Stereochemistry of Nucleic Acids and Their Constituents. XII. The Crystal and Molecular Structure of α-D-2′-Amino-2′-deoxyadenosine Monohydrate[1]

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Abstract: The structure of the α-nucleoside with a 2′-amino substituted ribose, α-D-2′-amino-2′-deoxyadenosine monohydrate, has been determined using three-dimensional diffractometer intensities collected with Cu Kα radiation. The crystals have an orthorhombic unit cell, space group $P2_12_12_1$. The unit cell constants are $a = 17.458$, $b = 10.157$, and $c = 6.8802$ A. The calculated (1.529 g cm^{-3}) and observed (1.531 g cm^{-3}) densities are consistent with the presence of a water per nucleoside molecule, which was subsequently confirmed by the X-ray analysis. The main conformational features are: the glycosidic torsional angle χ (Sundaralingam, 1969) is $-59.8°$ and is in the *anti* range, the purine ring is not planar, and the dihedral angle between the planes through the pyrimidine ring and the imidazole ring is 2.30, the sugar exhibits a C(3′)-*exo* puckering, and the conformation about the C(4′)–C(5′) bond is *gauche–trans*. The bases of the twofold screw axis related molecules are stacked on top of each other with considerable overlap of the pyrimidine rings, to form an infinite column approximately parallel to the *c* axis. There is an intramolecular hydrogen bond involving a hydrogen atom of the 2′-amino group and the O(3′) atom. Nitrogen-7 of the base is hydrogen bonded to the water. Similar hydrogen bonding may contribute to the hydration shell of the native nucleic acids. The ribose atom O(5′) appears to be involved in one donor and three acceptor hydrogen bonds, while the ring oxygen atom O(1′) probably is weakly hydrogen bonded to the water. Both these features are rather exceptional to this α-nucleoside.

The α-nucleosides and their analogs are of great interest because they are constituents of the vitamin B_{12} coenzyme and also occur as the pyrimidine components of the reduced and oxidized forms of nicotinamide adenine dinucleotide.[3] Therefore, it is important to have precise structural data on α-nucleosides to enable a comparison of their molecular dimensions and conformations with the more abundantly occurring β-nucleosides which are also present in coenzymes and are the sole constituents of the genetic material, the nucleic acids.

The structure analysis of α-D-2′-amino-2′-deoxyadenosine monohydrate represents the second example of an amino substituted ribose. In an earlier paper the 3′-amino analog derivative, puromycin dihydrochloride pentahydrate,[4] was reported.

Experimental Section

The late Professor M. L. Wolfram of Ohio State University supplied the synthetic sample of α-D-2′-amino-2′-deoxyadenosine[5] in powder form. Thin needle-shaped crystals were obtained by slow evaporation of an aqueous ethanol solution of the compound. A crystal with approximate dimensions 0.30 × 0.06 × 0.06 mm^3 was mounted on a glass fiber with the needle axis *a* parallel to the ϕ axis of the goniostat. Film and diffractometer data indicated that the systematic absenses were $h00$, $h = 2n + 1$; $0k0$, $k = 2n + 1$; and $00l$, $l = 2n + 1$; hence, the crystal belongs to the orthorhombic system with space group $P2_12_12_1$. Precise unit cell dimensions measured on the diffractometer are: $a = 17.4577 + 0.0020$, $b = 10.1568 \pm 0.0009$, and $c = 6.8802 \pm 0.008$ A. The density of the crystal measured by the method of flotation in CCl_4–$CHCl_3$ mixture is 1.531 g cm^{-3}, which is in good agreement with the calculated value of 1.529 g cm^{-3}, assuming one molecule of water of crystallization per nucleoside. Thus, there are four molecules of nucleoside monohydrate, $C_{10}H_6O_3H_{14} \cdot H_2O$, per unit cell.

The three-dimensional diffractometer intensities were collected up to a 2θ limit of 132° using the 2θ scan mode and a scan speed of 2°/min. A cutoff of $0.75\sigma(I)$ was used for an observed reflection. The data were corrected for Lorentz and polarization effects but no correction for absorption was made. Altogether 1266 reflections were scanned and 1074 were considered to be significantly above background.

Determination of Structure

The structure was solved by the direct method using the tangent formula.[6] The three origin-defining reflections and the enantiomorph fixing reflection are listed in Table I, where E is the normalized structure amplitude and ϕ is the phase angle. The phase refinement of the 250 largest E's, with $E > 1.2$, proceeded smoothly and the resulting E map showed all of the 19 nonhydrogen atoms of the nucleoside and the hydrate oxygen atom.

Table I. Origin and Enantiomorph-Defining Reflections for α-D-2′-Amino-2′-deoxyadenosine

	h	*k*	*l*	*E*	Phase
Origin	0	1	4	4.05	$\pi/2$
	12	0	5	2.91	$\pi/2$
	11	5	0	2.23	$\pi/2$
Enantiomer	13	0	1	2.36	$\pi/2$

Refinement of Structure

The coordinates of the 20 nonhydrogen atoms obtained from the E map were subjected to three cycles of full-matrix least-squares refinement[7] varying the in-

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[1] For part XI of this series see preceding article by D. C. Rohrer and M. Sundaralingam, *J. Amer. Chem. Soc.*, **92**, 4950 (1970).

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[3] S. F. Velick in "Light and Life," W. D. McElroy and H. B. Glass, Ed., Johns Hopkins Press, Baltimore, Md., 1961, p 106.

[4] M. Sundaralingam and S. K. Arora, *Proc. Nat. Acad. Sci., U.S.*, **64,** 1021 (1969).

[5] M. L. Wolfrom and M. W. Winkley, *J. Amer. Chem. Soc.*, **89,** 32 1823 (1967).

[6] J. Karle and I. L. Karle, *Acta Crystallogr.*, **21,** 849 (1966).

[7] W. R. Busing, K. A. Martin, and H. A. Levy, Oak Ridge National Laboratory Report ORNL-TM-305, Oak Ridge, Tenn., 1962.

dividual positional and isotropic thermal parameters and the overall scale factor. The resulting agreement index $R = \Sigma\,||F_o| - |F_c||/|F_o|$ was 0.099. A difference electron density map calculated at this point clearly showed all 16 hydrogen atoms. Including these atoms in another cycle of isotropic refinement, varying the positional and thermal parameters of all the atoms, lowered the R to 0.068. Two cycles of anisotropic least-squares refinement varying all the parameters except the thermal parameters of the hydrogen atoms gave the final R of 0.053 for the observed reflections.

In the least-squares refinement each reflection was given a weight (w) based on the counting statistics and given by the expression

$$\frac{1}{w} = \frac{1}{2\sqrt{\mathrm{Lp}}}\left[\frac{C_\mathrm{T} + C_\mathrm{B} + (0.05C_\mathrm{N})}{C_\mathrm{N}}\right]^{1/2}$$

where C_T is the total count for a reflection, C_B is the background count, and $C_\mathrm{N} = C_\mathrm{T} - C_\mathrm{B}$ is the net count. The scattering factors of C, N, and O used throughout the refinement are from the International Tables,[8] while that of H was from Stewart, *et al.*[9]

Results

A listing of the observed and calculated structure amplitudes (Table II) has been deposited with the ASIS–NAPS agency.[10] The atomic positional and thermal parameters are given in Tables III–V, respectively, for the nonhydrogen atoms and the hydrogen atoms. The thermal vibration ellipsoids are represented diagrammatically[11] in Figure 1.

Table III. Positional Parameters of α-D-2′-Aminodeoxyadenosine[a]

Atom	X/a	Y/b	Z/c
N(1)	0.28637 (24)	−0.15317 (39)	0.69804 (82)
C(2)	0.35809 (32)	−0.10261 (48)	0.69146 (114)
N(3)	0.38032 (24)	0.02236 (38)	0.69498 (82)
C(4)	0.31979 (31)	0.10163 (46)	0.69774 (87)
C(5)	0.24393 (29)	0.06771 (46)	0.70421 (87)
C(6)	0.22735 (28)	−0.06868 (49)	0.70183 (93)
N(7)	0.19703 (23)	0.17782 (41)	0.69814 (78)
C(8)	0.24516 (30)	0.27576 (48)	0.69485 (101)
N(9)	0.32062 (23)	0.23803 (35)	0.69631 (74)
N(6)	0.15638 (26)	−0.11578 (44)	0.70223 (86)
C(1′)	0.39001 (29)	0.31650 (46)	0.68369 (96)
C(2′)	0.39995 (31)	0.42235 (51)	0.84628 (85)
C(3′)	0.37338 (31)	0.54998 (50)	0.75163 (80)
C(4′)	0.39229 (34)	0.52849 (51)	0.53801 (87)
C(5′)	0.46942 (38)	0.57895 (58)	0.48058 (88)
O(1′)	0.39061 (27)	0.38761 (39)	0.50721 (60)
N(2′)	0.36416 (31)	0.38613 (50)	1.03129 (76)
O(3′)	0.29344 (23)	0.56852 (31)	0.78119 (74)
O(5′)	0.49051 (23)	0.54029 (38)	0.28777 (63)
O(W)	0.04390 (25)	0.23615 (44)	0.59789 (76)

[a] Estimated standard deviations in parentheses.

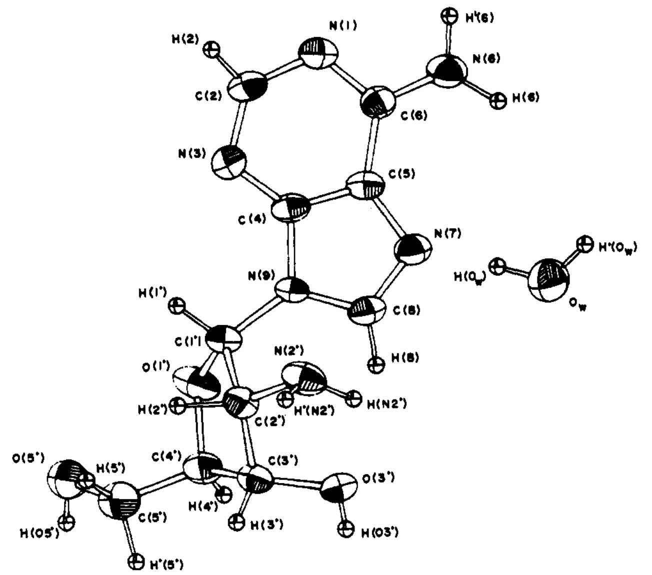

Figure 1. A computer plot of the thermal vibration ellipsoids[11] involving the nonhydrogen atoms.

Description of the Molecular Structure

Bond Distances and Bond Angles. The bond distances and bond angles involving the nonhydrogen atoms are shown in Table VI and Figure 2. The estimated standard deviations involving the bond distances of the base are about 0.006 Å, while those involving the

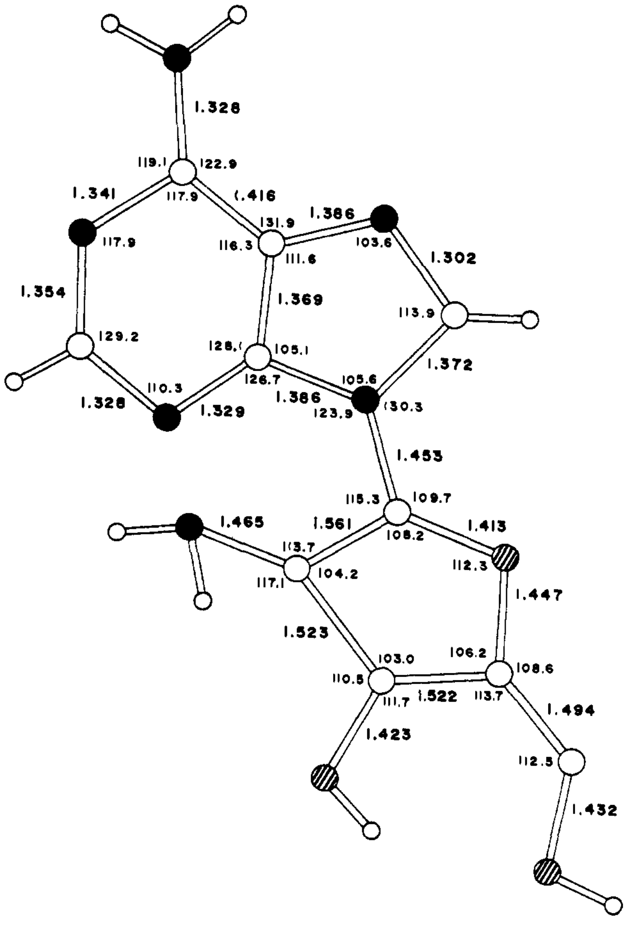

Figure 2. The bond distances and bond angles, in α-D-2′-amino-2′-deoxyadenosine.

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(8) "International Tables of Crystallography," Vol. III, Kynoch Press, Birmingham, England, 1962.

(9) R. F. Stewart, E. R. Davidson, and W. T. Simpson, *J. Chem. Phys.*, 42, 3175 (1965).

(10) Table II has been deposited as Document No. NAPS-01000 with the ASIS National Auxiliary Publications Service, c/o CCM Information Corp., 909 3rd Ave., New York, N. Y. 10022. A copy may be secured by citing the document number and by remitting $1.00 for microfiche or $3.00 for photocopies. Advance payment is required. Make checks or money orders payable to: ASIS–NAPS.

(11) C. K. Johnson, Oak Ridge National Laboratory Report ORNL-3794, Oak Ridge, Tenn., 1965.

Table IV. Thermal Parameters ($\times 10^4$)[a] of α-D-2′-Aminodeoxyadenosine

Atom	β_{11}	β_{22}	β_{33}	β_{12}	β_{13}	β_{23}
N(1)	231 (15)	429 (42)	1483 (123)	−1 (22)	0 (46)	0 (73)
C(2)	230 (19)	405 (48)	1912 (169)	6 (26)	0 (58)	−120 (94)
N(3)	191 (16)	496 (44)	1863 (137)	0 (21)	−9 (49)	101 (75)
C(4)	224 (18)	379 (47)	878 (124)	3 (24)	6 (49)	−32 (78)
C(5)	216 (18)	365 (45)	979 (128)	0 (24)	54 (49)	−32 (84)
C(6)	198 (18)	480 (49)	1104 (127)	−27 (24)	−14 (48)	157 (89)
N(7)	225 (16)	421 (40)	1350 (121)	2 (21)	−25 (44)	98 (75)
C(8)	211 (18)	372 (46)	1332 (146)	20 (24)	37 (53)	106 (86)
N(9)	173 (13)	279 (35)	1347 (123)	−30 (18)	−22 (43)	43 (67)
N(6)	227 (17)	485 (42)	1852 (134)	−49 (22)	70 (48)	152 (84)
C(1′)	203 (18)	342 (45)	1560 (156)	−26 (24)	−47 (56)	56 (81)
C(2′)	185 (18)	476 (53)	1189 (139)	−32 (27)	12 (43)	−83 (73)
C(3′)	229 (20)	382 (47)	867 (129)	−51 (26)	62 (41)	17 (70)
C(4′)	236 (21)	455 (53)	1062 (136)	16 (29)	37 (48)	−95 (75)
C(5′)	341 (25)	644 (63)	1011 (132)	−5 (33)	−156 (54)	32 (85)
O(1′)	461 (20)	526 (39)	1020 (92)	−183 (25)	−322 (41)	190 (56)
N(2′)	312 (20)	532 (48)	1106 (122)	−71 (26)	14 (32)	−177 (73)
O(3′)	220 (13)	381 (32)	1678 (105)	49 (18)	−56 (36)	−7 (63)
O(5′)	307 (16)	679 (40)	1342 (106)	−18 (22)	−147 (39)	46 (66)
O(W)	237 (15)	818 (48)	2357 (133)	2 (23)	17 (42)	147 (73)

[a] The temperature factor is of the form $T_1 = \exp[-(\beta_{11}h^2 + \beta_{22}k^2 + \beta_{33}l^2 + \beta_{12}hk + \beta_{13}hl + \beta_{23}kl)]$. Estimated standard deviations in parentheses.

Table V. Hydrogen Thermal and Positional Parameters of α-D-2′-Aminodeoxyadenosine[a]

Atom	X/a	Y/b	Z/c	B[b]
H(2)	0.3952 (27)	−0.1659 (46)	0.7020 (92)	2.63
H(8)	0.2343 (23)	0.3665 (41)	0.6765 (73)	1.04
H(6)	0.1087 (33)	−0.0639 (57)	0.7278 (103)	5.01
H′(6)	0.1445 (34)	−0.2069 (57)	0.6639 (104)	5.39
H(1′)	0.4344 (22)	0.2582 (38)	0.6786 (72)	1.42
H(2′)	0.4645 (23)	0.4244 (39)	0.8506 (63)	1.81
H(3′)	0.4033 (28)	0.6211 (49)	0.8141 (92)	3.36
H(4′)	0.3555 (31)	0.5735 (53)	0.4357 (84)	3.63
H(5′)	0.5186 (24)	0.5429 (45)	0.5885 (67)	1.51
H′(5′)	0.4572 (32)	0.6821 (54)	0.5036 (94)	4.15
H(N2′)	0.3108 (37)	0.4215 (61)	1.0082 (109)	5.87
H′(N2′)	0.3966 (37)	0.4205 (65)	1.1142 (95)	4.48
H(O3′)	0.2879 (38)	0.6378 (60)	0.7842 (139)	5.63
H(O5′)	0.4817 (34)	0.6119 (52)	0.2143 (98)	3.86
H(OW)	0.0995 (36)	0.2093 (54)	0.6267 (95)	4.21
H′(OW)	0.0108 (37)	0.1774 (65)	0.6331 (120)	6.22

[a] Estimated standard deviations in parentheses. [b] The temperature factor is of the form $T_i = \exp[-B \sin \theta/\lambda)^2]$.

Table VI. Bond Lengths and Angles of α-D-2′-Aminodeoxyadenosine[a]

Atoms	Length, Å	Atoms	Angle, deg
N(1)–C(2)	1.354 (7)	C(6)–N(1)–C(2)	117.9 (4)
N(1)–C(6)	1.341 (6)	N(1)–C(2)–N(3)	129.2 (4)
C(2)–N(3)	1.328 (6)	C(2)–N(3)–C(4)	110.3 (4)
N(3)–C(4)	1.329 (7)	N(3)–C(4)–C(5)	128.1 (4)
C(4)–C(5)	1.369 (7)	N(3)–C(4)–N(9)	126.7 (4)
C(4)–N(9)	1.386 (6)	C(5)–C(4)–N(9)	105.1 (4)
C(5)–C(6)	1.416 (7)	C(4)–C(5)–C(6)	116.3 (4)
C(5)–N(7)	1.386 (6)	C(4)–C(5)–N(7)	111.6 (4)
N(7)–C(8)	1.302 (6)	C(6)–C(5)–N(7)	131.9 (4)
C(8)–N(9)	1.372 (6)	N(1)–C(6)–C(5)	117.9 (4)
C(6)–N(6)	1.328 (7)	N(1)–C(6)–N(6)	119.1 (4)
N(9)–C(1′)	1.453 (6)	C(5)–C(6)–N(6)	122.9 (4)
		C(5)–N(7)–C(8)	103.6 (3)
		N(7)–C(8)–N(9)	113.9 (4)
C(1′)–C(2′)	1.561 (8)	C(4)–N(9)–C(8)	105.6 (3)
C(1′)–O(1′)	1.413 (7)	C(4)–N(9)–C(1′)	123.9 (4)
C(2′)–C(3′)	1.523 (7)	C(8)–N(9)–C(1′)	130.3 (4)
C(2′)–N(2′)	1.465 (7)		
C(3′)–C(4′)	1.522 (8)		
C(3′)–O(3′)	1.423 (7)	N(9)–C(1)′–O(1′)	109.7 (4)
C(4′)–C(5′)	1.494 (8)	N(9)–C(1′)–C(2′)	115.3 (4)
C(4′)–O(1′)	1.447 (6)	O(1′)–C(1′)–C(2′)	105.2 (4)
C(5′)–O(5′)	1.432 (7)	C(1′)–C(2′)–C(3′)	104.2 (5)
		C(1′)–C(2′)–N(2′)	113.7 (4)
		C(3′)–C(2′)–N(2′)	117.1 (4)
		C(2′)–C(3′)–C(4′)	103.0 (4)
		C(2′)–C(3′)–O(3′)	110.5 (4)
		C(4′)–C(3′)–O(3′)	111.7 (4)
		C(3′)–C(4′)–O(1′)	106.2 (4)
		C(3′)–C(4′)–C(5′)	113.7 (4)
		O(1′)–C(4′)–C(5′)	108.6 (4)
		C(4′)–C(5′)–O(5′)	112.5 (4)
		C(4′)–O(1′)–C(1′)	112.3 (3)

[a] Estimated standard deviations are in parentheses.

sugar are about 0.007 Å. The bond angles possess an error of about 0.4°.

The molecular dimensions of the adenine ring are generally in good agreement with the values found in 3′-O-acetyladenosine[12] and deoxyadenosine monohydrate.[13] On the other hand the glycosidic C(1′)–N(9) bond distance of 1.453 Å is shorter than the values commonly observed in the β-nucleosides.

The ribose ring C–C bonds are within the usual limits,[14] with the exception of C(1′)–C(2′) = 1.561 Å, which is about 0.035 Å greater than the average value, 1.525.[14] A similar but smaller lengthening of this bond was also found in α-pseudouridine.[15] This lengthening may have been influenced by the α linkage. The disproportionation of the intraring C–O bond distances, C(1′)–O(1′) = 1.413 Å, C(4′)–O(1′) = 1.447°, in comparison to the normal C–O single bond distance of 1.427 Å, is a feature that has consistently been observed in all of the accurately determined β-nucleosides and nucleotides.[14,16]

The ribose hydroxy bond C(3′)–O(3′) of 1.423 Å attached to the puckered carbon atom (see below) exhibits a normal value, and is in the quasi-axial orientation to the ribose ring. However, the amino group is in the quasiequatorial orientation to the ring and

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(12) S. T. Rao and M. Sundaralingam, *J. Amer. Chem. Soc.*, **92**, 4963 (1970).

(13) D. G. Watson, D. J. Sutor, and P. Tollin, *Acta Crystallogr.*, **19**, 111 (1965).

(14) M. Sundaralingam, *J. Amer. Chem. Soc.*, **87**, 599 (1965).

(15) See ref 1.

(16) M. Sundaralingam, *Biopolymers*, **6**, 189 (1968).

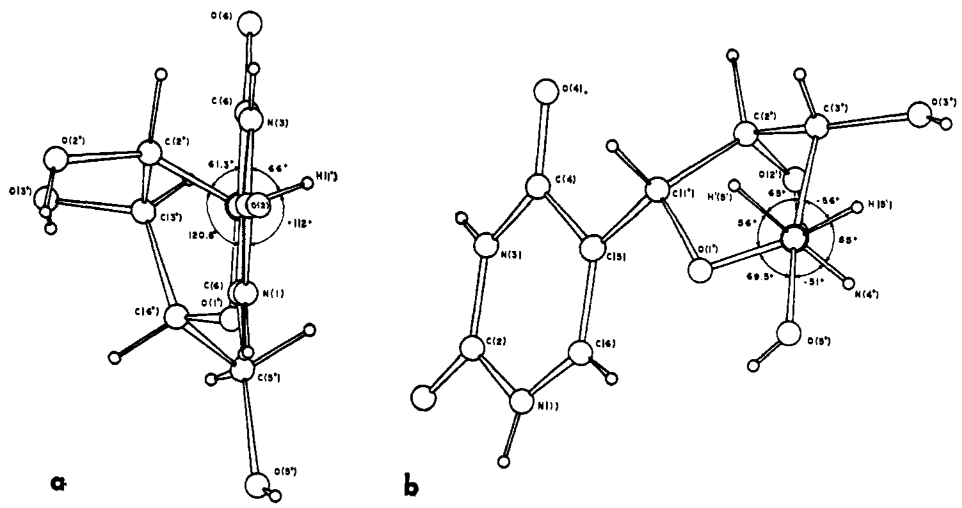

Figure 3. (a) A view down the glycosidic N(9)–C(1') bond showing the preferred *anti* conformation for the α nucleoside.[17] (b) A view down the exocyclic C(5')–C(4') bond illustrating the *gauche–trans* conformation of the C(5')–O(5') bond with respect to the O(1')–C(1') bond and the C(3')–C(4') bond, respectively

the C(2')–N(2') bond distance is 1.465 Å. This is about 0.035 Å longer than the C–OH bond normally present[14] in ribose.

Bond lengths and angles involving hydrogen atoms are shown in Table VII. Of interest are the angles at the amino nitrogen N(6) and N(2'). The C–N–H bond angles average 124° at the nitrogen (sp^2 hybridized) attached to the adenine ring, and average 101° at the nitrogen (sp^3 hybridized) attached to the ribose. The H–N–H is only 11° at N(6), but 124° at N(2').

Table VII. Bond Distances and Bond Angles Involving Hydrogen Atoms[a]

Bond	No.	Range	Av, A
sp^2 C–H	2	0.91–0.95	0.93
sp^2 N–H	2	0.98–1.00	0.99
sp^3 C–H	6	0.98–1.19	1.07
sp^3 N–H	2	0.88–1.01	0.96
sp^3 O–H	4	0.71–1.02	0.88
Angle	**No.**	**Range**	**Av, deg**
sp^2[b] N–C–H	4	113–128	119
sp^2 C–N–H	2	122–126	124
sp^2 H–N–H	1		111
sp^3 N–C–H	2	109–114	112
sp^3 C–C–H	9	98–117	107
sp^3 O–C–H	4	106–117	110
sp^3 C–N–H	2	100–101	101
sp^3 C–O–H	2	105–106	106
sp^3 H–N–H	1		124
sp^3 H–O–H	1		113

[a] Estimated standard deviations in bond distances and bond angles average 0.05 Å and 2°, respectively. [b] Denotes the hybridization state of the central atom.

Planarity of the Base. The least-squares planes through the nine atoms of the purine ring, the six atoms of the pyrimidine moiety, and the five atoms of the imidazole moiety are given in Table VIII. The latter two rings are planar within the errors of the structure determination. The dihedral angle between these planes is 2.3°; thus, the purine ring as a whole is distorted from being a perfect plane. The atoms C(2), C(5), and C(8) are displaced from the purine plane by about 3.5, 6, and 3 standard deviations, respectively. The amino substituent N(6) lies in the plane within experimental errors, while the sugar carbon atom C(1') is significantly displaced.

Table VIII. Least-Squares Planes[a,b,c] of Purine in α-D-2'-Aminodeoxyadenosine[d]

Atom	Displacement, Å Plane 1	 Plane 2	 Plane 3
N(1)	**−0.005** (6)	**0.007**	−0.077
C(2)	**−0.028** (8)	**−0.010**	−0.101
N(3)	**0.008** (6)	**0.010**	0.044
C(4)	**0.013** (6)	**−0.008**	−0.014
C(5)	**0.034** (6)	**0.005**	**0.014**
C(6)	**0.007** (6)	**0.004**	**−0.037**
N(7)	**−0.017** (5)	−0.071	**−0.008**
C(8)	**−0.022** (7)	−0.082	**−0.001**
N(9)	**0.009** (5)	−0.033	**0.009**
N(6)	−0.012	−0.030	−0.054
C(1')	−0.055	−0.096	−0.051
σ_{RMS}	0.018	0.008	0.0101
$\Delta(\sigma_{RMS})$	0.006	0.006	0.0059
l	0.0165	0.0268	0.0069
m	0.0040	−0.0110	0.0325
n	−0.9999	−0.9996	−0.9997
d	1.9959	−1.9325	−2.0026
ω			2.3°

[a] The equations of the planes are of the form $lx + my + nz = d$, where *l*, *m*, and *n* are the direction cosines of the normal to the plane, and *d* (Å) is the distance of the plane from the origin. [b] Displacements indicated in bold type denote atoms included in the calculation of the plane. All the atoms were given the same weight. [c] ω is the torsion angle between the six-member plane and the five-member plane. [d] Estimated standard deviations (Å) × 10^4 in parentheses.

Conformation of the Nucleoside

Glycosidic Torsional Angle. The glycosidic torsional angle, O(1')–C(1')–N(9)–C(8), is −59.8° and falls in the *anti* range generally found for the α-nucleosides,[17] Figure 3.

Conformation of the Amino Sugar. The ring puckering of the 2'-amino-2'-deoxyribose is C(3')-*exo*, with C(3') displaced by 0.459 Å, from the best four atom

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(17) M. Sundaralingam, *Biopolymers*, 7, 821 (1969).

Table IX. Least-Squares Planes[a,b,c] of Sugar in α-D-2′-Aminodeoxyadenosine[d]

Atom	Displacement, Å Plane 1	Plane 2	Plane 3	Plane 4	Plane 5	Plane 6	Plane 7
C(1′)	**0.093** (5)	**0.109**	**0.130**	**0.029**	**0.044**	0.239	**0.000**
C(2′)	**−0.169** (5)	**−0.175**	**+0.124**	**−0.017**	−0.435	**−0.093**	−0.148
C(3′)	**0.184** (5)	**0.178**	**0.079**	0.459	**0.039**	**0.149**	0.339
C(4′)	**−0.128** (6)	**−0.112**	−0.324	**0.019**	**−0.068**	**−0.157**	**0.000**
O(1′)	**0.021** (5)	0.050	**−0.086**	**−0.032**	**0.073**	**0.100**	**0.000**
N(9)	1.367	1.387	1.455	1.206	1.187	1.564	1.195
N(2′)	0.485	0.463	0.647	0.676	0.026	0.596	0.473
O(3′)	1.559	1.548	1.439	1.873	1.379	1.499	1.739
C(5)′	−1.513	−1.494	−1.761	−1.326	−1.374	−1.572	−1.337
RMS dev	0.1326	0.1474	0.1073	0.0251	0.0583	0.1281	
σ (RMS dev)	0.0054	0.0055	0.0052	0.0053	0.0053	0.0054	
l	−0.9965	−0.9958	−0.9846	−0.9966	−0.9885	−0.9869	−0.9998
m	−0.0839	−0.0905	−0.1573	0.0458	0.0580	−0.1608	0.0201
n	−0.0009	0.0133	−0.0766	−0.0690	−0.1400	−0.0103	−0.0034
d	−7.1491	−7.1517	−7.5067	−6.8177	−6.5677	−7.4984	−6.7500
ϕ	90.9°	88.3°	86.6°	86.9°	81.0°	90.4°	90.7°

[a] The equations of the planes are of the form $lx + my + nz = d$, where l, m, and n are the direction cosines of the normal to the plane, and d (Å) is the distance of the plane from the origin. [b] Displacements indicated in bold type denote atoms included in calculation of the plane. All atoms were given the same weight. [c] ϕ is the torsion angle between the plane and the purine nine-atom plane. [d] Estimated standard deviations in parentheses.

Table X. Some Torsional Angles[a]

Atoms	Angle, deg	Atoms	Angle, deg
C(6)-N(1)-C(2)-N(3)	2.7°	C(8)-N(9)-C(4)-N(3)	178.3
N(1)-C(2)-N(3)-C(4)	−2.8	C(8)-N(9)-C(4)-C(5)	−2.1
C(2)-N(3)-C(4)-C(5)	2.5	C(1′)-N(9)-C(4)-N(3)	2.5
C(2)-N(3)-C(4)-N(9)	−178.1	C(1′)-N(9)-C(4)-C(5)	−177.9
N(3)-C(4)-C(5)-C(6)	−2.1	C(4)-N(9)-C(1′)-O(1′)	114.9
N(3)-C(4)-C(5)-N(7)	−177.8	C(4)-N(9)-C(1′)-C(2′)	−126.5
N(9)-C(4)-C(5)-C(6)	178.4	C(8)-N(9)-C(1′)-C(2′)	58.8
N(9)-C(4)-C(5)-N(7)	2.7	N(9)-C(1′)-O(1′)-C(4′)	119.0
C(4)-C(5)-C(6)-N(1)	−1.5	N(9)-C(1′)-C(2′)-C(3′)	−98.8
C(4)-C(5)-C(6)-N(6)	−178.2	N(9)-C(1′)-C(2′)-N(2′)	29.9
N(7)-C(5)-C(6)-N(1)	176.2	O(1′)-C(1′)-C(2′)-N(2′)	151.0
N(7)-C(5)-C(6)-N(6)	−3.5	C(1′)-C(2′)-C(3′)-O(3′)	89.9
C(5)-C(6)-N(1)-C(2)	−1.8	N(2′)-C(2′)-C(3′)-C(4′)	−156.1
N(6)-C(6)-N(1)-C(2)	177.9	N(2′)-C(2′)-C(3′)-O(3′)	−36.7
C(4)-C(5)-N(7)-C(8)	−2.1	C(2′)-C(3′)-C(4′)-C(5′)	−92.6
C(6)-C(5)-N(7)-C(8)	−176.9	O(3′)-C(3′)-C(4′)-O(1′)	−91.8
C(5)-N(7)-C(8)-N(9)	0.6	O(3′)-C(3′)-C(4′)-C(5′)	148.8
N(7)-C(8)-N(9)-C(4)	0.9	C(5′)-C(4′)-O(1′)-C(1′)	109.2
N(7)-C(8)-N(9)-C(1′)	176.4		

[a] Estimated standard deviations in the torsional angles are about 0.8°.

plane, Table IX. This displacement is much smaller than the values (about 0.6 Å) normally observed. In fact, the ring is in a distorted half-chair conformation with C(3′) and C(2′) oppositely displaced by 0.339 Å and −0.148 Å, respectively, from the plane containing the remaining three ring atoms. The intraring torsional angles are: O(1′)→C(1′), −5.6; C(1′)→C(2′), 22.3°; C(2′)→C(3′), −29.5°; C(3′)→C(4′), 26.8°; C(4′)→O(1′), −13.4°.

The *exo* puckering of the ring appears to be the preferred mode of puckering of the α-nucleosides,[18] while the *endo* puckering is definitely favored for the β analogs.[14,17,19]

The torsional angles O(1′)-C(4′)-C(5′)-O(5′) and C(3′)-C(4′)-C(5′)-O(5′) are 53.3° and 171.2°, respectively, Figure 3. Therefore, the conformation about the C(4′)-C(5′) bond is *gauche–trans*,[14,20] which is similar to the conformation found in α-pseudouridine.[15]

The other torsional angles involving the nonhydrogen atoms are listed in Table X. One of the more interesting torsional angles (−36.7°) is that involving the adjacent ribose substituents N(2′) and O(3′). The torsional angles involving the bonds of the purine ring have also been tabulated to emphasize further the distortions from planarity of the ring.

The conformation of the amino group with respect to the sugar is such that the torsional angles H(2′)-C(2′)-N(2′)-H′(N2′) = 33° and H(2′)-C(2′)-N(2′)-H(N2′) = 161°. This conformation is preferred because it permits the intramolecular hydrogen bond between the 2′-amino group and the 3′-hydroxy group.

The torsional angles involving the hydrogen atoms on adjacent ring atoms are given in Table XI. These angles are of importance in determining the conformation of the sugar from nuclear magnetic resonance coupling constants.

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(18) M. Sundaralingam, to be published.
(19) M. Spencer, *Acta Crystallogr.*, **12**, 59 (1959).
(20) E. Shefter and K. N. Trueblood, *ibid.*, **18**, 1067 (1965).

Table XI. Torsional Angles Involving the Hydrogens of the Sugar[a]

Atoms	Angle, deg
H(1′)-C(1′)-C(2′)-H(2′)	26
H(2′)-C(2′)-C(3′)-H(3′)	−46
H(3′)-C(3′)-C(4′)-H(4′)	−98
H(4′)-C(4′)-C(′5)-H(5′)	176
H(4′)-C(4′)-C(5′)-H′(5′)	61
H(2′)-C(2′)-N(2′)-H(N2′)	161
H(2′)-C(2′)-N(2′)-H′(N2′)	33
H(3′)-C(3′)-O(3′)-H(O3′)	32
H(5′)-C(5′)-O(5′)-H(O5′)	−134
H′(5′)-C(5′)-O(5′)-H(O5′)	9
C(1′)-C(2′)-N(2′)-H(N2′)	−88
C(1′)-C(2′)-N(2′)-H′(N2′)	145
C(3′)-C(2′)-N(2′)-H(N2′)	34
C(3′)-C(2′)-N(2′)-H′(N2′)	−93
C(2′)-C(3′)-O(3′)-H(O3′)	150
C(4′)-C(3′)-O(3′)-H(O3′)	−96
C(4′)-C(5′)-O(5′)-H(O5′)	101

[a] The estimated standard deviation in the torsional angle is about 4°.

Hydrogen Bonding The hydrogen bond distances and bond angles in the crystal are given in Table XII. A view of the contents of the unit cell and the hydrogen bonding scheme is shown in Figure 4.

An interesting feature of the structure is the presence of the intramolecular hydrogen bond N(2′)-H(N2′)···O(3′) = 2.814 Å involving the amino group and the adjacent 3′ hydroxy group. The N(2′)-H(N2′)···O(3′) valence angle is 119°. Whereas intramolecular hydrogen bonds have been observed in the past for purine nucleosides involving O(5′)-H of the sugar and N(3′) of the base, this is the first time an intramolecular hydrogen bond between adjacent sugar ring substituents has been observed in a nucleoside in the solid state. It is of interest to note that in puromycin[4] the only hydrogen atom on the 3′ nitrogen atom was found to be hydrogen bonded to a water molecule.

There are no interbase hydrogen bonds. All the base nitrogen atoms, with the exception of N(3) which is not involved in hydrogen bonding, are involved in hydrogen bonding either to the sugar or the water molecule. The amino group on the base is involved in donor hydrogen bonds to the O(5′) atom and the amino nitrogen N(2′) atom of the sugar. The ribose hydroxy group O(3′)-H is hydrogen bonded to N(1) of the base, while N(7) is hydrogen bonded to the water molecule. The involvement of N(7) in hydrogen bonding to water is quite common.[21] This suggests that such hydrogen bonds are likely to occur in the nucleic acids, thus, placing water molecules in the broad groove of DNA. The second water hydrogen atom appears to be weakly hydrogen bonded both to the sugar hydroxy group O(5′)-H and the ring oxygen atom O(1′), Figure 5. Although the O(W)···O(5′) and O(W)···O(1′) distances of 3.061 ± 0.006 and 3.044 ± 0.006 Å, respectively, are greater than the sum of the van der Waals radii of the oxygen atoms, nevertheless, the H′(OW)···O(5′) and H′(OW)···O(1′) distances, 2.30 ± 0.07 and 2.40 ± 0.07 Å, respectively, are less than the sum of the van der Waals radii of the hydrogen and oxygen atoms. If O(1′) is an acceptor of a hydrogen bond, then this will represent a rare case of an hydrogen bond to the ring oxygen of a nucleoside. O(5′) is involved in an acceptor and a donor hydrogen bond of normal strength, and two weak acceptor hydrogen bonds involving the water and the 2′-amino group of the sugar, Table IX. Both the hydrogen bonding to O(1′) and the four hydrogen bonds to O(5′) represent rather unusual features in the structural chemistry of the nucleosides.

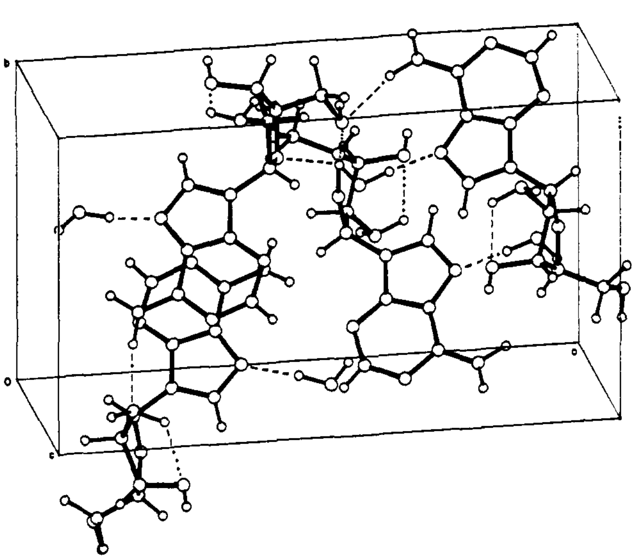

Figure 4. The contents of the unit cell showing the hydrogen bonding in the lattice and the base stacking.

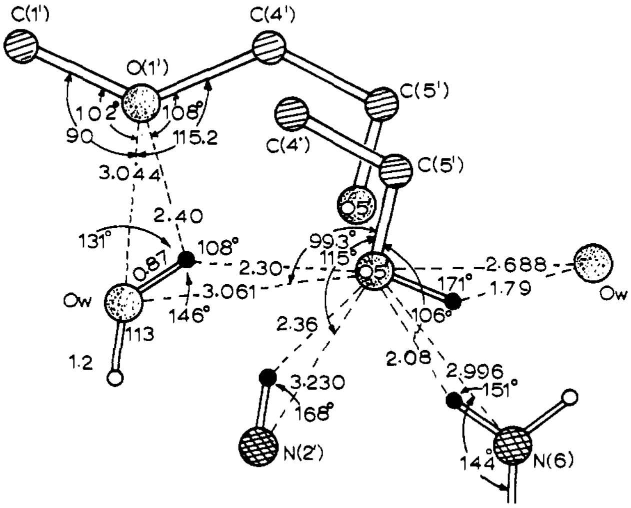

Figure 5. A schematic drawing showing the possible involvement of one of the water hydrogens in a bifurcated hydrogen bond, and the involvement of O(5′) in four hydrogen bonds (one donor and three acceptor hydrogen bonds). It should be pointed out that the hydrogen atoms have not been located very precisely, and therefore the conclusion on bifurcated hydrogen bonds is tentative. It is entirely possible that H′(OW) is really hydrogen bonded to only one of the atoms, O(1′) or O(5′). This may represent the first known case of at least a weak hydrogen bond to the ring O(1′) in the crystal chemistry of nucleosides and nucleotides. In a model of actinomycin·DNA complex the O(1′) atom has been involved in hydrogen bonding to the amino group of the actinomycin chromophore [L. Hamilton, W. Fuller, and E. Reich, *Nature* (*London*), **198**, 538 (1968)]. It should be pointed out that this hydrogen bonding is not preferred, and at the most it is a very weak hydrogen bond.

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(21) S. T. Rao and M. Sundaralingam, *J. Amer. Chem. Soc.*, **91**, 1210 (1968).

Table XII. Hydrogen Bond Lengths and Angles of α-D-2′-Aminodeoxyadenosine[a]

Sym. no.[b]	Translation			Atoms	Angle, deg	Length, Å	Length from hydrogen, Å
	X	Y	Z				
4	−1	0	1	N(6)–H(N6)···O(5′)	151	2.996 (6)	2.08 (6)
				C(6)–N(6)···O(5′)	144.0		
				N(6)···O(5′)–C(5′)	99.0		
				H(N6)···O(5′)–C(5′)	106		
3	0	0	0	N(6)–H′(N6)···N(2′)	167	3.009 (7)	2.04 (6)
				C(6)–N(6)···N(2′)	116.0		
				N(6)···N(2′)–C(2′)	128.3		
				H′(N6)···N(2′)–C(2′)	130		
1	0	0	0	N(2′)–H(N2′)···O(3′)	119	2.814 (6)	2.18 (7)
				C(2′)–N(2′)···O(3′)	59.4		
				N(2′)···O(3′)–C(3′)	64.5		
				H(N2′)···O(3′)–C(3′)	83		
1	0	0	−1	N(2′)–H′(N2′)···O(5′)	168	3.230	2.36 (6)[c]
				C(2′)–N(2′)···O(5′)	93.5		
				N(2′)···O(5′)–C(5′)	117.6		
				H′(N2′)···O(5′)–C(5′)	115		
1	0	1	0	O(3′)–H(O3′)···N(1)	161	2.887 (5)	2.20 (6)
				C(3′)–O(3′)···N(1)	98.2		
				O(3′)···N(1)–C(6)	130.9		
				O(3′)···N(1)–C(2)	109.8		
				H(O3′)···N(1)–C(6)	128		
				H(O3′)···N(1)–C(2)	111		
3	0	1	0	O(5′)–H(O5′)···O(W)	171	2.688 (6)	1.79 (6)
				C(5′)–O(5′)···O(W)	99.3		
1	0	0	0	O(W)–H(OW)···N(7)	173	2.824 (6)	1.80 (6)
				O(W)···N(7)–C(8)	116.5		
				O(W)···N(7)–C(5)	137.4		
				H(OW)···N(7)–C(8)	118		
				H(OW)···N(7)–C(5)	135		
4	0	0	−1	O(W)–H′(OW)···O(1′)	131	3.044 (6)	2.40 (7)[c]
				O(W)···O(1′)–C(1′)	89.9		
				O(W)···O(1′)–C(4′)	115.2		
4	0	0	1	O(W)–H′(OW)···O(5′)	146	3.061 (6)	2.30 (7)[c]
				O(W)···O(5′)–C(5′)	95.3		
				O(1′)···H′(OW)···O(5′)	107		

[a] Estimated standard deviations in parentheses. [b] Symmetry operations: (1) X, Y, Z; (2) $-X, \frac{1}{2} + Y, \frac{1}{2} - Z$; (3) $\frac{1}{2} - X - Y, \frac{1}{2} + Z$; (4) $\frac{1}{2} + X, \frac{1}{2} - Y - Z$. [c] These short contacts may only represent partial hydrogen bonds.

The conclusion that the hydrogen atom of the water is involved in a bifurcated hydrogen[22] bond, Figure 5, must be taken as being tentative since the hydrogen atoms in this structure have not been located precisely.

Base Stacking. The bases form an infinite stack of partially overlapping bases[23,24] involving the pyrimidine moieties about a twofold screw axis, with the amino group projected between alternate bases, Figure 4. Adjacent bases are rotated by 180° from each other, thus favoring dipole–dipole interaction. The interatomic contacts between the bases are all greater than 3.3 Å. The dihedral angle between adjacent stacked planes is 20°.

The following computer programs were used in this work: Busing, Martin, and Levy[7] least-squares program modified for the Univac 1107-1108 computers; ORTEP thermal ellipsoid program.[11] The phase refinement programs used in the direct method are those of Hall.[25] Most of the other programs[26] were written in these laboratories.

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(22) J. Donohue in "Structural Chemistry and Molecular Biology," W. H. Freeman, San Francisco, Calif., 1968, p 433.

(23) M. Sundaralingam, S. T. Rao, and C. E. Bugg, Abstracts, American Crystallography Association Meeting, Seattle, Wash., March 1969.

(24) C. E. Bugg, J. Thomas, M. Sundaralingam, and S. T. Rao, *Biopolymers*, in press.

(25) S. R. Hall, Abstracts, VIIth International Union of Crystallography Congress, Stonybrook, N. Y., Aug 1969.

(26) S. T. Rao, unpublished results.