

The Crystal Structure of Cytosine-5-Acetic Acid*

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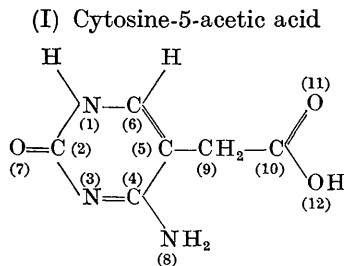
(Received 14 June 1961)

The crystal structure of cytosine-5-acetic acid has been determined and refined by three-dimensional Fourier and least-squares methods. The crystals are monoclinic with space group $P2_1/c$. The unit-cell dimensions are $a = 10.93$, $b = 5.02$, $c = 14.04$ Å, $\alpha = 114.7^\circ$.

An unusual feature of the structure is the formation of two 'symmetric' hydrogen bonds, each between a pair of equivalent atoms related to one another by centers of symmetry. As a result, in one half the molecules in the crystal the proton on oxygen atom O_{12} of the carboxyl group is transferred to the ring nitrogen atom N_3 , resulting in a zwitterion; the remaining half of the molecules are uncharged. The protons on the N_3 and O_{12} atoms appear not to lie on the centers of symmetry but to be randomly distributed between sites closer to one or the other atom in each pair, and the hydrogen bonds are only statistically symmetric.

Introduction

The current surge of interest in the structure of the nucleic acids has prompted attempts to determine the crystal structures of a considerable number of purines, pyrimidines, and related compounds. Recently Prof. James English of the Department of Chemistry, Yale University, made available to us a large number of organic chemicals prepared in the laboratories of the late Prof. Treat B. Johnson. Among them was the 5-acetic acid derivative of cytosine (I). (For its preparation, see Johnson, 1911). We have undertaken an X-ray diffraction investigation of the crystal structure of this compound, using three-dimensional techniques and Fourier and least-squares refinement methods.



Experimental

Repeated recrystallization from hot water yielded rectangular plates with principal faces (100); the plates were usually elongated in the b direction. The unit-cell dimensions and space group were determined

from oscillation and zero- and first-layer Weissenberg photographs about the b axis, calibrated with NaCl powder. The density was measured by flotation in a mixture of bromoform and carbon tetrachloride. The results are listed in Table 1, where the uncertainties are estimated standard deviations.

Table 1. *Crystal data for cytosine-5-acetic acid*

($\lambda_{Cu K\alpha} = 1.5418$ Å)

Monoclinic; space group, $P2_1/c$

$a = 10.930 \pm 0.006$ Å

$b = 5.016 \pm 0.008$ Å

$c = 14.042 \pm 0.005$ Å

$\beta = 114.69 \pm 0.03^\circ$

$V = 699.5$ Å³; $Z = 4$

$\rho_o = 1.611 \pm 0.006$ g.cm.⁻³

$\rho_c = 1.606 \pm 0.004$ g.cm.⁻³

For intensity purposes, layer lines 0–4 about the b axis and 0–9 about the a axis were recorded on equi-inclination Weissenberg photographs taken with copper radiation. By this means all of the effective copper diffraction sphere was surveyed; of a total of approximately 1500 reflections within the sphere, 1258 were of measurable intensity. Intensities were estimated visually by two authors (R. B. and R. M.) and were scaled independently. A comparison of the two resulting sets of observed structure factors showed that the pattern of differences could be approximated by the expression

$$|\Delta F| (= |F_{R.B.} - F_{R.M.}|) = 0.30 + 0.06|\bar{F}|;$$

the average discrepancy between the two sets of observations was about 9%. The foregoing expression was the basis of the weighting function used in the final least-squares refinements.

The quality of the photographs was not particularly good, especially for the higher layer lines about b . Apparently the crystals were slightly deformed, for

* Contribution No. 2713 from the Gates and Crellin Laboratories of Chemistry. This investigation was supported in part by Research Grant H-2143 from the National Heart Institute, Public Health Service.

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in certain regions the high-angle reflections were quite diffuse while in other regions they were exceptionally sharp. As a result, the agreement between the two sets of observations is somewhat worse than usual, and systematic errors in the estimated intensities are to be feared.

Determination of the structure

In an initial attempt to determine the approximate structure by two-dimensional methods, sharpened and unsharpened Patterson projections on (010) were calculated. The sharpened projections gave clear evidence as to the orientation of the pyrimidine ring and also indicated the probable positions of the atoms adjacent to the ring. Several peaks on the unsharpened projection were possible candidates for the inter-ring vector. One of these peaks was particularly promising in that the resulting structure had the hydrogen-bond system which we had anticipated, two carboxyl groups being paired about one center of symmetry and two *cis*-amide groups being paired about another center. A great deal of time and effort was spent in attempting to prove the correctness of this or of related structures, with no success. We finally abandoned hope of solving the structure by two-dimensional methods and calculated the sharpened three-dimensional Patterson function.

The three-dimensional function confirmed the assumed orientation of the pyrimidine ring. In addition, a peak along the line $u=w=0$ suggested that two atoms (by necessity, because of the shortness of the b axis and the geometry of the molecule, a carbon and oxygen atom of the carboxyl group) are superposed in the (010) projection. With this 'heavy atom' as a guide, the Patterson projection was again examined. The orientation of the entire molecule was now readily deduced and enough intermolecular vectors could be found to delineate the entire structure.

Two cycles of structure-factor electron-density calculations based on the $h0l$ data confirmed the structure and led to approximate x and z coordinates for all the atoms. Approximate y coordinates were deduced from geometric considerations in conjunction with the three-dimensional Patterson function. Attention was then turned to the three-dimensional data.

Refinement of the parameters

Initial refinement of the structure was carried out on a Burroughs 205 computer. Seven structure-factor least-squares cycles, including the weighting function suggested by Hughes (1941), were calculated, the R factor dropping from 0.28 to 0.15. During the first three cycles only the positional parameters of the heavy atoms were adjusted; individual anisotropic temperature parameters were included in the last four cycles.

Computations were then transferred to a Burroughs

220 computer. Two cycles of differential syntheses were followed by three structure-factor difference-map cycles during which preliminary parameters were assigned to the hydrogen atoms. On these difference maps, six of the seven hydrogen atoms showed up as pronounced maxima near the anticipated positions. The hydrogen atom of the carboxyl group, however, appeared only as a low, diffuse area near O_{12} . We had already noted that two O_{12} atoms related to one another by a center of symmetry are only about 2.5 Å apart, suggesting that there is one but not two protons between them; in addition, two N_3 atoms of the pyrimidine ring, also related by a center of symmetry, are only 2.8 Å apart, again suggesting that a single hydrogen atom is between them. This situation can arise if, in one-half the molecules in the crystal, the proton of the carboxyl group migrates from O_{12} to N_3 , leaving a single proton for each pair of O_{12} atoms and furnishing a single proton to each pair of N_3 atoms. These protons could either lie on the two centers of symmetries, forming symmetric hydrogen bonds between the two pairs of atoms, or be statistically distributed between two positions closer to one or the other atom in each pair.* The difference maps provided some indication that the second condition obtains, there being diffuse regions near O_{12} and N_3 rather than sharp peaks at the centers of symmetry. Accordingly, two sets of half-weight hydrogen atoms (labeled H_2 and H_3) were placed in general positions near N_3 and O_{12} .

Refinement was completed with seven least-squares cycles in which the positional parameters of all the atoms as well as anisotropic temperature parameters for the heavy atoms were adjusted; the temperature factors of the hydrogen atoms were held constant and isotropic, with $B=3.0$. The quantity minimized in the least-squares calculations was $\sum w(F_o^2 - F_c^2)^2$, and a weighting function was chosen to represent the uncertainties in F_o^2 ; the expression was

$$\sqrt{w} = 1/(0.6F_o + 0.12F_o^2)$$

(see Experimental). Auxiliary weights were assigned to individual reflections to allow for the number of observations or, to some extent, for abnormal spot shape.

At the conclusion of the refinement two Fourier syntheses were calculated: an electron-density projection onto (010) and a three-dimensional difference map for which the contributions of the hydrogen atoms were omitted from the F_c 's. These syntheses are shown in Figs. 1 and 2.

The final positional and temperature-factor parameters of the heavy atoms are listed in Table 2; the parameters of the hydrogen atoms are listed in Table 3.

* A third possibility—that the protons occupy ordered positions not at the centers of symmetry, and hence do not conform to the symmetry of the space group—can probably be ruled out by the complete absence of reflections extinguished by the space-group symmetry.

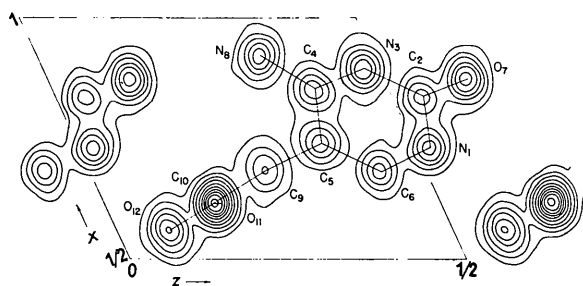


Fig. 1. The electron density projected onto (010). Contours are at intervals of $2 \text{ e.}\text{\AA}^{-2}$ beginning with $2 \text{ e.}\text{\AA}^{-2}$.

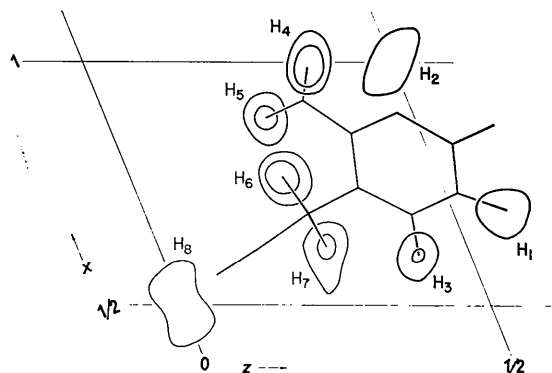


Fig. 2. A composite representation of the final three-dimensional difference map in which the hydrogen contributions were omitted from the F_c 's. Contours are at 0.2 and 0.4 $\text{e.}\text{\AA}^{-3}$.

The calculated and observed structure factors are listed in Table 4.

The final R factor for 1255 observed reflections of non-zero weight is 0.096, and the standard deviation of an observation of unit weight (Peterson & Levy, 1957) is 1.6. The deviation of this latter value from unity implies discrepancies that are not accounted for by the statistics of observation, and we feel that these discrepancies are primarily due to systematic observational errors caused by the deformed crystals. As a result, we fear that the temperature parameters in particular may be in error by amounts appreciably

larger than the standard deviations reported in Table 2, which were calculated from the least-squares residuals and hence imply random errors. More will be said of this later.

Table 3. *Hydrogen atom coordinates and their standard deviations*

All values have been multiplied by 10^3

Atom	Bonded to	$x (\sigma_x)$	$y (\sigma_y)$	$z (\sigma_z)$
H ₁	N ₁	700(6)	623(11)	565(5)
(½)H ₂	N ₃	973(14)	951(27)	489(13)
H ₃	C ₆	613(6)	352(11)	419(4)
H ₄	N ₈	993(6)	791(13)	356(5)
H ₅	N ₈	885(6)	606(12)	261(4)
H ₆	C ₉	763(6)	228(13)	255(4)
H ₇	C ₉	622(6)	190(12)	269(4)
(½)H ₈	O ₁₂	521(13)	500(29)	036(7)

The final parameters of the hydrogen atoms differ by a maximum of 0.1 Å from those originally derived from the difference map. The coordinates of H₂ and H₈ are very uncertain, and their inclusion as parameters in the least-squares calculations probably was not justified; however, the final values are not far from those that would be predicted from geometrical considerations.

Discussion of the results

(i) *The geometry of the molecule*

An outstanding feature of the crystal structure of cytosine-5-acetic acid is the partial transfer of the proton H₈ from the carboxyl group of the acetic acid side chain to the nitrogen atom N₃ of the pyrimidine ring. This transfer takes place in one-half of the molecules in the crystal; for the other half the proton remains on the carboxyl oxygen atom O₁₂. As a result, a single proton (H₂) is shared by a pair of nitrogen atoms N₃ related to each other by a center of symmetry; similarly, another proton (H₈) is shared by a pair of oxygen atoms O₁₂ related to each other by another center. Half the molecules in the crystal are zwitterions, and half are uncharged.

The bond distances and angles calculated from the

Table 2. *The final heavy-atom parameters and their standard deviations*

All values have been multiplied by 10^4 . The temperature factors are in the form

$$T_i = \exp(-\alpha_i h^2 - \beta_i k^2 - \gamma_i l^2 - \delta_i hk - \epsilon_i hl - \eta_i kl)$$

Atom	$x (\sigma_x)$	$y (\sigma_y)$	$z (\sigma_z)$	$\alpha (\sigma_\alpha)$	$\beta (\sigma_\beta)$	$\gamma (\sigma_\gamma)$	$\delta (\sigma_\delta)$	$\epsilon (\sigma_\epsilon)$	$\eta (\sigma_\eta)$
N ₁	7313(3)	6317(7)	5213(2)	76(4)	344(15)	27(2)	-73(11)	52(4)	-41(7)
C ₂	8351(4)	8027(7)	5434(3)	75(4)	301(16)	25(2)	-63(11)	51(4)	-24(8)
N ₃	8962(3)	8098(7)	4762(2)	83(4)	328(14)	24(2)	-69(10)	56(4)	-46(7)
C ₄	8526(4)	6586(7)	3883(2)	68(4)	261(14)	22(2)	-5(11)	39(4)	-5(7)
C ₅	7399(4)	4849(7)	3625(2)	79(4)	227(14)	23(2)	-15(10)	38(4)	2(7)
C ₆	6829(4)	4808(8)	4323(3)	81(4)	307(17)	32(2)	-74(12)	41(5)	-32(9)
O ₇	8726(3)	9523(6)	6217(2)	110(4)	453(15)	31(2)	-173(12)	84(4)	-102(8)
N ₈	9206(3)	6749(8)	3296(2)	80(4)	476(18)	28(2)	-67(13)	59(4)	-61(9)
C ₉	6857(4)	3236(7)	2638(3)	95(5)	224(14)	30(2)	-20(12)	43(5)	-33(8)
C ₁₀	6172(4)	4875(7)	1643(3)	65(4)	269(15)	30(2)	-16(11)	37(4)	-21(8)
O ₁₁	6181(3)	7331(5)	1680(2)	100(3)	232(11)	35(2)	55(9)	38(4)	-10(6)
O ₁₂	5601(3)	3545(6)	0783(2)	123(4)	310(13)	27(2)	-79(11)	26(4)	-51(6)

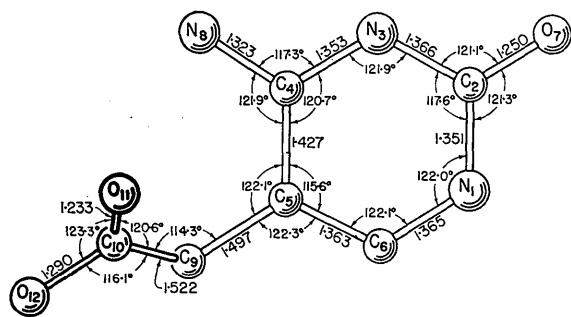


Fig. 3. Bond distances and angles. The distances have not been corrected for libration effects.

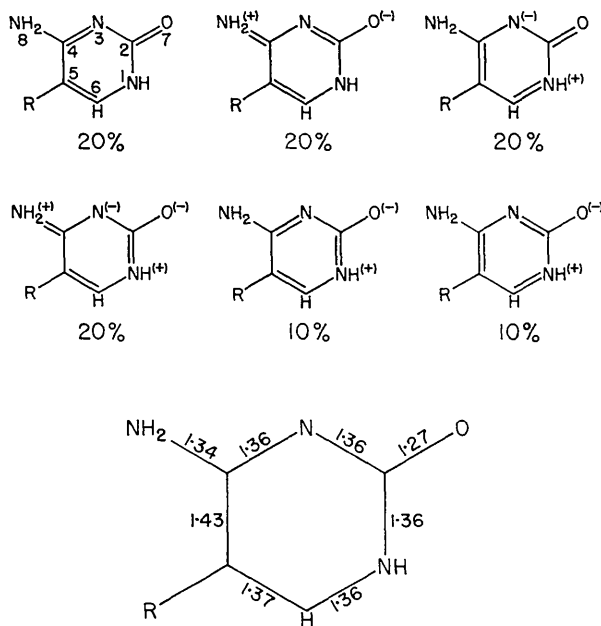


Fig. 4. Canonical structures for the pyrimidine ring in an uncharged molecule of cytosine-5-acetic acid, and the predicted bond distances.

drawing of Fig. 4. The calculated distances were obtained in the following way: the C-C distances, with bond numbers 1.3 and 1.7, were taken from Table 7-9 of Pauling (1960). The C-N (bond numbers 1.3 and 1.4) and C-O (bond number 1.4) distances were taken from two curves drawn through points representing observed C-N and C-O bond distances for bond numbers 1.0, 1.5, and 2.0. The values chosen for these points are listed in Table 6.

The four structures which are probably the major contributors to the carboxyl group are shown in Fig. 5. The observed C-O distances of 1.24 and 1.30 Å correspond to approximately 70% and 30% double-bond character. By adding the restrictions that structures III and IV contribute equally and that together they contribute 50% (since the molecule is a zwitterion half the time), we arrive at the numbers 45, 5, 25, and 25 as the percentage contributions of the four

Table 5. Bond distances and angles

The values in parentheses have been corrected for librations implied by the temperature parameters. The estimated standard deviations are approximately 0.006 Å and 0.3°

N ₁ -C ₂	1.351 Å	C ₅ -N ₁ -C ₂	122.0°
C ₂ -N ₃	1.366	N ₁ -C ₂ -N ₃	117.6
N ₃ -C ₄	1.353	C ₂ -N ₃ -C ₄	121.9
C ₄ -C ₅	1.427	N ₃ -C ₄ -C ₅	120.7
C ₅ -C ₆	1.363	C ₄ -C ₅ -C ₆	115.6
C ₆ -N ₁	1.365	C ₅ -C ₆ -N ₁	122.1
C ₂ -O ₇	1.250 (1.264)	N ₁ -C ₂ -O ₇	121.3
		N ₃ -C ₂ -O ₇	121.1
C ₄ -N ₈	1.323 (1.334)	N ₃ -C ₄ -N ₈	117.3
		C ₅ -C ₄ -N ₈	121.9
C ₅ -C ₉	1.497	C ₄ -C ₅ -C ₉	122.1
C ₉ -C ₁₀	1.522	C ₆ -C ₅ -C ₉	122.3
		C ₅ -C ₉ -C ₁₀	114.3
C ₁₀ -O ₁₁	1.233 (1.241)	C ₉ -C ₁₀ -O ₁₁	120.6
C ₁₀ -O ₁₂	1.290 (1.304)	C ₉ -C ₁₀ -O ₁₂	116.1
		O ₁₁ -C ₁₀ -O ₁₂	123.3

Table 6. Values of C-N and C-O distances for bond numbers *n*

<i>n</i>	C-N	References	C-O	References
1.0	1.48 Å	(a), (b), (d)	1.41 Å	(a), (d)
1.5	1.31	(a), (c)	1.26	(a), (b)
2.0	1.24	(a), (d)	1.21	(a), (d)

(a) Hahn, 1956. (b) Marsh, 1958. (c) Wheatley, 1955. (d) Pauling, 1960; Table 7-5.

structures. Perhaps a more correct description is to say that in one-half the molecules there is a carboxylate ion with C-O distances of 1.26 Å (see Table 6) while in the other half there is a carboxyl group with C-O distances of 1.22 and 1.36 Å, corresponding to 85 and 15% double-bond character (Pauling, 1960; p. 276); the observed bond distances are close to the average of these two sets of values. If this description is valid the apparent temperature factor for atom O₁₂ in the direction of the C-O bond should be larger than normal; however, the magnitude of the increase, about 0.2 in units of *B*, is too small to notice.

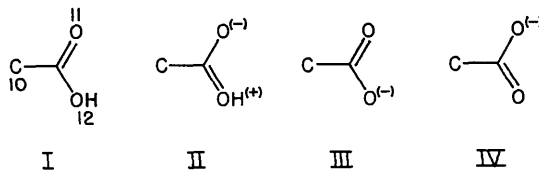


Fig. 5. Four canonical structures for the carboxyl group.

The equation for the best plane of the four atoms C₉, C₁₀, O₁₁, and O₁₂ of the carboxyl group is

$$0.8527X' + 0.0149Y - 0.5225Z' = 5.531 \text{ \AA},$$

where the coefficients are direction cosines relative to *a**, *b*, and *c*. The coordinates of Table 2 lead to exact coplanarity of these four atoms, no one being as much as 0.001 Å from the plane. The equation for the best plane of the six atoms N₁-C₆ of the pyrimidine ring is

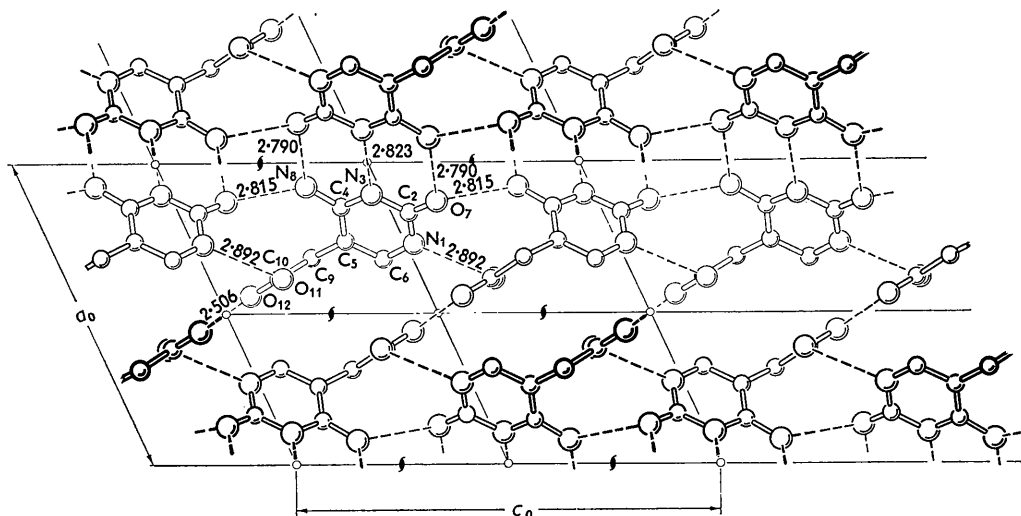


Fig. 6. The structure viewed down the b axis. The dashed lines represent hydrogen bonds.

$$-0.6220X' + 0.7341Y - 0.2723Z' = -3.258 \text{ \AA},$$

and the deviations from this plane are: N_1 , -0.017 ; C_2 , 0.015 ; N_3 , -0.003 ; C_4 , -0.009 ; C_5 , 0.007 ; C_6 , 0.006 ; O_7 , 0.082 ; N_8 , -0.059 ; C_9 , 0.057 Å. Thus the ring atoms are coplanar within experimental error but the atoms bonded to the ring lie significantly, and surprisingly, out of the plane. The situation is not appreciably improved by considering the best plane of all nine atoms. The dihedral angle between the plane of the carboxyl group and the plane of the pyrimidine ring is 68° .

Table 7. Bond distances and angles involving the hydrogen atoms

N_1-H_1	0.81 Å	$C_2-N_1-H_1$	116°
N_3-H_2	1.06	$C_6-N_1-H_1$	122
C_6-H_3	0.96	$C_2-N_3-H_2$	119
N_8-H_4	0.92	$C_4-N_3-H_2$	119
N_8-H_5	0.94	$C_4-N_8-H_4$	113
C_9-H_6	1.03	$C_4-N_8-H_5$	121
C_9-H_7	0.99	$H_4-N_8-H_5$	124
$O_{12}-H_8$	0.93	$C_5-C_9-H_6$	110
		$C_5-C_9-H_7$	109
		$C_{10}-C_9-H_6$	105
		$C_{10}-C_9-H_7$	110
		$H_6-C_9-H_7$	109
		$C_{10}-O_{12}-H_8$	96

The bond distances and angles involving the hydrogen atoms are given in Table 7. The distances are, on the average, about 0.1 Å shorter than the accepted values for the internuclear separations.

(ii) The intermolecular environment

A drawing of the structure of cytosine-5-acetic acid viewed down the b axis is shown in Fig. 6.

The molecules are held together by a three-dimensional network of hydrogen bonds involving all five

available protons: two on the amino nitrogen atom N_8 , one on the ring atom N_1 , and the two half-hydrogen atoms shared by pairs of O_{12} and N_3 atoms. All the hydrogen bonds are relatively short (Table 8), none being as long as the average values deduced by Fuller (1959) in a recent compilation of hydrogen-bond distances. The $O-H \cdots O$ and $N-H \cdots N$ distances, 2.51 and 2.82 Å, are slightly shorter than normal but not short enough to suggest symmetric hydrogen bonds, in agreement with the conclusions drawn from the difference maps (see Fig. 2).

Table 8. Hydrogen-bond distances and angles

$N_1 \cdots O_{11}$	2.892 Å	$C_6-N_1 \cdots O_{11}$	131.7°
$N_3 \cdots N_3$	2.823	$C_2-N_1 \cdots O_{11}$	104.8
$N_8 \cdots O_7$	2.790	$C_2-N_3 \cdots N_3$	115.5
$N_8 \cdots O_7'$	2.815	$C_4-N_3 \cdots N_3$	122.4
$O_{12} \cdots O_{12}$	2.506	$C_4-N_8 \cdots O_7$	119.8
		$C_4-N_8 \cdots O_7'$	136.3
		$O_7-N_8 \cdots O_7'$	100.6
		$C_{10}-O_{12} \cdots O_{12}$	113.1

The arrangement of pairs of cytosine nuclei about the center of symmetry between two N_3 atoms is the same as in a cytosine-guanine pair in the Watson & Crick (1953) structure of deoxyribonucleic acid. Another important point is the apparent ease with which the nitrogen atom N_3 has picked up a proton, thus becoming available as a hydrogen-bond donor rather than an acceptor. The possible existence of tautomeric or charged forms, not only of cytosine but of all four purine and pyrimidine bases, should not be overlooked in formulating structures for the nucleic acids.

(iii) The temperature factors

The magnitudes and direction cosines of the principal axes of thermal motion, as derived from the parameters of Table 2, are listed in Table 9.

Table 9. *The magnitudes B and direction cosines q relative to a*bc of the principal axes of the temperature-factor ellipsoids*

Atom	Axis i	B_i (\AA^2)	q_i^1	q_i^2	q_i^3
N ₁	1	4.02	0.584	-0.807	0.093
	2	2.47	0.812	0.579	-0.077
	3	1.39	0.008	0.121	0.993
C ₂	1	3.63	0.688	-0.724	0.036
	2	2.36	0.724	0.689	0.018
	3	1.28	-0.038	0.014	0.999
N ₃	1	4.01	0.690	-0.717	0.097
	2	2.64	0.723	0.678	-0.135
	3	1.14	0.031	0.163	0.986
C ₄	1	2.72	0.889	-0.452	-0.077
	2	2.61	0.445	0.891	-0.087
	3	1.31	0.108	0.043	0.993
C ₅	1	3.22	0.962	-0.175	-0.210
	2	2.26	0.186	0.982	0.032
	3	1.43	0.201	-0.070	0.977
C ₆	1	3.91	0.745	-0.660	-0.099
	2	2.62	-0.507	-0.656	0.559
	3	1.95	0.433	0.366	0.823
O ₇	1	6.28	0.674	-0.726	0.136
	2	2.75	0.738	0.664	-0.118
	3	1.13	-0.005	0.180	0.984
N ₈	1	5.12	-0.331	0.931	-0.155
	2	2.93	0.943	0.334	-0.009
	3	1.30	-0.044	0.149	0.988
C ₉	1	3.91	0.964	-0.061	-0.257
	2	2.51	0.090	0.838	0.538
	3	1.61	0.248	0.542	0.802
C ₁₀	1	2.83	-0.463	0.875	0.144
	2	2.55	0.852	0.394	-0.346
	3	1.82	0.246	0.283	0.927
O ₁₁	1	4.49	0.864	0.295	-0.408
	2	2.34	0.503	-0.506	0.700
	3	2.05	0.000	0.811	0.585
O ₁₂	1	5.71	0.894	-0.217	-0.392
	2	3.27	-0.024	-0.897	0.441
	3	1.45	0.448	0.385	0.807

A striking feature of the results presented in Table 9 is that the direction of minimum thermal motion for most of the atoms is approximately parallel to the c axis of the crystal, implying that there is considerably

smaller translational or lattice vibration (by about one B unit or 0.012 \AA^2 mean square displacement) of the molecules as a whole in the c direction than in the other two directions. The magnitude of this effect is rather surprising; for although hydrogen bonds hold adjacent molecules together to form chains along c (see Fig. 6) and would presumably restrict the motion in this direction, motion in the other directions should also be constrained (though to a somewhat smaller extent) by the hydrogen bonds between chains. It is possible that at least part of the effect may be due to systematic errors in the observed intensities caused by the deformations of the crystals (see Experimental), and the word of caution voiced by Lonsdale & Milledge (1960) concerning the reliability of thermal vibrations is clearly appropriate here.

The largest thermal motion is that of the carbonyl oxygen atom O₇ in a direction nearly perpendicular to the plane of the pyrimidine ring. The carboxyl oxygen atoms O₁₁ and O₁₂ similarly show large amplitudes of motion perpendicular to the plane of the carboxyl group, but the vibration of O₁₁ appears to be somewhat reduced by the out-of-plane hydrogen bond it accepts from N₁.

The amino nitrogen atom N₈ has a large amplitude of vibration in a direction 21° from the normal to the plane of the pyrimidine ring but nearly perpendicular to the C₄-N₈ bond.

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