

# The Crystal and Molecular Structure of Adeninium Phosphate, $C_5H_6N_3^+ \cdot H_2PO_4^-$

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## Abstract

The title compound is monoclinic,  $P2_1/c$ , with  $a = 10.904$  (3),  $b = 11.261$  (5),  $c = 7.234$  (3) Å,  $\beta = 94.36$  (3)°.  $Z = 4$ . The structure was refined to  $R = 0.068$  for 1394 counter reflexions. The adenine base is monoprotonated at N(1). There are hydrogen bonds between the adenine base and phosphate groups and between the adenine bases themselves.

## Introduction

The structure of adeninium phosphate has been determined as part of a study of the transfer of energy and information in nucleic acids and their components. Single crystals serve as a model suitable for the interpretation of optical measurements on polynucleotides, carried out at the Institute of Physics, Charles University, Praha. This communication is a continuation of our studies concerned with the structures of adeninium sulfate (Langer & Huml, 1978*a*), adenine hydrobromide hemihydrate (Langer & Huml, 1978*b*) and adeninium hemisulfate hydrate (Langer, Huml & Lessinger, 1978).

## Experimental

Crystals were grown on the basis of measurement of the solubility curve (solubility 1.09 g/100 ml phosphoric acid at 293 K; temperature factor of solubility  $\alpha = 9.3 \times 10^{-2}$  g/100 ml/K) by cooling the solution of adeninium phosphate in 2*N* phosphoric acid in a special crystallizer with reversible stirring of the crystal seeds (starting temperature in the range 302–311 K, cooling gradient 0.1 K/day, maximum crystal dimensions  $40 \times 4 \times 1$  mm). Crystals are colorless, very brittle and often twinned. The molecular formula was confirmed by elemental analysis. Crystal data are presented in Table 1.

Preliminary cell dimensions and systematic absences (for  $h0l$ :  $l = 2n + 1$ ; for  $0k0$ :  $k = 2n + 1$ ) were determined from photographs. Definitive parameters were obtained by refining 10 reflexions in the range  $71.8 \leq 2\theta \leq 85.1^\circ$ , measured with a Syntex  $P2_1$  automated diffractometer [ $\lambda(\text{Cu } K\alpha) = 1.5418$  Å, graphite monochromator, room temperature]. The crystal (dimensions  $0.30 \times 0.30 \times 0.20$  mm) was placed on a goniometer head in a general position. The density was measured by flotation in tetrachloromethane and bromoform.

## Intensity measurement

Intensities were measured with the same diffractometer by the  $\theta$ – $2\theta$  scan method under conditions described by Langer & Huml (1978*a*). The minimum scan rate was  $1^\circ \text{ min}^{-1}$  in  $2\theta$ . The whole measurement was corrected for the fluctuation of three standard reflexions (after each 50 reflexions) by the program *INTER* (Langer, 1973). In the range up to  $2\theta = 140^\circ$ , 1545 independent reflexions were measured, 1394 of which were observed ( $I > 1.96\sigma_I$ , where  $\sigma_I$  was calculated from counting statistics). Intensities and their e.s.d.'s were corrected for the Lorentz–polarization factor by  $L_p = [(1 + \cos^2 2\theta_M \cos^2 2\theta)/(1 + \cos^2 2\theta) + (1 + \cos 2\theta_M \cos^2 2\theta)/(1 + \cos 2\theta_M)]/2 \sin 2\theta$ , where  $2\theta_M$  is the diffraction angle of the monochromator ( $26.568^\circ$  for Cu  $K\alpha$  radiation). No correction for absorption was made.

Table 1. *Crystal data*

Monoclinic, $P2_1/c$	$C_5H_6N_3^+ \cdot H_2PO_4^-$
$a = 10.904$ (3) Å	$\mu(\text{Cu } K\alpha) = 2.886 \text{ mm}^{-1}$
$b = 11.261$ (5)	$D_m = 1.731$ (5) $\text{Mg m}^{-3}$
$c = 7.234$ (3)	$D_x = 1.748$ (1)
$\beta = 94.36$ (3)°	$Z = 4$
$V = 885.7$ (6) Å <sup>3</sup>	$F(000) = 480$
FW 233.13	

### Structure determination and refinement

The position of the P atom was determined from a Patterson function sharpened by the Lp factor. The subsequent Fourier map showed the phosphate anion. In the next step the positions of all the non-H atoms were determined.

The structure was refined by least squares in the block-diagonal approximation ( $9 \times 9$  matrix for the non-H atoms with anisotropic temperature factors and  $4 \times 4$  matrix for the H atoms with isotropic temperature factors);  $\sum w_F(|F_o| - |F_c|)^2$  was minimized. Scattering factors of all non-H atoms with correction for anomalous scattering were taken from *International Tables for X-ray Crystallography* (1974), those for H from Stewart, Davidson & Simpson (1965). Unobserved reflexions were excluded. The modified program NRC-10 (Ahmed, Hall, Pippy & Huber, 1966) was employed with the weighting scheme  $w_F = 1/[\sigma_F^2 + (0.02F_o)^2]$ . When  $R = \sum ||F_o| - |F_c|| / \sum |F_o|$  dropped to 0.12 for isotropically refined non-H atoms, a difference synthesis showed all H atoms. The refinement of all non-H (anisotropic) and H atoms (isotropic temperature factors) was stopped when the shifts of all parameters were  $< 0.15\sigma$ . The final  $R$  was 0.068. The

Table 2. Positional parameters ( $\times 10^4$ ) of the non-hydrogen atoms with e.s.d.'s

	x	y	z
P	1906 (1)	8918 (1)	8252 (1)
O(1)	1020 (2)	9758 (2)	7249 (4)
O(2)	2974 (3)	9596 (2)	9365 (4)
O(3)	2598 (3)	8153 (2)	6875 (5)
O(4)	1304 (3)	8109 (3)	9577 (4)
N(1)	1400 (3)	4226 (3)	7817 (4)
C(2)	2196 (4)	5097 (4)	8372 (6)
N(3)	3360 (3)	4959 (3)	8891 (5)
C(4)	3703 (4)	3790 (3)	8832 (6)
C(5)	2982 (3)	2839 (3)	8313 (6)
C(6)	1722 (3)	3056 (3)	7718 (6)
N(6)	926 (3)	2264 (3)	7080 (5)
N(7)	3650 (3)	1799 (3)	8439 (5)
C(8)	4752 (4)	2150 (4)	9030 (7)
N(9)	4843 (3)	3341 (3)	9271 (5)

Table 3. Positional parameters ( $\times 10^3$ ) of the H atoms with e.s.d.'s

	x	y	z
H(1)	48 (5)	439 (5)	744 (7)
H(2)	188 (3)	591 (3)	840 (4)
H(61)	24 (4)	258 (4)	685 (6)
H(62)	107 (7)	135 (7)	698 (10)
H(8)	521 (6)	161 (5)	936 (9)
H(9)	566 (4)	375 (4)	956 (7)
H(O2)	316 (5)	1027 (5)	877 (8)
H(O3)	179 (4)	767 (3)	639 (6)

coordinates of all non-H atoms are in Table 2, those of the H atoms in Table 3.\*

The residual electron density on the final difference map did not exceed  $\pm 0.45 \text{ e } \text{Å}^{-3}$ .

### Structure description

The numbering scheme, bond distances, valency angles and their e.s.d.'s are given in Fig. 1. The thermal ellipsoids at 50% probability for non-H atoms in projection along  $c$  (Soler, 1973) are given in Fig. 2. The analysis of the thermal vibration of the adenine moiety and of the phosphate group was carried out in the TLS

\* Lists of structure factors and thermal parameters have been deposited with the British Library Lending Division as Supplementary Publication No. SUP 34226 (20 pp.). Copies may be obtained through The Executive Secretary, International Union of Crystallography, 5 Abbey Square, Chester CH1 2HU, England.

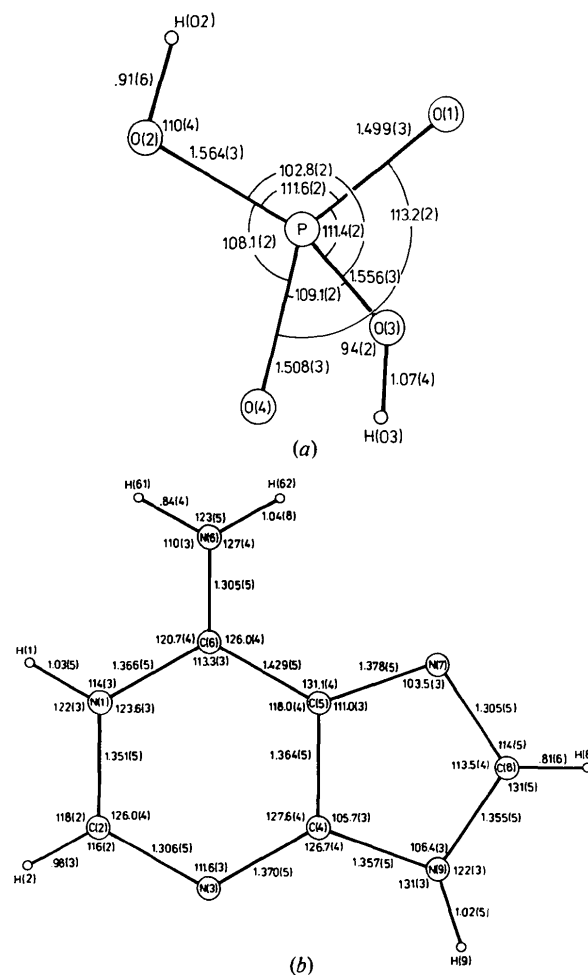


Fig. 1. Numbering scheme with bond distances (Å), valency angles ( $^\circ$ ) and their respective e.s.d.'s. (a) Phosphate group, (b) adenine base.

approximation to rigid-body motion (Schomaker & Trueblood, 1968). The correction of the bond distances for atomic libration was calculated by Cruickshank's (1956) method. The values of the tensors, **T**, **L**, **S**, their eigenvalues and direction cosines are given in Table 4. The criteria  $R.M.S. = [\sum (U_o - U_c)^2/n]^{1/2}$ ,  $E.S.D. = [\sum (U_o - U_c)^2/(n - s)]^{1/2}$  and  $(R.M.S.)' = [\sum \sigma^2(U_o)/n]^{1/2}$  show that the rigid-body approximation is acceptable for both the adenine moiety and the phosphate group. The bond distances for the

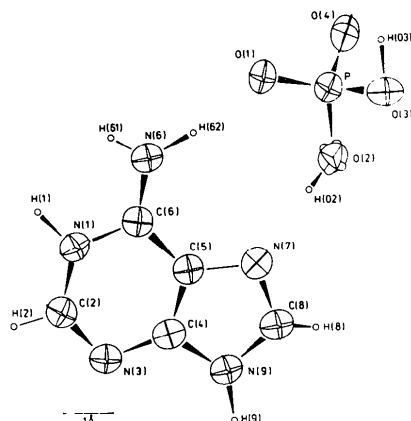


Fig. 2. Thermal ellipsoids at 50% probability for non-hydrogen atoms. The projection is along *c*. The H atoms are shown as small circles.

adenine base corrected for libration differ at most by the corresponding e.s.d.'s and have therefore been neglected. In the phosphate group changes in the bond distances are greater; they are summarized in Table 5. Only uncorrected values are used in the following discussion.

Table 6 shows deviations of the atoms from the weighted mean planes through the six-membered ring (plane I), the imidazole ring (plane II) and the whole base with the exception of N(6) (plane III).  $\chi^2$  values show the significant non-planarity of the six-membered ring, whereas the imidazole ring can be considered planar. The angle between planes (I) and (II) is  $0.68^\circ$ . The projection of the crystal structure along *c* is shown in Fig. 3. The adenine bases form parallel layers related by a center of symmetry; the overlap of imidazole rings and  $NH_2$  groups is caused by a *c*-glide plane. Fig. 4 shows the hydrogen-bonding scheme; the lengths and angles of the hydrogen bonds are in Table 7.

Table 5. Bond distances ( $\text{\AA}$ ) in the phosphate group corrected for rigid-body motion

	Uncorrected	Corrected
P—O(1)	1.499 (3)	1.507
P—O(2)	1.564 (3)	1.571
P—O(3)	1.556 (3)	1.567
P—O(4)	1.508 (3)	1.517

Table 4. Rigid-body motion parameters

The tensors are referred to a Cartesian coordinate system defined by  $X \parallel a$ ,  $Y \parallel b$ ,  $Z \parallel c^*$ ; the origin is at the center of mass.

Base				Phosphate group			
<b>T</b> =	$\begin{pmatrix} 372 (7) & -2 (6) & -27 (8) \\ & 406 (7) & -3 (8) \\ & & 493 (12) \end{pmatrix}$	$(\text{\AA}^2 \times 10^4)$	<b>T</b> =	$\begin{pmatrix} 367 (16) & -14 (8) & -65 (9) \\ & 392 (16) & 20 (8) \\ & & 545 (16) \end{pmatrix}$	$(\text{\AA}^2 \times 10^4)$		
<b>L</b> =	$\begin{pmatrix} 37 (5) & -4 (2) & 6 (3) \\ & 33 (4) & 7 (3) \\ & & 9 (3) \end{pmatrix}$	$(\text{rad}^2 \times 10^4)$	<b>L</b> =	$\begin{pmatrix} 86 (22) & 18 (5) & 34 (6) \\ & 63 (20) & -15 (5) \\ & & 46 (20) \end{pmatrix}$	$(\text{rad}^2 \times 10^4)$		
<b>S</b> =	$\begin{pmatrix} -5 (5) & -4 (5) & -12 (3) \\ & 3 (4) & 6 (4) \\ & & -5 (2) & 4 (2) & -1 (18) \end{pmatrix}$	$(\text{\AA rad} \times 10^4)$	<b>S</b> =	$\begin{pmatrix} 3 (19) & -15 (4) & -10 (5) \\ & 29 (5) & -1 (20) & -17 (5) \\ & & -14 (5) & -8 (4) & -2 (17) \end{pmatrix}$	$(\text{\AA rad} \times 10^4)$		
Eigenvalues of <b>T</b> ( $\text{\AA}^2 \times 10^4$ )	Direction cosines ( $\times 10^4$ )			Eigenvalues of <b>T</b> ( $\text{\AA}^2 \times 10^4$ )	Direction cosines ( $\times 10^4$ )		
499	-2101	-237	9774	569	-3118	1318	9410
406	-624	9980	107	389	-1066	9792	-1727
366	-9757	-576	-2112	344	-9442	-1537	-2913
Eigenvalues of <b>L</b> ( $\text{rad}^2 \times 10^4$ )	Direction cosines ( $\times 10^4$ )			Eigenvalues of <b>L</b> ( $\text{rad}^2 \times 10^4$ )	Direction cosines ( $\times 10^4$ )		
39	-8988	4303	-837	107	-8758	-2088	-4351
34	-3783	-8603	-3418	71	-243	-8759	4819
6	-2192	-2757	9359	16	-4818	4318	7625
Eigenvalues of <b>S</b> ( $\text{\AA rad} \times 10^4$ )	Direction cosines ( $\times 10^4$ )			Eigenvalues of <b>S</b> ( $\text{\AA rad} \times 10^4$ )	Direction cosines ( $\times 10^4$ )		
8	-5024	2852	8165	16	-4962	-7756	3852
2	144	9472	-3220	-3	-5561	6280	5443
-10	-8638	-1487	-4799	-12	-6663	604	-7459
R.M.S. = 0.0015 $\text{\AA}^2$ , E.S.D. = 0.0018 $\text{\AA}^2$ , (R.M.S.)' = 0.0017 $\text{\AA}^2$ .				R.M.S. = 0.0010 $\text{\AA}^2$ , E.S.D. = 0.0017 $\text{\AA}^2$ , (R.M.S.)' = 0.0013 $\text{\AA}^2$ .			

### Discussion of the structure

Comparison of the bond lengths and angles of the structure under study with those of other adenine bases monoprotonated at N(1) shows some significant differences: N(1)–C(2), 1.351 (5) Å, is somewhat shorter than the values found by Langer & Huml (1978*b*) [1.371 (5) Å] and Kistenmacher & Shigematsu (1974) [1.374 (4) Å], but is in good agreement with those of other structures (Langer, Huml & Lessinger, 1978; Table 7). This can be explained by different crystal packing of the hydrobromide and isomorphous hydrochloride. The same explanation is valid for the discrepancy of the angle N(1)–C(2)–N(3). C(5)–C(6) is significantly longer than in structures reported by us previously, but is in accord with

the mean value for monoprotonated adenines (Voet & Rich, 1970). Other distances and angles, showing discrepancies from some previously solved adenine structures, e.g. C(6)–N(1), C(5)–N(7), N(7)–C(8) and N(3)–C(4)–C(5), are also in good agreement with the respective mean values (Voet & Rich, 1970).

The effect of protonation of the adenine base at N(1) is reflected, as in all other cases, in a change of internal angles at N atoms in the pyrimidine ring.

The exocyclic angles of the imidazole ring show considerable departures from equality, as in adeninium hemisulfate hydrate (Langer, Huml & Lessinger, 1978) and adeninium sulfate *N*<sup>1</sup>-oxide (Prusiner & Sundaralingam, 1972).

Comparison of the bond distances for the phosphate group with those in *International Tables for X-ray Crystallography* (1962) shows O(1) to be a donor of a H atom (Table 7) and P–O(4) to be a double bond. H atoms were located at O(2) and O(3), and, accordingly, these P–O bonds are significantly longer.

Phosphate groups are hydrogen bonded to the adenine base by two means (Fig. 4 and Table 7): first *via* N(1)–H(1)···O(1<sup>ii</sup>) and N(6)–H(61)···O(4<sup>ii</sup>) bonds, and second *via* N(6)–H(62)···O(1<sup>iii</sup>) and

Table 6. *Weighted mean planes*

Equations are referred to a Cartesian coordinate system defined by  $X \parallel a$ ,  $Y \parallel b$ ,  $Z \parallel c^*$ . Deviations from planes (Å  $\times 10^3$ ) marked with a dagger indicate plane-defining atoms.

$$\begin{aligned} \text{(I)} \quad & 0.3075X + 0.1219Y - 0.9437Z + 4.3999 = 0 \quad (\chi^2 = 20.4) \\ \text{(II)} \quad & 0.3005X + 0.1120Y - 0.9472Z + 4.4834 = 0 \quad (\chi^2 = 5.3) \\ \text{(III)} \quad & 0.3058X + 0.1180Y - 0.9448Z + 4.4282 = 0 \quad (\chi^2 = 47.7) \end{aligned}$$

	(I)	(II)	(III)
N(1)	-4 (3)†	5 (3)	-2 (3)†
C(2)	-4 (4)†	-12 (4)	-8 (4)†
N(3)	5 (3)†	-11 (3)	-1 (3)†
C(4)	0 (4)†	-5 (4)†	-1 (4)†
C(5)	-10 (4)†	2 (4)†	-5 (4)†
C(6)	13 (4)†	33 (4)	19 (4)†
N(6)	82 (4)	118 (4)	94 (4)
N(7)	-16 (4)	1 (4)†	-9 (4)†
C(8)	-11 (5)	-7 (5)†	-7 (5)†
N(9)	15 (4)	5 (4)†	13 (4)†
H(1)	-28 (49)	-13 (49)	-25 (50)
H(2)	-21 (27)	-35 (28)	-28 (28)
H(61)	57 (41)	96 (41)	69 (41)
H(62)	73 (70)	118 (70)	88 (70)
H(8)	-157 (66)	-151 (66)	-152 (66)
H(9)	143 (48)	121 (48)	137 (48)

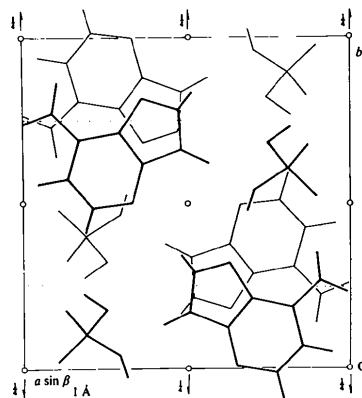


Fig. 3. Projection of the crystal structure along *c*.

Table 7. *Hydrogen bonds (A–H···B)*

A	H	B	A···B	B···H	$\angle A-H \cdots B$
N(1)	H(1)	O(1 <sup>ii</sup> )	2.703 (4) Å	1.72 (5) Å	157 (4)°
N(6)	H(61)	O(4 <sup>ii</sup> )	2.795 (4)	1.99 (4)	160 (4)
N(6)	H(62)	O(1 <sup>iii</sup> )	2.825 (4)	1.80 (8)	165 (6)
C(8)	H(8)	O(2 <sup>iv</sup> )	3.305 (5)	2.52 (7)	165 (6)
N(9)	H(9)	N(3 <sup>iv</sup> )	2.979 (5)	2.07 (5)	147 (4)
N(9)	H(9)	O(3 <sup>v</sup> )	2.978 (4)	2.33 (5)	120 (3)
O(2)	H(O2)	N(7 <sup>vi</sup> )	2.687 (4)	1.82 (6)	159 (5)
O(3)	H(O3)	O(4 <sup>vii</sup> )	2.533 (4)	1.63 (4)	138 (4)

Symmetry code

- (i)  $x, y, z$
- (ii)  $-x, -\frac{1}{2} + y, \frac{3}{2} - z$
- (iii)  $x, -1 + y, z$
- (iv)  $1 - x, 1 - y, 2 - z$
- (v)  $1 - x, -\frac{1}{2} + y, \frac{3}{2} - z$
- (vi)  $x, 1 + y, z$
- (vii)  $x, \frac{3}{2} - y, -\frac{1}{2} + z$

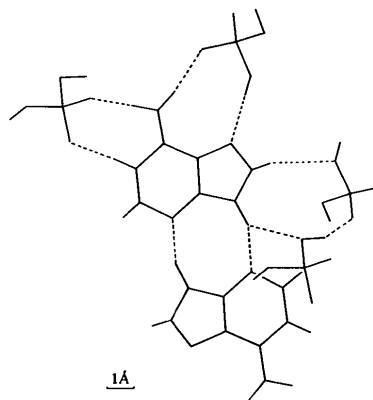


Fig. 4. Hydrogen-bonding scheme. The projection is along *c*.

O(2)—H(O2)···N(7<sup>v</sup>) bonds. The first is the more frequent for the interaction between the adenine base and phosphate (Sundaralingam, 1966). The sulfate can also interact in this way (Langer & Huml, 1978a; Langer, Huml & Lessinger, 1978). A mode of interaction similar to the second was observed between the phosphate and the protonated adenine base in nucleotides (Hecht & Sundaralingam, 1972) and for the sulfate (Langer & Huml, 1978a; Prusiner & Sundaralingam, 1972).

There are also hydrogen bonds between the adenine bases, *i.e.* N(9)—H(9)···N(3<sup>iv</sup>), and the bond related by the center of symmetry. This mode of adenine base pairing was described for the first time for adeninium hemisulfate hydrate (Langer, Huml & Lessinger, 1978).

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## The Crystal and Molecular Structure of $\alpha$ -D-manno-2-Heptulose

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#### Abstract

$\alpha$ -D-manno-2-Heptulose, C<sub>7</sub>H<sub>14</sub>O<sub>7</sub>, is monoclinic, space group *P2*<sub>1</sub>, with *a* = 6.626 (3), *b* = 7.049 (2), *c* = 9.499 (4) Å,  $\beta$  = 102.21 (4)°, *Z* = 2. The structure was refined to a final *R* of 0.026 for 837 counter reflexions. The molecule has the <sup>5</sup>C<sub>2</sub> chair conformation. Both primary alcoholic side chains have the *gauche*–*trans* conformation. The six OH groups participate in intermolecular hydrogen bonding and form a five-link finite chain, with a single-link branch, beginning at the anomeric O and ending at the ring O atom.

#### Introduction

Of the class of 2-ketoheptoses (2-heptuloses) two members,  $\alpha$ -D-*altro*-2-heptulose and  $\alpha$ -D-*manno*-2-

heptulose occur in nature as free sugars. The latter compound is known to occur in the Avocado pear (*Persea officinalis*). As part of our research programme on the conformation and hydrogen bonding of monosaccharides, we undertook the structure determination of  $\alpha$ -D-*manno*-2-heptulose.

#### Experimental

Crystals were grown at room temperature from a methanolic solution of a commercial product obtained through the Sigma Corporation. Photographs showed that the crystal is monoclinic with space group *P2*<sub>1</sub>. Cell dimensions and intensities were measured on a Nonius CAD-3 diffractometer with Zr-filtered Mo *K* $\alpha$  radiation with the  $\omega$ -scan technique. The crystal data are summarized in Table 1. Of 837 available reflexions