

## 3-Deazauridine: Crystal Structure, Conformational Parameters, and Molecular Orbital Calculations

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The cytostatic compound 3-deazauridine crystallizes in the orthorhombic space group  $P2_12_12_1$  with four molecules per unit cell of dimensions  $a=13.394$ ,  $b=8.335$ ,  $c=9.639$  Å. On a four-circle diffractometer 998 reflexions were measured. A trial structure was obtained by direct methods and refined by least-squares procedures to  $R = \sum ||F_o| - |F_c|| / \sum |F_o| = 4.0\%$ . The tautomeric form present in the crystal is the enol, 4-hydroxy-1-( $\beta$ -D-ribo-pentafuranosyl)-2-pyridone, which also predominates in solution. Conformational features of the nucleoside include a glycosidic bond conformation in the *anti* range, a ribose moiety in the C(2')-*endo* envelope form and a *gauche-gauche* arrangement about the C(4')-C(5') bond. Pyridone units form endless chains parallel to *c* firmly linked by O(4)-H...O(2) hydrogen bonds only 2.549 Å long. Base planes make a 21° angle with the *ac* plane; stacking interactions appear insignificant. Instead, the chains are tethered at the ribose oxygens by hydrogen bonds involving H(O3') in a bifurcated system as well as H(O2') and H(O5'). The bifurcated hydrogen bond involves a very unusual intramolecular O(3')-H...O(2') and an O(3')-H...O(4) hydrogen bond. Extended Hückel molecular orbital calculations of the electronic properties are reported.

### Introduction

The amino acid sequence of a protein is encoded in the nucleotide sequence of messenger ribonucleic acid (m-RNA). A sequence of three m-RNA nucleotides, the codon, directs the incorporation of one specific amino acid into the protein to be synthesized. The association of the proper amino acid with the m-RNA codon is accomplished at the ribosome with the mediation of transfer ribonucleic acids (t-RNA). Each t-RNA carries an amino acid and contains a nucleotide triplet, the anticodon, which is complementary to the codon specifying that amino acid.

The recognition of the codon by the anticodon involves the formation of three hydrogen-bonded base pairs. Two of the base pairs, those in the 5' and middle positions, must be of the Watson & Crick (1953) type. But the third, according to the 'wobble' theory (Crick, 1966), may be of a different type. The importance of a given proton donor or acceptor group in the formation of codon-anticodon base pairs can be investigated by incorporating chemically modified nucleobases into the codon.

3-Deazauridine, formally derived from uridine (U) by replacement of NH in the 3 position by CH<sub>2</sub>, is such a chemically modified nucleobase. In the binding of phenylalanine specific t-RNA from yeast with UUU as codon to the ribosome, 3-deazauridine may be substituted for U in the 5' and middle positions of the codon but not in the 'wobble' position (Gassen, Schettters & Matthaei, 1972). It was the aim of the X-ray analysis described below to obtain information on hydrogen bonding and stacking properties of 3-deazauridine and to compare them with those of U.

Furthermore, the analogue 3-deazauridine has powerful cytostatic properties (Robins, Currie, Robins & Bloch, 1969). X-ray (Schwalbe, Gassen & Saenger, 1972) and n.m.r. (Currie, Robins & Robins, 1970), evidence shows that the enol tautomer 4-hydroxy-1-( $\beta$ -D-ribo-pentafuranosyl)-2-pyridone is the form found in the crystalline state and predominates in solution. Computerized model studies (Schwalbe, Gassen & Saenger, 1972) demonstrated a possible base pair with two hydrogen bonds between this compound and guanosine or cytidine as well as a somewhat more contorted one with adenosine. Thus a possible role as a cytidine analogue should not be overlooked. We report here the detailed crystal structure parameters as well as a quantum-mechanical evaluation of charge densities and bond overlap populations by the extended Hückel method.

### Experimental

Crystals of 3-deazauridine were grown from water as colourless laths. Crystal data from X-ray photographs and diffractometer measurements are summarized in Table 1. One molecule constitutes the asymmetric unit. Intensity data were collected on a Stoe four circle diffractometer with graphite-monochromatized Cu  $K\alpha$  radiation by a  $\theta$ - $2\theta$  scan technique in which the scan width was  $(80 + 30 \tan \theta)$  steps of  $0.01^\circ$  in  $\theta$  and  $0.02^\circ$  in  $2\theta$ , at 0.6 sec per step. Stationary background counts were taken for 20 sec before and after the scan. By this method 1017 reflexions were measured out to  $\theta = 62.5^\circ$ . The data were corrected for Lorentz and polarization factors and assigned errors,  $\sigma$ , based on counting statistics as well as an allowance of 3% for machine instability (Stout & Jensen, 1968). Three reflexions

with negative net count were thrown out, as were eight reflexions with indices  $h21$  or  $h22$  where machine error was suspected. The remaining 1006 reflexions were used in structure determination. During the late stages of refinement an extinction correction based on a plot of  $I_c/I_o$  versus  $I_c$  was applied and eight reflexions showing serious extinction effects were omitted from the data set. No correction for absorption was made. With crystal dimensions  $0.3 \times 0.15 \times 0.08$  mm and  $\mu = 10.9$   $\text{cm}^{-1}$  the absorption factor applied to  $F$  for straight paths would be  $1.13 \pm 0.08$ .

Table 1. *Crystallographic data (estimated errors given in parentheses)*

Space group  $P2_12_12_1$  (systematic extinctions of  $h00$ ,  $0k0$ ,  $00l$  when non-zero index odd).

$a = 13.394$  (5) Å  
 $b = 8.335$  (3)  
 $c = 9.639$  (4)

Ambient temperature 21 (2)°  
 Graphite monochromatized Cu  $K\alpha$  radiation  $\lambda = 1.5418$  Å  
 Chemical formula  $\text{C}_{10}\text{H}_{13}\text{NO}_6$  (M.W. 243.22)  
 Measured density (cyclohexane/ $\text{CH}_3\text{I}$ ) 1.491 (4)  $\text{g cm}^{-3}$   
 Calculated density ( $Z=4$ ) 1.501  $\text{g cm}^{-3}$   
 $F_{000} = 512$

### Structure determination and refinement

Normalized structure factors (Karle & Hauptman, 1956) were computed by the equation  $E_n = (F_n^2 / \langle F^2 \rangle)^{1/2}$ , where  $\langle F^2 \rangle$  is a local average over  $\frac{1}{20}$  the total range of  $\sin \theta$ . The average values of 0.862 for  $E$  and 0.776 for  $(E^2 - 1)$  are close to the 0.886 and 0.736 expected (Hanic, 1966) for a non-centrosymmetric structure.

A multiple-solution procedure (Main, Germain & Woolfson, 1970) using the tangent formula (Karle & Hauptman, 1956) produced a trial structure very expeditiously from seven starting reflexions, two general and five of restricted phase. Out of 32 starting phase combinations, 2 led to different  $E$  maps (146  $E$ 's) that both revealed all 17 non-hydrogen atoms. Least-squares refinement (Busing, Martin & Levy, 1962) of coordinates as well as isotropic temperature factors in which the function  $\sum 1/\sigma^2 (|F_{\text{obs}}| - 1/K|F_{\text{calc}}|)^2$  was minimized proceeded to convergence at a discrepancy index  $R = \sum ||F_{\text{obs}}| - |F_{\text{calc}}|| / \sum |F_{\text{obs}}|$  of 0.139. Scattering factors were taken from *International Tables for X-ray Crystallography* (1962). Refinement with anisotropic thermal parameters reduced  $R$  to 0.082, at which point all hydrogen atoms appeared in a difference electron-density synthesis at  $0.28$ – $0.60$   $\text{e Å}^{-3}$  compared with background to  $0.27$   $\text{e Å}^{-3}$ . Further refinement of non-hydrogen atoms with anisotropic thermal parameters followed by hydrogen atom coordinates with thermal parameters fixed at those of the attached atoms converged at  $R = 4.0\%$ . At this point, all parameter shifts were  $\frac{1}{3}$  or less the standard deviation for hydrogens and  $\frac{1}{10}$  for non-hydrogen atoms.

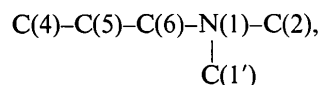
### Results

Observed and calculated structure factors are presented in Table 2, atomic coordinates and thermal parameters in Table 3, and bond angles involving hydrogen atoms in Table 4. Conformationally significant least-squares planes and dihedral angles appear in Tables 5 and 6, respectively. Table 7 characterizes the hydrogen bonds. Figs. 1 and 2 are sketches of 3-deazauridine (D) showing the numbering convention with all bond distances and non-hydrogen atom bond angles. Fig. 3 is a stereoscopic view (Johnson, 1965) of the molecule, in which the ellipsoids of thermal motion follow the 50% probability contour. Fig. 4 is a projection of the crystal structure along the  $b$  axis (molecules related by  $s_b$ , the screw axis with translation along  $\mathbf{b}$ , have been omitted for clarity). Fig. 5 shows a stereo view of the structure along  $c$ .

### Discussion

#### (a) The 3-deazauracil moiety

Inspection of the heterocycle reveals that there is a regular alternation in the C–C bond distances (Fig. 1, labelled D): 1.425 (6), 1.363 (6), 1.422 (6), and 1.361 (6) Å for C(2)–C(3), C(3)–C(4), C(4)–C(5), and C(5)–C(6) respectively. The range is not as great as that between C–C single [1.465 (5) Å], and double [1.336 (5) Å] bond lengths (Sutton, 1965) involving  $sp^2$  hybridized carbon in conjugated dienes; consequently there must be considerable delocalization of electrons. An aromatic C–C bond would be 1.394 (5) Å long. At nitrogen the N(1)–C(2) bond is 0.03 Å longer than N(1)–C(6) despite  $sp^2$  hybridization of both carbons, and 0.08 Å shorter than N(1)–C(1'), where the hybridization is  $sp^3$ . When one compares (Fig. 1) corresponding bonds in the following portion of the heterocycle common to 3-deazauridine (D), cytidine (C) and uridine (U) derivatives (Voet & Rich, 1970):



one finds a maximum variation of 0.02 Å. The changes in positions 3 and 4 have more of an effect on the C(2)–O(2) bond, where the 1.255 (5) observed in D is unusually long. Several observations show that 3-deazauridine exists as the 4-hydroxy tautomeric form in the crystalline state. The C(4)–O(4) distance in D, 1.341 (5) Å, suggests a single bond, although shorter than the aromatic C–OH distance (Sutton, 1965) of 1.36 (1) Å. Further evidence for the enol form is provided by the location and refinement of hydrogen atoms H(3) and H(O4), and by the strict planarity of the heterocyclic ring (Table 5). C(3) deviates only 0.028 Å from the C(4)–C(5)–C(6)–N(1)–C(2) plane, and H(3) is only 0.13 Å out of this plane. If there were a  $\text{CH}_2$  group at position 3, there would be no reason for C(3) to lie strictly in the plane, and its attached hydrogens should be at least 0.7 Å out of plane.

Table 2. Observed and calculated structure factors ( $\times 10$ )

Table with 48 columns (H, K, L, F\_OBS, F\_CAL) and 48 rows of numerical data representing structure factors.

Table 3. Fractional atomic coordinates and anisotropic thermal parameters in the form

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

Estimated standard deviations are in parentheses

	<i>x</i>	<i>y</i>	<i>z</i>	$\beta_{11}$	$\beta_{22}$	$\beta_{33}$	$\beta_{12}$	$\beta_{13}$	$\beta_{23}$
N(1)	0.0367 (2)	0.4422 (3)	0.1321 (2)	28 (1)	126 (4)	62 (2)	4 (2)	-0 (2)	-2 (3)
C(2)	0.1338 (2)	0.4893 (4)	0.1616 (3)	32 (1)	141 (5)	73 (3)	-7 (2)	8 (2)	-6 (3)
O(2)	0.1862 (2)	0.5465 (4)	0.0657 (2)	39 (1)	318 (7)	80 (3)	-37 (3)	3 (2)	18 (3)
C(3)	0.1658 (2)	0.4713 (4)	0.3017 (3)	28 (1)	145 (5)	78 (3)	-13 (2)	-1 (2)	-20 (4)
C(4)	0.1022 (2)	0.4172 (4)	0.4018 (3)	34 (1)	105 (4)	71 (3)	-0 (2)	-2 (2)	-6 (3)
O(4)	0.1270 (2)	0.4065 (3)	0.5362 (2)	36 (1)	170 (4)	65 (2)	-13 (2)	-9 (1)	-2 (3)
C(5)	0.0030 (2)	0.3720 (4)	0.3666 (3)	35 (2)	146 (5)	71 (3)	-7 (2)	4 (2)	3 (3)
C(6)	-0.0260 (2)	0.3856 (4)	0.2318 (3)	30 (2)	133 (5)	76 (3)	-7 (2)	0 (2)	1 (3)
C(1')	-0.0011 (2)	0.4572 (4)	-0.0102 (3)	29 (1)	117 (4)	67 (3)	-3 (2)	-0 (2)	9 (3)
O(1')	-0.0901 (2)	0.5456 (2)	-0.0073 (2)	48 (1)	111 (3)	99 (3)	17 (2)	-11 (2)	-9 (2)
C(2')	-0.0273 (2)	0.2974 (4)	-0.0777 (3)	34 (2)	115 (4)	69 (3)	9 (2)	2 (2)	-2 (3)
O(2')	0.0602 (2)	0.2305 (3)	-0.1360 (2)	40 (1)	181 (4)	90 (2)	26 (2)	-3 (2)	-30 (3)
C(3')	-0.1034 (2)	0.3502 (4)	-0.1849 (3)	34 (1)	132 (5)	67 (3)	-5 (2)	-0 (2)	8 (3)
O(3')	-0.0543 (2)	0.4116 (3)	-0.3049 (2)	42 (1)	206 (4)	67 (2)	9 (2)	3 (1)	23 (3)
C(4')	-0.1583 (2)	0.4867 (4)	-0.1119 (3)	33 (2)	146 (5)	80 (3)	10 (2)	1 (2)	29 (4)
C(5')	-0.2556 (3)	0.4402 (5)	-0.0457 (4)	40 (2)	193 (6)	117 (4)	31 (3)	15 (2)	31 (5)
O(5')	-0.2377 (2)	0.3097 (4)	0.0473 (3)	47 (1)	227 (5)	159 (4)	-2 (2)	20 (2)	81 (4)
H(3)	0.233 (3)	0.491 (5)	0.321 (4)	28	145	78	-13	-1	-20
H(O4)	0.188 (3)	0.428 (5)	0.558 (4)	36	170	65	-13	-9	-2
H(5)	-0.042 (3)	0.338 (5)	0.437 (4)	35	146	71	-7	4	3
H(6)	-0.095 (3)	0.358 (5)	0.198 (4)	30	133	76	-7	0	1
H(1')	0.050 (3)	0.509 (5)	-0.063 (4)	29	117	67	-3	-0	9
H(2')	-0.060 (3)	0.216 (4)	-0.017 (4)	34	115	69	9	2	-2
H(O2')	0.042 (3)	0.139 (5)	-0.155 (4)	40	181	90	26	-3	-30
H(3')	-0.154 (3)	0.271 (4)	-0.206 (4)	34	132	67	-5	-0	8
H(O3')	-0.001 (3)	0.354 (5)	-0.301 (4)	42	206	67	9	3	23
H(4')	-0.169 (3)	0.574 (5)	-0.187 (4)	33	146	80	10	1	29
H(5')	-0.282 (3)	0.542 (6)	0.006 (4)	40	193	117	21	15	31
H(5 <sub>1</sub> )	-0.304 (3)	0.417 (6)	-0.120 (5)	40	193	117	21	15	31
H(O5')	-0.301 (3)	0.274 (6)	0.061 (5)	47	227	159	-2	20	81

Table 4. Bond angles involving hydrogen atoms

H(3)—C(3)—C(2)	117°
H(3)—C(3)—C(4)	121
H(O4)—O(4)—C(4)	117
H(5)—C(5)—C(4)	120
H(5)—C(5)—C(6)	122
H(6)—C(6)—C(5)	124
H(6)—C(6)—N(1)	114
H(1')—C(1')—N(1)	107
H(1')—C(1')—O(1')	112
H(1')—C(1')—C(2')	110
H(2')—C(2')—C(1')	116
H(2')—C(2')—O(2')	109
H(2')—C(2')—C(3')	108
H(O2')—O(2')—C(2')	102
H(3')—C(3')—C(2')	115
H(3')—C(3')—C(4')	106
H(O3')—O(3')—C(3')	98
H(4')—C(4')—C(3')	105
H(4')—C(4')—O(1')	109
H(4')—C(4')—C(5')	111
H(5 <sub>1</sub> )—C(5')—C(4')	107
H(5 <sub>2</sub> )—C(5')—C(4')	108
H(5 <sub>1</sub> )—C(5')—O(5')	112
H(5 <sub>2</sub> )—C(5')—O(5')	114
H(5 <sub>1</sub> )—C(5')—H(5 <sub>2</sub> )	107
H(O5')—O(5')—C(5')	101

## (b) Ribose

The ribose conformation is a prime example of the C(2')-endo envelope form. No bond distance varies more than 0.017 Å from the average over three other C(2')-endo nucleosides (Saenger & Eckstein, 1970).

Table 5. Least-squares planes through heterocycles and riboses

The plane equations are of the form  $lX + mY + nZ + p = 0$  where  $X, Y, Z$  are along  $a, b$  and  $c$ . Atoms which define the planes are marked by \*.

Moiety	Plane coefficients	Atom	Deviation from plane (Å)
Heterocycle	$l = -0.3165$ $m = 0.9312$ $n = 0.1809$ $p = -3.5093$	N(1)*	-0.002
		C(2)*	0.003
		O(2)	0.058
		C(3)	-0.028
		C(4)*	-0.004
		O(4)	0.042
		C(5)*	0.005
		C(6)*	-0.002
		C(1')	0.026
		C(2')	-1.232
Ribose	$l = 0.3823$ $m = 0.6497$ $n = -0.6571$ $p = -2.5366$	H(3)	-0.13
		H(O4)	-0.01
		H(5)	0.06
		H(6)	0.02
		C(1')*	-0.002
		C(2')	-0.573
		C(3')*	0.002
		C(4')*	-0.003
		O(1')*	0.003
		O(2')	-0.119
		O(3')	1.345
		C(5')	-1.172
		O(5')	-2.376

The O(1')—C(4') bond is longer than the O(1')—C(1'), as usual. Bond angles (Fig. 2) differ from average values by no more than 1.0° except for the following angles,

Table 6. *Endocyclic and exocyclic dihedral angles within the ribose unit*

C(6)–N(1)–C(1')–C(2')	–65.3°
C(6)–N(1)–C(1')–O(1')	+52.3
C(2)–N(1)–C(1')–C(2')	+116.3
C(2)–N(1)–C(1')–O(1')	–126.2
N(1)–C(1')–C(2')–O(2')	–84.7
N(1)–C(1')–C(2')–C(3')	+155.3
O(1')–C(1')–C(2')–O(2')	+156.1
O(1')–C(1')–C(2')–C(3')	+36.1
C(1')–C(2')–C(3')–C(4')	–35.2
O(2')–C(2')–C(3')–O(3')	–35.2
C(1')–C(2')–C(3')–O(3')	+81.2
O(2')–C(2')–C(3')–C(4')	–151.7
C(2')–C(3')–C(4')–O(1')	+23.2
C(2')–C(3')–C(4')–C(5')	–98.0
O(3')–C(3')–C(4')–C(5')	+144.7
O(3')–C(3')–C(4')–O(1')	–94.1
O(1')–C(4')–C(5')–O(5')	–63.9
C(3')–C(4')–C(5')–O(5')	+55.1
C(3')–C(4')–O(1')–C(1')	+0.5
C(5')–C(4')–O(1')–C(1')	+124.0
C(4')–O(1')–C(1')–C(2')	–22.6
C(4')–O(1')–C(1')–N(1)	–145.2

which may well be influenced by the tug on hydrogen-bonded oxygens: C(1')–C(2')–O(2'), 108.9° (3) in *D* versus an average 112.1°; C(2')–C(3')–C(4'), 103.1° (3) vs. 101.1°; C(2')–C(3')–O(3'), 110.3° (3) vs. 108.3°; and C(4')–C(5')–O(5'), 108.5° (3) vs. 112.7°. One (least-squares) plane passes within 0.003 Å of atoms C(1'), O(1'), C(4'), and C(3') but misses C(2') by 0.57 Å. The dihedral angle O(2')–C(2')–C(3')–O(3') is –35.2°. Atom O(5') is located 'above' the ribose ring, as indicated by the dihedral angles O(5')–C(5')–C(4')–O(1') of –63.9° and O(5')–C(5')–C(4')–C(3') of 55.1°. The relation of ribose to base is specified by the dihedral angle C(2')–C(1')–N(1)–C(6), which is –65.3°. This value falls comfortably within the *anti* range (Saenger & Scheit, 1970), the usual one for pyrimidine nucleosides.

### (c) Packing arrangement

The segregation of hydrophobic and hydrophilic zones that is so frequently found in nucleoside crystals (Saenger & Suck, 1972) also occurs in 3-deazauridine but in an unusual manner. Whereas the hydrophobic zones are usually pillars of stacked bases, here the hydrophobic structural elements are undulating endless chains of bases produced by the action of  $s_c$ , the two-fold screw axis with translation along *c* (Fig. 4). Bases in the chain are linked by a short (2.549 Å) and presumably very strong hydrogen bond between the 4-hydroxyl

group and the 2-keto group of the screw-related neighbour molecule. The geometry of this hydrogen bond can be further described by the following distances: O(4)–H(O4), 0.94 Å; H(O4)–O(2<sub>s<sub>c</sub></sub>), 1.70 Å; and angles: H(O4)–O(4)–O(2<sub>s<sub>c</sub></sub>), 4°; C(4)–O(4)–O(2<sub>s<sub>c</sub></sub>), 109.9°. This arrangement, with H(O4) almost directly on the O(4)···O(2<sub>s<sub>c</sub></sub>) line and the bond angle at O(4) just a little greater than tetrahedral should be energetically favorable. Individual base planes in the hydrophobic bands, shaded in Fig. 4 to show their orientation, make 21° angles with the *ac* plane. Through the action of the twofold screw axis with translation along *b* an overlap of bases is produced (omitted from Fig. 4 for clarity), but at an angle of 42° which precludes the typical stacking interactions. These two bases form a pair of hydrophobic jaws that grasp the hydrophobic C(5') methylene group from a neighbouring ribose, but not the hydrophilic O(5'). Thus continuity of the hydrophobic region along the *b* direction is preserved. Most nucleoside crystals contain parallel-stacked bases; 5,6-dihydrouridine (Suck, Saenger & Zechmeister, 1972), does not because the planar aromatic system has been broken up, and 5'-methylammonium-5'-deoxyadenosine iodide monohydrate (Saenger, 1971) does not presumably because of interaction between adenine heterocycles and iodide ions. In the present case hydrogen bonding is optimized, hydrophobic interaction is preserved, but polarization interactions are sacrificed.

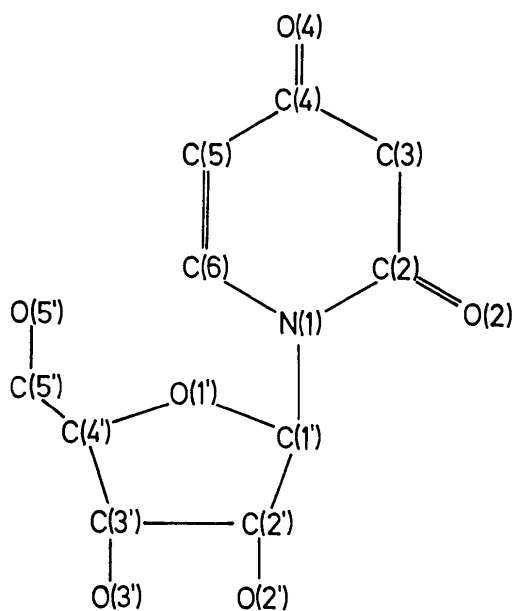
The hydrophilic groups form an intricate network of hydrogen bonds (Table 7) involving every hydroxyl group: O(2')–H(O2')···O(3'<sub>s<sub>b</sub></sub>), O(5')–H(O5')···O(2'<sub>s<sub>b</sub></sub>), and an unusual bifurcated system in which H(O3') is in the neighborhood both of O(2') in the same molecule and of O(4) in the molecule in the next unit cell along *c*. The intramolecular O(3')–H···O(2') hydrogen bond is most unusual and, to our knowledge, has not been observed in nucleoside crystal structures previously.

### Molecular orbital calculations

To investigate the electronic properties of 3-deazauridine, extended Hückel (Hoffman, 1963) calculations were carried out. Although it is well known that the charge separations obtained by this method are exaggerated and the total overlap populations depend significantly on the parametrization, comparisons among closely related molecules are reliable. Good comparison standards are available in uridine and cytidine (Jordan & Pullman, 1968, abbreviated JP)

Table 7. *Distances and angles that characterize the hydrogen bonds*

Donor (D)	Acceptor (A)	A position			Distance (Å) D···A	Distance (Å) H···A	Angle (°) H···A···D
		$\frac{1}{2}-x$	$1-y$	$\frac{1}{2}+z$			
O(4)	O(2)	$\frac{1}{2}-x$	$1-y$	$\frac{1}{2}+z$	2.549	1.70	4
O(2')	O(3')	$-x$	$-\frac{1}{2}+y$	$-\frac{1}{2}-z$	2.719	1.94	6
O(3')	O(2')	$x$	$y$	$z$	2.699	2.06	14
O(3')	O(4)	$x$	$y$	$-1+z$	2.871	2.36	15
O(5')	O(2')	$-\frac{1}{2}+x$	$\frac{1}{2}-y$	$-z$	2.858	1.99	7



and adenosine (Boyd & Lipscomb, 1969, abbreviated BL). Two calculations were performed, one with the input parameters of JP and one with those of BL (Table 8; results labelled JP and BL respectively in Fig. 6). Atomic coordinates were taken from the crystal structure, overlap integrals  $S_{ij}$  for the Slater basis orbitals were calculated directly, diagonal Hamiltonian matrix elements  $H_{ii}$  were set equal to the negative of the corresponding valence state ionization potential (VSIP), and off-diagonal elements  $H_{ij}$  were approximated by the Wolfsberg & Helmholz (1952) equation  $H_{ij} = 0.5 K \cdot S_{ij} \cdot (H_{ii} + H_{jj})$  with  $K = 1.75$  for JP and 2.00 for BL.

Table 8. Input parameters for extended Hückel calculations on 3-deazauridine

	Orbital exponent		VSIP (eV)			
	JP	BL	JP		BL	
	<i>s, p</i>	<i>s, p</i>	<i>s</i>	<i>p</i>	<i>s</i>	<i>p</i>
H	1.000	1.200	13.60		13.60	
C	1.625	1.625	21.40	11.40	21.40	11.40
N	1.950	1.950	26.00	13.40	26.00	13.40
O	2.275	2.275	35.30	17.76	37.59	14.62

The charge densities (Mulliken, 1955) calculated by these methods are presented in Fig. 6. Although the oxygen atoms attain a greater negative charge with JP parameters than with BL, there are no differences in the conclusions to be drawn. The base receives electron density from the ribose and carries a delocalized charge of  $-0.27 e$  for JP and  $-0.23 e$  for BL, virtually the same as the  $-0.27 e$  in C,  $-0.28 e$  in U, and  $-0.22 e$  in adenosine. Oxygen atom O(2) is definitely the most negative site in the molecule, followed by ribose

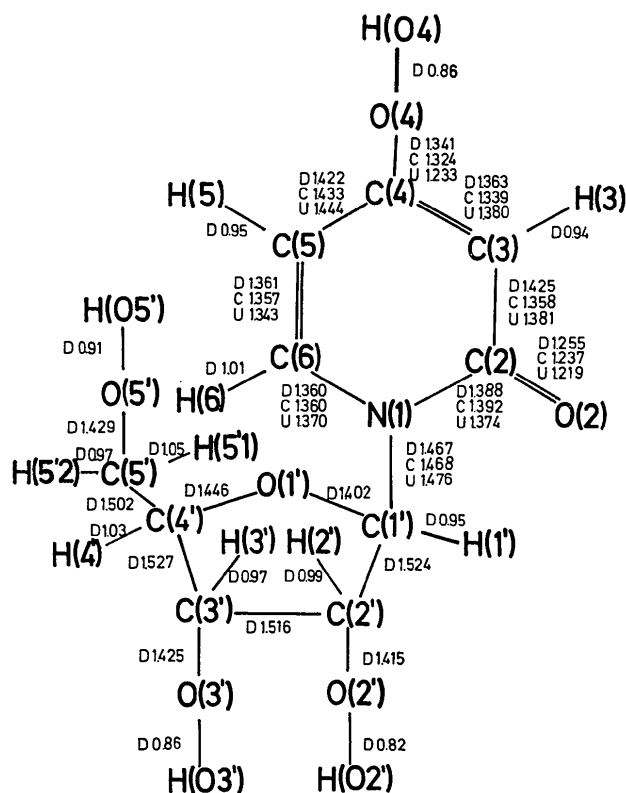


Fig. 1. Chemical structure, numbering convention, and bond distances in 3-deazauridine (Å). Estimated standard deviations are 0.005–0.006 Å except when a hydrogen atom is involved, when it is 0.05–0.08 Å. Average distances in cytosine (C) and uridine (U) derivatives (Voet & Rich, 1970) are given for comparison; C(3) is replaced by nitrogen in both C and U, and O(4) is changed to nitrogen in C.

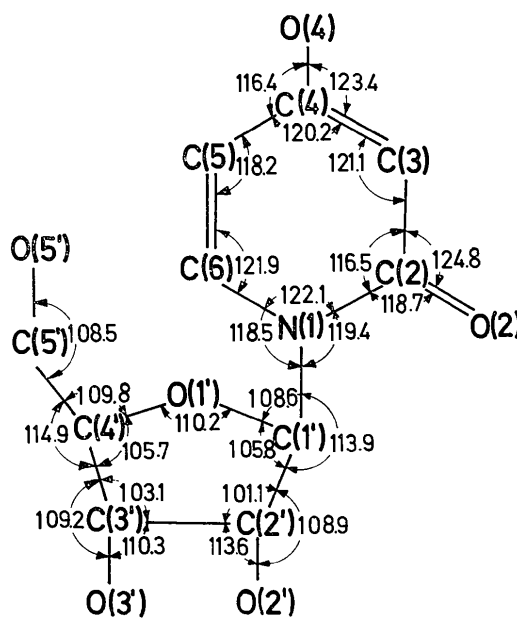


Fig. 2. Bond angles in 3-deazauridine (estimated standard deviations 0.3°).

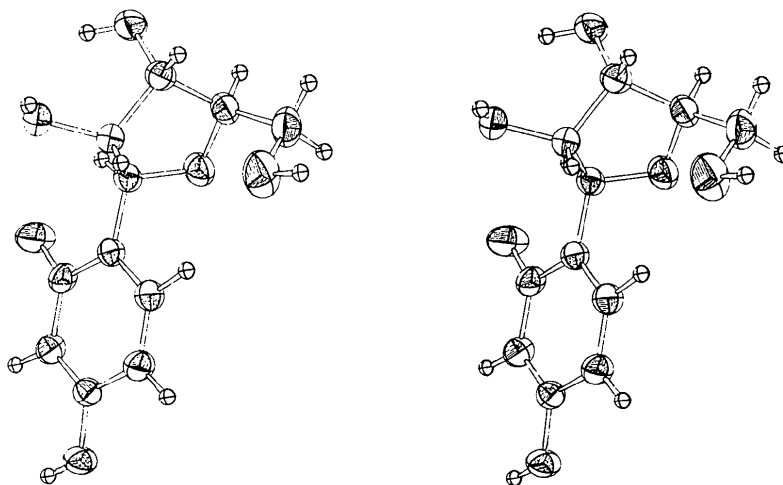


Fig. 3. Stereoview of 3-deazauridine drawn with the program *ORTEP* (Johnson, 1965). Thermal ellipsoids correspond to 50% probability.

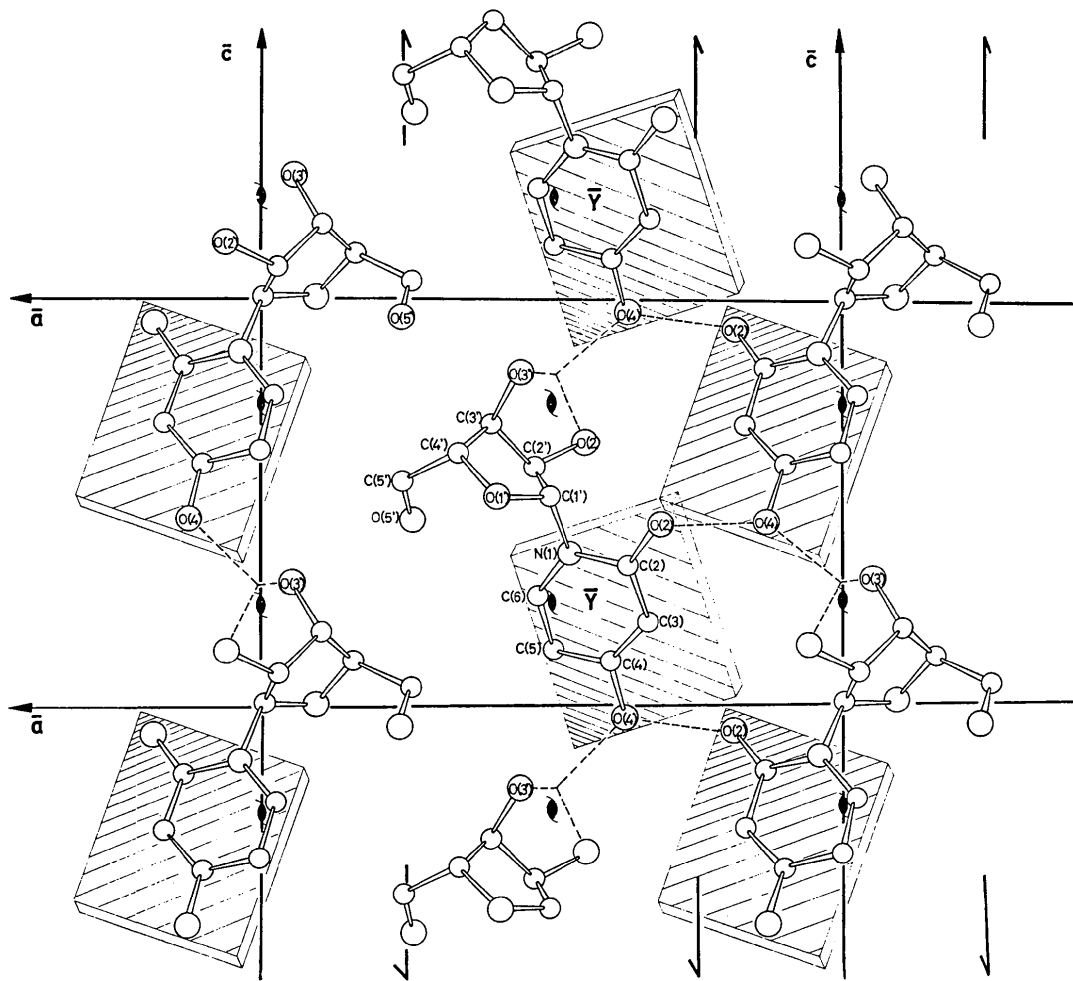


Fig. 4. Packing of molecules in the crystal as viewed along *b*. Molecules related by the screw axis with translation along *b* are not shown.

oxygens; O(4) is less negative. It is clear that O(2) can serve as an excellent hydrogen-bond acceptor for H(O4). The pattern of charges around the D heterocycle is not significantly different from C and U in the common C(5)–C(6)–N(1) portion. In D, carbon C(2) bears less of a positive charge than in C (+1.39 e) and U (+1.37 e). However, O(2) is similar in D, C (–1.42 e), and U (–1.42 e). At the 3-position of D the charge is similar to that on the imino nitrogen of U (–0.37 e) but not on the ring nitrogen of C (–1.02 e). On the other hand, conditions at the 4-position of D resemble those in C [+0.77 e on C(4), –0.67 e on N(4)] somewhat more than U [+1.18 e on C(4), –1.39 e on O(4)]. The H(O4) of D is more positive than either amino hydrogen of C (+0.36 e, +0.33 e).

Total overlap populations (Mulliken, 1955) show greater overlap to oxygen with BL than with JP parameters but excellent agreement otherwise (Fig. 6). The alternation in bond overlap population in the C–C bonds of the heterocycle follows that in bond distance; all these C–C bonds have greater overlap populations than the authentic C–C single bonds in the ribose. The overlap populations in the N(1)–C(2) and N(1)–C(6) bonds are almost equal despite the greater length of N(1)–C(2). The only unambiguous changes in bond-overlap populations among D, C and U involve bonds where a substitution of atoms has taken place.

In summary, the polar groups of D resemble those of C but with enhanced polarity at site 4. The ring system has characteristics all its own. The possibilities

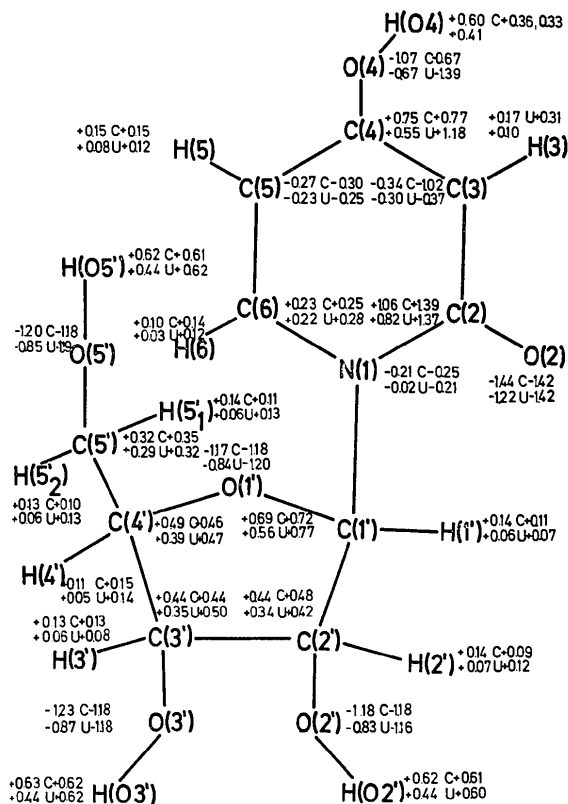


Fig. 6. Mulliken net charges for 3-deazauridine with JP (upper) and BL (lower) parameters, compared with those in C and U.

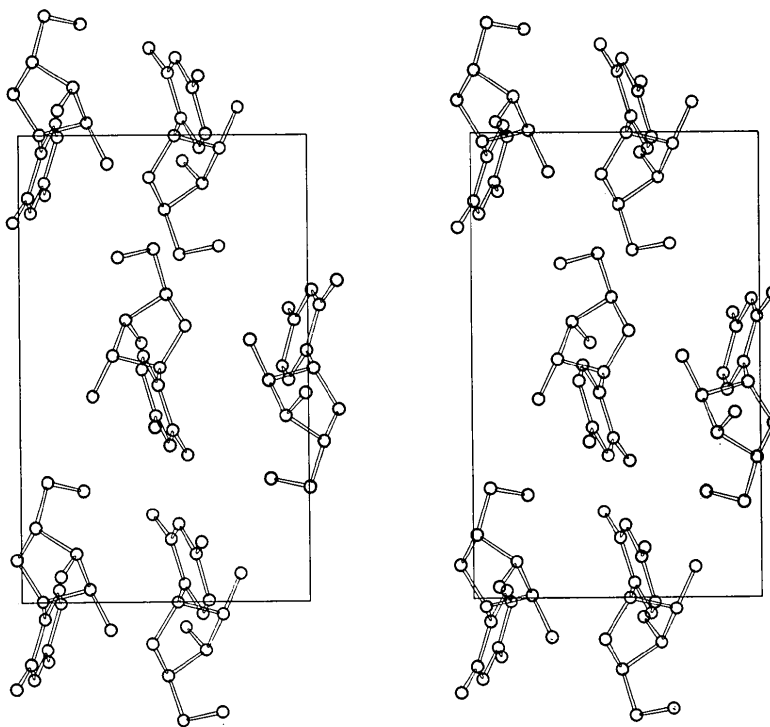


Fig. 5. ORTEP stereoview of the unit cell contents projected along *c*.



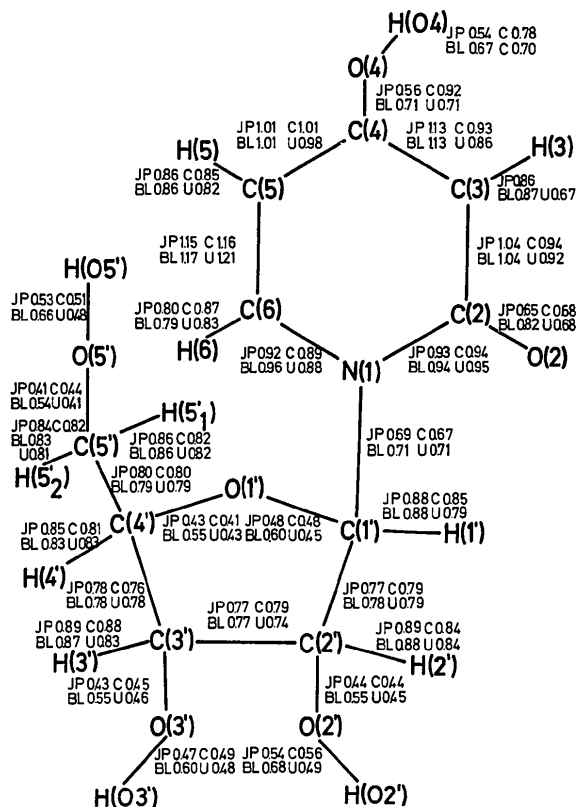


Fig. 7. Mulliken overlap populations in the bonds of 3-deaza-uridine with JP and BL parameters, compared with C and U.

for D to base pair with A, G and C have been discussed previously (Schwalbe, Gassen & Saenger, 1972).

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