

Single Crystal X-Ray Crystallography^{1,2}

You will use the program SHELXTL to unravel the structure of an organic compound (to be referred to as Ylid) from the data supplied by our x-ray diffractometer. The data, in the file *ylid.hkl*, consist of the x-ray intensities observed for reflections from many planes, identified by three index numbers, h, k, and l. The diffractometer automatically orients the crystal and the detector to pick up reflections from each plane, and records the number of counts per second as the intensity.

The empirical formula of Ylid is $C_{11}H_{10}O_2S$. Before you start, you should use MOE (or distance geometry and MM2) to construct several small molecules to give you an idea of what bond lengths to expect for C-C, C-O, C-S, O-S, C-H, O-H, and S-H single and (where feasible) double bonds, because you will have to try to recognize them. Try to get an idea of the variability of the bond lengths by building different environments.

There are four main programs in the SHELXTL suite. XPREP helps you make an initial decision about the space group and sets up the files to be used by the other programs. XS tries to find the positions of atoms directly from the x-ray diffraction data without using Patterson maps. XS will probably find more atoms than there actually are, and it may identify only a few of them. The atom positions of the real atoms it finds will most likely be displaced from the true positions. XSHELL allows you to visualize the structure at any point in the analysis. It allows you to determine distances and angles between atoms, to rename provisional atoms to real atoms, and to delete bad atoms from the list. XSHELL or XLS refines the structure, trying to find the best fit to the intensity data.

XPREP

From the Start menu and the BrukerAXS Programs group run SHELXTL. Pull down the project menu and choose New. Type in the project name: ylid. Under "Look in:" go to the directory D:\xray\ylid, and click on ylid.p4p. Set D:\Xray\ylid\ylid.* as the project path and click Open. SHELXTL returns to the main menu. Click on XPREP in the top menu bar.

Next you will be shown some information about lattice exceptions in order to choose the type of crystal lattice. The lattice types correspond to the positions of lattice points, repeating elements centered on some defined position in the unit cell. The simplest lattice (P, for primitive) has lattice points only on the corners. If the center is also a lattice point, it is designated I (body-centered cubic). If two opposite faces are lattice points, the designation is A if they are along the x-axis, B if the y-axis, and C if the z-axis. F designates a face-centered cubic lattice in which all faces are occupied. The abbreviations Rev and Obv (reverse and obverse) in XPREP refer to hexagonal unit cells, which we will not have to worry about. The type of lattice determines which planes should not yield any reflected intensity. Lattice exceptions are reflections that occurred anyway. For the correct lattice that number should be small. It must be zero for primitive lattices, since there are no exceptions. Allow the computer to choose the correct lattice for you by pressing Enter to accept the default choice.

You must next choose a crystal system (select H on the menu). The seven crystal systems are triclinic, monoclinic, orthorhombic, tetragonal, rhombohedral, hexagonal, and cubic. Rhombohedral and hexagonal systems are associated with hexagonal unit cells. You will be offered several possibilities. The default cell is triclinic ($a \neq b \neq c$, $\alpha \neq \beta \neq \gamma$), but it looks for possibilities with higher symmetry. Note how many possible cells you have. Let the program choose, but keep track of which lattice type and which crystal system you have chosen, because you will get asked again. You may go through XPREP again if you wish to try a different crystal system.

Let the program guide you through the remainder of the setup, including the space group assignment. For more on space groups, see Atkins. Note the number of molecules per unit cell, Z, and the unit cell volume, which should be near 18. If you go back through XPREP later and make different decisions you can choose a new name and work along two or more lines at once. XPREP writes an instruction file for XS (called *name.ins*, where *name* is the name you chose), and a set of intensities, possibly recalculated to fit the new crystal group and space group.

XS

This program runs virtually autonomously. Just click on XS in the top menu bar. There are many modifications one can make to XS, but it often works quite well without any. XS writes a *name.lst* file, which lists some information on the process, and a *name.res* file, which contains the results. The results file is read by XSHELL.

XSHELL

This is a powerful program to view the atoms in the positions found by XS. To start, click on XSHELL in the top menu bar. Most of the atoms are provisional, designated as Q1, Q2, etc. Your job will be to figure out which of them is a carbon, oxygen, sulfur. Hydrogen has such a small electron density that it is hard to locate, especially at the beginning of the process. There is a way to fill them in later in ideal calculated positions. If you are unsure if a given peak is in a correct position, the best approach is to delete it. If enough of the correct structure is included in the model, your next refinement of the structure will produce a better model that is easier to interpret.

You can display the atom list in compact form by pulling down the Atoms menu and choosing Info on All. Remember, that you have 14 heavy atoms. Scan down the atom list to see the 14 largest peak heights, so that you have a point of comparison. Real atoms tend to have larger peak heights. Atom coordinates are given as fractional coordinates relative to the unit cell dimensions a, b, and c. The atoms have colors, which are specified by the atom type in the **info** list. To start with, all or most all of your colors will be yellow, signifying provisional atoms. Orient the molecule by dragging with the left mouse button. As you move the mouse over possible atoms peak heights will be displayed in the upper left hand corner of the screen.

You will want to compare bond lengths and angles with those expected for sp^3 and sp^2 carbon, oxygen, and sulfur. To do this, position the mouse over a particular "bond." The bond length will appear in the upper left hand corner of the display. To determine the bond angles to a particular

atom, place the cursor over the central atom, click right and choose Bonds and Angles. For example, for Q3:

Bonds and Angles for Q3				
Q5	1.564			
Q8	1.387	107.06		
Q14	1.855	144.57	48.20	
Q1	1.226	119.07	133.66	88.17
	Q3	Q5	Q8	Q14
Peak Height: 160.67				

The bond angle Q1-Q3-Q5 is 119.07° and the Q3-Q5 bond length is 1.564\AA . Q8-Q3-Q5 is 107.06° . You may want to choose the atom to start with by picking some region of the molecule that looks like something reasonable. Such regions might be five or six membered rings or recognizable functional groups.

Assume you have selected Q1 from which to start tracing the molecule. Check the distances between Q1 and its neighbors. Suppose that Q1 is shown "bonded" to Q27. However, the bond length to Q27 may be too short for a reasonable bond. If everything still makes sense with Q27 out of the picture, then delete Q27. Deleting a false atom is done by placing the cursor over the suspect atom and pressing "K".

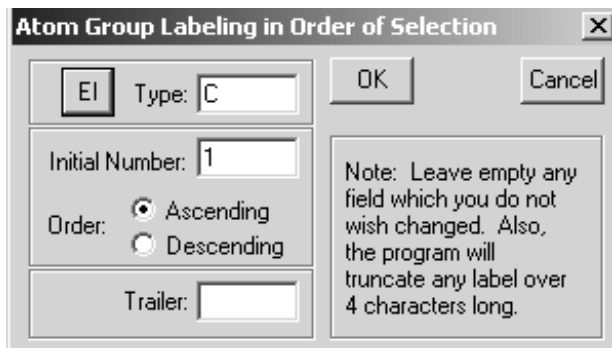
Note: If you mistakenly delete a peak, you can restore it with the Restore Killed Atoms feature. Deleted atoms (including Q peaks) go into a list. You can restore any atom in this list (and should probably do so immediately) by choosing Edit > Restore Killed Atom(s). The Undelete Atom(s) panel appears. Those atoms deleted last are at the top of the Deleted Atoms List. Highlight each atom you wish to restore, and click on the Restore button.

When you have a good guess for an atom, rename it. For example, if you would like Q1 to be oxygen, you might name it O1. To name an atom, first select it by placing the cursor over the atom and pressing the "S" key. The labels of selected atoms turn blue. Pull down the Select menu, slide right on Atoms, and choose Edit. In the Type dialog box enter the atom type, e.g. "O" or "C". If you know the atom hybridization, you can also enter it, as shown below.

Atom							
S1	Name	Q1	Type	O	EI	Occupancy	11.000000
Q1	XYZ	0.331100	0.198300	0.175100	<input type="checkbox"/>	Refine Occupancy	
Q2	Hybridization	s sp1 sp2 sp3			Charge	0	
Q3	<input type="checkbox"/>	Anisotropic					
Q4	Uij						
Q5	U11	U22	U33	U23	U13	U12	
Q6	0.050000	0.000000	0.000000	0.000000	0.000000	0.000000	
Q7	OK		Cancel				

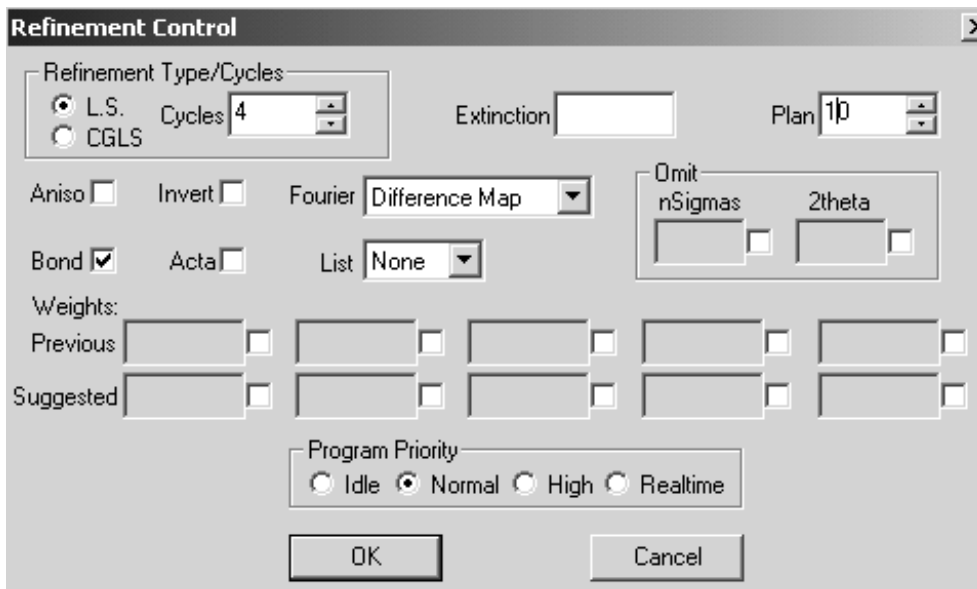
To deselect an atom, just place the cursor over the atom and press the "S" key again. Alternatively, you can pull down the Select menu and choose Deselect All. Another way to

rename and delete that is especially good when you have a whole bunch of the same element to do is to use the Labels > Group Labels command. For example, select Q atoms in the six membered ring. The labels of these selected atoms turn blue. Pull down the Labels menu and choose Group Labels. If not already shown type "C" in the label box, as shown below. The initial Number of 1 is fine for this example. In general it is best not to have two atoms with the same label so choose the initial number to avoid duplicate atom labels. Try to choose a numbering system that makes sense for the molecule as it is developing.



You have 11 carbon atoms, two oxygen atoms, and one sulfur atom to assign. It is not necessary to decide on all of them, but you should go through the provisional atom list and either rename or kill each atom. It is all right to finish this stage without all 14 atoms defined. Once you have pared down your list, XSHELL will prepare the instruction file for the next step.

Refining the Model: The next step is to refine your structure and look for missing atoms. XSHELL runs the XLS program, which will go through a least squares program to fit calculated x-ray intensities to the experimental intensities, varying atom positions to try to get the best fit. (XLS writes a *name.res* file that can again be used for further editing). The program also supplies a new list of provisional atoms, which you will have to dispose of one way or another. To begin click on the Refine menu. Change the value of Plan to 10 atoms. Plan is the maximum number of new provisional atoms that will be generated. Choosing a smaller number than the default value will decrease the number of Q atoms that you will need to delete. Set Fourier: to Difference Map; in doing so Q peaks will be generated from a Difference electron density map calculated after the fourth least squares cycle.



During its refinement, XLS is trying to reduce the R-value, similar to the R correlation coefficient you have used for plotting straight lines. For a good solution, R should be somewhere around 0.05. If you can get under 0.10 it can be taken to indicate that you have the correct structure. As the refinement proceeds the progress will be printed to the screen:

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+++++
+ XL - CRYSTAL STRUCTURE REFINEMENT - SHELXTL Ver. 6.12 W95/98/NT/2000/ME
+ Copyright(c) 2001 Bruker Analytical X-ray Solutions All Rights Reserved
+ ylid started at 10:06:49 on 10-Apr-2003
+++++

Read instructions and data
Data: 2293 unique, 0 suppressed R(int) = 0.0167 R(sigma) = 0.0209
Systematic absence violations: 6 Bad equivalents: 0
wR2 = 0.6066 before cycle 1 for 2293 data and 57 / 57 parameters
GooF = S = 6.593; Restrained GooF = 6.593 for 0 restraints
Mean shift/esd = 1.818 Maximum = -9.289 for U11 S1 at 10:06:50
Max. shift = 0.045 A for C4 Max. dU = 0.021 for C11
wR2 = 0.5229 before cycle 2 for 2293 data and 57 / 57 parameters
GooF = S = 5.272; Restrained GooF = 5.272 for 0 restraints
Mean shift/esd = 1.053 Maximum = 10.663 for U11 C11 at 10:06:50
Max. shift = 0.036 A for C11 Max. dU = 0.037 for C11
wR2 = 0.4658 before cycle 5 for 2293 data and 2 / 57 parameters
GooF = S = 4.490; Restrained GooF = 4.490 for 0 restraints
R1 = 0.1638 for 2239 Fo > 4sig(Fo) and 0.1658 for all 2293 data
wR2 = 0.4658, GooF = S = 4.490, Restrained GooF = 4.490 for all data
R1 = 0.1770 for 1380 unique reflections after merging for Fourier
Highest peak 5.06 at 0.8303 0.1216 0.2298 [ 1.80 A from S1 ]
Deepest hole -1.05 at 0.9425 0.7016 0.1974 [ 0.12 A from C11 ]

+++++
+ ylid finished at 10:06:51 Total CPU time: 1.2 secs +
+++++
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After the fourth cycle of least squares, the goodness of fit (GOOF) is 4.49 and the R1 value for all 1380 reflections is equal to 0.1770. Sometimes, you might get a message in the printout that says:

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** Absolute structure probably wrong - invert and repeat refinement **
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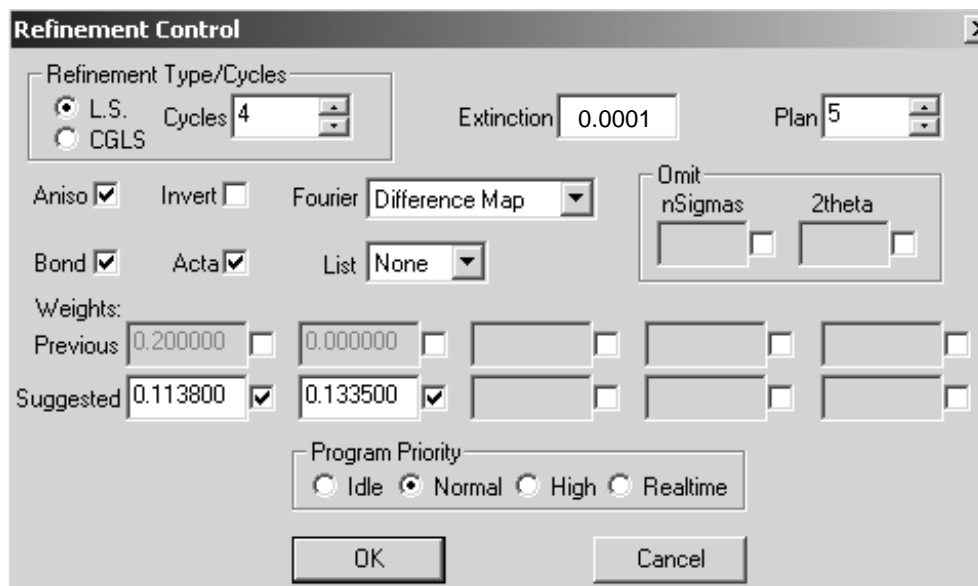
If so you should check the Invert check box in the Refinement Control the next time you do a refinement.

Look through the new Q peaks and decide which are real atoms and which are false atoms. Rename or kill all of the new Q peaks. You can delete all the remaining Q peaks by pulling down the Edit menu and choosing Kill All Q-Peaks. You can repeat the refinement process as many times as you like.

When you have the skeleton (C₁₁O₂S) figured out, you should add hydrogens pulling down the Atoms menu and choosing Hybridize All. Atoms colored yellow have s-type hybridization, atoms colored red have sp-type hybridization (none shown), atoms colored pink have sp²-type hybridization, atoms colored cyan have sp³-type hybridization, and atoms colored gray have no

assigned hybridization type. It will be very important whether a particular atom is sp^2 or sp^3 . If the automatic calculation gives the incorrect hybridization, you can change the hybridization using the Select > Atoms > Edit... dialog. Add hydrogens by pulling down the Atoms menu again and choosing Calculate Hydrogens. You must check that each carbon has the correct number of hydrogens, depending on the number of available bonding sites. If the incorrect number of hydrogens is assigned, check the hybridization of the attached atom.

Final Refinement: All atoms have now been located and labeled. So you can now refine all atomic parameters, including the anisotropic atomic displacement (or temperature) parameters. The temperature factors are a measure of how much the atom moves as the molecule vibrates. This process generates "thermal ellipsoids" that show graphically the extent of the motion of the atom. The bigger the thermal ellipsoid the greater the motion. Therefore, this time make sure to set the Aniso and Acta checkboxes. You can also set Plan to a smaller number, since all atoms should now be located. Also enter a 0.0001 in the Extinction box so that this parameter will be optimized. (This specific crystal is spherical so the Extinction should optimize to zero, but in general use the Extinction will be non-zero). Choose Invert if previous runs suggest doing so.



The final R1 value should now be much smaller than before. You should be able to get a value less than 0.05. Click right on the background and choose Thermal Ellipsoid. If any of the thermal ellipsoids are unusually small or large, you may have assigned the atom type incorrectly. If you change an atom type, adjust the number of attached hydrogens and refine again. If you get a better R1, you have made a better choice of atom assignments.

To print your structure, first do a print "preview" by pulling down the Render menu, slide right on Color, and choose To Screen... After the molecule is rendered press the space bar. To actually print the structure, repeat the process, except this time select To High-Quality JPEG... In the Bitmap Preferences Dialog leaving most of the directory path, type in a name for your file ending in .jpg; for example D:\XRay\pretty.jpg. Click OK. Once you quit ShelXTL, navigate to your file (in this example it will be on the D: drive in the XRay folder) and double click. The

picture will be opened in Internet Explorer or the Microsoft Photo Editor, from which you can print.

To see how the molecule packs into the unit cell, pull down the Atoms menu and choose Pack. To see the four molecules that constitute the unit cell, use the default X: 0 to 1, Y: 0 to 1, and Z: 0 to 1 setting. To return to a single molecule, pull down the Atoms menu and choose Trim. To see several complete unit cells, pull down the Atoms menu and choose Pack again. This time choose X: 0 to 2.0, Y: 0 to 2.0, and Z: 0 to 2.0

Literature Cited

1. Much of this writeup is taken from Patrick E. Hoggard, X-Ray Crystallography, Chem 6H Lab Santa Clara University.
2. Some parts of the XSHHELL section are taken from "XSHHELL User Guide: Tutorial," Bruker AXS, Bellerica, MA.