Crystal structure of 1,2,3,4-tetrahydroisoquinolin-2-ium (2S,3S)-3-carboxy-2,3-dihydroxypropanoate monohydrate

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The crystal structure of 1,2,3,4-tetrahydroisoquinolin-2-ium (2S,3S)-3-carboxy-2,3-dihydroxypropanoate monohydrate, $C_9H_{12}N^+ \cdot C_4H_5O_6^- \cdot H_2O$, at 115 K shows orthorhombic symmetry (space group $P2_12_12_1$). The hydrogen tartrate anions and solvent water molecules form an intricate diperiodic O—H⋯O hydrogen-bond network parallel to (001). The tetrahydroisoquinolinium cations are tethered to the anionic hydrogen-bonded layers through N—H⋯O hydrogen bonds. The crystal packing in the third direction is achieved through van der Waals contacts between the hydrocarbon tails of the tetrahydroisoquinolinium cations, resulting in hydrophobic and hydrophilic regions in the crystal structure.

1. Chemical context

1,2,3,4-Tetrahydroisoquinoline is a secondary amine derived from isoquinoline. Tetrahydroisoquinoline alkaloids represent a large and structurally diverse group of natural products with a wide range of biological activity (Kim *et al.*, 2023). The tetrahydroisoquinoline scaffold is also encountered in a number of approved drugs, for example in the angiotensin-converting-enzyme inhibitor quinapril and in the anti-muscarinic solifenacin. Thus far, few salts of 1,2,3,4-tetrahydroisoquinoline have been structurally characterized (see Section 4). Herein, we describe the crystal and molecular structure of 1,2,3,4-tetrahydroisoquinolinium hydrogen tartrate monohydrate [systematic name: 1,2,3,4-tetrahydroisoquinolin-2-ium (2S,3S)-3-carboxy-2,3-dihydroxypropanoate hydrate]. Hydrogen tartrate is a well-known anion in pharmaceutics (Bharate, 2021). The pK_a of the conjugate acid of tetrahydroisoquinoline is 9.3 (at 310 K; Bojarski *et al.*, 1995), and the pK_{a1} of tartaric acid is 2.9 (at 298 K; Dawson, 1959). According to the pK_a rule (Cruz-Cabeza, 2012), we can estimate $\Delta pK_a = pK_a[\text{protonated base}] - pK_a[\text{acid}] = 9.3 - 2.9 = 6.4$. Hence, proton transfer is expected when tetrahydroisoquinoline is reacted with tartaric acid.

2. Structural commentary

Fig. 1 shows a displacement ellipsoid plot of the molecular components of the salt in the solid state. The asymmetric unit comprises a 1,2,3,4-tetrahydroisoquinolin-2-ium cation, a
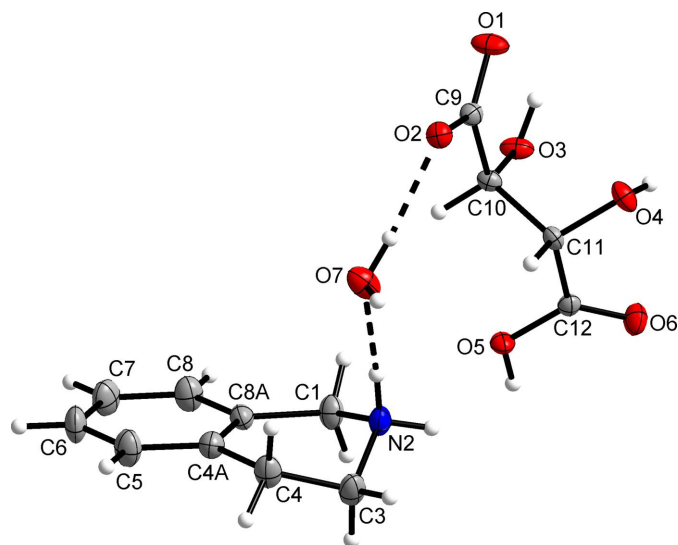
Figure 1
The asymmetric unit of the title compound with displacement ellipsoids at the 50% probability level. Hydrogen atoms are presented by small spheres of arbitrary radius. Dashed lines illustrate hydrogen bonds.

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

D—H⋯A	D—H	H⋯A	D⋯A	D—H⋯A
N2—H2A⋯O7	0.91 (2)	1.85 (2)	2.762 (3)	176 (2)
N2—H2B⋯O6^i	0.88 (2)	2.09 (2)	2.787 (2)	135 (2)
N2—H2B⋯O5	0.88 (2)	2.41 (2)	2.981 (2)	123 (2)
O3—H3⋯O4^{ii}	0.87 (2)	1.98 (2)	2.766 (2)	151 (3)
O4—H4⋯O2^{ii}	0.82 (2)	1.99 (2)	2.730 (2)	150 (3)
O5—H5A⋯O1^{iii}	0.89 (2)	1.60 (2)	2.480 (2)	173 (3)
O7—H7A⋯O2	0.87 (2)	1.91 (2)	2.782 (2)	173 (3)
O7—H7B⋯O3^{iv}	0.87 (2)	1.92 (2)	2.772 (2)	169 (3)

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

tartaric acid derivatives (Gawronski *et al.*, 2005). The carboxy group of the anion exhibits the *syn* conformation.

3. Supramolecular features

The solid state supramolecular structure features an intricate network of N—H⋯O and O—H⋯O hydrogen bonds (Fig. 2). Table 1 lists the corresponding geometric parameters, which are within expected ranges (Thakuria *et al.*, 2017). The hydrogen tartrate anions form hydrogen-bonded chains by translational symmetry in the *b*-axis direction through hydrogen bonding between the carboxy group and the carboxylate group of an adjacent molecule (O5—H5A⋯O1^{iii}). In the *a*-axis direction, the hydrogen tartrate ions are connected along a 2_1 screw axis *via* two hydrogen bonds with the two hydroxy groups as donors and a hydroxy group (O3—H3⋯O4^{ii}) and the carboxylate group (O4—H4⋯O2^{ii}) of a neighbouring molecule as acceptors. These O—H⋯O hydrogen-bonding interactions that extend in the *a*- and *b*-axis directions result in diperiodic hydrogen-bonded sheets parallel to (001). The protonated amino group of the tetrahydroisoquinolinium cation forms a bifurcated hydrogen bond to the carboxy groups of two adjacent hydrogen tartrate anions (N2—H2B⋯O5 and N2—H2B⋯O6^i) and another hydrogen bond to the solvent water molecule (N2—H2A⋯O7). The water molecule in turn acts as a hydrogen-bond donor towards the carboxylate group
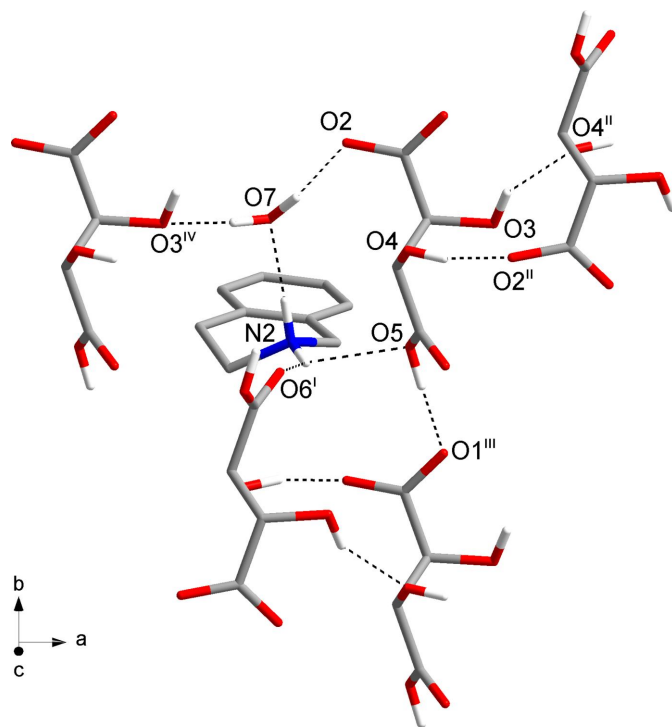

Figure 2
Section of the crystal structure, viewed along the [011] direction, showing the unique hydrogen bonds (dashed lines). Symmetry codes: (i) $x - \frac{1}{2}, -y + \frac{1}{2}, -z + 1$; (ii) $x + \frac{1}{2}, -y + \frac{3}{2}, -z + 1$; (iii) $x, y - 1, z$; (iv) $x - 1, y, z$.

(2*S*,3*S*)-hydrogen tartrate anion and a water molecule of crystallization. The axially chiral conformation of the tetrahydroisoquinolinium cation is left-handed, as revealed by the C4—C3—N2—C1 torsion angle of −65.8 (3)°. The carbon skeleton of the hydrogen tartrate anion adopts an antiperiplanar (*anti*) conformation [C9—C10—C11—C12 = 178.67 (15)°], which is known to be the predominant one in
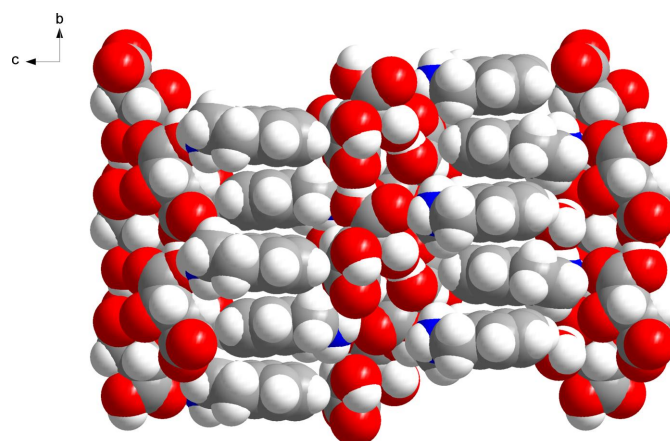

Figure 3
Space-filling representation of the crystal structure, viewed along the *a*-axis direction. Colour scheme: C, grey; H, white; N, blue; O, red.

(O7—HA···O2) and a hydroxy group (O7—HB···O3^{iv}) of two hydrogen tartrate anions. The hydrocarbon parts of the tetrahydroisoquinolinium cations are oriented approximately perpendicular to the diperiodic hydrogen-bonded sheets formed by the hydrogen tartrate anions. The crystal packing in the third dimension is achieved by stacking in the *c*-axis direction with interlocking of the hydrocarbon tails through van der Waals packing (Fig. 3). This affords hydrophobic and hydrophilic regions in the crystal structure.

4. Database survey

A survey of the Cambridge Structural Database (CSD, version 5.43, update of September 2022; Groom *et al.*, 2016) revealed that crystal structures of salts of tetrahydroisoquinolinium are scarce. Thus far, the crystal structures of a solvent-free hydrochloride (CSD refcode: GESVOR; Zia-ur-Rehman *et al.*, 2012), hydrogen squarate (TIGKIE; Kolev *et al.*, 2007), hexachloridostannate(IV) (AYAHAM; Dhanalakshmi *et al.*, 2021) and hexabromidostannate(IV) (AYAHEQ; Dhana-lakshmi *et al.*, 2021) as well as a violurate monohydrate (FUFPOM; Kolev *et al.*, 2009) have been reported. The solid-state structure of free-base tetrahydroisoquinolinium, which is liquid at ambient conditions, is hitherto unknown, as far as we are able to ascertain. In contrast, hundreds of crystal structures containing hydrogen tartrate anions can be found in the CSD. In the vast majority of these crystal structures, the carbon skeleton of the hydrogen tartrate anion exhibits the *anti* conformation. Exceptions are the crystal structure of quininium (*S*,*S*)-hydrogen tartrate hemihydrate (PUVTUV; Ryttersgaard & Larsen, 1998), lithium *meso*-hydrogen tartrate monohydrate (COFGAF10; Stouten *et al.*, 1988), potassium *meso*-hydrogen tartrate monohydrate (KHMTAR01; Currie *et al.*, 1975) and 1-(4′-cyano-4′-cyclohexyl-4′-phenylbutyl)piper-idinium (*S*,*S*)-hydrogen tartrate (EZOWUL; Jones, 2004) in which the hydrogen tartrate anions are found in the *gauche* conformation.

5. Synthesis and crystallization

Starting materials were obtained from commercial sources and used as received. A mixture of 1,2,3,4-tetrahydroisoquinoline (266 mg, 2 mmol) and excess (2*S*,3*S*)-tartaric acid (1.50 g, 10 mmol) in 60 mL of deionized water was stirred for four h at room temperature. Subsequently, the salt was isolated by filtration. Colourless crystals suitable for single-crystal X-ray diffraction were obtained from a water/methanol (3:1) solution of the salt, after the solvents were allowed to evaporate slowly at ambient conditions.

6. Refinement

Crystal data, data collection and structure refinement details are summarized in Table 2. Carbon-bound hydrogen atoms were placed in geometrically calculated positions and refined using the appropriate riding model with C—H$_{aromatic}$ = 0.95 Å, C—H$_{methylene}$ = 0.99 Å, C—H$_{methine}$ = 1.00 Å and U_{iso}(H) =

Table 2
Experimental details.

Crystal data	
Chemical formula	$C_9H_{12}N^+·C_4H_5O_6^-·H_2O$
M_r	301.29
Crystal system, space group	Orthorhombic, $P2_12_12_1$
Temperature (K)	115
a, b, c (Å)	7.0695 (3), 7.4842 (3), 26.9573 (10)
V (Å^3)	1426.30 (10)
Z	4
Radiation type	Mo $K\alpha$
μ (mm^{-1})	0.12
Crystal size (mm)	0.49 × 0.21 × 0.20
Data collection	
Diffractometer	Oxford Diffraction Xcalibur2
Absorption correction	Multi-scan (ABSPACK in *CrysAlis PRO*; Rigaku OD, 2023)
T_{min}, T_{max}	0.967, 1.000
No. of measured, independent and observed [$I > 2\sigma(I)$] reflections	16488, 3307, 2900
R_{int}	0.038
$(\sin\theta/\lambda)_{max}$ (Å^{-1})	0.671
Refinement	
$R[F^2 > 2\sigma(F^2)]$, $wR(F^2)$, S	0.037, 0.078, 1.04
No. of reflections	3307
No. of parameters	218
No. of restraints	7
H-atom treatment	H atoms treated by a mixture of independent and constrained refinement
$\Delta\rho_{max}$, $\Delta\rho_{min}$ (e Å^{-3})	0.25, −0.19
Absolute structure	The absolute structure was inferred from the known absolute configuration of the starting material.

Computer programs: *CrysAlis* system (Oxford Diffraction, 2009), *CrysAlis PRO* (Rigaku OD, 2023), *SHELXS97* (Sheldrick, 2008), *SHELXL2019/3* (Sheldrick, 2015), *DIAMOND* (Brandenburg, 2018) and *publCIF* (Westrip, 2010).

1.2 U_{eq}(C). Nitrogen- and oxygen-bound hydrogen atoms were located in difference-Fourier maps and subsequently refined semi-freely with the N—H and the O—H distances restrained to target values of 0.88 (2) Å and 0.84 (2) Å, respectively.

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supporting information

Crystal structure of 1,2,3,4-tetrahydroisoquinolin-2-ium (2*S*,3*S*)-3-carboxy-2,3-dihydroxypropanoate monohydrate

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Computing details

1,2,3,4-Tetrahydroisoquinolin-2-ium (2*S*,3*S*)-3-carboxy-2,3-dihydroxypropanoate monohydrate

Crystal data

$C_9H_{12}N^+ \cdot C_4H_5O_6^- \cdot H_2O$	$D_x = 1.403$ Mg m^{-3}
$M_r = 301.29$	Mo $K\alpha$ radiation, $\lambda = 0.71073$ Å
Orthorhombic, $P2_12_12_1$	Cell parameters from 5780 reflections
$a = 7.0695$ (3) Å	$\theta = 3.0–27.7°$
$b = 7.4842$ (3) Å	$\mu = 0.12$ mm^{-1}
$c = 26.9573$ (10) Å	$T = 115$ K
$V = 1426.30$ (10) Å^3	Prism, colourless
$Z = 4$	$0.49 \times 0.21 \times 0.20$ mm
$F(000) = 640$	

Data collection

Oxford Diffraction Xcalibur2 diffractometer	$T_{min} = 0.967$, $T_{max} = 1.000$
Radiation source: fine-focus sealed X-ray tube, Enhance (Mo) X-ray Source	16488 measured reflections
	3307 independent reflections
Graphite monochromator	2900 reflections with $I > 2\sigma(I)$
Detector resolution: 8.4171 pixels mm^{-1}	$R_{int} = 0.038$
ω scans	$\theta_{max} = 28.5°$, $\theta_{min} = 2.8°$
Absorption correction: multi-scan (ABSPACK in CrysAlisPro; Rigaku OD, 2023)	$h = -9 \rightarrow 9$
	$k = -9 \rightarrow 9$
	$l = -35 \rightarrow 35$

Refinement

Refinement on F^2	Hydrogen site location: mixed
Least-squares matrix: full	H atoms treated by a mixture of independent and constrained refinement
$R[F^2 > 2\sigma(F^2)] = 0.037$	
$wR(F^2) = 0.078$	$w = 1/[\sigma^2(F_o^2) + (0.0326P)^2 + 0.2898P]$ where $P = (F_o^2 + 2F_c^2)/3$
$S = 1.04$	
3307 reflections	$(\Delta/\sigma)_{max} < 0.001$
218 parameters	$\Delta\rho_{max} = 0.25$ e Å^{-3}
7 restraints	$\Delta\rho_{min} = -0.19$ e Å^{-3}
Primary atom site location: structure-invariant direct methods	Absolute structure: The absolute structure was inferred from the known absolute configuration of the starting material.
Secondary atom site location: difference Fourier map	

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 (Å²)

	x	*y*	*z*	U_{iso}*/U_{eq}
C1	0.4189 (3)	0.1694 (3)	0.34142 (7)	0.0239 (5)
H1A	0.464782	0.045500	0.345983	0.029*
H1B	0.528981	0.250520	0.344259	0.029*
C3	0.0946 (3)	0.1243 (4)	0.37283 (8)	0.0285 (5)
H3A	0.011223	0.144808	0.401784	0.034*
H3B	0.112372	−0.006161	0.368861	0.034*
C4	0.0045 (3)	0.2016 (4)	0.32647 (8)	0.0270 (6)
H4A	−0.108849	0.130433	0.317815	0.032*
H4B	−0.037111	0.325477	0.333300	0.032*
C4A	0.1392 (3)	0.2023 (3)	0.28289 (7)	0.0214 (5)
C5	0.0715 (3)	0.2181 (4)	0.23438 (8)	0.0304 (6)
H5	−0.060695	0.228797	0.228874	0.036*
C6	0.1933 (4)	0.2184 (4)	0.19427 (8)	0.0315 (6)
H6	0.144780	0.230122	0.161566	0.038*
C7	0.3856 (4)	0.2017 (4)	0.20182 (8)	0.0309 (6)
H7	0.469721	0.200425	0.174352	0.037*
C8	0.4550 (3)	0.1869 (3)	0.24957 (8)	0.0282 (5)
H8	0.587475	0.176093	0.254702	0.034*
C8A	0.3337 (3)	0.1876 (3)	0.29031 (7)	0.0194 (5)
C9	0.6220 (3)	0.8178 (3)	0.43005 (7)	0.0163 (4)
C10	0.6944 (3)	0.6256 (3)	0.43360 (7)	0.0150 (4)
H10	0.659059	0.561013	0.402479	0.018*
C11	0.6005 (3)	0.5311 (3)	0.47767 (7)	0.0149 (4)
H11	0.460966	0.528552	0.471655	0.018*
C12	0.6706 (3)	0.3389 (3)	0.47987 (7)	0.0151 (4)
N2	0.2809 (3)	0.2123 (3)	0.38108 (7)	0.0226 (4)
H2A	0.263 (4)	0.333 (3)	0.3823 (9)	0.029 (7)*
H2B	0.326 (3)	0.179 (3)	0.4103 (7)	0.024 (6)*
O1	0.7420 (2)	0.93738 (19)	0.43712 (6)	0.0257 (4)
O2	0.4493 (2)	0.8404 (2)	0.42043 (5)	0.0183 (3)
O3	0.8937 (2)	0.6193 (2)	0.43902 (6)	0.0204 (3)
H3	0.933 (4)	0.721 (3)	0.4501 (9)	0.039 (8)*
O4	0.6332 (2)	0.6239 (2)	0.52224 (5)	0.0206 (3)
H4	0.743 (3)	0.609 (4)	0.5316 (10)	0.041 (8)*
O6	0.7472 (2)	0.2755 (2)	0.51597 (5)	0.0242 (4)
O5	0.6396 (2)	0.25433 (19)	0.43803 (5)	0.0181 (3)
H5A	0.675 (4)	0.141 (3)	0.4404 (11)	0.055 (9)*
O7	0.2156 (3)	0.5762 (2)	0.38150 (6)	0.0290 (4)
H7A	0.296 (4)	0.651 (4)	0.3947 (11)	0.050 (9)*

| H7B | 0.108 (4) | 0.581 (5) | 0.3967 (11) | 0.063 (11)* |

Atomic displacement parameters (Å²)

	U^{11}	U^{22}	U^{33}	U^{12}	U^{13}	U^{23}
C1	0.0193 (11)	0.0331 (13)	0.0192 (10)	0.0045 (11)	−0.0019 (9)	0.0004 (9)
C3	0.0244 (13)	0.0404 (15)	0.0208 (10)	−0.0100 (12)	0.0004 (10)	0.0047 (10)
C4	0.0197 (12)	0.0395 (15)	0.0218 (11)	−0.0036 (11)	0.0000 (9)	0.0009 (10)
C4A	0.0236 (12)	0.0214 (11)	0.0190 (10)	−0.0013 (10)	−0.0003 (9)	0.0004 (8)
C5	0.0227 (12)	0.0440 (15)	0.0244 (11)	0.0006 (12)	−0.0051 (9)	0.0025 (10)
C6	0.0367 (14)	0.0433 (16)	0.0145 (10)	0.0000 (13)	−0.0045 (10)	0.0014 (10)
C7	0.0317 (13)	0.0413 (15)	0.0197 (11)	−0.0019 (13)	0.0062 (10)	−0.0009 (10)
C8	0.0221 (12)	0.0389 (15)	0.0235 (11)	0.0007 (11)	0.0011 (9)	−0.0017 (10)
C8A	0.0225 (11)	0.0188 (11)	0.0168 (9)	0.0003 (9)	−0.0021 (8)	−0.0012 (8)
C9	0.0179 (10)	0.0152 (10)	0.0159 (9)	0.0004 (9)	0.0013 (8)	−0.0004 (8)
C10	0.0124 (10)	0.0144 (10)	0.0182 (9)	0.0000 (8)	−0.0001 (8)	−0.0016 (8)
C11	0.0137 (10)	0.0169 (10)	0.0141 (9)	−0.0011 (8)	−0.0019 (8)	−0.0024 (8)
C12	0.0130 (10)	0.0175 (10)	0.0148 (9)	−0.0022 (8)	0.0011 (8)	0.0013 (8)
N2	0.0232 (10)	0.0298 (12)	0.0149 (8)	−0.0029 (9)	−0.0012 (8)	0.0027 (8)
O1	0.0202 (8)	0.0126 (7)	0.0443 (9)	0.0000 (7)	−0.0035 (8)	−0.0019 (7)
O2	0.0149 (7)	0.0195 (8)	0.0204 (7)	0.0019 (6)	0.0000 (6)	0.0001 (6)
O3	0.0141 (7)	0.0140 (8)	0.0331 (8)	0.0007 (6)	0.0014 (7)	−0.0021 (6)
O4	0.0169 (8)	0.0255 (8)	0.0194 (7)	0.0031 (7)	−0.0023 (7)	−0.0090 (6)
O6	0.0279 (8)	0.0260 (9)	0.0187 (7)	0.0051 (8)	−0.0050 (6)	0.0031 (6)
O5	0.0240 (8)	0.0116 (8)	0.0188 (7)	0.0018 (6)	−0.0029 (6)	−0.0008 (6)
O7	0.0222 (9)	0.0336 (10)	0.0312 (9)	−0.0026 (8)	0.0034 (8)	−0.0108 (8)

Geometric parameters (Å, º)

C1—N2	1.483 (3)	C8—H8	0.9500
C1—C8A	1.510 (3)	C9—O1	1.247 (2)
C1—H1A	0.9900	C9—O2	1.260 (3)
C1—H1B	0.9900	C9—C10	1.529 (3)
C3—N2	1.489 (3)	C10—O3	1.417 (2)
C3—C4	1.518 (3)	C10—C11	1.534 (3)
C3—H3A	0.9900	C10—H10	1.0000
C3—H3B	0.9900	C11—O4	1.407 (2)
C4—C4A	1.512 (3)	C11—C12	1.522 (3)
C4—H4A	0.9900	C11—H11	1.0000
C4—H4B	0.9900	C12—O6	1.211 (2)
C4A—C8A	1.393 (3)	C12—O5	1.312 (2)
C4A—C5	1.397 (3)	N2—H2A	0.91 (2)
C5—C6	1.382 (3)	N2—H2B	0.883 (19)
C5—H5	0.9500	O3—H3	0.87 (2)
C6—C7	1.380 (3)	O4—H4	0.82 (2)
C6—H6	0.9500	O5—H5A	0.89 (2)
C7—C8	1.382 (3)	O7—H7A	0.87 (2)
C7—H7	0.9500	O7—H7B	0.87 (2)

C8—C8A	1.393 (3)		
N2—C1—C8A	112.07 (18)	C8A—C8—H8	119.5
N2—C1—H1A	109.2	C4A—C8A—C8	119.6 (2)
C8A—C1—H1A	109.2	C4A—C8A—C1	122.13 (19)
N2—C1—H1B	109.2	C8—C8A—C1	118.22 (19)
C8A—C1—H1B	109.2	O1—C9—O2	126.43 (19)
H1A—C1—H1B	107.9	O1—C9—C10	115.97 (17)
N2—C3—C4	108.99 (18)	O2—C9—C10	117.60 (17)
N2—C3—H3A	109.9	O3—C10—C9	111.74 (16)
C4—C3—H3A	109.9	O3—C10—C11	109.57 (16)
N2—C3—H3B	109.9	C9—C10—C11	109.73 (16)
C4—C3—H3B	109.9	O3—C10—H10	108.6
H3A—C3—H3B	108.3	C9—C10—H10	108.6
C4A—C4—C3	112.13 (19)	C11—C10—H10	108.6
C4A—C4—H4A	109.2	O4—C11—C12	112.33 (16)
C3—C4—H4A	109.2	O4—C11—C10	111.24 (16)
C4A—C4—H4B	109.2	C12—C11—C10	108.98 (16)
C3—C4—H4B	109.2	O4—C11—H11	108.1
H4A—C4—H4B	107.9	C12—C11—H11	108.1
C8A—C4A—C5	118.6 (2)	C10—C11—H11	108.1
C8A—C4A—C4	120.63 (19)	O6—C12—O5	125.21 (19)
C5—C4A—C4	120.8 (2)	O6—C12—C11	123.19 (18)
C6—C5—C4A	121.3 (2)	O5—C12—C11	111.59 (16)
C6—C5—H5	119.4	C1—N2—C3	112.25 (17)
C4A—C5—H5	119.4	C1—N2—H2A	109.3 (17)
C7—C6—C5	119.9 (2)	C3—N2—H2A	108.7 (18)
C7—C6—H6	120.1	C1—N2—H2B	110.2 (16)
C5—C6—H6	120.1	C3—N2—H2B	109.1 (16)
C6—C7—C8	119.6 (2)	H2A—N2—H2B	107 (2)
C6—C7—H7	120.2	C10—O3—H3	109.0 (19)
C8—C7—H7	120.2	C11—O4—H4	110 (2)
C7—C8—C8A	121.0 (2)	C12—O5—H5A	111 (2)
C7—C8—H8	119.5	H7A—O7—H7B	110 (3)
N2—C3—C4—C4A	49.8 (3)	N2—C1—C8A—C8	167.3 (2)
C3—C4—C4A—C8A	−18.9 (3)	O1—C9—C10—O3	−6.6 (2)
C3—C4—C4A—C5	161.3 (2)	O2—C9—C10—O3	173.40 (17)
C8A—C4A—C5—C6	0.3 (4)	O1—C9—C10—C11	115.09 (19)
C4—C4A—C5—C6	−179.8 (2)	O2—C9—C10—C11	−64.9 (2)
C4A—C5—C6—C7	0.4 (4)	O3—C10—C11—O4	66.1 (2)
C5—C6—C7—C8	−0.8 (4)	C9—C10—C11—O4	−57.0 (2)
C6—C7—C8—C8A	0.3 (4)	O3—C10—C11—C12	−58.3 (2)
C5—C4A—C8A—C8	−0.8 (4)	C9—C10—C11—C12	178.67 (15)
C4—C4A—C8A—C8	179.4 (2)	O4—C11—C12—O6	−0.7 (3)
C5—C4A—C8A—C1	−179.8 (2)	C10—C11—C12—O6	123.1 (2)
C4—C4A—C8A—C1	0.4 (4)	O4—C11—C12—O5	−179.82 (16)
C7—C8—C8A—C4A	0.4 (4)	C10—C11—C12—O5	−56.1 (2)

C7—C8—C8A—C1	179.5 (2)	C8A—C1—N2—C3	46.4 (3)
N2—C1—C8A—C4A	−13.7 (3)	C4—C3—N2—C1	−65.8 (3)

Hydrogen-bond geometry (Å, º)

D—H···*A*	*D*—H	H···*A*	*D*···*A*	*D*—H···*A*
C1—H1*A*···O2ⁱ	0.99	2.53	3.263 (3)	131
C3—H3*A*···O1ⁱⁱ	0.99	2.63	3.343 (3)	129
N2—H2*A*···O7	0.91 (2)	1.85 (2)	2.762 (3)	176 (2)
N2—H2*B*···O6ⁱⁱⁱ	0.88 (2)	2.09 (2)	2.787 (2)	135 (2)
N2—H2*B*···O5	0.88 (2)	2.41 (2)	2.981 (2)	123 (2)
O3—H3···O1	0.87 (2)	2.14 (3)	2.612 (2)	114 (2)
O3—H3···O4ⁱᵛ	0.87 (2)	1.98 (2)	2.766 (2)	151 (3)
O4—H4···O2ⁱᵛ	0.82 (2)	1.99 (2)	2.730 (2)	150 (3)
O5—H5*A*···O1ⁱ	0.89 (2)	1.60 (2)	2.480 (2)	173 (3)
O7—H7*A*···O2	0.87 (2)	1.91 (2)	2.782 (2)	173 (3)
O7—H7*B*···O3ᵛ	0.87 (2)	1.92 (2)	2.772 (2)	169 (3)

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