

Fig. 2. Three-dimensional view of the crystal structure of 4-chloro-5-methylamino-2,3,6-pyridinetrione monohydrate.

The O-H...O distances are 3.001, 3.011, and 2.864 Å to O(1), O(2) and O(3) respectively. In addition, the amine [N(2)] hydrogen of a molecule related by $1-x, \frac{1}{2}+y, \frac{1}{2}-z$ forms an N-H...O bond of 2.808 Å to the H₂O oxygen. The basic molecule and that related by $x-1, \frac{1}{2}-y, z-\frac{1}{2}$ may also interact weakly through an N(1)-H...O(2) contact of 3.117 Å. We note that these hydrogen-bonded interactions are not only critical in determining the crystal structure of the monohydrate, but also may play an important role in stabilizing the valence structures inferred from the molecular bond lengths.

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The Crystal and Molecular Structure of the Tetraphenylarsonium Salt of the Monoanion of Adenine, [C₂₄H₂₀As]⁺[C₅N₅H₄]⁻. 3H₂O*

BY THOMAS J. KISTENMACHER

Department of Chemistry, The Johns Hopkins University, Baltimore, Maryland 21218, U.S.A.

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The tetraphenylarsonium salt of the monoanion of adenine crystallizes from aqueous solution as the trihydrate. The crystals are monoclinic, space group *P*2₁/n, with *a*=9.878 (4), *b*=21.347 (7), *c*=13.407 (4) Å, $\beta=103.19$ (3) $^\circ$ and *Z*=4. 2982 independent intensities (2418 above zero) were collected by counter methods. A structural solution was obtained by the heavy-atom method. The adenine anion is disordered in the crystal and accurate values for its bond lengths and angles have not been obtained. Full-matrix least-squares refinement based on the 2418 non-zero *F*'s led to an *R* value of 0.103 with all atoms treated isotropically.

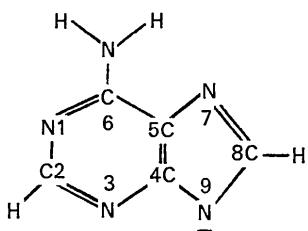
Introduction

Our recent interest in the coordination chemistry of purines and pyrimidines (Kistenmacher, Marzilli &

Chang, 1973) has led to the synthesis and structural investigation of several cobalt(III) complexes containing the monoanion of adenine (**I**) as a coordinated ligand. In an effort to compare the bond lengths and angles in the free anion *versus* those in the complexed anion, we have undertaken a structural study of the tetraphenylarsonium salt of the monoanion of adenine. Our efforts to obtain accurate dimensions have been thwarted by a disordering of the adenine anions.

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We are presently investigating other cations in an attempt to obtain crystals free of disorder.



Experimental

The crystals used in this study were prepared by Professor L. G. Marzilli and Mr C.-H. Chang. Clear, colorless crystals of the salt were obtained by slowly evaporating an aqueous solution. The crystals are ap-

proximately hexagonal prisms with the a axis coincident with the prism axis. Preliminary unit-cell constants and the space group were determined from Weissenberg photographs.

Intensities (hkl and $hk\bar{l}$) were measured on a Syntex

Table 1. Coordinates ($\times 10^4$) and isotropic temperature parameters of the heavy atoms

Estimated standard deviations are in parentheses.

	<i>x</i>	<i>y</i>	<i>z</i>	<i>B</i>
Tetraphenylarsonium ion				
As	2736 (1)	220 (1)	1615 (1)	3.45 (3)
C(11)	2910 (12)	- 409 (5)	655 (8)	4.0 (3)
C(12)	2463 (12)	- 286 (6)	- 374 (9)	4.8 (3)
C(13)	2526 (14)	- 763 (7)	- 1105 (10)	5.7 (3)
C(14)	3027 (13)	- 1348 (6)	- 792 (10)	5.5 (3)
C(15)	3471 (13)	- 1473 (6)	267 (10)	5.6 (3)
C(16)	3429 (13)	- 1014 (6)	1006 (9)	5.0 (3)
C(21)	1341 (12)	- 19 (5)	2315 (9)	4.0 (3)
C(22)	1131 (12)	383 (5)	3113 (9)	4.4 (3)
C(23)	94 (13)	203 (7)	3617 (9)	5.5 (3)
C(24)	- 627 (14)	- 373 (6)	3412 (10)	5.8 (3)
C(25)	- 358 (13)	- 754 (6)	2624 (9)	5.0 (3)
C(26)	627 (13)	- 588 (6)	2069 (9)	4.6 (3)
C(31)	2221 (11)	965 (5)	845 (8)	3.6 (2)
C(32)	3137 (14)	1199 (6)	307 (10)	5.5 (3)
C(33)	2707 (14)	1753 (6)	- 346 (10)	5.5 (3)
C(34)	1437 (14)	1988 (6)	- 390 (10)	5.3 (3)
C(35)	520 (13)	1763 (6)	157 (9)	5.0 (3)
C(36)	912 (12)	1223 (5)	805 (9)	4.1 (3)
C(41)	4413 (12)	349 (5)	2647 (8)	4.1 (2)
C(42)	4832 (13)	- 143 (7)	3326 (10)	6.0 (3)
C(43)	6065 (16)	- 44 (7)	4120 (11)	6.8 (4)
C(44)	6754 (14)	534 (6)	4200 (10)	5.5 (3)
C(45)	6274 (13)	1015 (6)	3512 (10)	5.0 (3)
C(46)	5104 (13)	926 (6)	2713 (9)	5.0 (3)

Adenine anion

N(1)	1870 (11)	2069 (5)	3461 (8)	5.2 (2)
N(3)	3450 (11)	2525 (5)	2600 (8)	5.7 (2)
N(6)	- 848 (13)	2282 (6)	2966 (9)	7.3 (3)
N(7)	- 204 (11)	3072 (4)	1453 (7)	4.8 (2)
N(9)	2068 (11)	3173 (5)	1269 (8)	5.3 (2)
C(2)	3156 (15)	2159 (6)	3327 (10)	5.5 (3)
C(4)	2224 (14)	2779 (6)	2078 (10)	4.7 (3)
C(5)	758 (21)	2705 (9)	2204 (15)	9.8 (5)
C(6)	640 (21)	2365 (9)	2833 (15)	10.7 (5)
C(8)	688 (14)	3318 (6)	983 (10)	5.1 (3)

Water molecules

O(1)	4033 (9)	3328 (4)	- 11 (7)	6.8 (2)
O(2)	6071 (9)	2573 (4)	2078 (7)	6.8 (2)
O(3)	7015 (9)	3371 (4)	504 (7)	7.3 (2)

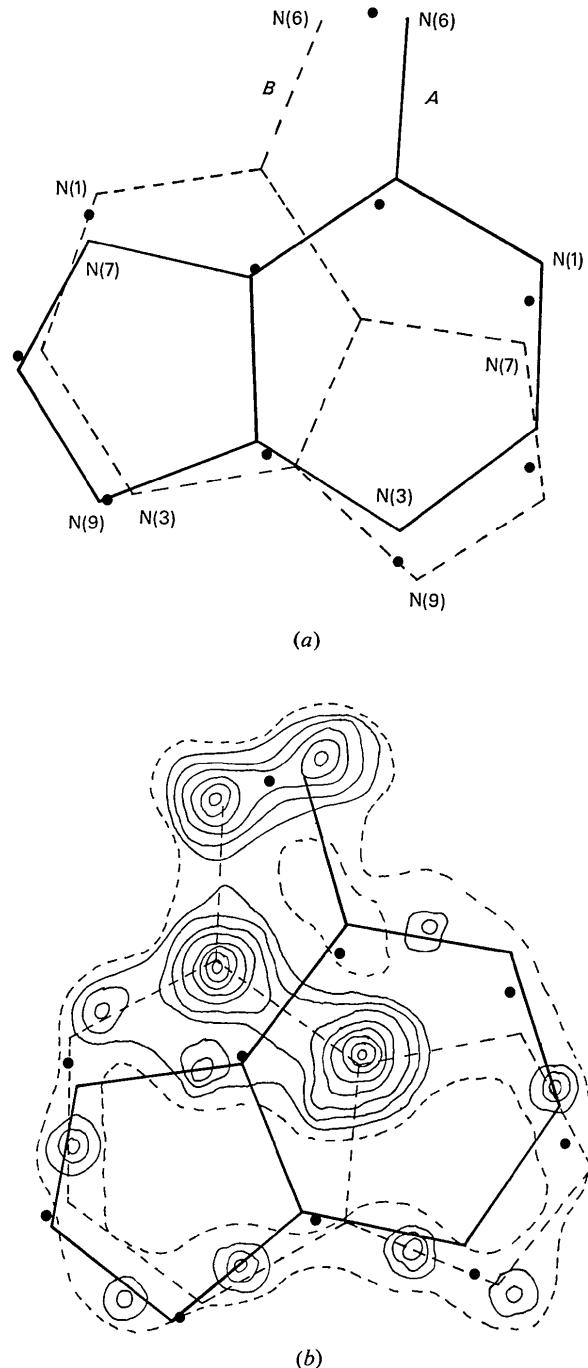


Fig. 1. (a) A schematic diagram of the proposed disorder model. The solid circles mark the final least-squares atomic positions. (b) Final difference Fourier map in the plane of the adenine ring.

*P*1 automated diffractometer with monochromated Mo $K\alpha$ radiation. The crystal studied was 0·20mm along the prism axis and varied from 0·16 to 0·18mm in cross section. A θ -2 θ scan technique was used in the data collection ($2\theta_{\max} = 45^\circ$). Cell constants, based on the complete angular setting of 12 reflections, and other crystal data are as follows: $a = 9\cdot878(4)$, $b = 21\cdot347(7)$, $c = 13\cdot407(4)$ Å, $\beta = 103\cdot19(3)^\circ$, space group $P2_1/n$ (systematic absences; $h0l$, $h+l=2n+1$; $0k0$, $k=2n+1$), $V = 2752\cdot5$ Å 3 , $Z = 4$, $D_c = 1\cdot38$, $D_m = 1\cdot38(1)$ g cm $^{-3}$, $\mu = 13\cdot5$ cm $^{-1}$.

2982 independent intensities (2418 above zero) were collected. Each reflection was assigned a variance, $\sigma^2(F)$, based on counting statistics plus a term $(0.03I)^2$

where I is the scan count. The 564 reflections with net intensities less than zero were assigned F and $\omega(F)$ of zero. The intensities were corrected for Lorentz and polarization effects. The calculated linear absorption coefficient ($\text{Mo } K\alpha$) is 13.5 cm^{-1} ; the maximum error due to neglect of absorption effects was estimated to be 5% in the intensities, which we considered to be sufficiently small to be ignored.

Determination and analysis of the structure

The coordinates of the As atom were determined from an unsharpened Patterson map. An electron density map based on signs derived from the known arsenic

Table 2. Observed and calculated structure factors

The three columns contain values of l , $10F(\text{obs})$ and $10|F(\text{calc})|$

Table 2 (*cont.*)

0	6	L	6	288	253	11	235	231	0	692	696	5	2	L	0	183	115	0	2	L	-12	178	174	-12	783	764	-12	327	305	4	2	L	-16	185	182	-16	559	521	-16	323	349	0	444	444	-16	323	349	0	124
0	364	359	8	168	168	11	191	214	0	855	831	2	235	262	0	134	165	6	6	L	166	204	-10	277	314	-10	358	308	-10	0	44	-10	40	-10	41	-1	452	1022	-10	301	349	-10	285	307	0	124			
0	488	479	7	141	144	3	2	L	0	183	115	0	250	269	0	195	209	2	120	248	0	472	494	-9	155	127	-9	2	6	L	0	183	115	0	262	291	0	124											
0	341	410	11	110	113	0	163	163	0	1014	995	10	170	202	3	323	351	1	380	357	2	122	102	-7	105	125	-13	81	85	-1	326	370	-10	539	521	-10	146	197	0	124									
0	347	416	0	10	10	0	227	207	0	177	207	0	120	125	1	5	229	245	0	253	263	0	177	207	-10	305	340	-10	146	197	-10	443	444	-10	124	197	0	124											
0	74	7	1	1	1	0	105	105	0	163	163	1	1	L	0	183	115	0	250	269	3	2	3	L	0	183	115	0	262	291	0	124	197	0	124	197	0	124											
0	102	108	0	82	74	5	712	751	9	115	77	1	303	289	0	114	114	0	190	190	0	212	150	-10	190	190	-10	12	55	-10	209	169	-10	443	444	-10	124	197	0	124									
0	187	157	1	150	150	0	580	532	6	149	187	10	350	416	2	272	172	0	94	92	0	163	163	-10	170	167	-10	167	163	-10	305	340	-10	539	521	-10	146	197	0	124									
0	12	130	175	4	162	206	0	103	103	0	134	134	5	5	L	0	183	115	0	250	269	2	120	140	0	1	L	0	183	115	0	262	291	0	124	197	0	124											
0	0	9	L	0	105	105	3	2	L	0	183	115	0	250	269	5	3	L	0	183	115	0	262	291	0	124	197	0	124	197	0	124																	
0	3	9	6	11	11	0	115	115	0	163	163	5	3	L	0	183	115	0	250	269	1	1	L	0	183	115	0	262	291	0	124	197	0	124															
0	375	355	7	133	133	3	2	L	0	183	115	0	250	269	5	3	L	0	183	115	0	262	291	0	124	197	0	124	197	0	124																		
0	284	750	9	120	120	2	4	L	0	183	115	0	250	269	5	3	L	0	183	115	0	262	291	0	124	197	0	124	197	0	124																		
0	446	499	11	243	212	0	163	163	0	250	269	2	4	L	0	183	115	0	250	269	4	171	159	-10	163	163	-10	305	340	-10	539	521	-10	146	197	0	124												
0	447	392	12	200	163	11	154	163	0	237	211	7	33	L	0	183	115	0	250	269	4	171	159	-10	163	163	-10	305	340	-10	539	521	-10	146	197	0	124												
0	700	21	1	7	L	0	163	163	8	80	70	1	150	163	163	0	163	163	0	250	269	4	171	159	-10	163	163	-10	305	340	-10	539	521	-10	146	197	0	124											
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0	11	310	1	444	488	6	731	771	11	280	312	4	166	153	0	250	269	0	163	163	0	250	269	4	171	159	-10	163	163	-10	305	340	-10	539	521	-10	146	197	0	124									
0	11	77	68	0	204	0	115	115	0	163	163	3	3	L	0	183	115	0	250	269	4	171	159	-10	163	163	-10	305	340	-10	539	521	-10	146	197	0	124												
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0	0	100	155	1	111	121	7	41	47	0	163	163	0	250	269	5	5	L	0	183	115	0	250	269	4	171	159	-10	163	163	-10	305	340	-10	539	521	-10	146	197	0	124								
0	11	207	280	1	120	120	0	163	163	0	250	269	5	5	L	0	183	115	0	250	269	4	171	159	-10	163	163	-10	305	340	-10	539	521	-10	146	197	0	124											
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0	477	477	0	10	10	0	163	163	0	250	269	5	5	L	0	183	115	0	250	269	4	171	159	-10	163	163	-10	305	340	-10	539	521	-10	146	197	0	124												
0	1	403	107	5	231	196	1	163	163	0	192	175	0	163	163	0	163	163	0	250	269	4	171	159	-10	163	163	-10	305	340	-10	539	521	-10	146	197	0	124											
0	213	462	0	10	10	0	163	163	0	250	269	5	5	L	0	183	115	0	250	269	4	171	159	-10	163	163	-10	305	340	-10	539	521	-10	146	197	0	124												
0	447	280	0	10	10	0	163	163	0	250	269	5	5	L	0	183	115	0	250	269	4	171	159	-10	163	163	-10	305	340	-10	539	521	-10	146	197	0	124												
0	347	318	0	10	10	0	163	163	0	250	269	5	5	L	0	183	115	0	250	269	4	171	159	-10	163	163	-10	305	340	-10	539	521	-10	146	197	0	124												
0	164	164	1	161	164	0	10	10	0	163	163	0	250	269	5	5	L	0	183	115	0	250	269	4	171	159	-10	163	163	-10	305	340	-10	539	521	-10	146	197	0	124									
0	75	53	1	9	L	0	163	163	0	250	269	5	5	L	0	183	115	0	250	269	4	171	159	-10	163	163	-10	305	340	-10	539	521	-10	146	197	0	124												
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0	321	219	11	11	110	163	0	163	163	0	250	269	5	5	L	0	183	115	0	250	269	4	171	159	-10	163	163	-10	305	340	-10	539	521	-10	146	197	0	124											
0	171	162	1	10	L	0	163	163	0	250	269	5	5	L	0	183	115	0	250	269	4	171	159	-10	163	163	-10	305	340	-10	539	521	-10	146	197	0	124												
0	171	162	1	10	L	0	163	163	0	250	269	5	5	L	0	183	115	0																															

atom position clearly revealed the carbons of the four phenyl rings of the arsonium ion. The position of the adenine anion was also indicated, but coordinates of individual atoms in the residue were unclear. A second electron density map based on the arsenic plus the 24 phenyl ring carbon atoms gave approximate positions for the atoms in the adenine ring system. Particular difficulty was encountered in finding suitable positions for atoms C(5) and C(6). This second map also gave coordinates for the three water molecules. Several cycles of isotropic, fullmatrix least-squares refinement, the quantity minimized being $\sum \omega(F_o - F_c)^2$, led to an *R* value, $\sum ||F_o|| - |F_c|| / \sum |F_o|$, of 0.103 (excluding rejects), and 0.142 (including rejects). The final

weighted R value, $[\sum \omega(F_o - F_c)^2 / \sum \omega F_o^2]^{1/2}$ is 0.091; the goodness of fit, $[\sum \omega(F_o - F_c)^2 / (n - p)]^{1/2}$ for $n = 2418$ observations of non-zero weight and $p = 153$ parameters, is 2.3. The maximum shift over error for any parameter was 0.6. The scattering factors for all atoms were taken from the compilation of Hanson, Herman, Lea & Skillman (1964). The final positional and thermal parameters are given in Table 1, and the observed and calculated structure factors in Table 2.

The least-squares refinement has led to a final set of thermal parameters and derived bond lengths and angles for the adenine ring which contain several anomalies. In particular, the thermal parameters for atoms C(5) and C(6) are about 10 \AA^2 (Table 1), and the bond

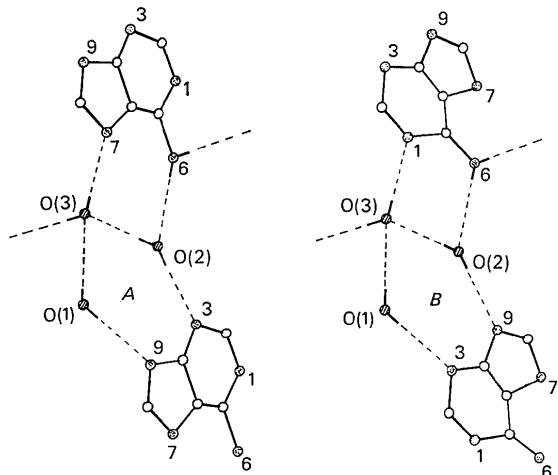


Fig. 2. Hydrogen bonding between the water molecules and translationally equivalent anions. Schemes *A* and *B* differ only in the orientation of the adenine ring system, see text.

lengths C(5)-C(6), 1.14 Å, C(4)-C(5), 1.50 Å, and N(6)-C(6), 1.53 Å, differ significantly from the expected values of about 1.4 Å (see Table 3). In an attempt to understand the reason for these anomalies, a difference Fourier map was computed with the atoms of the adenine ring removed. While several of the adenine anion atoms appeared as reasonably well-defined peaks, only broad maxima, about $2.9 \text{ e } \text{\AA}^{-3}$, were found for atoms C(5) and C(6) (all the maxima agreed within 2σ of the final least-squares values). The broad maxima were surrounded by diffuse density of the order of $1.5\text{--}2.0 \text{ e } \text{\AA}^{-3}$. A good account of the electron density could be made if the adenine system were assumed to be disordered such that the observed density is a 1:1 superposition of two adenine rings with their five- and six-membered rings interchanged. Fig. 1 contains (*a*) a schematic of the proposed disorder model, and (*b*) a final difference Fourier in the plane of the adenine molecule. The proposed disorder is very similar to that by Sletten (1969) in a dimeric copper complex containing a disordered adenine anion ligand. The near superpositioning of N(6) and the effective interchangeability of the sites occupied by atoms N(1) and N(7), and N(3) and N(9) in the two orientations of the disorder anion is obviously important in maintaining the hydrogen bonding in the structure. The hydrogen bonds which couple translationally related anions, along the *a* axis, are illustrated in Fig. 2. The hydrogen bonding is not markedly affected by whether the constituent rings of the adenine moiety are orientated imidazole-pyrimidine, *A* in Fig. 2, or pyrimidine-imidazole, *B* in Fig. 2. The hydrogen-bond distances are given in Table 4; the heavy-atom distances are the basis of the schematic positioning of the hydrogens in Fig. 2. The other important stabilizing force in the structure is the sandwiching of the adenine between screw-related tetraphenylarsonium cations, Fig. 3. A careful examination

of Fig. 3 and the interatomic contacts indicates that the interactions involved in this stacking are, like the hydrogen bonding, reasonably insensitive to the two different orientations of the adenine ring system.

Table 3. Bond lengths and angles in the adenine anion

Estimated standard deviations are in parentheses.

N(1)-C(2)	1.34 (2) Å	C(2)-N(1)-C(6)	124 (1)°
N(1)-C(6)	1.45 (2)	C(2)-N(3)-C(4)	107 (1)
N(3)-C(2)	1.33 (2)	C(5)-N(7)-C(8)	98 (1)
N(3)-C(4)	1.36 (2)	C(4)-N(9)-C(8)	107 (1)
N(6)-C(6)	1.53 (3)	N(1)-C(2)-N(3)	124 (1)
N(7)-C(5)	1.45 (2)	N(3)-C(4)-N(9)	126 (1)
N(7)-C(8)	1.31 (2)	N(3)-C(4)-C(5)	132 (1)
N(9)-C(4)	1.35 (2)	N(9)-C(4)-C(5)	103 (1)
N(9)-C(8)	1.36 (2)	N(7)-C(5)-C(4)	111 (1)
C(4)-C(5)	1.50 (2)	N(7)-C(5)-C(6)	134 (1)
C(5)-C(6)	1.14 (3)	C(4)-C(5)-C(6)	114 (2)
		N(1)-C(6)-N(6)	125 (1)°
		N(1)-C(6)-C(5)	119 (2)
		N(6)-C(6)-C(5)	115 (2)
		N(7)-C(8)-N(9)	121 (1)

Table 4. Hydrogen-bond distances

Donor atom	Acceptor atom	Symmetry†	Distance (donor-acceptor)
O(2)	N(3)*	<i>x</i> <i>y</i> <i>z</i>	2.83 Å
O(3)	N(7)*	1 + <i>x</i> <i>y</i> <i>z</i>	2.83
O(1)	O(3)*	<i>x</i> <i>y</i> <i>z</i>	2.87
O(3)	N(1)*	$\frac{1}{2} + x$ $\frac{1}{2} - y$ $-\frac{1}{2} + z$	2.87
O(1)	N(9)*	<i>x</i> <i>y</i> <i>z</i>	2.89
O(2)	O(3)*	<i>x</i> <i>y</i> <i>z</i>	3.02
N(6)*	O(1)	$\frac{1}{2} + x$ $\frac{1}{2} - y$ $-\frac{1}{2} + z$	3.03
N(6)*	O(2)	1 + <i>x</i> <i>y</i> <i>z</i>	3.07

† Transformation to be applied to the coordinates of the asterisked atom as listed in Table 1.

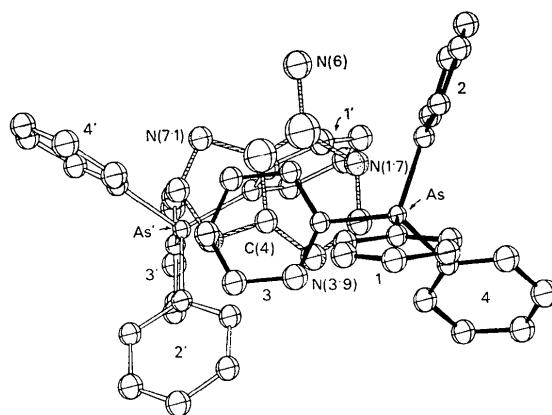


Fig. 3. Stacking of the adenine anion between two screw-related tetraphenylarsonium cations. The thermal ellipsoids are drawn at the 25% probability level [ORTEP; Johnson (1965)].

The dimensions of the tetraphenylarsonium cation are similar to those found in other crystal structure analyses. The ranges of bond lengths and angles are as follows:

As-C 1.90 (1)-1.92 (1) Å; C-As-C 106.2 (6)-113.2 (6)°; C-C 1.34 (2)-1.47 (2) Å; C-C-C 116.5 (15)-124.7 (15)°.

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The Prediction of the Stereochemistry of Polysulphate and Hydrogen Sulphate Ions

By I. D. BROWN

Institute for Materials Research, McMaster University, Hamilton, Ontario, Canada

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The angles in nine polysulphate and hydrogen sulphate ions are predicted to within 1.5° using two empirical relations, one involving the lengths of the bonds which define the angle, the other involving the configuration of the bonds around the bridging oxygen atom. Using, in addition, the bond strength relations of Brown & Shannon it is possible to predict *a priori* the complete geometry of the $\text{S}_2\text{O}_7^{2-}$ ion to an accuracy of 0.013 Å and 0.8°. The variations in angle can be understood equally well by assuming that they are caused by O-O repulsion or by variation in the strengths of the S-O bonds.

In most crystals the sulphate ion, SO_4^{2-} , shows a remarkable regularity, variations from $\bar{4}3m$ (Td) symmetry usually being quite small, but in the polysulphate and hydrogen sulphate ions much larger variations are found. The bond lengths can range from 1.36 to 1.83 Å and the angles from 97 to 128°. This paper shows that it is possible to make quantitative predictions of these effects.

The variations in bond length in SO_4 groups have been discussed in terms of π bonding by Cruickshank (1961), but they can also be understood in terms of the bond strength or bond valence theory by which it is assumed that the formal valence of an atom is shared among the bonds it forms. Thus in a regular SO_4^{2-} ion the valence, 6, of sulphur is shared equally between the four S-O bonds, each having a bond strength of 1.5 valence units (v.u.). The oxygen atoms have a valence of 2 and consequently form additional bonds with a total strength of 0.5 v.u. to other atoms in the crystal. Where the sulphur valence is shared unequally between the bonds the effect is manifest in the unequal lengths of the S-O bonds. Brown & Shannon (1973) have recently determined an empirical relationship between bond length (R) and bond strength (s) of the form:

$$s = (R/R_0)^{-N} \quad (1)$$

where $R_0 = 1.622$ and $N = 4.290$ for S-O bonds.

This relationship can be used either to determine bond strengths when the bond lengths are known or, if an *a priori* estimate of the bond strengths can be

made, it can be used to predict the bond lengths. The regularity of most SO_4^{2-} ions arises because the very weak bonds ($s \sim 0.15$) formed between most metallic cations and oxygen cause only small variations in the S-O bond strengths.

In the case of the polysulphate and hydrogen sulphate ions, at least one of the oxygen atoms (here designated as bridging) is bonded to two sulphur atoms or one sulphur and one hydrogen atom. Consequently its valence is more nearly equally shared between these two bonds giving rise to bonds of strength close to 1 v.u. with lengths of about 1.62 Å. The remaining oxygen atoms (here designated as terminal) are correspondingly more strongly bound with the bond-length shortening from the normal 1.47 to 1.43 Å. The effect is less marked in the hydrogen sulphate ions since the O-H bond typically has a bond strength of 0.85 v.u. (Brown & Shannon, 1973) so that the strength of the S-O bond will be 1.15 v.u. corresponding to a length of 1.57 Å.

Two different theories have been offered to explain the wide range of angles found in the SO_4 group. Baur (1970) assumes that the contact repulsion between the O atoms is sufficiently large to ensure that the oxygen atoms remain at the corners of a regular tetrahedron and the variation in angle is the result of the sulphur atom moving away from the centre of the tetrahedron. Thus the shortening of an S-O bond results in the increase of the angles between it and neighbouring bonds. On the other hand Louisnathan & Gibbs (1972) associate the increase in O-S-O angle with an increase