

Revision of the crystal structure of 'bis(glycine) squaric acid'¹

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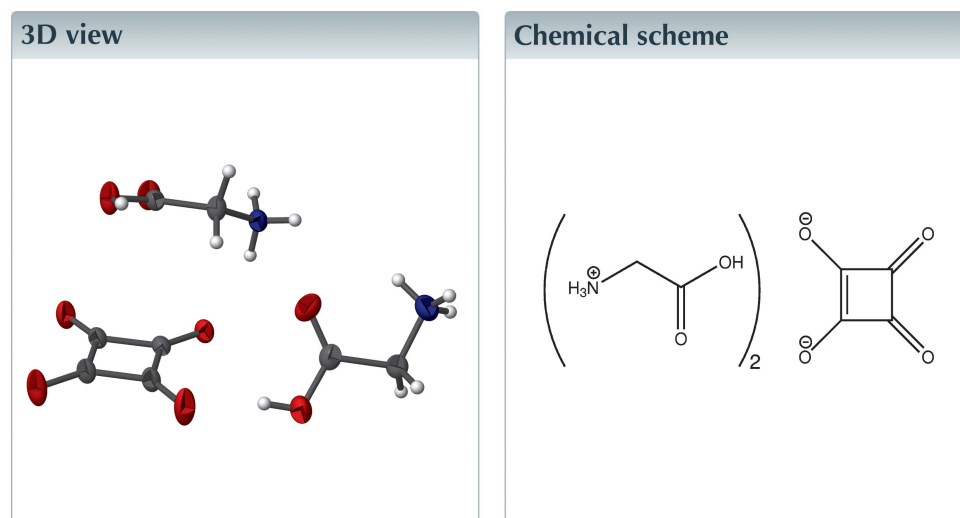
¹In the original publication by Tyagi *et al.* (2016), the compound was named 'bis glycine' squarate.

Keywords: crystal structure; redetermination; proton-transfer compound; squarate.

CCDC reference: 1832495

Structural data: full structural data are available from iucrdata.iucr.org

The crystal structure of 'bis(glycine) squaric acid' [Tyagi *et al.* (2016). *RSC Adv.* **6**, 24565–24576], is revised. Re-refinement of the structure against the original X-ray intensity data after correct placement of the donor H atoms proves that the compound is in fact the previously reported diglycinium squarate [systematic name: bis(carboxymethanaminium) 3,4-dioxocyclobut-1-ene-1,2-diolate; Anioła *et al.* (2014). *New J. Chem.* **38**, 3556–3568]. The findings are consistent with the pK_a rule.



Structure description

In a search of the Cambridge Structural Database (CSD Version 5.39 with February 2018 updates; Groom *et al.*, 2016) for salts of squaric acid ($H_2C_4O_4$) and α -amino acids, we stumbled upon CSD entries SIZKIX and SIZKIX01 (additional database identifier VABNUK). SIZKIX is diglycinium squarate, *i.e.* a 2:1 proton-transfer compound of glycine and squaric acid, and was reported by Anioła *et al.* (2014). SIZKIX01, however, is reportedly a 2:1 non-ionized acid–base complex of glycine and squaric acid (Tyagi *et al.*, 2016). In the original publication (Tyagi *et al.*, 2016), the compound was designated as 'bis glycine' squarate whereas in the CSD, 'bis(glycine) squaric acid' was assigned as the common name. Since squaric acid is a remarkably strong diprotic acid (Gilli *et al.*, 2001), the formation of a non-ionized acid–base complex rather than a salt with a glycinium cation would be very unusual. Considering that incorrect placement of H atoms is a common pitfall in crystal structure refinement (Spek, 2009; Bernal & Watkins, 2013; Schwalbe, 2018), this prompted us to scrutinize the structure and crystallographic data of SIZKIX01.

First of all, visual inspection of the original structural model for SIZKIX01 revealed that the hydrogen-bonding pattern is not sensible. Moreover, several *checkCIF/PLATON* (Spek, 2009) alerts concerning a strange C–O–H geometry (level A alert),

Table 1
Hydrogen-bond geometry (Å, °).

<i>D</i> —H··· <i>A</i>	<i>D</i> —H	H··· <i>A</i>	<i>D</i> ··· <i>A</i>	<i>D</i> —H··· <i>A</i>
N1—H1A···O4	0.89	2.08	2.9148 (15)	156
N1—H1A···O11 ⁱ	0.89	2.57	3.0297 (16)	113
N1—H1B···O3 ⁱⁱ	0.89	2.11	2.8933 (15)	146
N1—H1C···O4 ⁱⁱⁱ	0.89	1.98	2.7890 (15)	151
N2—H2A···O3 ⁱⁱ	0.89	2.33	3.1075 (19)	146
N2—H2A···O11 ⁱ	0.89	2.60	3.0591 (18)	113
N2—H2B···O3 ⁱ	0.89	1.93	2.8064 (17)	167
N2—H2C···O1 ^{iv}	0.89	2.48	3.1602 (18)	134
N2—H2C···O6 ⁱⁱ	0.89	2.13	2.8007 (16)	132
O6—H6···O2 ^v	0.82	1.64	2.4406 (16)	167
O9—H9···O1	0.82	1.75	2.5629 (15)	169

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

short intra- and intermolecular *D*—H···*H*—*D* (*D* = hydrogen-bond donor) contacts (level B alerts), positive and negative residual electron density at N and O atoms (level C alerts) and a C—O bond without an H atom attached longer than 1.3 Å, indicated incorrectly positioned hydrogen atoms.

It is instructive to inspect the $F_{\text{obs}} - F_{\text{calc}}$ difference electron-density map to identify incorrectly (and correctly) positioned H atoms. From Fig. 1 it is obvious that the positions of the N—H and O—H hydrogen atoms are incorrect, with the exception of that bonded to O6. After re-refinement of the crystal structure with correctly positioned donor H atoms against original diffraction data, *R*1 [$I > 2\sigma(I)$] dropped from 0.0589 to 0.0426. It should be noted that the *R* factors reported in the article by Tyagi *et al.* (2016) do not agree with those in the corresponding deposited CIF (CCDC 1052856). The residual difference electron densities after re-refinement are 0.35 and $-0.28 \text{ e} \text{ \AA}^{-3}$ (originally 0.63 and $-0.68 \text{ e} \text{ \AA}^{-3}$). Fig. 2 depicts the revised and re-refined structural model for SIZKIX01. A detailed description of the crystal structure of diglycinium squarate can be found in the article by Aniola *et al.* (2014). It is worth noting that the carboxy group of one glycinium ion adopts a *syn* conformation, whereas the other exhibits an *anti*

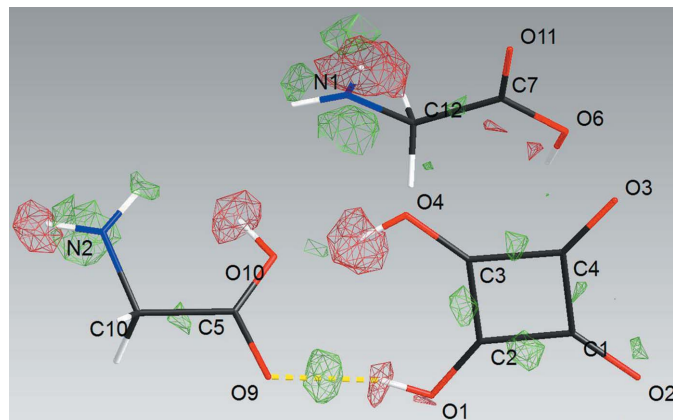


Figure 1
 $F_{\text{obs}} - F_{\text{calc}}$ difference electron density map 1.41 \AA around visible atoms for SIZKIX01: $0.11 \text{ e} \text{ \AA}^{-3}$ (green), $-0.11 \text{ e} \text{ \AA}^{-3}$ (red), $\sigma = 0.039$. Misplaced hydrogen atoms show up as negative density (red), and the correct positions appear as positive density (green).

conformation. The crystal packing of diglycinium squarate is governed by H bonds of the N—H···O and O—H···O type (Table 1). For other squarate salts of α -amino acids, see: Seidel & Zareva (2018), and references cited therein.

Considering that for $\Delta pK_a = pK_a[\text{protonated base}] - pK_a[\text{acid}] > 4$ ionized acid–base proton-transfer compounds were observed exclusively (Cruz-Cabeza, 2012), the formation of a non-ionized acid–base complex of glycine and squaric acid appears to be very unlikely. The pK_a value of the amino group in glycine is 9.6 (Dawson *et al.*, 1986), and for squaric acid, pK_{a1} values of 0.51 ± 0.02 and 0.55 ± 0.15 were obtained by conductometric determination (Gelb, 1971) and potentiometric titration (Schwartz & Howard, 1970), respectively, although based on earlier studies pK_{a1} values in the range of 1.2–1.7 were reported (Gilli *et al.*, 2001).

In conclusion, the crystal structure of the compound previously described as ‘bis(glycine) squaric acid’ (CSD refcode: SIZKIX01) is revised. It has been demonstrated that the structure is in fact the known proton-transfer compound diglycinium squarate and, thus, identical with CSD entry SIZKIX. Consequently, the results of Hirshfeld surface analysis in the original report by Tyagi *et al.* (2016), using the incorrect structure model, must be questioned. It is to be hoped that this contribution helps to avoid such errors in crystal structure refinement in the future.

Synthesis and crystallization

The crystallization of the compound was described by Tyagi *et al.* (2016).

Refinement

The original data (CCDC 1052856) were retrieved in CIF format from the Cambridge Crystallographic Data Centre (CCDC) via <http://www.ccdc.cam.ac.uk/structures>. The reflection data (*HKL*) and the *SHELXL* instruction file (*INS*) were

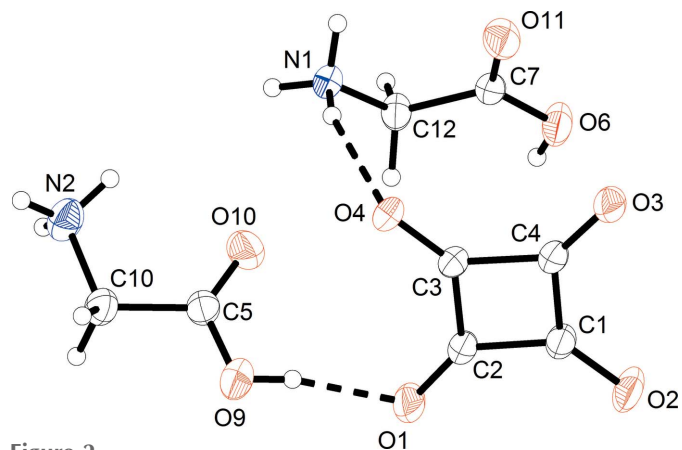


Figure 2
Revised and re-refined structural model for SIZKIX01, proving that the structure is indeed diglycinium squarate and thus identical with SIZKIX. Displacement ellipsoids are drawn at the 50% probability level. H atoms are represented by small spheres of arbitrary radii. Hydrogen bonds are represented by dashed lines.

Table 2
Experimental details.

Crystal data	
Chemical formula	C ₄ O ₄ ·2C ₂ H ₆ NO ₂
<i>M_r</i>	264.20
Crystal system, space group	Monoclinic, <i>C2/c</i>
Temperature (K)	293
<i>a</i> , <i>b</i> , <i>c</i> (Å)	16.8050 (16), 8.3008 (8), 15.7976 (13)
β (°)	100.259 (9)
<i>V</i> (Å ³)	2168.5 (3)
<i>Z</i>	8
Radiation type	Mo <i>K</i> α
μ (mm ⁻¹)	0.15
Crystal size (mm)	0.50 × 0.50 × 0.50
Data collection	
Diffractometer	Rigaku Oxford Diffraction Xcalibur, Sapphire3
Absorption correction	Multi-scan (ABSPACK in <i>CrysAlis PRO</i> ; Rigaku OD, 2014)
<i>T_{min}</i> , <i>T_{max}</i>	0.403, 1.000
No. of measured, independent and observed [<i>I</i> > 2 σ (<i>I</i>)] reflections	7067, 2570, 2277
<i>R_{int}</i>	0.036
(<i>sin</i> θ / λ) _{max} (Å ⁻¹)	0.692
Refinement	
<i>R</i> [<i>F</i> ² > 2 σ (<i>F</i> ²)], <i>wR</i> (<i>F</i> ²), <i>S</i>	0.043, 0.113, 1.04
No. of reflections	2570
No. of parameters	168
H-atom treatment	H-atom parameters constrained
$\Delta\rho_{\max}$, $\Delta\rho_{\min}$ (e Å ⁻³)	0.35, -0.28

Computer programs: *CrysAlis PRO* (Rigaku OD, 2014), *SHELXT2018/3* (Sheldrick, 2015a), *SHELXL2018/3* (Sheldrick, 2015b), *shelXle* (Hübschle *et al.*, 2011), *DIAMOND* (Brandenburg, 2014), *enCIFer* (Allen *et al.*, 2004) and *pubCIF* (Westrip, 2010).

extracted from the CIF using the program *shredCIF*, which is distributed with *SHELXL* (Sheldrick, 2015b). A structure factor file (FCF) was generated with *SHELXL2018/3* using the LIST 6 command, and the *F_{obs}*–*F_{calc}* difference electron-density map was visualized as a three-dimensional mesh (Fig. 1), using *shelXle* (Hübschle *et al.*, 2011).

A re-refinement against the original intensity data was carried out with *SHELXL2018/3* (Sheldrick, 2015b). For the sake of consistency, the chosen asymmetric unit and atom

labels, as shown in Fig. 1, were maintained. The positions of carbon-bound H atoms were calculated geometrically and refined using a riding model with $U_{\text{iso}}(\text{H}) = 1.2U_{\text{eq}}(\text{C})$. The C–H bond lengths were set at 0.97 Å. The initial torsion angles of the protonated amino groups and the carboxy O–H groups were determined *via* difference Fourier syntheses and subsequently refined while maintaining the tetrahedral angles, and with $U_{\text{iso}}(\text{H}) = 1.5U_{\text{eq}}(\text{N}, \text{O})$. The N–H bond lengths were set at 0.89 Å and the O–H bond lengths were set at 0.82 Å. Crystal data, data collection and structure refinement details are given in Table 2.

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full crystallographic data

IUCrData (2018). 3, x181324 [https://doi.org/10.1107/S241431461801324X]

Revision of the crystal structure of 'bis(glycine) squaric acid'

Rüdiger W. Seidel

Bis(carboxymethanaminium) 3,4-dioxocyclobut-1-ene-1,2-diolate

Crystal data

$C_4O_4 \cdot 2C_2H_6NO_2$

$M_r = 264.20$

Monoclinic, $C2/c$

$a = 16.8050$ (16) Å

$b = 8.3008$ (8) Å

$c = 15.7976$ (13) Å

$\beta = 100.259$ (9)°

$V = 2168.5$ (3) Å³

$Z = 8$

$F(000) = 1104$

$D_x = 1.619$ Mg m⁻³

Mo $K\alpha$ radiation, $\lambda = 0.71073$ Å

Cell parameters from 2994 reflections

$\theta = 3.6$ – 29.4 °

$\mu = 0.15$ mm⁻¹

$T = 293$ K

Prism, colourless

$0.50 \times 0.50 \times 0.50$ mm

Data collection

Rigaku Oxford Diffraction Xcalibur, Sapphire3 diffractometer

Radiation source: Enhance (Mo) X-ray Source

Detector resolution: 15.9853 pixels mm⁻¹

ω scans

Absorption correction: multi-scan

(ABSPACK in CrysAlisPro; Rigaku OD, 2014)

$T_{\min} = 0.403$, $T_{\max} = 1.000$

7067 measured reflections

2570 independent reflections

2277 reflections with $I > 2\sigma(I)$

$R_{\text{int}} = 0.036$

$\theta_{\max} = 29.5$ °, $\theta_{\min} = 3.6$ °

$h = -21 \rightarrow 22$

$k = -10 \rightarrow 11$

$l = -21 \rightarrow 19$

Refinement

Refinement on F^2

Least-squares matrix: full

$R[F^2 > 2\sigma(F^2)] = 0.043$

$wR(F^2) = 0.113$

$S = 1.04$

2570 reflections

168 parameters

0 restraints

Primary atom site location: structure-invariant

direct methods

Secondary atom site location: difference Fourier

map

Hydrogen site location: mixed

H-atom parameters constrained

$w = 1/[\sigma^2(F_o^2) + (0.0597P)^2 + 1.323P]$

where $P = (F_o^2 + 2F_c^2)/3$

$(\Delta/\sigma)_{\max} = 0.001$

$\Delta\rho_{\max} = 0.35$ e Å⁻³

$\Delta\rho_{\min} = -0.28$ e Å⁻³

Extinction correction: SHELXL-2018/3

(Sheldrick 2015b),

$F_c^* = kFc[1 + 0.001 \times Fc^2 \lambda^3 / \sin(2\theta)]^{-1/4}$

Extinction coefficient: 0.0281 (16)

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.

Fractional atomic coordinates and isotropic or equivalent isotropic displacement parameters (\AA^2)

	<i>x</i>	<i>y</i>	<i>z</i>	$U_{\text{iso}}^*/U_{\text{eq}}$
C1	0.09201 (8)	0.84696 (17)	-0.03393 (8)	0.0264 (3)
C2	0.09470 (9)	0.75825 (17)	0.04588 (8)	0.0277 (3)
C3	0.17481 (8)	0.82723 (16)	0.07796 (8)	0.0232 (3)
C4	0.17066 (8)	0.91641 (17)	-0.00344 (8)	0.0245 (3)
C5	0.10057 (8)	0.62754 (18)	0.28928 (9)	0.0274 (3)
C7	0.15012 (8)	1.19712 (16)	0.15276 (8)	0.0244 (3)
C10	0.11860 (9)	0.53370 (17)	0.37145 (8)	0.0295 (3)
H10A	0.071281	0.472052	0.378862	0.035*
H10B	0.162392	0.458753	0.368893	0.035*
C12	0.12634 (8)	1.10722 (18)	0.22754 (8)	0.0269 (3)
H12A	0.100022	1.180301	0.261757	0.032*
H12B	0.088457	1.022138	0.206253	0.032*
N1	0.19877 (7)	1.03746 (14)	0.28119 (7)	0.0270 (3)
H1A	0.218164	0.958976	0.252287	0.041*
H1B	0.185750	0.997609	0.329215	0.041*
H1C	0.236182	1.113628	0.294491	0.041*
N2	0.14146 (9)	0.64295 (17)	0.44486 (8)	0.0361 (3)
H2A	0.154562	0.738718	0.426043	0.054*
H2B	0.183654	0.602342	0.480560	0.054*
H2C	0.100009	0.654023	0.472474	0.054*
O1	0.04871 (8)	0.66282 (16)	0.07434 (7)	0.0471 (3)
O2	0.04301 (7)	0.85940 (16)	-0.10400 (6)	0.0408 (3)
O3	0.21416 (7)	1.01203 (14)	-0.03532 (6)	0.0353 (3)
O4	0.22470 (6)	0.81538 (12)	0.14578 (6)	0.0297 (3)
O6	0.09122 (6)	1.24195 (15)	0.09348 (6)	0.0366 (3)
H6	0.048364	1.209417	0.105110	0.055*
O9	0.09184 (8)	0.53179 (14)	0.22230 (7)	0.0443 (3)
H9	0.080061	0.585235	0.178194	0.066*
O10	0.09541 (7)	0.77080 (13)	0.28753 (7)	0.0392 (3)
O11	0.22034 (6)	1.22618 (15)	0.15001 (7)	0.0370 (3)

Atomic displacement parameters (\AA^2)

	U^{11}	U^{22}	U^{33}	U^{12}	U^{13}	U^{23}
C1	0.0260 (6)	0.0325 (7)	0.0201 (6)	-0.0021 (6)	0.0021 (5)	0.0027 (5)
C2	0.0307 (7)	0.0320 (7)	0.0188 (6)	-0.0057 (6)	0.0003 (5)	0.0025 (5)
C3	0.0262 (6)	0.0241 (6)	0.0186 (6)	-0.0007 (5)	0.0022 (5)	-0.0012 (4)
C4	0.0274 (6)	0.0275 (7)	0.0182 (6)	-0.0015 (5)	0.0028 (5)	-0.0003 (5)
C5	0.0206 (6)	0.0319 (7)	0.0284 (6)	-0.0028 (6)	0.0006 (5)	0.0048 (5)
C7	0.0277 (6)	0.0255 (6)	0.0200 (6)	-0.0034 (5)	0.0040 (5)	0.0002 (5)
C10	0.0318 (7)	0.0288 (7)	0.0262 (7)	0.0038 (6)	0.0006 (5)	0.0017 (5)
C12	0.0263 (6)	0.0312 (7)	0.0231 (6)	0.0006 (6)	0.0041 (5)	0.0054 (5)
N1	0.0319 (6)	0.0274 (6)	0.0201 (5)	-0.0015 (5)	0.0000 (4)	0.0018 (4)
N2	0.0432 (7)	0.0391 (7)	0.0257 (6)	0.0067 (6)	0.0057 (5)	-0.0018 (5)
O1	0.0467 (7)	0.0612 (8)	0.0289 (6)	-0.0282 (6)	-0.0053 (5)	0.0161 (5)

O2	0.0312 (5)	0.0648 (8)	0.0226 (5)	-0.0073 (5)	-0.0052 (4)	0.0123 (5)
O3	0.0364 (6)	0.0446 (6)	0.0238 (5)	-0.0150 (5)	0.0024 (4)	0.0059 (4)
O4	0.0319 (5)	0.0332 (5)	0.0207 (4)	-0.0029 (4)	-0.0049 (4)	0.0019 (4)
O6	0.0310 (5)	0.0514 (7)	0.0252 (5)	-0.0043 (5)	-0.0005 (4)	0.0130 (4)
O9	0.0659 (8)	0.0400 (6)	0.0237 (5)	-0.0044 (6)	-0.0012 (5)	0.0027 (4)
O10	0.0407 (6)	0.0306 (6)	0.0427 (6)	-0.0029 (5)	-0.0025 (5)	0.0086 (5)
O11	0.0291 (5)	0.0470 (7)	0.0350 (6)	-0.0088 (5)	0.0064 (4)	0.0080 (5)

Geometric parameters (Å, °)

C1—O2	1.2608 (16)	C10—N2	1.4684 (18)
C1—C4	1.4437 (18)	C10—H10A	0.9700
C1—C2	1.4538 (18)	C10—H10B	0.9700
C2—O1	1.2453 (18)	C12—N1	1.4724 (16)
C2—C3	1.4676 (18)	C12—H12A	0.9700
C3—O4	1.2413 (15)	C12—H12B	0.9700
C3—C4	1.4746 (17)	N1—H1A	0.8900
C4—O3	1.2447 (17)	N1—H1B	0.8900
C5—O10	1.1923 (18)	N1—H1C	0.8900
C5—O9	1.3106 (18)	N2—H2A	0.8900
C5—C10	1.4979 (18)	N2—H2B	0.8900
C7—O11	1.2126 (17)	N2—H2C	0.8900
C7—O6	1.2904 (16)	O6—H6	0.8200
C7—C12	1.5101 (18)	O9—H9	0.8200
O2—C1—C4	132.55 (13)	C5—C10—H10B	109.6
O2—C1—C2	135.85 (13)	H10A—C10—H10B	108.1
C4—C1—C2	91.59 (10)	N1—C12—C7	109.74 (11)
O1—C2—C1	135.23 (13)	N1—C12—H12A	109.7
O1—C2—C3	135.53 (12)	C7—C12—H12A	109.7
C1—C2—C3	89.24 (11)	N1—C12—H12B	109.7
O4—C3—C2	134.77 (12)	C7—C12—H12B	109.7
O4—C3—C4	135.42 (13)	H12A—C12—H12B	108.2
C2—C3—C4	89.81 (10)	C12—N1—H1A	109.5
O3—C4—C1	133.50 (12)	C12—N1—H1B	109.5
O3—C4—C3	137.14 (12)	H1A—N1—H1B	109.5
C1—C4—C3	89.35 (10)	C12—N1—H1C	109.5
O10—C5—O9	126.08 (13)	H1A—N1—H1C	109.5
O10—C5—C10	122.79 (13)	H1B—N1—H1C	109.5
O9—C5—C10	111.13 (12)	C10—N2—H2A	109.5
O11—C7—O6	122.84 (12)	C10—N2—H2B	109.5
O11—C7—C12	121.40 (12)	H2A—N2—H2B	109.5
O6—C7—C12	115.75 (12)	C10—N2—H2C	109.5
N2—C10—C5	110.32 (12)	H2A—N2—H2C	109.5
N2—C10—H10A	109.6	H2B—N2—H2C	109.5
C5—C10—H10A	109.6	C7—O6—H6	109.5
N2—C10—H10B	109.6	C5—O9—H9	109.5

O2—C1—C2—O1	-0.9 (3)	O2—C1—C4—C3	-178.53 (17)
C4—C1—C2—O1	-179.47 (19)	C2—C1—C4—C3	0.14 (11)
O2—C1—C2—C3	178.46 (18)	O4—C3—C4—O3	0.0 (3)
C4—C1—C2—C3	-0.14 (11)	C2—C3—C4—O3	179.65 (18)
O1—C2—C3—O4	-0.9 (3)	O4—C3—C4—C1	-179.79 (16)
C1—C2—C3—O4	179.79 (16)	C2—C3—C4—C1	-0.14 (11)
O1—C2—C3—C4	179.5 (2)	O10—C5—C10—N2	-9.3 (2)
C1—C2—C3—C4	0.14 (11)	O9—C5—C10—N2	170.58 (12)
O2—C1—C4—O3	1.7 (3)	O11—C7—C12—N1	-11.53 (19)
C2—C1—C4—O3	-179.66 (17)	O6—C7—C12—N1	169.34 (12)

Hydrogen-bond geometry (Å, °)

<i>D</i> —H \cdots <i>A</i>	<i>D</i> —H	H \cdots <i>A</i>	<i>D</i> \cdots <i>A</i>	<i>D</i> —H \cdots <i>A</i>
N1—H1A \cdots O4	0.89	2.08	2.9148 (15)	156
N1—H1A \cdots O11 ⁱ	0.89	2.57	3.0297 (16)	113
N1—H1B \cdots O3 ⁱⁱ	0.89	2.11	2.8933 (15)	146
N1—H1C \cdots O4 ⁱⁱⁱ	0.89	1.98	2.7890 (15)	151
N2—H2A \cdots O3 ⁱⁱ	0.89	2.33	3.1075 (19)	146
N2—H2A \cdots O11 ⁱ	0.89	2.60	3.0591 (18)	113
N2—H2B \cdots O3 ⁱ	0.89	1.93	2.8064 (17)	167
N2—H2C \cdots O1 ^{iv}	0.89	2.48	3.1602 (18)	134
N2—H2C \cdots O6 ⁱⁱ	0.89	2.13	2.8007 (16)	132
O6—H6 \cdots O2 ^v	0.82	1.64	2.4406 (16)	167
O9—H9 \cdots O1	0.82	1.75	2.5629 (15)	169

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