Chapter 3: X-ray crystallography case studies

Exercise 3.1

For case study 1, calculate the relative heights expected for non-overlapping Patterson peaks due to the following pairs of atoms: Hg–Hg, Hg–S, Hg–N, S–S. Confirm that the peaks listed in Table 3.1 have appropriate heights for Hg–Hg and Hg–S vectors. What should be the approximate height of the peaks appearing next in the list, and what atom pairs are responsible for them?

Atomic numbers: Hg 80, S 16, N 7. Patterson peak heights are proportional to the product of atomic numbers.

Hg–Hg 80 × 80 = 6400; Hg–S 80 × 16 = 1280; Hg–N 80 × 7 = 560; S–S 16 × 26 = 256. These are approximately in the ratio 20:4:2:1. In Table 3.1 peak 2 has height 403 and peaks 3–8 have heights between 99 and 132, the average being a factor of 3.6 lower than peak 2. These peaks may well overlap with some others, enhancing their heights above the expected non-overlapped value of 403/5 ≈ 80.

The next highest peaks should be due to Hg–N vectors (with Hg–C almost as high), with heights around 403 × 7 / 80 = 35.

Exercise 3.2

The Hg–S bond lengths in case study 1 are obtained, at the end of the refinement, with higher precision (lower s.u. values) than the N–C and C–C bond lengths. Why is this?

The precision of bond lengths depends on the precision of the atom positions (coordinates). In general (subject to any disorder or markedly different atomic displacement parameters), the coordinates of atoms with more electrons will be more precisely determined (have lower s.u. values) than those of lighter atoms. Hence the most precisely determined bond lengths here will be Hg–S.

Exercise 3.3

Why is it reasonable to expect that the $[Hg(SR)_3]^-$ anion of case study 1 will deviate significantly from showing perfect threefold rotation symmetry?

The anion is subject to interactions with the surrounding ions, and its environment has no crystallographic symmetry (the only symmetry is inversion, and none of the component ions lies on an inversion centre). The tendency of crystalline solid materials to be as closely packed as possible means that conformations usually adapt to enable this. Bond angles are more easily distorted from ideal values than bond lengths, and torsion angles are particularly strongly affected by intermolecular interactions.

Exercise 3.4

The triclinic space group for the complex $[(C_{18}H_{18}N_4S)HgBr_2]$ in Exercise 1.5 is $P\bar{1}$. For each mercury atom at a position (x, y, z) in the unit cell, space group symmetry requires that there is another mercury atom at the position ($-x, -y, -z$). Where, apart from the origin

(0, 0, 0), will the largest peaks be found in the Patterson map for this structure? The largest peaks found in the Patterson map calculated from the observed diffraction pattern are listed below (Table 3.5); there are also peaks at symmetry-equivalent positions. All other peaks are under 100 in height. Deduce the coordinates of one mercury atom in the structure. To what are peaks 3 and 4, and peaks 5 and 6, probably due?

Table 3.5 The largest Patterson peaks for Exercise 3.4

Peak number	*x*	*y*	*z*	Peak height	Vector length (Å)
1	0.000	0.000	0.000	999	0.00
2	0.358	0.374	0.540	336	8.23
3	0.118	–0.124	0.154	224	2.61
4	0.188	0.111	–0.094	223	2.50
5	0.452	0.514	0.558	223	8.46
6	0.471	0.243	0.689	222	6.76

Symmetry-equivalent atoms at (x, y, z) and ($-x$, $-y$, $-z$) give a Patterson peak at ($2x$, $2y$, $2z$) [and an equivalent peak at ($-2x$, $-2y$, $-2z$). The two largest non-origin Patterson peaks for this structure should be these for Hg atoms.

From Table 3.5, considering the highest non-origin peak in this way, ($2x$, $2y$, $2z$) for Hg is (0.358, 0.374, 0.540), so the Hg atom lies at (0.179, 0.187, 0.270) (just divide the Patterson peak coordinates by 2).

The next highest Patterson peaks should be due to Hg–Br bonds within a molecule and Hg…Br vectors between one molecule and its symmetry-equivalent related by inversion.

2.5 Å is a reasonable value for an Hg–Br bond length, so the bonds correspond to peaks 3 and 4, while the intermolecular vectors correspond to peaks 5 and 6 (the distances are similar to that for Hg…Hg).

Exercise 3.5

The monoclinic space group for the indium complex in Exercise 1.6 is $P2_1/c$. For each atom at a general position (*x*, *y*, *z*) in this space group, there must be three symmetry-equivalent atoms at positions (−*x*, −*y*, –*z*), (−*x*, ½+*y*, ½−*z*), and (*x*, ½−*y*, ½+*z*). Derive from these the positions of the corresponding Patterson vector peaks (similar to Table 3.2, but with different entries). The four largest peaks in the Patterson map for this compound are at positions given in Table 3.6, together with peaks at symmetry-equivalent positions. Propose (*x*, *y*, *z*) coordinates for one indium atom consistent with these peaks.

Table 3.6 The largest Patterson peaks for Problem 3.5

Peak number	*x*	*y*	*z*	Peak height	Vector length (Å)
1	0.000	0.000	0.000	999	0.00
2	0.000	0.888	0.500	348	8.45
3	–0.120	0.500	0.820	329	9.33
4	–0.120	0.388	0.320	179	8.77

	x, *y*, *z*	−*x*, −*y*, −*z*	−*x*, ½+*y*, ½−*z*	*x*, ½−*y*, ½+*z*
x, *y*, *z*	0, 0, 0	−2*x*, −2*y*, −2*z*	−2*x*, ½, ½−2*z*	0, ½−2*y*, ½
−*x*, −*y*, −*z*	2*x*, 2*y*, 2*z*	0, 0, 0	0, ½+2*y*, ½	2*x*, ½, ½+2*z*
−*x*, ½+*y*, ½−*z*	2*x*, ½, ½+2*z*	0, ½−2*y*, ½	0, 0, 0	2*x*, −2*y*, 2*z*

$x, \frac{1}{2}-y, \frac{1}{2}+z$	$0, \frac{1}{2}+2y, \frac{1}{2}$	$-2x, \frac{1}{2}, \frac{1}{2}-2z$	$-2x, 2y, -2z$	$0, 0, 0$

Use the first column and identify each of the entries with the corresponding peak in Table 3.6. Start at the bottom and work upwards, for simplicity.

$0, \frac{1}{2}+2y, \frac{1}{2}$ corresponds to peak 2, with $\frac{1}{2}+2y = 0.888$, so $y = 0.194$

$2x, \frac{1}{2}, \frac{1}{2}+2z$ corresponds to peak 3, with $2x = -0.120$ and $\frac{1}{2}+2z = 0.820$, so $x = -0.060$ and $z = 0.160$

In this case, we should find $2x, 2y, 2z$ is $-0.120, 0.388, 0.320$, and this is indeed peak 4, confirming that the assignments and calculations are correct.

Thus the In atom lies at $-0.060, 0.194, 0.160$.

Exercise 3.6

What difference is there in the following geometrical parameters for two enantiomers?

- bond lengths
- bond angles
- torsion angles

Two enantiomers have identical bond lengths and bond angles. Corresponding torsion angles have the same absolute values but opposite signs.

Exercise 3.7

Distinguish between isomers and polymorphs. Why is it important to investigate polymorphism and the formation of solvates for pharmaceutical compounds?

Isomers are two or more chemical compounds in which the same atoms are arranged with different connectivity (there are various kinds of isomerism depending on exactly what the difference in connectivity is). Polymorphs are two or more crystal structures adopted by the same chemical compound. (Strictly speaking, different solvates are not polymorphs.)

Different polymorphs and different solvates of a compound have different physical properties, including solubility, melting point, and (for a pharmaceutical compound) bioavailability; they are thus considered to be different materials. Not only do different polymorphs/solvates behave differently, they are also considered to be different for legal and patent purposes.

Exercise 3.8

What do you think might be the consequences of overlooking twinning in a diffraction pattern, and measuring and using only the reflections that fit the unit cell and orientation of one of the twin components?

The exact consequence will depend on the specific type of twinning present. For genuine twinning (as opposed to a split crystal having components with arbitrary unrelated orientations) at least some, if not all, reflections of the components overlap, so these have an intensity made up of contributions from two (or more) reflections that are not equivalent by symmetry. Depending on the proportion of overlapped reflections and the relative amounts of the components in the sample, the incorrect intensities may still allow the structure to be solved (albeit with greater difficulty than usual) but will prevent a fully successful refinement, leading to relatively high *R* values and possibly to atoms with physically unreasonable displacement parameters and poor molecular geometry.