7th European Crystallography School

Lisbon
July 10 – 15, 2022

Validation of results

Anthony Linden
Department of Chemistry, University of Zürich, Switzerland
anthony.linden@chem.uzh.ch

Contents

Validation of results

1 Introduction

When you have carefully finished the refinement of your structure, the structure looks pretty and you are confident that the work is correct, it agrees with the chemistry, the result is the best possible and everything is in order. Are you sure? Are you really sure? How do you know? Might you have overlooked something trivial or less trivial – easy to do, even for a really experienced crystallographer. Is there unexpected twinning? Have you accidentally assigned a C-atom as an N-atom? Did you add insufficient H-atoms to a C-atom? Should you really be considering disorder? There are a myriad of things one needs to keep an eye on during a structure determination and we cannot remember to check absolutely everything all of the time. We need aids to help us ensure we have not overlooked or forgotten anything and ultimately to help us avoid the risk of publishing something wrong, which makes us look silly. Structure validation is the tool that helps us ensure everything is as it should be. Crystallography is such a numerical science that it is relatively easy to develop software to help us detect unexpected "features" in our structures, alert us to them and give us an opportunity to correct or at least think about the issues. This chapter deals with the topic of validation and checking of crystal structures.

2 Validation and checking of crystal structures

An outline of the basic characteristics of the Crystallographic Information File (CIF) and its uses is provided as an separate document. This chapter is concerned with general issues of validation and checking of the quality and correctness of the results which arise from crystal structure determinations. It will provide an overview of validation in general as well as considering how different forms and levels of validation may be appropriate for work submitted to different journals. It will also examine the limits of validation by identifying issues which need to be considered independently: such issues will generally be referred to using the term checking.

Various degrees of validation can and should occur at all stages of a structure determination from initial assessment of the diffraction quality of a crystal onwards. This validation may be provided in various ways, for example by figures of merit output by structure solution software or an improvement in the fit of the least-squares refinement after the model has been changed. However, this section will focus on the validation which is carried out at the end of the structure refinement, at the point where a CIF has been generated. At this point any remaining shortcomings in the structure analysis must either be remedied or addressed by means of a scientifically valid explanation.

2.1 What is validation?

The process of validation involves a comparison against a set of test criteria (the validation suite), and the effectiveness of the validation procedure depends on how relevant and comprehensive the criteria are. Given the wide range of materials studied by diffraction methods, and the varying quality of the resulting determinations, there will inevitably be cases where it will be unclear whether or not a structure satisfies a particular

test criterion. One approach to this is to define different levels of agreement with the criterion (see Section 2.6), so that the validation software can indicate the likely seriousness of whatever problem it has detected. A minor discrepancy or a marginal failure to meet a criterion will attract less scrutiny than an intermediate or a major discrepancy.

2.2 Examples of validation criteria

A simple example of a validation criterion is whether the crystal colour has been specified: a warning will appear if a number appears instead of characters, if no colour is specified, or if the colour is not recognised. Another example of a criterion is the check on the unit cell volume against the six unit cell parameters a, b, c, α, β and γ. As the volume is a function of these parameters, validation software can calculate the unit cell volume and compare it with the value in the CIF. A slightly more complicated example is provided by the size of the crystal used in data collection, quoted as maximum, medial and minimum dimensions: in this case it is possible to check both the absolute values of the crystal dimensions (in some cases over-large crystals may cause problems) and whether the order is correct (*i.e.*, maximum ≥ medial ≥ minimum). In fact, many hundred different tests are possible, many of them relying on the interdependencies present in the data, for example between fractional coordinates and geometry parameters, while other tests refer to external criteria. Such tests might check whether bonded atoms have compatible U^{ij} values, whether the refinement has converged, whether the space group is correct and whether atoms have been assigned as the correct element.

2.3 *Valid*ation

The word "valid" has certain connotations which are helpful in understanding some of the purposes of validation:

(i) **Correct**. This implies that the right decision has been made between different possibilities, for example that the required absorption correction has been applied because the crystal contained lead (atomic number 82).

(ii) Appropriate. This implies that a sensible approach has been adopted or the most suitable option chosen, for example by choosing a static over a dynamic model for disorder when the disorder components are not well resolved.

(iii) Defensible. This might refer to any situation where the quality of the refinement is limited for some reason. For example, it is normal for all non-hydrogen atoms to be refined with anisotropic displacement parameters, but it might be reasonable to refine each atom of a minor disorder component with only an isotropic displacement parameter, especially if these atoms are of low atomic number (carbon or similar).

2.4 What is checking?

Checking refers to any testing of the quality of the structure that does not fall under the heading of formal validation (*i.e.*, comparison against specific test criteria) and is therefore – at least partly – distinct from validation. For example, does your structure make sense in chemical terms, both in relation to the product whose structure has been determined and its formation from its precursors? Does the structure "look right", or does some geometrical feature appear strange, anomalous or unusual? Do chemically equivalent bonds, which should not differ significantly, actually agree? Do such bonds

lie in the normal range expected, or does there appear to be a systematic shortening or lengthening? Do any atoms appear to have strangely-shaped ellipsoids which could indicate disorder or other problems? Are all CIF entries complete and correct, or are some of them derived from software defaults which are not relevant to this particular structure determination?

There are numerous situations where the validation and checking categories do overlap to some extent, and one example of this concerns atomic displacement parameters. Because the parameters used as input to validation software are also used to create ellipsoid plots, in many cases both the validation output and the plot may indicate a problem such as an excessively prolate ("rugby ball" shaped) ellipsoid. However, this overlap is incomplete and there are instances where only a visual inspection will identify the problem (see Section 2.17 for an example).

2.5 Resources available

Two papers on validation (Spek, 2003, 2009) are appended to this chapter and are essential reading.

The IUCr website for *Acta Crystallographica* contains extensive information to help you with topics related to CIFs and validation. All of this information can be found under the 'for authors' button for *Sections C* and *E* of *Acta Crystallographica* at *http://journals.iucr.org/c/services/authorservices.html* and includes:

- Downloads for CIF editing and preprint tools (*enCIFer, publCIF*, *printCIF*).
- The completion of CIFs, CIF data codes and keywords, *etc*.
- The preparation of CIFs for publication, including CIF templates and example CIFs.
- How to create special tables in CIFs, Greek characters and special symbols.
- Validation of CIFs and the meaning of validation alerts.
- Notes for authors.
- Author checklist for publication in *Acta Cryst*. *C* or *E*. These can also be used as a general checklist for the proper completion of CIFs and as a guide to information which might be relevant in the preparation of any structure report.

PLATON source code and Linux executables can be obtained from *https://www.platonsoft.nl/xraysoft/unix*. Easy instructions for compilation are provided. You can also compile and run the Linux version of *PLATON* on a Mac through the X11 (XQuartz) application. *WinGX* or Windows PC users can obtain a compiled version of *PLATON* from the *WinGX* website: *http://www.chem.gla.ac.uk/~louis/software/platon*. *PLATON* is updated almost daily and new features can appear at any time, so it is useful to download the newest version every few weeks.

2.6 Automated data validation

A major feature (and advantage) of the CIF standard (Hall *et al*., 1991; Hall, 1991) is that it provides crystallographic data in a standard format which can be read by any suitable software, including *checkCIF* (*http://checkcif.iucr.org*) and *PLATON* (Spek, 2003, 2009), which perform structure validation. Checks are carried out for CIF construction and syntax errors, missing information, parameters outside expected norms, missed symmetry and conformation with convention. The validation output can be

separated into three parts: firstly, it seeks to identify possible problems; secondly, it attempts to provide concise explanations of these problems; thirdly, it suggests interpretations and possible ways to deal with the problems. The second and third functions are particularly helpful to those with less experience of structure determination, but also provide advice for the more knowledgeable about problems which occur less frequently. *PLATON* validation duplicates most of the *checkCIF* tests and has a few additional tests, most notably tests for twinning and estimation of absolute structure using the Hooft parameter. *PLATON* allows the user to go beyond the numerical validation checks because its graphical features also can be used for other calculations and visual checks of molecular conformation, displacement ellipsoids and other features.

CIFs created by *SHELXL-2014* contain the .res file and the input .hkl reflection file embedded within the CIF under _shelx_res_file and _shelx_hkl_file, and in the case of the use of SQUEEZE, the .fab file under _shelx_fab_file. It is very important not to remove these sections, nor to change the data names to anything else, because validation can use this information to complete its tasks without the need to supply a separate structure factor file (.fcf file). If using *PLATON*, the only requirement for this to work is that *SHELXL* is on the known path of the computer, so *PLATON* can run it in the background.

2.7 Alert levels

The validation software *checkCIF* and *PLATON* are closely related and produce similar output. Possible problems are classified by their Alert level (A, B, C or G), corresponding to decreasing seriousness. Thus a type A Alert corresponds to a serious omission or a major deviation from the expected norm and, in general, attention is essential. Examples might include:

- no crystal dimensions have been given
- absorption correction required but none specified
- atom C5 has an extreme ellipsoid shape (max/min ratio 18.0)
- refinement has not converged (maximum shift/s.u. 1.5)
- no hydrogen atom geometry in the CIF

Although these are all clearly serious, this does not mean they are all relevant. For example, the absence of hydrogen atom geometry is spurious if the compound does not contain hydrogen and irrelevant if the intended journal does not insist on these geometric parameters being included.

If an Alert B is encountered, this is an indication of a significant problem or an unexpected outlier which requires investigation. Possible examples are:

- the formula has elements in wrong order
- possible missing symmetry: *Cc* to *Fdd*2 transformation?
- refined extinction parameter < 2.0*u* from zero
- structure contains voids of 180 Å^3

The first point in the list is only significant insofar as the elements should be in the correct order where the CIF is a route to publication; although the symmetry issue does need to be investigated carefully, it is more likely to be an indication of pseudosymmetry than of genuine missed symmetry; an extinction parameter whose value is less than about three times its standard uncertainty should probably be removed as a

refining parameter; finally, the distribution of voids in the structure needs to be analysed and accounted for.

Type C Alerts are the least significant, and may appear trivial, but should still be examined: an extensive list or a definite pattern may indicate problems which are more significant than the level of Alert might suggest. Examples are:

- moiety formula not given
- short intermolecular contact: O7···C1 2.96 Å
- low U_{eq} as compared with neighbours: C1
- D–H without acceptor: N2–H2?

The absence of a moiety formula is not a significant omission unless it is a journal requirement, but the remaining three examples merit closer scrutiny. In fact, taken together they expose a serious mistake in the assignment of element types: C1 and N2 should be a nitrogen and a carbon, respectively.

Type G Alerts are more of an informational nature, either highlighting a feature of the structure or the use of non-routine strategies, such as restraints. While they might not indicate a problem, it is useful to look at the G alert listing to ensure that everything is according to your expectations. For example, does a G alert indicating the *R*-configuration of a particular chiral centre agree with your expectation. If you were expecting the *S*-configuration, you then need to decide if the expected chemistry or model is at fault, what the absolute structure parameter says about the reliability of your model configuration, and so on.

2.8 Alert types

While the letters A, B or C indicate the seriousness of an Alert, the numbers 1–4 indicate what kind of Alert it is: type 1 refers to a CIF construction/syntax error or inconsistent/missing data; type 2 indicates that the structure model may be wrong or in some way deficient; type 3 that the quality of the data and/or structure model may be low; while type 4 Alerts involve cosmetic improvements, queries or suggestions. Thus an Alert identified as 2A is a serious indication of an incorrect structure, while 4C might be a mild suggestion for improvement. Some combinations, like 4A, are illogical.

2.9 Sources of outlier parameters

The parameters identified by the validation software as outliers may arise from a number of sources. One such source comprises unresolved problems in the structure analysis, for example disorder which has not been modelled correctly. There may be artefacts in the model due to the dataset being of limited extent or quality, or because of deficient procedures or corrections for effects such as absorption or extinction. There may be gross systematic errors in the refinement model, for example because of an incorrectly-assigned space group or element type. Finally, the outlier may comprise a genuinely rare and unusual observation, but this in itself implies a warning: such an observation is by definition infrequent, and other causes must be eliminated before it can be accepted.

2.10 Who uses validation software?

It is worth noting that it is not just authors who carry out validation checks. If you submit a paper containing one or more structure determinations, the crystallographic

referee is likely to download the CIF and check it before reading the paper. This use at an early stage of the manuscript assessment process is very sensible, because a serious flaw such as an incorrect space group can mean that the paper should be rejected immediately.

2.11 When to validate

As noted earlier, the software used for data collection, structure refinement, etc, should provide its own forms of validation. For post-refinement validation *checkCIF* or *PLATON* should be used, firstly on the raw CIF output from the refinement software, the purpose being to identify any major problems such as poor convergence or an incorrect space group. At this point, there may be a considerable number of Alerts due to missing values, as the refinement software may not know all of the required information, but these can be added once it has been established that the raw CIF exhibits no major problems. When the correct values are in place, the final version of the CIF should then be validated once more.

2.12 Looking at the structure

A visual examination can often be revealing. Fig. 1 shows some extreme ellipsoids which are also incompatible with a rigid bond model. This is clearly a structure with serious problems.

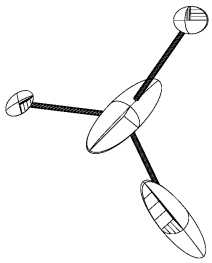


Fig. 1. A displacement ellipsoid plot showing some extreme ellipsoids.

Graphical tools can also be used to assess the molecular geometry. Fig. 2 shows a bromo-substituted diol with some of the bond lengths indicated: in this case the bond lengths match the values expected.

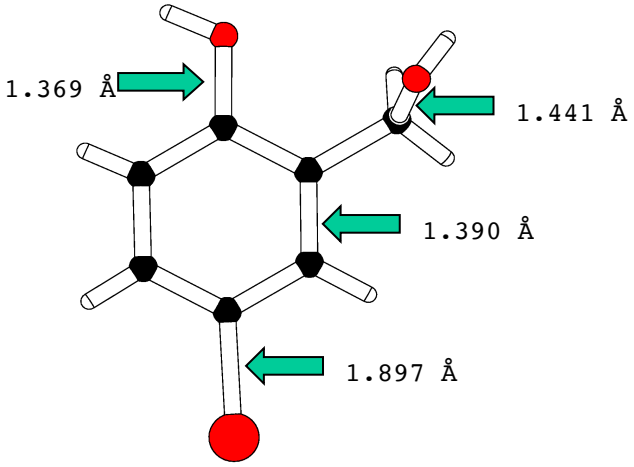


Fig. 2. A ball-and-stick representation of a molecule with selected bond lengths indicated. These lengths all lie within their expected ranges.

A less satisfactory situation is illustrated in Fig. 3, where the molecule contains two *tert*-butyl groups, only one of which is ordered, with all C–C distances clustered closely around 1.52 Å. In contrast, the C–C distances in the disordered group occupy a broad range from 1.49 to 1.60 Å. This may be the result of an inappropriate disorder model, an absence of restraints or a need for better restraints. In any case, further refinement is required.

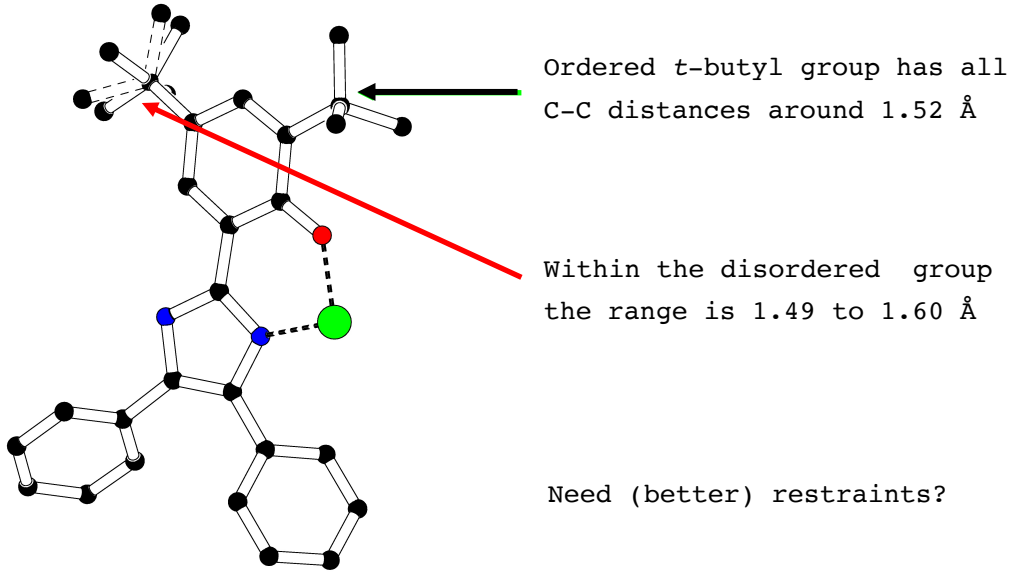


Fig. 3. A ball-and-stick representation of a molecule in which one *tert*-butyl group suffers from disorder and exhibits an unrealistically broad range of C—C distances.

2.13 Summary of a possible validation/checking strategy

- validate the raw CIF using *checkCIF* or *PLATON*
- look at ellipsoid plots from several directions
- check bond lengths are sensible and consistent
- augment the CIF using *e.g. Olex*^{2}, *XCIF*, *publCIF or enCIFer*
- re-validate the final version of the CIF
- whenever changes are made to the CIF, re-validate it

2.14 Validation and IUCr journals

Before the introduction of the CIF format in the early 1990s, results tables tended to be created largely by hand. The only methods for the checking of crystal data were manual, laborious and time-consuming. It was difficult to ensure that all structures were treated consistently, key points were not always checked and a revised submission had to undergo the same laborious checking procedure. In contrast, the CIF allows full electronic submission, automates many editorial tasks and thereby increases efficiency and reduces publication times. Most importantly, it also permits automated validation: authors can check their work before submission and the same validation tools are available to referees, editors and journal staff.

Persistent level A Alerts

If, despite attempts at remedial action, you still get A alerts, the paper may be

rejected immediately unless there is there a sound scientific basis for the outlier. If this is the case you should insert a Validation Response Form (VRF) into the CIF. The VRF will then be assessed and if the Alert has been addressed satisfactorily the paper will be allowed to proceed. The purpose of the VRF is to allow a degree of flexibility in the validation criteria, in part to accommodate non-standard cases, but any exercise of this flexibility must be justified on solid scientific grounds.

How to get a CIF through

- consider all the Alerts
- understand the validation criteria
- if your structure is not routine, explain clearly why not
- avoid casual or circular responses in the VRF
- demonstrate that you understand the causes of the outlier
- explain why the outlier is a real feature of the structure

What causes most problems?

Problems with the resolution or completeness of diffraction data comprise a common source of serious validation Alerts, and they are particularly troublesome because they may require reprocessing or even recollection. However, the criteria are not particularly stringent and they are met daily in laboratories across the world. Other common issues involve inappropriate treatment of hydrogen atoms, structures not at convergence, missing or inadequate absorption corrections and indications of a poor structure determination.

2.15 Validation and other journals

Standards and procedures vary widely, with some journals performing extensive checks, some doing only very basic checks and some doing none at all. In these last circumstances authors should perform their own validation to ensure there are no serious mistakes and that the quality of the determination is at least adequate: they should then submit a copy of the checking report with their paper.

Example of an ACS procedure

- the CIF must contain author names and paper title
- the authors check the CIF prior to submission
- the authors submit/upload the CIF along with the paper
- reviewers have Web access to the CIF

Another procedure

- the authors submit the paper to the journal
- the journal sends the authors a code for the paper
- the authors submit the CIF under this code

A third procedure

- the authors submit the CIF to the CCDC
- the CCDC then sends a deposition number to the authors
- the authors quote the deposition number in the paper
- reviewers can request access to the CIF *via* a web page of the CCDC

2.16 Dealing with "difficult" structures

If you wish to publish a "difficult" structure, that is one which has significant residual problems or which has required non-standard procedures, it is advisable to be very clear about the steps you have taken.

Identify and describe the problem

Referees dealing with a paper containing one or more difficult structures will be reassured if the authors make it clear that they have detected and correctly diagnosed the problems present. It is therefore vital that authors provide a clear description of the non-standard features of the refinement. The principal aim here is to prevent a difficult structure being perceived as problematic, deficient or unsafe.

Give details of the remedial action taken

Similarly, it is essential that the procedure used to deal with any problem is outlined in sufficient detail for the referee to be able to follow the exact actions taken and understand the reasons for these.

Describe the outcome

Perhaps less obviously, it is also important to describe the hopefully successful outcome of the remedial action, even if it is possible to deduce some of the information from various entries in the CIF. By doing so, authors reinforce the impression that they understand what they are doing and that it is unlikely that a better treatment could be devised.

Where and how?

- briefly in any experimental footnote
- at the top of the CIF using the `_refine_special_details` field
- in any other Supplementary Data

Example of text

Identify and describe the problem:

Disorder was identified in one of the two tetrafluoroborate anions. All the F atoms were affected and two orientations were identified.

Give details of remedial action:

Similarity restraints were applied to B–F distances, and to F–B–F angles. All F atoms were refined isotropically. The occupancies of each group of four partially-occupied F atoms were refined competitively. Each F atom was found to be disordered over two equally occupied sites, as shown by the converged group occupancies of 0.506(12) and 0.494(12). In the final cycles of refinement the occupancies of all F atoms were set at 0.5.

Describe the outcome:

In the final model the range of B–F distances was 1.36(2)–1.42(2) Å and the F–B–F angles spanned 105(2)–112(2)°. No difference electron density peak in the disorder region exceeded 0.6 e/Å^3.

2.17 The limits of validation

Automated validation procedures will not detect every problem or error with a structure, and this can occur for a number of reasons. It might be that the relevant test cannot be implemented as an automated test, or this has not yet been done. The required test may not be practical, perhaps because it is hard to differentiate between normal and discrepant values. Perhaps the error is not a validation issue, or the error cannot be detected from data in CIF. Finally, the CIF may contain inappropriate defaults or other nonsensical entries.

The test has not been implemented

Not all conceivable tests have been implemented, and occasionally this leads to a problem not being detected automatically. For example, we can consider the case of an isolated atom which is the only one of its type in the structure. The former feature obviously rules out any rigid-bond test, while the latter precludes any comparison with atoms of the same type. If the atom has a set of uniformly high displacement parameters it will not be detected by any test for extreme displacement parameters. In contrast, it is immediately obvious from the ellipsoid plot (Fig. 4) that there is a serious problem with the refinement model: the atom assigned as a chlorine is probably an oxygen, a conclusion which has serious consequences for the structure and the chemistry.

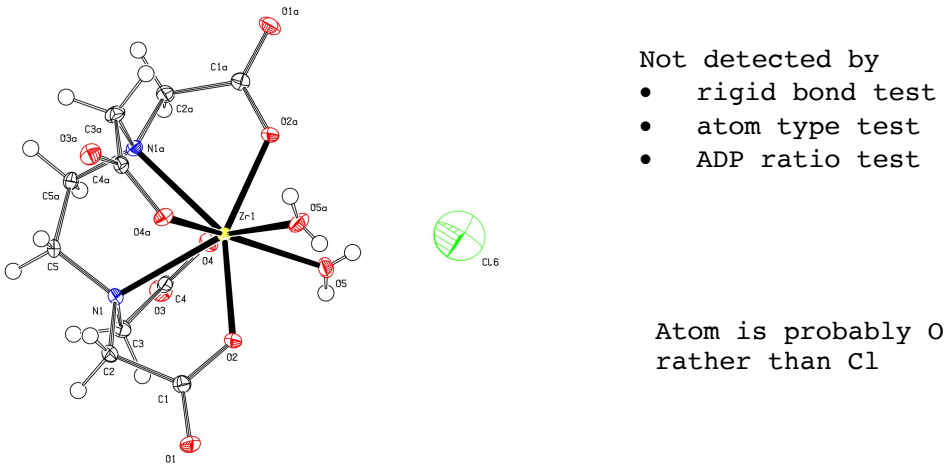


Fig. 4. An ellipsoid plot showing anomalously high but relatively isotropic displacement parameters for one isolated atom.

The test is not practical

Fig. 3 illustrates a molecule in which one *tert*-butyl group is affected by disorder and displays a wide range of C–C distances, from 1.49 to 1.60 Å. Although this range is clearly much wider than for the ordered *tert*-butyl group in the same molecule, no useful test based on C–C single bond distances can be applied because valid examples of these are found within this range. A more sophisticated test based on the geometry of the entire *tert*-butyl group is possible, but this is likely to be computationally demanding and therefore inconsistent with the requirement for rapid validation.

The error is not a validation issue

A CIF may contain errors, perhaps as a result of careless manual editing or the

inappropriate use of software defaults, which cannot be addressed by automatic validation. It may be necessary to rely on wider scientific knowledge to detect possible errors. In the example given below, it is helpful to be aware that iron seldom gives colourless compounds.

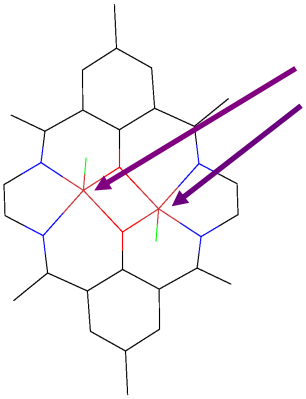
```
_chemical_formula_sum           'C24 H12 Fe O6'
_exptl_crystal_description      needle
_exptl_crystal_colour           colourless
_exptl_crystal_size_max         0.28
_exptl_crystal_size_mid         0.24
_exptl_crystal_size_min         0.03
```

This extract also contains another error, because the description of the crystal as a needle is inconsistent with the dimensions given.

The error cannot be detected from data in CIF unless the hkl data are embedded

In some cases a structure can be seriously in error without this being detectable from the CIF. This is especially so for older CIFs where the reflection data are not embedded in the CIF (*e.g. SHELXL* refinements prior to 2013) or the structure factors (*.fcf* file) are not available. One such situation is where an atom has been assigned as the wrong element: the least-squares refinement may converge to a plausible minimum with this wrong model. Fig. 5 is a chemical diagram of a dinuclear metal complex which was submitted for structure determination along with the prior chemical information that it was either a Ru(II)/Ru(II) or a Ru(II)/Zn(II) complex. The atomic numbers and therefore the relative scattering powers of zinc and ruthenium are 30 and 44, respectively.

Fig. 5. A chemical diagram showing two proposed structures for a dinuclear complex.



Prior chemical information: complex is either Ru / Ru or Ru / Zn

Refinement as Ru / Ru gave R_1 = 0.064; unusual five-coordinate Ru geometry

Alerts about negative residual e-density at metal sites

Refinement as Ru/Zn was ruled out because the two metals were related by symmetry and because this model gave a very high value for R_1. Refinement as Ru/Ru gave a plausible R_1 of 0.064 but with an unusual five-coordinate geometry at each Ru(II) centre. Validation of the CIF containing embedded reflection data would reveal problems of negative residual electron density at the metal atom sites. In the absence of the reflection data, validation provided no conclusive indications of any problem, but a difference electron density map reveals major negative electron density contours (shown as broken lines in Fig. 6) around the metal positions.

Such patterns can indicate that the model has placed too much electron density at these sites, suggesting that the metals might both be Zn rather than Ru. A refinement where both atoms were Zn converged at a much lower R_1 value of 0.022 and gave a much cleaner difference map (Fig. 7). Five-coordinate geometry at Zn(II) is unexceptional.

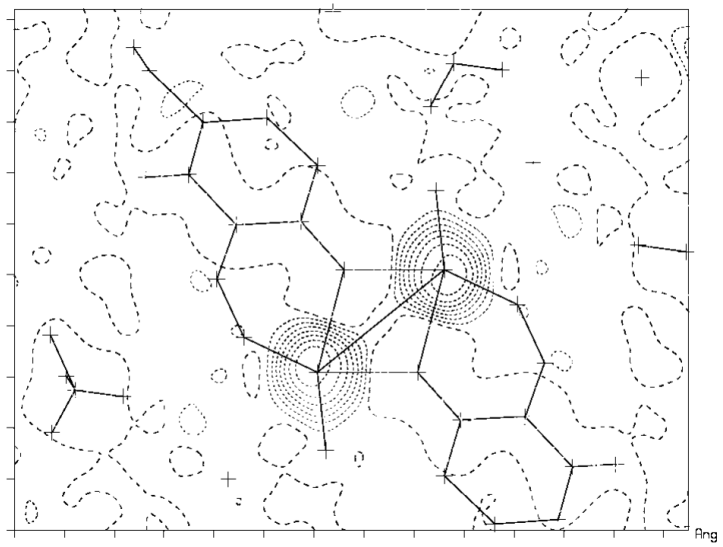


Fig. 6. A difference electron density map calculated using the Ru/Ru model which refines to give R_1 = 0.064. Solid contours indicate positive electron density, broken lines negative electron density and each contour step represents 1 e/Å^3.

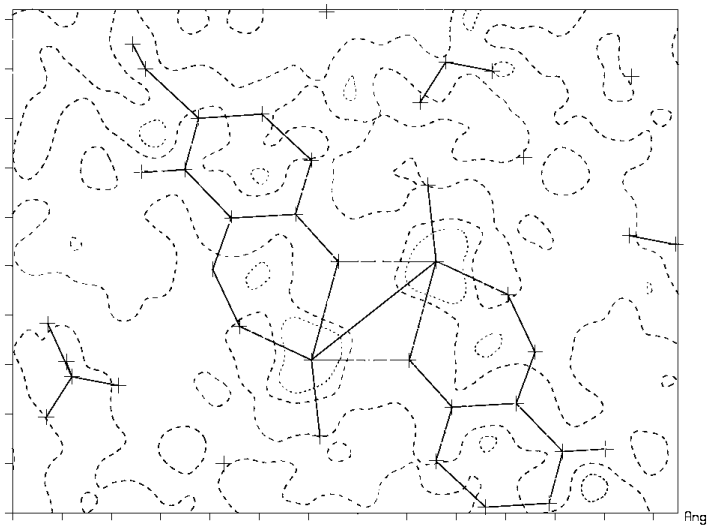


Fig. 7. A difference electron density map calculated using the Zn/Zn model which refines to give R_1 = 0.022. Solid contours indicate positive electron density, broken lines negative electron density and each contour step represents 0.1 e/Å^3

The main value of the difference map lies not in confirming the correct structure but in allowing the detection of the original error and guiding the choice of the correct refinement model. Another example of the application of difference maps include the investigation of the cyanide bridging (Ag–CN–Ag, Ag–NC–Ag or disordered) between two silver(I) ions. The method has also been used to distinguish the Ni (Z = 28) and Fe (Z = 26) centres in heterobimetallic complexes which are models for [NiFe] hydrogenase: if the structure is of high quality the difference maps serve to confirm the results of competitive refinement, but in poorer quality structures they provide the only reliable way to differentiate the metals.

There are circumstances where crystallography simply cannot resolve a particular structural question. An example of such a scenario is provided in Fig. 8 where the challenge is to identify the metal from three possibilities: these are the adjacent lanthanides erbium, thulium and ytterbium which have atomic numbers 68, 69 and 70, respectively.

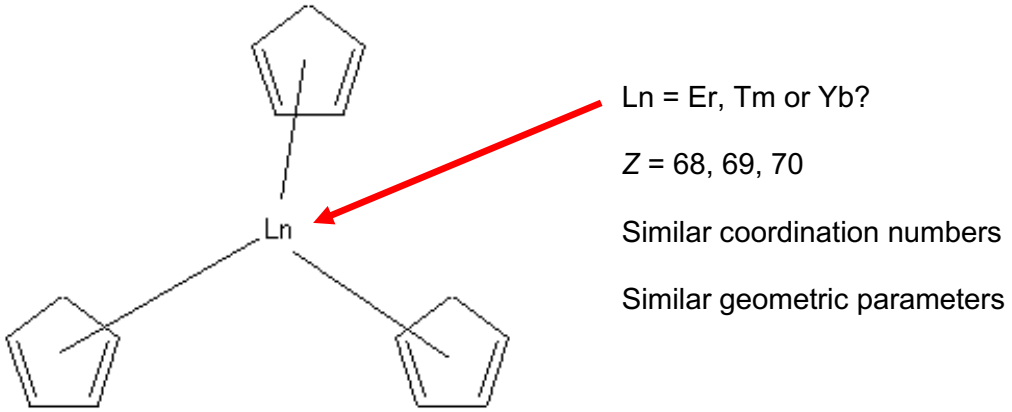


Fig. 8. A chemical diagram of tris(cyclopentadienyl)Ln, where Ln could be any one of the adjacent lanthanides Er, Tm or Yb.

Not only do these elements possess very similar scattering powers, they also exhibit very similar coordination geometries and geometric parameters. The alternative refinement models with the three different metals fit the diffraction data almost equally well, and it is unlikely that a comparison of the difference maps would be conclusive.

There are nonsense entries in the CIF

The issue of nonsensical entries in the CIF has been addressed in the literature (Clegg, 2003). Many of these arise from unsuitable defaults written to the CIF by the refinement software. The data affected include the space group notation, radiation used, data collection temperature, absorption correction factors, the total number of data collected, the index limits, R_{int}, the method of structure solution and the treatment of hydrogen atoms. Manual intervention is required to check and where necessary modify these entries.

2.18 Concluding remarks

Although standard, automated validation checks are vital and must be carried out on every completed structure, they cannot detect every possible problem. Additional checking, for example in the form of graphical visualisation of displacement parameters or difference electron density, is an essential complement, along with ancillary tests based on any relevant scientific knowledge. See Section 2.5 for a list of validation resources and the reprints appended to this chapter for further information on validation and examples.

3 References

Clegg, W. (2003). *Acta Cryst.* E**59**, e2–e5.
Hall, S. R. (1991). *J. Chem. Inf. Comput. Sci.* **31**, 326–333.
Hall, S. R., Allen, F. H. & Brown, I. D. (1991). *Acta Cryst.* A**47**, 655–685.
Spek, A. L. (2003). *J. Appl. Cryst.* **36**, 7–13.
Spek, A. L. (2009). *Acta Cryst.* D**65**, 148–155.