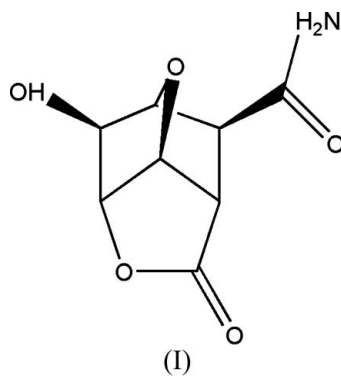


**(±)-*exo*-2-Hydroxy-5-oxo-4,8-dioxatricyclo-[4.2.1.0<sup>3,7</sup>]nonane-9-*exo*-carboxylic acid**Ali Sadeghi-Khomami,<sup>a</sup> Neil R. Thomas<sup>a</sup> and Claire Wilson<sup>b\*</sup><sup>a</sup>Centre for Biomolecular Sciences, School of Chemistry, University of Nottingham, Nottingham NG7 2RD, England, and <sup>b</sup>School of Chemistry, University of Nottingham, Nottingham NG7 2RD, EnglandCorrespondence e-mail:  
claire.wilson@nottingham.ac.uk**Key indicators**Single-crystal X-ray study  
*T* = 150 K  
Mean  $\sigma$ (C–C) = 0.002 Å  
*R* factor = 0.036  
*wR* factor = 0.096  
Data-to-parameter ratio = 12.5For details of how these key indicators were automatically derived from the article, see <http://journals.iucr.org/e>.

The title compound, C<sub>8</sub>H<sub>9</sub>NO<sub>5</sub>, was prepared as a by-product in synthetic efforts to prepare a carbasugar analogue of a putative intermediate, *viz.* (±)-6-hydroxymethyl-7-oxabicyclo[2.2.1]hept-2-*exo*-3-*endo*-diol, in the uridine diphosphate–galactopyranose mutase-catalysed reaction. The structure shows extensive hydrogen bonding involving N–H···O and O–H···O as well as C–H···O interactions.

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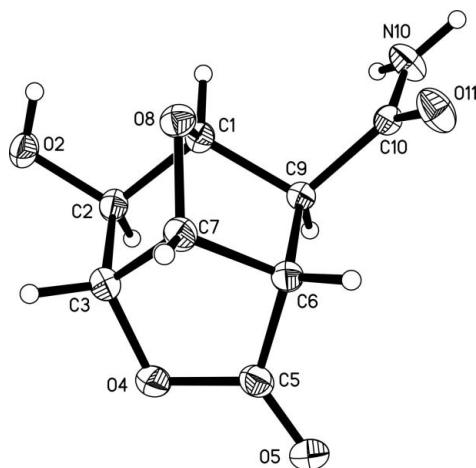
The title compound, (I), was prepared as a by-product in synthetic efforts to prepare a carbasugar analogue of a putative intermediate, *viz.* (±)-6-hydroxymethyl-7-oxabicyclo[2.2.1]hept-2-*exo*-3-*endo*-diol in the uridine diphosphate–galactopyranose mutase-catalysed reaction, and was synthesized from racemic *exo*-5,6-epoxy-7-oxabicyclo[2.2.1]heptan-*trans*-2,3-dicarboxylic acid dimethyl ester (Sadeghi-Khomami *et al.*, 2005) through treatment with concentrated ammonia solution (30% *w/v*).



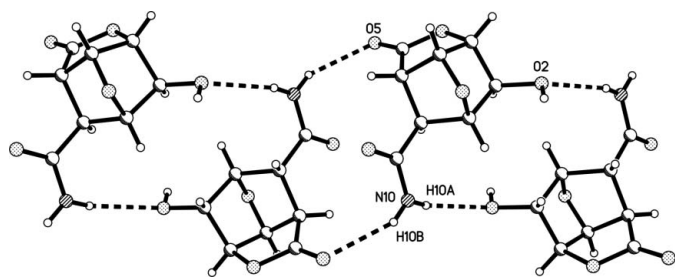
The molecular structure of (I) is shown in Fig. 1. There is extensive hydrogen bonding in the structure (see Table 1). N–H···O interactions form a ribbon structure (Fig. 2), which lies parallel to the *ac* plane and propagates along the *c*-axis direction. These ribbons can be considered to be linked by O–H···O interactions, forming a two-dimensional layer parallel to the *bc* plane (Fig. 3). In addition, there are C–H···O interactions in the structure (Table 1) which conform to the geometric conditions for the weak hydrogen bonds given by Desiraju & Steiner (1999).

**Experimental**

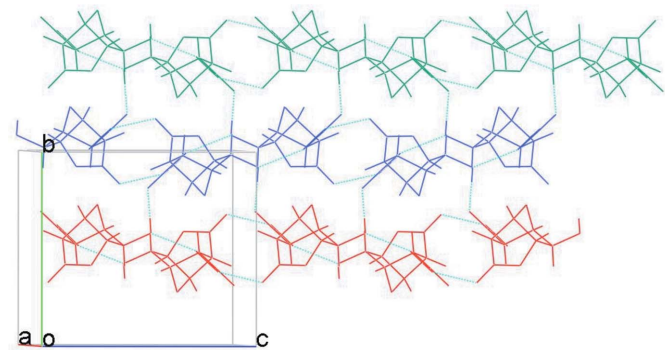
Formation of the title compound occurred *via* hydrolysis of the *endo*-methyl carboxylate, followed by a 5-*exo*-Tet lactonization on to the *exo*-epoxide. Concurrently, the *exo*-methyl carboxylate is hydrolysed



**Figure 1**  
View showing the molecular structure and atom-labelling scheme of the title compound. Displacement ellipsoids are drawn at the 50% probability level.



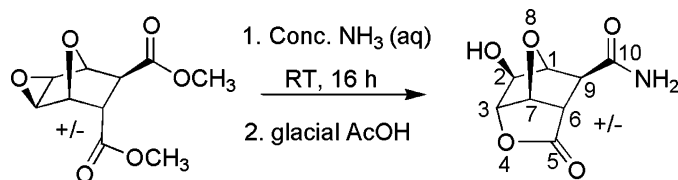
**Figure 2**  
View showing N—H...O hydrogen-bonding interactions (dashed lines), leading to a ribbon structure parallel to the *ac* plane and propagating parallel to the *c* axis.



**Figure 3**  
View showing linkage of the N—H...O ribbons (each shown as a single colour) by O—H...O interactions (dashed lines), forming a sheet in the *bc* plane.

and, somewhat surprisingly, forms the carboxamide rather than the expected ammonium salt of the carboxylic acid. The resulting solution was neutralized to pH 7.0 after 16 h at room temperature by dropwise addition of glacial acetic acid and the solvent removed by lyophilization (see scheme). This procedure gave the amide-lactone product ( $R_F = 0.5$ , 2-propanol/MeOH 2:1), which crystallized from methanol as colourless blocks. The IR spectrum of the title compound

clearly revealed carbonyl bands for the lactone ( $1780\text{ cm}^{-1}$ ) and carboxamide functional groups ( $1670\text{ cm}^{-1}$ ).



#### Crystal data

$\text{C}_8\text{H}_9\text{NO}_5$   
 $M_r = 199.16$   
Monoclinic,  $P2_1/c$   
 $a = 8.3843$  (6) Å  
 $b = 9.1844$  (6) Å  
 $c = 10.1638$  (7) Å  
 $\beta = 97.525$  (1)°  
 $V = 775.92$  (9) Å<sup>3</sup>

$Z = 4$   
 $D_x = 1.705\text{ Mg m}^{-3}$   
Mo  $K\alpha$  radiation  
 $\mu = 0.14\text{ mm}^{-1}$   
 $T = 150$  (2) K  
Block, colourless  
 $0.67 \times 0.49 \times 0.31\text{ mm}$

#### Data collection

Bruker SMART1000 CCD area-detector diffractometer  
 $\omega$  scans  
Absorption correction: none  
6671 measured reflections

1744 independent reflections  
1665 reflections with  $I > 2\sigma(I)$   
 $R_{\text{int}} = 0.051$   
 $\theta_{\text{max}} = 27.5^\circ$

#### Refinement

Refinement on  $F^2$   
 $R[F^2 > 2\sigma(F^2)] = 0.036$   
 $wR(F^2) = 0.096$   
 $S = 1.03$   
1744 reflections  
140 parameters  
H atoms treated by a mixture of independent and constrained refinement

$w = 1/[\sigma^2(F_o^2) + (0.0546P)^2 + 0.3811P]$   
where  $P = (F_o^2 + 2F_c^2)/3$   
 $(\Delta/\sigma)_{\text{max}} = 0.001$   
 $\Delta\rho_{\text{max}} = 0.40\text{ e \AA}^{-3}$   
 $\Delta\rho_{\text{min}} = -0.24\text{ e \AA}^{-3}$   
Extinction correction: *SHELXL97*  
Extinction coefficient:  $0.025$  (4)

**Table 1**

Hydrogen-bond geometry (Å, °).

D—H...A	D—H	H...A	D...A	D—H...A
N10—H10A...O2 <sup>i</sup>	0.84 (2)	2.30 (2)	3.0871 (15)	156.1 (17)
N10—H10B...O5 <sup>ii</sup>	0.88 (2)	2.39 (2)	3.1743 (15)	149.8 (16)
O2—H2...O11 <sup>iii</sup>	0.84 (2)	2.06 (2)	2.8841 (13)	167 (2)
C2—H2A...O11 <sup>iv</sup>	1.00	2.55	3.4779 (15)	154
C1—H1A...O11 <sup>iii</sup>	1.00	2.38	2.9723 (14)	117
C7—H7A...O4 <sup>v</sup>	1.00	2.43	3.2000 (14)	133
C7—H7A...O5 <sup>vi</sup>	1.00	2.60	3.2862 (15)	126

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

All H atoms could be located in a difference Fourier map. However, the H atoms bound to carbon were subsequently placed in idealized positions and included as part of a riding model, with C—H = 1.00 Å and  $U_{\text{iso}}(\text{H}) = 1.2U_{\text{eq}}(\text{C})$ . Positional and  $U_{\text{iso}}$  parameters were refined for H atoms bound to nitrogen and oxygen.

Data collection: *SMART* (Bruker, 2001); cell refinement: *SAINT* (Bruker, 2000); data reduction: *SAINT* and *SHELXTL* (Bruker, 2001); program(s) used to solve structure: *SHELXS97* (Sheldrick, 1997); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *MERCURY* (Version 1.4.1; Macrae *et al.*, 2006); software used to prepare material for publication: *SHELXL97* and *PLATON* (Spek, 2003).

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