

that observed in the previously analysed cinnamic acid derivatives in which nearest-neighbour  $>C=C<$  groups are parallel (related by translation) or antiparallel (related by centres of symmetry). The centre-to-centre distance of nearest-neighbour  $>C=C<$  groups is 3.93 Å; contacts between C(3) and C(4') and C(3') and C(4) of adjacent glide-plane related molecules are 3.53 Å and 4.33 Å respectively. It follows from these values that interaction between two molecules is possible and likely to take place in the first instance between C(3) and C(4').

The *p*-derivative displays the packing arrangement of the  $\alpha$  type in the cinnamic acid series since contacts between nearest-neighbour  $>C=C<$  groups occur across centres of symmetry. Three sets of such contacts are present (Fig. 4); the centre-to-centre distances across the inversion centres at  $(0\frac{1}{2}\frac{1}{2})$ ,  $(\frac{1}{2}\frac{1}{2}\frac{1}{2})$ , and  $(0\frac{1}{2}0)$  are 4.11, 5.29, and 5.74 Å respectively. In the light of our previous results we should expect photochemical interaction across the centre at  $(0\frac{1}{2}\frac{1}{2})$  with formation of the centrosymmetric dimer, dimethyl 4,4'-dibromo- $\alpha$ -truxillate.

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## The Crystal and Molecular Structure of D(+)-Barium Uridine-5'-Phosphate\*

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The crystal structure of hydrated barium uridine-5'-phosphate has been determined by three-dimensional Patterson and Fourier syntheses. The anomalous scattering of Cu *K* radiation by the barium (and phosphorus) atoms made it possible to confirm the absolute configuration of the molecule. The structure was refined by block diagonal least squares which made use of two unique octants of intensity data by incorporating the complex parts of the atomic scattering factors. The final *R* value was 9.8% for 1502 *hkl* and 1000 *hkl* intensity data.

The geometry and absolute configuration of the molecule are in accord with previous studies on nucleotides. The barium ions lie in two independent special positions and each ion is surrounded by ten oxygen atoms. The nucleotides pack compactly, with pairs of base planes nearly parallel but only partially overlapping, and a close contact of O(1') of one molecule with the pyrimidine ring of another. The conformation about the C(5')-C(4') bond in ribose derivatives and related molecules has been considered in detail, and its bearing on nucleotide conformation discussed. A suggested hydrogen-bonding scheme is illustrated.

### Introduction

Divalent metal ions, especially those of the alkaline earths, play a significant part in the combination and

the structural relationships of proteins and nucleic acids. The role of such ions in liberating DNA from nucleoproteins has been demonstrated by Kirby (1957, 1958). Dipositive cations are also known to act as catalysts in biological reactions of triphosphate nucleosides.

Various possibilities of coordination of dipositive cations with nucleotides have been discussed by Brint-

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zinger (1961), but the only previously reported structure of a salt of a nucleotide with such an ion is that of calcium thymidylate (Trueblood, Horn & Luzzati, 1961). The present determination of the structure and absolute configuration of barium uridine-5'-phosphate provides further data on the biologically significant coordination of alkaline earth ions with nucleotides.

### Experimental data and procedures

Barium uridine-5'-phosphate ( $C_9H_{11}N_2O_9P\text{Ba}$ ) was supplied to us by A. M. Michelson. It forms plate-like crystals, elongated along **b**, upon slow evaporation of aqueous solutions. When the crystals are taken from the solution they readily lose some water of hydration and start to show polycrystallinity within a few days. Crystals for data collection were therefore mounted in thin-walled boron-lithium glass capillaries.

Weissenberg and precession photographs with  $\text{Cu } K\alpha$  radiation gave the following systematic extinctions, which indicate the space group to be  $C222_1$ :  $hkl$ ,  $h+k=2n+1$ ;  $00l$ ,  $l=2n+1$ . The cell dimensions, determined from an  $h0l$  Weissenberg photograph calibrated with  $\text{CeO}_2$  ( $a_0=5.411 \text{ \AA}$ ) and from precession and oscillation photographs with the crystal mounted about **b**, were found to be:

$$a_0=21.11 \pm 0.02, b_0=9.06 \pm 0.03, c_0=20.98 \pm 0.02 \text{ \AA}.$$

The density of the freshly crystallized material, determined by flotation in chloroform and bromoform, was found to be  $2.05 \pm 0.01 \text{ g.cm}^{-3}$ . With the assumption that there are 8 formula weights of the salt in the unit cell, the volume and density then correspond to the presence of  $8.9 \pm 0.2$  molecules of water per molecule of nucleotide. However, as noted below, only seven water molecules were actually found; presumably the crystal effloresced slowly during the recording of the data.

The difficulty in obtaining good crystalline specimens made it necessary to use one crystal for collection of all the intensity data. The dimensions of this crystal were 0.61 mm along **b**, 0.12 mm along **a**, and 0.36 mm along **c**. Intensity data ( $h0l$  to  $h6l$ ) were collected on equiinclination Weissenberg photographs with a Nonius integrating camera, nickel-filtered  $\text{Cu } K\alpha$  radiation, and Ilford type-G industrial film. The photographs of the various layers were taken with the same exposure time in order to facilitate interlayer scaling.

Most of the intensities were measured with a Baird-Atomic microdensitometer (Model CB), but those too weak to be so determined were estimated visually with a calibrated integrated intensity strip. The integration process tended to blur together some of the weaker high-angle reflections, making it extremely difficult to determine their intensity, and consequently many reflections were considered undeterminable rather than unobservable and were not included in the analysis. In addition to the usual geometrical corrections, approximate absorption corrections were made with the pro-

gram of C. Burnham (ACA No. 338) and absorption coefficients from *International Tables* (1962).

The anomalous scattering effect of the barium atoms made it advantageous to measure the intensities of reflections in two octants; the indexing method of Peerdeman & Bijvoet (1956) was used. The numbers of  $hk\bar{l}$  and  $hkl$  reflections observed were 1502 and 1000 respectively, representing together approximately 53 per cent of the data in the  $\text{Cu } K\alpha$  sphere of reflection.

All calculations were made on an IBM 7090 computer. The form factors used for carbon, oxygen and nitrogen were those of Hoerni & Ibers (1954); that for phosphorus was Tomiie & Stam's (1958). The scattering curve for  $\text{Ba}^{2+}$  was approximated by using the curve for neutral Ba (Thomas & Umeda, 1957) above  $\sin \theta/\lambda=0.2$  and extrapolating this curve smoothly to 54 below this value. The anomalous dispersion corrections of Dauben & Templeton (1955) were applied to the atomic scattering factors of phosphorus and barium.

### Determination of the structure

Although there is, on the average, only one barium ion per asymmetric unit, there are in fact two independent  $\text{Ba}^{2+}$  each lying on a twofold axis. They were located from a three-dimensional Patterson synthesis. One lies on the twofold axis at  $(0, y, \frac{1}{4})$  and the other on that at  $(x, 0, 0)$ . The positions of the other atoms of the nucleotide were found in a three-dimensional Fourier synthesis phased on the two barium ions, which represent 62% of the scattering matter on a  $Z^2$ -basis. Successive Fourier syntheses phased on the barium ions and other atoms of the molecule showed seven water molecules per asymmetric unit, six of them lying in general positions and the other in two sets of special positions on the twofold axis parallel to **b** at  $(0, y, \frac{1}{4})$ . All of the  $(hk\bar{l})$  data, but not the  $(hkl)$  data, were used in all Fourier summations.

### Refinement

The observed anomalous scattering effect was sufficiently large that changes were made in the usual least-squares equations to permit using the independent  $(hk\bar{l})$  and  $(hkl)$  data. The least-squares equations were derived in the usual way from the appropriate expressions for  $F(hk\bar{l})$  and  $F(hkl)$  (e.g. Patterson, 1963).

After the positions of all the atoms with the exception of the water molecules at  $(0, y, \frac{1}{4})$  had been well defined by Fourier syntheses, three cycles of block-diagonal least-squares refinement were calculated with individual isotropic temperature factors in order to improve the interlayer scaling which was initially based only on relative exposure time. In these and all succeeding cycles the function minimized was  $\sum w(F_o - G|F_c|)^2$ , where  $G$  is the scale factor for the calculated structure factors. The least-squares program was that of Gantzel, Sparks & Trueblood (ACA No. 317). Hughes's weighting scheme (1941) was used throughout the re-

finement. The final layer scaling after this initial refinement required a maximum adjustment of about 20%, with the average change in relative scale only about 5%.

After the seventh water molecule was ascertained to be divided between the special positions along the two-fold axis at  $(0, y, \frac{1}{2})$ , block-diagonal least-squares refinement was carried out with all the data, with the barium and phosphorus atoms assigned anisotropic temperature factors. The shifts in the final cycle were less than one-third of the standard deviations estimated from the diagonal elements of the matrix of the least-squares normal equations. The final value of the usual discrepancy index,  $R$ , was 9.8% for 2502 observed reflections. Table 1 gives the final fractional coordinates and e.s.d.'s obtained from the final cycle of least squares. Table 6 contains a list of the observed ( $F_o$ ) and calculated ( $F_c$ ) structure factors for the  $(hkl)$  and  $(hkl)$  data.

### Absolute configuration

The absolute configuration of the compound was easily determined by comparison of the calculated structure

Table 1. Positional and thermal parameters and their estimated standard deviations\*

	$x$	$y$	$z$	$B$
Ba(1)	0	501(2)	2500	†
Ba(2)	489(1)	0	0	†
P	1264(2)	5719(7)	1609(2)	†
O(I)	1316(8)	7414(22)	1506(9)	4.3(0.3) Å <sup>2</sup>
O(II)	941(8)	5456(25)	2238(9)	4.7(0.3)
O(III)	955(8)	4807(26)	1089(9)	5.0(0.4)
O(2')	2006(6)	5197(19)	1678(6)	2.9(0.2)
C(5')	2177(9)	3675(26)	1767(9)	2.7(0.3)
C(4')	2873(11)	3673(33)	1759(12)	4.0(0.5)
C(3')	3219(8)	4723(29)	2247(9)	2.8(0.3)
C(2')	3384(8)	6012(28)	1804(9)	2.7(0.3)
C(1')	3511(8)	5314(26)	1139(8)	2.4(0.3)
O(1')	3102(6)	4057(19)	1124(7)	2.8(0.2)
O(3')	3777(7)	4052(19)	2458(8)	3.7(0.3)
O(2')	3890(7)	6813(21)	2037(7)	3.5(0.3)
N(3)	3658(7)	8005(21)	-135(7)	2.4(0.3)
C(2)	3858(8)	6901(27)	293(10)	2.7(0.3)
O(2)	4408(6)	6538(19)	367(7)	3.4(0.3)
N(1)	3351(7)	6302(21)	630(8)	2.4(0.3)
C(6)	2723(9)	6610(26)	497(9)	2.6(0.3)
C(5)	2560(7)	7588(28)	75(9)	2.2(0.3)
O(4)	2916(6)	9257(18)	-738(6)	2.8(0.2)
C(4)	3026(8)	8286(27)	-300(10)	2.7(0.3)
Water (1)	970(8)	7109(22)	-49(9)	4.3(0.3)
Water (2)	627(9)	1668(26)	1403(10)	5.2(0.4)
Water (3)	155(8)	8649(24)	1148(9)	5.0(0.4)
Water (4)	1590(7)	-140(23)	874(7)	3.9(0.3)
Water (5)	319(10)	5646(30)	4145(11)	6.2(0.5)
Water (6)	1297(7)	4467(22)	3334(8)	4.1(0.3)
Water (7)	0	3479(54)	2500	10(1)
Water (8)	0	7361(55)	2500	10(1)

\*  $x, y, z$  times  $10^4$ . The numbers in parentheses following each value are the e.s.d.'s.

† These three atoms were refined anisotropically; the final values of the coefficients,  $\times 10^4$ , with their e.s.d.'s were:

	$B_{11}$	$B_{22}$	$B_{33}$	$B_{12}$	$B_{13}$	$B_{23}$
Ba(1)	11(0.3)	79(3)	30(1)	0	-5(1)	0
Ba(2)	11(0.3)	99(4)	21(0.4)	0	0	25(2)
P	13(1)	81(10)	14(1)	-1(4)	1(1)	1(4)

factors for both enantiomorphs. The results are in accord with previous conclusions concerning the absolute configuration of D(+)-ribose. Table 2 lists some of the reflections showing large differences between the observed structure factor and that calculated for the L-form. Near the end of the refinement, the overall reliability factor for the D(+) form was significantly lower than that for the L(-) form (10.8% and 14.3% respectively).

### Results and discussion

The structural parameters found in this work have higher e.s.d.'s than those in most other reported investigations of nucleotides because of the presence of the barium ions. These ions not only dominate the scattering, but also cause large absorption errors, which are undoubtedly not entirely corrected. The e.s.d.'s average about 0.03 Å for the bonds between the light atoms, and about 2° for the angles involving these atoms. All the intramolecular bond distances and angles are shown in Fig. 1; the numbering system used is that of *Chemical Abstracts*.

The geometry found for the phosphate group in this molecule agrees, within the 95% confidence level of twice the e.s.d., with that found in calcium thymidylate (Trueblood, Horn & Luzzati, 1961), cytidylic acid (Alver & Furberg, 1959), adenosine-5'-phosphate (Kraut & Jensen, 1963) and 2-aminoethanol phosphate (Kraut, 1961). The conformation of the phosphate group in relation to the sugar is also of interest; Furberg (1960) has discussed the conformational possibilities, with emphasis on the consequent differences in extension of the molecule. It is noteworthy that in the known ribose and deoxyribose phosphates with the 5' linkage (calcium thymidylate, barium ribose-5-phosphate, adenosine-5'-phosphate, and the present molecule), the phosphate group is fully extended with the P-O ester bond nearly parallel to the C(4')-C(5') bond.

A parameter that appears even more significant concerns the conformation about the C(5')-C(4') bond (of a furanose). After the essence of the following discus-

Table 2. Comparison of  $F_o$  with  $|F_c|$  for D- and L-forms of barium uridine phosphate\*

$hkl$	$ F_o $	$ F_c _L$	$ F_c _D$
13 $\bar{1}$	156	112	141
42 $\bar{1}$	122	153	112
42 $\bar{1}$	159	112	153
91 $\bar{1}$	96	133	115
73 $\bar{1}$	171	213	194
44 $\bar{1}$	237	168	195
15 $\bar{1}$	47	89	49
15 $\bar{1}$	86	49	89
35 $\bar{1}$	213	175	197
35 $\bar{1}$	154	197	175
55 $\bar{1}$	171	126	150
91 $\bar{2}$	272	332	289
142 $\bar{2}$	111	171	129
93 $\bar{2}$	141	191	153
51 $\bar{3}$	180	135	179
75 $\bar{3}$	180	124	142

\* Near the end of the refinement

sion had been written we received an unpublished manuscript (Sundaralingam, 1964) concerned with the conformations of furanoside rings in which he had also considered the orientation of the C(5')-O(5') bond, and had made calculations for six of the compounds in Table 3, including two for which data were unavailable to us. Fig. 2 is a schematic view along the C(5')-C(4') bond showing the approximate conformation in the present molecule and other ribose derivatives. For convenience in comparing different structures we define two dihedral angles, as in Fig. 2:  $\varphi_{OO}$  between the projected C(5')-O(5') and C(4')-O(1') bonds, and  $\varphi_{OC}$  between the projected C(5')-O(5') and C(4')-C(3') bonds. When the conformation about the C(5')-C(4') bond is similar to that in Fig. 2 then both of these angles will be in the neighborhood of  $60^\circ$ , i.e. C(5')-O(5') is *gauche* to both C(4')-O(1') and C(4')-C(3'); in either of the other two possible staggered conformations, one of the two angles would be near  $180^\circ$ . Table 3 gives the values of these angles in a variety of ribose and deoxyribose derivatives, as well as in some hexoses with pyranose as well as furanose rings. The compounds vary widely; yet it is remarkable how similar the values of these angles turn out to be. Quite clearly the conformation of Fig. 2 is the preferred one for exocyclic -CH<sub>2</sub>O- groups in furanose derivatives, regardless of whether or not the oxygen atom is esterified or is involved in hydrogen bonding; it is the only conformation that has been reported for nucleotides, whether  $\beta$ - or  $\alpha$ -. The reason why this conformation seems preferred is not clear. It may be relevant that ethylene glycol and ethylene chlorohydrin (in the vapor phase) have the *gauche* rather than the *trans* conformation, with the dihedral angle about  $74^\circ$  (Bastiansen, 1949), while 1,2-dichloroethane (Ainsworth & Karle, 1952) is predominantly *trans*. Bastiansen has attributed this to intramolecular hydrogen bonding, even though the O-H...O angle would be in the neighborhood of  $110$ - $120^\circ$ ; in any event, that explanation cannot suffice for all the present compounds since many of them are esterified at O(5') (unless it is argued that the free sugars are in this conformation because of intramolecular hydrogen bonding and that after the esters are formed the barrier to rotation about these bonds is abnormally high so that other conformers do not form). Furthermore, this explanation would not suffice to eliminate *gt* conformers (Table 3).

Whatever the explanation of the preference for the *gg* conformation about C(5')-C(4') (Table 3), it has important implications for  $\beta$ -ribo- and  $\beta$ -deoxyribonucleotides. In the  $\beta$ -configuration, the glycosidic bond and the C(4')-C(5') bond are on the same side of the furanose ring, as is evident in Fig. 1. Because of the position taken by the O(5') atom, there is limited room for the bulkier parts of the purine or pyrimidine ring in different conformations about the glycosidic C(1')-N bond. Any bulky substituent on the atom adjacent to the glycosidic N atom interferes with O(5'), as is evident from models. It is apparently in part for

this reason that only *anti* conformations about the glycosidic C-N bond (Donohue & Trueblood, 1960) are found for  $\beta$ -nucleotides. The torsion angle about this bond is  $-43^\circ$  in the present molecule.

Another factor which may help to stabilize *anti* conformations of  $\beta$ -nucleotides is the possible contribution of C-H...O hydrogen bonding (Sutor, 1963), especially in the *anti* conformations of pyrimidine nucleotides, such as the present one. The possible interaction is between the hydrogen on C(6) of the pyrimidine ring and O(5') of the sugar. The C(6)...O(5') distance is  $3.17 \text{ \AA}$  in the present molecule, and although the hydrogen atom on C(6) has not been located, it must lie close to the C...O line; in the uridine residue of adenosine-uridine phosphate (Shefter, Barlow, Sparks & Trueblood, 1964), the corresponding

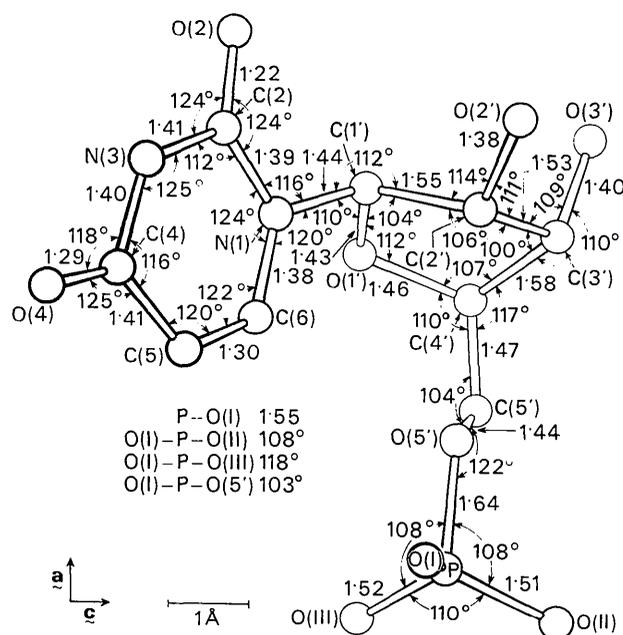


Fig. 1. Bond distances and angles in the nucleotide. The actual conformation of the molecule in the crystal is shown as viewed down b.

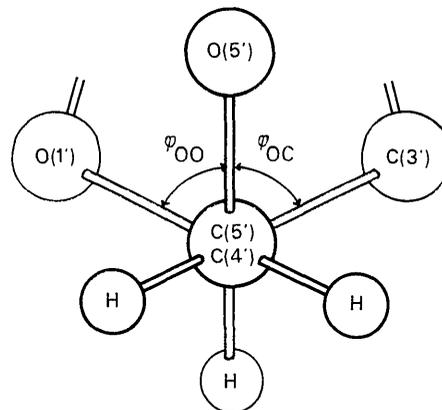


Fig. 2. Schematic projection down the C(5')-C(4') bond, showing the dihedral angles  $\varphi_{OO}$  and  $\varphi_{OC}$ .

C...O distance is 3.18 Å, with the H...O distance 2.3 Å, and the C-H...O angle 142°. In the calcium salt of thymidine-5'-phosphate (Trueblood, Horn & Luzzati, 1961), the corresponding distances and angle are 3.42 Å, 2.4 Å and 169°. All of these values agree quite plausibly with those suggested by Sutor (1963) as characteristic of C-H...O hydrogen bonding in analogous systems.

Sundaralingam (1964) has suggested that differences in furanose ring conformation may play a role in the variations of the glycosidic torsion angles in nucleosides and nucleotides.

Least-squares planes passing through the furanose ring of the present molecule were calculated for all five possible sets of four atoms; the combination giving the most satisfactory solution was the one with C(1'), C(3'), C(4'), and O(1') coplanar and C(2') out of the plane by 0.52 Å (Table 4). This result is in accord with the conformation in barium ribose-5-phosphate (Furberg & Mostad, 1960), and with the general conclusions of Spencer (1959) concerning the puckering of the ribose. None of the bond angles and distances in the ribose molecule differ from the values reported in other nucleotide and nucleoside structures by more than twice their e.s.d.'s.

The uracil ring has essentially the same bond angles and lengths as those found in calcium thymidylate, 5-fluoro-2'-deoxy- $\beta$ -uridine (FUDR), (Harris & Macintyre, 1964), uracil (Parry, 1954), thymine (Gerdil, 1961), the complex of *N*-methyluracil with *N*-ethyladen-

ine (Mathews & Rich, 1964), and  $\beta$ -adenosine-2'- $\beta$ -uridine-5' phosphoric acid (Shefter *et al.*, 1964). The C(4)-O(4) bond appears long, 1.29 Å, compared to the same bond in the above structures, average value 1.23 Å. However, this bond length has an e.s.d. of 0.03 Å, the position of C(4) being especially uncertain, so the difference is not significant. It is noteworthy that the C-C-O angle at C(4) is appreciably larger than the N-C-O angle here, just as it is in uracil itself, in *N*-methyluracil, and in the uracil residue of the above-cited adenosine-uridine phosphate, although in fluoro-deoxyuridine the angles are equal. This same difference in the corresponding angles in thymine and its derivatives has been attributed to repulsion of the methyl group on C(5) and the oxygen atom, but this explanation now seems specious.

The six atoms comprising the uracil ring are coplanar (plane II of Table 4), with none of the ring atoms displaced from the least-squares plane by more than twice its e.s.d. Atom C(1') of the ribose ring is 0.12 Å above the plane and O(2) is 0.14 Å below this plane, while O(4) is coplanar with the ring. The opposing displacement of O(2) and C(1') was also found in calcium thymidylate. This effect may be partly, if not wholly, due to steric hindrance between the sugar and the base. The dihedral angle between the plane of the furanose ring and the uracil ring is 67°, a value very similar to that in all other known nucleotide structures.

The packing of the bases and sugars is illustrated in part in Fig. 5. Because the base planes lie nearly

Table 3. Conformation about C(5')-C(4') bond\*

Compound	$\varphi_{00}$	$\varphi_{0C}$	Conformation†	Comment	Reference
Barium uridine-5'-phosphate	54°	70°	<i>gg</i>		This work
Cytidine-3'-phosphate	75	44	<i>gg</i>		Sundaralingam & Jensen (1964)
Adenosine-5'-phosphate	78	40	<i>gg</i>		Kraut & Jensen (1963)
Deoxyadenosine	68	173	<i>gt</i>	Deoxyribose	Watson, Sutor & Tollin (1963)
Calcium thymidine-5'-phosphate	63	57	<i>gg</i>	Deoxyriboside	Trueblood, Horn & Luzzati (1961)
Barium ribose-5-phosphate	67	56	<i>gg</i>		Furberg & Mostad (1962)
$\beta$ -Adenosine-2' $\beta$ -uridine-5'-phosphate	73	45	<i>gg</i>	Adenosine residue	Shefter <i>et al.</i> (1964)
	62	57	<i>gg</i>	Uridine residue	
5-Fluoro-2'-deoxyuridine	173	68	<i>tg</i>	Deoxyribose	Harris & Macintyre (1964)
Vitamin B <sub>12</sub> (air-dried)	60	66	<i>gg</i>	$\alpha$ -Riboside and 3'-phosphate linkage	Hodgkin <i>et al.</i> (1962)
$\alpha$ -D-glucose	66	172	<i>gt</i>	Glucopyranose	McDonald & Beevers (1952)
$\beta$ -D-glucose	61	58	<i>gg</i>	Glucopyranose	Ferrier (1963)
Sucrose‡	58	60	<i>gg</i>	Glucopyranose	Beevers & Cochran (1947)
	74	38	<i>gg</i>	Fructofuranose, C(6')-C(5')	
	51	64	<i>gg</i>	Fructofuranose, C(1')-C(2')	
Cellobiose	33	168	<i>gt</i>	Glucopyranose	Jacobson, Wunderlich & Lipscomb (1961)
	62	180	<i>gt</i>	Glucopyranose	

\* C(6')-C(5') in the hexoses, except as noted for fructose residue of sucrose. With the exception of the values for cytidine-3'-phosphate and deoxyadenosine, reported to us by Sundaralingam (1964), all values given were calculated by us from parameters in the references cited.

† The letters *g* and *t* refer to the terms *gauche* and *trans*, to signify whether the values of the dihedral angles of Fig. 2 are near 60° or near 180°; the first refers to  $\varphi_{00}$  and the second to  $\varphi_{0C}$ .

‡ In sucrose sodium bromide dihydrate, but the conformations are the same about C(6)-C(5) of both residues in crystalline sucrose (Brown & Levy, 1963), although differing by 135° around C(1')-C(2') of the fructose residue. It is noteworthy that C(2') in fructose has no hydrogen atoms, the lower hydrogen atom in the view analogous to Fig. 2 being replaced by a second (ether) oxygen atom, linked to the glucose residue.

parallel to **a** (Table 4), the pairs of bases related by the twofold axis along **a** at  $(x, \frac{1}{2}, 0)$  are nearly parallel to one another, as illustrated in the lower part of Fig. 5. The angle between them is just  $4^\circ$ ; O(4) of one ring is only 3.12 Å from O(4), and 3.27 Å from C(5), of the other. All other contacts are greater than 3.3 Å.

An even closer intermolecular contact is between O(1') of one molecule and the pyrimidine ring of a second related by the twofold axis along **a** at  $(x, 0, 0)$  which passes through Ba(2). This is also illustrated in Fig. 5; the base planes themselves are not close, but O(1') is seen to project toward the other base, being only 2.74 Å from C(4), 3.02 Å from N(3), and 3.14 Å from both C(5) and O(4). This arrangement is found also for both sugars and both bases in adenosine-uridine phosphate (Shefter *et al.*, 1964), although none of the contacts there is as short as the O(1')...C(4) distance here. Close contacts of this sort between carbonyl oxygen atoms and carbonyl carbon atoms in

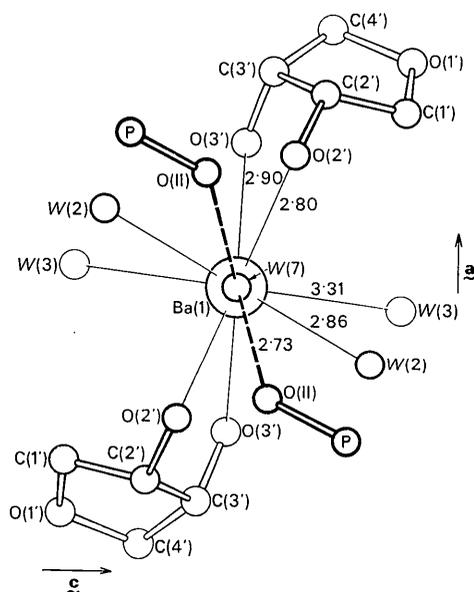


Fig. 3. The environment of Ba(1), viewed down **b**.

nearby molecules have been noted frequently (*e.g.* Bolton, 1963), although few as short as the present one have been reported.

### Barium coordination

The barium ions lie in two independent special positions in the structure. The ions in each of these positions have eight nearest-neighbor oxygen atoms at distances between 2.7 and 3.0 Å and two next-nearest neighbors at 3.3 Å; thus the total coordination number around the two unique barium ion positions is ten. The environments of the ions are illustrated in Figs. 3 and 5, and the Ba-O contact distances are listed in Table 5. The eight nearest oxygen neighbors of the barium ions are arranged in a distorted square Archimedean antiprism, with the two longer bonds extending out from triangular faces.

Ba(1), located on the twofold axis at  $(0, y, \frac{1}{4})$ , is coordinated directly to two hydroxyl groups in each of

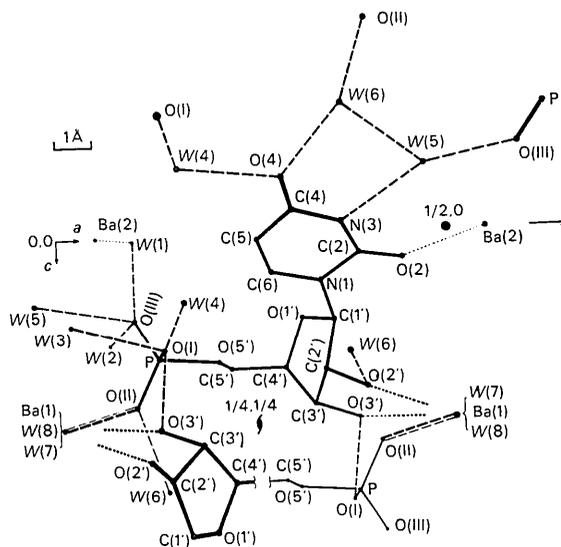


Fig. 4. Suggested hydrogen-bonding scheme and view of the molecule along **b**.

Table 4. Least-squares\* planes of ribose and uracil residues

Coefficients†	Atoms comprising the plane	Displacements	Displacements of other atoms
$A = 0.7737$	C(1')	-0.02 Å	C(2') -0.52 Å
$B = -0.6292$	O(1')	0.03	O(2') -0.11
$C = 0.0745$	C(3')	0.02	O(3') 1.34
$D = -2.900$	C(4')	-0.03	C(5') -1.16
			N(1) -0.92
			O(2) -0.14
$A = 0.0288$	N(1)	0.02	O(4) -0.04
$B = 0.7250$	C(2)	-0.04	C(1') 0.12
$C = 0.6882$	N(3)	0.05	
$D = -5.232$	C(4)	-0.04	
	C(5)	0.02	
	C(6)	-0.01	

\* All planes were calculated in a manner similar to that described by Schomaker, Waser, Marsh & Bergman (1959).

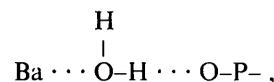
† These are coefficients for the equation of the plane in the form  $AX + BY + CZ + D = 0$ , with  $X$ ,  $Y$ , and  $Z$  in Å measured along **a**, **b**, and **c**\*

two ribose molecules. The Ba(1) to O(3') and O(2') distances are 2.90 and 2.80 Å, respectively. Brintzinger (1961) in his discussion of divalent metal complexes of nucleotides suggested the possibility of this type of coordination. A similar coordination of Ba<sup>2+</sup> has also been observed in barium ribose-5-phosphate (Furberg & Mostad, 1962), although there the Ba<sup>2+</sup> is coordinated also to the hydroxyl group on C(1'), not present here. Ba(1) is also bonded to four water molecules at distances of 2.7 to 2.9 Å and another two water molecules at 3.31 Å.

Ba(2), located on the twofold axis at (*x*, 0, 0), is coordinated with two O(2) atoms on different uracil rings. This separation is 2.78 Å. There are six water molecules at distances of 2.8 to 3.0 Å from this barium ion, and two more at 3.32 Å. The Ba–O distances and arrangements found here are consistent with those reported previously (Nardelli & Fava, 1962; Furberg & Mostad, 1962); the coordination number of barium with oxygen typically ranges from nine to twelve, with the average distance increasing as the coordination number increases.

The coordination polyhedra of the barium ions are linked together by the mutual bonding of the barium ions to waters (2) and (3). Water (2) is at 2.86 Å from Ba(1) and 3.32 Å from Ba(2), while water (3) is 2.79 Å from Ba(2) and 3.31 Å from Ba(1).

The barium ions are not linked directly to the phosphate oxygen atoms, but are connected to them through water bridges. These are of the type



which are similar to those found in the barium ribose-5-phosphate structure. This type of bonding, rather than the direct bonding of the metal ion to the phosphate oxygen atoms as found in calcium thymidylate, was suggested by Brintzinger, on the basis of equilibrium studies of the bonding of Co<sup>2+</sup>, Ni<sup>2+</sup>, and Zn<sup>2+</sup> in adenosine triphosphate systems. However, it should be noted (Furberg & Mostad, 1962) that deoxyribonucleotides, such as thymidine-5'-phosphate, have only one free sugar-hydroxyl group to coordinate with any cation present, while ribonucleotides have two (and ribonucleosides three).

### Hydrogen bonding

Some features of the network of hydrogen bonds remain uncertain because no effort was made to locate the hydrogen atoms. The most probable hydrogen bonds are listed in Table 5, with pertinent distances and angles, and many of them are illustrated in Figs. 4 and 5, where they are designated by dashed lines. We have avoided so designating any short interaction which forms the edge of a barium coordination polyhedron for, as Templeton (1960) and Clark (1963) have pointed out, it is unlikely that protons will lie along these edges, especially if other positions are available to them. Only two interactions of this sort are smaller

Table 5. *Barium–oxygen contacts and possible hydrogen bonds*

Atom A	Atom B	Distance*	Some relevant angles	
Ba(1)	O(2')	2.80 Å (2)		
	O(3')	2.90 (2)		
	W(2)	2.86 (2)		
	W(3)	3.31 (2)		
	W(7)	2.70 (1)		
	W(8)	2.85 (1)		
Ba(2)	O(2)	2.78 (2)		
	W(1)	2.81 (2)		
	W(2)	3.32 (2)		
	W(3)	2.79 (2)		
	W(4)	2.96 (2)		
O(I)	O(3')	2.64	C(3')–O(3') ··· O(I)	115°
	W(3)	2.80		
	W(4)	2.65		
O(II)	W(6)	2.58		
	W(7)	2.73	O(II) ··· W(7) ··· O(II)'	98
	W(8)	2.69	O(II) ··· W(8) ··· O(II)'	100
O(III)	W(1)	2.79		
	W(2)	3.00		
	W(5)	2.84		
	W(6)	2.56	C(2')–O(2') ··· W(6)	105
O(2')	W(6)	2.56	C(2)–N(3) ··· W(5)	120
N(3)	W(5)	2.91	C(4)–N(3) ··· W(5)	114
	W(3)	W(5)	2.96	O(I) ··· W(3) ··· W(5)
W(4)	O(4)	2.93	O(I) ··· W(4) ··· O(4)	119
W(6)	W(5)	2.88	O(III) ··· W(5) ··· W(6)	118
	O(4)	2.81	W(6) ··· W(5) ··· W(3)	118
			O(II) ··· W(6) ··· W(5)	101
			O(II) ··· W(6) ··· O(4)	131
			W(5) ··· W(6) ··· O(4)	81

\* The number in parentheses after each Ba–O distance gives the number of equivalent contacts of this sort.

than 3.0 Å:  $W(2) \cdots W(4)$ , 2.84 Å, and  $O(2') \cdots W(7)$ , 2.95 Å.

Each of the three phosphate oxygen atoms, O(I), O(II), O(III), appears to accept three hydrogen bonds. Each set of hydrogen-bonded neighbors is so arranged as to form with the phosphorus a distorted tetrahedron. The average lengths of the bonds to O(I) and O(II) are 2.7 Å whereas the three hydrogen-bonds to O(III) average 2.9 Å. The eight unique water molecules found in this structure are each involved in a hydrogen bond to a phosphate oxygen atom; the ninth bond comes from O(3') of the ribose. O(2') also appears to donate its hydrogen atom in a short hydrogen bond to water molecule  $W(6)$ .

The hydrogen atom on N(3) of the uracil ring is directed towards  $W(5)$ , 2.91 Å away. Water molecules (4) and (6) are 2.93 and 2.86 Å from O(4) of the uracil ring. From the angles around the water molecules it appears likely that there is a hydrogen bond between  $W(4)$  and O(4).  $W(5)$  and  $W(6)$  are the only two water molecules not coordinated to a barium ion, but each of them has four neighbors at reasonable distances for hydrogen bonds. The two water molecules in special positions,  $W(7)$  and  $W(8)$ , have very high temperature

factors, and may well be somewhat disordered, especially in view of their high apparent coordination numbers if they occupy the exact twofold position. Structure factor calculations with models containing disordered water molecules somewhat off the twofold axes were inconclusive.

As mentioned earlier, the fresh crystal appears to contain two more water molecules per asymmetric unit than were actually found in our Fourier syntheses. Furberg & Mostad (1962) reported that some water molecules appeared to be lost from crystals of barium ribose-5-phosphate during photography. We have not succeeded in unequivocally identifying regions in the present structure from which water molecules might have migrated, although there may be room for one along the *c* axis at  $(\frac{1}{4}, y, \frac{1}{4})$ . The molecule spirals about this axis, and water molecules might be trapped here initially but not held firmly. We attempted to measure the density of our single specimen after the collection of the intensity data, but because of apparent decomposition succeeded only in establishing that it was in the neighborhood of 1.9 g.cm<sup>-3</sup>. Since the crystals with nine water molecules per molecule of salt contain 26% water, the loss of two water molecules would reduce

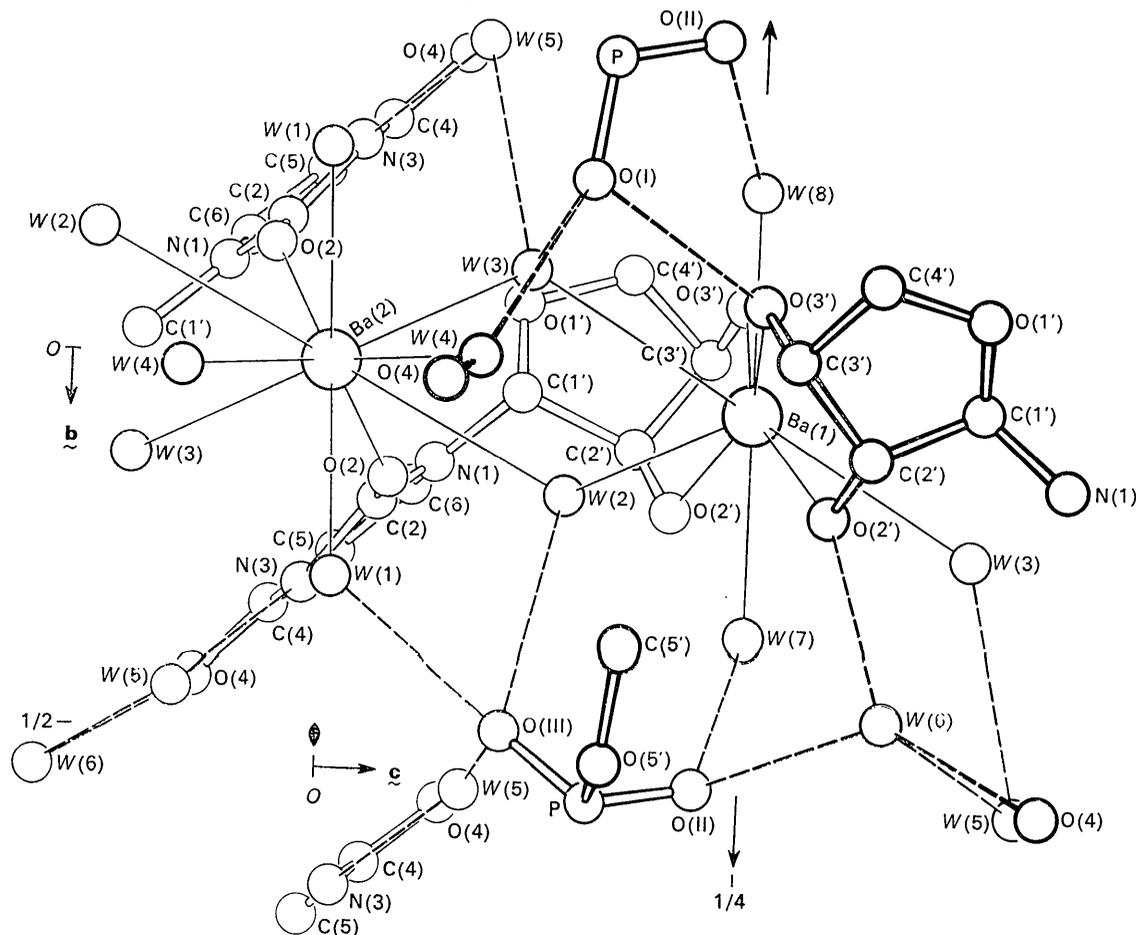


Fig. 5. A portion of the structure viewed down *a*, showing the coordination around the barium ions and some possible hydrogen bonds (dashed lines).

Table 6. Observed and calculated structure factor amplitudes. The three columns are, respectively, I, F<sub>o</sub>, and |F<sub>c</sub>|

Table with multiple columns containing numerical data for structure factor amplitudes. The table is organized into several sections, each with a header indicating the Miller indices (h, k, l) and the corresponding observed intensity (I), observed structure factor amplitude (F<sub>o</sub>), and calculated structure factor amplitude (|F<sub>c</sub>|). The data points are arranged in a grid-like format across the page.

Table 6 (cont.)

H <sup>+</sup> 21, k <sup>+</sup> 4	10 89 79	11 81 76	-2 31 24	-3 162 188	H <sup>+</sup> 11, k <sup>+</sup> 5	-4 58 34	-3 103 100	15 62 70	-3 103 101
-11 82 77	-10 82 80	-11 85 75	-3 56 59	-4 70 62	1 127 151	-4 52 32	-4 104 99	-15 51 75	-4 56 74
12 90 86	11 135 113	12 81 81	-3 58 64	-4 122 138	1 101 115	-3 91 80	-3 89 86	-17 43 26	-5 48 59
-12 96 99	-11 110 107	-12 37 43	-4 68 64	-5 139 135	1 94 101	-5 89 84	-5 81 66	-19 43 61	-5 50 67
13 104 94	12 94 94	13 50 51	-4 50 51	-5 140 140	1 87 94	-4 77 73	-4 77 73	-10 21 19	-10 21 19
-13 96 94	-13 61 60	-13 52 56	-5 58 59	-6 75 60	-2 98 104	-6 68 70	-6 64 102	-7 70 60	-7 70 60
14 104 94	13 90 76	14 56 51	-5 67 63	-6 74 61	3 41 48	-7 61 68	-7 90 78	-7 150 138	-7 58 59
-14 84 90	-14 78 85	-14 68 68	-6 75 68	-7 129 128	-1 57 57	-8 58 68	-8 77 79	-8 104 135	-8 37 44
-14 84 90	14 79 61	15 61 66	-6 36 36	-7 134 127	4 75 67	8 58 59	8 53 44	-1 114 131	4 102 86
-15 81 81	-15 61 61	-15 45 56	-7 40 44	-8 84 59	-8 39 43	-8 44 44	-8 44 44	-2 16 13	-2 16 13
-16 77 85	15 79 75	-16 40 40	-8 84 59	-9 77 65	5 77 65	4 40 42	9 127 104	-1 138 113	11 71 65
-16 45 55	-16 60 68	H <sup>+</sup> 16, k <sup>+</sup> 4	8 61 62	9 200 176	-5 59 61	-10 28 20	-10 110 104	-1 107 110	-11 57 58
-17 41 41	16 55 57	0 27 32	9 52 54	10 45 25	6 118 92	10 47 26	-11 41 43	-4 120 94	12 34 31
-18 31 37	-18 46 54	-2 27 18	11 116 116	11 80 70	-7 51 49	-11 75 68	-11 88 98	-5 117 119	-13 41 58
-20 26 45	-20 46 54	3 110 119	11 30 31	12 66 32	-8 108 87	-12 38 25	-12 55 52	6 131 107	14 10 26
H <sup>+</sup> 4, k <sup>+</sup> 4	0 37 21	1 121 132	4 115 121	-11 30 36	9 103 80	13 46 54	-16 41 29	7 112 81	15 64 64
0 28 207	-1 102 111	2 135 143	4 58 59	12 31 36	-9 107 95	-12 38 25	-15 43 40	-15 43 40	-15 43 40
-1 169 177	-2 149 177	-3 169 177	-4 57 54	-5 57 54	-10 103 76	14 31 27	14 31 27	8 114 91	-16 13 13
-2 83 84	-2 128 100	-3 149 177	5 66 69	6 66 69	-10 73 67	-14 20 20	-20 16 17	-8 80 88	-17 35 53
-3 237 232	-4 190 172	-5 273 255	H <sup>+</sup> 24, k <sup>+</sup> 4	11 79 81	11 97 100	-15 37 45	-15 37 45	-15 37 45	-15 37 45
-4 190 172	-5 273 255	-6 455 257	12 43 46	13 43 46	12 89 71	16 24 18	11 117 116	10 67 67	10 67 67
-6 79 62	-7 96 62	-8 140 118	14 52 55	15 42 45	-12 74 63	-17 54 56	0 74 70	10 67 67	10 67 67
-7 193 171	-8 182 174	-9 200 185	16 50 53	17 42 45	14 56 33	H <sup>+</sup> 10, k <sup>+</sup> 5	0 63 58	-2 146 137	-2 146 137
-9 197 186	-10 200 185	-11 200 185	18 46 49	19 36 39	-14 56 33	1 73 72	1 73 72	-2 146 137	-2 146 137
-10 200 185	-11 200 185	-12 200 185	20 32 35	21 22 25	-15 55 51	-1 73 72	-1 73 72	-2 146 137	-2 146 137
-11 200 185	-12 200 185	-13 200 185	22 18 21	23 8 11	-15 55 51	2 81 72	4 80 80	-1 14 12	-4 20 31
-12 200 185	-13 200 185	-14 200 185	24 4 7	25 0 3	-16 62 56	3 89 76	-4 81 60	-1 41 38	-5 25 03
-13 200 185	-14 200 185	-15 200 185	26 0 3	27 0 3	-17 62 56	4 97 86	-5 139 119	10 56 46	7 86 84
-14 200 185	-15 200 185	-16 200 185	27 0 3	28 0 3	-18 62 56	5 105 92	-6 152 124	-6 152 124	-6 152 124
-15 200 185	-16 200 185	-17 200 185	28 0 3	29 0 3	-19 62 56	6 111 98	-7 165 137	-7 165 137	-7 165 137
-16 200 185	-17 200 185	-18 200 185	29 0 3	30 0 3	-20 62 56	7 117 104	-8 178 146	-8 178 146	-8 178 146
-17 200 185	-18 200 185	-19 200 185	30 0 3	31 0 3	-21 62 56	8 123 110	-9 191 158	-9 191 158	-9 191 158
-18 200 185	-19 200 185	-20 200 185	31 0 3	32 0 3	-22 62 56	9 129 116	-10 204 166	-10 204 166	-10 204 166
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-20 200 185	-21 200 185	-22 200 185	33 0 3	34 0 3	-24 62 56	11 141 128	-12 230 182	-12 230 182	-12 230 182
-21 200 185	-22 200 185	-23 200 185	34 0 3	35 0 3	-25 62 56	12 147 134	-13 243 196	-13 243 196	-13 243 196
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-27 200 185	-28 200 185	-29 200 185	40 0 3	41 0 3	-31 62 56	18 188 170	-19 321 262	-19 321 262	-19 321 262
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-38 200 185	-39 200 185	-40 200 185	51 0 3	52 0 3	-42 62 56	29 265 236	-30 464 372	-30 464 372	-30 464 372
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-40 200 185	-41 200 185	-42 200 185	53 0 3	54 0 3	-44 62 56	31 279 248	-32 490 392	-32 490 392	-32 490 392
-41 200 185	-42 200 185	-43 200 185	54 0 3	55 0 3	-45 62 56	32 286 254	-33 503 402	-33 503 402	-33 503 402
-42 200 185	-43 200 185	-44 200 185	55 0 3	56 0 3	-46 62 56	33 293 260	-34 516 412	-34 516 412	-34 516 412
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-44 200 185	-45 200 185	-46 200 185	57 0 3	58 0 3	-48 62 56	35 307 272	-36 542 432	-36 542 432	-36 542 432
-45 200 185	-46 200 185	-47 200 185	58 0 3	59 0 3	-49 62 56	36 314 278	-37 555 442	-37 555 442	-37 555 442
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-50 200 185	-51 200 185	-52 200 185	63 0 3	64 0 3	-54 62 56	41 349 308	-42 620 492	-42 620 492	-42 620 492
-51 200 185	-52 200 185	-53 200 185	64 0 3	65 0 3	-55 62 56	42 356 314	-43 633 502	-43 633 502	-43 633 502
-52 200 185	-53 200 185	-54 200 185	65 0 3	66 0 3	-56 62 56	43 363 320	-44 646 512	-44 646 512	-44 646 512
-53 200 185	-54 200 185	-55 200 185	66 0 3	67 0 3	-57 62 56	44 370 326	-45 659 522	-45 659 522	-45 659 522
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-60 200 185	-61 200 185	-62 200 185	73 0 3	74 0 3	-64 62 56	51 419 368	-52 750 592	-52 750 592	-52 750 592
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-63 200 185	-64 200 185	-65 200 185	76 0 3	77 0 3	-67 62 56	54 440 386	-55 789 622	-55 789 622	-55 789 622
-64 200 185	-65 200 185	-66 200 185	77 0 3	78 0 3	-68 62 56	55 447 392	-56 802 632	-56 802 632	-56 802 632
-65 200 185	-66 200 185	-67 200 185	78 0 3						

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## Short Communications

*Contributions intended for publication under this heading should be expressly so marked; they should not exceed about 1000 words; they should be forwarded in the usual way to the appropriate Co-editor; they will be published as speedily as possible. Publication will be quicker if the contributions are without illustrations.*

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**On weights for a least-squares refinement.** By A. DE VRIES. *Laboratorium voor Kristalchemie der Rijksuniversiteit, Utrecht, The Netherlands.*

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### *The determination of the probable errors*

The object of a least-squares refinement is the minimization of a quantity such as

$$\sum w(hkl)\{F_{\text{obs}}(hkl) - F_{\text{calc}}(hkl)\}^2$$

in which the weight  $w(hkl)$  of each term should be taken inversely proportional to the square of the probable error of the corresponding  $F_{\text{obs}}$  (see *e.g.* Lipson & Cochran, 1957);  $F_{\text{obs}}$  and  $F_{\text{calc}}$  stand here and in the following for their moduli. The essential problem in the determination of weights is therefore how to get an estimate of the probable errors in the measurements. There are three basically different methods of doing this, which are briefly discussed.

One way is to determine experimentally the probable error in  $F_{\text{obs}}$  by repeated measurements. This determination is complicated, however, by the presence of various kinds of systematic error.

Another method is to calculate the probable error in  $F_{\text{obs}}$  on the basis of theoretical considerations (*e.g.* Evans, 1961). Here the systematic errors constitute an even larger problem.

The third method is to refine the structure first, using some arbitrary weighting scheme (*e.g.* the same weight for all reflexions), and next to take  $F_{\text{obs}} - F_{\text{calc}}$  as a measure for the error in  $F_{\text{obs}}$ .

None of these methods is quite correct. The first two for the reason that the weights as defined above are generally not those one really wants, for the deviations in  $F_{\text{calc}}$  due to approximations in the model (*e.g.* the omission of hydrogen atoms or the use of incorrect atomic scattering factors) should also be taken into account for the calculation of the weights (Kroon, 1962). The third method is not quite correct because errors in  $F_{\text{calc}}$  due to incorrect parameter values should not be included in the calculation of the weights,