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## (2*S*,4*R*)-4-Ammonio-5-oxopyrrolidine-2-carboxylate

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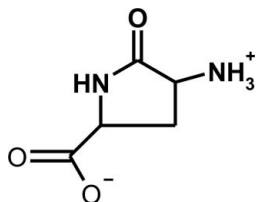
Received 1 February 2010; accepted 3 February 2010

 Key indicators: single-crystal X-ray study;  $T = 293$  K; mean  $\sigma(\text{C}-\text{C}) = 0.002$  Å;  $R$  factor = 0.027;  $wR$  factor = 0.069; data-to-parameter ratio = 9.4.

In the crystal structure of the title compound,  $\text{C}_5\text{H}_8\text{N}_2\text{O}_3$ , the molecules exist in the zwitterionic form. The pyrrolidine ring adopts an envelope conformation with the unsubstituted endocyclic C atom situated at the flap. The other four endocyclic atoms are coplanar with the exocyclic carbonyl O atom, with an r.m.s. deviation from the mean plane of 0.06 Å. The carboxylate substituent is located axially, while the ammonium group occupies an equatorial position. In the crystal structure, the molecules are linked through  $\text{N}-\text{H}\cdots\text{O}$  hydrogen bonds, forming a three-dimensional network.

### Related literature

For molecular recognition in *N*-methyl amino acids and proline residues, see: Dugave & Demange (2003). For the construction of modified amino acids, see: Dumy *et al.* (1997); Keller *et al.* (1998); Mutter *et al.* (1999); Tuchscherer & Mutter (2001); Paul *et al.* (1992). For pyroglutamic acid derivatives, see: Zabrocki *et al.* (1988); Kaczmarek *et al.* (2005). For the preparation of the title compound, see: Kaczmarek *et al.* (2001); Kaczmarek (2009). For asymmetry parameters, see: Griffin *et al.* (1984).



### Experimental

#### Crystal data

 $\text{C}_5\text{H}_8\text{N}_2\text{O}_3$   
 $M_r = 144.13$ 

 Orthorhombic,  $P2_12_12_1$   
 $a = 5.9790$  (3) Å

 $b = 9.3665$  (4) Å  
 $c = 11.3809$  (5) Å  
 $V = 637.36$  (5) Å<sup>3</sup>  
 $Z = 4$ 

 Cu  $K\alpha$  radiation  
 $\mu = 1.08$  mm<sup>-1</sup>  
 $T = 293$  K  
 $0.40 \times 0.40 \times 0.10$  mm

#### Data collection

 Bruker SMART APEX  
 diffractometer  
 Absorption correction: multi-scan  
 (SADABS; Bruker, 2003)  
 $T_{\min} = 0.707$ ,  $T_{\max} = 0.900$ 

 7227 measured reflections  
 1169 independent reflections  
 1168 reflections with  $I > 2\sigma(I)$   
 $R_{\text{int}} = 0.030$ 

#### Refinement

 $R[F^2 > 2\sigma(F^2)] = 0.027$   
 $wR(F^2) = 0.069$   
 $S = 1.08$   
 1169 reflections  
 125 parameters  
 H atoms treated by a mixture of  
 independent and constrained  
 refinement

 $\Delta\rho_{\text{max}} = 0.13$  e Å<sup>-3</sup>  
 $\Delta\rho_{\text{min}} = -0.17$  e Å<sup>-3</sup>  
 Absolute structure: Flack (1983),  
 461 Friedel pairs  
 Flack parameter: 0.1 (2)

**Table 1**

Hydrogen-bond geometry (Å, °).

$D-\text{H}\cdots A$	$D-\text{H}$	$\text{H}\cdots A$	$D\cdots A$	$D-\text{H}\cdots A$
$\text{N1}-\text{H1}\cdots\text{O2}^{\text{i}}$	0.82 (2)	2.07 (2)	2.8535 (15)	161.2 (18)
$\text{N2}-\text{H2}\cdots\text{O1}^{\text{ii}}$	0.88 (2)	1.87 (2)	2.7346 (16)	168.5 (17)
$\text{N2}-\text{H3}\cdots\text{O1}^{\text{iii}}$	0.897 (17)	1.886 (17)	2.7788 (14)	173.4 (17)
$\text{N2}-\text{H4}\cdots\text{O2}^{\text{iv}}$	0.868 (17)	1.935 (17)	2.7967 (15)	172.3 (17)

 Symmetry codes: (i)  $x + \frac{1}{2}, -y + \frac{1}{2}, -z + 1$ ; (ii)  $-x + 2, y + \frac{1}{2}, -z + \frac{3}{2}$ ; (iii)  $-x + \frac{3}{2}, -y, z + \frac{1}{2}$ ; (iv)  $-x + 1, y + \frac{1}{2}, -z + \frac{3}{2}$ .

Data collection: SMART (Bruker, 2003); cell refinement: SAINT-Plus (Bruker, 2003); data reduction: SAINT-Plus; program(s) used to solve structure: SHELXTL (Sheldrick, 2008); program(s) used to refine structure: SHELXTL; molecular graphics: SHELXTL and Mercury (Macrae *et al.*, 2008); software used to prepare material for publication: SHELXTL and publCIF (Westrip, 2010).

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Supplementary data and figures for this paper are available from the IUCr electronic archives (Reference: BT5187).

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## supporting information

*Acta Cryst.* (2010). E66, o831–o832 [doi:10.1107/S1600536810004277]

**(2*S*,4*R*)-4-Ammonio-5-oxopyrrolidine-2-carboxylate****Krzysztof Kaczmarek, Jakub Wojciechowski and Wojciech M. Wolf****S1. Comment**

*N*-methyl amino acids and proline residues in the peptide chain may cause the *cis-trans* isomerisation of the amide bond and lead to conformational changes, which influence the molecular recognition (Dugave & Demange, 2003). Importance of the *cis*-amide bonds for the peptide bioactivity led to the construction of modified amino acids, which could lock a peptide bond in the *cis*-geometry (Dumy *et al.*, 1997; Keller *et al.*, 1998; Mutter *et al.*, 1999; Tuchscherer & Mutter, 2001). In particular, Paul *et al.* (1992) designed mimetics of the *cis*-peptide bond based on the substituted pyroglutamic acid residue. In contrast with a tetrazole replacement for the peptide bond, the pyroglutamic acid derivatives are more rigid (Zabrocki *et al.*, 1988). Their carboxylic group could be either donor or acceptor of hydrogen bond without involving the polypeptide main chain amide moieties (Kaczmarek *et al.*, 2005).

The 4-aminopyroglutamic acid is a particularly useful residue for building the conformationally restricted peptide chains. Depending on the absolute configuration at both chiral centers it may be applied to construct the VIa or VIb  $\beta$ -turn mimetics.

The title compound may be obtained by two different methods elaborated by us, *i.e.* by electrophilic amination reaction of *N*-protected (*S*)-pyroglutamate ester, which gives separable 9:1 mixture of (2*S*,4*R*) and (2*S*,4*S*) diastereoisomers (Kaczmarek *et al.*, 2001) or through Michael addition of dehydroalanine derivatives to sodium salt of *N*-benzyloxycarbonylaminomalonate ester, which gives after hydrolysis and decarboxylation mixture of all four possible stereoisomers. The details of the last reaction and resolution of stereoisomers will be described elsewhere (Kaczmarek, 2009).

A view of the title compound is given in Fig. 1. The molecule has two chiral centres *viz.* C3 and C5. Their absolute configurations follow from the synthetic procedure and are *R* and *S*, respectively.

The pyrrolidine ring adopts an envelope conformation with N1, C2, C3 and C5 almost coplanar and the C4 situated at the flap.

Additionally, the former four endocyclic atoms are coplanar with the exocyclic carbonyl oxygen, the average r.m.s. deviation from the mean plane is 0.06 Å.

The three lowest ring asymmetry parameters (Griffin *et al.*, 1984) are:  $C_5(C4) = 1.26(14)$ ,  $C_2(C2) = 11.92(14)$ ,  $C_2(N1) = 15.46(14)^\circ$ . The carboxylate substituent is located axially in conformation stabilized by the short N1...O2 contact [2.787(2) Å], while the ammonium group occupies equatorial position.

In the crystal each molecule is linked through N—H...O hydrogen bonds with eight adjacent molecules, their details are shown in Table 2 and Fig. 2.

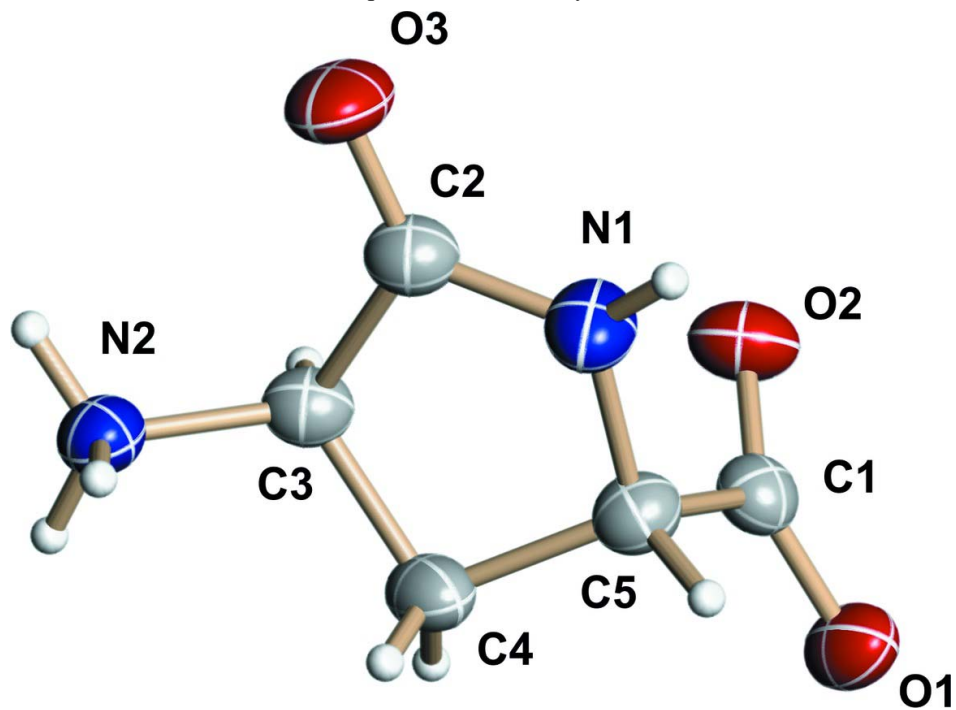
**S2. Experimental**

An optically pure (*ee*>99%) *N'*-benzyloxycarbonyl protected precursor of the title compound was hydrogenated in methanol solution over 10% palladium on charcoal, which resulted in precipitation of the final product. After filtration of

solids final product was washed out of the catalyst with the aim of water. The (2*S*,4*R*)-4-aminopyroglutamic acid crystals were grown from this water solution by slow evaporation.

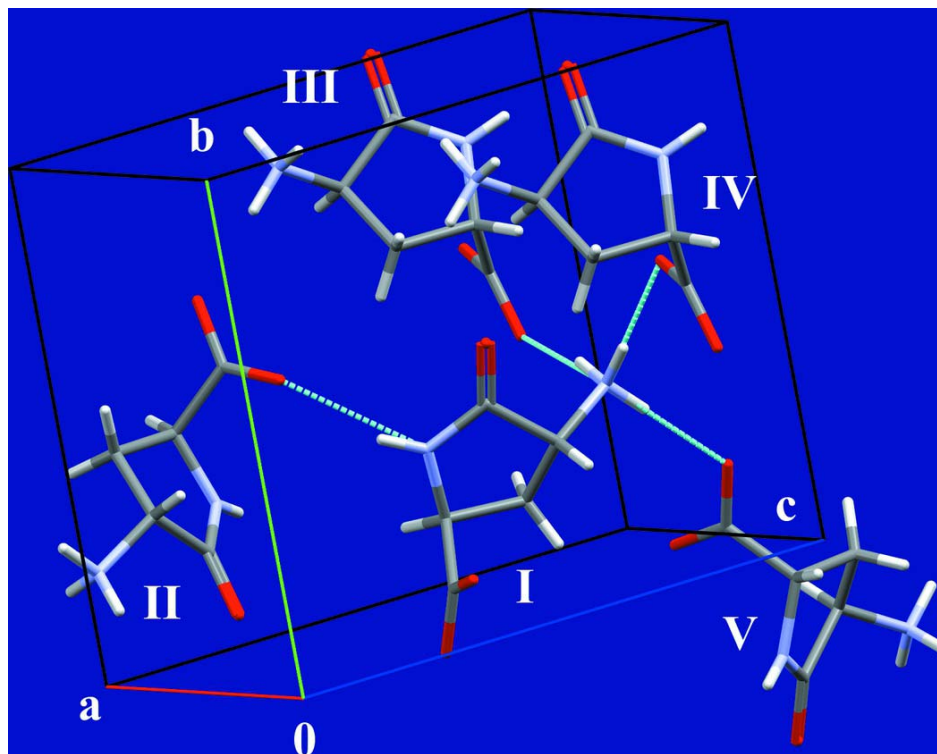
### S3. Refinement

All H atoms were located in difference Fourier maps and refined freely.



**Figure 1**

Molecule of the title compound. Displacement ellipsoids are drawn at the 50% probability level.

**Figure 2**

View of hydrogen bonding in the crystal of the title compound. Symmetry codes: I ( $x, y, z$ ); II ( $x + 1/2, -y + 1/2, -z + 1$ ); III ( $-x + 2, y + 1/2, -z + 3/2$ ); IV ( $-x + 1, y + 1/2, -z + 3/2$ ); V ( $-x + 3/2, -y, z + 1/2$ ).

### (2*S*,4*R*)-4-Ammonio-5-oxopyrrolidine-2-carboxylate

#### Crystal data

$C_5H_8N_2O_3$

$M_r = 144.13$

Orthorhombic,  $P2_12_12_1$

Hall symbol:  $P\ 2ac\ 2ab$

$a = 5.9790\ (3)\ \text{\AA}$

$b = 9.3665\ (4)\ \text{\AA}$

$c = 11.3809\ (5)\ \text{\AA}$

$V = 637.36\ (5)\ \text{\AA}^3$

$Z = 4$

$F(000) = 304$

$D_x = 1.502\ \text{Mg m}^{-3}$

Melting point:  $423\ (2)\ \text{K}$

$\text{Cu K}\alpha$  radiation,  $\lambda = 1.54178\ \text{\AA}$

Cell parameters from 7056 reflections

$\theta = 6.1\text{--}70.8^\circ$

$\mu = 1.08\ \text{mm}^{-1}$

$T = 293\ \text{K}$

Prism, colourless

$0.40 \times 0.40 \times 0.10\ \text{mm}$

#### Data collection

Bruker SMART APEX  
diffractometer

Radiation source: fine-focus sealed tube

Graphite monochromator

$\omega$  scans

Absorption correction: multi-scan

(*SADABS*; Bruker, 2003)

$T_{\min} = 0.707$ ,  $T_{\max} = 0.900$

7227 measured reflections

1169 independent reflections

1168 reflections with  $I > 2\sigma(I)$

$R_{\text{int}} = 0.030$

$\theta_{\max} = 70.8^\circ$ ,  $\theta_{\min} = 6.1^\circ$

$h = -6 \rightarrow 5$

$k = -11 \rightarrow 11$

$l = -13 \rightarrow 13$

*Refinement*Refinement on  $F^2$ 

Least-squares matrix: full

 $R[F^2 > 2\sigma(F^2)] = 0.027$  $wR(F^2) = 0.069$  $S = 1.08$ 

1169 reflections

125 parameters

0 restraints

Primary atom site location: structure-invariant  
direct methodsSecondary atom site location: difference Fourier  
mapHydrogen site location: inferred from  
neighbouring sitesH atoms treated by a mixture of independent  
and constrained refinement $w = 1/[\sigma^2(F_o^2) + (0.0468P)^2 + 0.0681P]$ where  $P = (F_o^2 + 2F_c^2)/3$  $(\Delta/\sigma)_{\max} < 0.001$  $\Delta\rho_{\max} = 0.13 \text{ e } \text{\AA}^{-3}$  $\Delta\rho_{\min} = -0.17 \text{ e } \text{\AA}^{-3}$ Extinction correction: *SHELXL97* (Sheldrick,  
2008),  $F_c^* = kF_c[1 + 0.001 \times F_c^2 \lambda^3 / \sin(2\theta)]^{-1/4}$ 

Extinction coefficient: 0.047 (3)

Absolute structure: Flack (1983), 461 Friedel  
pairs

Absolute structure parameter: 0.1 (2)

*Special details*

**Geometry.** All esds (except the esd in the dihedral angle between two l.s. planes) are estimated using the full covariance matrix. The cell esds are taken into account individually in the estimation of esds in distances, angles and torsion angles; correlations between esds in cell parameters are only used when they are defined by crystal symmetry. An approximate (isotropic) treatment of cell esds is used for estimating esds involving l.s. planes.

**Refinement.** Refinement of  $F^2$  against ALL reflections. The weighted  $R$ -factor  $wR$  and goodness of fit  $S$  are based on  $F^2$ , conventional  $R$ -factors  $R$  are based on  $F$ , with  $F$  set to zero for negative  $F^2$ . The threshold expression of  $F^2 > \sigma(F^2)$  is used only for calculating  $R$ -factors(gt) etc. and is not relevant to the choice of reflections for refinement.  $R$ -factors based on  $F^2$  are statistically about twice as large as those based on  $F$ , and  $R$ -factors based on ALL data will be even larger.

*Fractional atomic coordinates and isotropic or equivalent isotropic displacement parameters ( $\text{\AA}^2$ )*

	<i>x</i>	<i>y</i>	<i>z</i>	$U_{\text{iso}}^*/U_{\text{eq}}$
O1	0.85679 (17)	-0.10762 (9)	0.57781 (8)	0.0373 (3)
H2	0.838 (4)	0.3509 (18)	0.9130 (15)	0.042 (4)*
O2	0.57914 (17)	0.04638 (10)	0.55325 (8)	0.0383 (3)
O3	0.6519 (2)	0.46234 (9)	0.68254 (10)	0.0469 (3)
N1	0.8566 (2)	0.27436 (11)	0.61237 (10)	0.0353 (3)
H1	0.917 (4)	0.3094 (19)	0.5549 (17)	0.054 (5)*
C1	0.7725 (2)	0.01571 (13)	0.58351 (10)	0.0283 (3)
C5	0.9163 (2)	0.12935 (13)	0.64357 (11)	0.0304 (3)
H51	1.078 (3)	0.1140 (16)	0.6258 (13)	0.032 (4)*
C4	0.8646 (3)	0.12504 (13)	0.77672 (11)	0.0340 (3)
H41	0.807 (3)	0.0354 (17)	0.8009 (15)	0.045 (5)*
H42	0.995 (4)	0.156 (2)	0.8147 (18)	0.056 (5)*
C3	0.6848 (2)	0.23810 (12)	0.79144 (11)	0.0297 (3)
H31	0.541 (3)	0.1976 (15)	0.7877 (14)	0.030 (4)*
N2	0.7038 (2)	0.31400 (11)	0.90532 (10)	0.0310 (3)
H4	0.607 (3)	0.3822 (18)	0.9140 (14)	0.036 (4)*
H3	0.695 (3)	0.249 (2)	0.9630 (14)	0.042 (4)*
C2	0.7255 (2)	0.34135 (13)	0.68928 (11)	0.0319 (3)

Atomic displacement parameters ( $\text{\AA}^2$ )

	$U^{11}$	$U^{22}$	$U^{33}$	$U^{12}$	$U^{13}$	$U^{23}$
O1	0.0425 (6)	0.0262 (4)	0.0432 (5)	0.0027 (4)	-0.0079 (4)	-0.0062 (4)
O2	0.0334 (6)	0.0347 (5)	0.0466 (5)	-0.0016 (4)	-0.0093 (4)	0.0089 (4)
O3	0.0561 (7)	0.0309 (5)	0.0536 (6)	0.0133 (5)	0.0046 (5)	0.0104 (4)
N1	0.0451 (7)	0.0234 (5)	0.0374 (6)	-0.0044 (5)	0.0072 (5)	0.0050 (4)
C1	0.0331 (7)	0.0267 (6)	0.0251 (5)	-0.0021 (4)	0.0001 (5)	0.0034 (4)
C5	0.0311 (7)	0.0241 (6)	0.0361 (6)	-0.0008 (5)	0.0004 (5)	0.0004 (5)
C4	0.0435 (8)	0.0250 (6)	0.0335 (6)	0.0040 (5)	-0.0074 (6)	0.0002 (5)
C3	0.0294 (7)	0.0257 (5)	0.0340 (6)	-0.0027 (5)	-0.0020 (4)	0.0037 (5)
N2	0.0327 (7)	0.0257 (5)	0.0345 (5)	0.0022 (5)	0.0027 (4)	0.0029 (4)
C2	0.0321 (7)	0.0270 (6)	0.0367 (6)	-0.0015 (5)	-0.0022 (5)	0.0044 (5)

Geometric parameters ( $\text{\AA}$ ,  $^\circ$ )

O1—C1	1.2621 (16)	C4—C3	1.5187 (19)
O2—C1	1.2399 (17)	C4—H41	0.949 (17)
O3—C2	1.2179 (16)	C4—H42	0.94 (2)
N1—C2	1.3321 (17)	C3—N2	1.4826 (16)
N1—C5	1.4485 (15)	C3—C2	1.5318 (16)
N1—H1	0.82 (2)	C3—H31	0.939 (17)
C1—C5	1.5295 (17)	N2—H2	0.88 (2)
C5—C4	1.5470 (17)	N2—H4	0.867 (18)
C5—H51	0.997 (17)	N2—H3	0.898 (18)
C2—N1—C5	115.19 (10)	C3—C4—H41	109.0 (11)
O3—C2—N1	127.55 (12)	C5—C4—H41	112.3 (10)
O3—C2—C3	125.30 (12)	C3—C4—H42	108.7 (13)
N1—C2—C3	107.15 (11)	C5—C4—H42	106.1 (13)
N1—C5—C1	113.86 (10)	H41—C4—H42	116.4 (17)
N1—C5—C4	102.44 (10)	N2—C3—C4	112.11 (10)
C1—C5—C4	107.90 (10)	N2—C3—C2	110.40 (10)
C3—C4—C5	103.37 (10)	N2—C3—H31	107.7 (9)
C4—C3—C2	104.12 (10)	C4—C3—H31	111.1 (9)
C2—N1—H1	126.6 (13)	C2—C3—H31	111.5 (9)
C5—N1—H1	117.8 (13)	C3—N2—H2	110.3 (11)
O2—C1—O1	124.76 (12)	C3—N2—H4	113.6 (11)
O2—C1—C5	119.14 (11)	H2—N2—H4	107.9 (16)
O1—C1—C5	115.82 (11)	C3—N2—H3	108.0 (11)
N1—C5—H51	108.9 (9)	H2—N2—H3	104.4 (16)
C1—C5—H51	110.7 (9)	H4—N2—H3	112.3 (15)
C4—C5—H51	112.9 (8)		
N1—C5—C4—C3	26.38 (13)	O2—C1—C5—N1	-26.96 (16)
C5—C4—C3—C2	-25.98 (13)	O1—C1—C5—N1	158.87 (11)
C5—N1—C2—O3	-179.48 (14)	O2—C1—C5—C4	86.02 (13)
C5—N1—C2—C3	1.41 (16)	O1—C1—C5—C4	-88.15 (13)

C4—C3—C2—N1	16.23 (14)	C1—C5—C4—C3	-94.06 (11)
C4—C3—C2—O3	-162.91 (14)	C5—C4—C3—N2	-145.33 (10)
C2—N1—C5—C4	-17.99 (15)	N2—C3—C2—O3	-42.41 (18)
C2—N1—C5—C1	98.23 (14)	N2—C3—C2—N1	136.73 (12)

*Hydrogen-bond geometry (Å, °)*

<i>D—H...A</i>	<i>D—H</i>	<i>H...A</i>	<i>D...A</i>	<i>D—H...A</i>
N1—H1...O2 <sup>i</sup>	0.82 (2)	2.07 (2)	2.8535 (15)	161.2 (18)
N2—H2...O1 <sup>ii</sup>	0.88 (2)	1.87 (2)	2.7346 (16)	168.5 (17)
N2—H3...O1 <sup>iii</sup>	0.897 (17)	1.886 (17)	2.7788 (14)	173.4 (17)
N2—H4...O2 <sup>iv</sup>	0.868 (17)	1.935 (17)	2.7967 (15)	172.3 (17)

Symmetry codes: (i)  $x+1/2, -y+1/2, -z+1$ ; (ii)  $-x+2, y+1/2, -z+3/2$ ; (iii)  $-x+3/2, -y, z+1/2$ ; (iv)  $-x+1, y+1/2, -z+3/2$ .