

(average 4.7 and 5.5 Å²) than for the (C)–H atoms (average 0.8 and 1.5 Å²). No such trend was found in the neutron diffraction analysis of ascorbic acid.

Residual electron density

During the refinements of this structure no attempt was made to pick out one particular oxygen atom as carrier of the negative charge of the anion. The form factor was always the one given in *International Tables for X-ray Crystallography* (1962) for the free oxygen atom.

One extra electron is thus present in the anion in addition to those included in the calculations, and to conclude the analysis, a difference Fourier synthesis was evaluated. After omission of the uncertain 400 and 004 reflexions, the residual electron density in the region of the ascorbate anion is shown in Fig. 4. These maxima are clearly the largest in the unit cell, and some of them fall in the space between the carbon and oxygen atoms. This result is quite similar to that for ascorbic acid, but whether the peaks adjacent to the O(2), O(3) and O(4) atoms outside the bond area have relevance to the extra electron is questionable because of the low significance of such peaks in the present case.

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The Crystal Structure of Ribitol

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The crystal structure of ribitol, C₅H₁₂O₅, has been determined by means of a sign correlation procedure. The space group is *P*2₁/*c* with four molecules in a unit cell with *a* = 8.990, *b* = 4.946, *c* = 15.730 Å, β = 97.07°. The crystal is a racemate mixture of left and right-handed conformers, with non-planar carbon chains. These conformers appear to be favored over that with mirror symmetry because of the non-bonding interactions between the hydroxyl groups attached to alternate carbon atoms along the chain.

Introduction

Ribitol, C₅H₁₂O₅, is one of the four stereoisomeric pentitols. Like xylitol, it is a *meso* form; the other two pentitols are D- and L-arabinitol. Ribitol occurs in riboflavin (vitamin B₂) where it is combined with an isoalloxazine residue, and in certain plants. The structure of the ribitol residue has been studied in two crystal structure determinations; that of the *p*-bromophenylhydrazone of ribose by Bjåmer, Furberg & Petersen (1964), and of riboflavin hydrobromide monohydrate by Tanaka, Ashida, Sasada & Kakudo (1967). In both these structures the conformation of the polyol residue was that with a non-planar zigzag carbon chain, although the planar conformation has been found consistently in the other polyol crystal structures which have been

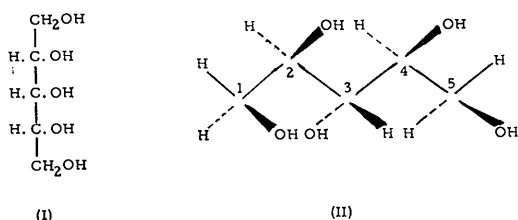
studied, *i.e.* *meso*-erythritol (Shimada, 1958; Bekoe & Powell, 1959), galactitol (Berman & Rosenstein, 1968), three forms of D-mannitol (Berman, Jeffrey & Rosenstein, 1968; Kim, Jeffrey & Rosenstein, 1968) and DL-arabinitol (Hunter & Rosenstein, 1968). Galactitol is also a *meso* form, in which the potential symmetry of the molecule is not used in the crystal symmetry. In that structure the observed conformation is very close to that of the symmetrical molecule, with small distortions which could be caused by the intermolecular forces characteristic of the crystal lattice.

The primary interest in this investigation was, therefore, to determine whether the non-planar carbon chain conformation found in the isoalloxazine and *p*-bromophenylhydrazone derivatives persisted in the structure of the uncombined ribitol, and could be a structural

property associated with the configuration of this particular carbohydrate molecule.

Molecular and crystal data

The Fischer projection of ribitol is shown in (I). The symmetrical conformation, shown in (II), has a mirror plane of symmetry, which includes the C(3).HOH atoms, normal to the plane of the zigzag carbon chain. In this conformation ribitol is optically inactive by intramolecular compensation. The conformation observed in the crystal structure is shown in Fig.1. It differs from (II) by a rotation of 120° about C(3)–C(4), which brings C(5) into the position of the OH on C(4). The crystals are optically inactive by reason of being a mixture of diastereoisomers.



Ribitol, $C_5H_{12}O_5$, M.W.152.15, m.p. $101^\circ C$.

Monoclinic.

Space group $P2_1/c$, from systematic absences $(0k0)$ absent k odd, $(h0l)$ absent l odd.

$a = 8.990(1) \text{ \AA}$

$b = 4.946(2)$

$c = 15.730(5)$

$\beta = 97.07(2)^\circ$

$V = 694.1(7)$.

$Z = 4$.

$D_m = 1.454 \text{ g.cm}^{-3}$

$D_x = 1.456 \text{ g.cm}^{-3}$.

$\mu_{Cu K\alpha} = 11.48 \text{ cm}^{-1}$.

(The standard deviations given in parentheses refer to the last figure)

Experimental

Large transparent tabular crystals with well-developed $\{100\}$ and $\{001\}$ faces were obtained by slow evaporation from solution in ethanol. The crystal density was measured at $23^\circ C$ by flotation in a benzene and carbon tetrachloride mixture. The cell parameters were measured on a Picker 4-circle diffractometer from the principal zone reflections and refined by least-squares by means of an IBM 1130 program (Shiono, 1968).

The intensities were obtained from a prism of dimensions $0.14 \times 0.25 \times 0.50 \text{ mm}$ with $Cu K\alpha$ radiation by a Picker diffractometer in the $\theta/2\theta$ scanning mode with the scan varying between 2° and 4° in low and high values of 2θ . Of the 1590 independent reflections within the $Cu K\alpha$ sphere, 1153 were recorded, of which 73 with intensities less than two standard deviations were given values of zero. No absorption corrections were applied. The intensities were reduced to structure amplitudes by the use of an IBM 1130 diffractometer data processing program (McGandy, 1968).

Determination and refinement of the structure

The structure was solved in three dimensions by a sign correlation procedure with the IBM 1620 program of Beurskens (1963). An interpretation of the first E map

Table 1. Fractional atomic coordinates and anisotropic thermal parameters in ribitol

Key to atomic numbering is given in Fig. 1. The estimated standard deviations in parentheses refer to the last decimal positions. The temperature expression used was

$$\exp [-(\beta_{11}h^2 + \beta_{22}k^2 + \beta_{33}l^2 + 2\beta_{12}hk + 2\beta_{13}hl + 2\beta_{23}kl)]$$

	x	y	z	β_{11}	β_{22}	β_{33}	β_{12}	β_{13}	β_{23}
C(1)	0.2613 (3)	0.5601 (6)	0.4722 (2)	0.0119 (4)	0.0422 (12)	0.0034 (1)	0.0005 (5)	0.0012 (1)	-0.0005 (3)
C(2)	0.3020 (2)	0.5814 (5)	0.5681 (1)	0.0072 (3)	0.0283 (10)	0.0036 (1)	-0.0003 (4)	0.0008 (1)	0.0009 (2)
C(3)	0.1708 (2)	0.5092 (4)	0.6176 (2)	0.0074 (3)	0.0202 (10)	0.0033 (1)	-0.0006 (3)	0.0002 (1)	-0.0008 (2)
C(4)	0.2008 (2)	0.5669 (4)	0.7135 (1)	0.0063 (3)	0.0250 (9)	0.0033 (1)	-0.0012 (4)	0.0005 (1)	-0.0005 (2)
C(5)	0.3302 (2)	0.4045 (5)	0.7589 (1)	0.0080 (3)	0.0368 (11)	0.0031 (1)	0.0021 (5)	-0.0003 (1)	-0.0012 (3)
O(1)	0.1625 (2)	0.7742 (4)	0.4415 (1)	0.0090 (2)	0.0496 (10)	0.0033 (1)	-0.0015 (3)	0.0002 (1)	0.0027 (2)
O(2)	0.3601 (2)	0.8426 (4)	0.5906 (1)	0.0072 (2)	0.0345 (9)	0.0042 (1)	-0.0039 (3)	-0.0005 (1)	0.0017 (2)
O(3)	0.1380 (2)	0.2311 (3)	0.6028 (1)	0.0085 (2)	0.0271 (9)	0.0039 (1)	-0.0021 (3)	0.0003 (1)	-0.0019 (2)
O(4)	0.0704 (2)	0.5044 (3)	0.7534 (1)	0.0084 (2)	0.0295 (9)	0.0039 (1)	0.0001 (3)	0.0019 (1)	-0.0001 (2)
O(5)	0.3621 (2)	0.5029 (4)	0.8440 (1)	0.0096 (3)	0.0603 (12)	0.0031 (1)	0.0074 (4)	-0.0005 (1)	-0.0023 (2)
H(C1)	0.348	0.570	0.437						
H'(C1)	0.210	0.400	0.455						
H(C2)	0.386	0.430	0.580						
H(C3)	0.070	0.610	0.590						
H(C4)	0.230	0.740	0.725						
H(C5)	0.306	0.190	0.748						
H'(C5)	0.420	0.420	0.733						
H(O1)	0.211	0.872	0.399						
H(O2)	0.279	0.956	0.588						
H(O3)	0.031	0.210	0.591						
H(O4)	-0.009	0.660	0.751						
H(O5)	0.461	0.411	0.869						

3. The C(4)–H(4) bond is then parallel to C(2)–O(2) and C(4)–O(4) is on the other side of the molecule. The other alternative (*Psc*) would bring C(5) into the position occupied by O(4) with parallel C(2)–O(2) and C(4)–C(5) bonds and an equally unfavorable O(2)...

C(5) approach. The observed ribitol conformation is, therefore, fully consistent with a model based on minimizing these third and fourth neighbour repulsive interactions, with the latter taking precedence over the former, because the non-bonding distance is shorter.

Table 3. Intramolecular distances and angles in ribitol.

The estimated standard deviations given in parentheses refer to the last decimal positions of respective values. The mean values are calculated from

$$l = \frac{\sum_i l_i}{\sum_i (\sigma_i^2)} \bigg/ \frac{1}{\sum_i (\sigma_i^2)}, \quad \sigma_{\text{mean}} = \left(\frac{\sum_i (l_i - l)^2}{N-1} \right)^{1/2}$$

<i>i</i>	<i>j</i>	<i>D</i> _{<i>ij</i>}	<i>D</i> _{<i>ij</i>} *	<i>i</i>	<i>j</i>	<i>k</i>	<(<i>ijk</i>)
C(1)	C(2)	1.510 (4) Å	[1.515] Å	C(1)	C(2)	C(3)	112.5 (2)°
C(2)	C(3)	1.534 (3)	[1.537]	C(2)	C(3)	C(4)	113.9 (2)
C(3)	C(4)	1.525 (3)	[1.530]	C(3)	C(4)	C(5)	113.5 (2)
C(4)	C(5)	1.518 (3)	[1.521]	O(1)	C(1)	C(2)	110.5 (2)
C(1)	O(1)	1.427 (3)	[1.430]	C(1)	C(2)	O(2)	110.4 (2)
C(2)	O(2)	1.421 (3)	[1.426]	O(2)	C(2)	C(3)	111.5 (2)
C(3)	O(3)	1.420 (3)	[1.424]	C(2)	C(3)	O(3)	107.4 (2)
C(4)	O(4)	1.429 (3)	[1.433]	O(3)	C(3)	C(4)	110.6 (2)
C(5)	O(5)	1.419 (3)	[1.424]	C(3)	C(4)	O(4)	109.8 (2)
C(1)	H(C1)	1.012		O(4)	C(4)	C(5)	107.5 (2)
C(1)	H'(C1)	0.939		C(4)	C(5)	O(5)	108.5 (2)
C(2)	H(C2)	1.063					
C(3)	H(C3)	1.078		Mean C–C			1.524 (10) Å
C(4)	H(C4)	0.907		Mean C–O			1.423 (5)
C(5)	H(C5)	1.092					
C(5)	H'(C5)	0.952		Mean C–C–C			113.3 (7)°
O(1)	H(O1)	0.969		Mean C–C–O			109.5 (15)
O(2)	H(O2)	0.917					
O(3)	H(O3)	0.962					
O(4)	H(O4)	1.045					
O(5)	H(O5)	1.032					
Non-bonded O...O distances							
O(1)	O(2)	2.782					
O(1)	O(3)	3.720					
O(2)	O(3)	3.642					
O(3)	O(4)	2.856					
O(4)	O(5)	2.826					

* Bond lengths corrected for libration.

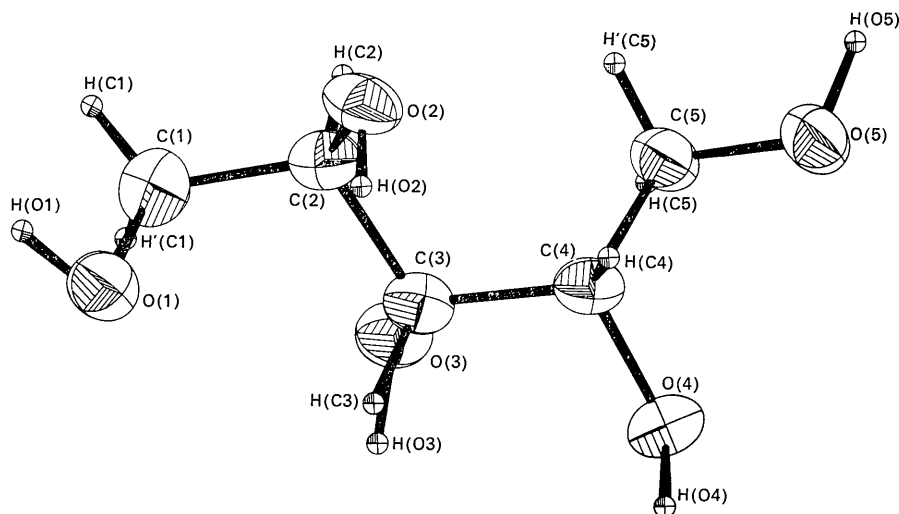


Fig. 1. Molecular conformation observed in the crystal structure of ribitol, showing atomic numbering used and the anisotropic thermal ellipsoids.

The same configuration is observed in the ribitol residue of the riboflavin monohydrate. In the ribose-*p*-bromophenylhydrazone, however, the conformation about C(3)–C(4) is (*Psc*), but this conformer is stabilized by the formation of an intramolecular hydrogen bond between O(2) and O(5).

Xylitol has parallel C(2) . . . O(2), C(4) . . . O(4) bonds in the planar carbon chain conformation in which the molecule is mirror-symmetrical. It is expected to have a non-planar carbon chain about C(3)–C(4) also, but in this case, the diastereoisomeric rotomers must be resolved on crystallization, since the crystal structure has symmetry $P2_12_12_1$. Of the ten hexitols, similar eclipsed C–O bonds on alternate carbon atoms occur in seven of the stereoisomers in the planar-chain conformation. These are D- and L-glucitol (sorbitol), D- and L-iditol, D- and L-talitol (altritol) and *meso*-allitol, none of which have yet been studied by crystal structure determination. In DL-arabinitol, galactitol and D-mannitol, which have been studied, the configurations are all such that the observed planar carbon chain conformation gives rise to no short interactions of the type O(*n*–1) . . . O(*n*+1) or C(*n*+2).

The extent to which the unsymmetrical rotomers of ribitol persist in solution depends upon the potential energy functions for rotation about the C–C bonds. In view of the arguments above, it seems likely that the symmetrical rotomer is a high energy form and that the unsymmetrical rotomers will predominate. As with the *meso*-tartrates (Kroon, Peerdeman & Bijvoet, 1965) and *meso*-tartaric acid (Bootsma & Schoone, 1967), lack of optical activity in solution, as well as in the solid, probably results more from compensation by conformational antipodes than from the mirror or centric symmetry in the molecules. This is in contrast to the crystal structures of the various forms of D-mannitol and of galactitol, where the conformation in the solid is very close to the symmetrical average of those of the

rotomers expected to occur in solution. Some recent nuclear magnetic resonance spectroscopic data also support the view that in solution the planar carbon chain conformation is favored, except for those roto-

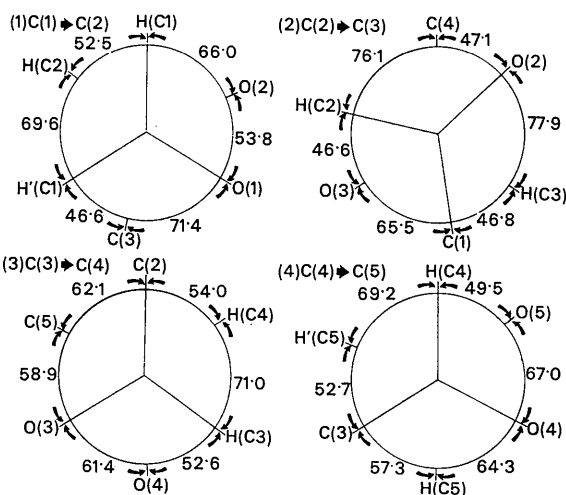


Fig. 2. Newman projections down the C–C bonds in ribitol, showing the conformation angles in degrees.

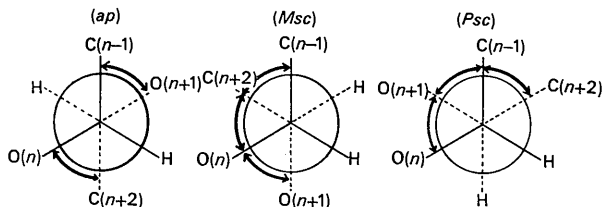


Fig. 3. Newman projections for the three preferred conformations down a C(*n*)–C(*n*+1) bond in a polyol. The (*ap*) conformers have the linear carbon chain.

Table 4. *Least-squares planes in ribitol*

Equation for plane: $Ax + By + Cz = D$, where x, y, z are in Å.

Atoms in plane		Distance from best plane		Given constant
A	C(1)	C(1)	+0.050 Å	$A = -0.319$ $B = 0.943$ $C = -0.054$ $D = 1.412$
	C(2)	C(2)	-0.049	
	C(3)	C(3)	-0.051	
	C(4)	C(4)	+0.050	
	O(4)	O(4)	+0.098	
B	C(1)	C(1)	+0.055	$A = -0.278$ $B = 0.957$ $C = -0.055$ $D = 1.537$
	C(2)	C(2)	-0.028	
	C(3)	C(3)	-0.084	
	C(4)	C(4)	+0.031	
	O(4)	O(4)	+0.026	
C	C(3)	C(3)	+0.050	$A = 0.682$ $B = 0.691$ $C = -0.323$ $D = -0.398$
	C(4)	C(4)	-0.055	
	C(5)	C(5)	-0.048	
	O(5)	O(5)	+0.052	
	O(4)	O(4)	-1.099	

mers where it gives rise to eclipsed oxygen atoms on alternate carbon atoms (El Khadem, Horton & Page, 1968). This non-bonding interaction is usually referred to as a 1-3 interaction by the organic chemists.

The hydrogen bonding

The hydrogen bonding is all intermolecular and is illustrated in Fig.4. Each hydroxyl group forms

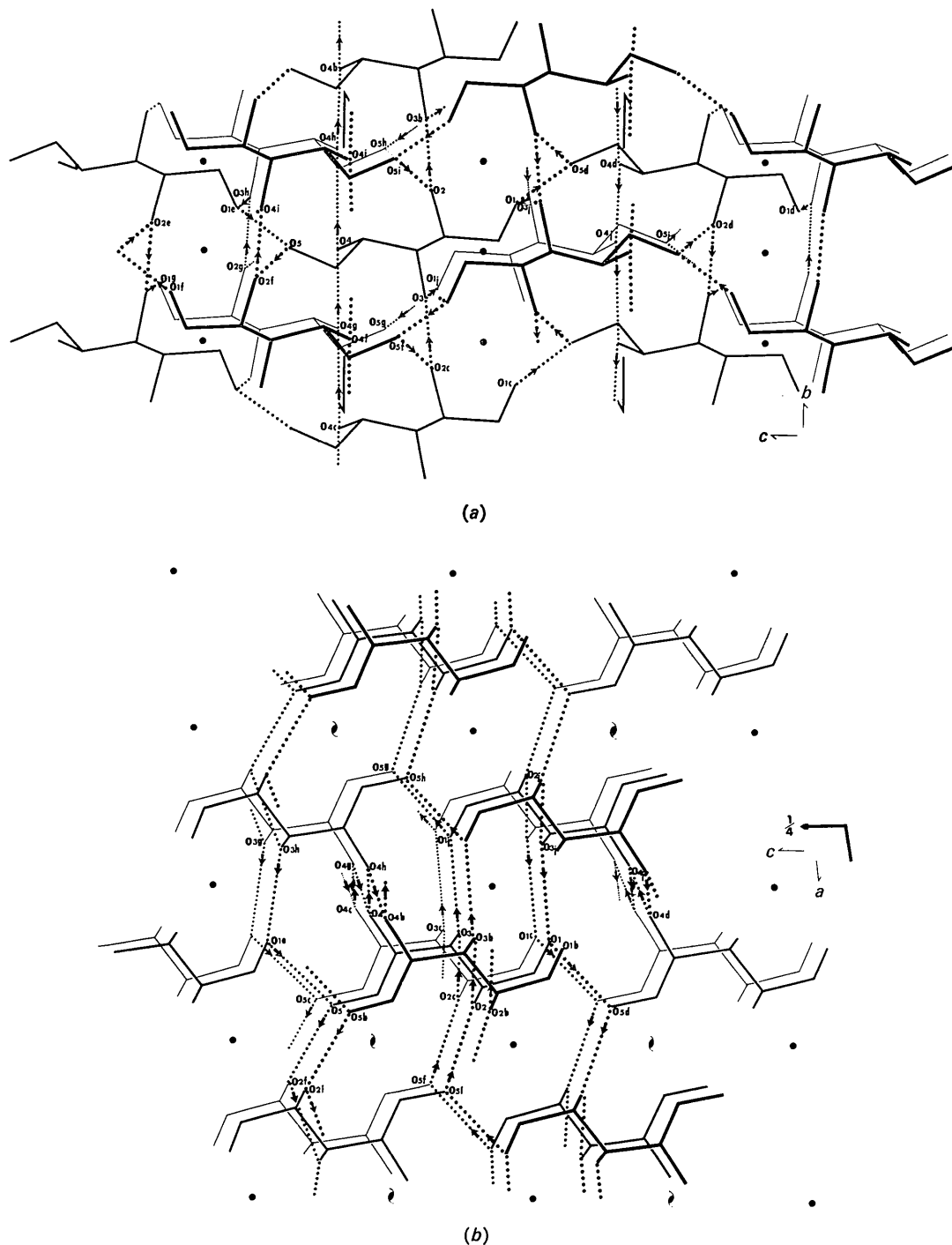


Fig.4. The crystal structure of ribitol. Solid lines indicate primary C-C and C-O bonds. Dotted lines indicate hydrogen bonds with arrows pointing in the donor direction. (a) view down the *a* axis; (b) view down the *b* axis.

Table 5. Intermolecular hydrogen-bond distances and angles in ribitol

<i>i</i>	<i>j</i>	<i>k</i>	<i>l</i>	<i>D_{jk}</i>	\angle_{ijk}	\angle_{jkl}
C(1)	O(1) →	O(5 <i>d</i>)	C(5 <i>d</i>)	2.732 Å	93.7°	126.7°
C(2)	O(2) →	O(3 <i>b</i>)	C(3 <i>b</i>)	2.794	113.5	122.8
C(3)	O(3) →	O(1 <i>j</i>)	C(1 <i>j</i>)	2.705	103.4	129.8
C(4)	O(4) →	O(4 <i>h</i>)	C(4 <i>h</i>)	2.773	100.7	124.8
C(5)	O(5) →	O(2 <i>f</i>)	C(2 <i>f</i>)	2.700	109.2	130.9

Symmetry code:

<i>a</i>	<i>x</i>	<i>y</i>	<i>z</i>
<i>b</i>	<i>x</i>	1 + <i>y</i>	<i>z</i>
<i>c</i>	<i>x</i>	-1 + <i>y</i>	<i>z</i>
<i>d</i>	<i>x</i>	1½ - <i>y</i>	-½ + <i>z</i>
<i>e</i>	<i>x</i>	1½ - <i>y</i>	½ + <i>z</i>
<i>f</i>	1 - <i>x</i>	-½ + <i>y</i>	1½ - <i>z</i>
<i>g</i>	- <i>x</i>	-½ + <i>y</i>	1½ - <i>z</i>
<i>h</i>	- <i>x</i>	½ + <i>y</i>	1½ - <i>z</i>
<i>i</i>	1 - <i>x</i>	½ + <i>y</i>	1½ - <i>z</i>
<i>j</i>	- <i>x</i>	1 - <i>y</i>	1 - <i>z</i>

→: direction of O-H...O bond.

two hydrogen bonds, one as donor and one as acceptor. As is commonly observed, the spread of C-O-H angles at the donor oxygen atom of the hydrogen bond is less than those of H...O-C at the acceptor oxygen, being 100.7 to 129.8° versus 93.7 to 130.9° respectively. The O...O distances are given in Table 5. They vary over the range 2.701 to 2.795 Å which is narrower than usually found in carbohydrates. The hydrogen atoms deviate from the line of O...O centers by less than 0.28 Å, which is consistent with the small variation in hydrogen-bond distances.

The hydrogen bonds form infinite spirals and zigzag chains parallel to the *a* and *b* axes respectively, as shown in Fig. 4. The sequences are O(5*f*)→O(2*c*)→O(3)→O(1*j*)→O(5*g*)→*etc.* parallel to the *a* axis and O(4*c*)→O(4*g*)→O(4)→O(4*h*)→O(4*b*)→*etc.* parallel to the *b* axis. In common with the other polyol structures which have been studied, the molecules are arranged in a very regular and elegant pattern which utilizes their full potential for hydrogen-bond formation.

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