

Crystallographic Studies of Metal–Nucleotide Base Complexes. IV.* Tetraaquo-(9-methyladenine)copper(II) Sulphate Monohydrate

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(Received 29 May 1974; accepted 24 June 1974)

Tetraaquo-(9-methyladenine)copper(II) sulphate monohydrate is triclinic, space group $P\bar{1}$, with $Z=2$, $a=14.079$, $b=7.150$, $c=7.853$ Å, $\alpha=100.52$, $\beta=75.87$, $\gamma=107.98^\circ$. The structure was determined from counter intensities measured with Nb-filtered Mo $K\alpha$ radiation. Final $R=0.026$ for the 2911 reflexions above the threshold value. The copper ion is octahedrally surrounded, the equatorial positions being occupied by one adenine molecule coordinated through N(7), Cu–N(7)=1.995 Å, the other three sites being occupied by water molecules. The axial positions are occupied by the sulphate group and a water molecule. Centrosymmetrically related adenine molecules are hydrogen-bonded through N(1) and the amino group. The adenine ligands are stacked the same way as in the crystal structure of the uncomplexed molecule. The amino group is hydrogen-bonded to the coordinated sulphate oxygen, thus completing an indirect chelate formation involving N(6)···SO₄²⁻–Cu²⁺–N(7).

Introduction

A systematic investigation of metal bonding to nucleic acid components is in progress at this laboratory. Recently the crystal structure of the copper complex of a nucleoside analogue of hypoxanthine has been published (Sletten, 1974; see this paper for references to related crystal investigations).

The present paper presents the crystal structure of a copper–adenosine analogue, 1:1 copper–9-methyladenine.

Experimental

The compound was synthesized by dissolving 9-methyladenine in 1*N* H₂SO₄ and adding saturated CuSO₄ solution (Weiss & Venner, 1963). The mixture was heated under dropwise addition of 1*N* NaOH until pH~4. The green solution was filtered and ethanol was added. After approximately 4 h, turquoise crystals appeared. The crystal used had dimensions 0.3 × 0.5 × 0.1 mm.

Crystal data

[(C₆H₇N₅)Cu(H₂O)₄]SO₄·H₂O, F.W. 398.8, space group $P\bar{1}$, $a=14.079$ (3), $b=7.150$ (3), $c=7.853$ (2) Å, $\alpha=100.52$ (2), $\beta=75.87$ (2), $\gamma=107.98$ (2)^o. $D_m=1.83$, $D_x=1.83$ g cm⁻³, $Z=2$, $\lambda(\text{Mo } K\alpha)=0.71069$ Å, $\mu=17.58$ cm⁻¹.

Integrated intensities were measured on an off-line Siemens four-circle diffractometer. The experimental procedure has been described elsewhere (Sletten, 1974). Within the sphere of reflexion limited at $\sin \theta/\lambda=0.64$, 3156 unique reflexions were recorded. Of these, 245

were less than the threshold value of $2\sigma_c$, where σ_c is the error due to counting statistics. The two standard reflexions monitored during data collection showed individual fluctuations of $\pm 2\%$. After collecting approximately 1000 reflexions the intensities suddenly dropped by about 4%. Since the crystal would not be expected to deteriorate abruptly the incident must be ascribed to electronic instability.

The expression $\sigma_I=[\sigma_c^2+(0.02\sigma_c^2)]^{1/2}$ was used to calculate the random error in any one reflexion. The standard deviations in the structure factors were calculated according to $\sigma_F=\sigma_I/2(I \text{ Lp})^{1/2}$. The data were corrected for Lorentz and polarization effects according to normal beam geometry. Absorption correction was carried out by a modified Busing & Levy (1957) procedure. The crystal was divided in a Gaussian grid of $8 \times 10 \times 10$ points, and six boundary planes were defined. The transmission coefficients lay in the range 0.83–0.94.

The structure was solved by the heavy-atom method and refined by full-matrix least-squares calculations to an R of 0.026 ($R=\sum||F_o|-|F_c||/\sum|F_o|$). All non-hydrogen atoms were refined isotropically. H(11) on the water molecule with highest thermal motion did not refine satisfactorily and is probably disordered.

The final difference map showed the usual pattern of electron densities in the middle of each bond, ranging from 0.15 to 0.25 e Å⁻³. Several negative regions of as much as 0.2 e Å⁻³ were found in the map. The positions of the four oxygen atoms in the sulphate group had positive peaks of roughly 0.2 e Å⁻³, while the sulphur position was surrounded by three distinct, negative regions of 0.2 e Å⁻³.

Scattering factors used for Cu, O, N, C, S are those given in *International Tables for X-ray Crystallography* (1962), and for H the curve published by Stewart, Davidson & Simpson (1965).

* Part III: *Acta Cryst.* B30, 1961–1966

Table 1. Observed and calculated structure factors ($\times 10$)

Table with multiple columns of numerical data representing observed and calculated structure factors. The table is organized into several columns, likely representing different hkl reflections. The data is presented in a grid-like format with some rows containing additional identifiers or indices.

Table 1 (cont.)

A large table of numerical data, likely representing crystallographic parameters or coordinates, organized in a grid format with multiple columns and rows.

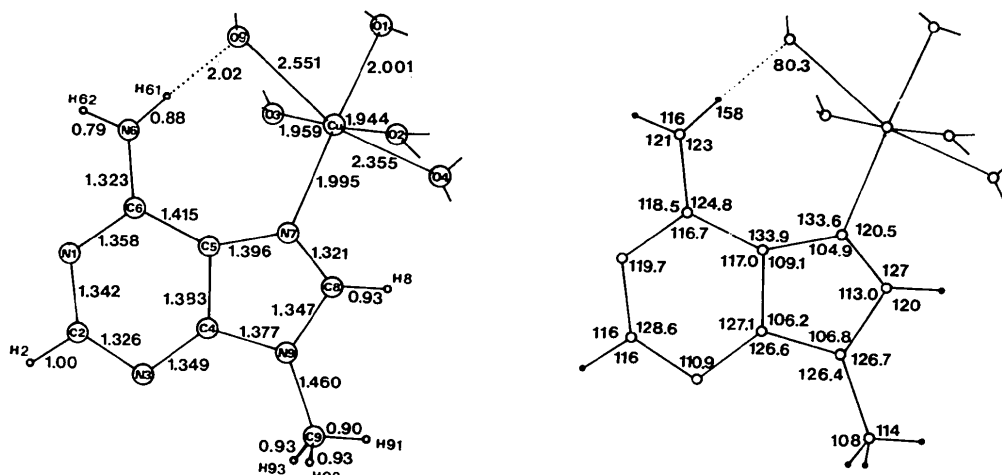


Fig. 1. Bond lengths and angles in the Cu(ade)(H₂O)₂⁺ ion. The σ 's in bond lengths are: Cu-O(N) 0.001–0.002 Å, C-C(N) 0.002–0.003 Å, H-C(N) (O) 0.02–0.04 Å. The σ 's in angles are in the range 0.05–0.14°.

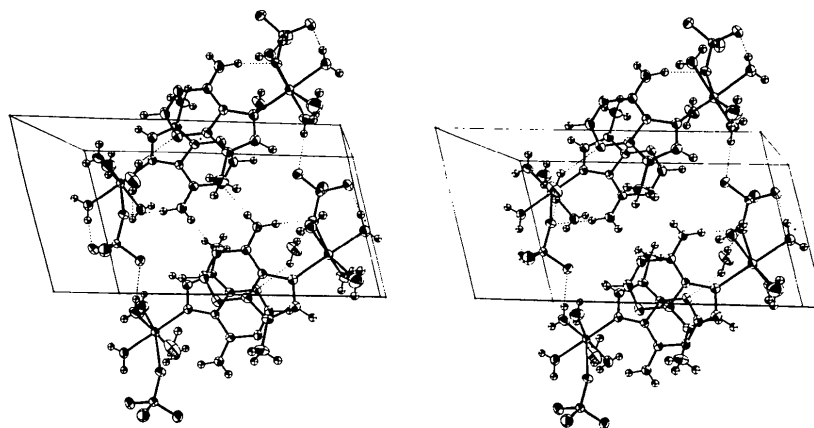


Fig. 2. Stereoscopic drawing of the crystal packing of tetraaquo-(9-methyladenine)copper(II) sulphate monohydrate viewed perpendicular to the *ac* projection.

Table 2. *The final atomic parameters*

(a) Non-hydrogen atoms. Temperature parameters $\times 10^4$. Standard deviations are given in parentheses. Anisotropic temperature factor = $\exp[-2\pi^2(U_{11}h^2a^{*2} + U_{22}k^2b^{*2} + U_{33}l^2c^{*2} + 2U_{12}hka^*b^* + 2U_{23}klb^*c^* + 2U_{13}hla^*c^*)]$.

	<i>X/a</i>	<i>Y/b</i>	<i>Z/c</i>	<i>U</i> ₁₁	<i>U</i> ₂₂	<i>U</i> ₃₃	<i>U</i> ₁₂	<i>U</i> ₂₃	<i>U</i> ₁₃
Cu	0.14291 (2)	0.22381 (4)	0.25332 (3)	171 (1)	309 (1)	227 (1)	87 (1)	66 (1)	-11 (1)
S	0.13615 (4)	0.53693 (8)	0.68570 (6)	194 (2)	386 (3)	182 (2)	132 (2)	36 (2)	-15 (2)
O(1)	0.00316 (11)	0.19007 (22)	0.40407 (19)	211 (7)	345 (8)	295 (7)	90 (6)	75 (6)	-30 (6)
O(2)	0.11991 (13)	0.40779 (28)	0.12398 (21)	450 (10)	636 (11)	274 (8)	374 (9)	209 (8)	115 (7)
O(3)	0.17066 (11)	0.07569 (22)	0.41348 (20)	252 (7)	340 (8)	353 (8)	122 (6)	118 (6)	-9 (6)
O(4)	0.06232 (15)	-0.06837 (29)	0.09097 (25)	478 (11)	550 (11)	431 (10)	-13 (9)	30 (8)	-133 (8)
O(5)	0.29627 (13)	0.84942 (25)	0.32513 (24)	478 (13)	418 (9)	577 (11)	236 (8)	196 (8)	196 (8)
O(6)	0.13313 (12)	0.74488 (24)	0.74018 (22)	355 (9)	396 (9)	404 (9)	148 (7)	-100 (7)	-128 (7)
O(7)	0.19460 (12)	0.48026 (30)	0.78822 (21)	331 (8)	827 (13)	278 (8)	291 (9)	173 (8)	-33 (7)
O(8)	0.02845 (11)	0.40754 (23)	0.71399 (20)	216 (7)	419 (8)	305 (8)	98 (6)	69 (6)	28 (6)
O(9)	0.18039 (11)	0.51176 (22)	0.49477 (18)	263 (7)	349 (7)	187 (7)	104 (6)	51 (5)	9 (5)
N(1)	0.52218 (13)	0.38112 (27)	0.26363 (24)	201 (8)	383 (10)	287 (9)	95 (7)	-7 (7)	-65 (7)
N(3)	0.54184 (13)	0.24083 (26)	-0.04107 (23)	201 (8)	339 (9)	277 (9)	100 (7)	34 (7)	15 (7)
N(6)	0.37148 (13)	0.42541 (30)	0.43741 (24)	229 (8)	522 (11)	236 (9)	146 (8)	-90 (8)	-68 (7)
N(7)	0.27956 (12)	0.23399 (26)	0.09914 (22)	198 (8)	341 (9)	221 (8)	83 (7)	17 (7)	-38 (6)
N(9)	0.38254 (13)	0.14758 (27)	-0.14601 (22)	273 (9)	381 (9)	174 (8)	121 (7)	-29 (7)	-29 (6)
C(2)	0.57482 (15)	0.32067 (32)	0.10744 (30)	205 (9)	359 (11)	333 (11)	93 (8)	36 (8)	-25 (8)
C(4)	0.44145 (15)	0.22225 (28)	-0.01944 (26)	228 (9)	233 (9)	218 (9)	69 (7)	39 (7)	-9 (7)
C(5)	0.37730 (14)	0.27584 (28)	0.13291 (25)	165 (8)	239 (9)	211 (9)	62 (7)	36 (7)	-25 (7)
C(6)	0.42131 (15)	0.36238 (29)	0.28268 (26)	210 (9)	254 (9)	226 (9)	70 (7)	18 (7)	-35 (7)
C(8)	0.28760 (16)	0.15867 (34)	-0.06863 (28)	258 (10)	417 (12)	243 (10)	106 (9)	-19 (8)	-75 (8)
C(9)	0.41716 (20)	0.07455 (40)	-0.32986 (30)	485 (14)	568 (15)	208 (11)	227 (12)	-62 (10)	-20 (10)

Table 2 (cont.)

(b) Hydrogen atoms (parameters $\times 10^3$). Isotropic temperature factor = $\exp[-8\pi^2 U \sin^2 \theta/\lambda^2]$.

	X/a	Y/b	Z/c	U
H(2)	649 (2)	341 (3)	101 (3)	30 (6)
H(8)	235 (2)	109 (3)	-131 (3)	36 (6)
H(11)	-33 (2)	218 (3)	361 (3)	41 (6)
H(12)	5 (2)	269 (4)	512 (3)	56 (8)
H(21)	84 (2)	450 (3)	165 (3)	36 (6)
H(22)	139 (2)	427 (3)	36 (3)	47 (7)
H(31)	202 (2)	12 (3)	381 (3)	41 (7)
H(32)	121 (2)	18 (4)	475 (3)	49 (7)
H(41)	75 (3)	-112 (5)	0 (5)	214 (26)
H(42)	36 (3)	-133 (6)	146 (6)	126 (14)
H(51)	321 (3)	816 (6)	222 (6)	125 (14)
H(52)	272 (3)	762 (5)	374 (5)	83 (10)
H(61)	306 (2)	419 (4)	459 (3)	46 (7)
H(62)	400 (2)	476 (3)	516 (3)	40 (6)
H(91)	366 (3)	-5 (5)	-382 (5)	114 (13)
H(92)	460 (3)	168 (5)	-403 (5)	98 (12)
H(93)	437 (3)	-39 (5)	-332 (5)	99 (12)

A list of observed and calculated structure factors is given in Table 1. Atomic parameters are listed in Table 2. All the above calculations were carried out on a UNIVAC 1110 computer. The main programs used originate from the Weizmann Institute of Science, Rehovoth, Israel, and were modified by Dr D. Rabinovich, cand. real. L. Milje and cand. real. K. Åse. The ORTEP program was used for making the stereo drawings (Johnson, 1970).

Results and discussion

Environment of copper

The copper ion has octahedral (4+2) coordination (Fig. 1). The equatorial positions are occupied by N(7) of the adenine ligand and by three water molecules. The Cu-N(7) distance, 1.995 Å, is significantly shorter than the corresponding distance, 2.054 Å, in the copper-hypoxanthine complex (Sletten, 1974). The copper ion is displaced 0.045 Å from the equatorial plane towards a fourth water molecule, O(4), in the axial position. The coordination sphere is completed by one of the sulphate oxygens, the distance Cu-O(9) = 2.551 Å indicating a very weak interaction.

In Table 3 the angles around copper are listed. The sulphate ligand is shown to be 'pushed' away from the adenine ligand to accommodate an intramolecular hydrogen bond to the amino group. This indirect chelate formation involving N(6)···O(9)-Cu-N(7) seems to be a characteristic feature in complex formation between copper and purine bases.

The coordination pattern described above is the normal arrangement for copper(II) complexes which have no crystallographic symmetry restraints. The preference for water molecules rather than the sulphate ion in equatorial positions has also been found in the tri- and pentahydrate of CuSO₄ (Zahrobsky & Baur, 1968; Bacon & Curry, 1962).

Table 3. Bond angles (°) in the coordination sphere of copper ($\sigma = 0.05-0.07^\circ$)

O(1)-Cu-O(2)	90.63
O(1)-Cu-O(3)	87.74
O(4)-Cu-O(1)	83.25
O(4)-Cu-O(2)	96.69
O(4)-Cu-O(3)	92.36
O(4)-Cu-N(7)	92.85
O(4)-Cu-O(9)	162.94
N(7)-Cu-O(2)	92.19
N(7)-Cu-O(3)	90.06
N(7)-Cu-O(9)	103.65
O(9)-Cu-O(1)	80.08
O(9)-Cu-O(2)	87.12
O(9)-Cu-O(3)	83.44

Table 4. Bond lengths (Å) and angles (°) in the sulphate ion

$\sigma(l) = 0.001-0.002 \text{ \AA}$, $\sigma(\text{angle}) = 0.1^\circ$			
O(6)-S-O(7)	111.3	S-O(6)	1.481
O(6)-S-O(8)	107.9	S-O(7)	1.462
O(7)-S-O(8)	110.0	S-O(8)	1.500
O(9)-S-O(6)	109.3	S-O(9)	1.477
O(9)-S-O(7)	110.6		
O(8)-S-O(9)	107.7		
S-O(9)-Cu	132.2		

Geometry of the adenine ligand

The bond lengths and angles of the adenine ligand are given in Fig. 1. To assess the influence of metal bonding, a comparison with the molecular dimensions of un-

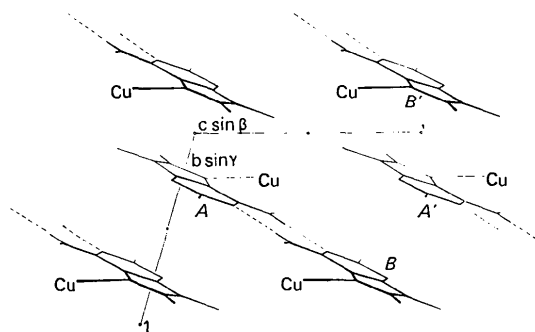
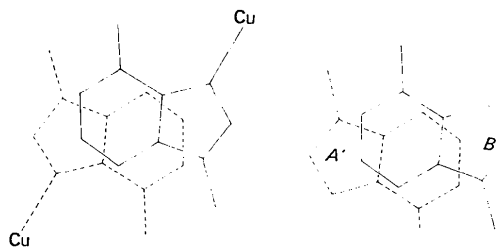
Fig. 3. Base stacking of the adenine ligands projected along the *a* axis.Fig. 4. Base stacking of: (a) 9-methyladenine ligands $D = 3.39 \text{ \AA}$, (b) uncomplexed 9-methyladenine $D = 3.33 \text{ \AA}$.

Table 5. *Hydrogen-bond distances and angles*

Bond	Position of acceptor atom	Distances (Å)		Angle (°)
		D...A	H...A	D-H...A
O(1)-H(11)···O(6)	$\bar{x}, 1-y, 1-z$	2.643 (3)	1.89 (3)	173 (2)
O(1)-H(12)···O(8)	x, y, z	2.677 (2)	1.76 (3)	170 (2)
O(2)-H(21)···O(8)	$\bar{x}, 1-y, 1-z$	2.742 (2)	2.09 (3)	177 (2)
O(2)-H(22)···O(7)	$x, y, z-1$	2.671 (2)	1.97 (3)	178 (3)
O(3)-H(31)···O(5)	$x, y-1, z$	2.639 (3)	1.95 (3)	171 (2)
O(3)-H(32)···O(1)	$\bar{x}, \bar{y}, 1-z$	2.840 (2)	2.06 (2)	167 (2)
O(4)-H(41)···O(6)	$x, 1-y, z-1$	2.916 (2)	2.19 (3)	171 (4)
O(4)-H(42)···O(8)	$\bar{x}, \bar{y}, 1-z$	2.889 (3)	2.26 (4)	165 (4)
O(5)-H(51)···N(3)	$1-x, 1-y, \bar{z}$	2.914 (2)	2.20 (4)	145 (4)
O(5)-H(52)···O(9)	x, y, z	2.819 (2)	2.09 (3)	170 (3)
N(6)-H(61)···O(9)	x, y, z	2.856 (3)	2.02 (3)	158 (2)
N(6)-H(62)···N(1)	$\bar{x}, \bar{y}, \bar{z}$	2.986 (3)	2.20 (3)	179 (2)

complexed 9-methyladenine may be made. The structure determination of 9-methyladenine is not of comparable accuracy, being based on film data and without hydrogen refinement (Stewart & Jensen, 1964). However, differences between corresponding bond lengths and angles are less than 0.02 Å and 2.1°, respectively. The bonds adjacent to the coordination site show a small *trans* effect consistent with that found in the corresponding copper-hypoxanthine complex (Sletten, 1974). The indirect chelate ring involving the hydrogen bond between the amino group and the sulphate ion is formed without imposing noticeable strain in the adenine geometry. The angles N(6)-C(6)-C(5) and C(6)-C(5)-N(7) are only slightly adjusted relative to the uncomplexed adenine geometry.

The adenine ligand shows the characteristic bend around the C(4)-C(5) bond found in most purine structures. The angle between the planes through the pyrimidine ring and the imidazole ring is 0.96°. The amino group is slightly bent out of the pyrimidine plane, but shows no twist around the C(6)-N(6) bond. The copper ion is located 0.312 Å from the plane through the purine ring.

The sulphate ion

Bond lengths and angles in the sulphate ion are listed in Table 4. The shape of the sulphate group is seen to be irregular. In the crystal structure of CuSO₄·3H₂O the longest S-O bond is the one coordinated to copper (Zahrobsky & Baur, 1967). However, in the present compound the variation in bond lengths is not related to coordination effects. The oxygen atoms of the sulphate group are involved in relatively strong hydrogen bonds and there seems to be a correlation between the number of hydrogen bonds established and the S-O bond lengths. Thus, the longest bond, S-O(8) = 1.500 Å, participates in three hydrogen bonds, while the shortest, S-O(7) = 1.462 Å, participates only in one. The two intermediate S-O bonds are each involved in two hydrogen bonds.

Molecular packing and hydrogen bonding

A stereographic drawing of the molecular packing is shown in Fig. 2. Centrosymmetrically related adenine

ligands are hydrogen-bonded in a DNA-like pattern, the distance N(6)-H(62)···N(1) being 2.986 Å and the angle at H(62) being 179°. The uncomplexed 9-methyladenine molecule is found to be hydrogen-bonded through N(6)-H(61)···N(7). This change in hydrogen bonding corroborates the assumption that N(7) rather than N(1) is the preferring binding site for metal ions in adenine.

The adenine ligands stack pairwise on top of each other in the usual pattern found in the uncomplexed purines (Fig. 3). The interplanar distance between molecules *A'* and *B* is 3.396 Å. The degree of overlap is shown in Fig. 4 together with the corresponding projection of the uncomplexed 9-methyladenine molecule. The similarity of the two projections is remarkable considering the differences in crystallographic and ionic environment.

The hydrogen-bonding network in the crystal is extensive, with all the available hydrogen donors occupied. A complete list of hydrogen bonds is given in Table 5; in addition some of the bonds are indicated as dashed lines in the stereo drawing (Fig. 2). There are two intramolecular hydrogen bonds in the complex; one between the amino group and the coordinated sulphate oxygen O(9), and one between water molecule O(1) and sulphate oxygen O(8).

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