

QUESTIONNAIRE FOR the
STRUCTURE DETERMINATION BY POWDER DIFFRACTOMETRY ROUND ROBIN - 3

d

Please answer all questions as completely as possible. Provide one filled questionnaire for each data (samples 1 and 2).

Preferably, attach the results as one PDF file or as a MS Word document compressed by Winzip.

It is advised to complete the form as the structure determination progress.

0.0 Precise date of

- data download : Fri, 1 Feb 2008 afternoon
- results submission : Fri, 8 Feb 2008

0.1 Is the first sample structure solvable with this quality of data ? Yes [*] No []

0.2 Is the second sample structure solvable with this quality of data ? Yes [*] No []

0.3 If not, what data would be required ?

Then, for each sample :

1. Preliminary work

1.1 Did you obtained additional informations ? No.
(for instance from CSD or ICSD or ICDD databases)

1.2 Did you obtained additional informations from the powder pattern ? If yes, how and what information ? No.
(for instance using the JCPDS-ICDD database)

1.3 Did you extract the structure factors ? Yes [*] No []

I extracted intensities using the Le Bail method with GSAS and used for input to Shelxs or Sir2002. Later on, I tried to perform whole pattern decomposition with EXPO, also without much success.

1.3.1 If yes, which program(s) did you use ?

1.3.2 Give the angular range: 8-50 in 2theta

1.3.3 Give the number of extracted structure factors: 180

1.3.4 Give the Rp and Rwp (conventional Rietveld, background subtracted): 0,0649 and 0,0658 with Manually determined background points

1.3.5 Give the Rp and Rwp (background not subtracted): 0,0279 and 0,0383

1.3.6 If not, did you use the whole pattern ?

1.3.7 Or a partial pattern (if yes, give the angular range):

1.3.8 If you use the whole or a partial pattern, did you keep fixed the profile parameters, and if yes, how did you obtained them ?

2- Structure solution

2.1 Did you use direct methods ? Yes [*] No []

2.1.1 If yes, was it on the whole dataset ? On the extracted reflections

2.1.2 Or on a partial dataset ?

2.1.3 Give the number of reflections: 180

2.1.4 Which program(s) did you use ? Shelxs, Sir2002

2.1.5 Did you modified intensities of closely neighbouring reflections ? If yes, explain how. No.

2.2 Did you use Patterson methods ? Yes [*] No []

2.2.1 If yes, was it on the whole dataset ? On the same set of extracted intensities.

2.2.2 Or on a partial dataset ?

2.2.3 Give the number of reflections: 180

2.2.4 Which program(s) did you use ? Shelxs

2.2.5 Did you modified intensities of closely neighbouring reflections ? If yes, explain how. No.

2.3 Did you use another method ? Yes [*] No []

2.3.1 If yes, which method(s) (give details : molecule location by direct space - genetic algorithm, Monte Carlo, Simulated annealing, scratch, charge flipping, other) ? Paralell tempering

2.3.2 Which program(s) did you use (name and reference) ? Fox, version 1.7.1.1 Dec 4 2007

2.3.3 If you used direct space methods, how many independent molecules did you use (give details on these molecules)? How many degrees of freedom (total) ? How many torsion angles ?

A few different attempts. (1) tartarate treated as a molecule, calcium and four oxygen atoms all treated independently of each other; dof: 24 torsions 3 . (2) only with two or three oxygen atoms bonded to calcium atom; dof: 18, torsions 3 (3) as 1 with more than four not bonded oxygen atoms dof: around 30, torsions 3.

2.4 Did you first locate the whole structure ? Yes [*] No []

2.4.1 If not, how many atoms did you locate ?

2.4.2 Give their name and initial atomic coordinates

Atom	x	y	z
------	---	---	---

C1	0.5050	0.3701	0.8419
----	--------	--------	--------

C2	0.3201	0.3840	0.7142	
C3	0.0878	0.3767	0.7444	
C4	-0.1148	0.3542	0.6100	
O5	-0.2115	0.2242	0.5179	
O6	-0.1985	0.4861	0.5947	
O7	0.4499	0.2166	0.8786	
O8	0.7007	0.4790	0.9012	
O9	0.4197	0.5381	0.6720	
O10	0.1210	0.5314	0.8256	
H11	0.2846	0.2732	0.6370	
H12	0.0252	0.2653	0.7966	_____atoms above: tartarate
Ca1	0.1592	0.3120	0.2280	
O1	0.8055	0.1218	0.2725	
O2	0.6237	0.8175	0.8893	
O3	0.1132	0.8025	0.0111	
O4	0.3191	0.1516	0.3977	

2.4.3 Were the initial atomic coordinates taken from a known structure ? Not to me at least. Yes [] No [*]
 If yes, which one (give reference) ?

3- Structure completion

3.1 Did you performed Fourier difference syntheses before refining the structure by the Rietveld method ? Yes [] No [*]

3.2 If yes, with what program ?

3.3 If yes, how many additional atoms did you obtained from Fourier difference syntheses ?

3.4 Give their name and atomic coordinates as they were obtained

Atom	x	y	z
.....			
.....			
.....			

3.5 Did you made first Rietveld refinements without preliminary Fourier difference syntheses ? Yes [*] No []

3.5.1 If yes, with what program ? GSAS

3.5.2 What were the Rp and Rwp (background subtracted AND not subtracted) and RB and RF that you obtained at the first Rietveld application ?

Haven't written it down. As I recall Rwp~0,11; Rwp(-bknd)~0,15

3.5.3 Did you get the structure factors from this result and performed a Fourier difference synthesis ? No.

3.5.4 Did you locate additional atoms at this stage ? No.

3.5.5 And which one ?

Atom	x	y	z
.....			
.....			
.....			

3.5.6 If you repeated Rietveld refinements and Fourier syntheses several times before to complete the model, give the number of times and which atoms you locate and the Rp, Rwp RB, RF at each times.

Atom	x	y	z
.....			
.....			
.....			

4- Final refinement

- Give the final atomic coordinates, thermal parameters, standard deviations, Reliability factors.....

Atom	x	y	z	B
C1	0.4969(21)	0.3622(16)	0.8337(14)	1.0 0.0498(9)
C2	0.3004(28)	0.3898(16)	0.7160(13)	1.0 0.0498(9)
C3	0.0801(26)	0.3716(18)	0.7534(13)	1.0 0.0498(9)
C4	-0.0971(25)	0.3551(15)	0.6281(15)	1.0 0.0498(9)
O5	-0.2034(13)	0.2052(11)	0.5360(9)	1.0 0.0498(9)
O6	-0.1787(15)	0.4757(11)	0.5900(8)	1.0 0.0498(9)
O7	0.4271(14)	0.2031(12)	0.8697(8)	1.0 0.0498(9)
O8	0.6845(15)	0.4753(10)	0.9007(8)	1.0 0.0498(9)
O9	0.4214(15)	0.5354(11)	0.6732(8)	1.0 0.0498(9)
O10	0.1388(15)	0.5293(11)	0.8434(9)	1.0 0.0498(9)
H11	0.265(11)	0.277(7)	0.623(6)	1.0 0.0498(9)
H12	0.095(13)	0.255(7)	0.798(7)	1.0 0.0498(9)
CA13	0.1630(5)	0.3127(4)	0.22960(31)	1.0 0.0498(9)
O14	0.8067(13)	0.1226(9)	0.2715(8)	1.0 0.0498(9)
O15	0.6339(12)	0.8471(10)	0.8812(7)	1.0 0.0498(9)
O16	0.1216(14)	0.8148(10)	0.0100(9)	1.0 0.0498(9)
O17	0.3194(11)	0.1478(9)	0.3969(7)	1.0 0.0498(9)

- Give details about constraints, restraints

I used restraints on bond lengths and angles.

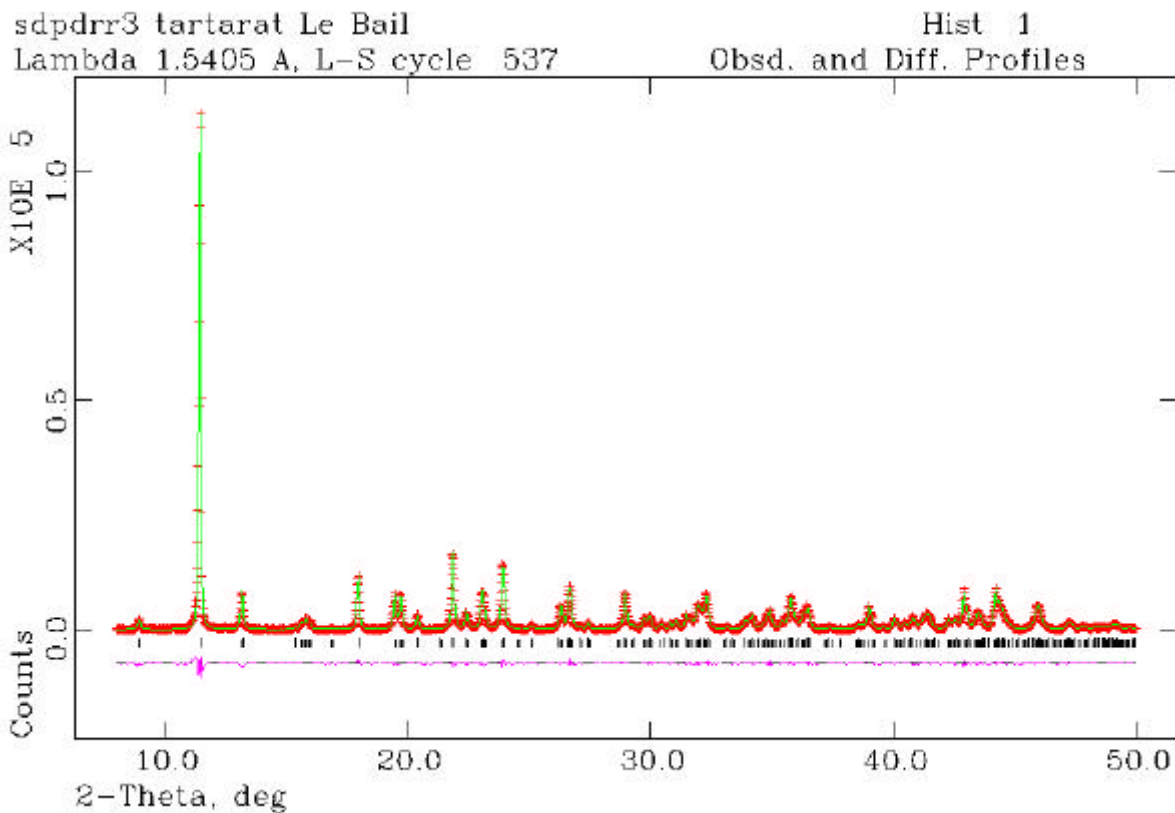
5- Feel free to add any intermediate results (list of extracted structure factors, software decisive input and output data...) or comments you might consider as essential (details on hardware, time for solving the structure, number of moves by Monte Carlo or molecule position trial, any picture...).

I strongly believe that this is the correct structure. I had a few doubts as it is stated on the website that this is a polymorph of enantiomerically pure calcium tartarate. This structure I got to is a racemate. I have tried to find initial model using all of the above named methods in P1 space group but with no meaningful results. And I would be very surprised to find that I could get a Rietveld fit this good and chemically very sensible structure with a wrong structure. Additionally, this structure model didn't show a hint of divergence in least squares.

I hope I've answered all questions. I will be happy to answer if I left something that needs clarification.

With kind regards,

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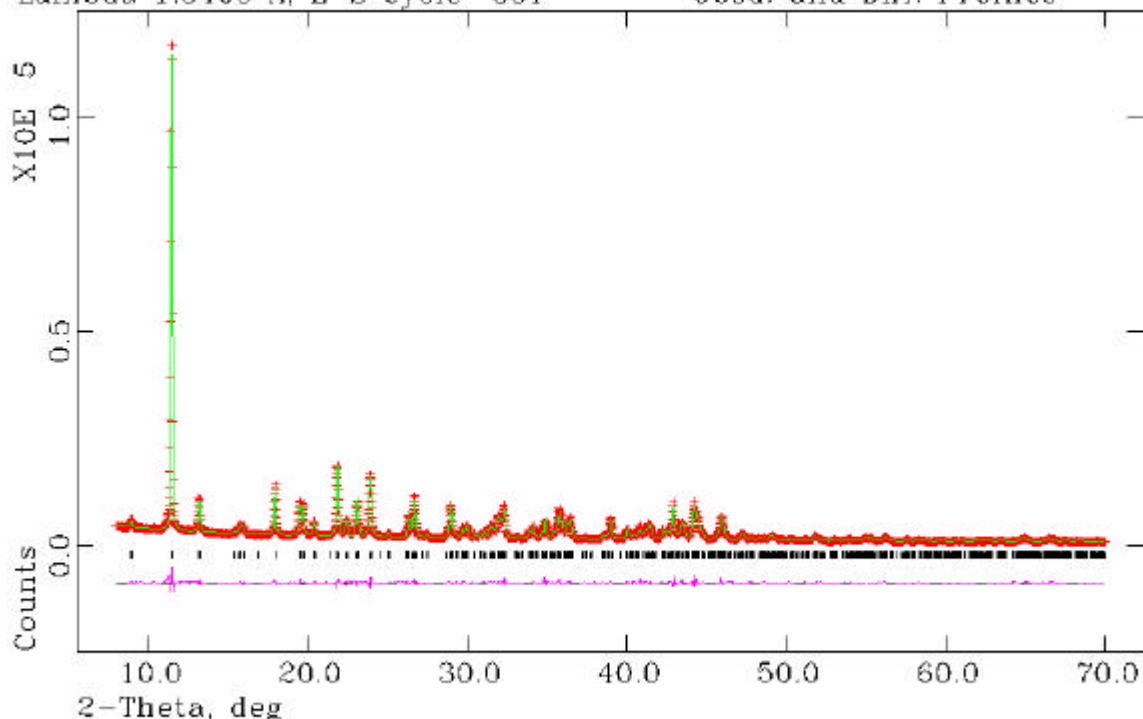
```

C:\ genes TART
Cycle 541 There were 2471 observations.
Total before-cycle CHI**2 (offset/sig) = 8.8192E+03 < 9.0792E+01>
Reduced CHI**2 = 3.591 for 15 variables
CPU times for matrix build 0.45 sec; matrix inversion 0.00 sec
Final variable sum((shift/esd)**2) for cycle 541: 0.47 Time: 0.45 sec
Restraint data statistics:
No restraints used
Powder data statistics
Bank Ndata Sum(w*d**2) Fitted wRp Rp -Bknd Rp Dwd Average
Integral
Hstgm 1 PKC 1 2471 8816.9 0.0382 0.0278 0.0657 0.0648 0.484 0.946
Powder totals 2471 8816.9 0.0382 0.0278 0.0657 0.0648 0.484
Cycle 542 There were 2471 observations.
Total before-cycle CHI**2 (offset/sig) = 8.8169E+03 < 9.0759E+01>
Reduced CHI**2 = 3.590 for 15 variables
CPU times for matrix build 0.47 sec; matrix inversion 0.00 sec
Final variable sum((shift/esd)**2) for cycle 542: 0.41 Time: 0.47 sec
STOP GENLES terminated successfully statement executed
Press any key to continue . . .

```

sdpdrr3 tartarat Rietveld
 Lambda 1.5405 A, L-S cycle 831

Hist 1
 Obsd. and Diff. Profiles



data_TART_publ

_pd_block_id
 2008-02-08T12:31|TART|Ivan_Halasz|Overall

_audit_creation_method "from EXP file using GSAS2CIF"
 _audit_creation_date 2008-02-08T12:31
 _audit_author_name "Ivan Halasz"
 _audit_update_record
 ; 2008-02-08T12:31 Initial CIF as created by GSAS2CIF
 ;

```

=====
# this information describes the project, paper etc. for the CIF #
# Acta Cryst. Section C papers and editorial correspondence is generated #
# from the information in this section #
# #
# (from) CIF submission form for Rietveld refinements (Acta Cryst. C) #
# Version 14 December 1998 #
=====
# 1. SUBMISSION DETAILS

```

_publ_contact_author_name ? # Name of author for correspondence
 _publ_contact_author_address # Address of author for correspondence
 ; ?
 ;

```

_publ_contact_author_email      ?
_publ_contact_author_fax       ?
_publ_contact_author_phone     ?

_publ_contact_letter
; ?
;

_publ_requested_journal         ?
_publ_requested_coeditor_name   ?
_publ_requested_category       ?   # Acta C: one of CI/CM/CO/FI/FM/FO

```

#=====

2. PROCESSING SUMMARY (IUCr Office Use Only)

```

_journal_data_validation_number  ?

_journal_date_recd_electronic    ?
_journal_date_to_coeditor        ?
_journal_date_from_coeditor      ?
_journal_date_accepted           ?
_journal_date_printers_first     ?
_journal_date_printers_final     ?
_journal_date_proofs_out         ?
_journal_date_proofs_in         ?
_journal_coeditor_name           ?
_journal_coeditor_code           ?
_journal_coeditor_notes         ?
; ?
;

_journal_techeditor_code         ?
_journal_techeditor_notes       ?
; ?
;

_journal_coden_ASTM             ?
_journal_name_full              ?
_journal_year                   ?
_journal_volume                 ?
_journal_issue                  ?
_journal_page_first             ?
_journal_page_last              ?
_journal_paper_category         ?
_journal_suppl_publ_number      ?
_journal_suppl_publ_pages       ?

```

#=====

3. TITLE AND AUTHOR LIST

```

_publ_section_title
; ?
;

_publ_section_title_footnote
; ?
;

```

The loop structure below should contain the names and addresses of all
authors, in the required order of publication. Repeat as necessary.

loop_


```

    _publ_author_name
    _publ_author_footnote
    _publ_author_address
?                                     #<--'Last name, first name'
; ?
;
; ?
;

#=====

# 4. TEXT

_publ_section_synopsis
; ?
;
_publ_section_abstract
; ?
;
_publ_section_comment
; ?
;
_publ_section_exptl_prep             # Details of the preparation of the sample(s)
                                     # should be given here.
; ?
;
_publ_section_exptl_refinement
; ?
;
_publ_section_references
; ?
;
_publ_section_figure_captions
; ?
;
_publ_section_acknowledgements
; ?
;

#=====

# 5. OVERALL REFINEMENT & COMPUTING DETAILS

_refine_special_details
; ?
;
_pd_proc_ls_special_details
; ?
;

# The following items are used to identify the programs used.
_computing_molecular_graphics      ?
_computing_publication_material   ?

_refine_ls_weighting_scheme        ?
_refine_ls_weighting_details       ?
_refine_ls_hydrogen_treatment      ?
_refine_ls_extinction_method       ?
_refine_ls_extinction_coef         ?
_refine_ls_number_constraints      ?

_refine_ls_restrained_S_all        ?

```

```

_refine_ls_restrained_S_obs      ?

#=====
# 6. SAMPLE PREPARATION DATA

# (In the unusual case where multiple samples are used in a single
# Rietveld study, this information should be moved into the phase
# blocks)

# The following three fields describe the preparation of the material.
# The cooling rate is in K/min. The pressure at which the sample was
# prepared is in kPa. The temperature of preparation is in K.

_pd_prep_cool_rate              ?
_pd_prep_pressure               ?
_pd_prep_temperature            ?

_pd_char_colour                 ?      # use ICDD colour descriptions
data_TART_overall

_refine_ls_shift/su_max         0.00
_refine_ls_shift/su_mean       0.00
_computing_structure_refinement GSAS
_refine_ls_number_parameters    1
_refine_ls_goodness_of_fit_all  5.30
_refine_ls_number_restraints    35
_refine_ls_matrix_type         full

# pointers to the phase blocks
loop_   _pd_phase_block_id
        2008-02-08T12:31|TART_phase1|Ivan_Halasz||
# pointers to the diffraction patterns
loop_   _pd_block_diffraction_id
        ?

# Information for phase 1
data_TART_phase_1

_pd_block_id
        2008-02-08T12:31|TART_phase1|Ivan_Halasz||

#=====
# 7. CHEMICAL, STRUCTURAL AND CRYSTAL DATA

_pd_char_particle_morphology    ?

_chemical_name_systematic
; ?
;
_chemical_name_common           ?
_chemical_formula_moiety        ?
_chemical_formula_structural    ?
_chemical_formula_analytical    ?
_chemical_melting_point         ?
_chemical_compound_source       ?      # for minerals and
                                     # natural products

_symmetry_space_group_name_Hall ?

_exptl_crystal_F_000           ?
_exptl_crystal_density_diffn    ?
_exptl_crystal_density_meas    ?

```

```

_exptl_crystal_density_method      ?

_cell_measurement_temperature      ?

_cell_special_details
; ?
;

_geom_special_details              ?

# The following item identifies the program(s) used (if appropriate).
_computing_structure_solution      ?

#=====

# 8. Phase information from GSAS

_pd_phase_name                     tart
_cell_length_a                     6.25092(15)
_cell_length_b                     8.22598(23)
_cell_length_c                     10.43844(20)
_cell_angle_alpha                  94.9368(15)
_cell_angle_beta                   105.9512(16)
_cell_angle_gamma                  107.5183(17)
_cell_volume                       483.732(20)
_symmetry_cell_setting              triclinic
_symmetry_space_group_name_H-M     "P -1"
loop_ _symmetry_equiv_pos_site_id  _symmetry_equiv_pos_as_xyz
    1  +x,+y,+z
    -1 -x,-y,-z

# ATOMIC COORDINATES AND DISPLACEMENT PARAMETERS

loop_
  _atom_site_type_symbol
  _atom_site_label
  _atom_site_fract_x
  _atom_site_fract_y
  _atom_site_fract_z
  _atom_site_occupancy
  _atom_site_thermal_displace_type
  _atom_site_U_iso_or_equiv
  _atom_site_symmetry_multiplicity

C
C1      0.505      0.3701      0.8419      1.0      Uiso      0.025      2
C
C2      0.3201     0.384       0.7142     1.0      Uiso      0.025      2
C
C3      0.0878     0.3767     0.7444     1.0      Uiso      0.025      2
C
C4     -0.1148     0.3542     0.61       1.0      Uiso      0.025      2
O
O5     -0.2115     0.2242     0.5179     1.0      Uiso      0.025      2
O
O6     -0.1985     0.4861     0.5947     1.0      Uiso      0.025      2
O
O7      0.4499     0.2166     0.8786     1.0      Uiso      0.025      2
O
O8      0.7007     0.479      0.9012     1.0      Uiso      0.025      2
O

```

O9	0.4197	0.5381	0.672	1.0	Uiso	0.025	2
O							
O10	0.121	0.5314	0.8256	1.0	Uiso	0.025	2
H							
H11	0.2846	0.2732	0.637	1.0	Uiso	0.025	2
H							
H12	0.0252	0.2653	0.7966	1.0	Uiso	0.025	2
Ca							
CA13	0.1592	0.312	0.228	1.0	Uiso	0.025	2
O							
O14	0.8055	0.1218	0.2725	1.0	Uiso	0.025	2
O							
O15	0.6237	0.8175	0.8893	1.0	Uiso	0.025	2
O							
O16	0.1132	0.8025	0.0111	1.0	Uiso	0.025	2
O							
O17	0.3191	0.1516	0.3977	1.0	Uiso	0.025	2

```

loop_  _atom_type_symbol
      _atom_type_number_in_cell
      C 8.0
      O 20.0
      H 4.0
      Ca 2.0

```

```

# If you change Z, be sure to change all 3 of the following
_chemical_formula_sum          "C4 H2 Ca O10"
_chemical_formula_weight      250.13
_cell_formula_units_Z         2

```

MOLECULAR GEOMETRY

```

loop_
  _geom_bond_atom_site_label_1
  _geom_bond_atom_site_label_2
  _geom_bond_distance
  _geom_bond_site_symmetry_1
  _geom_bond_site_symmetry_2
  _geom_bond_publ_flag
C1      C2      1.54427(4) .      1_555 N
C1      O7      1.324280(30) .      1_555 N
C1      O8      1.22913(4) .      1_555 N
C1      CA13    3.10524(8) .      -1_666 N
C2      C1      1.54427(4) .      1_555 N
C2      C3      1.55368(4) .      1_555 N
C2      O9      1.400090(30) .      1_555 N
C2      H11     1.087610(30) .      1_555 N
C3      C2      1.55368(4) .      1_555 N
C3      C4      1.56332(4) .      1_555 N
C3      O10     1.39269(4) .      1_555 N
C3      H12     1.130050(30) .      1_555 N
C4      C3      1.56332(4) .      1_555 N
C4      O5      1.24407(4) .      1_555 N
C4      O6      1.342440(30) .      1_555 N
C4      CA13    3.22394(8) .      -1_566 N
O5      C4      1.24407(4) .      1_555 N
O6      C4      1.342440(30) .      1_555 N
O6      CA13    2.28459(5) .      -1_566 N
O7      C1      1.324280(30) .      1_555 N
O8      C1      1.22913(4) .      1_555 N
O8      CA13    2.38398(5) .      -1_666 N

```

O9	C2	1.400090(30)	.	1_555	N
O9	H11	2.04463(6)	.	1_555	N
O9	CA13	2.41932(7)	.	-1_666	N
O10	C3	1.39269(4)	.	1_555	N
O10	H12	2.05885(6)	.	1_555	N
O10	CA13	2.44622(5)	.	-1_566	N
H11	C2	1.087610(30)	.	1_555	N
H11	O9	2.04463(6)	.	1_555	N
H12	C3	1.130050(30)	.	1_555	N
H12	O10	2.05885(6)	.	1_555	N
CA13	C1	3.10524(8)	.	-1_666	N
CA13	C4	3.22394(8)	.	-1_566	N
CA13	O6	2.28459(5)	.	-1_566	N
CA13	O8	2.38398(5)	.	-1_666	N
CA13	O9	2.41932(7)	.	-1_666	N
CA13	O10	2.44622(5)	.	-1_566	N
CA13	O14	2.48174(6)	.	1_455	N
CA13	O15	2.45658(5)	.	-1_666	N
CA13	O16	2.51192(7)	.	-1_565	N
CA13	O17	2.47000(5)	.	1_555	N
O14	CA13	2.48174(6)	.	1_655	N
O15	CA13	2.45658(5)	.	-1_666	N
O16	CA13	2.51192(7)	.	-1_565	N
O17	CA13	2.47000(5)	.	1_555	N

loop_

	_geom_angle_atom_site_label_1						
	_geom_angle_atom_site_label_2						
	_geom_angle_atom_site_label_3						
	_geom_angle						
	_geom_angle_site_symmetry_1						
	_geom_angle_site_symmetry_2						
	_geom_angle_site_symmetry_3						
	_geom_angle_publ_flag						
C2	C1	O7	114.1749(20)	1_555	.	1_555	N
C2	C1	O8	126.3713(18)	1_555	.	1_555	N
O7	C1	O8	119.0339(17)	1_555	.	1_555	N
C1	C2	C3	110.4558(17)	1_555	.	1_555	N
C1	C2	O9	108.0528(20)	1_555	.	1_555	N
C1	C2	H11	106.7168(20)	1_555	.	1_555	N
C3	C2	O9	112.1487(16)	1_555	.	1_555	N
C3	C2	H11	109.3994(19)	1_555	.	1_555	N
O9	C2	H11	109.9149(19)	1_555	.	1_555	N
C2	C3	C4	110.5267(18)	1_555	.	1_555	N
C2	C3	O10	109.9851(18)	1_555	.	1_555	N
C2	C3	H12	112.3067(15)	1_555	.	1_555	N
C4	C3	O10	107.3331(20)	1_555	.	1_555	N
C4	C3	H12	107.5796(20)	1_555	.	1_555	N
O10	C3	H12	108.9514(19)	1_555	.	1_555	N
C3	C4	O5	126.5707(17)	1_555	.	1_555	N
C3	C4	O6	116.6538(17)	1_555	.	1_555	N
O5	C4	O6	116.7299(18)	1_555	.	1_555	N
C4	O6	CA13	123.3521(15)	1_555	.	-1_566	N
C1	O8	CA13	114.6948(18)	1_555	.	-1_666	N
C2	O9	CA13	117.7954(17)	1_555	.	-1_666	N
C3	O10	CA13	121.8789(18)	1_555	.	-1_566	N
O6	CA13	O8	94.4849(20)	-1_566	.	-1_666	N
O6	CA13	O9	74.6355(21)	-1_566	.	-1_666	N
O6	CA13	O10	66.1752(17)	-1_566	.	-1_566	N
O6	CA13	O14	87.8266(21)	-1_566	.	1_455	N
O6	CA13	O15	144.4202(11)	-1_566	.	-1_666	N

