

X-Ray Crystallography

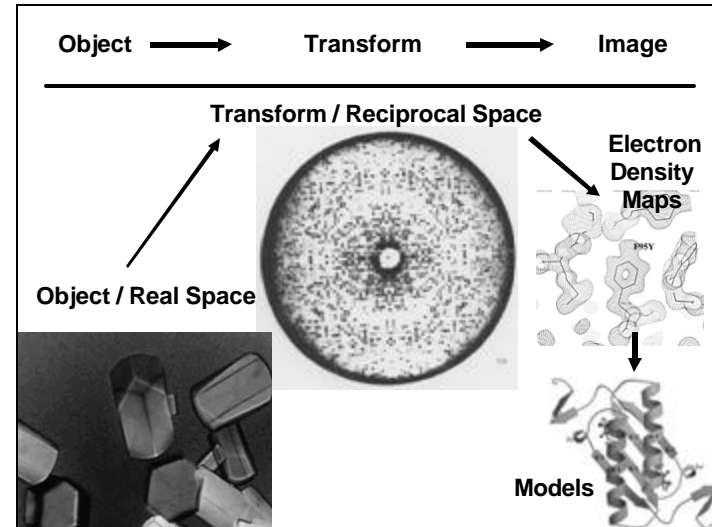
“If a picture is worth a thousand words, then a macromolecular structure is priceless to a physical biochemist.” – van Holde

Topics:

1. Protein Data Bank (PDB)
Data mining and Protein Structure Analysis Tools
2. Image Formation
Resolution / Wavelength (Amplitude, Phase) / Light Microscopy / EM / X-ray / (NMR)
3. X-Ray Crystallography (after NMR)



- e) Data Collection – Methods / Detectors / Structure Factors
- f) Structure Solution – Phase Problem: MIR / MR / MAD
- h) Refinements and Models
- i) Analysis and presentation of results



X-Ray Crystallography

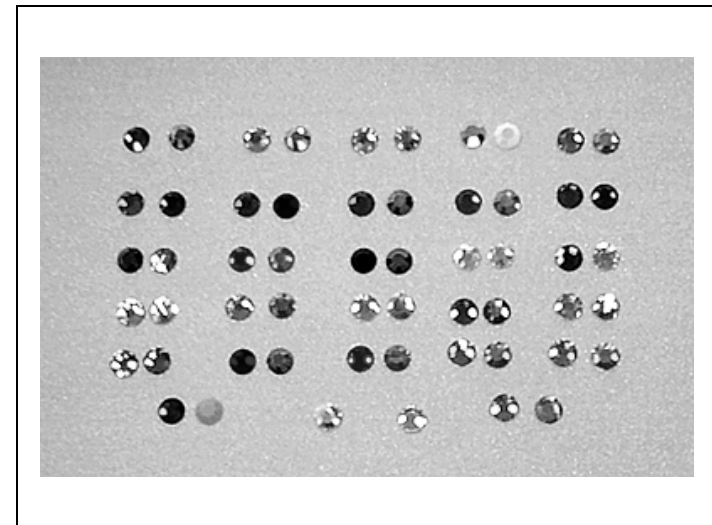
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- b) Crystal Lattices - Lattice Constants / Space Groups / Asymmetric Unit
- c) X-ray Sources – Sealed Tube / Rotation Anode / Synchrotron
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Common Compounds used in Crystallization

Ammonium or sodium sulfate
 Sodium or ammonium citrate
 Sodium or ammonium acetate
 Magnesium sulfate
 Cetyltrimethyl ammonium salts
 Polyethylene glycol 400, 1000, 4000, 6000, 15,000 (now also 2,000, 8,000, etc.)

Methods for protein crystallization

Batch crystallization (simply dump reagents together)
 Liquid-liquid diffusion in a capillary tube
 Vapor diffusion-the most successful method (hanging drop, sitting drop), typically using a Limbro plate. Equilibration occurs between the liquid and vapor phase.
 Dialysis

Hampton Crystal Screen Solutions

☐

Note :

A mini-screen can be set up from the most successful conditions. Those are indicated in the column labeled **Miniscreen**.

- a nice list of [detergents](#) commonly used in crystallization experiments
- [pretty pictures](#)
- [CRYSTCOOL](#) efficient random screen made for you here on the WEB.

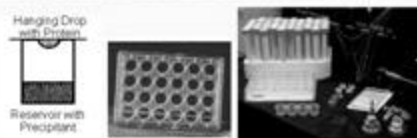
Tube #	SALT	BUFFER	Precipitant	Miniscreen	Tube #
1	0.02M Calcium Chloride	0.1M Na Acetate pH 4.6	30% w/v 2-methyl-2,4-pentanediol	Y	1
2	None	None	0.4M K ₂ Na Tartrate tetrahydrate		2
3	None	None	0.4M Ammonium dihydrogen phosphate		3
4	None	0.1M Tris-HCl pH 8.5	2.0M Ammonium Sulfate	Y	4
5	0.2M Tris-sodium citrate	0.1M Na HEPES pH 7.5	30% w/v 2-methyl-2,4-pentanediol		5
6	0.2M Magnesium chloride	0.1M Tris-HCl pH 8.5	30% w/v PEG 4000		6
7	None	0.1M Na Cacodylate pH 6.5	1.4M Sodium acetate trihydrate		7
8	0.2M Tris-sodium citrate	0.1M Na Cacodylate pH 6.5	30% w/v 2-propanol		8
9	0.2M Ammonium acetate	0.1M Na Citrate pH 5.6	30% w/v PEG 4000	Y	9
10	0.2M Ammonium acetate	0.1M Na Acetate pH 4.6	30% w/v PEG 4000	Y	10
11	None	0.1M Na Citrate pH 5.6	1.0M Ammonium dihydrogen phosphate		11
12	0.2M Magnesium chloride	0.1M Na HEPES pH 7.5	30% w/v 2-propanol		12
13	0.2M Tris-sodium citrate	0.1M Tris-HCl pH 8.5	30% w/v PEG 400		13
14	0.2M Calcium Chloride	0.1M Na HEPES pH 7.5	28% w/v PEG 400	Y (best)	14
15	0.2M Ammonium acetate	0.1M Na Cacodylate pH 6.5	30% w/v PEG 8000		15
16	None	0.1M Na HEPES pH 7.5	1.5M Lithium sulfate monohydrate	Y	16
17	0.2M Lithium sulfate	0.1M Tris-HCl pH 8.5	30% w/v PEG 4000	Y (2nd best)	17



Hanging Drop Method - Crystal Screening

The Experimental Setup

In order to obtain a crystal, the protein molecules must assemble into a periodic lattice. One starts with a solution of the protein with a fairly high concentration (2-30 mg/ml) and adds reagents that reduce the solubility down to spontaneous precipitation. By slow further concentration, and under conditions suitable for the formation of a few nucleation sites, small crystals **may** start to grow. Often, many many conditions have to be tested to succeed. That is usually done by **plate** assessing, followed by a systematic optimization of conditions. Crystals should be for a few tests of a run in each direction to be useful for the diffraction experiments.



Right: The hanging drop technique. Center: 24-well hanging drop experiments are set up in a Labin plate. Right: A lot of different screening solutions, a set up Labin plate, delivery bottles and a micro batch plate behind a glass cover lead.

The most common setup to grow protein crystals is by the **hanging drop** technique. A few microliters of protein solution, are mixed with an about equal amount of reservoir solution containing the precipitants. A drop of this mixture is put on a glass slide which covers the reservoir. As the protein/precipitant mixture in the drop is less concentrated than the reservoir solution, reservoir we used the protein solution with the reservoir solution about 1:1, water evaporates from the drop into the reservoir. As a result the concentration of both protein and precipitant in the drop slowly increases, and crystals may form. There is a variety of other techniques available such as sitting drops, diffusion tubes, and gel and microbatch-techniques. Before we could do the automatic assessing and optimization of crystallization conditions. We have implemented a web computing service of [Hampton Crystal Screen](#), an advanced efficient random screen for crystallization conditions that you can customize. The main advantage is the small sample size a crystallization **screen** can handle reproducibly, but it needs some effort to set it up. Click here to learn more about the [MPLC](#) screen.

Using Oryx 6 for Crystallization with Microbatch

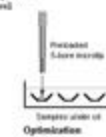
Microbatch operation is identical to [MPLC 1-5](#)

<http://www.douglas.co.uk/oryx.htm>

Very Fast- 240 wells-hour
 over 300 wells-hour for screening



Uses little protein
 0.1 - 1 µl per well



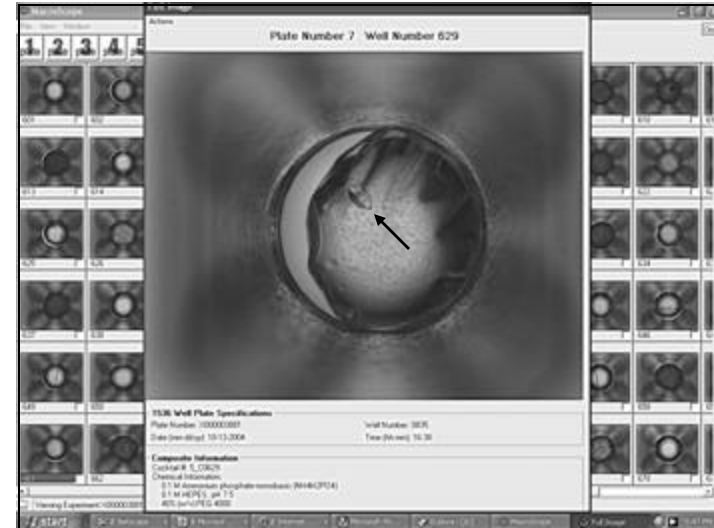
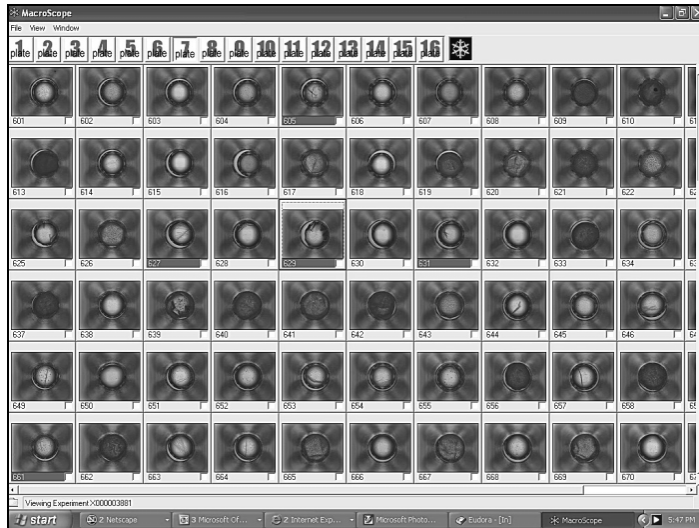
Microbatch screening finds more leads
 than VFD in a given time

	Automated MPLC	Manual VFD
Protein consumed	3	3
Screening conditions	40	40
Time	3	1
Volume per well	1 + 1 µl	4 + 1 µl
Total volume used	900 µl	1170 µl
Condition time	7 hr	24 hr
Crystallization conditions found	40	40
Crystallization conditions	17	13

Large diffraction
 crystals



90 series crystals for X-ray data collection for 10 years and was awarded the 1997 Nobel Prize in Chemistry. Oryx 6 is a 240 well microbatch crystallization robot. Oryx 6 is a 240 well microbatch crystallization robot. Oryx 6 is a 240 well microbatch crystallization robot.



His J- His complex:

Tetanus Toxin C Fragment:

http://www.ccp14.ac.uk/ccp/web-mirrors/lnlrupp/crystal_lab/Cryst_lab.html

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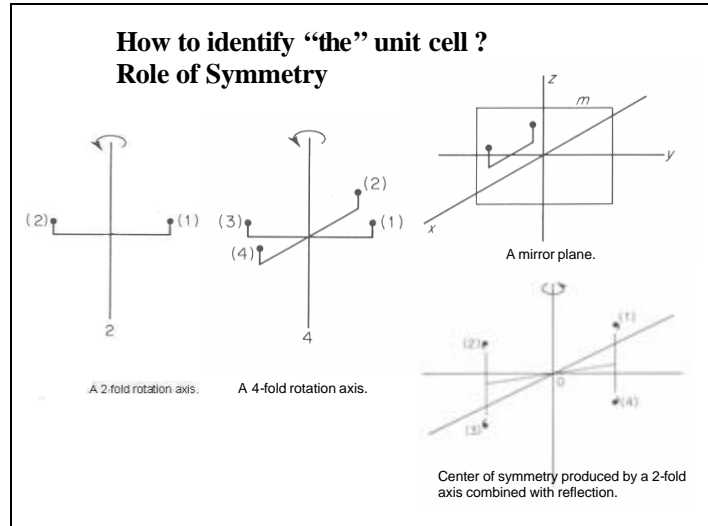
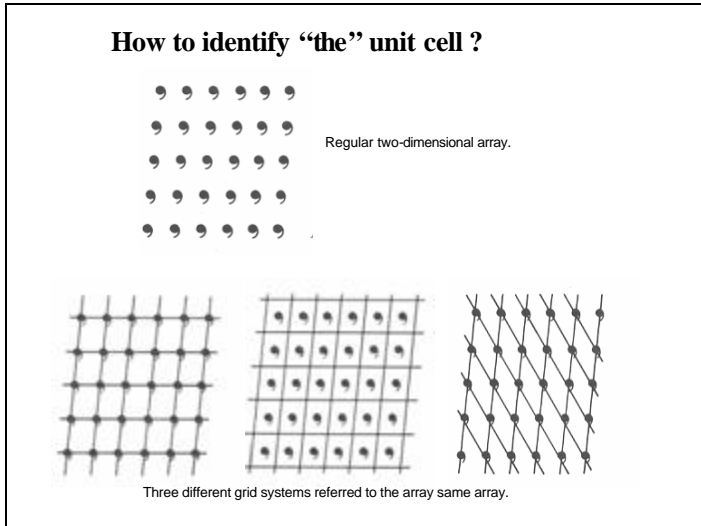
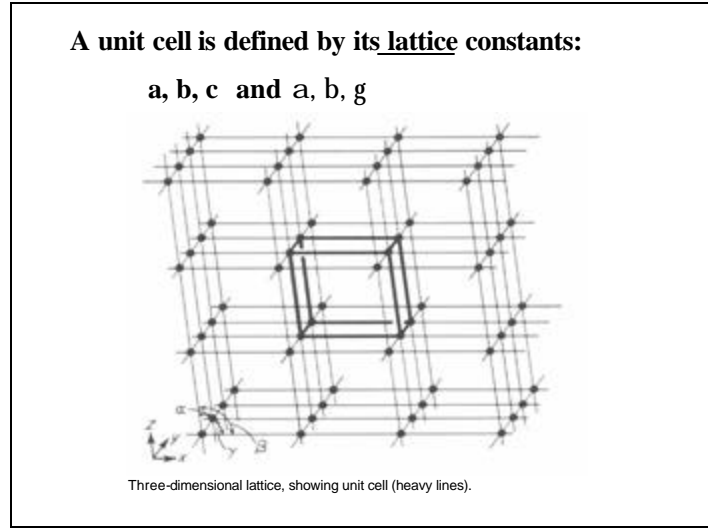
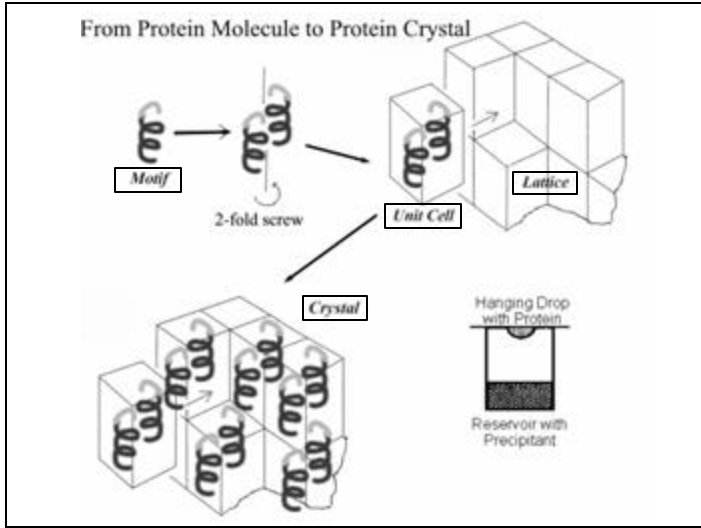


TABLE 18-5 The 65 "Biological" Space Groups

CRYSTAL SYSTEM	LATTICE	MINIMAL SYMMETRY OF UNIT CELL	UNIT CELL EDGES AND ANGLES ^a	DIFFRACTION PATTERNS SYMMETRY ^b	SPACE GROUP ^c
Triclinic	P	None	$a \neq b \neq c$ $\alpha \neq \beta \neq \gamma$	1	P1
Monoclinic	P	2-fold axis parallel to b	$a \neq b \neq c$ $\alpha = \beta = \gamma = 90^\circ$	2m	P2, P2 ₁ , C2
	C				
Orthorhombic	P	3 mutually perpendicular 2-fold axes	$a \neq b \neq c$ $\alpha = \beta = \gamma = 90^\circ$	mmm	P22 ₂ , P2 ₂ 2 ₁ , P22 ₁ , P2 ₁ 2 ₂ , C22 ₂ , C22 ₁ , (P22 ₂ , P2 ₁ 2 ₁)
	C				
	F				
Tetragonal	P	4-fold axis parallel to c	$a = b \neq c$ $\alpha = \beta = \gamma = 90^\circ$	4m	P4, P4 ₁ , P4 ₂ , P4 ₃ , I4, I4 ₁
	F			4mm	P42 ₁ , P42 ₂ , P42 ₁ 2 ₁ , P42 ₂ 2 ₁ , P42 ₁ 2 ₁ , P42 ₂ 2 ₁ , P42 ₁ 2 ₁
Trigonal/rhombohedral	R ^d	3-fold axis parallel to c	$a = b \neq c$ $\alpha = \beta = \gamma = 120^\circ$	3	R3
	R ^e			3m	R3 ₂ , R3 ₁ , R3 ₁ , R3 ₂ , R3 ₁ , R3 ₂ , R3 ₁ , R3 ₂ , R3 ₁ , R3 ₂ , R3 ₁ , R3 ₂
Hexagonal	P	6-fold axis parallel to c	$a = b \neq c$ $\alpha = \beta = 90^\circ$ $\gamma = 120^\circ$	6/m	P6, (P6 ₁ , P6 ₅)
	F			6/mmm	P6 ₁ , (P6 ₁ , P6 ₅) P62 ₂ , (P62 ₂ , P62 ₂) P63 ₂ , (P63 ₂ , P63 ₂) P63
Cubic	P	3-fold axes along cube diagonals	$a = b = c$ $\alpha = \beta = \gamma = 90^\circ$	m3	P2 ₁ (I23, I213)
	I				I23
	F			m3m	P432, (P432, P432) P432 I432, I432 F432, F432

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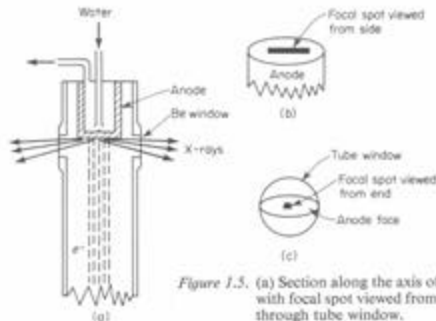
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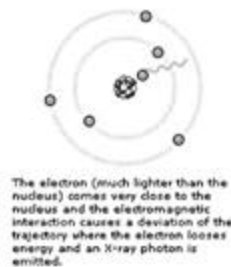
X-ray tubes: the "sealed" tube



Origin of Non-characteristic X-rays

Bremsstrahlung X-rays

In an X-ray tube the electrons emitted from the anode are accelerated towards the metal target cathode by an accelerating voltage of typically 50 kV. The high energy electrons interact with the atoms in the metal target. Sometimes the electron comes very close to a nucleus in the target and is deviated by the electromagnetic interaction. In this process, which is called bremsstrahlung (braking radiation), the electron loses much energy and a photon (X-ray) is emitted. The energy of the emitted photon can take any value up to a maximum corresponding to the energy of the incident electron.



Origin of characteristic X-rays

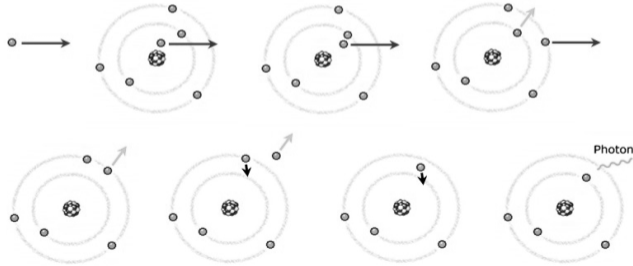
Related Laureate



The Nobel Prize in Physics 1917 - Charles Glover Barkla »

Characteristic X-ray Lines

The high energy electron can also cause an electron close to the nucleus in a metal atom to be knocked out from its place. This vacancy is filled by an electron further out from the nucleus. The well defined difference in binding energy, characteristic of the material, is emitted as a monoenergetic photon. When detected this X-ray photon gives rise to a characteristic X-ray line in the energy spectrum. C. Barkla observed these lines in 1908-09 and was given the 1917 Nobel Prize for this discovery. He also made the first experiments suggesting that the X-rays are electromagnetic waves.



Characteristic X-rays arise from electronic transitions

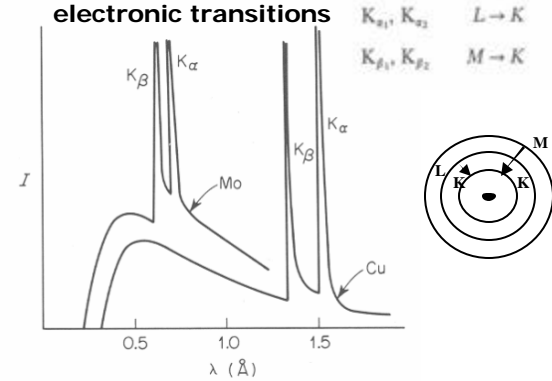


Figure 1.2. X-ray spectra with characteristic peaks: MoK α , 50 Kv; CuK α , 35 Kv.

Characteristic X-rays have defined l

Table 1.1. Target Materials and Associated Constants

	Cr	Fe	Cu	Mo
Z	24	26	29	42
α_1 , Å	2.2896	1.9360	1.5405	0.70926
α_2 , Å	2.2935	1.9399	1.5443	0.71354
$\bar{\alpha}$,* Å	2.2909	1.9373	1.5418	0.71069
β_1 , Å	2.0848	1.7565	1.3922	0.63225
β , filt.	V, 0.4 mil†	Mn, 0.4 mil	Ni, 0.6 mil	Nb, 3 mils
α , filt.	Ti	Cr	Co	Y
Resolution, Å	1.15	0.95	0.75	0.35
Critical potential, kV	5.99	7.11	8.98	20.0
Operating conditions, kV:	30-40	35-45	35-45	50-55
half- or full-wave-	10	10	20	20
rectified, mA				
constant potential, mA	7	7	14	14

* $\bar{\alpha}$ is the intensity-weighted average of α_1 and α_2 and is the figure usually used for the wavelength when the two lines are not resolved.

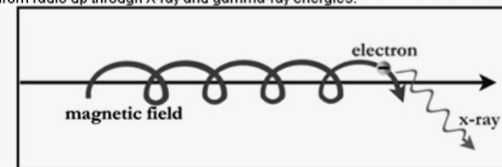
† 1 mil = 0.001 inch = 0.025 mm.

Another Source of "X-rays"

Synchrotron Radiation

X-ray photons can also be created under different conditions. When physicists were operating the first particle accelerators, they discovered that electrons can produce photons without colliding at all. This was possible because the magnetic field in the accelerators was causing the electrons to move in large spirals around magnetic field lines of force. This process is called synchrotron radiation.

In the cosmos particles such as electrons can be accelerated to high energies— near the speed of light— by electric and magnetic fields. These high-energy particles can produce synchrotron photons with wavelengths ranging from radio up through X-ray and gamma-ray energies.



Synchrotron Radiation: Electrons moving in magnetic field radiate photons.

“X-ray” Sources: Beyond X-ray tubes

The **brilliance** of a light source is defined as the number of photons emitted per second, per unit source size, per unit open angle and for a bandwidth of 1/1000 of the photon energy.

The comparison between various sources of X-rays shows large differences in their brilliance.

X-ray tubes

While Conrad Roentgen discovered X-rays in 1895 while working with cathode-ray tubes. Using the principle of fast electrons hitting a metallic target, a first substantial gain in brilliance was not obtained until the introduction of rotating anode sources (~1980).

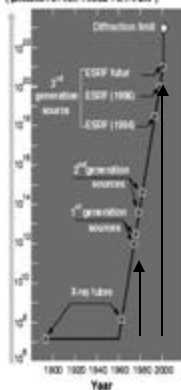
Synchrotron Radiation Facilities

The progress of high energy physics, with the construction of powerful particle accelerators gave birth to what we now call third generation synchrotron sources (~1970). Using the deflection of high energy electrons by a magnetic field for the production of X-rays proved as promising that a number of dedicated second generation sources were built (~1980). Relying on the combination of undulators and insertion devices, third generation synchrotron sources (~2000) are now emitting synchrotron X-ray beams that are a billion (10^9) times more brilliant than those produced by X-ray tubes.

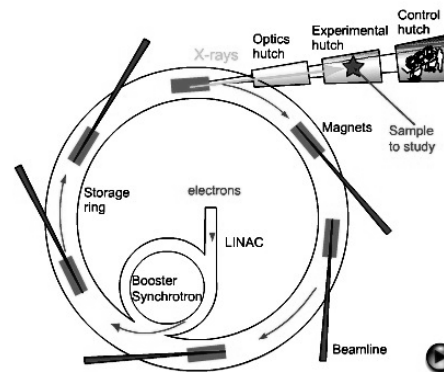
Free Electron X-ray Lasers

Coupling electron and X-ray beams together, the Free Electron X-ray Lasers currently on the drawing boards could be the next generation of X-ray sources. While they promise to achieve an increase in peak brilliance by another factor of a billion, the first prototypes may be operational around the year 2010.

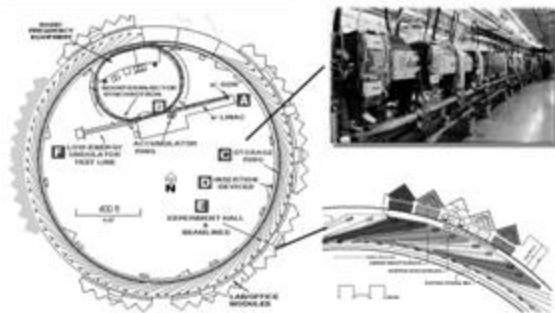
Brilliance of the X-ray beams
(photons / s / mm² / mrad² / 0.1% BW)



How synchrotron light is produced?



APS - Advanced Photon Source
Argonne National Laboratory



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X-RAYS
Bragg, What Are They? 6-7

More About the Bragg Formula

X-rays scattered from different layers of atoms can interfere with each other. The interference depends on the wavelength of the X-ray and on the distance between the atom layers. An X-ray with well-known wavelength can be used to explore the structure of the crystal. For a well-known crystal, the X-ray properties can be examined.

$d = 0.3 \text{ nm}$

Crystal planes, in NaCl, ordinary salt. Other planes are also possible.

X-ray scattering from three crystal planes, separated by the distance d . For constructive interference in a direction θ the path difference must be an even number of wavelengths.

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

Related Laureates

The Nobel Prize in Physics 1915 - Sir William Henry Bragg >

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The Nobel Prize in Physics 1901 - Wilhelm Conrad Röntgen >	The Nobel Prize in Physics 1914 - Max von Laue >	The Nobel Prize in Physics 1915 - Sir William Henry Bragg >
The Nobel Prize in Physics 1915 - William Lawrence Bragg >	The Nobel Prize in Physics 1917 - Charles Glover Barkla >	The Nobel Prize in Physics 1924 - Karl Manne Georg Siegbahn >
The Nobel Prize in Physics 1927 - Arthur Holly Compton >	The Nobel Prize in Chemistry 1916 - Paul Peter Rudolph Debye >	The Nobel Prize in Chemistry 1942 - Max Ferdinand Perutz >
The Nobel Prize in Chemistry 1962 - John Cowdery Kendrew >	The Nobel Prize in Chemistry 1962 - Francis Harry Compton Crick >	The Nobel Prize in Physiology or Medicine 1962 - James Dewey Watson >
The Nobel Prize in Physiology or Medicine 1962 - Maurice Hugh Frederick Wilkins >	The Nobel Prize in Physiology or Medicine 1962 - Dorothy Crowfoot Hodgkin >	The Nobel Prize in Physiology or Medicine 1976 - William K. Lipscomb >
The Nobel Prize in Physiology or Medicine 1979 - Allan M. Cormack >	The Nobel Prize in Physiology or Medicine 1979 - Godfrey H.ounsfield >	The Nobel Prize in Physics 1991 - Kai M. Siegbahn >
The Nobel Prize in Chemistry 1985 - Herbert A. Hauptman >	The Nobel Prize in Chemistry 1985 - Jenö Károlyi >	The Nobel Prize in Chemistry 1988 - Johann Drenth >
The Nobel Prize in Chemistry 1988 - Robert Huber >	The Nobel Prize in Chemistry 1988 - Hartmut Michel >	

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Image Formation
Abbe (~1873):
Limit Res. $\sim \lambda/2$

- Light Photography
 $l \sim 400 - 700 \text{ nm}$
- Electron Microscopy
 $l \sim 0.001 - 0.1 \text{ nm}$
- X-Ray or NMR
 $l \sim 0.1 \text{ nm}$

SOURCE **SCATTERING** **RECOMBINATION** **EXAMPLE**

OBJECT **LENS** **IMAGE**

light source object lens image

object slit image

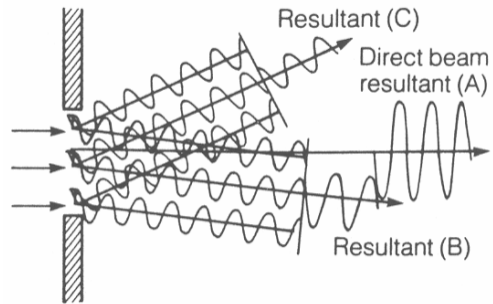
micro-magnetic lens

diffraction pattern

crystal X-ray film calculated image

Single Hole Scattering Experiment

Transforms / Reciprocal Space



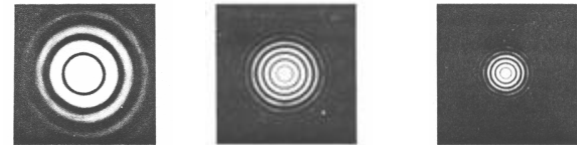
(b)

Single Hole Scattering Experiment

Transforms / Reciprocal Space

Different size holes

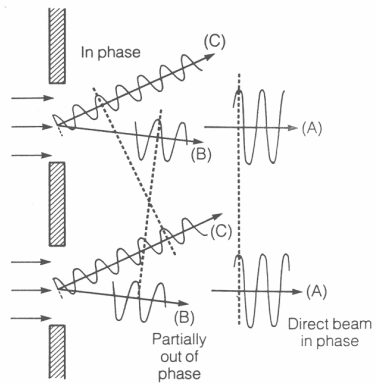
(a) • (b) • (c) •



(a) (b) (c)

Effect of Multiple "Scatterers"

Transforms / Reciprocal Space

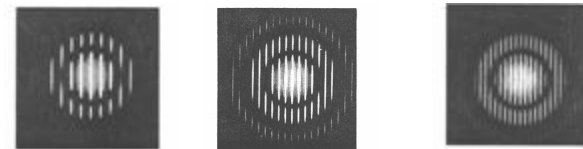


(c)

Transforms / Reciprocal Space

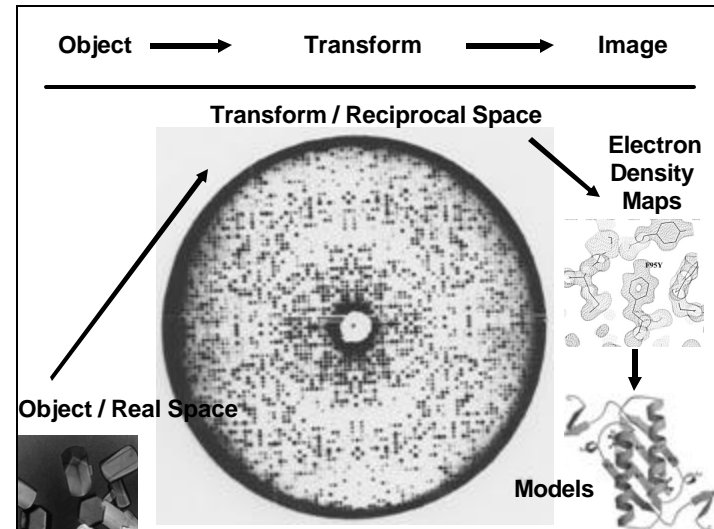
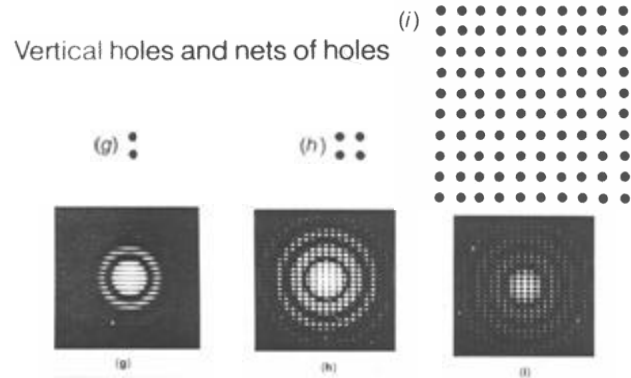
Five horizontal holes with various spacings

(j) ••••• (k) ••••• (l) • • • • •



(j) (k) (l)

Transforms / Reciprocal Space



Kevin Cowtan's Book of Fourier Transformations

Kevin Cowtan's Book of Fourier

This is a book of pictorial 2-D Fourier Transforms. These are particularly relevant to my own field of X-ray crystallography, but should be of interest to anyone involved in signal processing or frequency domain calculations.

<http://www.ysbl.york.ac.uk/~cowtan/fourier/fourier.html>

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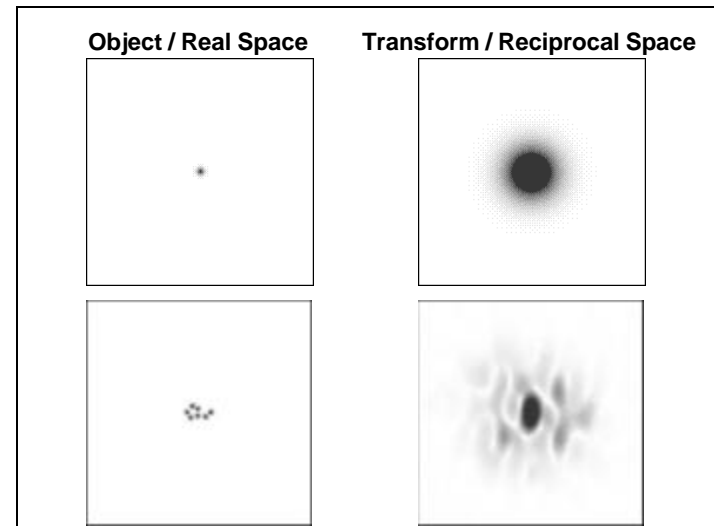
- Introduction
- Book of Convolutions
- Dock Tables and missing data.
- A Little Animal Maps and cross phasing.
- A Tale of Two Cities and image restoration.
- Animal Liberation and free-ions.
- The Gallery: Other interesting pictures.

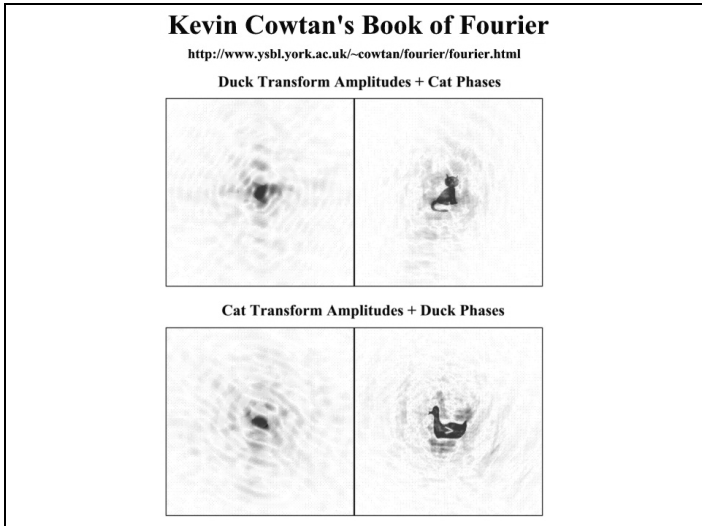
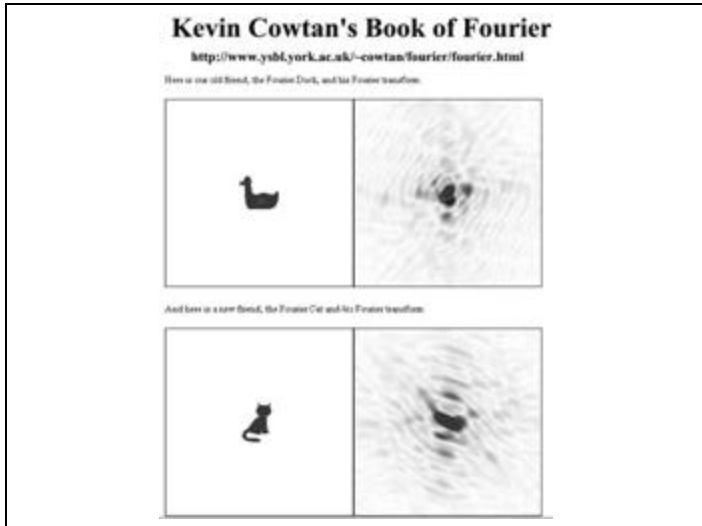
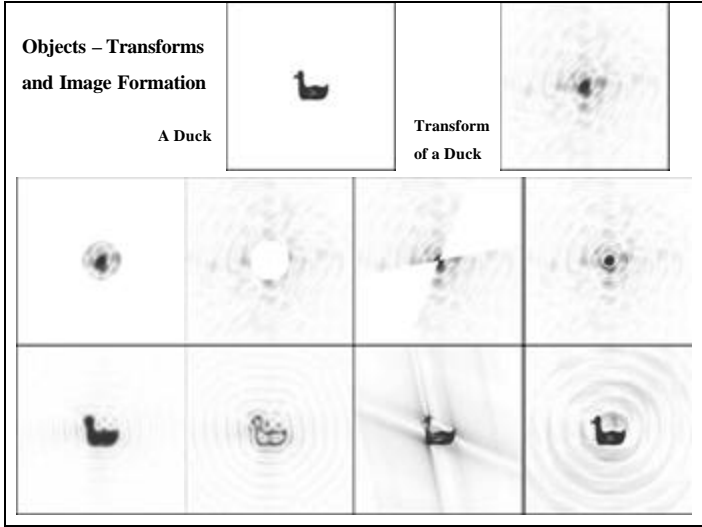
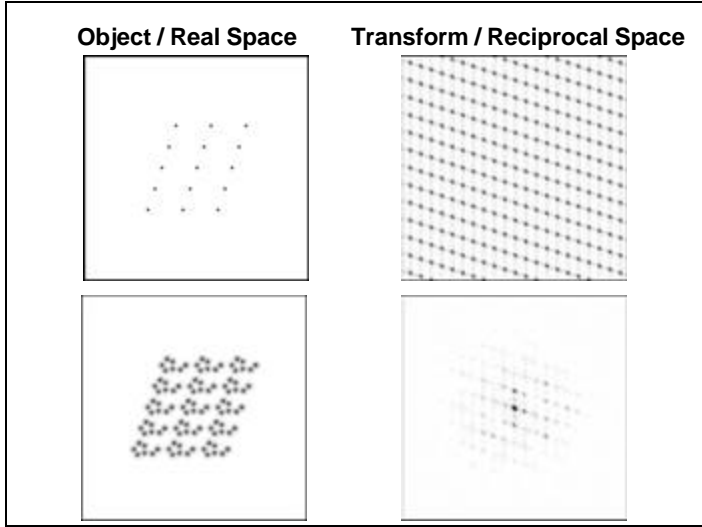
Other topics:

The Interactive Structure Factor Tutorial: Learn about structure factors and maps.

An introduction to crystallography: [Fourier transforms](#): The mathematical link between [scattering theory](#) and Fourier theory. An explanation of the [convolution theorem](#).

Teaching materials elsewhere





Kevin Cowtan's Book of Fourier

<http://www.york.ac.uk/~cowtan/fourier/fourier.html>

