

gree of anisotropic vibration, assuming that systematic errors in the experimental data are insignificant.

Table 6. *Ellipsoids of vibration to the unit-cell axes (neutron refinement)*

	<i>i</i>	$(\overline{r_i^2})^{1/2}$	<i>a<sub>ia</sub></i>	<i>a<sub>ib</sub></i>	<i>a<sub>ic</sub></i>
Y(1)	1	0.078 Å	0.577	0.577	0.577
	2	0.040	0.816	-0.408	-0.408
	3	0.040	0.000	0.707	-0.707
Y(2)	1	0.082	0.000	0.403	0.915
	2	0.066	1.000	0.000	0.000
	3	0.047	0.000	0.915	-0.403
O	1	0.080	-0.468	0.837	-0.282
	2	0.060	0.355	0.471	0.808
	3	0.045	0.809	0.278	-0.518

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## The Crystal Structure of 5-Methyluridine\*

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5-Methyluridine was crystallized from aqueous ethanol as the hemihydrate in the form of orthorhombic needles, space group  $P2_12_12$  with  $a=14.026$ ,  $b=17.302$ ,  $c=4.861$  Å and four molecules per cell. The crystal structure has been determined by a three-dimensional, X-ray diffraction analysis. Intensity data were collected on photographic film and estimated visually. The structure was solved from the Patterson function with the help of Fourier techniques and packing considerations. Refinement by a full-matrix, least-squares method has led to a final  $R$  value of 0.075 for 1294 reflections and to estimated standard deviations in bond lengths for the non-hydrogen atoms between 0.006 and 0.007 Å. The torsion angle describing the relative orientations of the sugar residue and the pyrimidine base is  $-29.4^\circ$ . Atom C(3') of the sugar residue is displaced by about 0.60 Å from the least-squares plane through the other four ring atoms and lies on the same side of the plane as C(5'). This plane also makes an angle of  $71.9^\circ$  with the least-squares plane through the six ring atoms of the pyrimidine base. Of the twelve atoms within, or bonded to, the pyrimidine ring, only C(1') deviates significantly, by 0.083 Å, from the least-squares plane through the six ring atoms.

### 1. Introduction

The structure of 5-methyluridine (Fig. 1) has been determined as one in a series of compounds being studied in these laboratories to provide accurate bond lengths and angles and conformational information useful in structural studies of the nucleic acids.

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As far as the authors are aware, ten X-ray analyses have been reported, to date, for uridine and thymidine derivatives (Huber, 1957; Trueblood, Horn & Luzzati, 1961; Harris & McIntyre, 1964; Shefter, Barlow, Sparks & Trueblood, 1964; Shefter & Trueblood, 1965; Camerman & Trotter, 1965; Haschemeyer & Sobell, 1965; Iball, Morgan & Wilson, 1966, 1968). The most accurate determinations seem to be for  $\beta$ -adenosine-2'-uridine-5'-phosphoric acid (Shefter *et al.*, 1964) and 5-fluorodeoxyuridine (Harris & MacIntyre, 1964) for which the estimated standard deviations (e.s.d.'s) are slightly larger than those reported here for 5-methyluridine.

## 2. Experimental procedure

5-Methyluridine was obtained as a powder from Mann Research Laboratories Inc., New York, N.Y. and crystallized from aqueous ethanol as orthorhombic needles, elongated along *c*. Weissenberg photographs showed systematic absences only amongst *h*00 for  $h=2n+1$  and *0k*0 for  $k=2n+1$  indicating the space group to be  $P2_12_12$ .

Unit-cell parameters were obtained from Straumanis type Weissenberg photographs taken about the *a* and *c* axes. A least-squares routine minimizing

$$\sum_n w_n (\sin^2\theta_{\text{obs}} - \sin^2\theta_{\text{calc}})^2 (4/\lambda^2)$$

was used,  $w_n$ , the weight of an observation, being proportional to  $1/\sin^2 2\theta$ . Systematic corrections for eccentricity and absorption were applied (Klug & Alexander, 1954) and the values obtained were:

$$\begin{aligned} a &= 14.026 \pm 0.003 \text{ \AA} \\ b &= 17.302 \pm 0.001 \\ c &= 4.861 \pm 0.001 . \end{aligned}$$

The indicated eccentricity and absorption corrections are small and the confidence limits cited are subjective, being approximately ten times the standard deviations obtained from the least squares. The calculated density, assuming four molecules of  $C_{10}H_{14}N_2O_6$  and two molecules of water per unit cell is  $1.504 \text{ g.cm}^{-3}$ ; the density measured by flotation is  $1.503 \text{ g.cm}^{-3}$ .

Intensity data were collected by the multi-film, equi-inclination Weissenberg technique with Cu  $K\alpha$  radiation and Eastman No-screen film. Reflection intensities for layers *hk*0–*hk*4 and *0kl*–*5kl* were estimated visually by comparison with calibrated ‘wedges’. Two crystals were used, both cut from needles to give rough cubes of side 0.10 mm, though slightly elongated in the *c* direction. Empirical film factors (corrected for equi-inclination angle) ranged from 2.8 to 4.5; since experience in this laboratory has indicated an average value of 3.8 for this brand of film, this latter value (adjusted for equi-inclination angle) was used in scaling the obser-

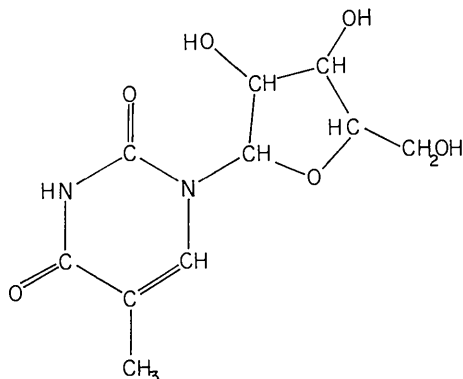


Fig. 1. 5-Methyluridine.

vations together. The variation of the empirical film factors probably arose from a systematic under-estimation of the very strong intensities.

Each intensity reading was allotted a standard deviation according to the formulae

$$\begin{aligned} \sigma(I) = \sigma(\text{ext}) \left\{ \left[ \frac{I_{\text{min}}}{3} + bI + \left( \frac{0.1I^2}{I_{\text{max}}} - I \right)^2 \right] \right. \\ \left. \times \left[ 1 + 0.25 \exp [-50(0.5 - \sin^2\theta)^2] \right] \right\}, \end{aligned}$$

where  $I_{\text{min}}$  and  $I_{\text{max}}$  are the limits within which an intensity can be reliably estimated and  $b$  was determined from a statistical analysis of the consistency between reflections multiply observed in the sensitive region of the intensity ‘wedge’.  $\sigma(\text{ext})$  is a subjective parameter. The exponential term is designed to take account of  $\alpha_1$ ,  $\alpha_2$  splitting. The data were then corrected for Lorentz and polarization effects and placed on a common arbitrary scale after a least-squares determination of inter-layer scale factors. The final total of 1499 independent reflection intensities (of which 192 were too small to be observed) were then scaled absolutely by the method of Wilson (1942). In view of the size of the crystal and the fact that the calculated absorption coefficient is  $11.1 \text{ cm}^{-1}$  it was considered unnecessary to make absorption corrections. All calculations were carried out on an IBM 7094 computer using subprograms operating under the *CRYRM* system (Duchamp, 1964).

## 3. Structure determination

A three-dimensional, origin-removed Patterson function was computed with sharpened coefficients,

$$\begin{aligned} \left[ \frac{(k|F_{\text{obs}}|)^2}{\exp(-2B\sin^2\theta/\lambda^2) \cdot \sum n_i f_i^2} - 1 \right] \cdot 2^{16} \cdot \left( \frac{\sin\theta}{\lambda} \right)^4 \\ \times \exp\left(-19.36 \frac{\sin^2\theta}{\lambda^2}\right), \end{aligned}$$

$n_i$  being the number of atoms of type *i* having atomic scattering factor  $f_i$  and  $B$  the overall isotropic temperature factor. The approximate orientation of the pyrimidine base was determined from a visual investigation of the heights and positions of the peaks close to the origin of the Patterson function. The location of the base in the unit cell was determined from the Patterson projection,  $P(u, v)$ , where a large peak was to be expected corresponding to the ‘ring–ring’ vector from molecules related by the twofold axis. Of several possible peaks, one was selected that corresponded to reasonable packing conditions in the crystal and that best matched the three-dimensional Patterson function. This interpretation turned out to be correct.

Iterative Fourier methods then led to a complete trial structure with an agreement index of  $R_{hk0} = 0.51$ . Full-matrix least-squares refinement of the *x* and *y* coordinates, a scale factor, and in later cycles isotropic temperature parameters reduced  $R_{hk0}$  to 0.15. As ex-

pected from the density measurements the unit cell contains two water molecules, these being situated on the twofold axes at (0,0) and  $(\frac{1}{2}, \frac{1}{2})$ .

The  $z$  coordinate of the oxygen atom of the water molecule was estimated from the Harker line  $P(\frac{1}{2}, \frac{1}{2}, w)$ . To determine trial  $z$  coordinates for the remaining atoms it was assumed that the nitrogen atom of the pyrimidine ring participated in a hydrogen bond with the oxygen atom at (0,0). From the Fourier projection it seemed that this geometry was favourable and so the molecule was adjusted in  $z$  until the oxygen atom of the water molecule was in the plane of the ring. At this stage a three-dimensional structure factor calculation gave an agreement index of  $R_{hkl}=0.19$ .

#### 4. Refinement

Atomic coordinates, a scale factor and isotropic tem-

perature factors were refined with a full-matrix, least-squares routine minimizing

$$\sum w(|F_{\text{obs}}|^2 - 1/k^2|F_{\text{calc}}|^2)^2,$$

where  $k$  is the scale factor and  $w=1/\sigma^2(|F_{\text{obs}}|^2)$  was derived from  $\sigma(I)$  defined in § 2. Refinement for three cycles reduced  $R$  to 0.15 and was then continued with anisotropic temperature factors of the form

$$\exp[-(h^2b_{11} + k^2b_{22} + l^2b_{33} + hkb_{12} + hlb_{13} + klb_{23})].$$

Three further cycles reduced  $R$  to 0.10 whereupon difference Fourier syntheses were calculated in the planes where hydrogen atoms were expected to lie. Peaks ranging from 0.1 to 0.6 e.Å<sup>-3</sup> were observed in reasonable positions for all hydrogen atoms; these positions with isotropic temperature factors of 4.0 Å<sup>2</sup> were included in subsequent structure-factor calculations but were not refined. For the hydrogen atoms, scattering

Table 1. *The heavy-atom parameters and their estimated standard deviations*

All entries have been multiplied by 10<sup>4</sup>.

	X	Y	Z	$b_{11}$	$b_{22}$	$b_{33}$	$b_{12}$	$b_{13}$	$b_{23}$
C(5)	2669 (4) Å	1916 (3) Å	4207 (10) Å	29 (3)	19 (1)	288 (18)	9 (4)	-12 (13)	-22 (9)
C(6)	2397 (4)	2457 (3)	2379 (10)	27 (3)	17 (1)	342 (20)	-4 (3)	24 (13)	-35 (9)
N(1)	1537 (3)	2463 (2)	1087 (8)	31 (3)	15 (1)	291 (16)	-2 (3)	-8 (11)	-16 (7)
C(2)	0860 (4)	1905 (3)	1593 (11)	27 (3)	16 (1)	351 (22)	-1 (4)	-35 (14)	-18 (10)
N(3)	1132 (3)	1362 (2)	3509 (9)	31 (3)	16 (1)	436 (21)	-4 (3)	-15 (13)	25 (9)
C(4)	1998 (4)	1317 (3)	4868 (10)	32 (3)	17 (1)	381 (23)	8 (4)	-24 (14)	24 (9)
C(7)	3619 (5)	1924 (3)	5555 (11)	38 (3)	33 (2)	363 (24)	0 (5)	-50 (16)	40 (12)
O(1) (water)	0	0	5605 (11)	27 (3)	31 (2)	401 (24)	3 (5)	0	0
O(2)	0094 (3)	1900 (2)	0508 (8)	30 (2)	25 (1)	566 (20)	-9 (3)	-76 (13)	42 (9)
O(4)	2130 (4)	0795 (2)	6517 (9)	52 (3)	27 (1)	601 (24)	-3 (4)	-73 (15)	122 (9)
C(1')	1262 (4)	3096 (3)	-0803 (10)	29 (3)	20 (1)	244 (17)	0 (4)	-47 (13)	-17 (9)
C(2')	0751 (4)	3767 (3)	0639 (10)	29 (3)	19 (1)	305 (20)	0 (3)	-4 (13)	-14 (9)
O(1')	2091 (3)	3400 (2)	-2039 (6)	43 (2)	18 (1)	247 (13)	3 (3)	54 (10)	-26 (6)
C(3')	1583 (4)	4307 (3)	1177 (9)	31 (3)	19 (1)	205 (18)	7 (3)	-9 (12)	-8 (8)
C(4')	2170 (4)	4221 (2)	-1391 (9)	41 (3)	16 (1)	198 (17)	2 (3)	-31 (13)	0 (7)
O(2')	0100 (3)	4070 (2)	-1280 (8)	37 (2)	24 (1)	492 (19)	15 (3)	-124 (13)	-30 (8)
C(5')	3207 (5)	4438 (3)	-1203 (12)	41 (4)	25 (2)	373 (24)	-1 (4)	67 (17)	26 (11)
O(5')	3682 (3)	4102 (2)	1067 (8)	29 (2)	28 (1)	410 (17)	9 (3)	4 (11)	-29 (8)
O(3')	1257 (3)	5072 (2)	1638 (7)	35 (2)	19 (1)	442 (17)	5 (3)	-18 (12)	-77 (7)

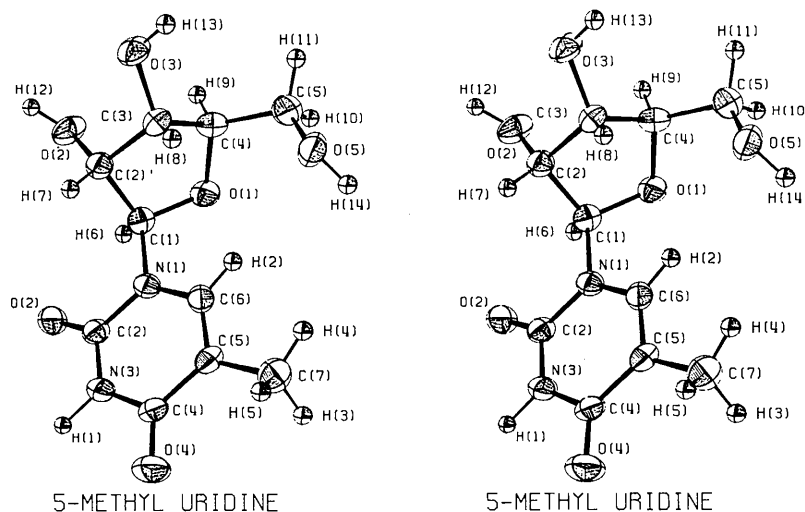


Fig. 2. A stereoscopic view of the molecule. The atoms are represented by ellipsoids (drawn at the 50% probability level) defined by the principal axes of thermal motion (Table 4).

factors calculated by Stewart, Davidson & Simpson (1965) were used and the remaining scattering-factor tables were taken directly from *International Tables for X-ray Crystallography* (1962). At the stage when parameter shifts were less than one fifth of their e.s.d.'s, hydrogen-atom positions alone were refined for four cycles. With the two largest amplitudes (121 and 350) excluded from the calculations and two final cycles of heavy-atom refinement,  $R$  converged to 0.075 with a 'goodness of fit'  $[\sum w(|F_{\text{obs}}|^2 - |F_{\text{calc}}|^2/k^2)^2/(m-s)]^{1/2}$ , of 1.29, where  $s$  is the number of parameters refined and  $m$  the number of observations ( $m=1294$ ; 'less thans' were only included if  $|F_{\text{calc}}| > |F_{\text{obs}}|$ ). All parameter shifts were now less than one tenth of their e.s.d.'s.

### 5. Results and discussion

For the heavy atoms, the final atomic parameters and their e.s.d.'s are listed in Table 1. The corresponding values for the hydrogen atoms appear in Table 2. Table 3 lists the observed and calculated structure factors and a stereoscopic view of the molecule is shown in Fig. 2 together with the numbering scheme adopted.

Table 4 shows the magnitudes and direction cosines of the principal axes of the thermal ellipsoids which are also represented in Fig. 2. Atoms C(5), C(2'), C(3') and C(5') are not significantly anisotropic on the basis that

none of their  $b_{ij}$  terms (Table 1) differ by more than three e.s.d.'s from the values they would have assuming isotropic motion with  $B$  equal to the mean value of the principal axis  $B_{ij}$ 's. Atoms O(2), O(4), O(2'), and O(3') appear to be highly anisotropic. As expected, O(2) and O(4) have their maximum amplitudes in a direction approximately perpendicular to the plane of the pyrimidine ring.

Table 2. *Hydrogen-atom coordinates and their estimated standard deviations ( $\times 10^3$ )*

	<i>X</i>	<i>Y</i>	<i>Z</i>
H(1)	061 (4)	089 (3)	370 (11)
H(2)	277 (5)	287 (3)	183 (11)
H(3)	400 (4)	146 (3)	497 (11)
H(4)	393 (5)	244 (3)	554 (11)
H(5)	354 (5)	188 (3)	726 (11)
H(6)	089 (5)	285 (3)	-208 (11)
H(7)	052 (4)	357 (3)	256 (12)
H(8)	190 (4)	419 (3)	259 (11)
H(9)	184 (5)	452 (3)	-279 (12)
H(10)	346 (5)	430 (3)	-301 (12)
H(11)	327 (4)	500 (4)	-122 (10)
H(12)	-038 (4)	435 (3)	-041 (11)
H(13)	170 (5)	537 (3)	198 (11)
H(14)	417 (4)	374 (3)	072 (11)
H(15)(water)	-052 (4)	032 (3)	660 (11)

Intramolecular bond distances and angles for the heavy atoms are shown respectively in Fig. 3(a) and (b). The values in parentheses in Fig. 3(a) include estimated corrections for thermal motion on the basis of a riding model (Busing & Levy, 1964). In the discussion that follows, bond lengths referred to are those uncorrected for thermal motion. The average C-H and O-H distances and the N-H distance are respectively 0.95, 0.94, and 1.10 Å. The average e.s.d.'s in bond lengths are:

$$\begin{aligned} \text{C-C} &= 0.007 \text{ \AA} \\ \text{C-N} &= 0.006 \\ \text{C-O} &= 0.006 \\ (\text{C, N, O})\text{-H} &= 0.06, \end{aligned}$$

with the corresponding average e.s.d.'s of bond angles not involving hydrogen atoms being of the order of 0.5°. Fig. 4 is a composite difference electron density map excluding the contributions of the hydrogen atoms to the calculated structure factors.

#### (a) Packing and hydrogen bonding

The view of the crystal structure projected down the  $c$  axis (Fig. 5) shows the packing arrangement, the hydrogen-bond scheme (broken lines) and the hydrogen bond distances. Some intermolecular contacts less than 3.5 Å are listed in Table 5, where proposed hydrogen bonds are identified by an asterisk. All potential hydrogen-atom donors seem to fulfill that role and O(3'), O(5'), and O(1) (water) also act as acceptors. Some angles associated with the hydrogen bonds are listed in Table 5.

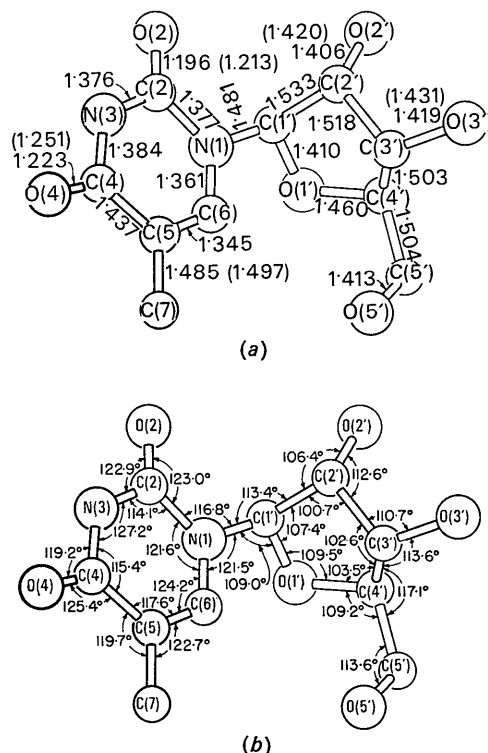


Fig. 3. (a) Bond distances (in Å) for the non-hydrogen atoms. Values in parentheses include an approximate correction for the effects of thermal motion. (b) Bond angles in degrees for the non-hydrogen atoms.

Table 3. Observed and calculated structure factors

The four rows in each column are k, 10F<sub>o</sub>, 10F<sub>c</sub> and the phase angle in degrees. Negative values for 10F<sub>o</sub> indicate 'less than' reflections; asterisks indicate reflections omitted from the final least-squares cycle.

Table with multiple columns containing numerical data for structure factors (k, 10F<sub>o</sub>, 10F<sub>c</sub>) and phase angles in degrees. The table is organized into a grid of rows and columns, with some cells containing asterisks to indicate omitted reflections.

Each water molecule is surrounded by two diad-related oxygen atoms [O(5')] and two diad-related nitrogen atoms [N(3)], all presumably participating in hydrogen bonding with the water molecule. The distance N(3)-O(1) of 3.019 Å is, however, rather long compared with similar nitrogen to water distances of

2.78 Å in calcium thymidylate (Trueblood *et al.*, 1961) and 2.91 Å in barium uridine-5'-phosphate (Shefter & True blood, 1965). Except for those of H(1) and H(13) it appears that none of the positions listed for the hydrogen atoms are significantly displaced from the donor-acceptor line. It is estimated that the standard devia-

Table 4. *The magnitudes and direction cosines (with respect to the crystallographic axes) of the principal axes of the thermal ellipsoids*

Axis					Axis						
(i)	$B_i$	$q_i^a$	$q_i^b$	$q_i^c$	(i)	$B_i$	$q_i^a$	$q_i^b$	$q_i^c$		
C(5)	1	3.10 Å <sup>2</sup>	-0.432	-0.532	0.728	C(1')	1	3.01 Å <sup>2</sup>	-0.635	-0.315	0.705
	2	2.35	0.663	0.360	0.656		2	2.33	-0.398	0.916	0.051
	3	1.77	-0.611	0.766	0.197		3	1.60	0.662	0.248	0.707
C(6)	1	3.58	0.256	-0.377	0.890	C(2')	1	2.97	-0.070	-0.318	0.946
	2	2.06	-0.943	0.104	0.315		2	2.30	-0.935	0.351	0.049
	3	1.80	0.212	0.920	0.329		3	2.19	0.347	0.881	0.322
N(1)	1	2.83	-0.181	-0.223	0.958	O(1')	1	3.75	0.878	-0.054	0.475
	2	2.41	0.966	-0.223	0.131		2	2.49	-0.342	-0.765	0.546
	3	1.67	0.184	0.949	0.255		3	1.57	-0.334	0.642	0.690
C(2)	1	3.54	-0.320	-0.167	0.933	C(3')	1	2.79	-0.733	-0.647	0.212
	2	2.06	0.846	-0.493	0.203		2	2.02	0.680	-0.707	0.193
	3	1.77	0.426	0.854	0.299		3	1.89	0.025	0.286	0.958
N(3)	1	4.22	-0.130	0.188	0.973	C(4')	1	3.32	-0.959	-0.060	0.278
	2	2.46	0.960	-0.224	0.171		2	1.92	-0.019	0.989	0.145
	3	1.84	-0.250	-0.956	0.152		3	1.75	0.283	-0.133	0.950
C(4)	1	3.74	-0.198	0.179	0.964	O(2')	1	5.89	-0.521	-0.259	0.813
	2	2.74	0.836	0.545	0.071		2	2.78	0.169	0.903	0.396
	3	1.67	0.512	-0.819	0.258		3	1.73	0.837	-0.344	0.426
C(7)	1	4.52	-0.284	0.724	0.628	C(5')	1	4.38	0.608	0.231	0.759
	2	3.43	-0.633	-0.634	0.445		2	3.12	-0.473	0.874	0.113
	3	2.38	0.720	-0.271	0.638		3	2.32	-0.638	-0.427	0.641
O(1)	1	3.79	-0.011	-0.075	0.997	O(5')	1	4.17	-0.100	-0.526	0.845
	2	3.70	-0.106	-0.994	0.000		2	3.20	0.392	0.760	0.519
	3	2.13	-0.994	0.106	0.000		3	2.05	-0.915	0.383	0.130
O(2)	1	5.90	-0.303	0.268	0.914	O(3')	1	4.87	-0.153	-0.446	0.882
	2	2.81	0.155	-0.933	0.325		2	2.75	0.984	0.016	0.179
	3	2.01	0.940	0.241	0.241		3	1.56	-0.093	0.895	0.436
O(4)	1	7.14	-0.297	0.454	0.840						
	2	3.90	0.936	0.315	0.160						
	3	2.02	0.192	-0.834	0.518						

Table 5. *Some close contacts less than 3.5 Å and hydrogen atom-donor-acceptor angles ( $\theta$ ) where appropriate*

Proposed hydrogen bonds are denoted by an asterisk. Other angles relevant to the hydrogen bonds are also shown.

Atom 1	Atom 2	Distance (Å)	$\theta^\circ$
O(1) (water)	N(3)	3.019*	17
O(2') ( $-x, -y+1, z$ )	O(2')	3.232	
O(2') ( $-x, -y+1, z$ )	O(3')	2.800*	4
C(5') ( $-x+\frac{1}{2}, y-\frac{1}{2}, -z+1$ )	O(4)	3.305	
O(5') ( $-x+\frac{1}{2}, y-\frac{1}{2}, -z+1$ )	O(1)	2.906*	7
O(5') ( $-x+\frac{1}{2}, y-\frac{1}{2}, -z+1$ )	O(4)	3.354	
O(3') ( $-x+\frac{1}{2}, y-\frac{1}{2}, -z+1$ )	C(7)	3.486	
O(3') ( $-x+\frac{1}{2}, y-\frac{1}{2}, -z+1$ )	O(4)	2.735*	13
O(1') ( $x, y, z+1$ )	C(5)	3.252	
O(1') ( $x, y, z+1$ )	C(6)	3.195	
O(2') ( $x+\frac{1}{2}, -y+\frac{1}{2}, -z$ )	C(7)	3.404	
O(2) ( $x+\frac{1}{2}, -y+\frac{1}{2}, -z$ )	O(5')	2.742*	6
O(2) ( $x+\frac{1}{2}, -y+\frac{1}{2}, -z+1$ )	C(7)	3.476	
Other hydrogen-bond angles			
O(5') ( $-x+\frac{1}{2}, y-\frac{1}{2}, -z+1$ )-O(1)-O(5') ( $x-\frac{1}{2}, -y+\frac{1}{2}, -z+1$ )			112.4°
C(5')-O(5')-O(2) ( $x+\frac{1}{2}, -y+\frac{1}{2}, -z$ )			112.5
C(2)-N(3)-O(1)			127.9
C(4)-N(3)-O(1)			104.9
C(3')-O(3')-O(4) ( $-x+\frac{1}{2}, y+\frac{1}{2}, -z+1$ )			102.2
C(2')-O(2')-O(3') ( $-x, -y+1, z$ )			107.6

tions for the 'hydrogen-donor-acceptor' angles are of the order of  $3.5^\circ$ . The hydrogen atoms of the bonds  $N(3)-H(1)\dots O(1)$  and  $O(3')-H(13)\dots O(4)$  ( $\frac{1}{2}-x, \frac{1}{2}+y, 1-z$ ) lie respectively  $17^\circ$  and  $13^\circ$  off the donor-acceptor line.

Because of the tilt ( $42.5^\circ$ ) of the base plane with respect to (001) there is little overlap between bases and stacking interactions will be small. The closest contact between parallel bases is  $3.598 \text{ \AA}$  for  $C(2)-O(4)$  ( $x, y, z-1$ ).

### (b) The pyrimidine ring

Within the accuracy of this determination, the pyrimidine ring is planar but with  $C(1')$  significantly displaced ( $0.083 \text{ \AA}$ ) to the same side of the plane as  $C(2')$ . The data for the least-squares plane are given in Table 6 and show that the other five exocyclic atoms are not significantly displaced from the plane. Fig. 6 provides a view of the  $C(7)$  hydrogen atoms looking down the bond  $C(7)-C(5)$ . As might be expected, the conformation adopted is staggered with respect to  $O(4)$ .

Table 6. Deviations from the least-squares plane of the pyrimidine ring

The equation of the least-squares plane is

$$-0.3730X + 0.5629Y + 0.7375Z = 1.9841$$

where the coefficients are the direction cosines of the plane normal with respect to the crystallographic axes.

	Deviation ( $\text{\AA}$ )		Deviation ( $\text{\AA}$ )
N(1)	0.000	O(2)*	-0.001
C(2)	-0.008	O(4)*	0.012

Table 6 (cont.)

	Deviation ( $\text{\AA}$ )		Deviation ( $\text{\AA}$ )
N(3)	0.009	C(7)*	-0.013
C(4)	-0.001	C(1')*	0.083
C(5)	-0.006	H(1)*	-0.11
C(6)	0.007	H(2)*	0.02

\* Atoms not included in the calculation of the plane.

The bond lengths in the pyrimidine base agree quite well with those of previous determinations of comparable accuracy (Harris & MacIntyre, 1964; Camerman

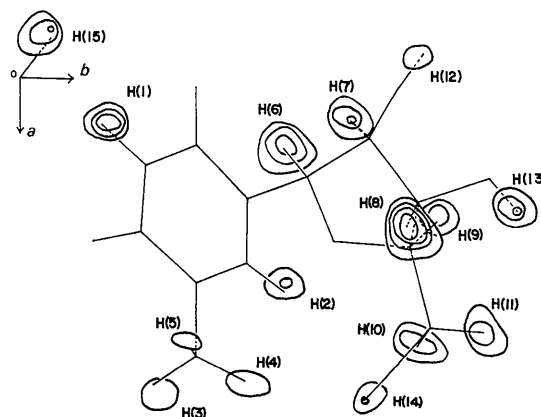


Fig. 4. The composite difference electron density map, for which the contributions of the hydrogen atoms were excluded from the calculated structure factors. Contours are drawn at intervals of  $0.1 \text{ e.\AA}^{-3}$  starting at  $0.3 \text{ e.\AA}^{-3}$ .

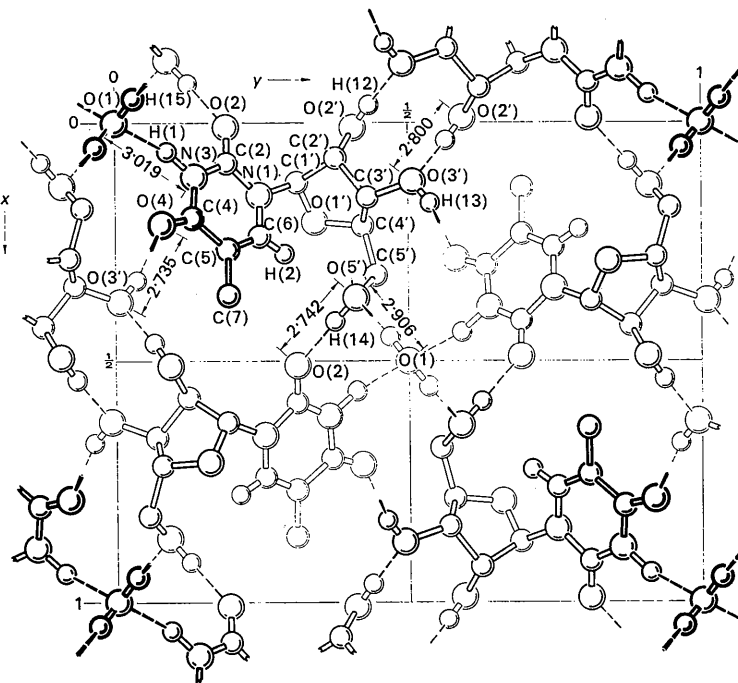


Fig. 5. The crystal structure viewed down the  $c$  axis. Not all the hydrogen atoms are shown.

& Trotter, 1965; Trueblood *et al.*, 1961; Shefter & Trueblood, 1965; Haschemeyer & Sobell, 1965; Iball *et al.*, 1966, 1968; Parry, 1954; Gerdil, 1961; Reeke & Marsh, 1966). The e.s.d.'s in bond lengths for 5-fluoro-2'-deoxyuridine (FUDR)\* (Harris & MacIntyre, 1964) and thymine monohydrate (Gerdil, 1961) were quoted† as 0.008–0.011 and 0.006–0.009 Å respectively. There are no significant differences between the lengths of the bonds common to the pyrimidine bases of 5-methyluridine and FUDR. The agreement of thymine monohydrate with 5-methyluridine is similar except for the bond C(2)–O(2), which is 0.038 Å longer in the free base than in the nucleoside. The significance of this difference would probably be reduced if the effects of thermal motion were taken into account. For the bond angles, the agreement is nearly as good except around C(4), C(5) and C(6). The respective values of the internal angles at these atoms for 5-methyluridine and FUDR are 115.4, 117.6, 124.2, and 112.6(0.7), 122.7(0.7), 120.3(0.7)°; the differences are not surprising in view of the different substituent at C(5) in the two compounds. The values for 5-methyluridine agree much better with those of thymine monohydrate (115.6,

118.2, 121.8°) where the calculated standard deviations of the bond angles vary from 0.3 to 0.5°.

### (c) The sugar residue

The conformation adopted by the sugar ring can be described with respect to the plane through the atoms C(1'), C(2'), C(4'), and O(1') (Table 7). C(3') is displaced 0.605 Å out of this plane on the same side as C(5'), a conformation commonly observed amongst pyridine nucleosides and referred to as C(3') *endo*.

Table 7. Deviations from a least-squares plane of the sugar residue

The equation of the least-squares plane is

$$0.5055X - 0.2103Y + 0.8367Z = -0.5713.$$

	Deviation (Å)
C(1')	0.012
C(2')	-0.007
C(3')	0.605*
C(4')	0.008
C(5')	0.741*
O(1')	-0.013
O(2')	-1.360*
O(3')	0.283*
O(5')	2.123*

\* Atoms not included in the calculation of the plane.

\* The abbreviation of the original authors.

† For thymine monohydrate, the figures given here are confidence limits estimated by Gerdil and equal to twice the e.s.d.'s obtained from the least-squares method.

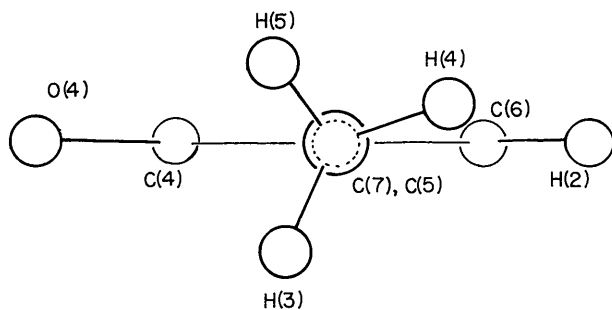


Fig. 6. The view of the C(7) hydrogen atoms looking down the bond C(7)–C(5).

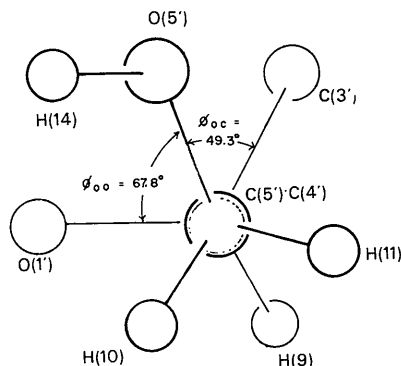


Fig. 7. The conformation of the bond C(5')–C(4').

The torsion angle (Sundaralingam & Jensen, 1965*a*) describing the relative orientation of the sugar and base residues with respect to the glycosidic bond [N(1)–C(1')] is  $-29.4^\circ$ , the *anti* conformation; it lies within the range of values previously observed for pyrimidine nucleosides (Haschemeyer & Rich, 1967). The dihedral angle between the least-squares plane through the six ring atoms of the base and that through the ring atoms of the sugar residue, excluding C(3'), is  $71.9^\circ$ .

For comparison purposes, the structure of the ribose in cytidine (Furberg, Peterson & Rømming, 1965) seems appropriate, and, in fact, the similarities in the geometries of the two residues are striking. Cytidine is also in the *anti* conformation with a torsion angle of  $-18.3^\circ$  (our calculation); and C(3') is displaced *endo* by 0.58 Å. The e.s.d.'s in bond lengths and angles are quoted as about 0.006 Å and 0.5° respectively. Only one of the ribose bond lengths in 5-methyluridine is significantly different from that in cytidine. The bond C(3')–C(4') is 0.030 Å shorter in 5-methyluridine (1.503 Å) than in cytidine (1.533 Å). The next largest difference is 0.019 Å for C(2')–O(2') which is 1.406 Å in 5-methyluridine and 1.425 Å in cytidine. This difference is probably not significant.

The internal ring angles of the ribose in 5-methyluridine do not differ significantly from those determined for cytidine, but four of the external bond angles in the two nucleosides differ by approximately three e.s.d.'s. These angles are, for 5-methyluridine and cytidine in each case, N(1)–C(1')–C(2') (113.4, 111.4°), C(1')–C(2')–O(2') (106.4, 108.9°), C(2')–C(3')–O(3') (110.7,



112.7°) and C(3')-C(4')-C(5') (117.1, 114.8°). Presumably, these quite small differences arise from the different hydrogen-bonding and packing schemes in the crystals. That the modes of puckering of the five-membered rings of the two nucleosides are similar can be seen from a comparison of the torsion angles – the dihedral angle between the planes defined by a bond and its two adjacent ring bonds (Brown & Levy, 1963). These angles are given in Table 8.

Table 8. *Torsion angles in the ribose rings of 5-methyluridine (MUR) and cytidine*

Furberg *et al.* (1965) did not list signs for the torsion angles; we have allocated signs according to the definition of Brown & Levy (1963).

Bond	MUR	Cytidine
C(1')→O(1')	+2.5	+6.1
C(1')→C(2')	-25.5	-28.1
C(2')→C(3')	+38.5	+37.6
C(3')→C(4')	-38.2	-35.1
C(4')→O(1')	+22.5	+18.3

For 5-methyluridine the conformation about the bond C(4')-C(5') can be seen in Fig. 7, which also shows the two projected valency angles  $\varphi_{OO}$  and  $\varphi_{OC}$  (Shefter & Trueblood, 1965). For 5-methyluridine  $\varphi_{OO}=67.8^\circ$  and  $\varphi_{OC}=49.3^\circ$ , the conformation is *gauche-gauche*, with C(5')-O(5') on the same side of the bonds O(1')-C(4') and C(3')-C(4'). Sundaralingam & Jensen (1965*b*) and Shefter & Trueblood (1965) have noted that the *gauche-gauche* conformation occurs most frequently in nucleosides and nucleotides. For cytidine (Furberg *et al.* 1965) we have calculated  $\varphi_{OO}=70.4^\circ$  and  $\varphi_{OC}=47.1^\circ$  with the C(5')-C(4') bond also in the *gauche-gauche* conformation.

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