

Structure validation in the submission, review and publication process

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APD - IV,
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Part 1

IUCr

CIF (Crystallographic Information File)

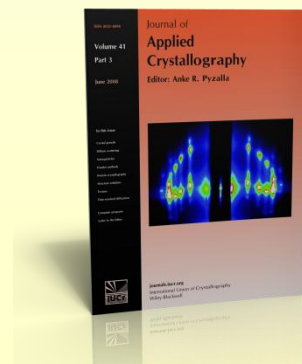
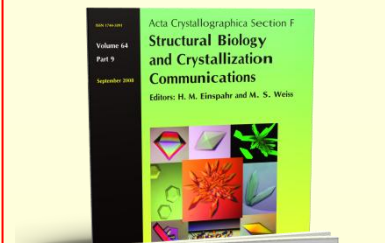
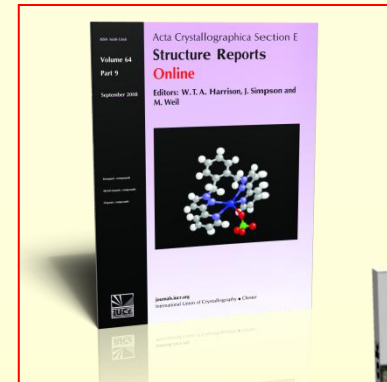
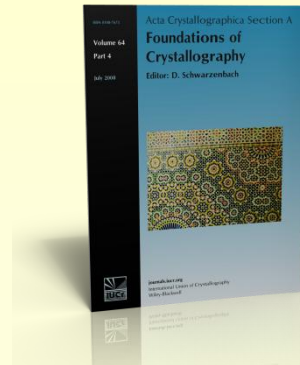
Validation

checkCIF

Tools

International Union of Crystallography

- International Scientific Union
- Publishes 8 research journals:
 - New title in preparation: IUCrJ
- Major reference work *International Tables for Crystallography*
- *Volume H: Powder Diffraction*
- Promotes standard crystallographic data file format (CIF)





IUCrJ

www.iucrj.org

Volume 1 | Part 1 | 1 January 2014 | Pages 1-106



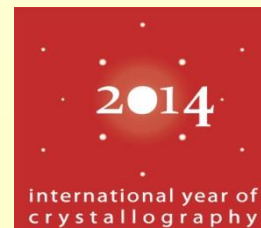
International Union of
CRYSTALLOGRAPHY

ISSN 2052-2525

IUCrJ

The new open-access
high-influence journal
from the IUCr
www.iucrj.org to
celebrate the
**International Year of
Crystallography**

Inaugural issue to be published in 2014



Crystallography
Journals
Online

CIF – A timeline (1)

- 1983, 1988 – Standard Crystallographic File Structure
I.D. Brown
- 1990 – Checking of data in *Acta Cryst. C* papers
- 1991 – Publication of first CIF dictionary
- 1991 – Techniques developed for processing CIF data
First article typeset from a CIF file. Willis *et al.*
- 1992 – First unsolicited CIF submission
- 1994 – Faster processing for CIF submissions
- 1994 – First email versions of checkCIF/printCIF
- 1996 – *Acta Cryst. C* – CIF submission only

CIF – A timeline (2)

- 1997 – Release of powder CIF dictionary (ver. 1.0)
- 1998 – Automated submission by email – use of the VRF (validation response form)
- 1998/9 – web version of checkCIF/printCIF
- 1997-2000 – Electronic only section in *Acta Cryst. C*
- 2001 – Expanded checkCIF to include full PLATON validation test
- 2001 – First edition of *Acta Cryst. E*
- 2007 – Full online submission of CIF, structure factors and figures
- 2008 – *Acta Cryst. E* became an open-access journal

CIF dictionaries

- core CIF 1991
- powder diffraction CIF (pdCIF) 1997
- modulated and composite structures (msCIF) 2002
- electron density (rhoCIF) 2003
- restraints 2011

CIF as a vehicle for article submission

```
_publ_section_title
;\
Diaqua-hexa-μ2-dichloroacetato-
tetrahydrofuran-diiron(III)
;
loop_
  _publ_author_name
  _publ_author_address
  'Sadeghi, Omid'
; Department of Chemistry
  General Campus
  Shahid Beheshti University
  Tehran 1983963113
  Iran
;
  'Ng, Seik Weng'
; Department of Chemistry
  University of Malaya
  50603 Kuala Lumpur
  Malaysia
;
  _publ_section_abstract
; In the oxido-centered
[Fe2Mn(C2HCl2O2)6(H2O)2],
the central O atom is
which are themselves each
dichloroacetate anions
configuration. Two of the
coordinated by a water
is coordinated by a tetrahydrofuran
the crystal, adjacent molecules
O---H...O and O---H...O
centers of inversion, generating a
chain along the c-axis. The MnII
atoms, and the same metal site is
occupied by 1/3Mn + 2/3FeIII.
```

metal-organic compounds

Acta Crystallographica Section E
Structure Reports
Online
ISSN 1600-5368

Diaqua-hexa-μ₂-dichloroacetato-μ₃-oxido-tetrahydrofuran-diiron(III)-manganese(II)

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Correspondence e-mail: seikweng@um.edu.my

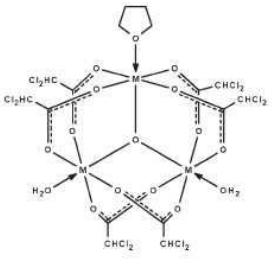
Received 17 December 2009; accepted 17 December 2009

Key indicators: single-crystal X-ray study; T = 295 K; mean σ(C—C) = 0.012 Å; disorder in main residue; R factor = 0.063; wR factor = 0.207; data-to-parameter ratio = 19.4.

In the oxido-centered title compound, [Fe₂Mn(C₂HCl₂O₂)₆(H₂O)(C₄H₈O)(H₂O)₂], the central O atom is linked to three metal atoms, which are themselves each linked to four dichloroacetate anions, and is in a triangular configuration. Two of the metal atoms are each coordinated by a water molecule, whereas the third is coordinated by a tetrahydrofuran molecule. In the crystal, adjacent molecules are linked by O—H...O and O—H...Cl hydrogen bonds across centers of inversion, generating a hydrogen-bonded chain along the c axis. The Mn^{II} atoms are disordered with respect to the Fe^{III} atoms, and the same metal site is occupied by 1/3Mn + 2/3Fe.

Related literature

For aquabis(tetrahydrofuran)hexakis(trifluoroacetato)(μ₃-oxido)M(II)diiron(III) (M = copper, zinc, see: Amini *et al.* (2004a,b)).



M = 1/3Mn^{II} + 2/3Fe^{III}

Experimental

Crystal data
[Fe₂Mn(C₂HCl₂O₂)₆(C₄H₈O)(H₂O)₂]
M_r = 1058.34
Triclinic, P1
a = 9.580 (1) Å
b = 13.316 (1) Å
c = 15.432 (1) Å
α = 90.131 (1)°
β = 100.067 (1)°
γ = 97.677 (1)°
V = 1880.1 (2) Å³
Z = 2
Mo Kα radiation
μ = 2.01 mm⁻¹
T = 295 K
0.35 × 0.15 × 0.15 mm

Data collection
Bruker SMART APEX diffractometer
Absorption correction: multi-scan (SADABS; Sheldrick, 1996)
T_{min} = 0.540, T_{max} = 0.753
15425 measured reflections
8543 independent reflections
5788 reflections with I > 2σ(I)
R_{int} = 0.025

Refinement
R[F² > 2σ(F²)] = 0.063
wR(F²) = 0.207
S = 1.03
8543 reflections
440 parameters
35 restraints
H atoms treated by a mixture of independent and constrained refinement
Δρ_{max} = 1.64 e Å⁻³
Δρ_{min} = -0.90 e Å⁻³

Table 1

Hydrogen-bond geometry (Å, °)

D—H...A	D—H	H...A	D...A	D—H...A
O1w—H11...O3 ⁱ	0.85 (1)	2.01 (3)	2.809 (6)	158 (5)
O2w—H22...O8 ⁱ	0.85 (1)	2.08 (4)	2.821 (5)	149 (7)
O2w—H21...O13 ⁱ	0.84 (6)	2.19 (7)	2.950 (6)	150 (6)
O1w—H12...Cl1 ⁱ	0.85 (3)	2.47 (4)	3.288 (4)	160 (6)

Symmetry codes: (i) -x+1, -y+1, -z; (ii) -x+1, -y+1, -z+1.

Data collection: APEX2 (Bruker, 2008); cell refinement: SAINT (Bruker, 2008); data reduction: SAINT; program(s) used to solve structure: SHELXS97 (Sheldrick, 2008); program(s) used to refine structure: SHELXL97 (Sheldrick, 2008); molecular graphics: X-SEED (Barbour, 2001); software used to prepare material for publication: publCIF (Westrip, 2010).

The authors thank Shahid Beheshti University and the University of Malaya for supporting this study.

Supplementary data and figures for this paper are available from the IUCr electronic archives (Reference: CI2991).

References

Amini, M. M., Yadavi, M. & Ng, S. W. (2004a). *Acta Cryst.* E60, m492–m494.
Amini, M. M., Yadavi, M. & Ng, S. W. (2004b). *Acta Cryst.* E60, m495–m497.
Barbour, L. J. (2001). *J. Supramol. Chem.* 1, 189–191.
Bruker (2008). APEX2 and SAINT. Bruker AXS Inc., Madison, Wisconsin, USA.
Sheldrick, G. M. (1996). *SADABS*. University of Göttingen, Germany.
Sheldrick, G. M. (2008). *Acta Cryst.* A64, 112–122.
Westrip, S. P. (2010). *publCIF*. In preparation.

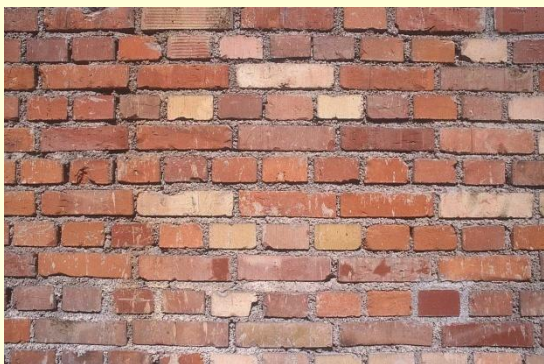
Acta Cryst. (2010). E66, m101
doi:10.1107/S1600536809054518
Sadeghi *et al.* m101

```
SHELXL-97
c
oacetato-μ3-oxido-
(II)manganese (II)
) 6 O (C4 H8 O) (H2 O)2 ]'
C16 H18 Cl12 Fe2 Mn O16'
1058.34
triclinic
me_H-M 'P -1'
me_Hall '-P 1'
xyz
z'
```

9.380 (1)
13.316 (1)
15.432 (1)
90.131 (1)
100.067 (1)
97.677 (1)
1880.1 (2)

Crystallography
Journals
Online

Validation with checkCIF



Brick Wall

OR



Useful set of
tools



What is validation?

Comparison against a set of test criteria

- Are all the usually expected data and information present?
- Are related parameters consistent?
- Is the space group correct?
- Has the refinement converged?
- Are the assigned atom types correct?
- Is the structure reasonable?
- Has the structure been determined before?

Is validation needed?

CIF made possible the automated checking of structure determinations.

- Incomplete CIFs
- Syntax errors in CIFs
- Too many avoidable oversights
- Doesn't meet accepted standards
- More non-experts determining structures

- Still some avoidable mistakes

Automation of validation

- Allows authors to get anonymous and instant feedback
- Detect and fix problems prior to submission
- Fewer and shorter revision cycles
- Consistent application of criteria
- Known application of criteria (**no hidden hurdles to jump**)
- Allows editors and referees to focus on the science

- **Benefit – faster publication times!**

What does validation software do?

- Identifies possible problems via ALERTs
- Provides explanations of ALERTs
- Suggests interpretations and possible solutions
- A tool to help the author
 - efficiently check their work
 - avoid simple mistakes

- Not intended as a hurdle to make life difficult
- Not intended to hinder publication of correct results
- Also a useful tool for reviewers

Alert indicators

380 ALERT 4 C Likely Unrefined X(sp²)-Methyl Moiety C18
412 ALERT 2 C Short Intra XH3 .. XHn : H19B .. H30A = 1.81 Ang.
720 ALERT 4 C Number of Unusual/Non-Standard Label(s) 1

Alert numbers 1-5
indicate the type of issue

Alerts levels A, B, C and G indicate
the severity of the issue

Alert levels and types

ALERT level A = Most likely a serious problem – resolve or explain

ALERT level B = A potentially serious problem, consider carefully

ALERT level C = Check. Ensure it is not caused by an omission or oversight

ALERT level G = General information/check it is not something unexpected

ALERT type 1 CIF construction/syntax error, inconsistent or missing data

ALERT type 2 Indicator that the structure model may be wrong or deficient

ALERT type 3 Indicator that the structure quality may be low

ALERT type 4 Improvement, methodology, query or suggestion

ALERT type 5 Informative message, check

Alert level A

Alert A Most likely a serious problem – resolve or explain

Required item omitted, large deviation from usually expected value, or inconsistent values

Alert A No crystal dimensions have been given

Alert A Atom C58A ADP max/min Ratio 18.00

Alert A H...A calc 5.82(3); rep 1.915; dev 3.91 Å

Alert A Space group symbol does not match sym. ops.

Alert level B

Alert B A potentially serious problem, consider carefully

Item is a significant or unexpected outlier

- Alert B The formula has elements in wrong order
- Alert B ADDSYM detects Cc to Fdd2 transformation
- Alert B Refined extinction parameter $< 1.9\sigma$
- Alert B Structure contains VOIDS of 130.00 \AA^3

Validation Response Form

- Indicates that there are issues which have triggered a level A alert
- Provides a field for the author to respond to the alert

PLAT355_ALERT_3_A Long O-H Bond (0.82A) O22 - H220 ... 1.14 Ang.

_vrf_PLAT355_I

; PROBLEM: Long O-H Bond (0.82A) O22 - H220 ... 1.14 Ang.

RESPONSE: The H220 atom participates in a very strong nearly symmetric hydrogen bond which is discussed in details in the paper.

;

Example of an unsuitable VRF

- Alert A** Given & expected crystal density differ
- Alert A** Given & expected absorption co-efficient differ
- Calculated density = 3.377 density in CIF = 1.689
- Calculated mu = 2.063 mu in CIF = 1.031

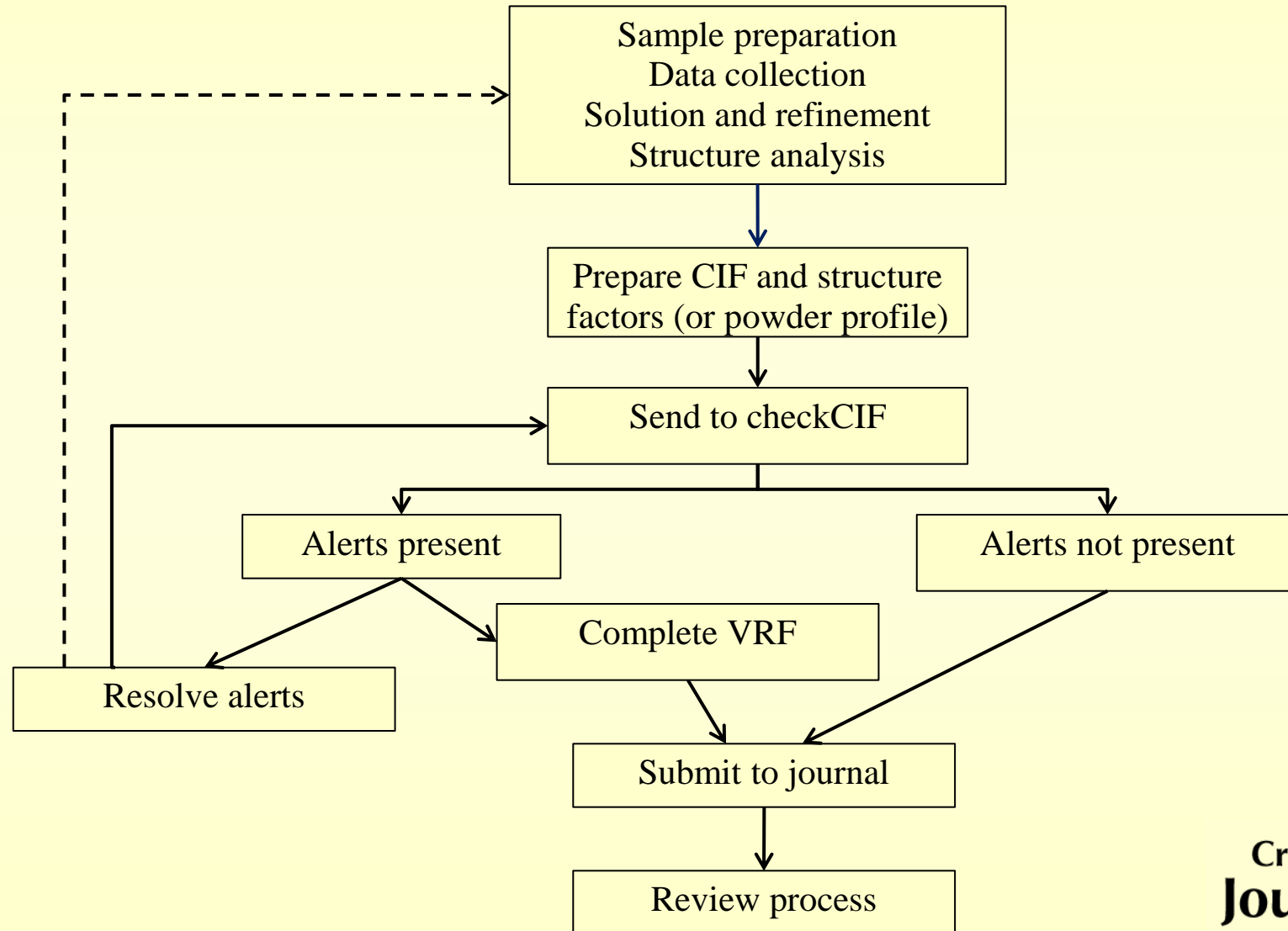
Author Response:

It appears that the absmu- and the density-problem are related. No explanation other than it is related to the disordered triflate groups and the refinement over several partially occupied sites

Actual cause of alert:

Molecule sits over inversion centre in $P2_1/n$
Z given as 4, instead of 2

checkCIF workflow



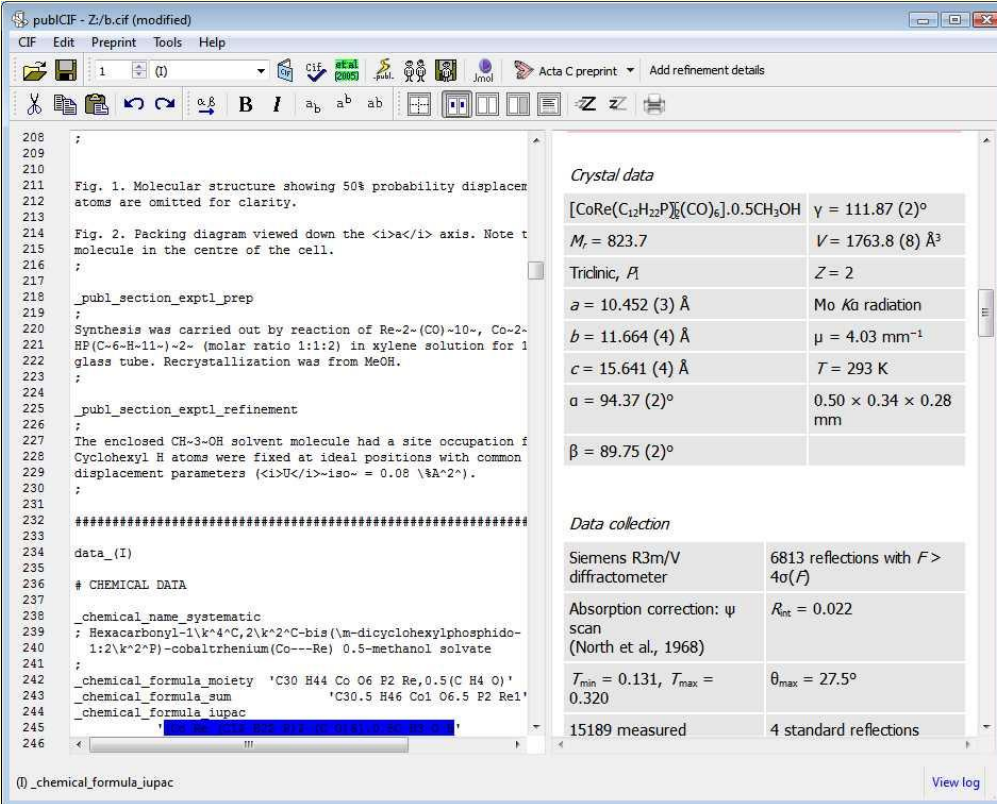
Limitations of validation

- Test is not yet implemented
- Test is not practical in these circumstances
- Error is not a validation issue
- Mistake cannot be detected from data in the CIF
- Nonsense entries in the CIF

Authoring tools

(1) *publCIF*

Desktop CIF publishing editor, validator and formatter for small-molecule, powder, modulated and incommensurate structure CIFs



The screenshot shows the publCIF software interface. The main window displays the CIF file content, which includes figure captions, synthesis details, and chemical data. The right-hand panel shows the following information:

Crystal data	
$[\text{CoRe}(\text{C}_{12}\text{H}_{22}\text{P})_2(\text{CO})_6] \cdot 0.5\text{CH}_3\text{OH}$	$\gamma = 111.87 (2)^\circ$
$M_r = 823.7$	$V = 1763.8 (8) \text{ \AA}^3$
Triclinic, $P1$	$Z = 2$
$a = 10.452 (3) \text{ \AA}$	Mo $K\alpha$ radiation
$b = 11.664 (4) \text{ \AA}$	$\mu = 4.03 \text{ mm}^{-1}$
$c = 15.641 (4) \text{ \AA}$	$T = 293 \text{ K}$
$\alpha = 94.37 (2)^\circ$	$0.50 \times 0.34 \times 0.28 \text{ mm}$
$\beta = 89.75 (2)^\circ$	

Data collection	
Siemens R3m/V diffractometer	6813 reflections with $F > 4\sigma(F)$
Absorption correction: ψ scan (North et al., 1968)	$R_{int} = 0.022$
$T_{min} = 0.131$, $T_{max} = 0.320$	$\theta_{max} = 27.5^\circ$
15189 measured	4 standard reflections

<http://journals.iucr.org/services/cif/publCIF/>

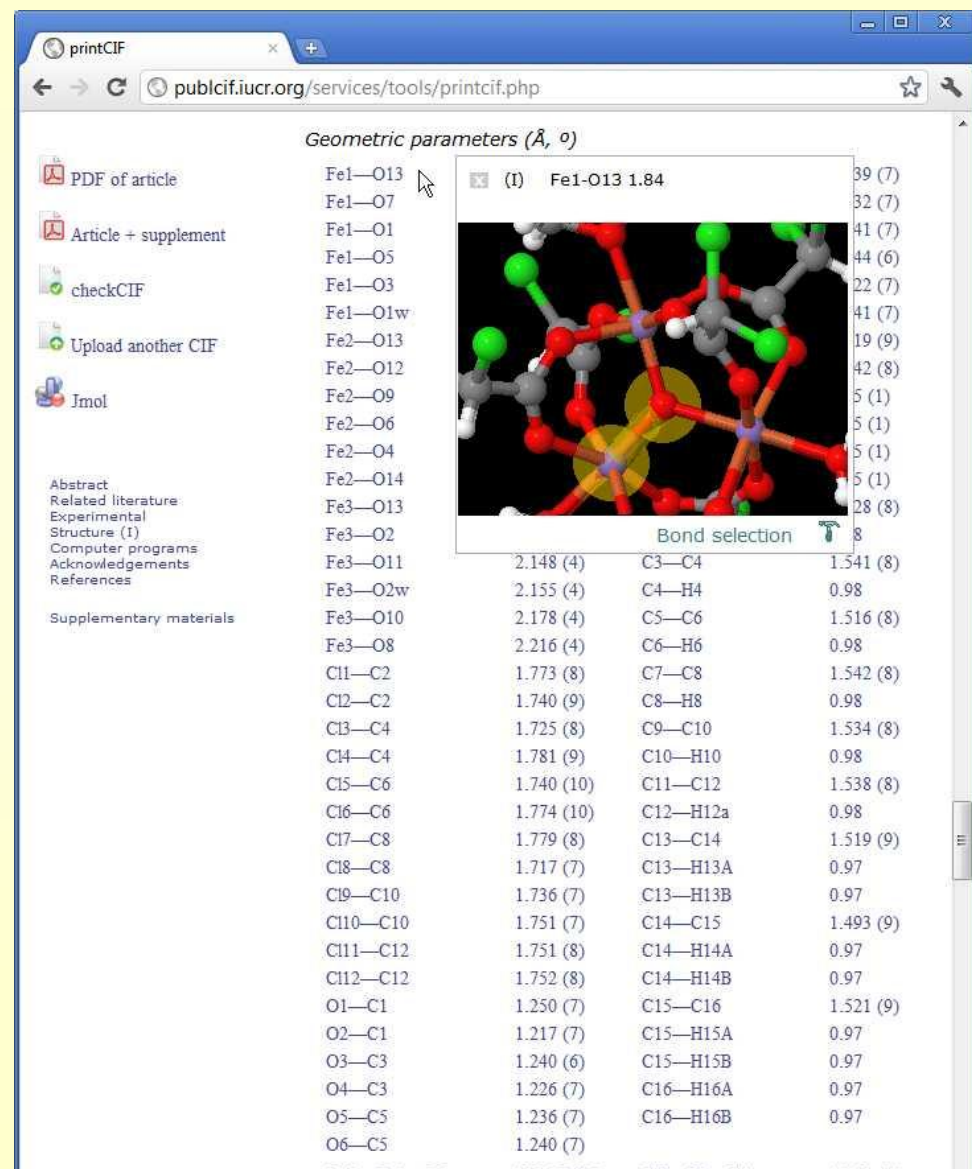
Crystallography
Journals
Online

Authoring tools

(2) *printCIF*

Online CIF publishing validator and formatter for small-molecule, powder, modulated and incommensurate structure CIFs

<http://publCIF.iucr.org/services/tools/printcif.php>



The screenshot displays the printCIF web application interface. The browser address bar shows the URL `publCIF.iucr.org/services/tools/printcif.php`. The page title is "printCIF".

On the left side, there is a navigation menu with the following items:

- PDF of article
- Article + supplement
- checkCIF
- Upload another CIF
- Jmol
- Abstract
- Related literature
- Experimental
- Structure (1)
- Computer programs
- Acknowledgements
- References
- Supplementary materials

The main content area is titled "Geometric parameters (\AA , $^\circ$)". It contains a table of bond lengths and angles. A mouse cursor is hovering over the "Fe1—O13" entry, which has opened a pop-up window showing a 3D ball-and-stick model of the crystal structure with the selected bond highlighted in yellow. The pop-up window also displays the bond length "Fe1—O13 1.84" and the label "Bond selection".

Geometric parameters (\AA , $^\circ$)	
Fe1—O13	1.84 (7)
Fe1—O7	2.02 (7)
Fe1—O1	2.04 (7)
Fe1—O5	2.04 (6)
Fe1—O3	2.02 (7)
Fe1—O1w	2.04 (7)
Fe2—O13	2.04 (9)
Fe2—O12	2.02 (8)
Fe2—O9	2.04 (1)
Fe2—O6	2.04 (1)
Fe2—O4	2.04 (1)
Fe2—O14	2.04 (1)
Fe3—O13	2.02 (8)
Fe3—O2	2.04 (8)
Fe3—O11	2.148 (4)
Fe3—O2w	2.155 (4)
Fe3—O10	2.178 (4)
Fe3—O8	2.216 (4)
Cl1—C2	1.773 (8)
Cl2—C2	1.740 (9)
Cl3—C4	1.725 (8)
Cl4—C4	1.781 (9)
Cl5—C6	1.740 (10)
Cl6—C6	1.774 (10)
Cl7—C8	1.779 (8)
Cl8—C8	1.717 (7)
Cl9—C10	1.736 (7)
Cl10—C10	1.751 (7)
Cl11—C12	1.751 (8)
Cl12—C12	1.752 (8)
O1—C1	1.250 (7)
O2—C1	1.217 (7)
O3—C3	1.240 (6)
O4—C3	1.226 (7)
O5—C5	1.236 (7)
O6—C5	1.240 (7)
C3—C4	1.541 (8)
C4—H4	0.98
C5—C6	1.516 (8)
C6—H6	0.98
C7—C8	1.542 (8)
C8—H8	0.98
C9—C10	1.534 (8)
C10—H10	0.98
C11—C12	1.538 (8)
C12—H12a	0.98
C13—C14	1.519 (9)
C13—H13A	0.97
C13—H13B	0.97
C14—C15	1.493 (9)
C14—H14A	0.97
C14—H14B	0.97
C15—C16	1.521 (9)
C15—H15A	0.97
C15—H15B	0.97
C16—H16A	0.97
C16—H16B	0.97

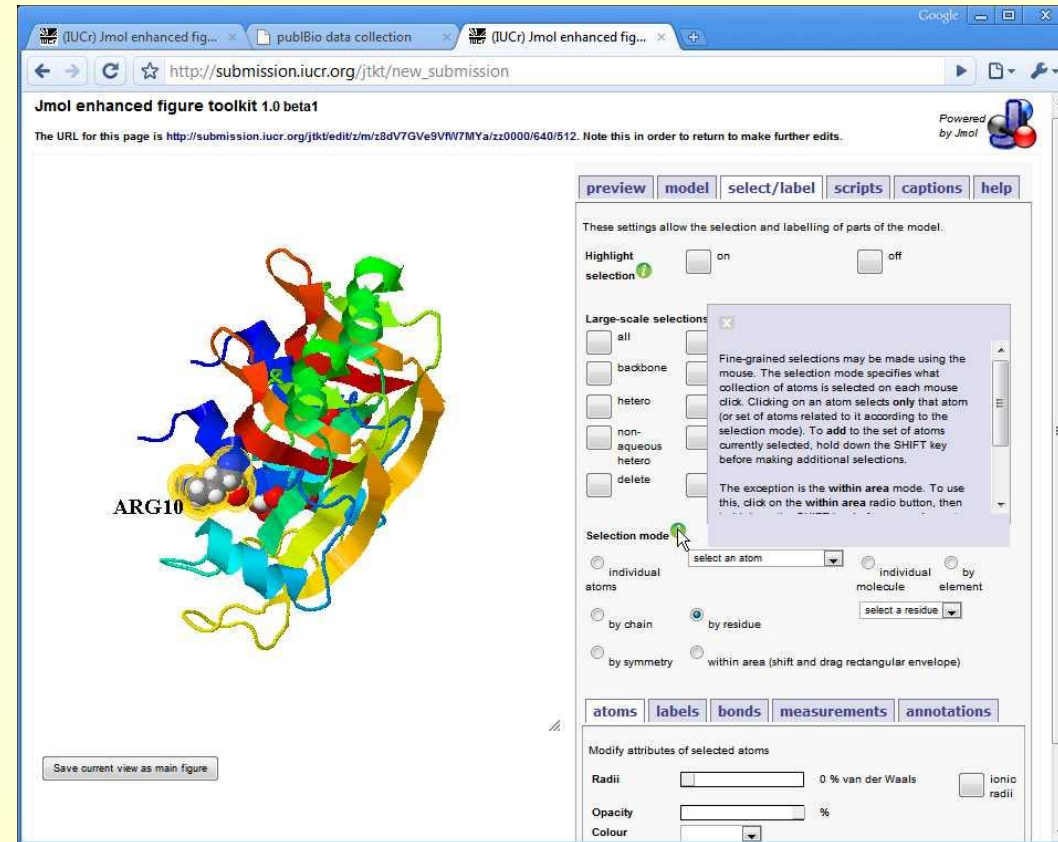
Authoring tools

(3) *Enhanced figure toolkit*

Create interactive three-dimensional visualisations with *Jmol*, a viewer that allows direct interaction with the underlying data

These figures form an *integral* part of the online published article

<http://submission.iucr.org/jtk>



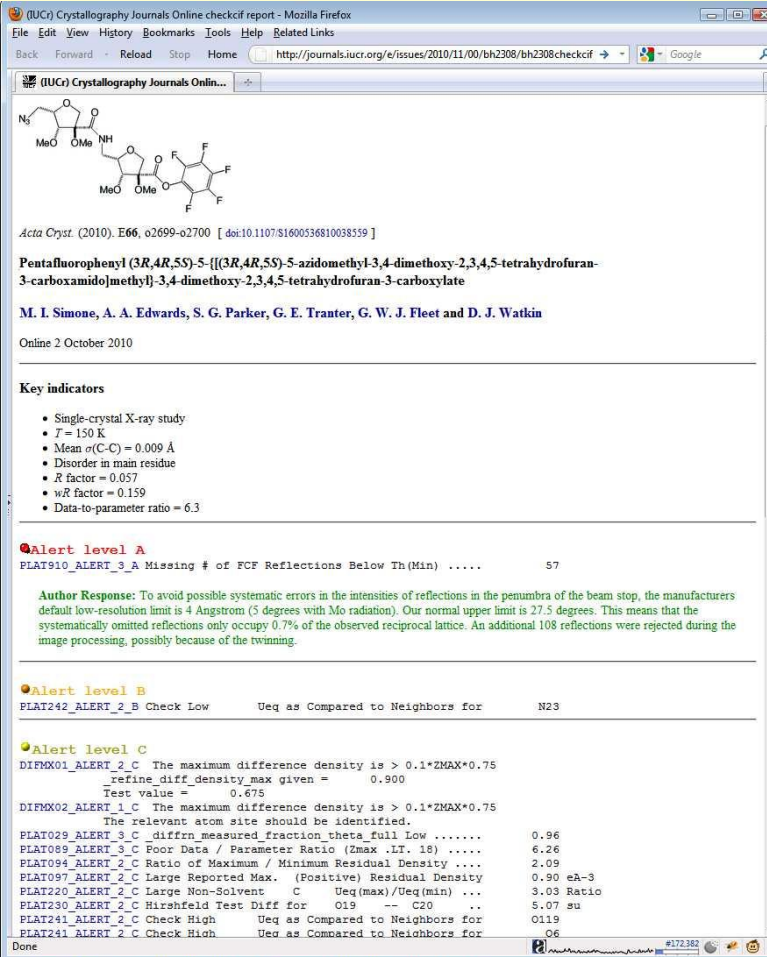
The screenshot displays the Jmol enhanced figure toolkit interface. The main window shows a 3D ribbon representation of a protein structure with a specific residue labeled ARG10. The interface includes a navigation bar with tabs for 'preview', 'model', 'select/label', 'scripts', 'captions', and 'help'. A control panel on the right allows for selection and labeling of parts of the model, with options for 'Highlight selection' (on/off), 'Large-scale selections' (all, backbone, hetero, non-aqueous hetero, delete), and 'Selection mode' (individual atoms, by chain, by symmetry, individual molecule/element, by residue, within area). A tooltip explains fine-grained selections. At the bottom, there are controls for 'atoms', 'labels', 'bonds', 'measurements', and 'annotations', along with a 'Save current view as main figure' button.

Authoring tools

(4) *checkCIF*

- checkCIF reports are generated following the upload of a CIF to the checkCIF service
 - For single-crystal studies the structure factors are also validated
- Within the submission system the checkCIF report is made available to the reviewers

<http://checkcif.iucr.org/>



(IUCr) Crystallography Journals Online checkcif report - Mozilla Firefox

Back Forward Reload Stop Home <http://journals.iucr.org/e/issues/2010/11/00/bh2308/bh2308checkcif> Google

(IUCr) Crystallography Journals Online

COC1OC(COC2=CC=CC=C2F)N(C1)C3=CC=CC=C3F

Acta Cryst. (2010), E66, o2699-o2700 [doi:10.1107/S1600536810038559]

Pentafluorophenyl (3*R*,4*R*,5*S*)-5-[[*(*3*R*,4*R*,5*S*)-5-azidomethyl-3,4-dimethoxy-2,3,4,5-tetrahydrofuran-3-carboxamido]methyl]-3,4-dimethoxy-2,3,4,5-tetrahydrofuran-3-carboxylate

M. I. Simone, A. A. Edwards, S. G. Parker, G. E. Tranter, G. W. J. Fleet and D. J. Watkin

Online 2 October 2010

Key indicators

- Single-crystal X-ray study
- $T = 150$ K
- Mean $\sigma(\text{C-C}) = 0.009$ Å
- Disorder in main residue
- R factor = 0.057
- wR factor = 0.159
- Data-to-parameter ratio = 6.3

Alert level A

PLAT910_ALERT_3_A Missing # of FCF Reflections Below Th (Min) 57

Author Response: To avoid possible systematic errors in the intensities of reflections in the penumbra of the beam stop, the manufacturers default low-resolution limit is 4 Angstrom (5 degrees with Mo radiation). Our normal upper limit is 27.5 degrees. This means that the systematically omitted reflections only occupy 0.7% of the observed reciprocal lattice. An additional 108 reflections were rejected during the image processing, possibly because of the twinning.

Alert level B

PLAT242_ALERT_2_B Check Low Ueq as Compared to Neighbors for N23

Alert level C

DIFMX01_ALERT_2_C The maximum difference density is > 0.1*ZMAX*0.75
refine_diff_density_max given = 0.900
Test value = 0.675

DIFMX02_ALERT_1_C The maximum difference density is > 0.1*ZMAX*0.75
The relevant atom site should be identified.

PLAT029_ALERT_3_C diffn_measured_fraction_theta_full Low	0.96
PLAT089_ALERT_3_C Poor Data / Parameter Ratio (Zmax .LT. 18)	6.26
PLAT094_ALERT_2_C Ratio of Maximum / Minimum Residual Density	2.09
PLAT097_ALERT_2_C Large Reported Max. (Positive) Residual Density	0.90 eA-3
PLAT220_ALERT_2_C Large Non-Solvent C Ueq(max)/Ueq(min) ..	3.03 Ratio
PLAT230_ALERT_2_C Hirshfeld Test Diff for O19 -- C20 ..	5.07 su
PLAT241_ALERT_2_C Check High Ueq as Compared to Neighbors for	0.119
PLAT241_ALERT_2_C Check High Ueq as Compared to Neighbors for	0.06

Done

Authoring tools

(5) *Experimental tables*

Online service for formatting complex geometry and experimental tables for small-molecule, powder, modulated and incommensurate structure CIFs

Output available in rtf format

<http://publCIF.iucr.org/services/tools/>

CIF geometry data tables - Mozilla Firefox

Show/hide non-selected geometry Select... Change layout Download RTF document

Prepare table of experimental details Upload another CIF

Select/deselect a single parameter by clicking it; select/deselect a group of parameters by dragging the mouse over them.
Move a single parameter by dragging its icon
Move a group of parameters that have the same selection state by holding down the SHIFT key before dragging the icon of the first parameter in the group.
Move a structure block by dragging its icon

(I) Co-Re-C1 134.8

Bonds Angles Hydrogen bonds

Select... Jmol

Co—Re—P1	46.4(1)	Co—P2—C41	120.1(2)
Co—Re—P2	46.5(1)	C31—P2—C41	109.3(2)
Co—Re—C1	134.8(2)	Re—C1—O1	177.6(5)
Co—Re—C2	86.9(2)	Re—C2—O2	178.7(5)
Co—Re—C4	135.1(2)	Re—C3—O3	180.0(9)
P1—Re—P2	92.9(1)	Re—C4—O4	178.3(5)
P1—Re—C1	88.4(2)	Co—C5—O5	175.5(7)
P1—Re—C2	90.4(2)	Co—C6—O6	176.2(6)
P1—Re—C3	87.6(2)	P1—C11—C12	117.1(4)
P1—Re—C4	177.4(1)	P1—C11—C16	114.2(3)
P2—Re—C1	178.6(2)	C12—C11—C16	110.5(5)
		C11—C12—C13	111.3(5)

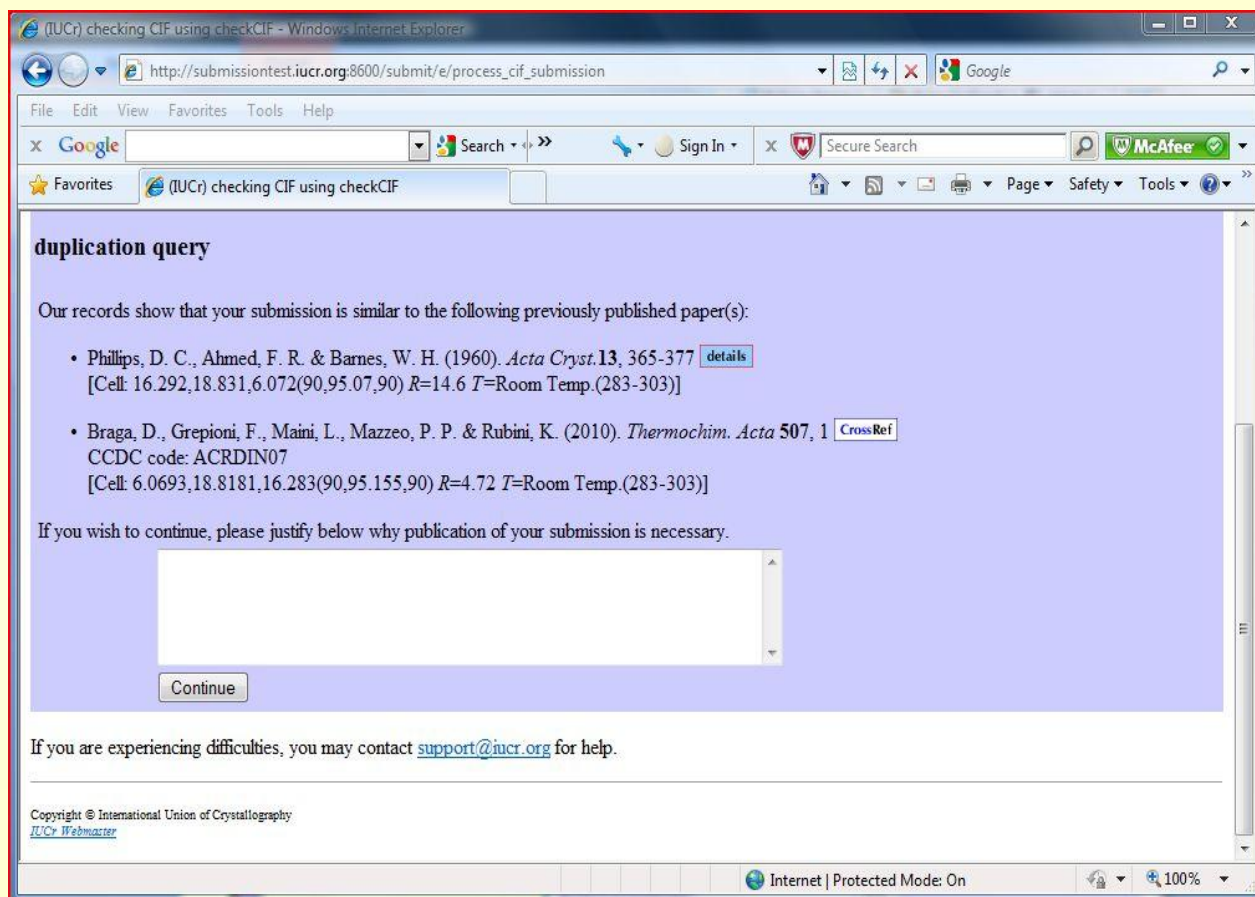
Angle selection

Duplication query

The system checks the article against an internal database to determine if the structure has been submitted to or published by the IUCr previously.

In addition an automated check is performed against the CCDC database.

If duplicates occur, then the author is able to note why their article should be considered for publication.



The screenshot shows a web browser window titled "(IUCr) checking CIF using checkCIF - Windows Internet Explorer". The address bar displays the URL http://submissionstest.iucr.org:8600/submit/e/process_cif_submission. The page content is as follows:

duplication query

Our records show that your submission is similar to the following previously published paper(s):

- Phillips, D. C., Ahmed, F. R. & Barnes, W. H. (1960). *Acta Cryst.* **13**, 365-377 [details](#)
[Cell: 16.292,18.831,6.072(90,95.07,90) R=14.6 T=Room Temp.(283-303)]
- Braga, D., Grepioni, F., Maini, L., Mazzeo, P. P. & Rubini, K. (2010). *Thermochim. Acta* **507**, 1 [CrossRef](#)
CCDC code: ACRDIN07
[Cell: 6.0693,18.8181,16.283(90,95.155,90) R=4.72 T=Room Temp.(283-303)]

If you wish to continue, please justify below why publication of your submission is necessary.

If you are experiencing difficulties, you may contact support@iucr.org for help.

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Internet | Protected Mode: On

Why publish data?

Some reasons:

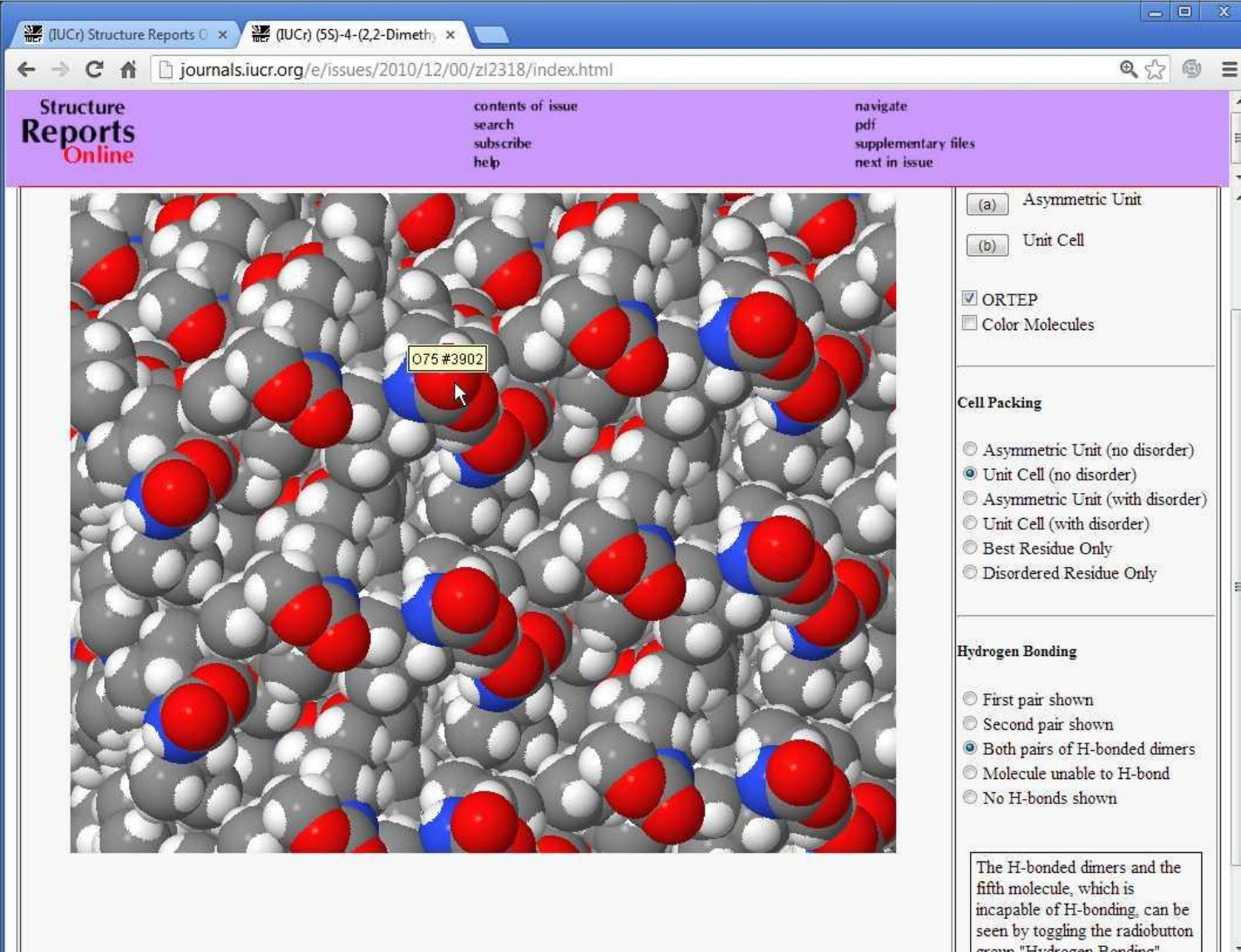
- To enhance the reproducibility of a scientific experiment
- To verify or support the validity of deductions from an experiment
- To safeguard against error
- To safeguard against fraud
- To allow other scholars to conduct further research based on experiments already conducted
- To allow reanalysis at a later date, especially to extract 'new' science as new techniques are developed
- To provide example materials for teaching and learning
- To provide long-term preservation of experimental results and future access to them
- To permit systematic collection for comparative studies

Reading the data

Interactive figures as an *integral* part of the article

Author views

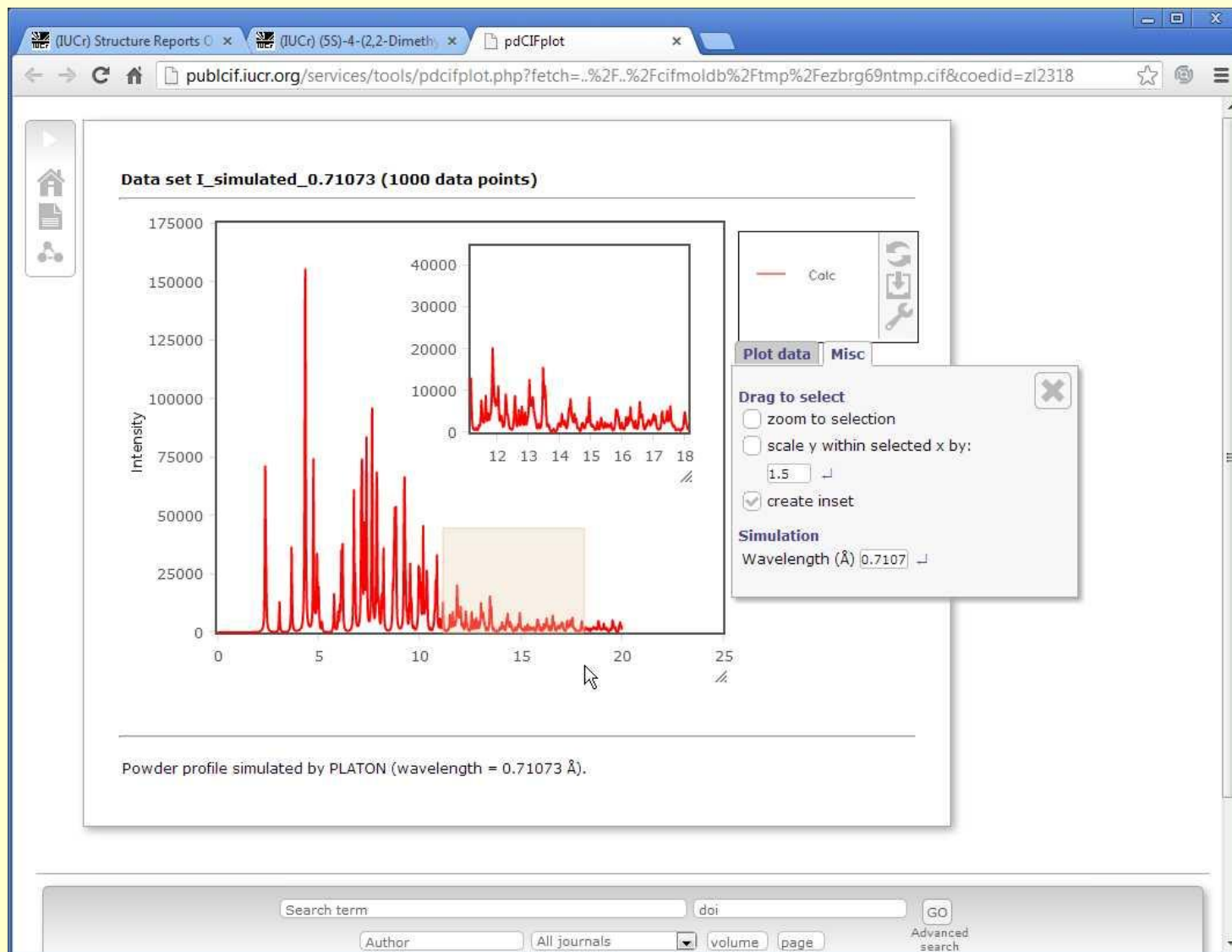
Reader freedom to explore



The screenshot displays the IUCr Structure Reports Online interface. The browser address bar shows the URL: journals.iucr.org/e/issues/2010/12/00/zi2318/index.html. The page header includes the IUCr logo and navigation links: contents of issue, search, subscribe, help, navigate pdf, supplementary files, and next in issue. The main content area features a 3D molecular model of a crystal structure, with a tooltip indicating the molecule ID "O75 #3902". The right sidebar contains interactive controls for the model, including radio buttons for (a) Asymmetric Unit and (b) Unit Cell, a checked checkbox for ORTEP, and an unchecked checkbox for Color Molecules. Below these are options for Cell Packing: Asymmetric Unit (no disorder), Unit Cell (no disorder) (selected), Asymmetric Unit (with disorder), Unit Cell (with disorder), Best Residue Only, and Disordered Residue Only. Further down are options for Hydrogen Bonding: First pair shown, Second pair shown, Both pairs of H-bonded dimers (selected), Molecule unable to H-bond, and No H-bonds shown. A text box at the bottom right explains that the H-bonded dimers and the fifth molecule, which is incapable of H-bonding, can be seen by toggling the radiobutton group "Hydrogen Bonding".

Working with the data

For *any* published structure, the reader can *generate* a predicted powder diffraction pattern



Part 2

CIF for powder studies Current perspective The future

Advantages of CIF for powder studies


- Data in CIF ideally written directly by refinement software – fewer errors
- Forms a complete record of the experiment
- Data validation possible
- Can use to typeset experimental details, coordinates, bond lengths, angles etc. for journal article or thesis – fewer errors
- Easier and quicker for authors

Successful?

- Single-crystal studies – yes (aided by a small number of refinement programs)
- Single phase
- Single data set
- Straightforward experiment
- Can validate with checkCIF – useful results

Powder studies

- Several refinement programs
- Different output (different residuals etc.)
- One phase/multiple phases
- One data set/multiple data sets (and weighting)
- Multiple wavelengths (Cu K α , synchrotron, neutron, time of flight...)
- Diverse experiments (but all can be described using the powder CIF dictionary)

- 
- Refinement program might not write all necessary details to CIF
 - CIF may have to be created by hand – errors!
 - checkCIF struggles with multiple phase studies, time of flight experiments, ‘non-standard’ wavelengths...
 - Powder diffractionists go elsewhere...

Short term – improve checkCIF

- Suppress irrelevant tests
- Add powder-specific tests
- Develop checkCIF so can handle multiple data blocks/`non-standard' wavelengths
- Expertise requested for validation of powder data based structures and incommensurate structures
- Feedback and suggestions welcome

Long-term measures

- Could existing refinement programs write more details to the CIF?
- Could we ask for other file formats as a record of the experiment?
- Develop a tool to read the most common file formats (which are these?) and convert them to powder CIF

Data deposition

- Raw data? (Too unwieldy?)
- Profile (not necessarily in CIF format)
- Structure factors, if available?
- IUCr Data Deposition Working Group – suggestions welcome

International Tables for Crystallography

- Volume H on powder diffraction
- Editors: Chris Gilmore, Jim Kaduk and Henk Schenk
- Due 2014
(International Year of Crystallography)



Thank you

