

Small Molecule Structure Solution and Refinement

Defining formula

Structure solution and refinement of organic and inorganic molecules and peptides can be performed in the *HKL-3000SM* command center. This part of *HKL-3000* is integrated with *SHELXS* and *SHELXL* from the *SHELX-97* package, written by Prof. George Sheldrick. These programs can be acquired directly from the author at <http://shelx.uni-ac.gwdg.de/SHELX/>. The structure solution process can be simplified if the chemical composition of the molecule under study is known. Exact knowledge of the chemical composition is not necessary, but a precise definition of the chemical composition will make all subsequent steps straightforward. The chemical content can be entered in the **Project** panel. In the **Project** box click the **EDIT PROJECT** button (Figure 1). A new window, **Setup Project**, will appear. Click the **DEFINE FORMULA** button and the periodic table of elements will appear (Figure 2). To build the formula of the compound, click on the symbol for each element present in the compound and change the number of atoms using the arrows or by typing directly into the box. Close the **Element Composition** box, click **DONE** in the **Setup Project** window to close it, and, if your data are already collected and reduced, you can go to the **Structure** tab.

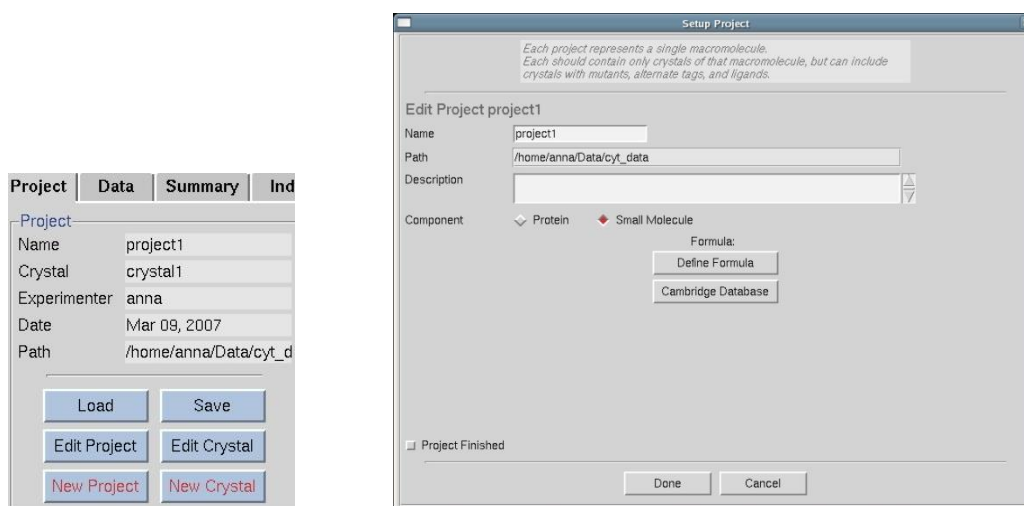


Figure 1. Edit and Setup Project windows

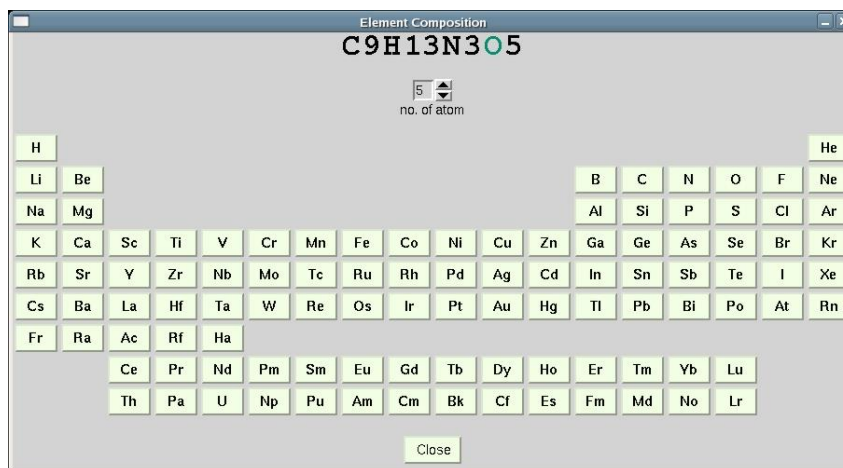


Figure 2. The periodic table that is used to define element composition

I don't want to lose time solving structures that have already been solved. Any suggestions?

Search databases! Over 390,000 carbon-containing structures analyzed with X-ray or neutron diffraction methods are provided by the Cambridge Structural Database (CSD). If you have a license to access the CSD, click the **CAMBRIDGE DATABASE** button in the right lower corner of the **Index** panel, you can check the indexed pre-scaled unit cell parameters, or check the parameters of the unit cell after scaling your data. In the latter case find the **CAMBRIDGE DATABASE** button under the **Project** tab and click on it (Figure 3). You will also find the **CAMBRIDGE DATABASE** button in the **Setup Project** window (Figure 1). A new window (Figure 4) entitled **Check Cambridge Database** will open. In this window you will see what parameters will be taken under consideration while searching through the CSD. By default, the formula you defined is treated as the formula of an individual molecule (if your compound consists of more than one type of ion or molecule, you should select **All Molecules in Structure** to find a result). Other defaults are: **tolerance** of 1.5% (expressed as a percentage of the longest cell dimension), searching on the **reduced cell** and choice of the **primitive (P)** lattice type. The **tolerance** value is changeable in the **Check Cambridge Database** window and other parameters can be changed after opening the **Build Queries** tab in **CCDC ConQuest** window. The results, sorted by identifiers called **refcodes**, are shown in the **View Results** window. You can toggle between the **Author/Journal**, **Chemical**, **Crystal**, **Experimental**, **Diagram**, **3D Visualizer** and **CSD Internals** tabs to find out if the structure has previously been solved. For more details see the CCDC web page at <http://www.ccdc.cam.ac.uk/>.

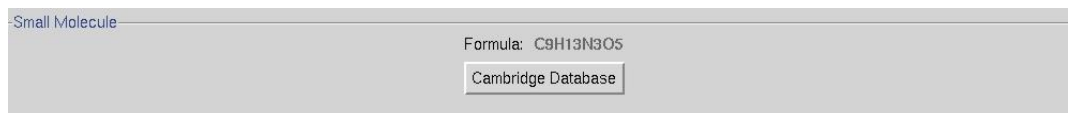


Figure 3. A button that opens the CSD window

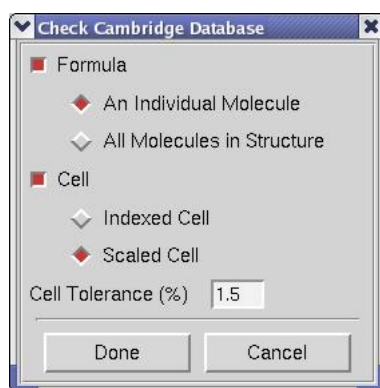


Figure 4. The Check Cambridge Database window

Structure solution

Before you click the **SOLVE STRUCTURE** button the following information should already be correctly entered in the other tabs:

1. the molecular formula (in this context, molecule means the whole formula unit, which may actually consist of more than one chemically discrete entity),
2. the space group, and
3. the number of molecules per AU (asymmetric unit). The default value is 1.0.

You may overwrite the previously established values by inputting them in the **Structure** tab. You can also change the structure solution method from direct methods (default) to the Patterson method by toggling the **DIRECT METHOD** checkbox off (Figure 5). Now, when you click the **SOLVE STRUCTURE** button, the program will use the Patterson method to solve the structure.



Figure 5. The solving method buttons

I made a mistake and accidentally solved the structure with direct methods when I wanted to use the Patterson method. Can I undo this?

Just click the **ABORT** button in the **Controls** panel (Figure 6). The previous solution will be abandoned. Don't worry if some graphics remain in the **Molecule View** – they won't be taken into consideration during the solving process. Change the solving option to the Patterson method by unchecking the **DIRECT METHOD** checkbox (Figure 5) and click the **SOLVE STRUCTURE** button again.



Figure 6. The middle part of the Control panel

Where will I find the space group?

Under the **Scale** tab. The lattice type is determined in *Denzo*, then the integrated data are scaled in the primary space group in *Scalepack*. Unless you are sure the crystal structure is centrosymmetric, scale your data using the **ANOMALOUS SCALING** option. Before using the **REJECTIONS ON NEXT RUN** option, make sure the space group is correct. To do this, click on the **CHECK SPACE GROUP** button from the **Controls** menu of the **Scale** tab. This option is available only for licensees of the *XPREP Software* (which is available from Bruker AXS Inc.). The **Space Group Probability** box appears (Figure 7). In its upper part, the most probable space groups and their probability values are seen. The table below shows systematic absence exceptions. In the first row, symmetry elements that could cause systematic absences are listed. The number of reflections (*N*), percentage of reflections with intensity higher than 3σ ($\%I > 3s$), average intensity ($\langle I \rangle$) and average $I/\sigma I$ ($\langle I/s \rangle$) are presented for all symmetry elements. In the lower part a slider with the $\langle E^2 - 1 \rangle$ value is shown. The expected value for a centrosymmetric space group is 0.968 and 0.736 for a non-centrosymmetric one. The position of the slider indicates if the space group is more likely to be centro- or non-centrosymmetric.

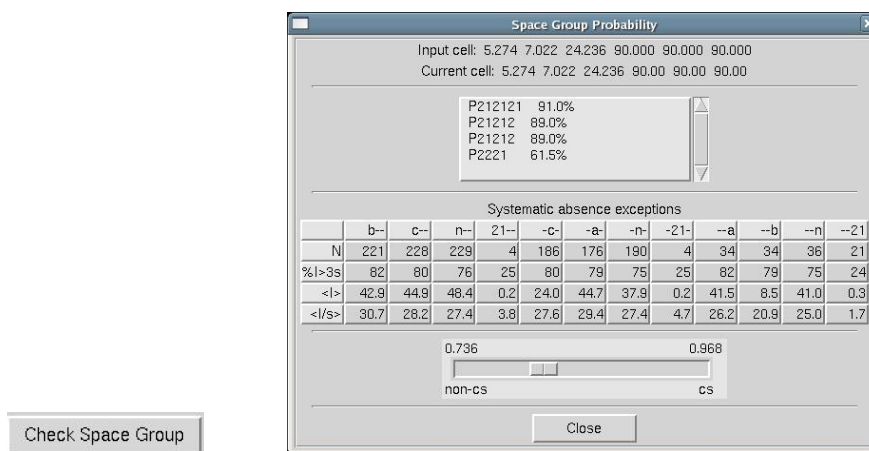


Figure 7. The Check Space Group button and the Space Group Probability box

- Note that unless you fill in the space group name box (Figure 8) manually, the program will import it from *Scalepack* (marked on a blue background under the **Scale** tab), which means it will be one of the 65 space groups available for protein crystals.

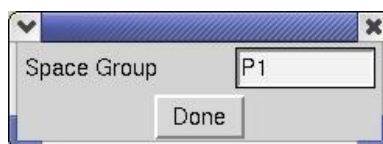


Figure 8. The Space Group box

When the structure is solved, I see only atoms that are in the asymmetric unit contents. Can I see more? How can I maneuver the picture?

In order to display symmetrically dependent molecules, click on the **SYMMETRY** button in the lower left corner of the **Molecule View** window (Figure 9). Now you can examine the unit cell contents. The mouse can be used to manipulate the 3-dimension representation of both the AU and unit cell. Use the left mouse button to rotate and the right one to increase or decrease the size of the structure. When you want to return to the view of the asymmetric unit just click the **SYMMETRY** button again. If you check the **CENTER** option in the **Molecule View** window (Figure 9) and then click on some atom with the middle mouse button, the atom will become the new center of rotation and will be moved to the center of the window.

- Note that if you choose an atom from a symmetry-related molecule to center on, the structure will be centered on the corresponding atom from the molecule visible in **Molecule View** window when **SYMMETRY** is switched off. This molecule has white colored bonds to distinguish it from the symmetry-related molecules whose bonds are colored blue.

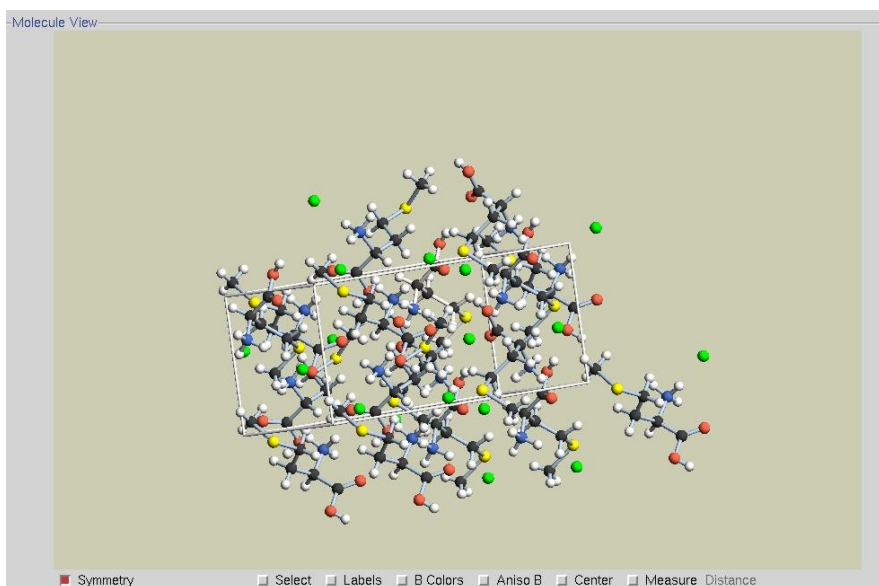


Figure 9. The Molecule View window

How do I modify the model of the solved structure? I want to delete some atoms and change the type or labels of others.

When you use the middle mouse button to click on any atom a new gray window will appear (Figure 10). At the top of the window, three pieces of information are given: the label of that particular atom, the residual electron density (in $\text{e}\text{\AA}^{-3}$) on a difference Fourier map for the atom, and the B factor. These are followed by the list of elements that are present in the molecular formula, which can be used to change the selected atom to a different element (simply select the new element for the atom).

Next is the **Rename** option to change the label of a particular type of the atom (Figure 11). To check the default atom label click the **LABELS** button at the bottom of the **Molecule View** window (Figure 9). When you choose the **Rename** option, the new box will open (Figure 11) where you can change the atom label (according to *SHELX-97* requirements, the atom name should not be longer than 4 characters). If you choose a number that is already assigned to the same type of atom, the program will switch the numbers between these two atoms.

In order to delete an atom, place the cursor on this atom, click the middle mouse button, and select the **Delete** option. The last two options are **Symm Atom** and **Symm Molecule**. **Symm Atom** (or **Molecule**) is used when a particular atom or molecule, selected in the **Molecule View** window, is assigned a symmetry related position but should be part of the main structure. To change this assignment, follow the same general procedure as for deleting and renaming, but choose **Symm Atom**, and choose the atom you wish to reassign using the mouse middle button.

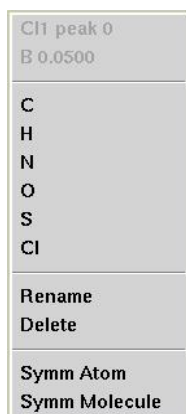


Figure 10. The atoms information box

How do I check the distances and angles between atoms?

Check the option **MEASURE DISTANCE/ANGLE** (the angle option is active after clicking on the word **DISTANCE**) on the lower right corner of the **Molecule View** window (see Figure 9). Using the middle mouse button, choose the atoms between which you want to know the distance or bond angle. The radii of the selected atoms will enlarge and the value of the distance (in angstroms) or bond angle (in degrees) will appear in the lower right corner of the **Molecule View** window.

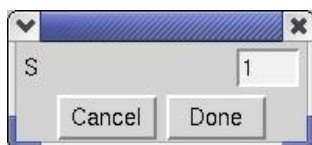


Figure 11. The Rename window

What does the **B COLORS** option do?

When you switch on **B COLORS** (Figure 9), colored discs will appear around the atoms (Figure 12). The more intense the color, the greater the B factor. A large B factor may be a warning that the position of the atom is wrong, the group of atoms is disordered or that a lighter atom should occupy the site.

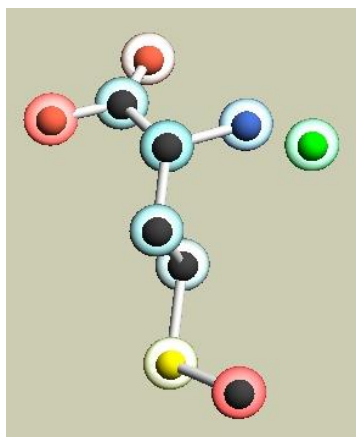


Figure 12. The B Colors option

The solved structure looks nice and colorful but I am used to looking at log files or *.lst files. How I can see them?

Go to the **Controls** box and click **SHOW LOG** (see *Figure 13*). A new editor window will open with the log file loaded. The default editor is Emacs, but you can choose between several common editors under **Options** in the top menubar of the *HKL-2000* window. When you click **Save Options**, your favorite editor and setup will be used in the future. Now you can inspect and manually edit the *SHELX-97 *.lst* file. Note that manual editing of *.lst files is necessary only in very rare circumstances, and should not be used as a standard method for structure solution.

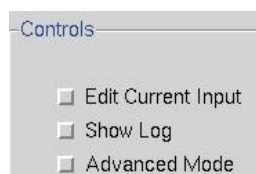


Figure 13. The left part of the Controls panel

Structure refinement

The first round of refinement is very strongly coupled to structure solution, as you may not have all atoms present and/or atom assignments may be incorrect. First, decide if you want to add or delete atoms or leave the solved structure as it is. If you want to add additional atoms click **ADD NEW ATOMS**. The program will propose the exact number of atoms to complete the molecular formula known from the **EXPECTED FORMULA** field. To change the amount of atoms, edit the box **NUMBER OF ATOMS TO ADD**, as shown in *Figure 14*. Enter the desired number of atoms and click **DONE**, and afterwards click **REFINE**. The values of the conventional and weighted residuals (R-factors), goodness of fit (GooF) and the Flack parameter, with its estimated standard deviation (esd), are shown in the upper part of the **Structure** tab after every refinement cycle.

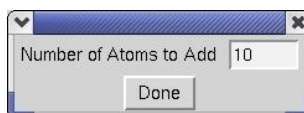


Figure 14. The Add New Atoms window

When all non-hydrogen atoms are found and refined it's time to calculate the anisotropic atomic displacement parameters. Check the **ANISOTROPIC B-FACTOR REFINEMENT** checkbox in the **Controls** box (*Figure 15*), and then click **REFINE**. If you are satisfied with the anisotropic refinement of the “heavy” atoms of the structure, you can then identify hydrogen atoms using the difference Fourier map. Use the **ADD NEW ATOMS** button to add the desired number of hydrogen atoms (*Figure 14*). **REFINE** the structure again. With high quality data, that is almost all you should have to do; all that is left is to critically examine the final result. Looking carefully at the refined structure will save you time during final report generation, deposition to the Cambridge Structural Database or final preparation of the structure publication.

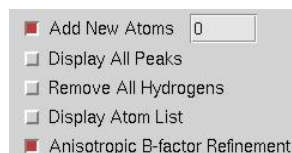


Figure 15. The right part of the Control panel

The Display All Peaks and Display Atom List options

The **DISPLAY ALL PEAKS** button (*Figure 15*) in the **Controls** menu shows the highest difference Fourier peaks (*Figure 16*), which are listed at the end of *SHELX-97 *.res* file and given names beginning with ‘Q’ followed by a

number. The number of peaks is defined by the `PLAN` command of *SHELX-97*. The default value is 20 but can be changed in the `*.ins` file (see page 9). The unique peaks are displayed as spheres smaller in radius smaller than the atoms that have already been labeled.

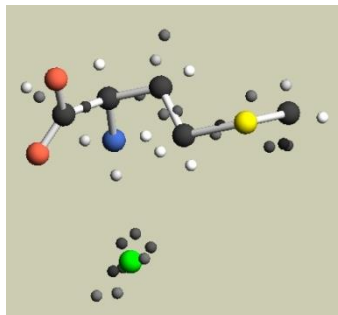


Figure 16. The Display All Peaks window

The **DISPLAY ATOM LIST** button (Figure 15) in the **Controls** menu opens a new window with two tables: an atom list and a new peak list. It is possible to sort the data in tables by atom names, residual electron density and B-factor value by clicking on the column headers of the table: **name**, **peak** or **Bf**. In the **Atom List** table you may mark atoms – the rows with marked atoms become highlighted in blue and white disks will appear around these atoms in the **Molecule View** window (Figure 17). This way you can delete or change the type of all marked atoms without having to click on each of them individually in the **Molecule View** window.

name	peak	Bf
Cl1	0.14	0.017
S1	0.18	0.018
N1	0.09	0.016
O1	0.21	0.018
C3	0.20	0.014
C4	0.18	0.015
C5	0.11	0.015
O2	0.00	0.026
C7	0.15	0.018
C8	0.00	0.028

Figure 17. The Atom List window – Atom List table

In the **New Peak List** table, when you check each of the numbered peaks, white disks matching the peaks will appear in the **Molecule View** window. This can be used to decide if each selected peak is an atom you are looking for or not. If they are, click the **ADD** button; each selected peak will be assigned a new name and its white disk will become a sphere in the **Molecule View** window (Figure 18). If they are not, select the peaks to reject and click the **DELETE** button; the peaks will disappear from the **Molecule View** window and will not be considered as atoms during the next refinement cycle.

name	peak	add
21	0.61	0
22	0.49	0
23	0.48	0
24	0.48	0
25	0.48	0
26	0.46	0
27	0.43	0
28	0.42	0
29	0.39	0
30	0.39	0

Figure 18. The Atom List window – New Peak List

What is the **SELECT** button for?

The **SELECT** button placed at the bottom of the **Molecule View** window (Figure 9) works like the **DISPLAY ATOM LIST** button (Figure 15) and opens the **Atom List** window but also allows selecting atoms not only from the list but from the molecules in the **Molecule View** window.

How should I deal with hydrogen atoms that I cannot locate on a difference Fourier map?

You can generate idealized coordinates for hydrogen atoms. Use the **ADD IDEAL HYDROGENS** option (Figure 19) after selecting the **ADVANCED MODE** option (Figure 13) in the **Controls** menu to open the **Advanced Mode** window. In the newly opened window, choose the chemical environment (**ATOM TYPE**) and a constraint (**CONNECTION MODE**) for refinement of the desired ideal H atom. Then click **SELECT ATOM** and with the middle mouse button select any non-hydrogen atoms you wish to add hydrogen atoms to. For better visualization, the radii of spheres representing the selected atoms will increase. Now click **APPLY**. The selected spheres will return to their standard size, and their chosen **ATOM TYPE** will be highlighted in blue (Figure 19). Now you can refine the structure again or select another **ATOM TYPE**.

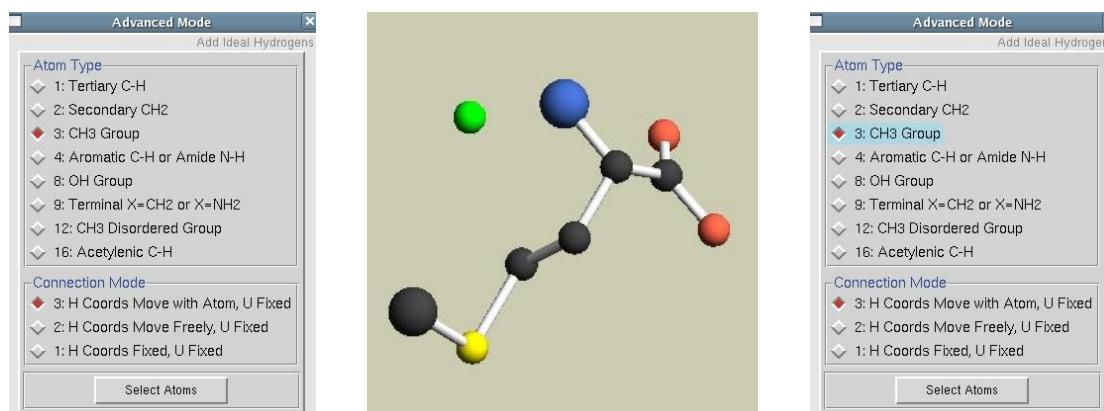


Figure 19. Idealized hydrogen window

How can I add a hydrogen bond to the refined structure?

The **DEFINE H BONDS** button from the **Advanced Mode** window (Figure 21) lets you find the H-bonds in the structure and will open a new window (Figure 20) with a list of them.

Number of Hydrogen bonds found: 4						
	D-H	d(D-H)	d(H...A)	<DHA	d(D...A)	A
1:	N1-H2	0.974	2.333	176.42	3.305	C11
2:	N1-H4	0.919	2.291	160.86	3.173	C11 [-x, y+1/2, -z+1/2]
3:	N1-H5	0.879	2.294	172.64	3.168	C11 [x-1, y, z]
4:	O2-H11	0.832	2.214	164.40	3.024	C11 [x, y+1, z]

Figure 20. The list of hydrogen bonds

How can I deal with twinned or disordered structures?

If the structure is twinned then the semi-automatic mode of structure solution may not be adequate. The **TWIN** and **BASF** commands must be manually added to the **SHELX-97 *.ins** file. If you want to add the commands for only one round of refinement (i.e. it won't be saved in the ***.ins** file for the next round) then go to the **Controls** panel and hit **EDIT CURRENT INPUT** (see Figure 13). A new window is opened in which you can complete and extend the current **SHELX-97 *.ins** file. If you want to add the commands and have it saved for further routine use the **MANUAL MODE** option

(Figure 21) of the **Advanced Mode** window to update the input file. For more details see the *SHELX-97* web page at <http://shelx.uni-ac.gwdg.de/SHELX/>.

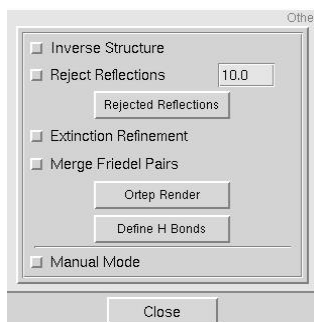


Figure 21. Additional options in the **Advanced Mode** window

Semi-automatic refinement of partially disordered structures is still in the developmental stage, and until it is fully tested, using the **MANUAL MODE** option and adding the **PART** command to the *.ins file is recommended.

I heard that when I use Cu radiation during the diffraction experiment I should especially worry about extinction.

To apply an empirical extinction correction factor to be refined with other parameters, select **EXTINCTION REFINEMENT** in the **Advanced Mode** window (Figure 21). You can also analyze the *.lst file to check how strongly this correction is recommended.

The value of the Flack parameter is 0.90(3). Shouldn't it be equal to 1 or 0?

Values of the Flack parameter between zero and unity describe the degree of racemic twinning. Values of (or close to) 0 value suggest that the correct enantiomorph was chosen, and a value close to 1 indicates that the structure should be inverted. To invert the structure click **INVERSE STRUCTURE** from the **Other** menu of the **Advanced Mode** window (Figure 21). During the next cycle of the refinement, the structure will be inverted.

- Structure inversion is performed by the *SHELXL* instruction 'MOVE 1 1 1 -1'. According to the *SHELX-97* manual, the instruction 'MOVE 1 1 1 -1' works for most but not all space groups. The 11 enantiomorphous pairs (e.g. P6₁ and P6₅) also require an inversion of the translation parts of the symmetry operators (the **SYMM** instruction). As well, for 7 space groups, inversion in the origin doesn't invert the absolute structure. The **MOVE** instructions for these 7 space groups are as follows:

```
I 4 2d  MOVE 1 .5 .25 -1
Fdd2   MOVE .25 .25 1 -1
I41    MOVE 1 .5 1 -1
I4122  MOVE 1 .5 .25 -1
I41md  MOVE 1 .5 1 -1
I41cd  MOVE 1 .5 1 -1
F4132  MOVE .25 .25 .25 -1.
```

It is possible that for structures consisting of only light atoms like C, H, N and O, the anomalous signal is too weak to be detected and the absolute configuration cannot be defined. For these structures the value of the Flack parameter will be much more ambiguous (e.g. a value of 0.59 with an esd of 0.69!). In such cases the Friedel pairs should be averaged and the **MERGE FRIEDEL PAIRS** option in the **Advanced Mode** window (Figure 21) selected. This will cause the instruction 'MERG 4' to be executed in the *SHELX-97* *.ins file.

The structure refines well but I still cannot observe the value of Flack parameter.

Is the space group of the structure centrosymmetric? If so, the value is not shown.

It's nice that I can edit the input file but it is worth nothing when I don't know how the names of atoms in the file correspond with the atoms shown in the molecules in the viewer.

Selecting the **LABELS** checkbox at the bottom of the *Molecule View* window (Figure 9) will label the atoms in the display (Figure 22).

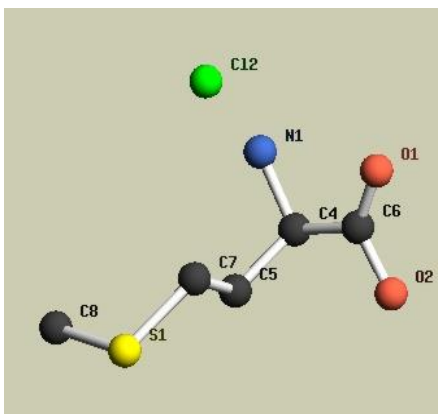


Figure 22. Labeling mode

I am not sure about the atom assignment. I think that I need to exchange the placement of one nitrogen and one carbon atom.

Inspecting the electron density map and manipulating molecular coordinates is handled by the program Coot, written by Paul Emsley. This program can be obtained from the Coot website (<https://www2.mrc-lmb.cam.ac.uk/personal/pemsley/coot/>), but is also distributed with CCP4 and Phenix. Click the **DISPLAY MAP** button from the *Controls* menu (Figure 6). A new window will be opened and **Coot** will run (see Figure 23). The blue, green, and red colored maps of electron density are displayed. The blue maps show the observed electron density. The more spherical the contours of this map are, the “better” the map is. The difference maps (red and green) illustrate difference between your model and the electron density. The red regions indicate a deficit of electron density on the map (e.g. when too “heavy” of an atom is placed in a position). The green regions show an excess of electron density (e.g. when an atom is too “light” for a position).

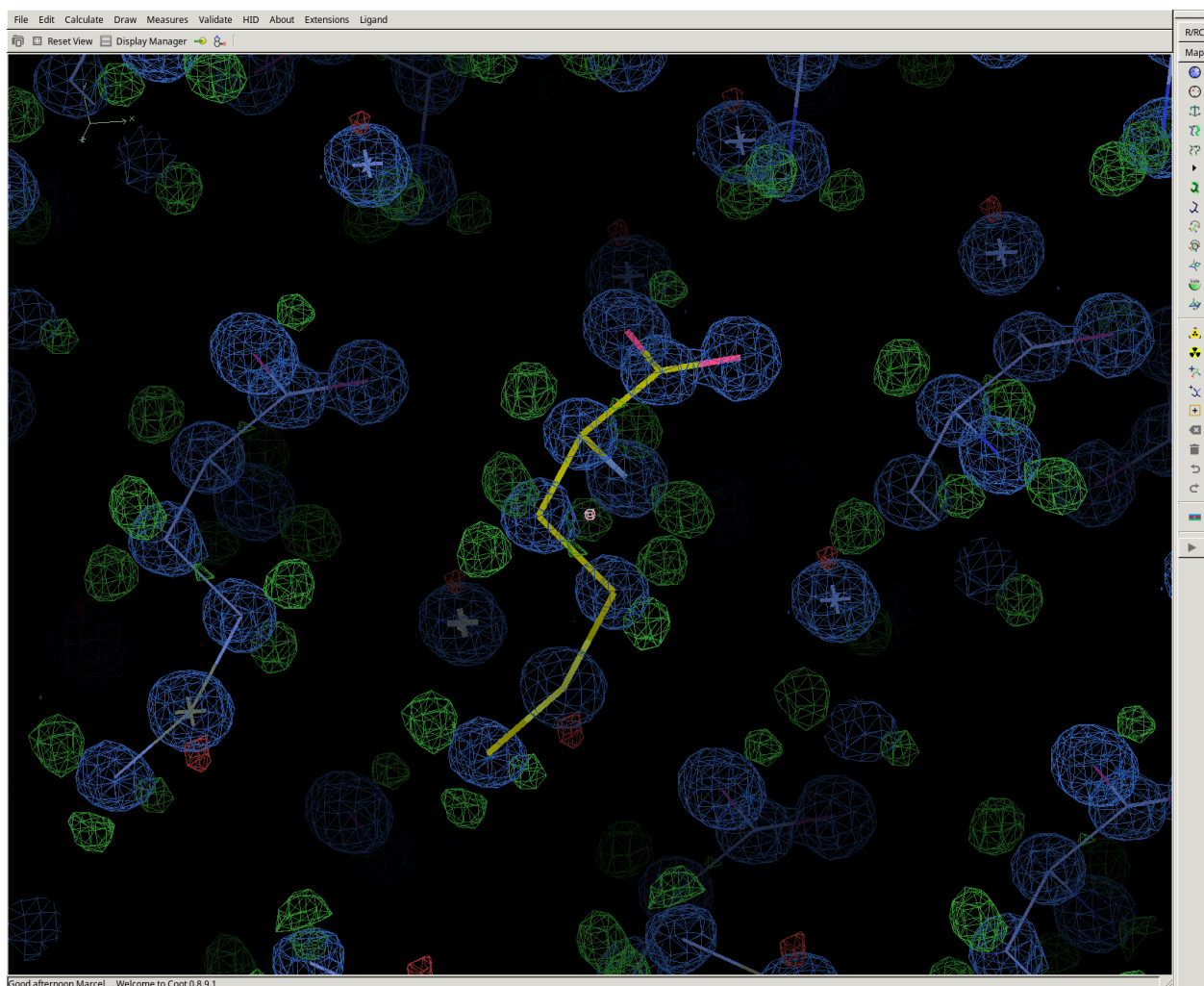


Figure 23. The electron density map and structure in the Coot window with hydrogen atoms removed.

I want to return to e.g. the third round of refining and continue in a different way. Can I do this?

What you should do is use one of the two blue square buttons surrounding the **HISTORY** caption (see *Figure 6*). The one marked “–” lets you go back to the previous step of the structural analysis and “+” enables to go forward. If you place the cursor on the **HISTORY** caption, the path to the current working directory will appear highlighted in yellow.

Should I reject any reflections during refinement?

Generally, you should not reject any reflections during the refinement procedure. Occasionally, some reflections can be affected by ‘zingers’ (only in the case of CCD detectors) or moving blind regions. During the last stages of refinement you may examine a list of the “most disagreeable reflections”: those with a high value of $\Delta F^2/\sigma$ are suspicious. Choosing the option **REJECT REFLECTIONS** in the *Advanced Mode* window (see *Figure 21*) allows you to exclude reflections with $\Delta F^2/\sigma \geq 10$ (by default) during the next cycle of refinement. Remember that removal of more than a few reflections indicates some serious problem and should not be done even though this procedure does decrease the crystallographic R-factor. If you want to change the cutoff value of $\Delta F^2/\sigma$ for rejecting reflections, click on the box with the current number. A new window (*Figure 24*) will open where you can place the desired value of $\Delta F^2/\sigma$.

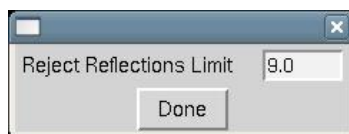


Figure 24. Reject Reflections Limit window

The **REJECTED REFLECTIONS** button allows you to see the list of reflections rejected during the last cycle of refinement without editing the *.lst file (Figure 25).

	h	k	l	Fo ²	Fc ²	Delta(F ²)/esd	Fc/Fc(max)	Resolution(A)
1:	1	2	3	134.45	3.02	11.97	0.014	2.75
2:	2	0	3	33.45	1.47	9.83	0.010	2.51
3:	0	1	7	834.40	75.01	9.62	0.069	3.11
4:	0	3	11	114.18	10.16	9.28	0.025	1.60
5:	0	1	2	35.30	2.39	11.28	0.012	6.08
6:	7	1	3	23.03	136.87	9.35	0.091	0.72
7:	0	1	3	30.53	5.16	9.09	0.018	5.30

Figure 25 .The list of rejected reflections

I would like to present some screen shots illustrating the refinement of my crystal structure but I really would prefer atoms to be shown as thermal ellipsoids, not as isotropic spheres.

If you want to do it very quickly, select the **ANISO B** checkbox located along the bottom of the **Molecule View** window (Figure 9); thermal ellipsoids are immediately shown (Figure 26). However, when you are preparing a crystallographic publication, use the **ORTEP RENDER** button in the **Advanced Mode** window (Figure 21). If you have a valid license it will open a new window with Ortep-3 for Windows by Louis J. Farrugia. According the Ortep-3 webpage (<http://www.chem.gla.ac.uk/~louis/software/ortep3>), the program “is a MS-Windows version of the current release of Ortep-III written by Michael N. Burnett and Carroll K. Johnson (<http://www.ornl.gov/sci/ortep/ortep.html>), which incorporates a Graphical User Interface (GUI) to make production of thermal ellipsoid plots much easier”.

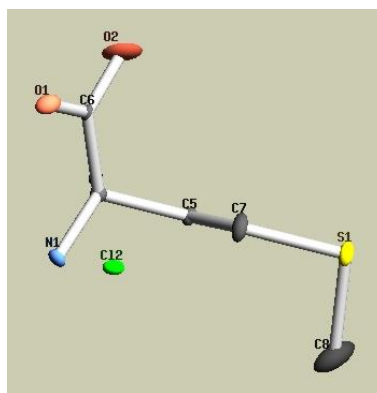


Figure 26. The thermal ellipsoids window

- To use Ortep-3 for Windows on any Linux machine you will have to install the Wine Windows emulator first.

Crystallographic Information File

You will find a very useful tool under the **Publication** tab (Figure 27). It is used to create, complete, check and print the Crystallographic Information File (CIF), which is an essential component of all papers describing small molecule crystallographic structures.

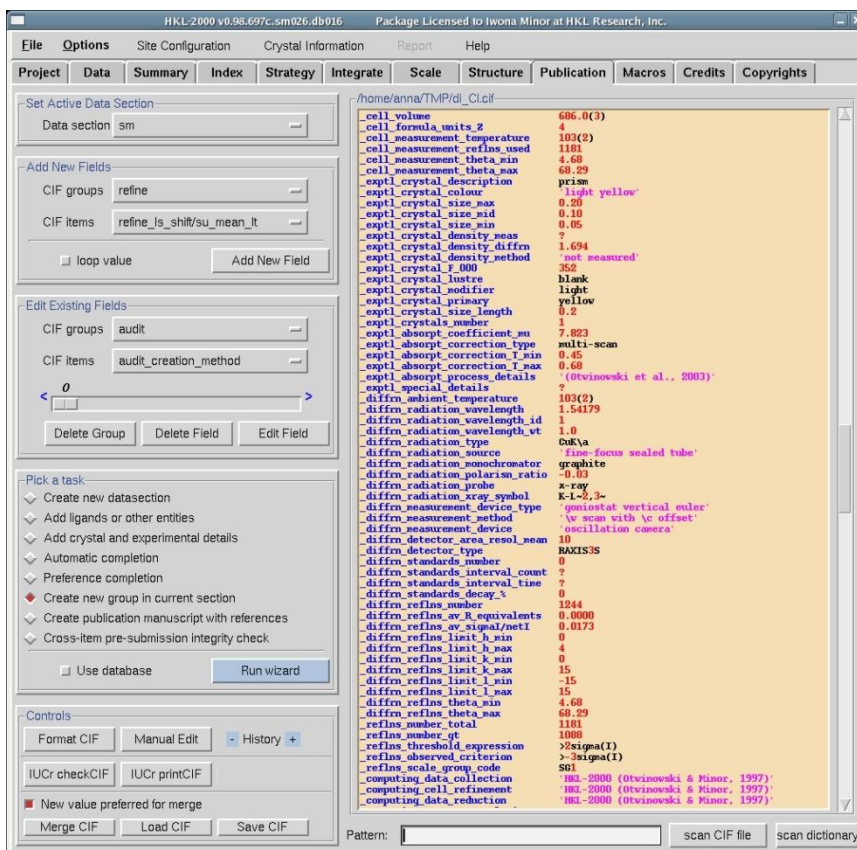


Figure 27. The Publication window

How do I start?

When you open the **Publication** tab after finishing structure solution and refinement in the **Structure** window, a partially filled CIF template will appear in the right half of the window. At the top of the CIF body, the path to the directory where the file will be saved is shown. CIF template program primarily uses the `sm.cif` file from the last refine subdirectory placed in the `structure_sm` directory to generate the initial template.

Can I use a *.cif file other than the generated template in the Publication panel?

Yes, you can. In the lower left corner of the **Controls** menu, click the **LOAD CIF** button (Figure 28). Then you will be prompted to select the *.cif file you wish to use.

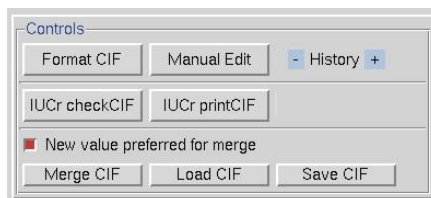


Figure 28. The CIF Controls menu

Can I use the data from two different *.cif files? I had prepared the whole file before, but I managed to further refine the structure. Now I do not want to waste time filling out the template once again .

In this case you can use the **MERGE CIF** button (Figure 28) in the **Controls** menu. A new window **CIF merge datasection name assignment** is opened (Figure 29). It is important to carefully assign the names of the merged data sections, especially when the same block of data is named differently in the files to be merged. Otherwise instead of merging values of the same fields, the program will add a new data section at the end of the old file. For example, if the new file has a data section data_I, and the existing file has the same items in a data section named data_sm, choose the **MERGE TO SM** option instead of choosing **KEEP CURRENT NAME**.



Figure 29. The CIF merge datasection name assignment window

New values are preferred for merging (i.e. the values in the new CIF file) but you can change this behavior by unselecting the **New value preferred for merge** option (Figure 28). The program will inform you if “nothing suspicious is found;” otherwise a new window will open (Figure 30). This window will list data items which are present in both *.cif files but differ in value. For each one you can select the value to keep.

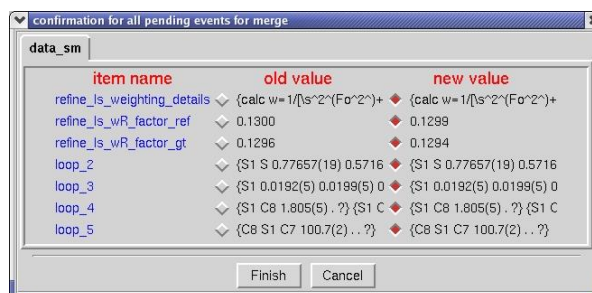


Figure 30. The Merge CIF window

What is the **Pick a task** box for?

The options from the **Pick a task** window (Figure 31) let you, generally, do two things. The first is to fill in data in the CIF file using information already calculated by *HKL-3000*. These include replacing question marks with proper data taken from *Denzo* and *Scalepack* programs (the **AUTOMATIC COMPLETION** button), or from a personally created database (**PREFACE COMPLETION** button), or using your knowledge about the crystal description (**ADD CRYSTAL AND EXPERIMENTAL DETAILS** button). The second is to add additional data sections, which are required parts of CIF but are not provided in a “raw” CIF produced by the instruction ACTA in the *SHELXL* *.ins file. These additional fields can be created by picking the following options: **CREATE NEW DATASECTION**, **CREATE NEW GROUP IN CURRENT SECTION**, **CREATE PUBLICATION MANUSCRIPT WITH REFERENCES**. After choosing a task, click the **RUN WIZARD** button to execute it.

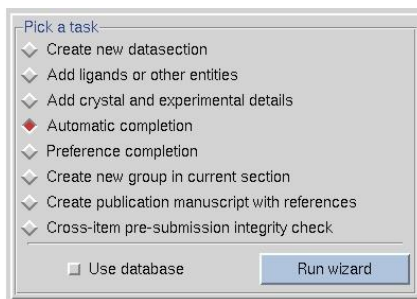


Figure 31. The Pick a task window

How do I make the right part of the **Publication** window editable?

Use the **MANUAL EDIT** button from **Controls** menu (Figure 28), and when you finish click the red **DONE EDIT** button (Figure 32) to make manual CIF editing inactive again. The manual editing mode is designed to modify the body of CIF fields but not the names of fields themselves.

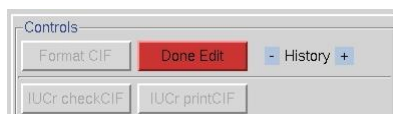


Figure 32. The Done Edit button

An alternative way of manually editing data items editing is using the **Edit Existing Fields** menu (Figure 33). The slider there allows you to scroll through all existing items in a chosen data section (the name of the current data section is given in the upper left corner of the **Publication** tab, see Figure 38). You can also jump directly to a given item by selecting the **CIF group**, and within the that group the **CIF item**.

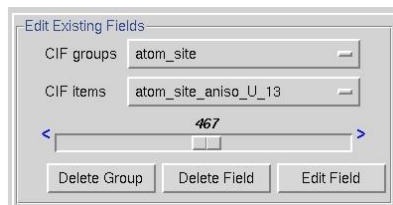


Figure 33. The Edit Existing Fields window

The chosen field is highlighted in blue in the CIF body window. You can edit the field clicking the button **EDIT FIELD** or pressing the middle mouse button on the highlighted item. In both cases a new window will open. How the window looks depends whether the CIF item is part of a loop (Figure 34) or not (Figure 36). In either case, the upper part of the window will show the name of the item along with a blue question mark sign, which can be used to find information about the item, its definition and some examples. The lower part will let you change, add or delete an value(s) for the item. You can also use **Edit Existing Fields** menu to delete CIF item(s). When you click the **DELETE FIELD** or **DELETE GROUP** button you will be asked to confirm removing the field or group with its value or values before the program executes the command.

e_label	type_sy	fract_x	fract_y	fract_z	U_iso	adp_type	occupa	symmet	calc_fla	refinem	disorde
S1	S	0.77657	0.57165	0.01295	0.0175	Uani	1	1	d	.	.
Cl2	Cl	1.28285	0.42714	0.18535	0.0162	Uani	1	1	d	.	.
O2	O	1.1446	0.9372	0.1989	0.0172	Uani	1	1	d	.	.
N1	N	0.7664	0.6847	0.2044	0.0156	Uani	1	1	d	.	.
O1	O	0.9539	1.1206	0.1355	0.0256	Uani	1	1	d	.	.
C4	C	0.7313	0.8503	0.1658	0.0136	Uani	1	1	d	.	.
C5	C	0.6616	0.7820	0.1071	0.0143	Uani	1	1	d	.	.
C6	C	0.9689	0.9709	0.1686	0.0140	Uani	1	1	d	.	.
C7	C	0.8588	0.6519	0.0818	0.0178	Uani	1	1	d	.	.
C8	C	0.5154	0.4140	0.0282	0.0299	Uani	1	1	d	.	.

Figure 34. The CIF edition of looped item

If you realize that some parts of the CIF file are missing, you can use the **ADD NEW FIELDS** menu (Figure 35) which works analogously to the **EDIT FILE** menu.

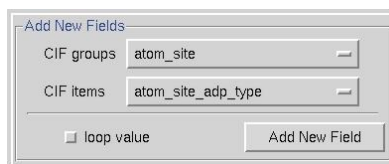


Figure 35. The Add New Fields window

What are these strange blue marks ">" in the editing windows for?

Click on this mark to expand the editing area for the field (Figure 36). This is useful when you wish to add a longer sentence or just more than one word or symbol.

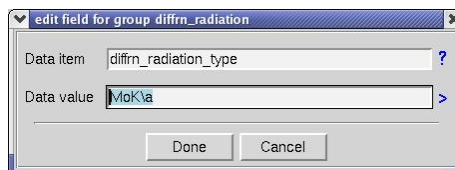


Figure 36. The CIF edition of the common item

Is there a search function in the **Publication** panel?

Below the window with the main body of the CIF file, you will find a keyword searching tool (Figure 37) which helps locate a particular word in the whole CIF body or in a CIF item from the dictionary (CIF items are these written in blue in the right half of the main window). Type the keyword in the **Pattern** window and click the **SCAN CIF FILE** or **SCAN DICTIONARY** button. A new window will appear with all CIF items containing the keyword. Choose the proper item – it will be highlighted in blue in the new window as well as in the main CIF contents.



Figure 37. The CIF key word searching tool

How can I validate my CIF file?

Once you have created your CIF you should check both the format and essential components of the *.cif file. Use the **FORMAT CIF** button in **Controls** menu (Figure 28) and the number of marks on each line and the presence of the proper punctuation marks will be checked. After corrections, if your computer is connected to the Internet, click the **IUCR CHECK CIF** button. Your structure will be checked using the *checkCIF/PLATON* service at <http://journals.iucr.org/services/cif/checkcif.html>. Using **IUCR PRINT CIF** lets you preview your article before submission using the *printcif* service at <http://journals.iucr.org/services/cif/print>.



Figure 38. The current data section name window

