X-ray Crystallography

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Introduction

When X-rays strike a crystal, they are diffracted by the ordered atoms in the crystal, via elastic scattering from the electrons. Measurements of the angles and intensities of these diffracted rays are used to obtain the three-dimensional arrangement of the atoms. This is called X-ray crystallography, and this technique is widely used to determine the structure of a variety of organic, inorganic and biological substances. A timeline of major discoveries and advances in X-ray crystallography is shown in Table 1 below.

Year(s)	*Discovery/Advance*	*Notes*
1895	X-rays discovered by Wilhelm Röntgen	First Nobel Prize in Physics (1901)
1912	Diffraction of X-rays by crystals discovered by Paul Ewald and Max von Laue	Nobel Prize in Physics (1914) to von Laue for working out the relationship between diffraction angles and unit cell parameters
1912-1913	William Lawrence Bragg develops an equation for determining spacings between crystal planes by X-ray diffraction	Nobel Prize in Physics (1915) to Bragg and his father, William Henry Bragg, for their contributions to X-ray crystallography
1940s-1960s	Dorothy Crowfoot Hodgkin obtains the crystal structures of several important small biomolecules by X-ray crystallography	Nobel Prize in Chemistry (1964)
2000s	Structures of large molecules (~10^5 g/mol) routinely solved by X-ray crystallography	Mostly made possible by prodigious improvements in computer technology

Table 1. *Timeline of developments in X-ray crystallography.*

Single-crystal X-ray diffraction patterns are obtained using a diffractometer. A schematic diagram of one is shown in Fig. 1(a) below. The diffraction pattern (angles, positions and intensities) of spots on the detector screen obtained by rotating the single crystal mounted on a goniometer is analyzed by computer to provide the arrangements of atoms in the crystal, called

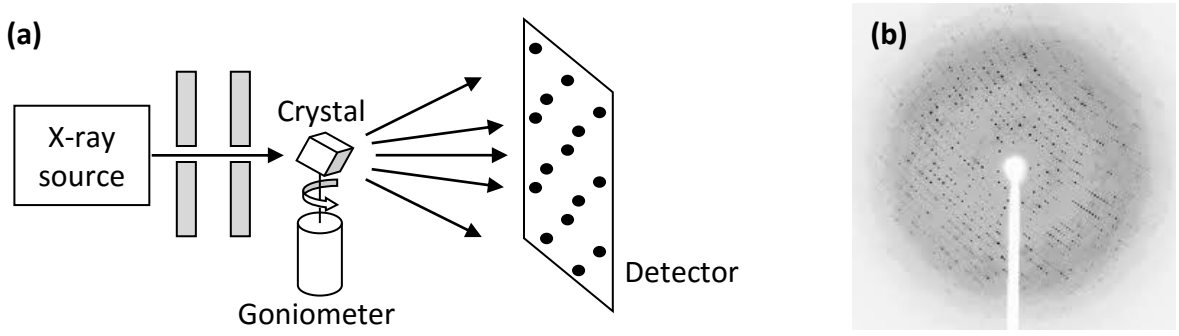


Figure 1. *(a) Schematic diagram of a single crystal X-ray diffractometer. (b) A sample diffraction pattern (adapted from http://departments.colgate.edu/chemistry).*

"solving the crystal structure." Hundreds of thousands of crystal structures of elements, metals, alloys, organic molecules, inorganic complexes, biological molecules and other chemical entities have been solved by X-ray crystallography. Besides providing fundamental physical data such as bond lengths, bond angles and atomic radii, these structures have yielded insights into the very nature of chemical bonding and the relationship between chemical structure and function.

The number of solved structures increases every year, and there exist journals devoted to nothing but crystal structure reports. These structural data are often freely available for research and study, commonly as a standard Crystallographic Information File (CIF), from the major international crystal structure databases shown in Table 2 below.

Crystallography Database	*Scope and Content*
Cambridge Structural Database, CSD http://www.ccdc.cam.ac.uk/products/csd/	Small organics and organometallics
Crystallography Open Database, COD http://www.crystallography.net	Small organics and organometallics, inorganics, and minerals
Protein Data Bank, PDB http://www.rcsb.org/pdb/	Proteins, polypeptides and polysaccharides
Nucleic Acid Database, NDB http://ndbserver.rutgers.edu/	Oligonucleotides
Inorganic Crystal Structure Database, ICSD http://www.fiz-karlsruhe.de/icsd.html	Purely inorganic compounds
CRYSTMET® http://www.tothcanada.com/databases.htm	Metals, alloys and minerals
Crystallography Open Database http://www.crystallography.net	Organics, inorganics, organometallics, and minerals

Table 2. *Major international crystal structure databases.*

In this exercise, you will be exploring some aspects of the CSD (top entry in Table 2 above) using a small teaching version of the complete database. After learning the basics of how to access and manipulate crystal structure data though the WebCSD interface, you will extract actual chemical information from selected structures stored in the teaching database.

Exercises

You can access the main CSD page from **http://www.ccdc.cam.ac.uk/products/csd/**. Read the introductory material and answer the following questions.

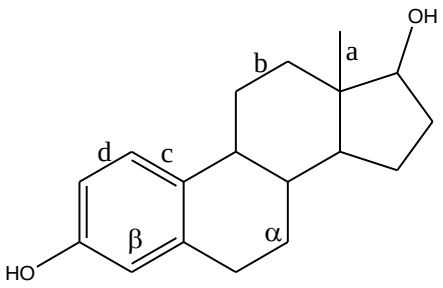
1. Which of the following would you expect to find structures for in the CSD?

Copper	Propane	Sodium chloride	Acetanilide	Aspirin	Heroin
Ferrocene	Glucose	Hemoglobin	Serine	DNA	Steel

2. Approximately how many crystal structures does the CSD contain?

   a. 8,500
   b. 85,000
   c. 850,000
   d. 8,500,000

The demo version, **http://webcsd.ccdc.cam.ac.uk/teaching_database_demo.php**, is a restricted set of 742 structures selected from the full CSD for teaching purposes. Go to this page, then type the refcode "ESTDOL10" into the "Find Entry" box in the upper left to examine the crystal structure of estradiol hemihydrate. You can check its chemical formula by clicking on the Diagram tab (upper right). Explore different views of the crystal by selecting different packing options. Manipulate the structure on the screen with the mouse and the Shift and Control keys. Right click the display for more options and features.



3. (i) What are the carbon-carbon bond lengths marked a, b, c and d in estradiol?

   a _____ b _____ c _____ d _____

   Measure the bond angles α and β: α _____ β _____

   (ii) Are these bond lengths and angles what you would expect? Explain.

   _____

   _____

Display the unit cell for the crystal structure of citric acid monohydrate, refcode CITARC.

4. (i) How many citric acid molecules are there in the unit cell? _____
   How many water molecules? _____

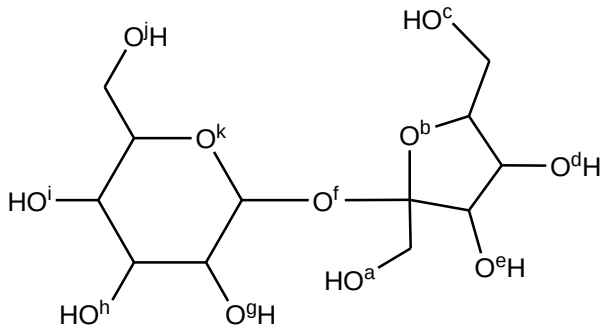
   (ii) What is the total mass of these molecules, in grams? _____

   (iii) Find the unit cell volume, in cm^3. _____

   (iv) Calculate the density of this crystal in g/cm^3. _____

Hydrogen bonds are ca. 20 kJ/mol non-bonding interactions between a hydrogen bond donor X–H and a hydrogen bond acceptor Y, where X and Y are strongly electronegative atoms and Y bears a lone pair of electrons [1]. Generally, in such interactions, denoted X–H---Y, the H---Y distance is about 1.2 – 2.2 Å and the X-Y distance is about 2.5 – 3.2 Å [2]. Enter refcode SUCROS01 to display the crystal structure of sucrose.

5. Using the labeling scheme shown below, identify two O–H---O *intra*molecular hydrogen bonding interactions, and one OH group involved in *inter*molecular hydrogen bonding.



   Intramolecular H-bonds _____ _____

   Intermolecular H-bonding OH group _____

The crystal structure of a compound may sometimes have been determined repeatedly, for a variety of reasons. Open all structures corresponding to refcodes beginning with QAXMEH.

6. What is a crystal polymorph? How many polymorphs of 5-methyl-2-((2-nitrophenyl)amino)-3-thiophenecarbonitrile are there in the teaching database?

   _____

   _____

   _____

Solvent molecules are often incorporated into crystals during crystallization, the most common example being waters of hydration in simple inorganic salts. Dichloromethane is found as a solvate in the structures given by refcodes BEJKUW, (η^2-C_{70} fullerene) bis(triphenylphosphine) palladium; DAMROY, (μ_2-chloro) bis(pentafluorophenyl) xenon(II) hexafluoroarsenate; and NOCHUI, 2,2'-bis(adamant-2-ylidene) chloronium hexachloroantimonate.

7. Explain why the dichloromethane solvate looks so unusual in the NOCHUI structure.

Open refcodes TPASTB, tetraphenylarsonium tribromide; CLPYSB, 2-chloropyridinium pentabromoantimonate(III); and SOBWAH, tetramethylammonium pentafluoroxenate(IV).

8. Draw the Lewis dot structure of Br_3^- to explain its geometry using VSEPR theory.

9. (i) How many lone pairs does Sb have in the $SbBr_5^{2-}$ anion?

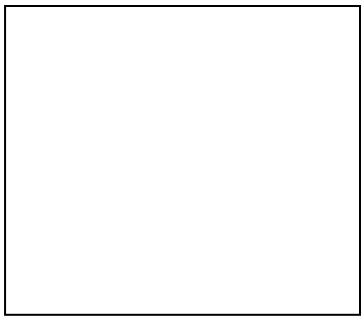
   a. 0
   b. 1
   c. 2
   d. 3

   (ii) What is the geometry of this ion? _____

   (iii) Draw the 3-D structure of this ion (including any lone pairs) using wedge bonds.

10. (i) What is the geometry of the XeF_5^- ion? _____

(ii) Draw its Lewis dot structure and use it to explain its shape by VSEPR theory.



The molecule 1,3,5,7-tetramethylcyclooctatetraene (refcode TMCOTT) is tub-shaped, but the corresponding dianion (refcode TMOCKE) is planar.

11. Explain this difference in shape.

References

1. P. W. Atkins and J. De Paula, *Physical Chemistry*, 9th ed., p. 637 (W. H. Freeman & Co., 2010).
2. G. A. Jeffrey, *An Introduction to Hydrogen Bonding*, p. 12 (Oxford University Press, 1997).