

through the crystal, and could also help to explain the yellow colour of pyridazino[4,5-d]pyridazine.

Table 9. Shortest intermolecular distances

Values less than 3.5 Å for contacts involving C and N atoms, and less than 3.0 Å for contacts involving C or N and H atoms.

	<i>x</i> ;	<i>y</i> ;	<i>z</i>
(I)			
(II)	1+ <i>x</i> ;	<i>y</i> ;	<i>z</i>
(III)	- <i>x</i> ;	$\frac{1}{2}+y$ ;	$\frac{1}{2}-z$
(IV)	<i>x</i> ;	<i>y</i> ;	$\frac{1}{2}+z$
(V)	1- <i>x</i> ;	- <i>y</i> ;	- <i>z</i>
(VI)	1- <i>x</i> ;	$\frac{1}{2}+y$ ;	$\frac{1}{2}-z$
(VII)	1- <i>x</i> ;	$-\frac{1}{2}+y$ ;	$\frac{1}{2}-z$
(VIII)	- <i>x</i> ;	1- <i>y</i> ;	- <i>z</i>
N(1) (I)-C(1) (II)		3.457 Å	
-C(1) (VIII)		3.477	
-C(2) (III)		3.425	
N(2) (I)-C(1) (IV)		3.451	
-C(2) (VI)		3.349	
C(2) (I)-C(3) (V)		3.473	
N(1) (I)-H(1) (VII)		2.63	
-H(2) (VII)		2.79	
-H(2) (III)		2.94	
N(2) (I)-H(2) (VI)		2.52	

## References

- ADEMBRI, G., DE SIO, F., NESI, R. & SCOTT, M. (1967). *Chem. Comm.* p. 1006.  
 ALBANO, V., BELLON, P. L., POMPA, F. & SCATTURIN, V. (1963). *Ric. Sci.* 3A, 1067.  
 BERTINOTTI, F., GIACOMELLO, G. & LIQUORI, A. M. (1956). *Acta Cryst.* 9, 510.  
 CRUICKSHANK, D. W. J. (1956). *Acta Cryst.* 9, 754.  
 CRUICKSHANK, D. W. J. (1957). *Acta Cryst.* 10, 504.  
 CRUICKSHANK, D. W. J. (1961a). *Acta Cryst.* 14, 896.  
 CRUICKSHANK, D. W. J. (1961b). In *Computing Methods and the Phase Problem in X-ray Crystal Analysis*, p. 32. Oxford: Pergamon Press.  
 HAMEKA, H. F. & LIQUORI, A. M. (1956). *Proc. K. Ned. Akad. Wetensch.* B59, 242.  
 HIGGS, P. W. (1955). *Acta Cryst.* 8, 99.  
 HUGHES, E. W. (1941). *J. Amer. Chem. Soc.* 63, 1737.  
*International Tables for X-ray Crystallography* (1962). Vol. III, p. 202. Birmingham: Kynoch Press.  
 STEWART, J. M. (1964). Technical Report TR-64-6, Univ. of Maryland Computer Science Center.  
 WHEATLEY, P. J. (1953). *Acta Cryst.* 6, 369.

*Acta Cryst.* (1969). B25, 2236

## The Crystal and Molecular Structure of Guanosine-5'-phosphate Trihydrate

BY WATARU MURAYAMA, NOBUYA NAGASHIMA AND YOKO SHIMIZU

Central Research Laboratories, Ajinomoto Company, Inc., 2964 Suzuki-cho, Kawasaki, Japan

(Received 15 December 1968)

The crystal structure of guanosine-5'-phosphate trihydrate has been determined by a three-dimensional sharpened Patterson function and a Fourier synthesis, and was refined by the block-diagonal matrix least-squares method to a final *R* index of 0.086 for non-zero intensity reflexions. The space group is *P*2<sub>1</sub>2<sub>1</sub>2<sub>1</sub>, and the unit-cell dimensions are *a*=10.64, *b*=6.18 and *c*=25.58 Å with four molecules per unit cell. Of a total of 20 hydrogen atoms in an asymmetric unit, 15 atoms are located by difference Fourier synthesis. The conformation of the guanosine-5'-phosphate molecule in the crystal is similar to that of adenosine-5'-phosphate, and differs significantly from that of the disodium salt of inosine-5'-phosphate. The conformation of purine nucleotides in the solid state is discussed in connexion with that in an aqueous solution.

### Introduction

Guanosine-5'-phosphate (9-β-5'-phospho-D-ribofuranosylguanine, 5'-GMP) is one of the important ribonucleic acid constituents. To date only the hydrogen-bonded helical structure of dried GMP gel has been reported (Gellert, Lipsett & Davies, 1962). While it is of fundamental importance to determine accurate molecular dimensions for this biochemically important material, the conformation of the molecule in the solid state is also of interest.

The conformation of the ribose or deoxyribose moiety in nucleotides and nucleosides in aqueous solution has been investigated by nuclear magnetic resonance spectra (Jardetzky, 1962, 1960; Lemieux, 1961) but the

results do not always coincide with those for the solid state obtained by X-ray diffraction methods. As Jardetzky points out, the conformations of the ribose or deoxyribose moiety should be affected by the crystal field.

The molecular structure of 5'-GMP established by this investigation is compared with those of analogous purine nucleotides, *i.e.* adenosine-5'-phosphate (5'-AMP; Kraut & Jensen, 1963) and the disodium salt of inosine-5'-phosphate (disodium 5'-IMP; Nagashima & Iitaka, 1968), in which the intramolecular interactions between various substituents of the ribose ring are expected to be similar. Comparison of the molecular structures of these compounds may give some information on the factors determining the stable conformation of

purine nucleotides in the solid state and in an aqueous solution.

The conventional formula of 5'-GMP and the numbering system used is illustrated in Fig. 1.

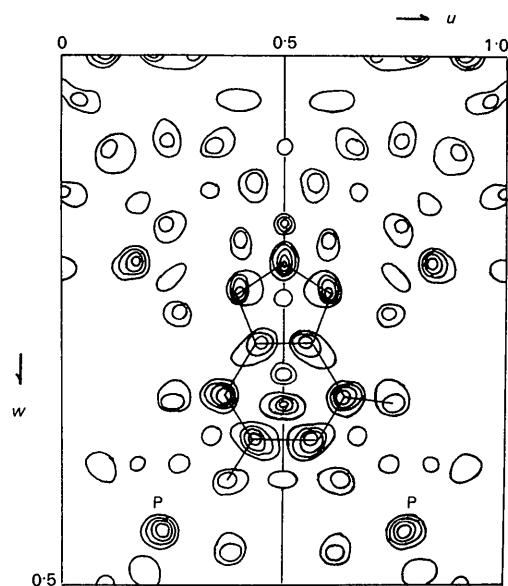


Fig. 1. Patterson map at  $v = \frac{1}{2}$ , the peak denoted by P corresponds to the vector between two equivalent phosphorus atoms.

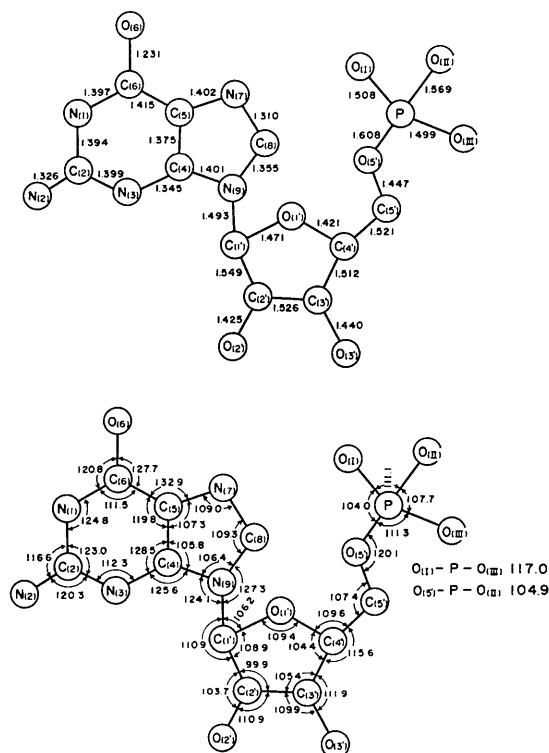


Fig. 2. The bond lengths ( $\text{\AA}$ ) and angles ( $\sigma$ ) of the 5'-GMP molecule.

## Experimental

An aqueous solution of the sodium salt of 5'-GMP was treated with a cation exchange resin (DOWEX-50W), concentrated at 50°C and slowly cooled to room temperature. Fine needle-shaped crystals were separated from the solution.

The lattice constants and the space group were determined by Weissenberg and precession photographs rotated around the  $b$  axis. The crystal belonged to the orthorhombic system, and the systematic absences were  $h, k$  and  $l$  odd for  $h00, 0k0$  and  $00l$  reflexions. The space group was determined as  $P2_12_12_1$ . Unit-cell parameters were:  $a = 10.64$ ,  $b = 6.18$ ,  $c = 25.58 \text{ \AA}$ ,  $V_c = 1680 \text{ \AA}^3$ . The observed density of the crystals measured by the flotation method was  $1.644 \text{ g.cm}^{-3}$ , and the calculated value with four molecules per unit cell was  $1.650 \text{ g.cm}^{-3}$ .

The intensity data were recorded by the multi-film Weissenberg method from the zero to fifth layers around the  $b$  axis, and measured visually.

Of the possible 2100 reflexions within the limiting sphere of  $\text{Cu K}\alpha$  radiation, 1876 reflexions were recorded on the films, 220 of which were too weak to be measured. Lorentz and polarization corrections were applied and the approximate scale and temperature factors for each layer were estimated by Wilson's method. No absorption corrections were applied.

## Determination of the structure

A three-dimensional sharpened Patterson function with  $F_0^2 \exp[5.0(\sin \theta/\lambda)^2]$  as Fourier coefficient was calculated. From packing considerations it was anticipated that the 5'-GMP molecule might be elongated along the  $c$  axis with its guanine base plane parallel to (010), since the conformation of the 5'-GMP molecule was expected to be similar to those of 5'-AMP and 5'-IMP.

On the  $(u, \frac{1}{2}, w)$  Patterson section the form of the guanine base appeared clearly (Fig. 2). The Patterson peaks were assigned to the vectors from a phosphorus atom to each atom of the guanine base. The map indicates that the  $y$  coordinate of the guanine-base plane differs by one half of the  $b$  axis period from that of a phosphorus atom, and that the difference between the  $x$  coordinates of a phosphorus atom and the C(8) atom of the guanine base is one half of the  $a$  axis period.

The positional parameters of the phosphorus atom were determined as  $(0.117, 0.200, 0.029)$  from  $(\frac{1}{2}, v, w)$ ,  $(u, \frac{1}{2}, w)$  and  $(u, v, \frac{1}{2})$  Harker sections. From Fig. 2 the fractional coordinates of each of the atoms belonging to the guanine base could be determined relative to the phosphorus atom. Two sets of positional parameters were possible for the guanine base next to the phosphorus atom, but only one of them could lead to a reasonable result.

Structure factors were calculated by the use of the positional parameters of the phosphorus atom and the

atoms belonging to the guanine base (one oxygen, five nitrogen and five carbon atoms) which were determined as described above; the  $R$  value at this stage was 0.53.

A Fourier synthesis with the weighting system of Sim (1961) revealed the positions of the atoms in the ribose ring. All the remaining atomic coordinates were subsequently obtained. The  $R$  value for the complete trial structure with isotropic temperature factors was 0.277.

#### Refinement of the structure

After three cycles of block-diagonal matrix least-squares refinement with isotropic temperature factors, the  $R$  value was decreased to 0.137. Two cycles of isotropic, and then three cycles of anisotropic, block-diagonal matrix least-squares refinements were carried

out, and the  $R$  value was reduced to 0.095. The weighting scheme at this stage was  $W=30/F_o$  for  $F_o > 30$ ,  $W=1.0$  for  $30 \geq F_o > 10$  and  $W=0.5$  for  $F_o \leq 10$ .

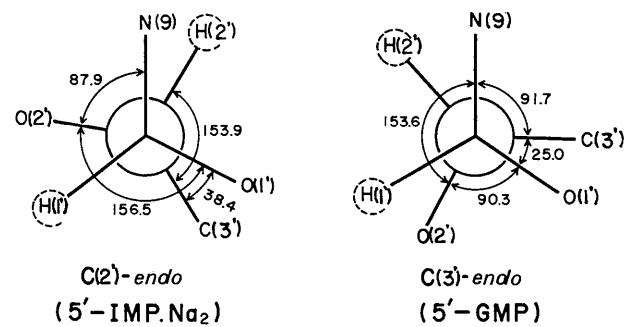


Fig. 3. Internal rotation around the  $C(1')-C(2')$  bond.

Table 1. Positional parameters in fractional coordinates and their estimated standard deviations in Å

	$x/a$	$y/b$	$z/c$	$S(x)$	$S(y)$	$S(z)$
P	-0.11468	0.70290	0.47390	0.0026	0.0030	0.0022
N(1)	-0.05452	0.31851	0.16132	0.0081	0.0101	0.0076
C(2)	-0.18500	0.31774	0.16167	0.0098	0.0113	0.0085
N(2)	-0.24202	0.30849	0.11549	0.0085	0.0110	0.0076
N(3)	-0.25347	0.31762	0.20572	0.0078	0.0102	0.0075
C(4)	-0.18109	0.32620	0.24877	0.0092	0.0121	0.0088
C(5)	-0.05212	0.32773	0.25214	0.0090	0.0118	0.0092
C(6)	0.02113	0.32290	0.20597	0.0089	0.0115	0.0083
O(6)	0.13647	0.32700	0.20229	0.0068	0.0086	0.0070
N(7)	-0.02097	0.32783	0.30536	0.0076	0.0093	0.0069
C(8)	-0.12448	0.33299	0.33306	0.0091	0.0106	0.0086
N(9)	-0.22493	0.33146	0.30046	0.0076	0.0095	0.0072
C(1')	-0.36056	0.34063	0.31521	0.0088	0.0116	0.0084
O(1')	-0.36566	0.30476	0.37003	0.0072	0.0086	0.0061
C(2')	-0.41698	0.56615	0.30306	0.0086	0.0114	0.0086
O(2')	-0.54860	0.52274	0.29515	0.0067	0.0087	0.0071
C(3')	-0.39472	0.67807	0.35543	0.0095	0.0129	0.0096
O(3')	-0.38155	0.85054	0.36326	0.0075	0.0089	0.0075
C(4')	-0.40887	0.50299	0.39630	0.0099	0.0133	0.0096
C(5')	-0.33437	0.53678	0.44637	0.0108	0.0146	0.0104
O(5')	-0.20871	0.60111	0.43128	0.0071	0.0086	0.0065
O(I)	-0.01391	0.81049	0.44160	0.0076	0.0094	0.0069
O(II)	-0.06075	0.50326	0.50447	0.0086	0.0099	0.0075
O(III)	-0.18384	0.84208	0.51232	0.0081	0.0086	0.0073
O(IV)	0.222353	0.30855	0.33350	0.0071	0.0092	0.0074
O(V)	0.29167	0.29713	0.43776	0.0080	0.0096	0.0075
O(VI)	0.03282	0.23140	0.43793	0.0079	0.0088	0.0078

Table 2. Positional parameters of hydrogen atoms in fractional coordinates and their estimated standard deviations in Å

	$x/a$	$y/b$	$z/c$	$S(x)$	$S(y)$	$S(z)$
H(N1)	-0.010	0.322	0.128	0.13	0.16	0.12
H(N2)	-0.189	0.288	0.092	0.13	0.16	0.12
H'(N2)	-0.330	0.337	0.114	0.13	0.16	0.12
H(C8)	-0.142	0.323	0.372	0.13	0.15	0.12
H(C1')	-0.407	0.227	0.291	0.12	0.15	0.12
H(C2')	-0.381	0.642	0.271	0.13	0.14	0.12
H(C4')	-0.494	0.453	0.408	0.14	0.15	0.12
H(O2')	-0.567	0.480	0.271	0.13	0.15	0.13
H(C5')	-0.322	0.347	0.467	0.12	0.15	0.12
H'(C5')	-0.395	0.650	0.462	0.12	0.15	0.12
H(O IV)	0.242	0.317	0.371	0.13	0.16	0.12
H(O V)	0.326	0.175	0.447	0.12	0.16	0.12
H'(O V)	0.323	0.390	0.463	0.13	0.15	0.12
H(O VI)	0.100	0.185	0.434	0.12	0.15	0.12
H'(O VI)	0.043	0.347	0.471	0.13	0.15	0.12

A difference Fourier synthesis was then calculated. Of a total of 20 hydrogen atoms in the asymmetric unit, 15 were actually located at stereochemically reasonable positions. The peak heights ranged from 0·35 to 0·66 e. $\text{\AA}^{-3}$ . The positional parameters of the hydrogen atoms were then adjusted by block-diagonal matrix least-squares with their isotropic temperature factors fixed at 3·0 (a slightly higher value than the isotropic temperature factors of non-hydrogen atoms). The  $R$  value after this final refinement was 0·086 for 1656 observed reflexions.

Atomic scattering factors used for phosphorus, oxygen, nitrogen, carbon and hydrogen atoms were those of

*International Tables for X-ray Crystallography* (1962).

The final parameter shifts of the non-hydrogen atoms, in terms of their standard deviations, were on average 0·30 $\sigma$  and the maximum shift was 0·66 $\sigma$ .

The refined atomic parameters are given in Tables 1, 2 and 3. The observed and calculated structure factors are listed in Table 4.

### Results and discussion

The bond lengths and angles of the 5'-GMP molecule are shown in Fig. 1. The e.s.d.'s of the bond lengths are: P–O, 0·008; C–O, 0·012; C–N, 0·012 and C–C, 0·015 Å,

Table 3. Thermal parameters of non-hydrogen atoms and their estimated standard deviations (in parentheses),  $\times 10^5$

$B_{ij}$  is defined by

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

	$B_{11}$	$B_{22}$	$B_{33}$	$B_{12}$	$B_{13}$	$B_{23}$
P	431 (18)	1055 (76)	39 (3)	-84 (39)	16 (7)	-34 (13)
N(1)	468 (70)	848 (276)	69 (11)	44 (130)	33 (24)	-70 (50)
C(2)	601 (86)	343 (304)	55 (12)	40 (145)	8 (27)	4 (54)
N(2)	562 (76)	1315 (293)	55 (11)	-44 (147)	-14 (24)	5 (52)
N(3)	409 (66)	1208 (281)	53 (10)	-91 (130)	14 (23)	48 (51)
C(4)	423 (80)	810 (341)	64 (13)	-28 (146)	20 (27)	1 (56)
C(5)	286 (70)	710 (334)	85 (13)	94 (139)	-27 (26)	-52 (56)
C(6)	379 (72)	926 (314)	45 (11)	115 (141)	13 (25)	-15 (54)
O(6)	400 (59)	1531 (254)	99 (11)	46 (114)	35 (22)	7 (47)
N(7)	368 (62)	822 (267)	44 (10)	-42 (117)	9 (21)	-9 (45)
C(8)	275 (70)	741 (315)	70 (12)	144 (139)	-4 (26)	-10 (51)
N(9)	352 (63)	949 (277)	50 (10)	72 (67)	-40 (22)	13 (46)
C(1')	297 (73)	1226 (350)	53 (12)	-90 (133)	3 (24)	22 (51)
O(1')	588 (65)	1227 (234)	53 (9)	-56 (122)	13 (20)	46 (41)
C(2')	246 (72)	1486 (358)	42 (11)	-12 (124)	49 (24)	18 (52)
O(2')	255 (56)	1966 (268)	89 (11)	-18 (104)	-17 (22)	-71 (46)
C(3')	340 (76)	1426 (359)	90 (14)	-38 (162)	-41 (29)	15 (61)
O(3')	491 (64)	1343 (282)	112 (12)	149 (114)	6 (24)	-112 (47)
C(4')	379 (86)	1885 (392)	62 (13)	44 (147)	45 (28)	-36 (60)
C(5')	440 (89)	2879 (469)	77 (15)	-309 (171)	97 (32)	-18 (69)
O(5')	413 (59)	2080 (263)	48 (9)	-87 (108)	30 (20)	-87 (41)
O(I)	648 (70)	1489 (267)	80 (10)	-274 (131)	2 (23)	68 (50)
O(II)	768 (79)	2211 (296)	74 (11)	-138 (134)	24 (26)	110 (49)
O(III)	830 (79)	918 (272)	102 (12)	-124 (123)	81 (25)	-77 (45)
O(IV)	435 (63)	1599 (264)	116 (12)	-20 (123)	-34 (23)	51 (53)
O(V)	686 (72)	1429 (259)	104 (12)	-144 (130)	-56 (25)	-44 (51)
O(VI)	644 (75)	1435 (289)	126 (12)	205 (119)	43 (27)	-4 (48)

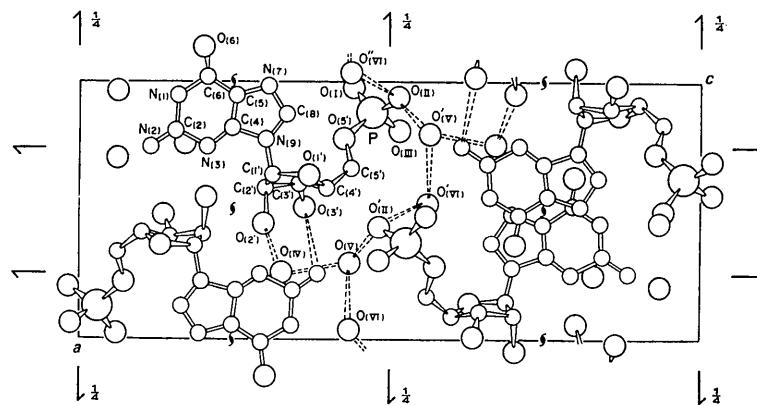


Fig. 4. The crystal structure projected along the  $b$  axis.

and that of the bond angles about 1°. Table 5 contains bond lengths and angles of covalent bonds involving hydrogen atoms.

#### (a) The phosphate group

The bond lengths and angles in the phosphate group are as expected in an organic monophosphate. Com-

Table 4. Observed and calculated structure factors

L	FO	FC	L	FO	FC	L	FO	FC	L	FO	FC	L	FO	FC	L	FO	FC
H <sub>2</sub> K <sub>2</sub> 0 0	18 0 5	24 0 4	12 83 74	11 414 413	9 210 191	15 223 246	11 69 76										
2 318 355	19 161 143	25 0 6	11 0 31	12 207 105	10 259 290	16 179 181	12 65 76										
4 284 323	20 0 38	26 150 136	13 229 227	13 355 343	12 182 171	17 147 167	13 43 44										
6+878 959	21 128 118	27 119 98	14 0 6	14 148 134	12 211 198	18 132 136	14 97 87										
8+912 925	22 0 33	26 65 53	15 0 3	15 232 215	13 175 163	19 134 135	15 121 112										
10 104 91	23 379 425	29 74 61	16 126 110	16 173 161	14 0 20	20 93 94	16 159 120										
12+475 499	24 87 123	H <sub>2</sub> K <sub>2</sub> 7 0	17 242 245	17 155 131	14 252 254	21 0 8	17 85 91										
14+432 434	25 66 70	1 118 63	18 65 83	18 71 47	16 73 59	22 70 80	18 102 93										
16+617 630	26 116 108	2 273 249	19 126 84	19 237 254	17 342 397	23 78 105	H <sub>2</sub> K <sub>2</sub> 12 1										
18+200 198	27 135 127	3 131 109	20 95 107	20 145 143	18 59 97	24 51 65	0 0 4										
20 313 332	28 245 238	4 0 48	21 104 99	21 119 106	18 189 202	25 98 111	1 0 36										
22+712 848	29 66 57	5 376 381	H <sub>2</sub> K <sub>2</sub> 11 0	22 221 239	20 0 27	26 87 81	2 215 203										
24+ 0 17	30 102 111	6 239 224	1 173 147	23 141 129	21 129 136	27 51 53	3 191 161										
26 296 300	31 97 88	7 233 213	2 289 254	24 133 128	22 121 128	H <sub>2</sub> K <sub>2</sub> 8 1	4 161 177										
28 179 162	H <sub>2</sub> K <sub>2</sub> 4 0	8 373 398	3 59 66	25 257 269	23 296 350	0 105 79	5 0 40										
30 353 340	0 401 314	9 273 260	4 59 81	26 76 73	24 102 93	1 202 196	6 72 81										
H <sub>2</sub> K <sub>2</sub> 1 0	1 323 300	10 164 137	5 52 37	27 289 276	25 99 97	2 71 55	7 82 80										
14+441 417	2 304 293	11 374 405	6 142 123	28 198 180	26 123 114	3 279 308	8 0 16										
2 321 285	3 0 71	12 269 246	7 57 72	H <sub>2</sub> K <sub>2</sub> 0 1	27 0 14	4 53 54	9 69 69										
3 227 198	4 198 187	13 131 95	8 115 128	29 175 58	28 59 65	5 229 221	10 0 27										
4+ 0 39	5+531 505	14 389 424	9 0 16	30 219 83	29 58 60	6 231 214	11 0 7										
5+874 947	6+533 500	15 119 113	10 247 206	31 86 126	30 38 38	7 223 204	12 54 55										
6+444 457	7 258 234	16 174 167	11 0 11	32 130 56	H <sub>2</sub> K <sub>2</sub> 5 1	8 278 315	13 44 48										
7+648 770	8+534 553	17 0 32	12 141 149	H <sub>2</sub> K <sub>2</sub> 2 1	0 16	9 175 167	H <sub>2</sub> K <sub>2</sub> 13 1										
8+ 94 87	9 412 214	18 0 39	13 62 76	0+452 399	1 130 82	10 132 129	0 0 34										
9 154 130	10+ 69 36	19 87 87	14 0 51	1 188 171	2 121 104	11 215 259	1 33 69										
10 229 164	11+ 67 86	20 0 47	15 0 18	2+782 833	3+696 693	12 216 235	2 47 59										
11+634 579	12 117 66	21 219 202	16 234 215	3+475 459	4 371 332	13 219 217	3 33 43										
12 172 174	13 145 134	22 0 0	17 51 58	4+762 729	5 211 209	14 246 300	4+ 0 1										
13 370 334	14+497 479	23 0 0	H <sub>2</sub> K <sub>2</sub> 12 0	5 238 226	6 177 141	15+ 0 44	5+ 86 84										
14 400 385	15 458 250	24 111 117	0 322 229	6 273 262	7 163 167	16 175 193	6 103 124										
15 139 113	16 405 418	25+ 0 29	1+ 63 87	7 243 227	8 311 305	17 225 228	7+ 0 16										
16 363 359	17+ 0 5	26 167 106	2+ 0 29	8+527 482	9 114 120	18+ 85 108	8+ 84 94										
17 120 109	18 361 359	27+ 0 13	3+ 89 84	0+566 534	10+552 565	19 161 155	9+ 91 95										
18+ 0 22	19+ 0 23	28 130 133	4+ 71 70	10+614 580	11+501 498	20 171 166	H <sub>2</sub> K <sub>2</sub> 0 2										
19 137 113	20 321 330	H <sub>2</sub> K <sub>2</sub> 8 0	5+ 87 87	11 353 349	12+537 581	21+ 78 94	2 219 206										
20+443 468	21+ 0 25	0 291 253	6 121 102	12+692 655	13 141 138	22+ 98 71	3+466 507										
21 281 241	22 126 116	1 222 203	7+ 0 31	13 207 196	14 162 143	23+422 495	12 192 194										
22+ 0 17	23 167 185	2+ 0 42	8+ 81 82	14+ 43 57	15 209 205	24+ 46 41	5+660 791										
23 385 460	24 163 179	3 366 360	9+ 73 73	15 202 194	16 269 278	25+107 106	6 305 333										
24 101 115	25 118 125	4 229 251	10 107 99	17 111 108	18+ 55 69	0 137 142	8 304 294										
25+87 123	26+ 79 66	5 197 187	11 73 56	17 111 108	18+ 55 69	0 137 142	8 304 294										
26 274 249	27+ 94 70	6 195 215	12+ 79 75	13 365 389	15 251 257	1 157 146	9 228 224										
27 164 146	31+ 51 59	7+ 0 19	13 160 97	15 166 111	20 187 221	2+ 55 73	10+682 646										
28 230 189	H <sub>2</sub> K <sub>2</sub> 5 0	8 121 111	14+ 33 25	20 402 424	21 178 196	3 112 112	11 132 120										
29 307 279	1+712 701	9 271 251	15+ 0 104	21+ 0 23	22 110 102	4+422 495	12 192 194										
30 170 140	2+819 756	10 154 133	H <sub>2</sub> K <sub>2</sub> 13 0	22 113 94	23 244 248	5 243 238	13 210 227										
31 217 207	3 138 136	11 155 175	1+ 65 61	23 249 248	24 73 57	7 121 122	15+443 441										
H <sub>2</sub> K <sub>2</sub> 2 0	4 256 236	12 178 475	2+ 55 45	25 109 107	26 161 158	B+ 0 33	15+ 53 44										
5+ 220 291	5 228 234	13+539 319	J+ 42 45	25 109 107	26 161 158	B+ 0 33	15+ 53 44										
1 374 321	6+ 401 299	14+ 104 104	4+ 26 126	27 182 168	28+ 94 82	10 223 262	18 250 241										
2 217 137	7 196 195	15+ 89 62	5+ 54 131	28+ 0 24	29+ 81 67	12 175 180	19 185 192										
2 307 268	8+ 258 230	16+ 87 134	6+ 60 15	29+ 0 24	29+ 81 67	12 175 180	19 185 192										
4 223 219	9+ 77 615	17 150 128	7+ 71 101	29+ 61 68	30+ 115 138	12 122 131	20 275 278										
5+ 0 033 153	10 123 93	18 149 251	7+ 77 149	30+ 38 41	31+ 99 72	H <sub>2</sub> K <sub>2</sub> 6 1	15+ 77 63	21 194 197									
6+ 111 109	11 325 326	19 237 223	9+ 99 104	31+ 99 72	0+533 508	14+ 77 77	22 404 467										
7 395 371	12 67 56	20 263 240	H <sub>2</sub> K <sub>2</sub> 9 0	8+ 134 99	8+ 512 484	15+ 106 128	23 257 240										
8 112 93	13 249 263	21 126 224	9+ 139 644	6+498 458	9+ 259 255	23+ 78 66	31+ 81 69										
16+ 35 35	23 232 269	22 176 156	10 184 145	7+454 429	10+ 99 83	H <sub>2</sub> K <sub>2</sub> 10 1	H <sub>2</sub> K <sub>2</sub> 1 2										
17 303 319	24 192 180	3 124 115	11 163 299	8+435 375	11+ 0 34	H <sub>2</sub> K <sub>2</sub> 1 2	18+37 765										
18 244 218	25+ 0 14	4 203 193	12 311 284	9+ 178 161	12 281 273	16+ 175 175	18+951 033										
19 112 104	24+ 0 22	5 239 228	13+ 0 9	10 154 141	13 297 317	2 112 101	2+818 644										
20 223 242	25+ 0 7	6+ 89 86	14 169 143	11 187 213	14 270 280	3 159 164	3+ 85 50										
21 314 364	26+ 0 37	7 7431 485	15 114 96	12 448 407	14 269 407	4+144 162	4+462 300										
13+ 130 96	27 137 128	8 214 224	16 104 98	13 185 186	15+ 0 69	5+ 55 49	5+70 787										
23 224 230	28 115 106	9 135 132	17+ 56 61	14 311 358	17 207 217	6+ 0 22	6 150 152										
24+ 92 89	29 152 49	10+ 0 21	18+ 87 74	23 126 119	26+ 53 44	15+ 0 33	16+ 242 251										
25+ 0 13	30+ 53 63	11 373 411	19 143 131	24 169 188	27 143 116	16+ 66 87	16+ 330 342										
26+ 56 66	H <sub>2</sub> K <sub>2</sub> 6 0	12+ 0 16	20+ 0 34	17 199 189	20+ 97 80	9+ 73 72	9+491 487										
27+ 92 97	0+ 20 20	13+ 0 47	21+ 312 325	18 198 220	21 134 150	18 120 108	10+463										

pared with the values for the phosphate groups in some organic phosphates so far determined by the X-ray diffraction method (Table 6), it can be concluded

that the un-ionized OH in the phosphate group corresponds to O(II) and that the phosphate group exists as a monovalent anion.

Table 4 (cont.)

L	FO	FC	L	FO	FC	L	FO	FC	L	FO	FC	L	FO	FC	L	FO	FC	L	FO	FC
1 245 230	6 492 287	17 116 115	5 158 158	10 577 586	21 144 136	H <sub>2</sub> K= 11 3	16 72 68													
2 270 299	7 148 135	18 121 131	6 131 138	11 144 133	22 144 194	0+ 0 46	17 114 121													
3 562 527	8 434 220	19 72 78	7 367 379	12 254 240	23 120 197	1+ 73 73	18 187 183													
4 280 291	9 189 132	20 128 133	8+ 98 711	13+ 89 89	24+ 68 62	2 167 155	19 197 193													
5 281 247	10 215 185	21+ 48 50	9 238 254	14 214 186	25+ 68 71	3+ 0 48	20+ 71 61													
6 363 391	11 336 354	22+ 56 90	10+ 97 61	15 302 299	H <sub>2</sub> K= 7 3	4+ 88 84	21+ 0 19													
7 375 360	12+ 0 45	23 116 105	11+ 46 58	16 177 175	0 275 283	5 190 144	22 133 139													
8+ 93 518	13 273 257	24+ 92 73	12 387 397	1+ 77 72	1+ 59 42	6 135 141	23 108 111													
9 225 203	14 267 274	25+ 90 84	13 191 185	18 148 146	2 363 420	7 117 111	24+ 0 41													
10 680 626	15 175 172	H <sub>2</sub> K= 9 2	14+ 44 433	19 176 185	3 297 289	8+ 0 5	25+ 43 49													
11 246 232	16 130 121	0 152 170	19+ 461 476	20 279 297	4 149 145	9+ 86 83	26+ 55 55													
12 235 185	17 170 139	1 192 200	16 200 189	21 187 196	5 114 133	10+ 96 88	27+ 81 77													
13 416 390	18+ 100 91	22+ 274 276	17 262 269	22+ 0 45	6 262 231	11+ 92 85	H <sub>2</sub> K= 3 4													
14 316 343	19+ 83 76	3 305 323	18+ 50 532	23+ 83 98	7 323 353	12+ 0 38	0+ 71 70													
15 281 270	20+ 0 33	4 193 211	19+ 88 106	24+ 79 99	8 154 144	13 116 102	1+ 92 80													
16+ 60 62	21 125 132	5 125 109	20 290 271	25 107 117	9 230 237	1+ 54 65	2 212 213													
17 297 314	22 403 198	6 147 163	21 126 130	26 142 135	10+ 62 60	H <sub>2</sub> K= 12 3	3+ 467 495													
18 283 277	23+ 81 72	7 186 206	22+ 0 37	27 156 138	1+ 0 24	0+ 40 64	4 220 225													
19 137 115	24 117 116	8 141 130	23+ 0 18	28+ 96 77	12 273 265	1+ 97 96	5 107 71													
20+ 87 94	25 198 184	9 159 153	24+ 0 16	H <sub>2</sub> K= 4 3	13 262 266	2 146 178	6 148 131													
21 139 141	26 143 120	10 157 136	25+ 0 2	0 346 247	14 167 151	3+ 0 31	7 252 245													
22 186 178	27 144 138	11 228 240	26 207 194	1 218 218	15 154 166	4+ 61 69	8 162 145													
23 305 338	28 162 153	12 120 111	27+ 0 3n	2+ 464 467	16+ 86 70	5+ 90 99	9+ 0 30													
24 160 173	29+ 81 94	13 196 224	28+ 0 38	3 207 194	17+ 83 82	6+ 0 33	10+ 0 29													
25 141 133	H <sub>2</sub> K= 6 2	14+ 63 72	29+ 67 46	4 126 116	18+ 85 87	7+ 92 119	11 292 299													
26 137 156	0 210 196	15 200 216	30 105 149	5 278 317	19+ 0 28	8+ 53 72	12 265 253													
27 103 95	1+ 430 416	16+ 59 76	H <sub>2</sub> K= 1 3	6 203 188	20 183 186	9+ 27 36	13 263 253													
28+ 0 32	2 199 195	17+ 0 20	0+ 520 562	7+ 43 50	21+ 66 93	H <sub>2</sub> K= 0 4	14 114 120													
29+ 0 32	3 101 78	18+ 86 105	1 193 223	6+ 427 413	22+ 62 63	2 256 395	15 237 227													
30 132 121	4 215 178	19+ 47 57	2+ 550 581	9 212 195	23+ 42 47	3 226 233	16 102 101													
H <sub>2</sub> K= 3 2	5 316 293	20+ 89 89	3 122 126	10+ 492 433	24 127 112	4+ 92 92	17 261 280													
0+ 0 14	6 283 271	21 118 121	4 205 227	11+ 54 37	25+ 50 59	5 282 309	18+ 92 101													
1 341 308	7 144 125	22 123 125	5 111 99	12+ 56 40	H <sub>2</sub> K= 8 3	6 149 138	19 149 177													
2+ 584 575	8 117 116	23+ 88 87	6 182 167	13 257 237	0+ 62 72	7 128 121	20+ 74 87													
3+ 542 526	9+ 74 50	H <sub>2</sub> K= 10 2	7 247 250	14 127 122	1 216 218	+ 0 0 4	21+ 53 63													
4 176 185	10 272 265	10+ 86 72	8 194 173	15 130 129	2 216 215	9+ 546 570	22+ 45 56													
5 292 304	11 129 111	1 157 176	9 189 205	16 175 177	3 144 141	10+ 0 57	23+ 78 84													
6+ 466 463	12 256 253	2 147 151	10 272 284	17 148 127	4 161 192	11 270 240	24 188 177													
7 356 351	13+ 76 103	3+ 86 95	11+ 51 59	18 137 119	5 204 218	12+ 85 91	25 143 141													
8+ 440 493	14 225 243	4 192 206	12 257 257	19 137 147	6 195 188	13+ 463 470	26 125 128													
9 316 318	15 267 250	5 209 224	13 383 388	20+ 0 30	7 157 144	14+ 0 44	27+ 82 100													
10 379 376	16 194 189	6 186 172	14 236 221	21 157 193	8 286 309	15+ 455 455	H <sub>2</sub> K= 4 4													
11 111 95	17 188 191	7+ 59 55	15 281 281	22 214 224	9 204 220	16+ 79 79	0 123 100													
12 250 230	18+ 66 58	8 182 198	16 160 164	23 114 113	10 156 160	17+ 57 46	1 333 334													
13+ 433 427	19 160 178	9+ 0 48	17 279 291	24 118 123	11 277 321	18 195 172	2 100 103													
14+ 56 54	20 199 220	10 123 118	18 327 330	25 123 125	12+ 67 95	19+ 72 91	3 166 171													
15 264 235	21 253 263	11+ 97 98	19 266 269	26 138 117	13 118 125	20+ 0 23	4 102 92													
16 276 266	22+ 79 67	12+ 0 27	20 135 113	27+ 0 28	14 220 235	21 342 408	5 333 318													
17 324 350	23+ 76 99	13+ 58 81	21+ 85 79	24 152 151	15+ 0 37	22+ 0 0 6	6+ 0 33													
18 169 142	24+ 0 19	14 102 110	6 222 225	H <sub>2</sub> K= 3 3	15 185 173	23 316 291	7 313 286													
19 171 166	25+ 88 64	15+ 49 57	23 149 145	0+ 0 28	17+ 60 73	24 105 291	8 164 152													
20 186 172	26 109 88	16+ 46 59	24 114 101	1 258 262	18 101 112	25 323 289	9 206 199													
21 162 167	27+ 89 90	17 194 189	25+ 66 69	6 204 370	19+ 0 29	26+ 0 41	10+ 41 19													
22 152 153	28+ 49 58	18 148 125	26+ 0 23	3+ 501 504	20+ 79 88	27 133 149	11 272 247													
23 189 183	H <sub>2</sub> K= 7 2	19+ 0 30	27 120 120	28 133 108	5 185 176	10+ 103 101	H <sub>2</sub> K= 1 4	12 123 107												
24+ 184 158	0 175 141	20 111 122	28 133 108	5+ 91 95	6 286 285	22 128 117	0 214 222	13+ 90 82												
25+ 81 70	1 352 346	H <sub>2</sub> K= 11 2	29+ 65 63	6 100 101	1 277 245	14+ 71 117	17 127 117	2 184 159												
26+ 54 27	2 412 193	8+ 92 109	6 223 243	15 294 313	7 227 245	10+ 237 257	23 314 314													
27+ 50 49	3 177 162	1+ 56 73	7 200 182	16 119 117	8+ 61 88	11 168 129	24 109 96													
28 184 148	4 320 328	2 181 165	8 130 123	17+ 68 59	9+ 85 93	12 309 310	25 154 146													
29 143 131	5+ 441 407	3 221 220	1 175 144	10 277 270	2+ 0 44	5+ 84 83	18 151 150													
30 232 217	7 156 146	4+ 42 42	2+ 531 506	11 198 182	3+ 0 10	6 132 111	19+ 24 26													
1+ 518 510	8+ 10 546	5 54 62	3 331 326	12 281 277	4 124 116	7 219 204	20+ 0 20													
2+ 213 221	9 257 241	7 106 105	4 139 115	13 160 148	5+ 238 259	8 218 203	21 173 173													
3+ 348 313	10 161 119	6 143 139	2+ 587 616	14 250 235	14+ 71 117	16+ 70 64	1+ 106 98					</								

Table 4 (cont.)

L	FO	FC	L	FO	FC	L	FO	FC	L	FO	FC	L	FO	FC	L	FO	FC
3 173 176	H <sub>2</sub> K <sup>#</sup> 8 4	2 119 104	20 237 239	11 142 155	3* 51 52	H <sub>2</sub> K <sup>#</sup> 6 5	1* 34 63										
4 303 306	0* 60 55	3* 83 76	21* 72 68	12 201 196	4 232 265	0 172 185	2* 68 92										
5* 70 87	1* 57 53	4 176 152	22* 0 33	13 298 311	5* 57 62	1 178 193	3* 0 28										
6 342 401	2* 98 108	5* 36 37	23* 0 26	14* 36 41	6* 67 75	2 182 202	4* 0 22										
7 127 136	3 127 123	6 212 200	24* 0 10	15 115 103	7 131 131	3 115 116	5 122 104										
8 171 167	4* 80 55	7* 76 103	25* 55 57	16 129 113	8 189 183	4* 100 78	6* 0 27										
9 185 193	5 180 203	8 158 135	H <sub>2</sub> K <sup>#</sup> 1 5	17* 0 22	9 107 96	5 152 165	7 152 130										
10 237 223	6 188 185	9 118 118	9 255 346	18* 0 43	10 273 267	6* 93 92	8 282 293										
11 109 94	7* 0 37	10 171 170	1 213 238	19* 0 14	11* 51 59	7 165 180	9 123 117										
12 115 115	8* 96 100	11 173 165	2* 48 48	20* 66 81	12* 86 76	8 110 110	10* 53 56										
13* 62 70	9 293 265	12* 61 62	3 263 320	21* 0 49	13* 0 7	9 131 137	11 200 196										
14 234 248	10 150 108	13* 59 78	4* 0 10	22 112 90	14* 93 92	10* 0 26	12* 78 94										
15* 0 10	11 228 190	14 149 195	5 246 245	23 184 206	15* 0 18	11 116 96	13 102 81										
16 272 273	12* 188 187	15* 89 95	6 278 278	24 133 157	16* 75 77	12* 55 65	14 214 219										
17* 53 65	13 276 233	H <sub>2</sub> K <sup>#</sup> 11 4	7 231 241	25 103 114	17 103 111	13 195 183	15 127 118										
18 134 136	14 106 84	8* 0 28	8 305 333	H <sub>2</sub> K <sup>#</sup> 3 5	18* 78 86	14* 75 94	H <sub>2</sub> K <sup>#</sup> 9 5										
19 129 126	15* 77 94	1* 63 61	9 163 145	0 304 374	19* 0 19	15 178 159	0* 85 95										
20 103 95	16* 73 64	2 119 129	10 121 112	1* 0 23	20* 41 68	16 165 146	1* 85 81										
21* 73 83	17* 0 38	3 182 202	11 151 137	2* 289 362	21 107 78	17* 78 53	2 174 154										
22* 0 41	18* 68 86	4* 0 17	12 123 114	3 135 121	22 115 101	18 151 124	3* 0 36										
23 133 128	19* 61 65	5* 0 23	13 126 141	4 110 114	23 121 106	19 129 113	4 117 109										
24* 81 77	20* 96 101	6* 0 39	14 239 227	5 131 121	H <sub>2</sub> K <sup>#</sup> 5 5	20 110 97	5 204 215										
H <sub>2</sub> K <sup>#</sup> 7 4	H <sub>2</sub> K <sup>#</sup> 9 4	7 117 111	15 227 210	6 176 187	* 42 48	21 102 114	6* 74 57										
0 150 144	8* 54 48	8* 71 69	16 124 115	7* 64 49	1 275 311	H <sub>2</sub> K <sup>#</sup> 7 5	7* 88 90										
1 301 331	1* 77 95	9 28 27	17 123 119	8 148 128	2* 95 81	0 191 208	8* 70 75										
2 146 274	2 21 194	10* 87 96	18 145 148	9* 68 62	3 288 334	1* 0 45	9* 75 63										
3 248 244	3 246 184	H <sub>2</sub> K <sup>#</sup> 0 5	19 234 239	10 244 262	4* 99 114	2 182 181	10* 0 35										
4 127 131	4 215 202	2* 67 90	20 152 133	11 187 188	5 132 112	3* 72 75	11* 37 48										
5 127 125	5* 0 41	3* 93 98	21 159 120	12 232 233	6* 50 57	4* 0 41	12* 83 72										
6 147 139	6* 0 23	4* 0 39	22 116 104	13 187 165	7 117 114	5 140 140	13* 96 104										
7* 0 21	7* 0 40	5 147 139	23* 27 47	14 151 139	8* 93 104	6 114 103	H <sub>2</sub> K <sup>#</sup> 10 5										
8 228 273	8 241 236	9 31 38	24* 66 67	15 197 199	9 165 171	7* 6 21	0 114 93										
9 109 167	9 206 188	7 160 168	25* 69 51	16* 99 84	10 169 165	8* 83 81	1* 94 76										
10 194 187	10 155 119	8 280 295	H <sub>2</sub> K <sup>#</sup> 2 5	11 133 128	11* 63 74	9 133 136	2 105 69										
11 134 135	11* 33 64	9* 83 63	12 160 149	12* 48 37	12 138 146	10 142 140	11* 88										
12* 92 101	12* 92 101	10 292 279	13 174 184	13* 47 47	13* 76 71	10 200 171	4* 23 44										
13* 138 125	13* 34 28	11 172 172	14 87 104	20 254 262	14 115 110	12 280 253	5 123 96										
14* 119 182	14 173 173	12 257 263	15* 64 79	21 149 139	15* 50 54	13 134 109	6* 76 65										
15* 23 41	15* 83 88	13 243 248	16 118 115	22 133 29	16 156 166	14* 83 81	7* 94 80										
16* 97 91	16 100 86	14 171 159	17 258 286	23* 38 38	17* 0 19	15 156 135	8* 85 72										
17 136 141	17* 41 40	15* 81 77	6 110 105	24 136 140	16* 85 89	16 166 133											
18* 0 41	18 131 148	16 115 83	7 259 278	H <sub>2</sub> K <sup>#</sup> 4 5	17 138 116	17* 68 49											
19 113 105	H <sub>2</sub> K <sup>#</sup> 10 4	17* 43 21	8 190 178	0 165 211	20 173 166	18 135 120											
20 141 181	0* 0 53	18* 57 71	9 253 261	1 143 167	21 237 234	H <sub>2</sub> K <sup>#</sup> 6 5											
21* 63 80	1 167 153	19 110 108	10 239 287	2 246 285	22 103 103	0* 0 36											

Table 5. Bond lengths and angles involving hydrogen atoms

Bond lengths			
N(1)-H(N1)	0.97 Å	C(5')-H(C5')	1.30 Å
C(8)-H(C8)	1.01	C(5')-H'(C5')	1.03
N(2)-H(N2)	0.83	O(IV)-H(O IV)	0.99
N(2)-H'(N2)	0.95	O(V)-H(O V)	0.87
C(1')-H(C1')	1.06	O(V)-H'(O V)	0.92
C(2')-H(C2')	1.03	O(VI)-H(O VI)	0.78
C(4')-H(C4')	1.01	O(VI)-H'(O VI)	1.10
		O(2')-H(O2')	0.70

Bond angles			
H(N1)-N(1)-C(6)	116°	H(C2')-C(2')-C(3')	116°
H(N1)-N(1)-C(2)	119	H(C4')-C(4')-C(3')	121
H(C8)-C(8)-N(7)	133	H(C4')-C(4')-O(1')	102
H(C8)-C(8)-N(9)	128	H(C4')-C(4')-C(5')	105
H'(N2)-N(2)-H(N2)	131	H(C5')-C(5')-H'(C5')	121
H'(N2)-N(2)-C(2)	119	H(C5')-C(5')-C(4')	106
H(N2)-N(2)-C(2)	110	H(C5')-C(5')-O(5')	106
H(C1')-C(1')-N(9)	106	H'(C5')-C(5')-C(4')	95
H(C1')-C(1')-C(2')	107	H(C5')-C(5')-O(5')	120
H(C1')-C(1')-O(1')	113	H(O V)-O(V)-H'(O V)	101
H(C2')-C(2')-C(1')	115	H(O VI)-O(VI)-H'(O VI)	105
H(C2')-C(2')-O(2')	111	H(O2')-O(2')-C(2')	118

Hydrogen bonding at the phosphate group will be discussed later.

#### (b) The guanine ring

The bond lengths and angles in the guanine group of 5'-GMP are very close to the corresponding values

of guanine bases and their derivatives determined so far by X-ray crystal structure analysis.

The C(6)-O(6) bond length of 1.231 Å corresponds to a C-O double bond. It shows that the guanine base is in a lactam form. The C(2)-N(2) bond (1.326 Å) has a considerable amount of double bond character. Simi-

Table 6. Bond lengths ( $\text{\AA}$ ) and angles ( $^\circ$ ) in some organic phosphates

	P=O	P-O <sup>-</sup>	P-OH	P-OR
2-Aminoethyl phosphate	(1) 1.493	1.503	1.557	1.591
L-Serine phosphate	(2) 1.497	1.517	1.560	1.608
3'-CMP(monoclinic form)	(3) 1.480	1.498	1.588	1.610
3'-CMP(orthorhombic form)	(4) 1.483	1.504	1.551	1.611
3'-AMP	(5) 1.477	1.486	1.579	1.612
5'-AMP	(6) 1.495	1.514	1.566	1.610
5'-GMP	(7) 1.499	1.508	1.569	1.608
O=P-O <sup>-</sup>	O=P-OH	O=P-OR	HO-P-O <sup>-</sup>	RO-P-O <sup>-</sup>
2-Aminoethyl phosphate	117.4	109.8	103.9	109.6
3'-CMP(monoclinic form)	117.5	112.5	105.5	110.9
3'-CMP(orthorhombic form)	116.0	113.6	110.1	106.1
3'-AMP	117.2	107.1	110.7	112.3
5'-AMP	118.2	106.4	105.7	110.2
5'-GMP	117.0	107.7	111.3	111.1
RO-P-OH				
(1) Kraut (1961)			(2) McCallum, Robertson & Sim (1959)	
(3) Bugg & Marsh (1967)			(4) Sundaralingam (1965)	
(5) Sundaralingam (1966)			(6) Kraut & Jensen (1963)	
(7) This investigation.				

lar values have been reported for the length of the C-N bond between an amino group and a purine or pyrimidine base, *i.e.* 1.331  $\text{\AA}$  in deoxyguanosine (Haschemeyer & Sobell, 1965), 1.312  $\text{\AA}$  in 5'-AMP (Kraut & Jensen, 1963), 1.332  $\text{\AA}$  in cytosine (Jeffrey & Kincshita, 1963) and 1.331  $\text{\AA}$  in cytidine-3'-phosphate (3'-CMP; Bugg & Marsh, 1967).

The deviation of the glycosidic bond N(9)-C(1') from the guanine-base plane is 0.067  $\text{\AA}$  at the C(1') atom position (see Table 7). A similar small deviation from the plane has also been encountered in calcium thymidylate (0.050  $\text{\AA}$ ; Horn & Luzatti, 1961). In contrast, this deviation is large in 5'-AMP (0.211  $\text{\AA}$ ; Kraut & Jensen, 1963).

Table 7. Deviations from the least-squares plane of the guanine ring

The equation of the least-squares plane, with coefficients equal to the direction cosines with respect to the crystallographic axes is:

$$-0.0034X + 0.9998Y - 0.0213Z = 1.880 \text{ \AA}.$$

Deviation	Deviation
N(1) 0.003 $\text{\AA}$	N(7) 0.020 $\text{\AA}$
C(2) 0.002	C(8) 0.001
N(3) 0.020	N(9) 0.013
C(4) 0.007	O(6)* 0.026
C(5) 0.010	N(2)* 0.028
C(6) 0.003	C(1')* 0.067

\* Atoms excluded from the calculation of the least-squares plane.

### (c) Conformation of the molecule

The ribose ring puckering in 5'-GMP is described as C(3')-endo, in which the C(3') atom is displaced by 0.515  $\text{\AA}$  from the plane formed by the remaining four ring atoms (see Table 8). This deviation from the plane is rather small compared with the values of 0.66  $\text{\AA}$  in 5'-AMP (Kraut & Jensen, 1963) and 0.62  $\text{\AA}$  in disodium 5'-IMP (Nagashima & Iitaka, 1968).

Table 8. Deviations from the least-squares plane of the ribose ring of 5'-GMP

The equation of the least-squares plane, with coefficients equal to the direction cosines with respect to the crystallographic axes is:

$$0.9279X + 0.3703Y + 0.0443Z = -2.457 \text{ \AA}.$$

Deviation	Deviation
C(1') 0.035 $\text{\AA}$	N(9)* 1.336 $\text{\AA}$
C(2') -0.020	O(2')* -1.428
C(3')* 0.515	O(3')* 0.062
C(4') 0.021	C(5')* 0.891
O(1') -0.036	

\* Atoms excluded from the calculation of the least-squares plane.

Conformational aspects of the 5'-GMP molecule in the solid state are summarized in Table 9 together with those of the other two purine nucleotides, disodium 5'-IMP and 5'-AMP. As is seen in the Table, the whole molecular structure of 5'-GMP resembles 5'-AMP and differs significantly from 5'-IMP.

Internal rotation of the ribose ring around the C(1')-C(2') bond is illustrated in Fig. 3. In the C(2')-endo conformation (disodium 5'-IMP) H(1') and H(2) are *trans*, and in the C(3')-endo conformation they are *gauche* with respect to their central bond, C(1')-C(2').

Proton spin-spin coupling constants between H(1') and H(2') of 5'-GMP and 5'-IMP in aqueous solution (pH 7) have been obtained in our laboratory, and the corresponding value in 5'-AMP was reported by Jardetzky (1962). These values are listed in Table 10. The dihedral angle H(1')-C(1')-C(2')-H(2') was estimated as shown in the Table. These results suggest that both these purine nucleotides have the same ribose conformation as each other, *i.e.* C(2')-endo, in aqueous solution. In the C(3')-endo conformation the dihedral angle H(1')-C(1')-C(2')-H(2') is expected to be about 90° as is seen in Fig. 3. If this were also the case in aqueous solution the spin-spin coupling constant between them would be much smaller.

Table 9. Conformation of crystalline purine 5'-nucleotides

	Ribose conformation	$\varphi_{CN}^*$	$\varphi_{OO}^\dagger$	$\varphi_{OC}^\ddagger$
5'-GMP	C(3')-endo	-12·4	71·9	45·9
5'-AMP	C(3')-endo	-18	78	40
5'-IMP. Na <sub>2</sub>	C(2')-endo	-43	60·5	56

\* The dihedral angle O(1')-C(1')-N(9)-C(8); the sign of the angle is as defined by Donohue & Trueblood (1960), Sundaralingam & Jensen (1965).

† The dihedral angle O(5')-C(5')-C(4')-O(1').

‡ The dihedral angle O(5')-C(5')-C(4')-C(3'). The notations  $\varphi_{OO}$ ,  $\varphi_{OC}$  are those of Shefter & Trueblood (1965).

Table 10. H(1')-H(2') proton spin-spin coupling constants in an aqueous solution and the estimated dihedral angle between them

	pH	$J_{H(1')-H(2')}$	Dihedral angle	Ribose conformation
5'-GMP	7	5·1 c.p.s.	140	C(2')-endo
5'-IMP	7	5·1	140	C(2')-endo
5'-AMP	1~2	4·6	135	C(2')-endo
	7~8	5·0	140	C(2')-endo

The C(3')-endo ribose conformation in 5'-GMP is probably the result of packing and hydrogen bonding requirements. In fact, the OH group attached to the C(3') atom is hydrogen-bonded to the amino nitrogen atom of the guanine base, and the C(3')-endo conformation may be favourable for the formation of the hydrogen bond. On the other hand, in crystalline disodium 5'-IMP the ribose conformation is C(2')-endo, which is the same as would be expected in aqueous solution. The alkali-metal salt crystals of the nucleotides contain a comparatively large number of water molecules of crystallization, and it might be supposed that in these crystals the environments around the nucleotide molecules are somewhat similar to those in aqueous solution.

In purine nucleotides or nucleosides which have the C(3')-endo ribose conformation, only the *anti* region is allowed with respect to the internal rotation around the glycosidic bond ( $-150^\circ < \varphi_{CN} < +20^\circ$ ; Haschemeyer & Rich, 1967). In fact the  $\varphi_{CN}$  values are small when the ribose puckering is C(3')-endo; for instance  $-20^\circ$  in 5'-AMP (Kraut & Jensen, 1963),  $-4^\circ$  in 3'-AMP (Sundaralingam, 1966) and  $-11^\circ$  in adenosine (Haschemeyer & Sobell, 1965). The C(3')-H(3') bond is approximately in the axial position with respect to the ribose ring when the ribose conformation is C(3')-endo. The non-bonded repulsion between an axial hydrogen atom H(3') of the ribose ring and the H(8) atom of the purine base will cause a rotation around the glycosidic bond to reduce the  $\varphi_{CN}$  value.

#### (d) Description of the structure and the hydrogen bonding

The crystal structure viewed along the *b* axis is shown in Fig. 4. The guanine bases are stacked with their planes parallel to (010). The perpendicular distance between two parallel guanine bases is 3·09 Å corresponding half of the *b* axis period. The closest intermolecular distance is 3·18 Å, which is found between N(7) of one guanine base and C(6) of another guanine

base, separated by one half of the *b* axis period by the twofold screw axis symmetry operation along this direction.

Three oxygen atoms of water molecules are linked with each other by hydrogen bonds. The O(V) atom of one water molecule makes a hydrogen bond with O(II) of one phosphate group, and the O(VI) atom of the same water molecule is hydrogen bonded to O(II) of the other phosphate group; thus an infinite hydrogen bond chain is formed along the *a* axis (Fig. 4). O(VI) is also hydrogen bonded along the *b* axis to O(I) of the phosphate group in the adjacent unit cell, and two phosphate groups are linked with each other along the *b* axis by the bonding sequence P-O(I)-O(VI)-O(II)-P (not shown in Fig. 4).

The O(2') atom of the ribose OH group is hydrogen bonded to O(IV) of the water molecule. The distance between O(3') of the ribose OH group, which is attached to the out-of-plane carbon atom in the ribose ring, and N(2) of the guanine amino group of the adjacent molecule is 3·00 Å, indicating a hydrogen bond between these two atoms. Hydrogen bonds between the ribose OH group and nitrogen atoms of the purine bases have been reported also in 3'-AMP (Sundaralingam, 1966) and 5'-AMP (Kraut & Jensen, 1963).

Hydrogen bond lengths and angles are given in Table 11.

Table 11. Hydrogen bond lengths and angles

The suffices i and ii denote atoms which belong to the adjacent unit cell along the *b* axis.

Bond length			
O(2')-O(IV)	2·931 Å	O'(II)—O'(VI)	2·591 Å
O(IV)-O(V)	2·766	O''(VI) <sup>i</sup> -O(I) <sup>ii</sup>	2·649
O(V)-O(VI)	2·784	O(3')—N(2)	3·002
O(V)-O'(II)	2·845		

Bond angles			
C(2')-O(2')—O(IV)		148·9°	
O(2')-O(IV)—O(V)		96·8	

Table 11 (cont.)

Bond angles	
O(IV)–O(V) —O(VI)	75·3
O(IV)–O(V) —O'(II)	131·5
O(VI)–O(V) —O'(II)	116·8
O(V) —O'(II) —O'(VI)	97·5
O'(II) —O'(VI) —O'(V)	106·6
O(II) <sup>i</sup> —O''(VI)—O(I) <sup>ii</sup>	122·8
P——O(II) —O'(V)	124·8
P <sup>i</sup> ——O(II) —O''(VI)	108·8
P <sup>i</sup> ——O(I) —O''(VI) <sup>ii</sup>	125·9
C(3') —O(3') —N'(2)	125·8
O(3') —N'(2) —C'(2)	106·3

We wish to express our thanks to Professor Yoichi Itika of the University of Tokyo for reading the manuscript of this paper.

All the crystallographic computations were carried out on a CDC 3600 computer with the *UNICS* programs (Sakurai, 1967).

#### References

- BUGG, E. & MARSH, R. E. (1967). *J. Mol. Biol.* **25**, 67.  
 DONOHUE, J. & TRUEBLOOD, K. N. (1960). *J. Mol. Biol.* **2**, 363.  
 GELLERT, M., LIPSETT, M. N. & DAVIS, D. R. (1962). *Proc. Nat. Acad. Sci. Wash.* **48**, 2013.
- HASCHEMEYER, A. E. V. & RICH, A. (1967). *J. Mol. Biol.* **27**, 369.  
 HASCHEMEYER, A. E. V. & SOBELL, H. M. (1965). *Acta Cryst.* **19**, 125.  
*International Tables for X-ray Crystallography* (1962). Vol. III, p. 202. Birmingham: Kynoch Press.  
 JARDETZKY, C. D. (1960). *J. Amer. Chem. Soc.* **82**, 229.  
 JARDETZKY, C. D. (1962). *J. Amer. Chem. Soc.* **84**, 62.  
 JEFFREY, G. A. & KINOSHITA, Y. (1963). *Acta Cryst.* **16**, 20.  
 KRAUT, J. (1961). *Acta Cryst.* **14**, 1146.  
 KRAUT, J. & JENSEN, L. H. (1963). *Acta Cryst.* **16**, 79.  
 LEMIEUX, R. U. (1961). *Canad. J. Chem.* **39**, 116.  
 McCALLUM, G. H., ROBERTSON, J. M. & SIM, G. A. (1959). *Nature, Lond.* **184**, 1863.  
 NAGASHIMA, N. & IITAKA, Y. (1968). *Acta Cryst.* **B24**, 1136.  
 SAKURAI, T. (1967). *UNICS Program System*. Japan Crystallographic Association.  
 SHEFTER, E. & TRUEBLOOD, K. N. (1965). *Acta Cryst.* **18**, 1067.  
 SIM, G. A. (1961). In *Computing Methods and the Phase Problem in X-ray Crystal Analysis*, p. 227. Oxford: Pergamon Press.  
 SUNDARALINGAM, M. (1966). *Acta Cryst.* **21**, 495.  
 SUNDARALINGAM, M. & JENSEN, L. H. (1965). *J. Mol. Biol.* **13**, 914.  
 TRUEBLOOD, K. N., HORN, P. & LUZZATI, V. (1961). *Acta Cryst.* **14**, 965.

*Acta Cryst.* (1969). **B25**, 2245

## Five-Coordinate Adducts of Cupric $\beta$ -Diketone Complexes: the Structure of 4-Methylpyridine bis-(*o*-hydroxyacetophenonato)copper (II)

BY V. F. DUCKWORTH AND N. C. STEPHENSON

School of Chemistry, University of New South Wales, Sydney, Australia

(Received 1 August 1968)

4-Methylpyridine bis-(*o*-hydroxyacetophenonato)copper(II) is the first 'stable' 1:1 adduct of a cupric  $\beta$ -diketone to have its structure determined by X-rays. The copper atom is five-coordinated and has a tetragonal pyramidal environment. Four oxygen atoms form an approximate square-planar arrangement about the copper atom, which is raised slightly out of this plane towards the apical nitrogen atom. The discrete molecule has a twofold axis of symmetry. Copper–oxygen and carbon–oxygen bond distances indicate that the  $\pi$ -electron system of the coordinated  $\beta$ -diketone framework has been largely destroyed by the presence of a benzene ring in the *o*-hydroxyacetophenone residue. The crystals, which decompose during irradiation, crystallize in the orthorhombic system, space group *Pbcn*, with lattice constants  $a = 9.23 \pm 0.05$ ,  $b = 13.99 \pm 0.07$ ,  $c = 15.59 \pm 0.08$  Å. The intensities of three-dimensional equi-inclination Weissenberg data were estimated visually and the structure was solved by Patterson and Fourier techniques. Refinement of atomic parameters was carried out by the method of least-squares.

#### Introduction

Cupric complexes with  $\beta$ -diketones have been extensively investigated in recent years, and X-ray crystallographic studies have shown that their structures are essentially square-planar, although in some cases there

is evidence of weak axial interactions (Boyko, 1963; Barclay & Cooper, 1965; Hall, McKinnon & Waters, 1965). Graddon (1959) observed changes in the visible spectra of these compounds in chloroform, produced by increasing the concentrations of various heterocyclic bases, and he proposed the formation of