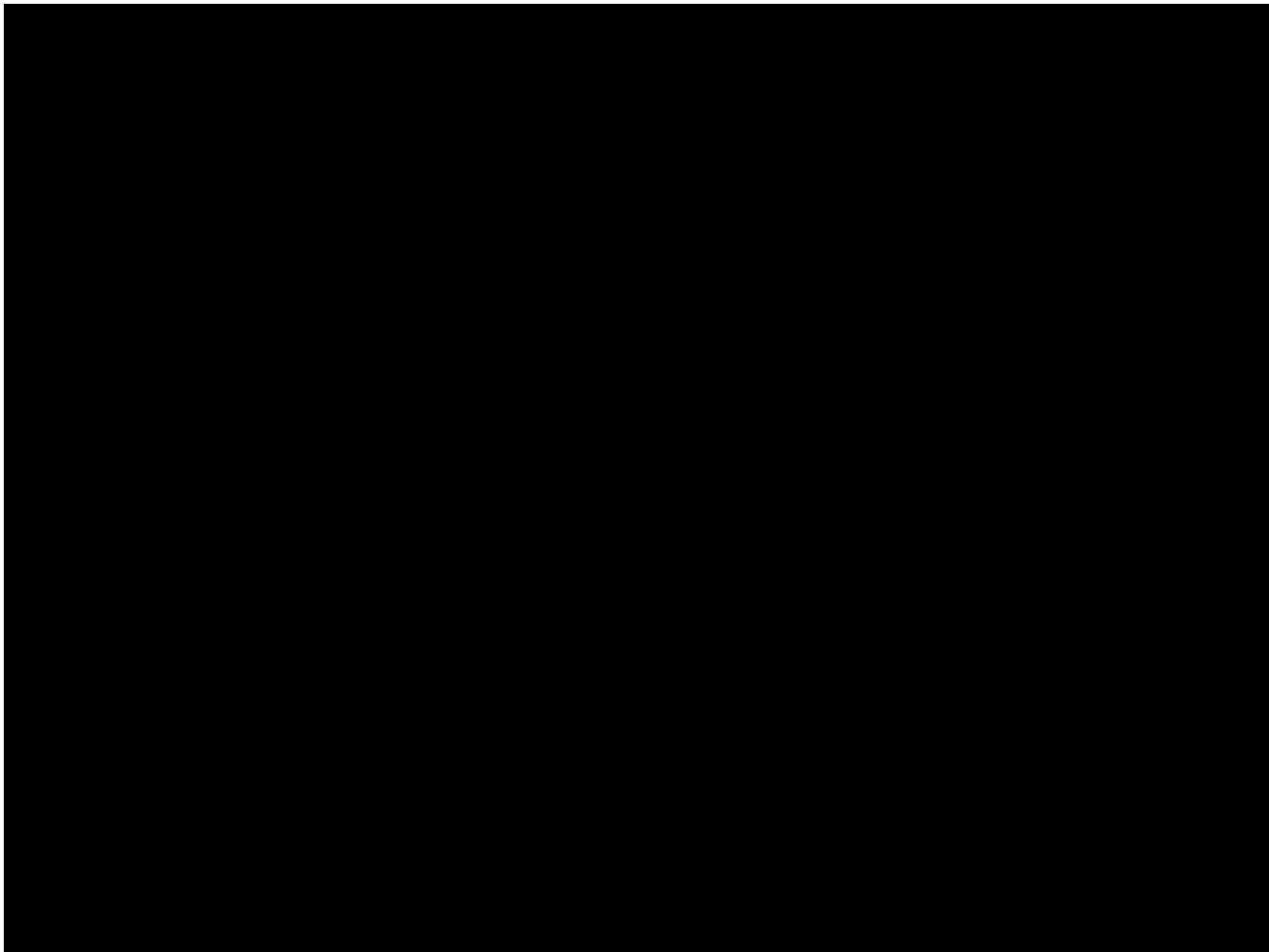


The second step for determining the molecular structure by crystallography is to get the **diffraction data**.

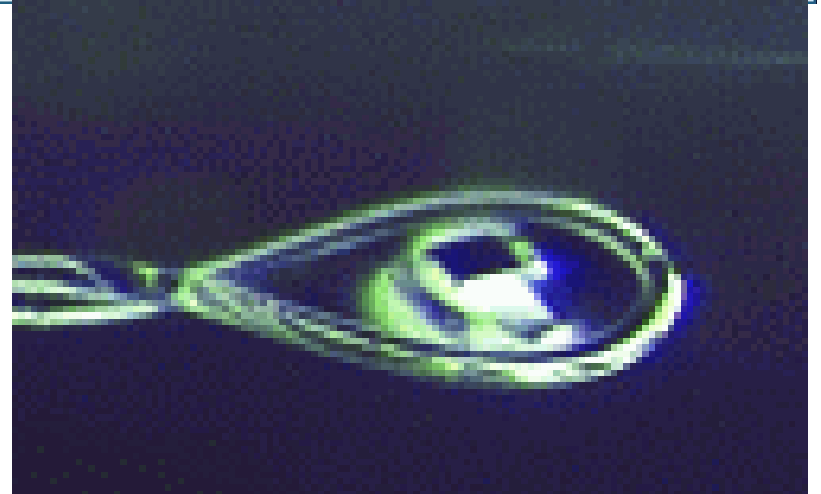
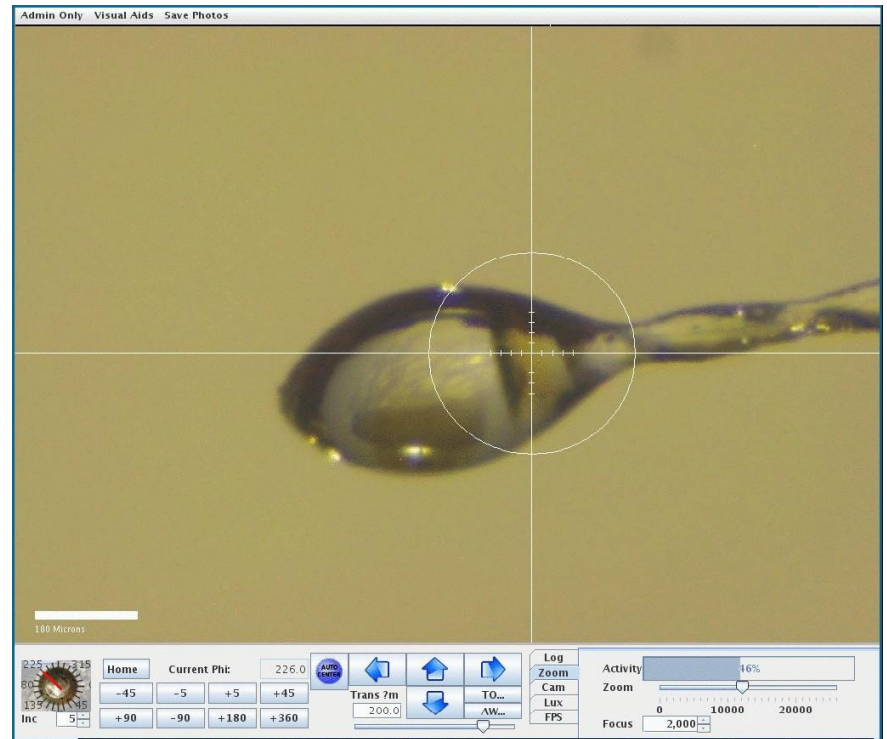
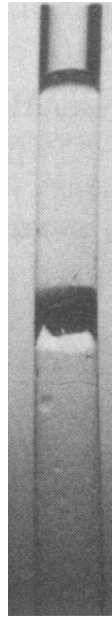
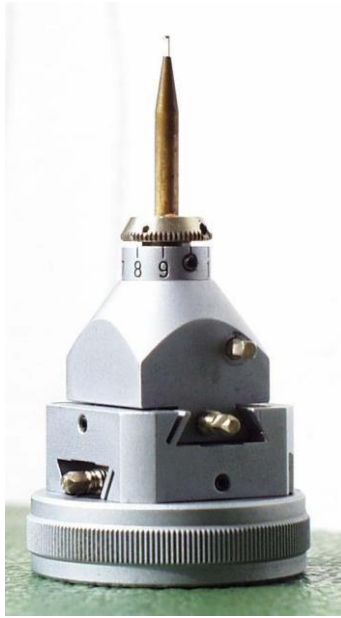
1. **Select and mount the crystal on goniometer head.**

2. **Set the goniometer head in the goniometer of the diffractometer**



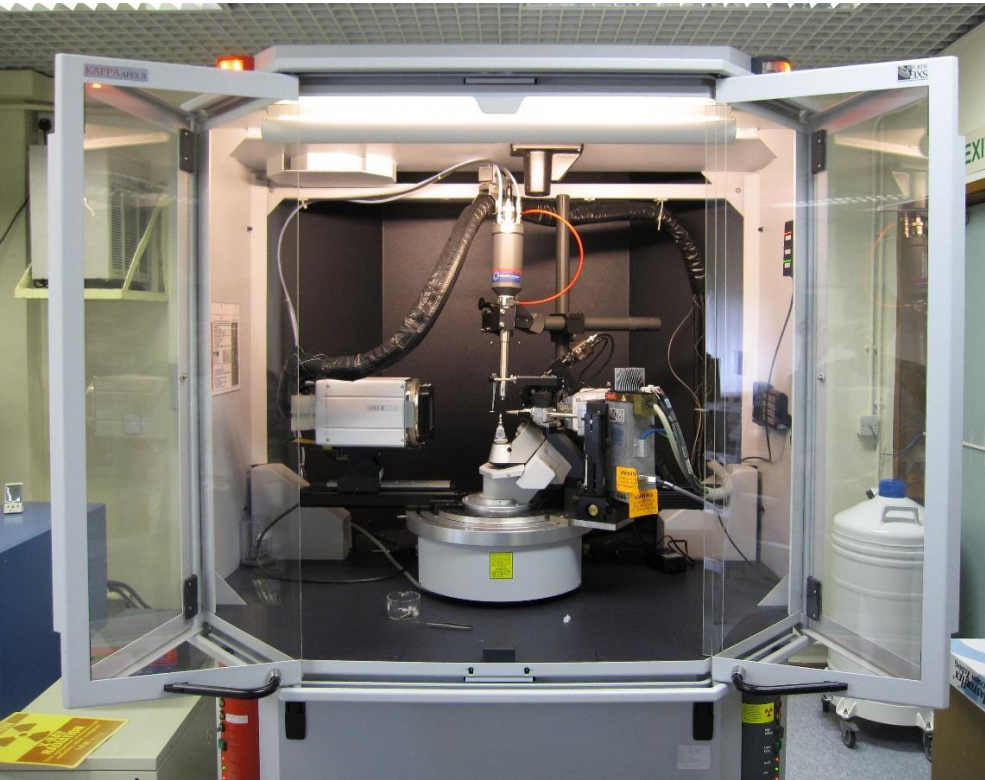


# Crystal Mount

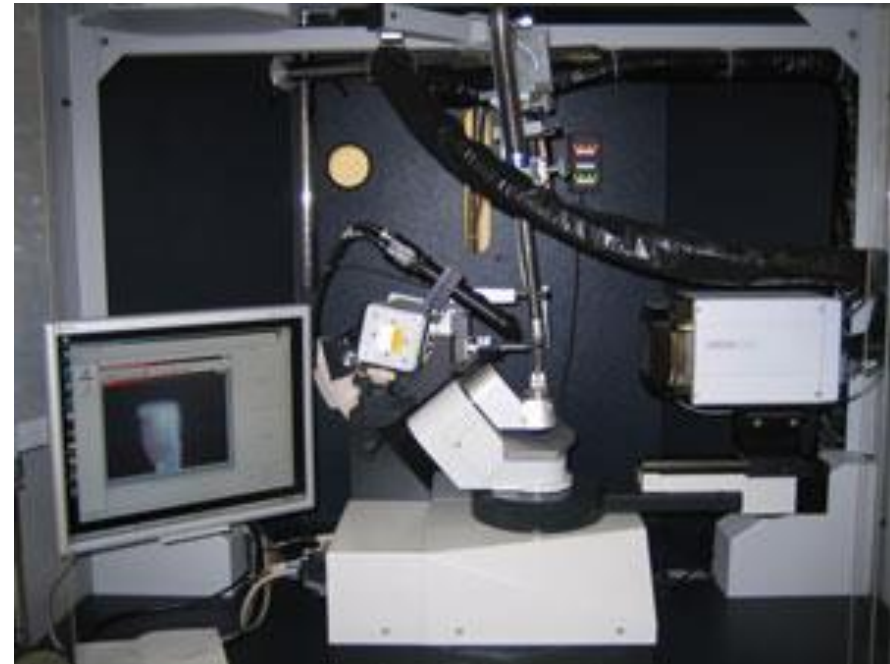




# Instruments for measuring intensity: diffractometers with area detector



The complete diffraction pattern is measured and stored as a photographic film



## Advantages:

- Fast measurement (simultaneous measurement of multiple reflections)
- smaller crystals (highest sensitivity)
- Weak crystals measurement (twinned crystals)
- Super structures can be easily detected

# Collect diffraction data

- ✓ Collect:
  - 1) An image: Screen the sample quality
  - 2) A preliminary set of frames: Determine the unit cell
- ✓ Index the reflections, refine and convert to crystal system
- ✓ Perform the intensity data collection

## Reflections:

Adequate intensity  
Good shape(sharp and not split)

## Incremental scan method:

Crystal moves through small angles (0.1 - 0.3°) with an image recorded at each step

# Data collection, data reduction and absorption correction

## Diffraction software package

- ✓ Integrate the images into a single file (list of intensities)
- ✓ Merge (identify same peaks in two or more images)
- ✓ Scale the relative images

## 5. Solve structure

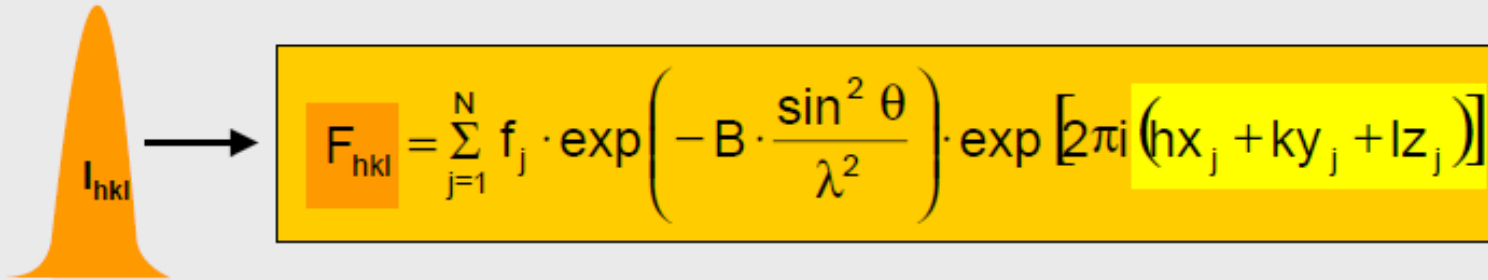
### Atom assignments

- ✓ Transfer final data to structure determination software package - WINGX and SHELXL program suites
- ✓ Perform the Direct Methods calculations: programs SIR92, SIR97 or SIR2004

### Assignment process:

Heavier elements are associated to higher intensities  
Distances and angles between intensity centres

## Structure solution: Introduction



$I_{hkl}$

$$F_{hkl} = \sum_{j=1}^N f_j \cdot \exp\left(-B \cdot \frac{\sin^2 \theta}{\lambda^2}\right) \cdot \exp\left[2\pi i (hx_j + ky_j + lz_j)\right]$$

What is needed for a structure determination?

- The intensity of each reflection (from intensity measurement)
- The phase of each reflection (Get lost in the intensity measurement (called “Phase problem“ ?))
- The phase of each reflection is determined by structure solution

# Phase determination

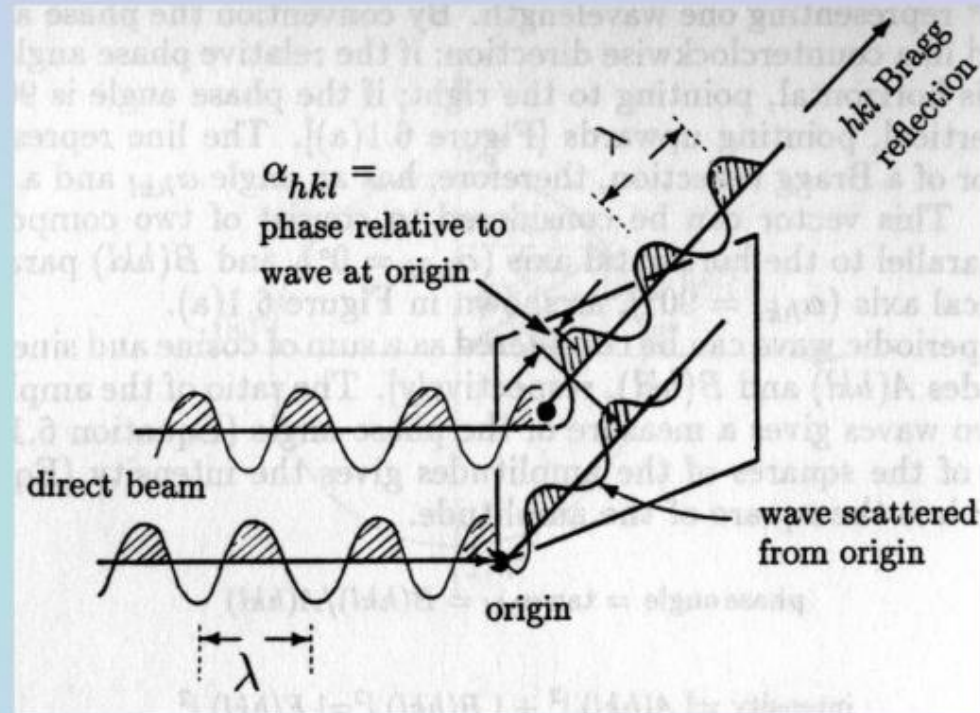
This is the famous "phase problem" of crystallography

Each reflection (diffraction point) is described mathematically by a vector designated by a design factor (F) which may be represented by:

$$\mathbf{F} = |\mathbf{F}| e^{i\alpha}$$

↑  
amplitude

← phase



The reflection intensity is proportional to the square of the amplitude factor of the structure:  $I = |\mathbf{F}|^2$

Thus, although the scale of the structure factor can be directly calculated intensity of reflection, the phase can not.

# Phase determination

---

The next step for the determination of molecular structure is to solve the crystallography **Phase Problem**

- ☀ To reconstruct the image you need phases (even if approximate). Therefore is necessary to build a model; we use this model to calculate the reciprocal lattice and compare with the true diffraction data.

There are several methods for solving the structures:

- Direct methods (the most used) - statistical method for determining the phase angles
  - Works in general for all atoms
  - The phase angles are estimated with some probability
- Patterson methods (when there is a heavy atom)
  - Interpretation of interatomic vectors for the determination of the phase angles
  - heavy atoms must be present in the structure

## Electronic density $\rho$

---

**X-rays are scattered by the electrons of the atoms; therefore the result of a determination of structure is the distribution of electrons in the crystal (asymmetric unit)**

The electron density in a crystal is a periodic function.

The electron density map is calculated by a Fourier synthesis:

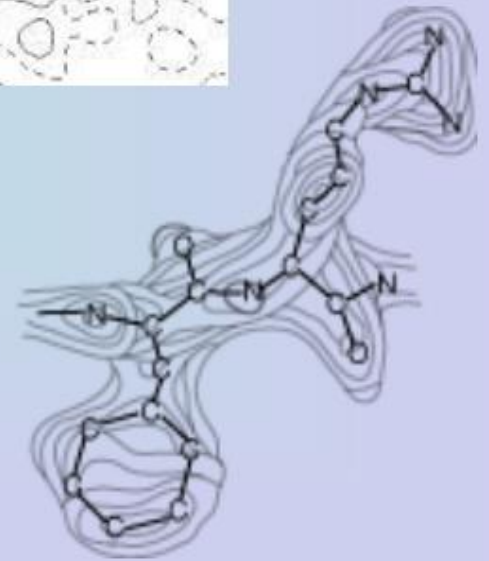
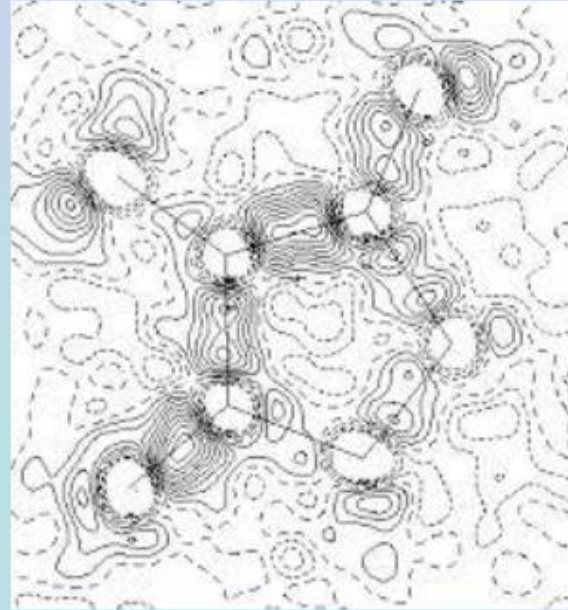
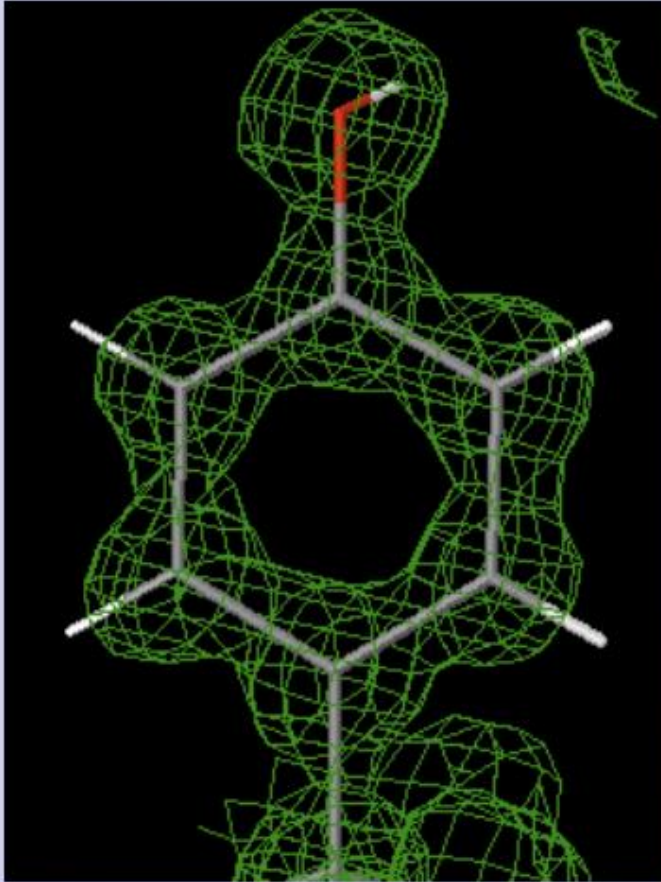
If the intensity and the phase angle of each (structure factor) reflection is known, the E-map means that the crystal structure can be calculated.

$$\rho_{xyz} = (1/V) \sum_{hkl} |F_{hkl}| \exp[2\pi i(hx+ky+lz) + i\alpha_{hkl}]$$

The electron density ( $e/\text{\AA}^3$ ) can be calculated at each point in the asymmetric unit

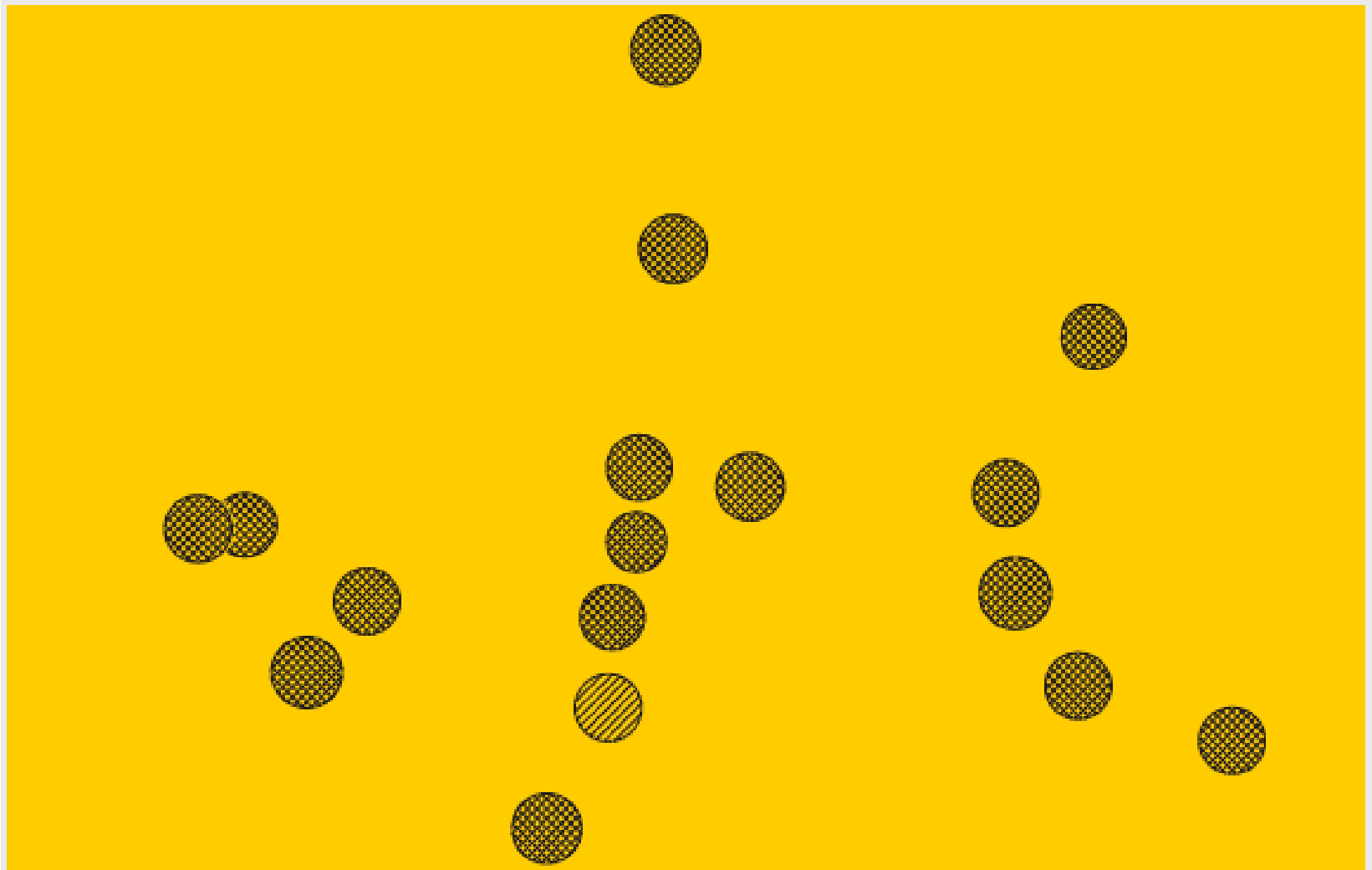


# Electron density maps

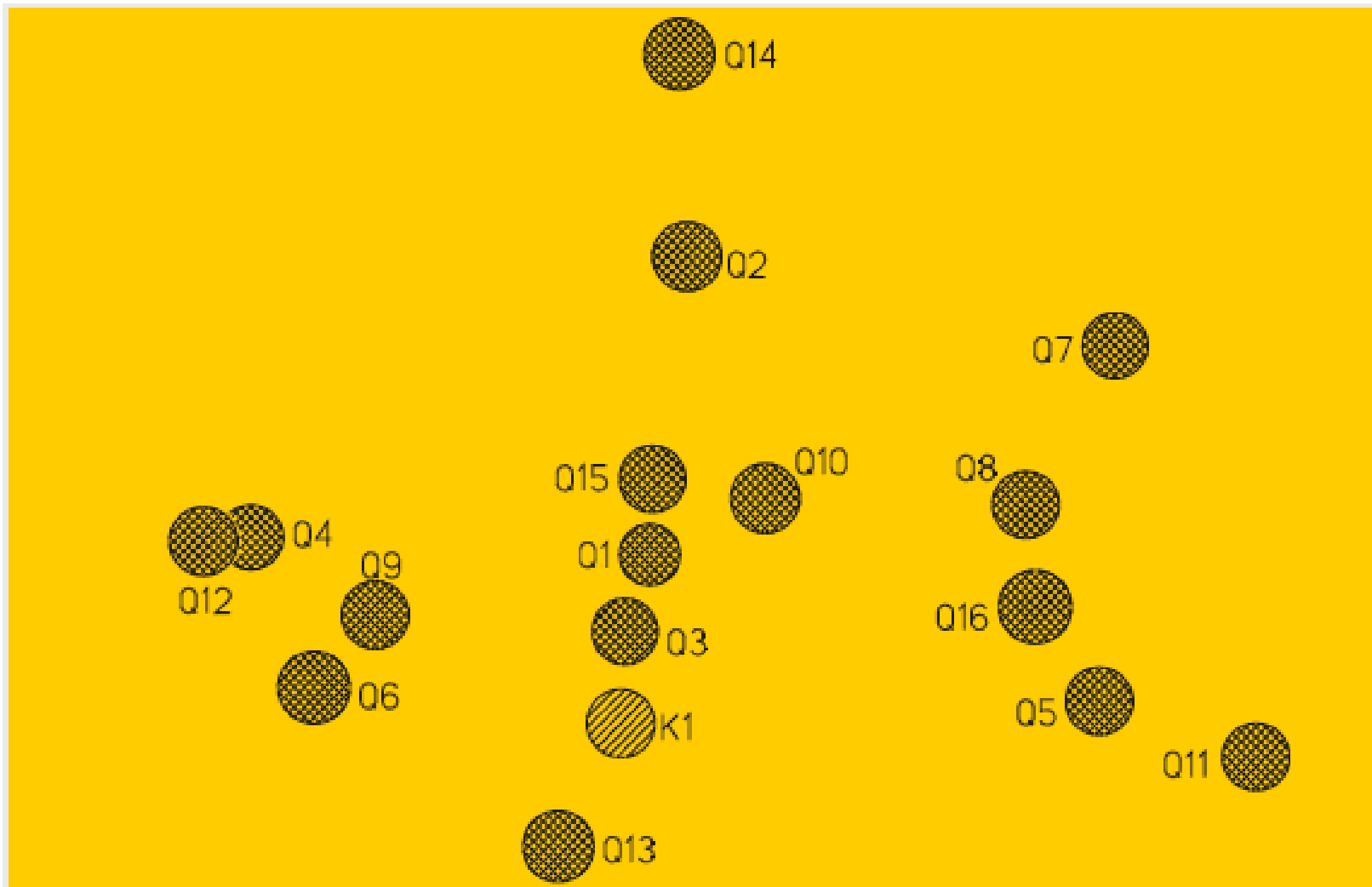


# Assignment of atoms to the maxima in the electron density map

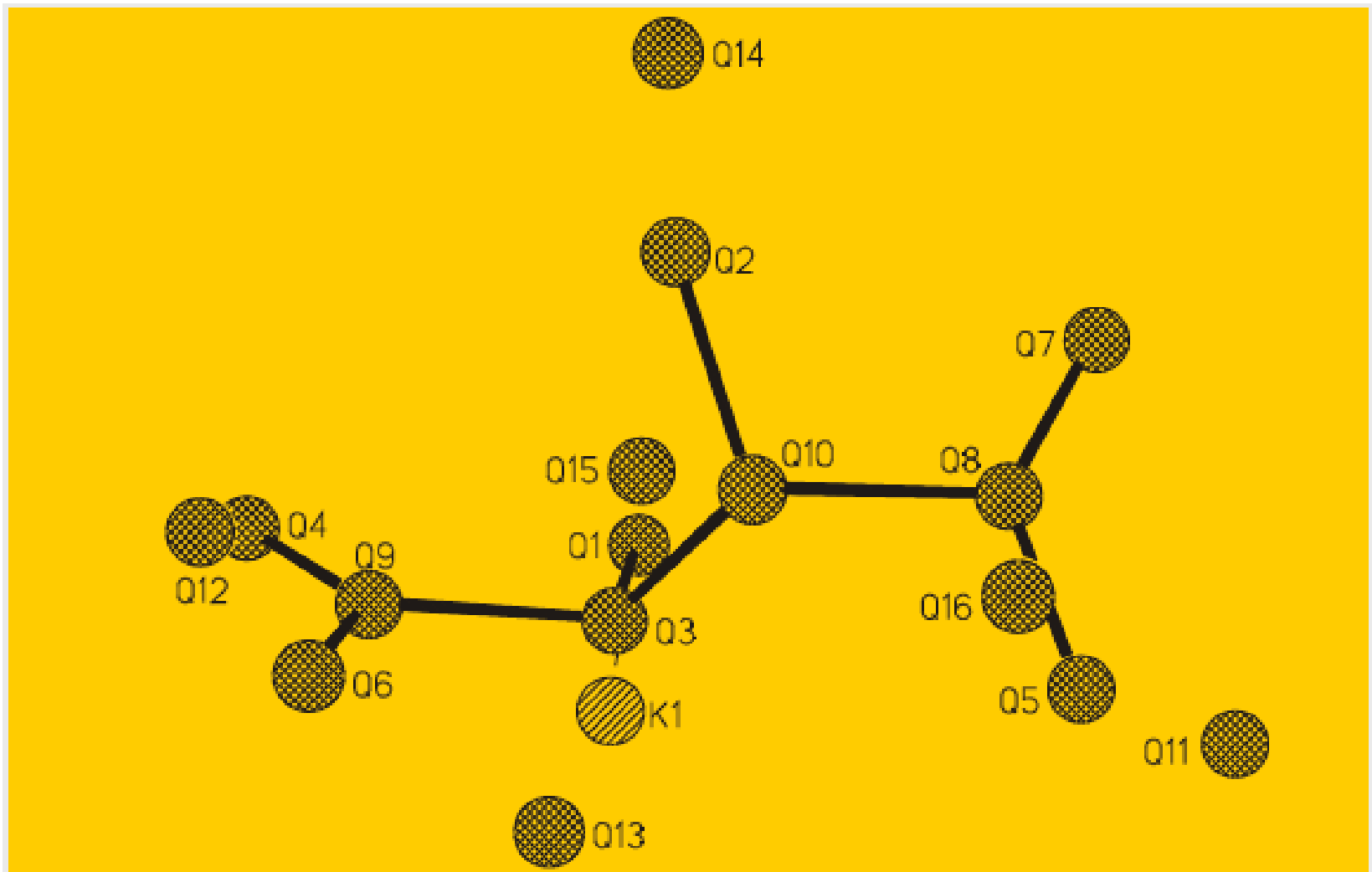
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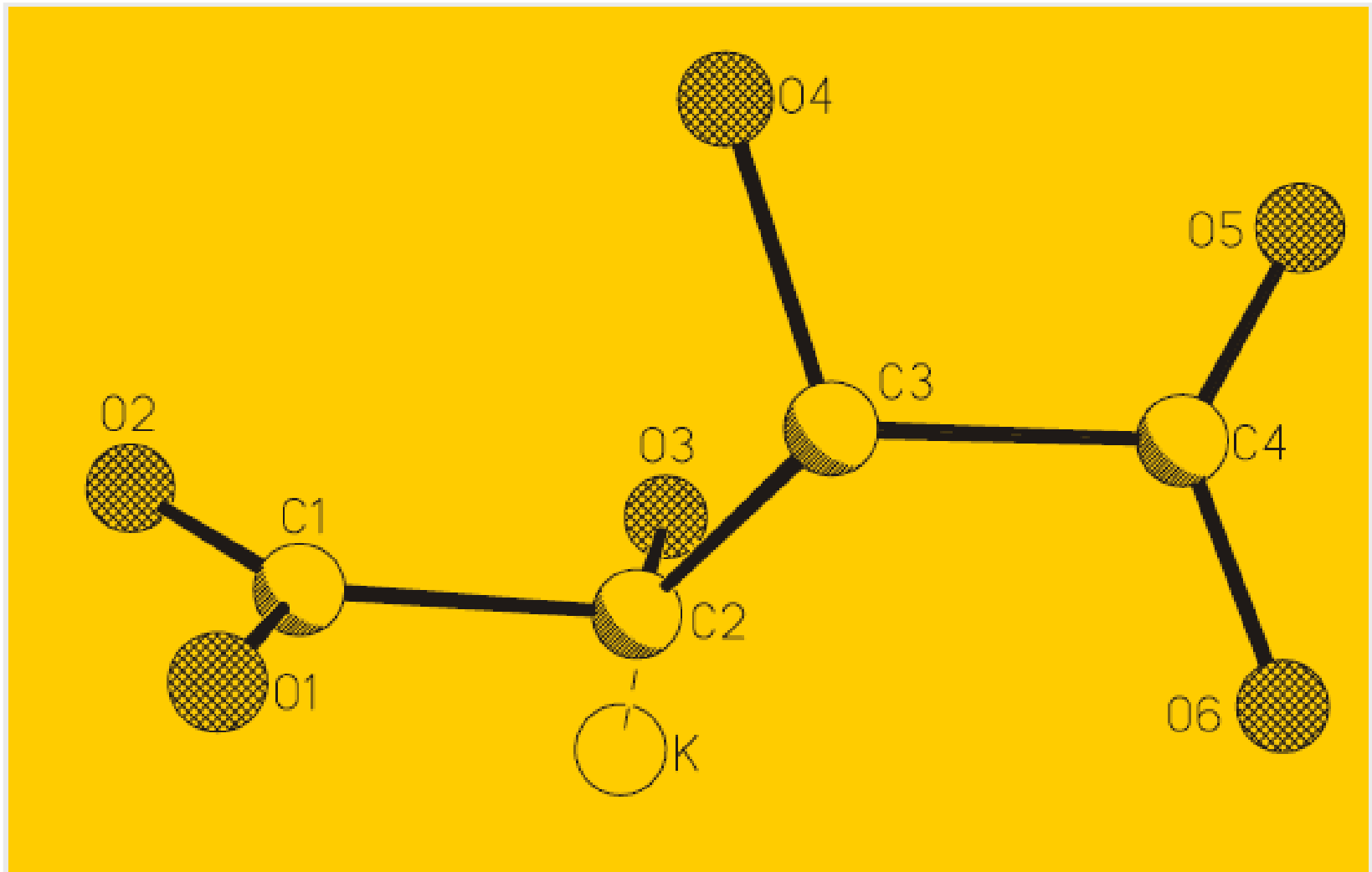
# Assignment of atoms to the maxima in the electron density map



# Assignment of atoms to the maxima in the electron density map



# Assignment of atoms to the maxima in the electron density map



## 6. Refinement - accurate determination of atomic coordinates and temperature factors

Remove some errors in the model through least-squares

- ✓ Atoms are allowed to move slightly from previous positions
- ✓ Thermal factors are applied to each atom

Diffraction pattern calculated  
=  
Experimental diffraction pattern

# Structure refinement

---

- **Problem:**

- The structure model obtained from the E-map contains some errors in the atomic coordinates and therefore, the position of the atoms is inaccurate

- **Solution:**

- Variation of the parameters in a way that the difference between the experimental structure factors and those calculated becomes smaller

- **Method:**

- Method of Least-squares

- Structure refinement

- Which parameters must be refined ?

- 1. Atomic coordinates  $x, y, z$

- 2. Isotropic and anisotropic displacement parameters (A measure for the electron

- distribution of an atom which depends on thermal motion, disorder and the atomic number)

The model is therefore improved to give a better concordance between the structure factors observed and calculated.

Currently, this is done by computer, however the role of the crystallographer is to interpret the result and decide if the changes made are the right ones or if the model got worse!

# R factor

---

- The process of refinement of the structure is followed by the agreement between observed data (data which is acquired in the diffractometer) and calculated data (data calculated from the model). =

## Factor R

$$R = \frac{\sum (|F_{obs}| - |F_{calc}|)}{\sum |F_{obs}|}$$

- R=0% => Perfect agreement between observed and calculated intensities.
- In practice this is not achieved due to random errors in the experimental measurements.
- A good structure should have a factor R smaller than 8%.



## Other statistical factors

---

**$wR_2$**  - R is a weighted factor that uses all the diffraction data and allows the crystallographer follow the refining process. The numerator of  $wR_2$  equation is the function that is minimized in refining.

$$wR_2 = \left\{ \frac{\sum [w (F_o^2 - F_c^2)^2]}{\sum [w (F_o^2)^2]} \right\}^{1/2}$$

**S** - Another statistical factor that is known as the goodness of fit. Theoretically, goodness of fit is "the standard deviation of a observation with a weight 1." In practice the goodness of fit shows how reliable are the deviations of the positional and thermal parameters of atoms. This factor ranges from 0 to 1. For a refinement on F2 the goodness of fit is determined by:

$$GoF = S = \left\{ \frac{\sum [w(F_o^2 - F_c^2)^2]}{(n-p)} \right\}^{1/2}$$

where n = is the number of measured data,

and

p = is the number of parameters.

## The structure is completed when ...

---

1. The bonds in the model must make sense chemically. Similar bonds should have similar geometries, and all distances and bond angles, etc., should have similar values in the literature.
2. There can be no atoms with temperature factors with values too high or too low. Values should range between 00:03 and 00:15 depending on the type of atom.
2.  $R_1$  and end  $wR_2$  The structure must be refined to convergence, i.e., the ratio shift / error should be  $<0.05$ .
4. The goodness of fit,  $S$ , must have a value close to 1.0.
5. The final difference Fourier map should not be very large or very small peaks.
6. Final  $R_1$  and  $wR_2$  values should be reasonably low compared to data quality.

## 7. Validate and check structure

Online service available by the International Union of Crystallography

- ✓ Reports the consistency and integrity of the crystal structure

# Structural analysis

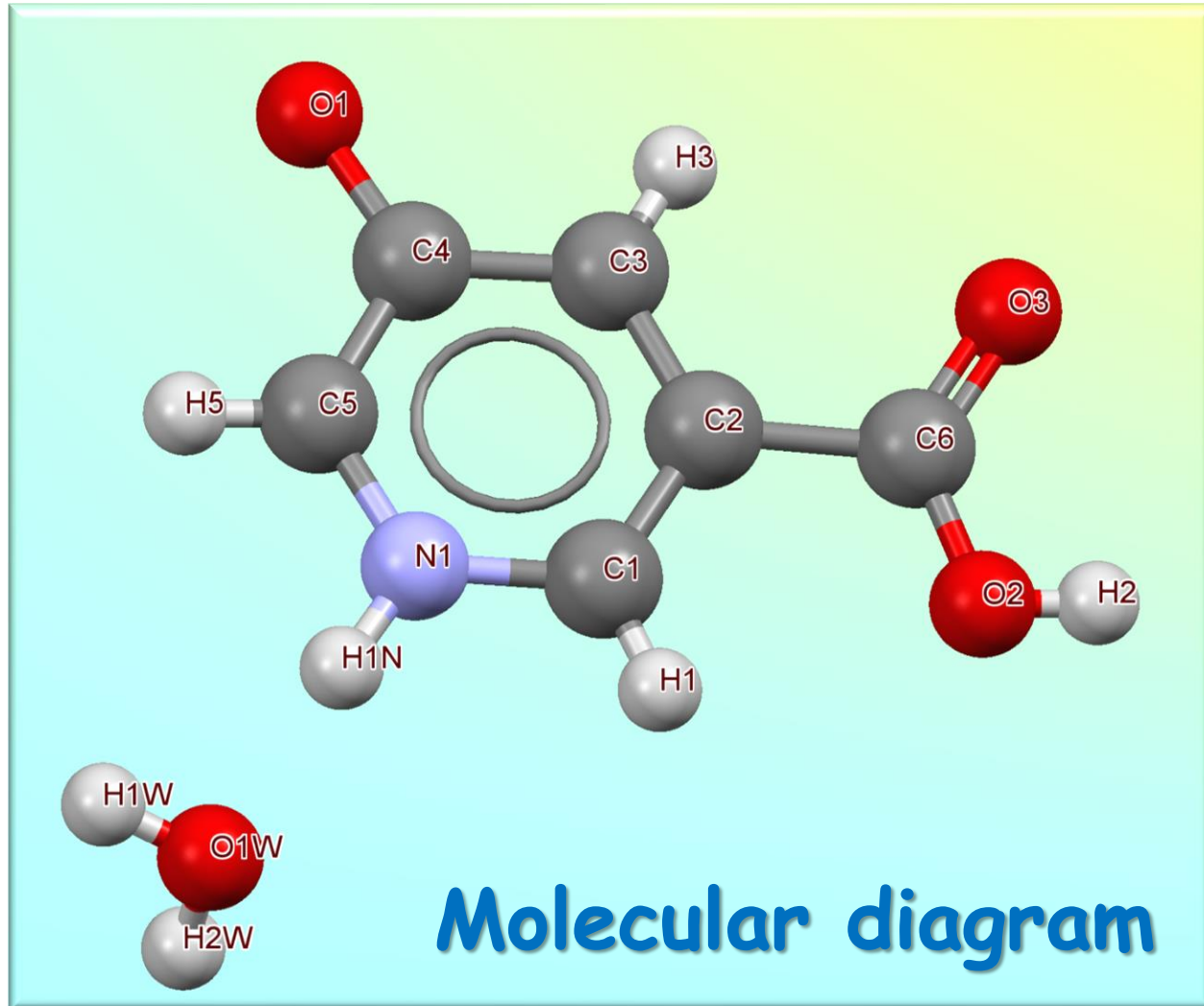
---

What are actually the results of crystal structure determination?

- **Atomic coordinates**
- **Temperature Factors**
- **Unit cell geometry**
- **Unit cell symmetry**
- **Bond lengths**
- **Bond angles**
- **Torsion angles**
- **Ring conformation**
- **Association degree**
- **Intermolecular Interactions (ex: hydrogen bond)**

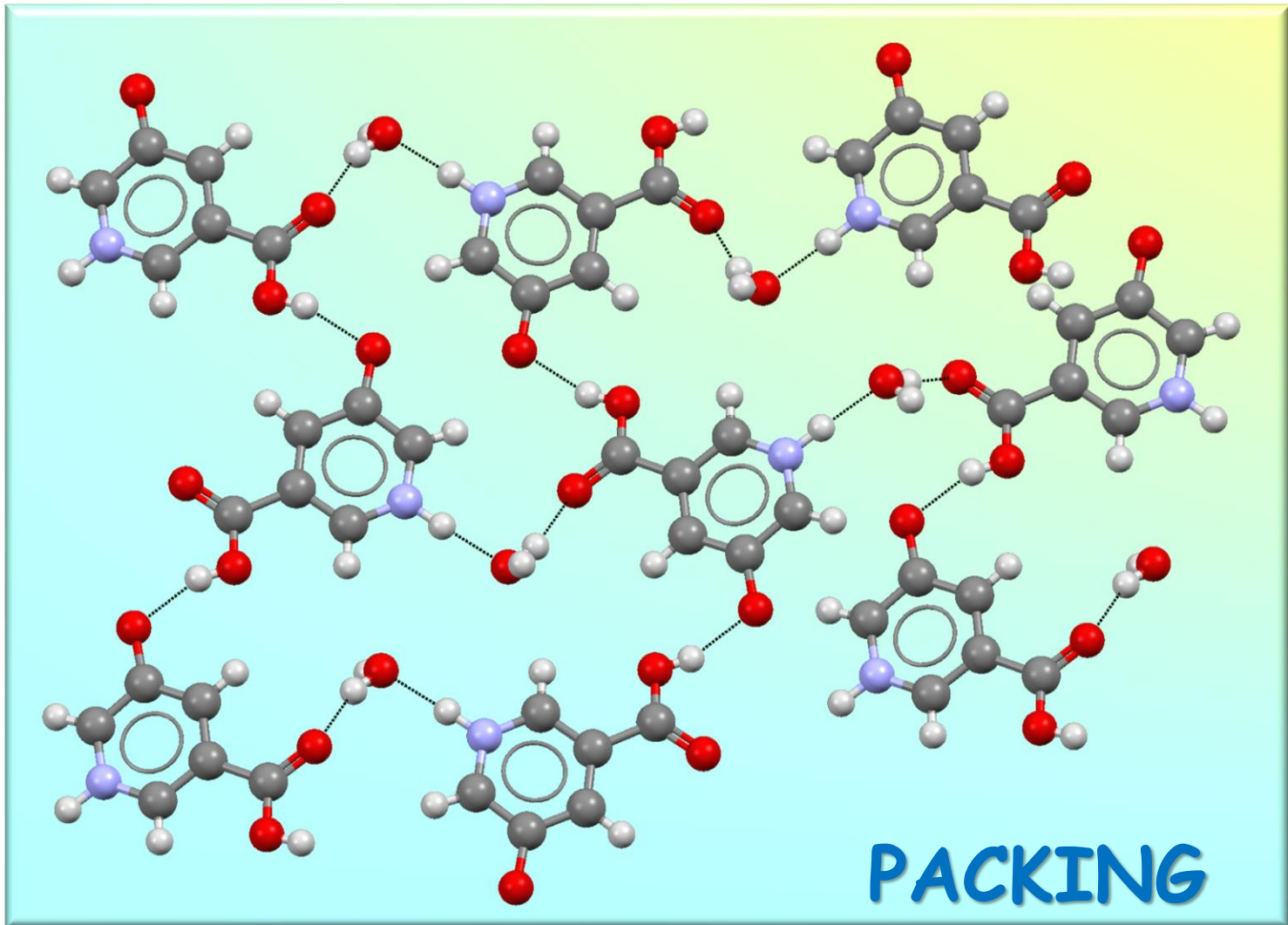
# Structural analysis

What are actually the results of crystal structure determination?



# Structural analysis

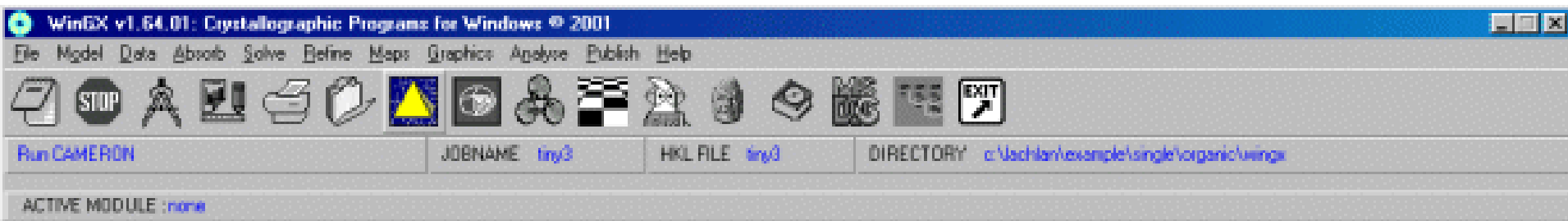
What are actually the results of crystal structure determination?



# Computer programs used in structures determinations

The most used GUI is :

**WinGX – An Integrated System of Windows Programs for the Solution, Refinement and Analysis of Single Crystal X-Ray Diffraction Data**  
de Louis Farrugia, Dept. Of Chemistry, University of Glasgow.



✓ **WinGX** is a system of programs to solve and analyze data refine X-ray diffraction of single crystal, for small molecules.

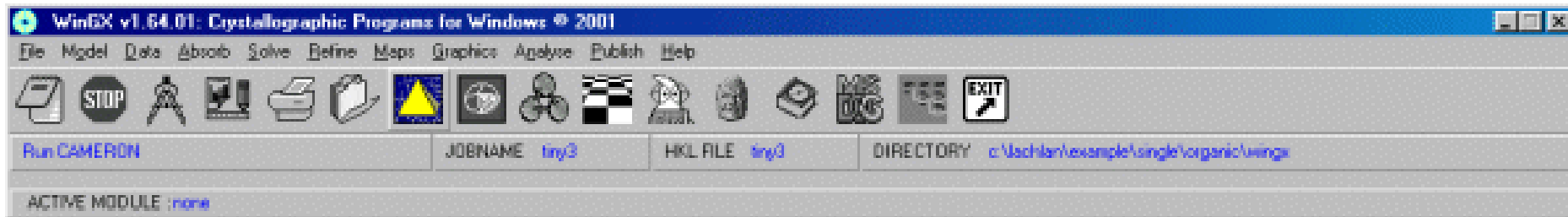
It provides a consistent graphical user interface and easy to use for some of the best crystallography programs available to the public, and has interfaces with other popular programs such as SIR-97 / SIR-2002.

<http://www.chem.gla.ac.uk/~louis/software/wingx>

# Computer programs used in structures determinations

**A interface gráfica mais utilizada é:**

**WinGX – An Integrated System of Windows Programs for the Solution, Refinement and Analysis of Single Crystal X-Ray Diffraction Data**  
**de Louis Farrugia, Dept. Of Chemistry, University of Glasgow.**



✓ It provides a consistent graphical user interface and easy to use for some of the best publicly available crystallographic programs, Such As:

- Data reduction - (CAD4 /Siemens P4/ *KappaCCD*/ *SMART*)
- Data Analysis - Graphics reciprocal network, peak profiles
- Absorption correction (analytical, semi-empirical, ref-DELF)
- Structure resolution - SHELXS Programs, DIRDIF, SIR
- Refinement structure - SHELXL-97 (CRYSTALS / Jana2000)
- Analysis of results - THMA, PLATON, PARST, GEOM
- Graphics - ORTEP, CAMERON (Schakal, RasMol, POV-Ray ...)
- Publication - CIF creation, validation (CIFtbx tools)



# Crystallographic database - Cambridge DataBase

## CONQUEST- The Interface for searching structures in the CSD System .

The screenshot displays the CONQUEST software interface for searching structures in the Cambridge Structural Database (CSD). The main window is titled "CCDC ConQuest (1) : search2 [Search]" and shows a "Combine Hitlists" dialog box. The dialog box has a "Combine Hitlist" section with "Combination Name: combination1", "List A: search1", and "List B: search2". Below this, there are options to "Include deselected entries in:" with checkboxes for "List A" and "List B". The "Generate a List of Entries:" section has three options: "combine to List A and List B", "in either List A or List B", and "in List A but not in List B". The "OK" button is visible at the bottom right of the dialog box.

The main window displays the results for the "nocontact (199 Entries)" search. The text reads: "nocontact (199 Entries) Full overview" and "Entries containing thymine but no interaction with N-H". Below this, there are two chemical structures. The first structure is labeled "Search : search1" and shows a thymine molecule (SMILES: CC1=CNC(=O)NC1=O). The second structure is labeled "Search : search2" and shows a thymine molecule with an N-H group (SMILES: CC1=CNC(=O)NC1=O), with a red line indicating the N-H bond. The word "not" is written in red between the two structures.

At the bottom of the main window, there is a table with columns "Name", "Hits", and "Type". The table contains the following data:

Name	Hits	Type
search2	42	Search
nocontact	199	Combine
search1	241	Search

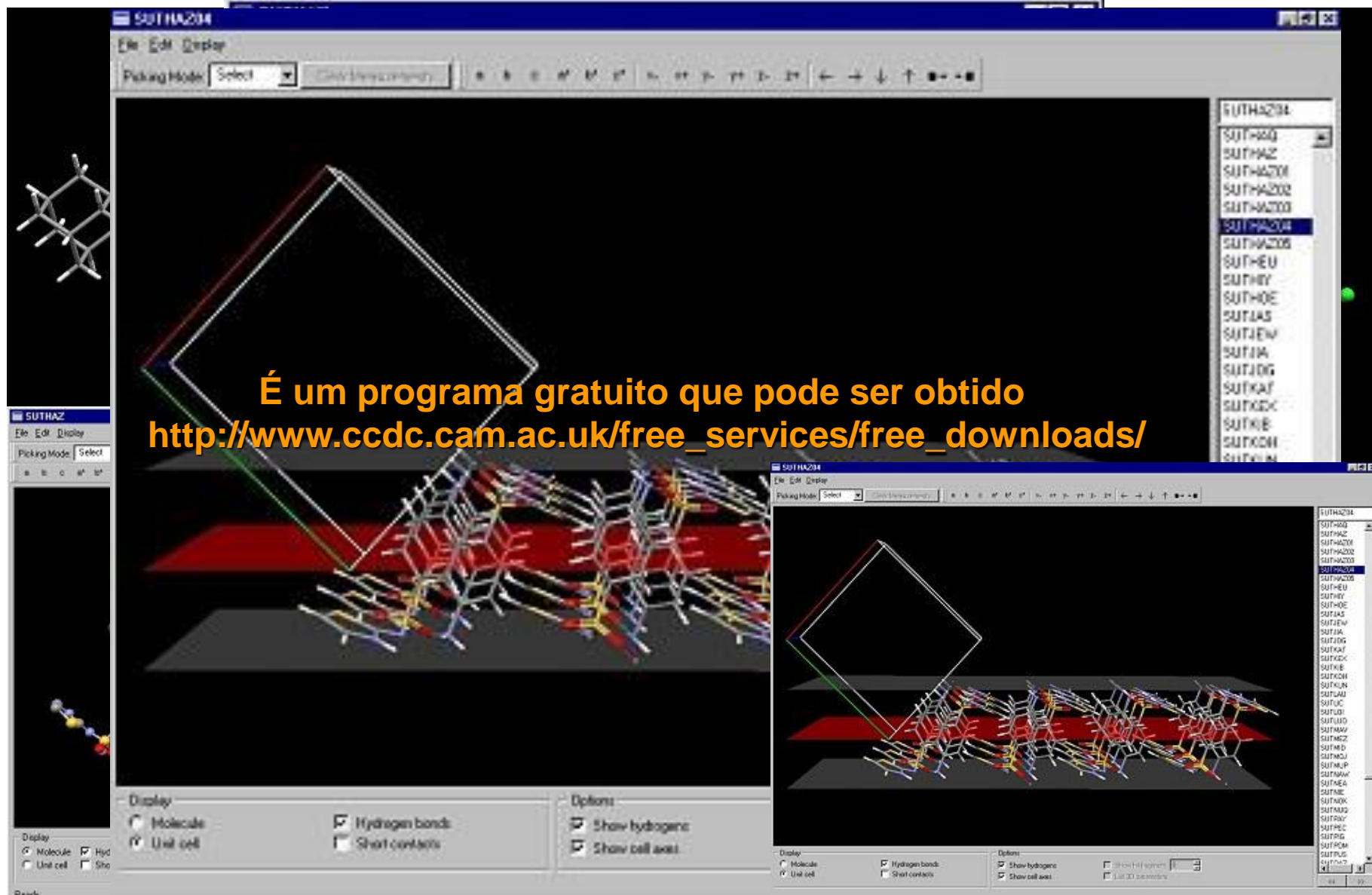
At the bottom of the table, there are buttons for "Delete", "Rename", "Notes...", and "View".

On the left side of the interface, there is a vertical toolbar with buttons for "DRAW", "EDIT", "ERASE", "ADD 3D", and "CONTACT". Below these are icons for "Templates" and "RingMaker".

On the right side of the interface, there is a vertical toolbar with buttons for "Zoom", "Info", and "Search".

# Crystallographic database - Cambridge DataBase

MERCURY- Crystal Structure Visualisation and Exploration Made Easy.



The image displays two overlapping screenshots of the MERCURY software interface. The main window shows a 3D ball-and-stick model of a crystal structure with a red plane and a white unit cell outline. A smaller window in the bottom right shows a list of databases, including SUTHA201, SUTHA00, SUTHA2, SUTHA201, SUTHA200, SUTHA200, SUTHA200, SUTHA204, SUTHA200, SUTHEU, SUTHEU, SUTHEU, SUTHOE, SUTLAS, SUTLEW, SUTIA, SUTJOG, SUTKAT, SUTKDC, SUTKE, SUTKOH, and SUTKOH.

É um programa gratuito que pode ser obtido  
[http://www.ccdc.cam.ac.uk/free\\_services/free\\_downloads/](http://www.ccdc.cam.ac.uk/free_services/free_downloads/)

Display:  Molecule  Unit cell  Hydrogen bonds  Short contacts  Show hydrogen  Show cell axis

## Information in a single crystal structure determination

---

- **Crystal system, Bravais symmetry, space group, lattice parameters**
- **Electronic density and "chemistry composition"**
- **Symmetry of the molecules**
- **Constitution and absolute configuration of the compound**
- **Three-dimensional structure and crystal packing**
- **Precise and sometimes accurate lengths and bond angles**
- **Conformation of molecules (torsion angles)**
- **Intermolecular and intramolecular interactions**
- **Van der Waals Radius**
- **Volume of molecules**
- **Electronic Distribution**
- **Dynamics in crystalline solids**
- **Static and dynamic disorder in crystalline solids**

### Exercise:

The spacing of one set of crystal planes in NaCl (table salt) is  $d = 0.282 \text{ nm}$ . A monochromatic beam of X-rays produces a Bragg maximum when its glancing angle with these planes is  $\theta = 7^\circ$ . Assuming that this is a first order maximum ( $n = 1$ ), find the wavelength of the X-rays.

The Bragg law is

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

$$\lambda = 2d \sin \theta = 2 \times (0.282 \text{ nm}) \times \sin 7^\circ = 0.069 \text{ nm}$$

# Powder X-ray diffraction

Allows :

- Do phase identification
- To detect phase transition
- Follow a reaction path
- Identify and compare molecular and crystal structures
- Study polymorphism
- Study micro and mesoporous materials

*And sometimes*

to **determine** the molecular structure

*(need synchrotron source; accurate equipment)*