

9(*R*)-[6(*R*)-Hydroxymethyl-1-oxa-4-thiacyclohexan-2-yl]hypoxanthine-water (4/3), a nucleoside analogueG. Mazumder,<sup>a</sup> M. De,<sup>a\*</sup> S. K. Mazumder,<sup>a</sup>  
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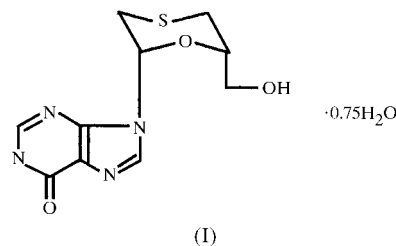
The title compound, 9(*R*)-[6(*R*)-hydroxymethyl-1-oxa-4-thiacyclohexan-2-yl]-1,9-dihydro-6*H*-purin-6-one-water (4/3), C<sub>10</sub>H<sub>12</sub>N<sub>4</sub>O<sub>3</sub>S·0.75H<sub>2</sub>O, crystallizes in the triclinic space group *P*1 with four molecules in the asymmetric unit and 0.75 waters of hydration per molecule. The structure was refined to an *R* value of 0.072 for 3382 observed reflections. The four crystallographically independent molecules are designated *A*, *B*, *C* and *D*. All four oxathiane rings adopt the chair conformation and the purine bases are in an *anti* orientation with respect to the sugar moieties. Molecules *A* and *D* and molecules *C* and *B* are base paired by a single hydrogen bond of the type N—H···N. These base pairs are again hydrogen bonded to their translated pairs in the direction of a cell diagonal.

## Comment

A number of sugar-modified nucleosides display antiviral activity because of their ability to interfere with virally encoded enzymes. The structure analysis of the title compound, (I), is a continuation of our earlier work involving systematic conformational studies on modified nucleosides with the aim of understanding structure–function relationships. The synthesis of (I) has been described (Van Aerscht *et al.*, 1990).

The crystal structure of (I) (Fig. 1) has been determined and the absolute configuration is indicated by a Flack parameter of 0.04 (9) (Flack, 1983). There are four crystallographically independent molecules in the crystal structure, designated *A*, *B*, *C* and *D*. All bond lengths and angles of the four hypoxanthine residues agree well with the values quoted by Taylor and others (Taylor & Kennard, 1982). The C6–O6 bond

lengths in the four molecules vary from 1.204 (6) to 1.242 (6) Å, with an average value of 1.217 (6) Å, which agrees well with the quoted value of 1.215 Å for C=O (Taylor & Kennard, 1982). The pyrimidine and imidazole rings in the four molecules are planar within experimental error. The dihedral angles between pyrimidine and imidazole rings are 0.7 (2), 2.1 (1), 1.3 (2) and 0.2 (2)° in molecules *A*, *B*, *C* and *D*, respectively. The bond lengths and angles of the sugar moieties of the four molecules agree well with each other within experimental error. The N-glycosidic bond lengths



N9–C2' are in the range 1.443 (6)–1.465 (6) Å, with an average value of 1.451 (6) Å, which agrees well with the normal value of 1.464 (6) Å. In all four molecules, the C2'–O1' bond lengths lie in the range 1.402 (5)–1.422 (5) Å, with an average value of 1.413 (5) Å. This is shorter than the adjacent bond lengths C6'–O1', which lie in the range 1.420 (5)–1.444 (5) Å, with an average value of 1.430 (6) Å. Similar shortening of bond lengths has been found in glucosides with an equatorial substituent at the anomeric C atom C1' (Berman *et al.*, 1967; Jeffrey *et al.*, 1978). This anomeric effect is commonly observed in other nucleosides (Birnbaum *et al.*, 1984; Thewalt *et al.*, 1970; Watson *et al.*, 1965). The orientation of O7' with respect to the sugar moiety described by the torsion angle  $\gamma$  (O7'–C7'–C6'–C5') is different for all four molecules. In molecules *A*, *B* and *D*, the  $\gamma$  values are –168.3 (5), 175.4 (5) and –179.3 (6)°, respectively, and they are in the *gauche*–*trans* (*ap*) orientation, whereas molecule *C* has  $\gamma = -70.2$  (6)°, which corresponds to a *trans*–*gauche* (*–sc*)

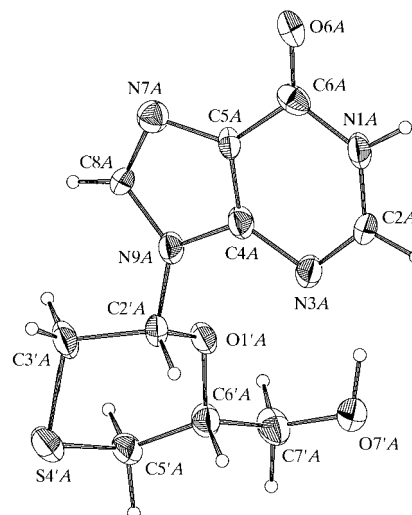


Figure 1

An ORTEP (Johnson, 1976) plot of one of the molecules shown with 30% probability ellipsoids.

orientation. The puckering parameters (Cremer & Pople, 1975) for the sequence  $C2'-C3'-S4'-C5'-C6'-O1'$  in the oxathiane ring are  $Q = 0.631$  (5) Å,  $\varphi_2 = -134$  (5)° and  $\theta_2 = 175.2$  (5)° for molecule *A*,  $Q = 0.629$  (5) Å,  $\varphi_2 = -71$  (4)° and  $\theta_2 = 172.9$  (4)° for molecule *B*,  $Q = 0.623$  (6) Å,  $\varphi_2 = -44$  (6)° and  $\theta_2 = 173.9$  (5)° for molecule *C*, and  $Q = 0.663$  (8) Å,  $\varphi_2 = -117$  (3)° and  $\theta_2 = 170.1$  (7)° for molecule *D*, giving an average value of  $Q = 0.639$  (6) Å for the total puckering amplitude; this value is close to that of 0.63 Å for an ideal cyclohexane ring (Cremer & Pople, 1975). Each molecule of the title compound has two H atoms capable of participating in hydrogen bonds and these are from N1 of the purine bases and the hydroxyl O7' atom of the sugar ring. There are hydrogen bonds between purine rings. The purine rings form *AD* and *BC* base pairs by a single hydrogen bond of the type N1—H···N7 and these base pairs are hydrogen bonded to their translated pairs in the direction of a cell diagonal. The bases in each pair are nearly parallel to each other, the dihedral angles between them being 170.9 (2)° for the *AD* and 171.1 (1)° for the *BC* base pairs.

## Experimental

The synthesis of the title compound has been described by Van Aerschot *et al.* (1990). Colorless prismatic crystals were grown by slow evaporation from methanol at room temperature (293 K).

### Crystal data

$C_{10}H_{12}N_4O_3S \cdot 0.75H_2O$   
 $M_r = 281.81$   
 Triclinic, *P*1  
 $a = 7.995$  (2) Å  
 $b = 9.261$  (2) Å  
 $c = 18.062$  (2) Å  
 $\alpha = 98.290$  (10)°  
 $\beta = 94.470$  (10)°  
 $\gamma = 101.210$  (10)°  
 $V = 1290.4$  (4) Å<sup>3</sup>

$Z = 4$   
 $D_x = 1.451$  Mg m<sup>-3</sup>  
 Mo *K*α radiation  
 Cell parameters from 25 reflections  
 $\theta = 9.6$ – $14.4$ °  
 $\mu = 0.265$  mm<sup>-1</sup>  
 $T = 293$  (2) K  
 Prism, colorless  
 $0.25 \times 0.21 \times 0.12$  mm

### Data collection

Enraf–Nonius CAD-4 diffractometer  
 $\omega$ – $2\theta$  scans  
 Absorption correction: empirical via  $\psi$  scan (North *et al.*, 1968)  
 $T_{\min} = 0.848$ ,  $T_{\max} = 0.973$   
 4559 measured reflections  
 4559 independent reflections

3382 reflections with  $I > 2\sigma(I)$   
 $\theta_{\max} = 25.05$ °  
 $h = -9 \rightarrow 9$   
 $k = -11 \rightarrow 10$   
 $l = 0 \rightarrow 21$   
 3 standard reflections every 100 reflections  
 intensity decay: negligible

### Refinement

Refinement on  $F^2$   
 $R[F^2 > 2\sigma(F^2)] = 0.072$   
 $wR(F^2) = 0.155$   
 $S = 0.958$   
 4559 reflections  
 673 parameters  
 H atoms treated by a mixture of independent and constrained refinement

$w = 1/[\sigma^2(F_o^2) + (0.1004P)^2]$   
 where  $P = (F_o^2 + 2F_c^2)/3$   
 $(\Delta/\sigma)_{\max} = -0.007$   
 $\Delta\rho_{\max} = 0.42$  e Å<sup>-3</sup>  
 $\Delta\rho_{\min} = -0.53$  e Å<sup>-3</sup>  
 Absolute structure: Flack (1983)  
 Flack parameter = 0.04 (9)

**Table 1**

Hydrogen-bonding 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>
O1W—H1W1···O2W	0.83	2.07	2.804 (7)	148
O1W—H2W1···N3B	0.84	2.06	2.901 (6)	174
N1A—H1A···N7D <sup>i</sup>	0.86 (6)	1.96 (6)	2.816 (7)	176 (4)
O7'A—H7'A···O1W <sup>ii</sup>	0.99	1.78	2.734 (7)	163
O7'C—H7'C···O7'A <sup>iii</sup>	0.83	2.20	2.769 (8)	126
N1B—H1B···N7C <sup>iv</sup>	0.86 (5)	2.00 (6)	2.858 (6)	172 (4)
O2W—H2W2···O6C <sup>v</sup>	1.05	1.95	2.753 (7)	130
O7'B—H7'B···O6D <sup>vi</sup>	0.84	1.92	2.728 (6)	162
N1C—H1C···N7B <sup>vii</sup>	0.86 (6)	2.02 (6)	2.882 (6)	178 (4)
N1D—H1D···N7A <sup>viii</sup>	0.86 (6)	1.97 (6)	2.829 (7)	174 (5)
O7'D—H7'D···O6B <sup>ix</sup>	0.83	2.14	2.802 (8)	137
O2W—H1W2···O7B <sup>ix</sup>	0.82	2.20	2.938 (8)	150
O3W—H1W3···O6A <sup>x</sup>	0.85	2.00	2.833 (7)	167
O3W—H2W3···O7D <sup>xi</sup>	0.91	1.89	2.793 (9)	167

Symmetry codes: (i)  $x-1, y-1, z-1$ ; (ii)  $x-1, y, z$ ; (iii)  $1+x, 1+y, z$ ; (iv)  $x, y-1, z-1$ ; (v)  $x, y, z$ ; (vi)  $x, y, z-1$ ; (vii)  $x-1, y, 1+z$ ; (viii)  $x, y, 1+z$ ; (ix)  $x, y-1, z$ ; (x)  $x, 1+y, 1+z$ ; (xi)  $x-1, 1+y, z$ .

H atoms of hydroxyl groups and water molecules were located from a difference map and not refined. Other H atoms were obtained from stereochemical considerations and were refined with fixed isotropic displacement parameters ( $C-H = 0.93$ – $0.98$  Å).

Data collection: *CAD-4 Software* (Enraf–Nonius, 1989); cell refinement: *CAD-4 Software*; data reduction: *CAD-4 Software*; program(s) used to solve structure: *SHELXS86* (Sheldrick, 1990); program(s) used to refine structure: *SHELXL93* (Sheldrick, 1993); molecular graphics: *ORTEPII* (Johnson, 1976); software used to prepare material for publication: *SHELXL93*.

Supplementary data for this paper are available from the IUCr electronic archives (Reference: DE1134). Services for accessing these data are described at the back of the journal.

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