Temperature parameters are given in Table 4. Calculations of the thermal ellipsoids yielded very little of value. No clear evidence was to be seen of any rigidbody motions, and the only general feature of note was the larger amplitudes of vibration of the hydroxyl and nitro groups.

The observed and calculated structure amplitudes. the calculated phase angles and the e.s.d's of the observed amplitudes are listed in Table 5.

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 - The 5-Hydroxyl Configuration in Dialuric Acid Monohydrate by Neutron Crystal Structure Determination

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The crystal structure of dialuric acid monohydrate (5,6-dihydroxyuracil) has been reinvestigated with three-dimensional neutron diffraction data, in order to obtain more accurate hydrogen atom positions than in Bolton's X-ray determination. The crystal data of Bolton (Acta Cryst. (1965) 19, 1051) were assumed, i.e. a = 12.714, b = 3.676, c = 12.949 Å, $\beta = 94^{\circ}24'$, space group $P_{2_1/n}$, with four formula units, C4H4O4N2.H2O, in the unit cell. With 871 neutron data above background, least-squares refinement of positional and anisotropic thermal parameters for all atoms gave a final R index of 0.05. Molecular association in this crystal structure is dominated by conventional hydrogen bonds (two NH---OC bonds and three hydrogen bonds involving the water molecule) and van der Waals interactions within stacks of parallel, almost flat, dialuric acid molecules. Averaged over time, the O-H bond of the 5-hydroxyl group is found to be restricted to a range of about 50° of the full rotation about the C–O bond. In its mean position, this bond is twisted 67° from the configuration of molecular coplanarity in which the hydrogen atom is nearest the 4-position of the pyrimidine ring. There are weak hydrogen bonding interactions of the 5-hydroxyl group throughout the observed range of O-H twist, with no position seeming to be particularly favourable. For the non-hydrogen atoms, the greatest discrepancy between X-ray and neutron bond lengths is 0.014 Å for N(1)–C(6) for which the estimated standard deviation is 0.005 Å.

Introduction

An X-ray crystal structure determination of dialuric acid monohydrate (5,6-dihydroxyuracil, I) was first reported by Alexander & Pitman (1956) for the structure in projection. Bolton (1965), using three-dimensional X-ray intensity data, confirmed the earlier work and reported the location of the imine hydrogen atoms.

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The remaining hydrogen atoms were not precisely determined. For atoms H(5) and H(2, W),* only tenta-



tive positions were assigned on the basis of difference

Fig. 1. Fourier synthesis projection of neutron scattering den-sity, down b. Contours are on an arbitrary scale with negative contours dotted.

* The atom labelling in this paper is the same as that of Bolton (1965), except for the water molecule atoms O(W), H(1, W), H(2, W), which Bolton labelled O(7), H(7), H(8), respectively.

Table 1. Atomic parameters with their e.s.d.'s

The positional parameters x, $\sigma(x)$ etc. are expressed as fractions of the lattice translations. The thermal parameters are defined by the expression $2kkR_{12} \pm 2klB_{12} + 2klB_{23}$ -.....

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

The atoms listed here correspond to those in Table 1 of Bolton (1965).

	x	у	Z	β_{11}	β_{22}	β_{33}	β_{12}	β_{13}	β_{23}
	$\sigma(x)$	$\sigma(y)$	$\sigma(z)$	$\sigma(\beta_{11})$	$\sigma(\beta_{22})$	$\sigma(\beta_{33})$	$\sigma(\beta_{12})$	$\sigma(\beta_{13})$	$\sigma(\beta_{23})$
N(1)	0.10945	0.4548	0.24209	0.00228	0.0211	0.00225	-0.0008	0.00052	0.0008
.,	0.00015	0.0005	0.00016	0.00013	0.0013	0.00010	0.0003	0.00009	0.0003
H(1)	0.16791	0.5424	0.19942	0.00366	0.0801	0.00399	0.0012	0.00134	0.0034
	0.00049	0.0017	0.00049	0.00038	0.0047	0.00036	0.0010	0.00030	0.0009
C(2)	0.13869	0.2968	0.33435	0.00174	0.0424	0.00215	0.0006	0.00032	-0.0006
- ()	0.00020	0.0006	0.00019	0.00014	0.0016	0.00014	0.0004	0.00011	0.0003
O(2)	0.23098	0.2394	0.36440	0.00189	0.0690	0.00275	0.0025	0.00025	-0.0013
- ()	0.00026	0.0009	0.00026	0.00019	0.0025	0.00018	0.0002	0.00014	0.0005
N(3)	0.05925	0.2030	0.39117	0.00198	0.0469	0.00195	0.0006	0.00036	0.0011
- (-)	0.00014	0.0005	0.00014	0.00011	0.0015	0.00012	0.0003	0.00008	0.0003
H(3)	0.07997	0.0744	0.46125	0.00322	0.0694	0.00325	0.0013	0.00039	0.0044
	0.00043	0.0012	0.00043	0.00033	0.0039	0.00033	0.0008	0.00026	0.0009
C(4)	-0.04612	0.2625	0.36335	0.00196	0.0358	0.00182	0.0009	0.00039	0.0009
- ()	0.00019	0.0006	0.00019	0.00016	0.0016	0.00014	0.0003	0.00011	0.0003
O(4)	-0.11178	0.1665	0.42273	0.00236	0.0612	0.00289	0.0009	0.00100	0.0020
- (-)	0.00026	0.0009	0.00026	0.00019	0.0024	0.00018	0.0005	0.00014	0.0005
C(5)	-0.07194	0.4287	0.26560	0.00197	0.0363	0.00214	-0.0004	0.00011	0.0014
- (-)	0.00020	0.0006	0.00019	0.00012	0.0012	0.00014	0.0003	0.00011	0.0003
O(5)	-0.17328	0.2081	0.23329	0.00291	0.0285	0.00358	0.0021	-0.00029	0.0031
~ /	0.00030	0.0009	0.00029	0.00021	0.0024	0.00020	0.0006	0.00016	0.0005
H(5)	-0.21470	0.3053	0.21840	0.00731	0.0820	0.02115	0.0011	-0.00800	-0.0058
	0.00089	0.0026	0.00124	0.00074	0.0069	0.00159	0.0017	0.00093	0.0025
C(6)	0.00672	0.5235	0.20694	0.00269	0.0361	0.00162	-0.0007	0.00037	0.0009
- (-)	0.00021	0.0006	0.00018	0.00016	0.0012	0.00014	0.0004	0.00011	0.0003
O(6)	-0.00345	0.6841	0.11734	0.00394	0.0662	0.00253	-0.0011	0.00042	0.0028
- (-)	0.00031	0.0010	0.00027	0.00026	0.0025	0.00020	0.0006	0.00017	0.0005
H(6)	-0.07781	0.7632	0.09436	0.002	0.0791	0.00372	0.0006	-0.00071	0.0024
	0.00054	0.0017	0.00048	0.00048	0.0048	0.00037	0.0011	0.00033	0.0009
O(W)	-0.31514	0.4551	0.44486	0.00573	0.1337	0.00571	0.0072	-0.00280	-0.0186
- (')	0.00046	0.0016	0.00045	0.00040	0.0020	0.00036	0.0011	0.00028	0.0011
H(1, W)	-0.25194	0.3492	0.42966	0.00644	0.1070	0.00612	0.0028	-0.00111	-0.0051
	0.00075	0.0023	0.00065	0.00065	0.0071	0.00051	0.0016	0.00047	0.0014
H(2, W)	-0.30120	0.5751	0.50940	0.00896	0.1264	0.00488	0.0023	-0.00119	-0.0122
	0.00078	0.0025	0.00071	0.00074	0.0076	0.00051	0.0017	0.00048	0.0016

Table 2. Observed and calculated structure factors for dialuric acid monohydrateColumns are: l index, 100|Fobs|, 100Fcalc.

* Indicates an unobserved reflexion.

Fourier peaks which were not greatly different from the highest background noise peaks.

The X-ray studies showed that at distances less than 2.84 Å from the hydroxyl oxygen atom O(5), there are four oxygen atoms which might participate in hydrogen bonding through the hydrogen atom H(5). These distances are to two atoms O(5) in neighbouring molecules (2.73 Å), to a water oxygen atom (2.84 Å) and to the oxygen atom O(4) of the same molecule. It is difficult to reach reliable conclusions from the wellestablished heavier atom geometry concerning the orientation of the 5-hydroxyl group in the crystal, since no postulated H(5) position gives a collinear hydrogen bonding arrangement O(5)-H(5)---O'.

The present three-dimensional neutron diffraction study was undertaken primarily in order to provide experimental evidence for the averaged position of the H(5) proton at room temperature.

Experimental

The crystal data were assumed to be those reported by Bolton (1965), *i.e.*

$a = 12.714 \pm 0.003 \text{ Å}$,	$\beta = 94^{\circ}24 \pm 5'.$
$b = 3.676 \pm 0.003$,	Z=4 formula units/cell.
$c = 12.949 \pm 0.004$;	Space group: $P2_1/n$.

The crystal used for neutron data collection measured 3.6 mm along **b**, with a somewhat irregular cross section of average area 0.6 mm^2 . This crystal, supplied by



Fig.2. The three-dimensional Fourier synthesis of the neutron scattering density showing the environment of atom H(5). The positive direction of x is toward the viewer, normal to the page. Water molecule peaks are shown shaded. Only the ring atoms C(4), C(5), C(6) and their substituent carbonyl or hydroxyl group atoms are shown for each molecule. The atoms heavily contoured correspond to the shaded molecule in the centre of Fig.5. The screw axis along y which runs through the centre of the Figure is at $x = -\frac{1}{4}$.

Dr Bolton, was the largest in the same batch from which the crystal used for his X-ray data collection was selected.

The diffracted intensity data were obtained using a monochromatic neutron beam $(\lambda = 1.09 \text{ Å})$ from the HIFAR reactor, of flux 6×10^6 n.cm⁻²sec⁻¹ at the specimen. The diffractometer was operated in the $\theta:2\theta$ step-scanning mode, the crystal being mounted with **b** along the φ axis. The intensities were measured for 1174 non-symmetry related reflexions with $\sin \theta/\lambda < 0.6$, of which 303 reflexions were unobservably weak. The latter were assigned intensities one half the minimum observable value. The data were not corrected for the neutron absorption effect arising from the incoherent scattering by the hydrogen atoms.

The refinement of the structure parameters

Initially, the Fourier synthesis of nuclear scattering density (Fig. 1) was calculated with phases for the observed *h0l* neutron structure amplitudes based on the X-ray results. Coherent neutron scattering lengths were assumed to be H, -0.378; C, 0.661; N, 0.940; O, 0.577×10^{-12} cm (*International Tables for X-ray Crystallography*, 1962). The crescent of negative scattering density surrounding the atom O(5) in this projection may be attributed in part to diffraction ripple, but there is also a strong indication that H(5) is not in a well-localized position. A three-dimensional structure determination was then undertaken.

A cycle of full-matrix least-squares, in which the atomic positional and thermal parameters reported by Bolton (1965) were varied, was calculated with threedimensional data. In addition, anisotropic thermal parameters were varied for the hydrogen atoms, with initial values assumed to be the same as those of the heavier atoms to which they are covalently bonded. From the large increase in thermal parameters for atom H(5), it was suspected that this atom might not be in the position suggested by Bolton. Also, a shift of 0.28 Å in the position of the water oxygen nucleus revealed an error in the listing of Bolton's positional parameters for this atom.* A three-dimensional Fourier synthesis of neutron scattering density was calculated, using calculated structure factor phases based on the revised atomic parameters, but with atom H(5) omitted. In this map (Fig.2), atom H(5) corresponded to the elongated trough of negative neutron scattering density with a centre corresponding to a dihedral angle of about 70° between the planes of the pyrimidine ring and the hydroxyl group C(5)-O(5)-H(5). This represents a twist of about 80° from the orientation suggested by Bolton.

Full-matrix least-squares refinement was then carried out with standard deviations in observed structure

^{*} Bolton (1965) gives the y coordinate for atom O(7) (H_2O) incorrectly in Table 1 as 0.5407 instead of 0.4593. The reported interatomic distances involving this atom are correct.

amplitudes given by

$$\sigma(F) = \sigma_c + 0.05F,$$

where σ_c = estimated standard deviation derived from experimental counting statistics. Atomic positional and anisotropic thermal parameters were varied for all atoms, including H(5). After four cycles of least squares, convergence was obtained with an *R* index of 0.092 including all reflexions, or 0.067 excluding the unobserved reflexions. With the unobserved reflexions given zero weight in the least-squares calculations, two cycles of least-squares refinement again gave convergence with an *R* index of 0.05. The final atomic positional and thermal parameters, with e.s.d.'s derived from this final refinement, are given in Table 1 and the observed and calculated structure factors are listed in Table 2.

Discussion of the structure

(i) The molecular geometry

Neutron diffraction confirms the molecular structure as 2,4-dioxo-5,6-dihydroxypyrimidine (*i.e.* 5,6-dihydroxyuracil). A dihedral angle of 67° is observed between the plane of the 5-hydroxyl group C(5)O(5)H(5), and the best least-squares plane through the pyrimidine ring (Table 3). The molecular configuration is shown in Fig. 3, to gether with ellipsoidal representations of atomic thermal vibration. It is emphasized that the

Table 3. Least squares planes with atomic displacements

The planes, referred to the crystallographic axes, are in the form AX+BY+CZ=D, with X, Y, Z in Å units. Planes (1) and (2) are best least-squares planes, with all atoms equally weighted. The planes are as follows:

(1) Plane through the atoms of the pyrimidine ring (present neutron analysis).

(2) Plane through the atoms of the pyrimidine ring (X-ray analysis; Bolton, 1965).

(3) Plane through the atoms of the 5-hydroxyl group, *i.e.* C(5), O(5), H(5) (present neutron analysis).

(4) Plane through the atoms of the 5-hydroxyl group, *i.e.* C(5), O(5), H(5) (X-ray analysis; Bolton, 1965).

(5) Plane through the atoms of the water molecule.

(6) The crystallographic plane (010).

(i) Plane coefficients

	A	· B	С	D
(1)	0.02067	0.89837	0.43485	2.89513
(2)	0.01443	0.89783	0.43679	2.89718
(3)	-0.32140	-0.02452	0.07267	3.60057
(4)	0.13672	0.95052	0.26483	2.27015
(5)	-0.28145	0.83358	0.49967	3.94497
(6)	0	1.0	0	0
(ii) D	ihedral angles			
Pla	anes A	ngle	Planes	Angle
(1)	(3) +	- 67·3°*	(1) (6)	26·1 °
(2)	(4) -	-12	(2) (6)	26.1
(1)	(5) +	-17·9 *	(3) (6)	91.4
			(5) (6)	33.5

(iii) Displacements of atoms and symmetry elements from the planes

Positive displacements are in the sense outwards from the crystallographic origin towards the plane. The e.s.d.'s in atomic displacements are shown in brackets. Displacements and their e.s.d.'s are in units of $Å \times 10^3$.

Atoms forming the planes

$\begin{array}{c|cccc} Plane (1) & Plane (2) \\ neutron & X-ray \\ N(1) & -1 (2) & +6 (3) \\ C(2) & +4 (2) & -5 (3) \end{array}$

1 ((3)	· (-)	1 (3)
C(4)	+6(2)	+6(3)
C(5)	-3(2)	-6(3)
C(6)	+1(2)	0 (3)

Other displacements from plane (1)

O(2)	+8(3)	H(1)	+ 63 (6)
O(4)	+6(3)	H(3)	-31(6)
O(5)	+51(3)	H(5)	-714(10)
0(6)	+24(4)	H(6)	+136(6)

Crystallographic centre at $(0, 0, \frac{1}{2})$: -80 Crystallographic centre at (0, 1, 0): +407

* The planes making this angle intersect in a line approximately parallel to a. When viewed from the crystallographic origin along the positive direction x, a positive angle is a clockwise twist with respect to the plane (1).

dihedral angle of 67° is an average value calculated using the position of the 'thermal' centroid of the H(5)proton.

The pyrimidine ring atoms are very nearly coplanar (Table 3). There are small but highly significant out of plane displacements of all ring substituent atoms, except possibly O(4), which give more nearly collinear intermolecular hydrogen bonds than would otherwise be the case.

The bond lengths in dialuric acid and the water molecule are listed in Table 4 with minimum possible values after correction for anisotropic thermal motion and with corrections assuming the 'riding' mode of thermal motion (Busing & Levy, 1964). The latter assumption provides a reasonable model for the hydrogen atom behaviour and at least an indication of the expected lengthening for the bonds between the heavier atoms. Thus the bond length corrections within the pyrimidine ring appear to be negligibly small, those for the C-O bonds are about 0.01 Å, those for N-H and O-H bond lengths somewhat greater, and for the O(5) H(5) bond length a very large correction (0.11 Å) is obtained. The difference between the two O-H bond lengths in the water molecule is insignificant after thermal corrections are applied. The bond lengths and angles without thermal corrections are shown in Fig. 4(a) and (b) for the neutron and X-ray analyses, re-



Fig.3. The molecular configuration with ellipsoidal representations of the anisotropic thermal parameters. These are 50% probability ellipsoids.



spectively. The results are the same within experimental error, except possibly for the bond length N(1)-C(6) for which the difference (0.014 Å) has an e.s.d. of 0.005 Å.

Table 4. Thermal corrections to the bond lengths

Column (1): uncorrected values; (2): the minimum values with corrections assuming the anisotropic thermal parameters given in Table 1; (3): the corrected values assuming the 'riding' mode of thermal motion.

(1)	(2)	(3)
1·349 Å	1·349 Å	1·352 Å
1.349	1.349	1.350
1.372	1.372	1.375
1.416	1.416	1.416
1.357	1.357	1.357
1.366	1.366	1.370
1.219	1.220	1.228
1.238	1.239	1.250
1.349	1.350	1.360
1.297	1.299	1.311
1.019	1.021	1.038
1.035	1.036	1.050
0.923	0.965	1.035
1.007	1.008	1.019
0.930	0.930	0.941
0.947	0.947	0.949
	(1) 1·349 Å 1·349 1·372 1·416 1·357 1·366 1·219 1·238 1·349 1·297 1·019 1·035 0·923 1·007 0·930 0·947	(1)(2) $1 \cdot 349$ Å $1 \cdot 349$ Å $1 \cdot 349$ $1 \cdot 372$ $1 \cdot 372$ $1 \cdot 416$ $1 \cdot 357$ $1 \cdot 357$ $1 \cdot 357$ $1 \cdot 366$ $1 \cdot 366$ $1 \cdot 219$ $1 \cdot 220$ $1 \cdot 238$ $1 \cdot 239$ $1 \cdot 349$ $1 \cdot 350$ $1 \cdot 297$ $1 \cdot 299$ $1 \cdot 019$ $1 \cdot 021$ $1 \cdot 035$ $1 \cdot 036$ $0 \cdot 923$ $0 \cdot 965$ $1 \cdot 007$ $1 \cdot 008$ $0 \cdot 930$ $0 \cdot 930$ $0 \cdot 947$ $0 \cdot 947$

(ii) The molecular packing and hydrogen bonding

The molecular packing and hydrogen bonding in dialuric acid monohydrate are shown in Figs. 2 and 5. The b projection of the crystal structure was shown by Bolton (1965, Fig. 2). The hydrogen bonding distances and angles and other close intermolecular distances are listed in Table 5.

(iii) The environment of the 5-hydroxyl group

1.357.44

120.6,3

120.6.3

123.3,

С

19.0.2

115.5

0

(r)

C 1.350,4

1,218.44

120.23

115 8 3

125.9.3

1.347 54

121 9,3

O

123

120.3.3

1.371.44

From qualitative considerations, the planar conformation I is expected for the isolated dialuric acid molecule. This would maximize the attractive interac-

127 0 :

112.5.3

1.352.4

.308.44



tions between the protons H(5) and H(6) and the lone pair electrons on oxygen atoms O(4), O(5) and O(6), and permit the most effective participation of atoms O(5) and O(6) in the delocalized π -bonding of the oxopyrimidine system.

In the crystal structure, the O(6) H(6) hydroxyl group forms a strong hydrogen bond with a water molecule [O(6) - O(W)] distance 2.57 Å; H(6) - O(W) distance 1.57 Å] with atoms O(6) and H(6) only slightly displaced from the pyrimidine ring plane (Table 3, iii). For this hydroxyl group, the predicted conformation for an isolated molecule and that which is observed in the crystalline hydrate are closely similar.

For the O(5) H(5) hydroxyl group, however, the postulated planar conformation would result in a close intermolecular approach (2.0 Å) between atoms H(5) and the water hydrogen atom H(1, W) which is hydrogen bonded to the carbonyl oxygen atom O(4). This would be a repulsive interaction, since the H---H distance is considerably less than the van der Waals distance (2.4 Å; Pauling, 1960). Other intermolecular interactions involving H(5) in this postulated position. would be with two oxygen atoms O(5), at distances 1.4 and 2.2 Å along the positive and negative y directions. These interactions might be described as forming a weak bifurcated hydrogen bond. The hydrogen

Table 5. Intermolecular distances and angles with e.s.d.'s

The e.s.d.'s are shown in brackets as 1000 $\sigma(d)$ Å and $10\sigma(\theta)^\circ$. Atoms not in the crystal chemical unit (*i.e.* not listed in Table 1) are specified by a subscript. The four-digit subscript denotes how the atomic parameters can be derived from the corresponding atom in the crystal chemical unit. The first three digits code a lattice translation, e.g. 564 means a translation of (5-5)a + (6-5)b + (5-5)a + (6-5)b + (5-5)a + (6-5)a +(4-5)c or (b-c). The fourth digit specifies one of following operations:

1:	x, y, z	3:	$\frac{1}{2} - x, \frac{1}{2} + y, \frac{1}{2} - z$
2:	-x, -y, -z	4:	$\frac{1}{2} + x, \frac{1}{2} - y, \frac{1}{2} + z$

(i) Hydrogen bonds, excluding interactions involving O(5) H(5)

Distance	$d, \sigma(d)$	Angle	$\theta, \sigma(\theta)$
N(1)O(2)5553	2·764 (4) Å	$N(1)-H(1)\cdots O(2)_{5553}$	173.4 (6)
H(1)O(2)5553	1.749 (7)	$H(1) \cdots O(2)_{5553} - C(2)_{5553}$	130.5 (3)
N(3)O(4)5562	2·792 (4)	$N(3)-H(3)\cdots O(4)_{5562}$	176.8 (5)
H(3)O(4)5562	1.758 (6)	$H(3) \cdots O(4)_{5562} - C(4)_{5562}$	124.1 (3)
$O(6) - O(W)_{4553}$	2.571(7)	$O(6) - H(6) \cdots O(W)_{4553}$	169.8 (7)
$H(6) - O(W)_{4553}$	1.574 (9)	$H(6) \cdots O(W)_{4553} - H(1, W)_{4553}$	118.9 (8)
		$H(6) \cdots O(W)_{4553} - H(2, W)_{4553}$	125.3 (8)
		$H(6) \cdots O(W)_{4553} \cdots H(5)_{4653}$	98·7 (5)
$O(W) - O(2)_{5662}$	2.830 (7)	$O(W) - H(2, W) \cdots O(2)_{5662}$	162.3 (9)
$H(2, W) - O(2)_{5662}$	1.913 (10)	$H(2, W) \cdots O(2)_{5662} - C(2)_{5662}$	124.7 (4)
O(<i>W</i>)O(4)	2.834 (7)	$O(W) - H(1, W) \cdots O(4)$	169.8 (9)
H(1, W) O(4)	1.914 (7)	$H(1, W) \cdots O(4) - C(4)$	127.9 (4)
		$O(2)_{5662} \cdots O(W) \cdots O(4)$	87.9 (2)
s involving the 5-hydrox	kyl group*		

(ii) Interactions

Distance	$d, \sigma(d)$	Angle	$\theta, \sigma(\theta)$
O(5)O(5) ₄₅₅₃	2·744 (5) Å	$C(5) - O(5) \cdots O(5)_{4553}$	$140.2(3)^{\circ}$
O(5)O(5)4453	2·744 (5)	$C(5) - O(5) \cdots O(5)_{4453}$	118.6 (3)
$O(5) - O(W)_{4453}$	3.068 (7)		
$O(5) O(W)_{4553}$	2.825 (7)	$C(5)-O(5)\cdots O(W)_{4553}$	110.7 (3)
H(5)O(5) ₄₅₅₃	3.043 (11)		
H(5)H(5)4553	2.23	$H(5)_{4553} \cdots H(5) \cdots H(5)_{4453}$	111
H(5)O(5)4453	1.945 (13)	$O(5)-H(5)\cdots O(5)_{4453}$	143.7 (11)
		$H(5) \cdots O(5)_{4453} - C(5)_{4453}$	136.7 (5)
$H(5) - O(W)_{4453}$	2.534 (16)	$O(5)-H(5)\cdots O(W)_{4453}$	117.2 (10)
		$H(5) \cdots O(W)_{4453} - H(1, W)_{4453}$	80·6 (7)
		$H(5) \cdots O(W)_{4453} - H(2, W)_{4453}$	118·0 (8)

 $H(5) - - O(W)_{4553}$ 3.236 (16)

(iii) Close non-bonded intermolecular interatomic distances†

Distance	d	Distance	d
C(2)N(1) ₅₄₅₁	3·326 Å	$H(1) C(2)_{5553}$	2·705 Å
$N(3) - C(6)_{5451}$	3.475	$H(3) C(4)_{5562}$	2.657
$C(4) - C(5)_{5451}$	3.321	$H(6) H(1, W)_{4553}$	2.181
$C(4) - C(6)_{5451}$	3.491	$H(6) H(2, W)_{4553}$	2.258
C(6)O(6)5451	3.295		
O(6)O(6) ₅₆₅₂	3.335	$O(W) O(5)_{4453}$	2.825
		$O(W) O(5)_{4553}$	3.068
		O(W)O(5)	3.424

* Distances and angles are with respect to the position of the thermal centroid of atom H(5).

† This list includes all distances which are within 0.2 Å of the sum of the appropriate van der Waals radii (C, 1.7; N, 1.5; O, 1.4; H, 1.2 Å; Pauling, 1960).

atom H(5) would be about 0.6 Å from the plane containing the donor O(5) atom and the two acceptor O(5) atoms. The repulsive interaction H(5)---H(1, W) presumably outweighs the weak attractive hydrogen bonding interaction, since the hydrogen atom is not found in this postulated position.

With the hydrogen atom H(5) in its observed mean position, a zigzag chain of weak intermolecular hydrogen bonds is formed, --O(5)-H(5)--O(5)-H(5)--O(5)-H(5), in which the distance H(5)---O(5) is 1.95 Å and the angle at H(5) is 144°. Atom H(5) is also involved in a very weak attractive interaction with the water oxygen atom O(W) shown at the bottom righthand corner of Fig.2. The distance H(5)---O(W) is 2.53 Å, only slightly less than the van der Waals distance (2.6 Å; Pauling, 1960) and the angle O(5)---H(5)---O(W) is 117°.

These distances and angles were calculated assuming atoms to be located at their thermal centroids. It should be noted that the anisotropic thermal parameters reported for atom (H5) indicate an exceptionally large root mean square amplitude of vibration (0.47 Å) in a direction compatible with an intramolecular vibration of the bond O(5)-H(5) about the C(5)-O(5) axis. This corresponds to a restriction of the O-H bond to a range of about 50° of the full rotation about the C-O bond. Since the neutron diffraction data give information concerning only the time average positions of atomic nuclei in the crystal structure, atom H(5) could also be described as disordered with respect to two sites displaced about 0.4 Å on either side of the 'thermal' centroid, or in terms of other descriptions, ranging between the extremes of normal thermal vibration and disorder.

From Fig.2, it appears that stronger hydrogen bonds O(5)-H(5)--O(5') would be formed if the O(5)-H(5) bond were to twist about the C(5)-O(5) bond towards the line of centres O(5)--O(5'), *i.e.* the H(5)--O(5') distance would be decreased and the angle at H(5) increased. However, within a chain of hydrogen bonds, this movement leads to increasingly unfavourable H(5)--H(5') repulsions, since the H(5) atoms would become closer together than the separation (2·23 Å) between their thermal centroids, which is already slightly less than the van der Waals distance (2·4 Å). This is probably the reason why ordered hydrogen



Fig. 5. The molecular packing and hydrogen bonding. The structure is viewed down the normal to the pyrimidine ring of the central shaded molecule. This molecule, together with the shaded water molecule, constitutes the crystal chemical unit, for which the atomic parameters are listed in Table 1. Circles of decreasing radii represent oxygen, nitrogen, carbon and hydrogen atoms, respectively. Atom H(5) is shown as the thermal ellipsoid derived from the least-squares anisotropic thermal parameters.

bonded chains with H(5) atoms in such positions are not observed.

A twist of the O(5)-H(5) bond in the opposite sense, *i.e.* away from the line of centres O(5)---O(5'), would weaken the hydrogen bond O(5)-H(5)---O(5'), but would strengthen the attractive interaction O(5)-H(5)---O(W) with the water oxygen atom at the bottom right of Fig.2, by decreasing the H(5)---O(W) distance from 2.5 Å and increasing the angle at H(5) from 117°. The water molecule would then become involved in four, rather than three, hydrogen bonds, and these would be tetrahedrally disposed.

It appears that, within the observed range of twist of the O(5)-H(5) bond about the C(5)-O(5) bond, no one position is particularly favourable for intermolecular hydrogen bonding.

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The Crystal Structures of Two Polymorphs of 5,5'-Diethylbarbituric Acid (Barbital)

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Crystal morphological, X-ray and infrared spectral data are presented for the identification of three (I, II and IV) of the four reported polymorphs of 5,5'-diethylbar bituric acid (barbital). Three-dimensional X-ray crystal structure determinations of barbital I and II are reported. The crystal data are: I (trigonal, m.p. 190°C) a = 26.921, c = 6.828 Å (hexagonal lattice), space group R3, with 18 molecules per cell; II (monoclinic, m.p. 183 °C) a = 7.120, b = 14.162, c = 9.810 Å, $\beta = 89^{\circ}14'$, space group C2/c with 4 molecules per cell. For barbital I X-ray intensity data were collected from two different crystals and two independent structure determinations (Ia, Ib) were carried out. These agreed within experimental error. The X-ray intensity data (1526, 1617 and 840 reflections in Ia, Ib and II) were collected with a fourcircle automatic diffractometer. Refinement of atomic positional and anisotropic thermal parameters was by full-matrix least-squares, resulting in final R values of 0.057, 0.041 and 0.062 for Ia, Ib, II, excluding the unobservably weak reflections. All hydrogen atoms were found. The molecule is in the 2.4,6-trioxo tautomeric form in both I and II. The molecular point symmetry is approximately 2 mm, but with distortions in the barbiturate ring and hydrocarbon chain which are most marked in I. Molecules are linked by NH...OC hydrogen bonds to form ribbons in which the barbiturate rings are almost coplanar, although the mode of hydrogen bonding is different in I and II. Van der Waals interactions are of greater importance in the stable form I. Variations of 0.014 Å in C-N ring bond lengths are near the limit of experimental error, but appear to be systematic and may be related to hydrogen bonding effects. The atomic thermal vibrational behaviour is strikingly similar in I and II.

Introduction

Since 1903 when Fischer and von Mering discovered the hypnotic action of 5,5'-diethylbarbituric acid (also known as barbital, veronal, or diemal, Fig. 1⁺), the relationship between chemical structure and drug action

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 $[\]dagger$ The atomic nomenclature in the present work was chosen to conform as closely as possible to the chemical nomenclature. A twofold rotation axis of crystallographic symmetry passes through atoms O(2), C(2) and C(5) in the case of barbital II.