

## The Crystal and Molecular Structure of Purine\*

BY DAVID G. WATSON†

*Department of Biological Structure, University of Washington, Seattle, Washington, U.S.A.*

AND ROBERT M. SWEET AND RICHARD E. MARSH

*Gates and Crellin Laboratories of Chemistry, California, U.S.A.‡*

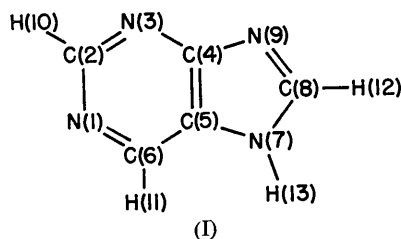
(Received 18 December 1964)

The crystal structure of purine,  $C_5H_4N_4$ , has been determined by X-ray diffraction techniques. Two entirely independent investigations were carried out. In each case complete three-dimensional intensity data were collected using  $Cu K\alpha$  X-radiation and the structural parameters, including anisotropic temperature parameters for the heavy atoms, were refined by full-matrix least-squares techniques. The final  $R$  values for the two investigations are 0.048 and 0.070.

The unit cell is orthorhombic, space group  $Pna2_1$ , with  $a=15.55$ ,  $b=9.37$ , and  $c=3.66$  Å; there are four molecules in the unit cell. The values of the bond distances found in the two investigations agree within experimental error (about 0.01 Å), and are in general agreement with values found in adenine derivatives. A proton is attached to atom N(7) of the five-membered ring rather than to N(9). The molecules are planar, and are joined together by relatively short (2.85 Å)  $N(7)-H \cdots N(9)$  hydrogen bonds.

### Introduction

This paper presents the results of two entirely independent investigations of the structure of purine (I).



The duplication of effort was discovered only when both three-dimensional studies were almost complete (Watson, 1964). Since different experimental techniques had been used, it was considered appropriate to publish both sets of results in the same paper and to make the necessary comparison between them. It has been a comfort to both parties that, except for systematic differences in the temperature factors, the two sets of results differ by less than their standard deviations.

In both laboratories the investigation was undertaken for essentially the same reasons. It was thought worthwhile to establish accurately the geometry of the purine ring system, which is the structural backbone of adenine and guanine, important components of the nucleic

acids. Another interesting aspect of the study was the question of possible tautomerism of the atom H(13) between atoms N(7) and N(9).

For convenience, we shall divide the experimental portions of this paper into two parts, describing first the methods used by Watson (W) and then those used by Sweet and Marsh (SM).

### Unit cell and intensity measurements

*W*

Considerable difficulty was experienced in attempting to recrystallize a commercial sample of purine. However, sublimation yielded a crop of rather poor crystals in the form of very thin plates elongated along  $c$ .

The crystal used for the determination of approximate unit-cell parameters and for the collection of intensity data had dimensions of the order of  $0.03 \times 0.3 \times 1.5$  mm. The final unit-cell parameters (Table 1) were measured with a Picker diffractometer using a smaller crystal.

Intensities on unidimensionally-integrated Weissenberg photographs were measured with a microdensitometer (Jensen, 1954) and recorded with a logarithmic slide-wire recorder. Within the linear response range of the film, the area under the recorder tracing is proportional to the integrated intensity. Data were collected for the layers  $hk0$ ,  $hk1$ ,  $hk2$ , and  $hk3$  with  $Cu K\alpha$  radiation. 327 reflections were of measurable intensity, corresponding to 44% of the total number of reflections within the  $Cu K\alpha$  sphere. The usual Lorentz and polarization factors were applied but no corrections were made for absorption.

*SM*

Again, crystals were obtained only with difficulty, in this case by slow evaporation of methanol-water solu-

\* This work was supported in part by a grant (AM-3288) from the National Institute of Arthritis and Metabolic Diseases, U.S. Public Health Service, and in part by a grant (G-21608) from the National Science Foundation, U.S.A.

† Present address: University Chemical Laboratories, Lensfield Road, Cambridge, England.

‡ Contribution No. 3197 from the Gates and Crellin Laboratories of Chemistry.

tions. They were considerably smaller than W's, about  $0.02 \times 0.1 \times 1.5$  mm. One crystal was mounted along the needle axis ( $c$ ); a second was mounted along  $b$  and reduced to approximately square cross-section by rubbing with moist tissue paper.

Unit-cell dimensions were obtained from least-squares treatment of measurements on  $hk0$  and  $h0l$  Weissenberg photographs prepared with the film in the asymmetric position. Intensities were estimated visually from multiple-film equi-inclination Weissenberg photographs of layers 0–3 about  $c$  and 0–5 about  $b$ , taken with Cu  $K\alpha$  radiation. After correction for Lorentz and polarization effects, they were correlated by means of a least-squares routine; since the spots on the  $b$ -axis photographs were somewhat misshapen, indicating a deformed crystal, their intensities were given half weight in the scaling procedure. Of a total of 730 reflections within the effective copper sphere, 640 were recorded, 570 being of measurable intensity. Most of the unrecorded reflections are of the type  $hk4$  which, because of their general weakness and diffuseness (due to the deformed crystal), could not be measured on the  $b$ -axis photographs.

A statistical comparison of  $F^2$  values for equivalent reflections measured from the two crystals indicated that the pattern of uncertainties  $F_o^2$  (on an absolute scale) could be approximated by the expression

$$\sigma(F_o^2) = 2.44 - 0.64F_o + 0.213F_o^2;$$

this expression was the basis of the weighting function used in the final least-squares refinements.

The crystal data are summarized in Table 1.

Table 1. *Crystal data*

Purine,  $C_5N_4H_4$ . M.W. 120.11.  $\mu(\text{Cu } K\alpha)$ ,  $9.8 \text{ cm}^{-1}$

	W	SM
$a$	$15.553 \pm 3 \text{ \AA}$	$15.551 \pm 2 \text{ \AA}$
$b$	$9.374 \pm 1$	$9.375 \pm 1$
$c$	$3.664 \pm 1$	$3.663 \pm 1$

( $\lambda \text{ Cu } K\alpha = 1.5418$ )

Systematic absences:  $h0l$ ,  $h = 2n + 1$ ;  $0kl$ ,  $(k+l) = 2n + 1$ .  
Space group,  $Pna2_1$  or  $Pnam$ ;  $Pna2_1$  selected on the basis of packing considerations.  
 $Z = 4$ .  $D_x = 1.493 \text{ g.cm}^{-3}$ ;  $D_m(\text{SM}) = 1.491 \text{ g.cm}^{-3}$ .

Table 2. *Synopsis of three-dimensional refinement of purine (W)*

In this table  $X$ ,  $Y$ ,  $Z$  and  $x$ ,  $y$ ,  $z$  denote coordinates of heavy atoms and hydrogen atoms, respectively.  $K_{1-4}$  denotes the four separate level scale factors and  $K$  is the composite scale factor.

Calculation	Refining or determining	Discrepancy index $R(\%)$	$\Sigma w(\Delta F)^2$	Remarks
Structure factors and 3-D $F_o$ map		35.4		$X$ , $Y$ , $B$ from 2-D refinement. Trial $Z$ coordinates.
LS cycles 1–4	$X$ , $Y$ , $Z$ , $B$ , $K_{1-4}$	33.8–16.0	3526–1542	
LS cycles 5–6	$X$ , $Y$ , $Z$ , $\beta_{ij}$	16.5–9.1	669–135	Anisotropic thermal refinement commenced. No refinement of scale.
3-D diff. map	$x$ , $y$ , $z$			Hydrogen peaks of $0.27$ – $0.33 \text{ e. \AA}^{-3}$ .
LS cycles 7–9	$x$ , $y$ , $z$	7.0–7.0	99–96	
LS cycles 10–11	$X$ , $Y$ , $Z$ , $\beta_{ij}$	7.0–5.5	96–63	
LS cycles 12–13	$x$ , $y$ , $z$ , $K$	5.0–4.9	49–47	Single scale $K$ applied and data edited.
LS cycles 14–15	$X$ , $Y$ , $Z$ , $\beta_{ij}$ , $K$	4.9–4.8	47–44	

### Determination and refinement of the structure

W

With such a very short  $c$  axis and four molecules per unit cell, it was decided to proceed on the assumption that the space group is  $Pna2_1$ . This space group has been confirmed by the solution and refinement of the structure. From packing considerations and a study of the strong reflections, a trial model was proposed for the centrosymmetric (001) projection. Structure factors calculated for this model gave  $R = 63\%$  and the corresponding Fourier synthesis showed that, although the six-membered ring was reasonably located, the manner of fusion of the five-membered ring was in error. Reassignment of the positions of atoms N(7) and C(8) resulted in a drop in  $R$  to 41% and the use of improved coordinates from a Fourier map further decreased  $R$  to 34%. Two cycles of isotropic least-squares refinement reduced  $R$  to 21%, at which stage the two-dimensional studies were terminated.

Since the 011 reflection was very intense, preliminary  $y$  coordinates were assigned assuming the molecule to be in this plane; atom C(6) was arbitrarily placed at  $z = 0$  to determine the origin. Structure factors corresponding to this model gave  $R = 35\%$  and the associated three-dimensional Fourier syntheses seemed very satisfactory. At this point the refinement process was initiated.

In the process of solution and refinement of the structure, the atomic scattering factors for nitrogen and carbon were those given by Berghuis, Haanappel, Potters, Loopstra, MacGillavry & Veenendaal (1955), and for hydrogen those of McWeeny (1951). The structure was refined by least-squares analysis based on the observed reflections only; at an intermediate stage, a three-dimensional difference synthesis was computed to determine the positions of the hydrogen atoms.

The least-squares program used in these calculations was the Busing, Martin & Levy (1962) full-matrix FORTRAN program adapted for our IBM 709 crystallographic system by Dr James M. Stewart. The function minimized was  $\Sigma w(F_o - F_c)^2$ , and the weighting scheme was that suggested by Hughes (1941). Seven

low-order reflections for which  $|F_o|$  was less than  $|F_c|$  were given zero weight since they were considered to be affected by extinction. A summary of the refinement procedure is presented in Table 2.

At the outset an attempt was made to refine the four individual level scale factors but a singular matrix resulted. Thus for the first eleven cycles the individual scale factors were adjusted between each cycle but not refined in the least-squares process. After least-squares cycle 11 the data were placed on a common scale and this single scale factor was then refined.

The peaks corresponding to hydrogen atoms in the three-dimensional difference synthesis were reasonably well defined except for the hydrogen attached to N(7). Since there is a possibility of tautomerism of the hydrogen between N(7) and N(9), particular attention was given to this problem. Two least-squares cycles, not quoted in Table 2, were computed in which a half-hydrogen was assigned to each of N(7) and N(9). Refinement of H(10), H(11), H(12) and the two half-hydrogens resulted in the half-hydrogen attached to N(9) shifting to a position about 1 Å from N(7) of the neighbouring hydrogen-bonded molecule. On this basis it seemed fairly certain that the hydrogen was indeed located on N(7). However, the final 3-D difference map indicates that the electron density distribution of H(13) is much more smeared than those for the other hydrogen atoms. In these calculations each hydrogen atom was assigned an isotropic  $B$  value of 3.0 Å<sup>2</sup> but no refinement of the thermal parameters was attempted.

The final  $R$  index, from which the extinguished reflections and the unobserved reflections were excluded, was 4.8%. The maximum coordinate shift in least-squares cycle 15 was 0.45 of its standard deviation and the maximum temperature parameter shift was 1.10  $\sigma$ .

### SM

A trial structure was derived on the basis of packing considerations and with the assumption that a hydrogen bond would be formed between atoms N(7) and N(9) of adjacent molecules (whichever of these atoms is protonated, the other has increased electronegativity and hence becomes a good hydrogen-bond acceptor). Structure factors calculated by hand for 15 low-order  $hk0$  reflections showed satisfactory agreement with the observed values; these 15 reflections were included in an electron-density projection which led to improved  $x$  and  $y$  coordinates. Two-dimensional least-squares refinement, during which individual anisotropic temperature factors were introduced, led to an  $R$  value of 0.10; a difference map calculated towards the end of the refinement clearly showed the positions of the hydrogen atoms and in particular H(13), which lay near N(7) rather than N(9).

Three-dimensional least-squares refinement was carried out on an IBM 7094 computer under the CRYRM crystallographic system (Duchamp, 1964). The form factors were from *International Tables for X-ray Crystallography* (1962), and the quantity minimized was  $\sum w(F_o^2 - KF_c^2)^2$ . Various weighting functions were used, depending on the stage of refinement; during the last few cycles, when it appeared that the discrepancies between  $F_o^2$  and  $KF_c^2$  lay within the observational uncertainties, weights were taken equal to the inverses of the squares of the standard deviations in  $F_o^2$  (see *Intensity measurements*). Unobserved reflections were included only if the values of  $KF_c^2$  exceeded the threshold value of  $F_o^2$ . The full matrix of the normal equations was collected and inverted. Since the  $c$  axis is polar, the matrix is in principle singular; however, round-off effects were apparently large enough to remove the

Table 3. *The final heavy-atom coordinates and their estimated standard deviations*

All values have been multiplied by 10<sup>4</sup>. The temperature factor is of the form  
 $\exp \{ -(\beta_{11}h^2 + \beta_{22}k^2 + \beta_{33}l^2 + 2\beta_{12}hk + 2\beta_{13}hl + 2\beta_{23}kl) \}$

		$x$	$y$	$z$	$\beta_{11}$	$\beta_{22}$	$\beta_{33}$	$\beta_{12}$	$\beta_{13}$	$\beta_{23}$
N(1)	W	30(4)	3047(6)	1274(30)	35(3)	81(6)	562(70)	6(4)	12(9)	-15(21)
	SM	37(3)	3041(4)	1257(*)	61(2)	128(4)	1057(46)	0(2)	-2(8)	6(15)
C(2)	W	154(6)	1693(7)	2402(31)	40(4)	81(8)	530(82)	-13(5)	-7(12)	-10(19)
	SM	160(3)	1689(5)	2390(*)	58(2)	133(6)	1172(69)	-12(3)	8(9)	21(16)
N(3)	W	888(4)	947(5)	2406(25)	41(3)	49(5)	398(53)	-12(4)	8(10)	17(13)
	SM	889(3)	960(4)	2462(*)	66(2)	103(4)	840(36)	-13(2)	6(7)	44(11)
C(4)	W	1561(4)	1701(7)	1205(34)	28(4)	51(6)	389(56)	1(3)	-18(11)	22(16)
	SM	1561(3)	1700(4)	1223(*)	60(2)	80(4)	825(40)	-1(2)	-11(8)	36(11)
C(5)	W	1505(4)	3117(7)	-46(29)	34(3)	44(6)	278(61)	-5(4)	-12(10)	28(15)
	SM	1501(3)	3103(4)	-41(*)	59(2)	82(4)	733(42)	-2(2)	-24(8)	25(11)
C(6)	W	701(5)	3772(7)	0(*)	38(4)	58(7)	566(73)	11(4)	-8(12)	33(17)
	SM	704(2)	3761(4)	13(*)	68(2)	97(4)	1065(56)	11(3)	-23(10)	31(13)
N(7)	W	2325(4)	3467(5)	-1105(27)	29(3)	57(6)	636(63)	-10(4)	-11(11)	20(16)
	SM	2316(3)	3465(5)	-1151(*)	60(2)	99(4)	921(42)	-10(2)	-9(8)	78(11)
C(8)	W	2809(5)	2330(8)	-447(37)	24(3)	124(10)	531(61)	2(5)	-16(12)	-14(24)
	SM	2812(2)	2332(4)	-465(*)	54(2)	132(5)	896(45)	-1(3)	1(10)	17(15)
N(9)	W	2399(4)	1232(5)	927(28)	36(3)	48(5)	566(60)	6(4)	-17(11)	11(14)
	SM	2396(3)	1241(5)	929(*)	59(2)	106(4)	946(40)	8(2)	-15(8)	53(11)

\* In W, the  $z$  coordinate of C(6) was constrained to the value 0 and was omitted from the refinement. In SM, all coordinates were included in the full-matrix refinement and no meaningful standard deviations in the  $z$  coordinates are available. The  $z$  coordinates of SM have been incremented so that the average values of  $z$  are the same for both determinations.

singularity and in no refinement cycle did the program fail to win a satisfactory inverse. Accordingly, the  $z$  coordinates refined satisfactorily; however, their standard deviations are without meaning.

The positional coordinates of all 13 atoms and the anisotropic temperature parameters of the 9 heavy atoms were adjusted; the temperature factors of the hydrogen atom were assumed to be isotropic, with  $B=3.5 \text{ \AA}^2$ . In the last refinement cycle the largest shift in any heavy-atom parameter was 12% of its standard deviation and in a hydrogen-atom coordinate, 35%. The final  $R$  value for 568 observed reflections of non-zero weight is 0.070. The 'goodness of fit' -  $\Sigma w(F_o^2 - F_c^2)^2 / (n-p)$  - is 0.76. That this value is less than unity suggests that, in general, the observational errors are smaller than the values reflected by the weighting function.

At the conclusions of the refinement, an electron density map and a difference map were calculated in the plane of the purine molecule. These maps are shown in Fig. 1.

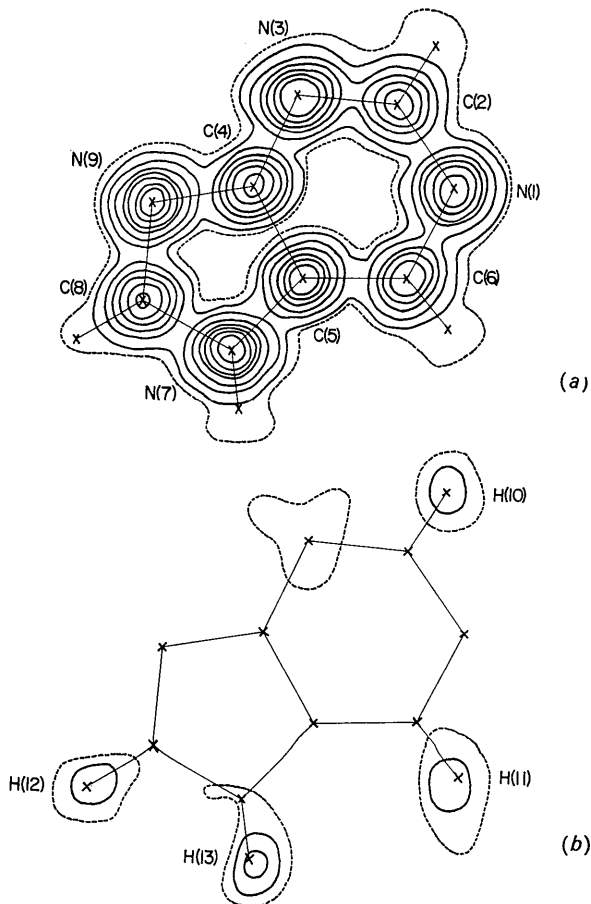


Fig. 1. (a) The electron density in the plane of the purine molecule, calculated at the conclusion of the refinement (SM). Contours are at intervals of  $1 \text{ e.}\text{\AA}^{-3}$  beginning at  $1 \text{ e.}\text{\AA}^{-3}$  (dashed). (b) The final difference map (SM) in the plane of the molecule; the contributions of the hydrogen atoms were omitted from the  $F_{\text{cal}}$ 's. Contours are at  $0.1 \text{ e.}\text{\AA}^{-3}$  beginning with  $0.1 \text{ e.}\text{\AA}^{-3}$  (dashed).

Table 4. Final hydrogen coordinates and their standard deviations

Atom		$x$	$y$	$z$
H(10)	W	-0.033(4)	0.112(8)	0.383(24)
	SM	-0.034(3)	0.125(5)	0.352
H(11)	W	0.061(4)	0.476(7)	-0.096(22)
	SM	0.056(3)	0.464(5)	-0.104
H(12)	W	0.342(5)	0.233(8)	-0.068(19)
	SM	0.346(4)	0.232(4)	-0.130
H(13)	W	0.241(4)	0.430(7)	-0.219(26)
	SM	0.246(3)	0.420(5)	-0.229

The final heavy-atom parameters, and their standard deviations, for the two structure determinations are given in Table 3. Coordinates of the hydrogen atoms are given in Table 4, and the observed and calculated structure factors in Table 5.

### Molecular dimensions

The bond distances and angles for the two determinations, calculated from the parameters in Tables 3 and 4, are shown in Fig. 2. The estimated standard deviations in the distances and angles involving the heavy atoms are about  $0.01 \text{ \AA}$  and  $0.8^\circ$  (W) and  $0.006 \text{ \AA}$  and  $0.5^\circ$  (SM), the differences between the two sets of standard deviations being a reflection of the larger number of intensities observed by SM (570 vs. 327); the uncertainties in values involving hydrogen atoms

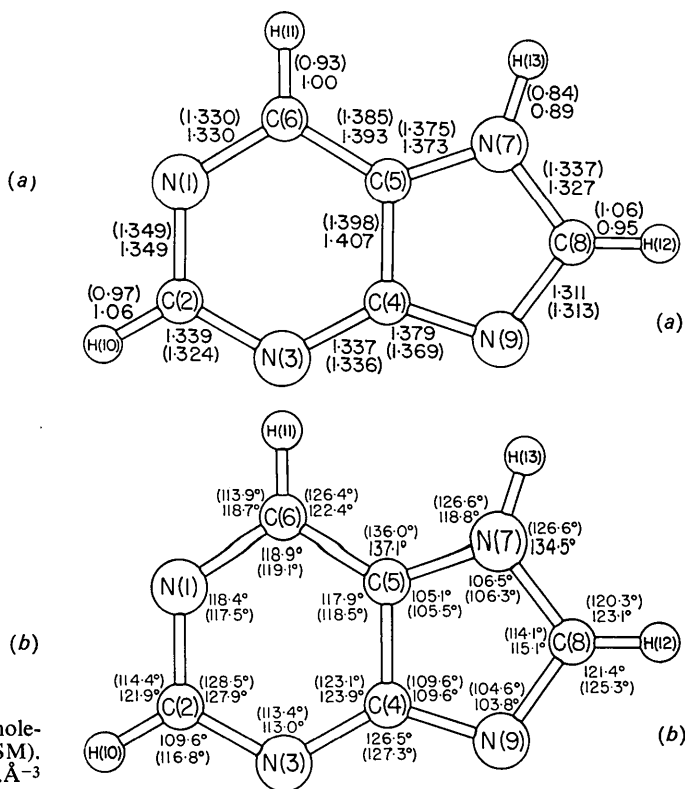


Fig. 2. The bond distances (a) and angles (b) calculated from the final coordinates. The values in parentheses are those of SM; the others, W.



are roughly ten times larger. Vibrational corrections appear to be small, and were neglected.

We find it extremely comforting that the two sets of values agree within their uncertainties. In view of this agreement, we shall discuss the various structural features in terms of the averages of the two sets of values.

These studies have definitely established that, in the crystal state at least, the proton H(13) is attached to N(7) rather than to N(9). In spite of the different numbers of ligands of these two nitrogen atoms, the C(5)-N(7) bond is the same length as the C(4)-N(9) bond and C(8)-N(7) is only slightly longer than C(8)-N(9). Equivalence of the C(4)-N(9) and C(5)-N(7) bonds has also been reported in studies of adenine derivatives (Watson, Sutor & Tollin, 1965; Kraut & Jensen, 1963; Hoogsteen, 1963); in these compounds, however, the C(8)-N(9) bond is considerably longer than in purine. This lengthening is undoubtedly associated with the presence of a substituent group on N(9).

Pullman & Pullman (1958) have carried out a simple Hückel-type molecular orbital calculation for purine; their predicted bond distances are compared with our observed values in Table 6. The maximum difference between the two sets of values, 0.02 Å, is certainly within the range of error to be expected in such a calculation.

Within experimental error, the purine molecule is planar. The least-squares plane, with all heavy atoms

Table 6. Comparison of average observed bond distances with those calculated by the method of molecular orbitals (Pullman & Pullman, 1958)

Bond	<i>d</i> (obs.)	<i>d</i> (calc.)
N(1)-C(2)	1.349 Å	1.34 Å
C(2)-N(3)	1.332	1.32
N(3)-C(4)	1.337	1.35
C(4)-C(5)	1.403	1.41
C(5)-C(6)	1.389	1.40
C(6)-N(1)	1.330	1.32
C(5)-N(7)	1.374	1.37
N(7)-C(8)	1.330	1.35
C(8)-N(9)	1.312	1.32
N(9)-C(4)	1.374	1.36

weighted equally, was calculated for both sets of parameters; the results are given in Table 7. It is interesting to note that the deviations of the hydrogen atoms from the plane of the heavy atoms are in the same sense for both determinations; however, these deviations are probably not significant.

### Packing of the molecules

The structure as viewed down the *c* axis is shown in Fig. 3. Strong N(7)-H(13)···N(9) hydrogen bonds, 2.85 Å in length, hold molecules together to form chains along [011], and presumably account for the relatively high melting point of purine (213°C) com-

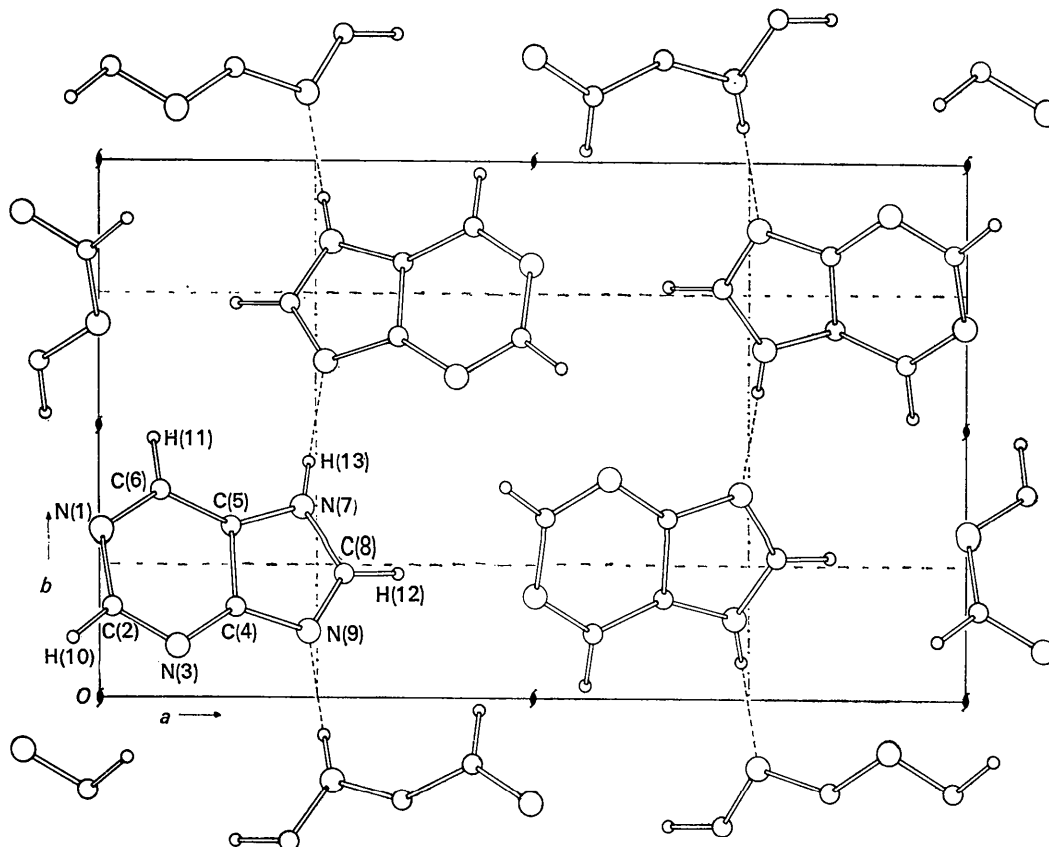


Fig. 3. The structure viewed along the *c* axis.

Table 7. Deviations of the atoms from the best plane through the ring atoms of purine

W:  $0.1852X + 0.3319Y + 0.9250Z = 1.382 \text{ \AA}$   
 SM:  $0.1861X + 0.3390Y + 0.9221Z = 1.398 \text{ \AA}$

Atom	W	SM
N(1)	-0.007 Å	-0.001 Å
C(2)	-0.004	0.008
N(3)	0.016	0.004
C(4)	-0.005	-0.008
C(5)	-0.006	-0.009
C(6)	0.006	-0.006
N(7)	0.008	0.015
C(8)	-0.001	0.000
N(9)	-0.007	-0.004
H(10)	-0.17	-0.09
H(11)	0.05	0.11
H(12)	0.10	0.10
H(13)	0.09	0.13

pared with pteridine ( $140^\circ$ ) and pyrimidine ( $21^\circ$ ), where there are no opportunities for hydrogen bonds.

As in crystals of other purine and pyrimidine compounds, purine molecules pack on top of one another – in contrast to aromatic hydrocarbons, which tend to form staggered arrays. The interplanar spacing between purine molecules stacked along  $c$  is  $3.39 \text{ \AA}$ ; the shortest interatomic distances between these molecules are  $N(1) \cdots C(6)$ ,  $3.43 \text{ \AA}$ ,  $N(3) \cdots C(4)$ ,  $3.46 \text{ \AA}$ , and  $C(8) \cdots N(9)$ ,  $3.39 \text{ \AA}$ . Other short intermolecular contacts are  $C(2) \cdots N(3)$ ,  $3.48 \text{ \AA}$ , between molecules related by screw axes and  $C(6) \cdots N(1)$ ,  $3.47 \text{ \AA}$ , between molecules related by the  $b$  glide.

It is pertinent to point out the striking similarity (Fig. 4) between the crystal structures of purine and pyrimidine (Wheatley, 1960). Pyrimidine also crystallizes in space group  $Pna2_1$  with  $b$  and  $c$  axial lengths approximately the same as in purine; the  $a$  axis in purine is lengthened to accommodate the five-membered ring. The dimensions of the pyrimidine rings in the two compounds are not significantly different.

#### Anisotropic thermal vibrations

The magnitudes and directions of the principal axes of thermal vibration have been calculated from the two sets of anisotropic temperature parameters; the results are listed in Table 8. The agreement between the two determinations is not good. In particular, the  $B$  values of SM are, on the average, about 2 units greater than those of W – an effect which is apparent even at a casual glance at Table 5. We suspect that the disagreement is due in part to the fact that W used a relatively large crystal, for which absorption effects may have been important, but in larger part to the poor quality of crystals obtained by SM, resulting in diffuse high-angle reflections. We take some solace in the observation that the overall patterns of anisotropy are quite similar in the two determinations; and while we have not undertaken a rigid-body treatment of the thermal vibrations, it is apparent that the predominant motions are a lattice vibration parallel to the long

axis of the molecule and in-plane libration about the center of mass. This latter motion appears to be too small to affect appreciably the observed bond lengths.

Table 8. Magnitudes and direction cosines (relative to the crystal axes) of the principal axes of the thermal vibration ellipsoids

Atom		Axis $i$	$B_i$	$C_{ia}$	$C_{ib}$	$C_{ic}$
N(1)	W	1	3.61	0.895	0.331	0.300
		2	3.15	-0.049	-0.595	0.802
		3	2.49	-0.444	0.733	0.516
SM	1	1	5.93	0.978	0.001	-0.210
		2	5.67	0.209	0.070	0.975
		3	4.50	-0.016	0.998	-0.069
C(2)	W	1	4.28	0.884	-0.464	-0.054
		2	2.92	-0.132	-0.359	0.924
		3	2.36	0.448	0.810	0.379
SM	1	1	6.35	0.129	0.111	0.985
		2	5.98	0.870	-0.489	-0.059
		3	4.22	0.476	0.865	-0.160
N(3)	W	1	4.17	0.962	-0.269	0.055
		2	2.24	0.047	0.359	0.932
		3	1.42	0.271	0.894	-0.358
SM	1	1	6.61	0.966	-0.256	-0.016
		2	4.79	0.119	0.392	0.912
		3	3.13	0.227	0.883	-0.410
C(4)	W	1	2.92	0.882	-0.079	-0.464
		2	2.14	0.401	0.644	0.652
		3	1.54	-0.247	0.761	-0.599
SM	1	1	5.89	0.981	-0.043	-0.189
		2	4.52	0.193	0.273	0.942
		3	2.69	-0.011	0.961	-0.277
C(5)	W	1	3.40	0.966	-0.189	-0.177
		2	1.80	0.259	0.707	0.659
		3	1.13	0.001	-0.682	0.732
SM	1	1	5.85	0.958	-0.062	-0.281
		2	3.88	0.287	0.295	0.911
		3	2.79	-0.026	0.953	-0.301
C(6)	W	1	3.90	0.947	0.319	-0.033

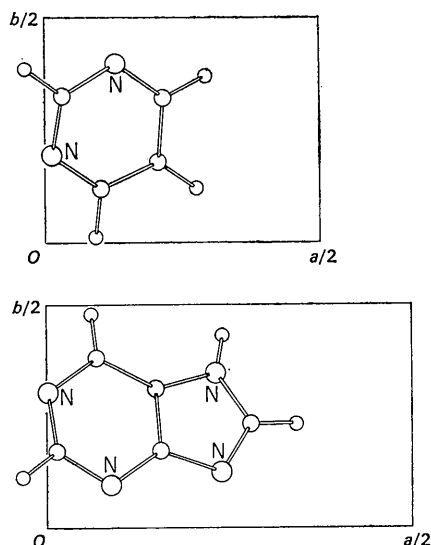


Fig. 4. A comparison of the crystal structures of pyrimidine (top) and purine (bottom). In each case only one asymmetric unit is shown. Nearly exact superposition of the two six-membered rings can be obtained if the origin of either structure is taken at the alternative position  $x = \frac{1}{2}$ ,  $y = 0$  (see Fig. 3).

Table 8 (cont.)

Atom	Axis <i>i</i>	<i>B<sub>i</sub></i>	<i>C<sub>ia</sub></i>	<i>C<sub>ib</sub></i>	<i>C<sub>ic</sub></i>	
	2	3.21	-0.076	0.324	0.943	
	3	1.65	-0.311	0.891	-0.331	
SM	1	6.86	0.921	0.118	-0.372	
	2	5.65	0.332	0.265	0.905	
	3	3.20	-0.205	0.957	-0.205	
N(7)	W	1	3.65	-0.456	0.301	0.837
		2	2.89	0.769	-0.339	0.541
		3	1.69	0.447	0.891	-0.077
SM	1	6.17	0.815	-0.361	-0.453	-0.453
	2	5.20	0.560	0.293	0.775	-0.775
	3	2.86	0.147	0.885	-0.441	-0.441
C(8)	W	1	4.40	0.081	0.987	-0.142
		2	3.00	-0.445	0.163	0.880
		3	2.14	0.892	-0.008	0.453
SM	1	5.26	0.994	-0.112	0.011	0.011
	2	4.97	0.056	0.571	0.819	-0.819
	3	4.47	0.098	0.813	-0.574	-0.574
N(9)	W	1	3.73	0.878	0.116	-0.464
		2	2.89	0.430	0.235	0.872
		3	1.59	-0.210	0.965	-0.156
SM	1	5.92	0.949	0.111	-0.294	-0.294
	2	5.37	0.216	0.447	0.868	0.868
	3	3.26	-0.228	0.888	-0.400	-0.400

\* One of us (DGW) would like to thank Drs J. Stewart and D. High for the use of their computer programs, the Research Computer Laboratory at the University of Washington for a grant of computer time, and the National Institute of Arthritis and Metabolic Diseases

for financial support. He would also like to thank Professor L. H. Jensen for his continued support and encouragement throughout the course of this work.

The work described by SM was carried out as an undergraduate research project (RMS) sponsored by the National Science Foundation.

## References

- BERGHUIS, J., HAANAPPEL, IJ. M., POTTERS, M., LOOPSTRA, B. O., MACGILLAVRY, C. H. & VEENENDAAL, A. L. (1955). *Acta Cryst.* **8**, 478.
- BUSING, W. R., MARTIN, K. O. & LEVY, H. A. (1962). U.S. Atomic Energy Commission Report ORNL-TM-305.
- DUCHAMP, D. J. (1964). Program and Abstracts, Amer. Cryst. Assoc. Meeting, Bozeman, Montana; paper B-14.
- HOOGSTEEN, K. (1963). *Acta Cryst.* **16**, 907.
- HUGHES, E. W. (1941). *J. Amer. Chem. Soc.* **63**, 1737.
- International Tables for X-Ray Crystallography* (1962). Vol. II, pp. 202-203. Birmingham: Kynoch Press.
- JENSEN, L. H. (1954). *J. Amer. Chem. Soc.* **76**, 4663.
- KRAUT, J. & JENSEN, L. H. (1963). *Acta Cryst.* **16**, 79.
- MCWEENY, R. (1951). *Acta Cryst.* **4**, 513.
- PULLMAN, A. & PULLMAN, B. (1958). *Bull. Soc. Chim. Fr.*, p. 766.
- WATSON, D. G. (1964). Program and Abstracts, Amer. Cryst. Assoc. Meeting, Bozeman, Montana; paper F-2.
- WATSON, D. G., SUTOR, D. J. & TOLLIN, P. (1965). *Acta Cryst.* **19**, 111.
- WHEATLEY, P. J. (1960). *Acta Cryst.* **13**, 80.

*Acta Cryst.* (1965). **19**, 580

## Structures Cristallines des Dérivés 2 et 2,3 de la Naphtoquinone-1,4.

### II. Chloro-2-hydroxy-3-naphtoquinone-1,4

PAR JACQUES GAULTIER ET CHRISTIAN HAUW

Laboratoire de Minéralogie et Cristallographie, Faculté des Sciences de Bordeaux, France

(Reçu le 9 février 1965)

Crystals of  $C_{10}O_3H_5Cl$  are monoclinic, space group *Pc*, two molecules in a unit cell with lattice constants:

$$a = 8.25, b = 3.92, c = 14.39 \text{ \AA}; \beta = 113^\circ 20'$$

Least-squares refinement on visually estimated intensities was used to obtain optimum values for 14 positional and 14 isotropic thermal parameters. The value of *R* is 0.11.

The molecular packing is discussed in the following article together with that of  $C_{10}O_2NH_6Cl$ .

Miller (1911) et Fieser (1926) ont montré que les hydroxy-3-naphtoquinone-1,4 sont des mélanges en équilibre de deux formes tautomères: leurs points de fusion varient avec le temps car l'équilibre n'est atteint que lentement à l'état solide et deux éthers peuvent aisément être identifiés. Ils attribuent à ces composés les formules représentées sur la Fig. 1.

La chloro-2-hydroxy-3-naphtoquinone que nous étudions ici se comporte comme une antivitamine K et à ce titre peut être comparée à des composés comme la bromo-2-naphtoquinone-1,4 de structure connue.

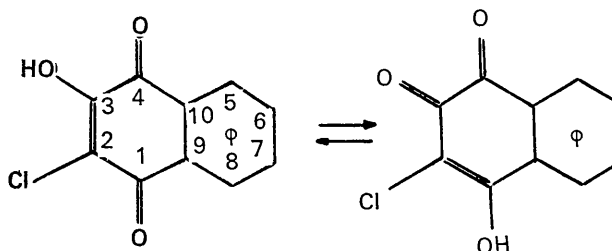


Fig. 1. Formes tautomères de la chloro-2-hydroxy-3-naphtoquinone-1,4.