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Keyphrases

Methoxysulfanilamidodiazines—hydrolyses
Hydrolyses—acid catalyzed
TLC—identity
IR spectrophotometry—structure
UV spectrophotometry—structure

Crystal and Molecular Structure of 6-Thiopurine Riboside

By ELI SHEFTER

The molecular structure of 6-thiopurine riboside (commonly known as 6-mercaptopurine riboside) has been determined by X-ray crystallographic analysis. The material crystallizes from water as orthorhombic needles (space group $P2_12_12_1$) with unit cell dimensions of $a = 8.622$ Å., $b = 13.624$ Å., and $c = 20.262$ Å. There are two unique molecules in the asymmetric unit of the cell. The structure was solved by the heavy atom technique and refined by block diagonal least squares. The final R index is 0.067. In general, the bond lengths and angles agree with those found in other nucleoside structures. The C6-S distances of the two molecules (average 1.669 ± 0.002 Å.) together with the presence of a hydrogen on each of the N1 atoms indicates that the molecules are in the thiolactam configuration rather than the mercapto form. The glycosidic torsion angles (ϕ_{CN}) are +135° and +144° for the two molecules. The *syn* conformation about each of the CN bonds is stabilized by O5′-H...N3 intramolecular hydrogen bonds. The furanose rings are puckered; C2′ being displaced *endo* in both molecules. Each of the unique sulfurs is involved in a C-H...S interaction, while one is also participating in an O-H...S hydrogen bond.

6-Thiopurine (commonly known as 6-mercaptopurine) has been well established as an effective antineoplastic agent. It has been postulated that the compound exerts its effect at an enzymatic level., *i.e.*, through the purine metabolic pathway (1). In order to act as an inhibitor, it must first be converted to its active form, the ribonucleotide. In the hope of providing information on the electronic and steric configuration of this active species, the crystal and molecular structure of the riboside has been investigated.

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EXPERIMENTAL

The compound was obtained from Sigma Chemical Co. (St. Louis, Missouri) and crystallized from water. Orthorhombic needles so derived have the following data:

$a = 8.622 \pm 0.002$ Å. $D_M = 1.589 \pm 0.005$ Gm./-cm.^{3} (by flotation)

$b = 13.624 \pm 0.002$ Å. $D_{calcd.} = 1.586$ for $Z = 8$

$c = 20.262 \pm 0.004$ Å. Space group $P2_12_12_1$

TABLE I—FINAL POSITIONAL AND THERMAL PARAMETERS FOR NONHYDROGEN ATOMS AND THEIR ESTIMATED *SD*'S IN PARENTHESES, × 10^4[a]

Name	x/a	y/b	z/c	b_{11}	b_{22}	b_{33}	b_{12}	b_{13}	b_{23}
1S	9356(2)	−6936(1)	2913(1)	133(2)	47(1)	22(1)	−25(3)	−20(2)	−14(1)
1N1	7708(7)	−7216(4)	1808(3)	127(8)	35(3)	19(1)	4(8)	11(6)	−5(3)
1C2	6872(9)	−6943(4)	1267(3)	153(10)	30(3)	14(1)	26(10)	−16(6)	8(3)
1N3	6710(7)	−6059(4)	1056(2)	131(8)	34(3)	13(1)	8(8)	−4(5)	−3(3)
1C4	7490(7)	−5406(4)	1430(3)	90(7)	27(3)	14(1)	9(8)	10(5)	5(3)
1C5	8348(7)	−5586(4)	1993(3)	91(8)	35(3)	13(1)	1(9)	18(5)	2(3)
1C6	8472(7)	−6562(4)	2224(3)	88(7)	30(3)	17(1)	−11(8)	15(6)	−1(3)
1N7	8948(7)	−4745(4)	2259(3)	107(7)	40(3)	18(1)	−7(8)	−18(5)	12(3)
1C8	8455(8)	−4052(4)	1847(3)	117(9)	26(3)	20(2)	−3(9)	−17(6)	14(3)
1N9	7576(6)	−4397(4)	1337(2)	107(7)	26(2)	14(1)	−2(7)	5(5)	6(3)
1C1′	7096(8)	−3822(4)	779(3)	102(8)	24(3)	16(1)	−6(8)	−6(6)	3(3)
1O1′	5517(5)	−3992(3)	643(2)	98(6)	43(2)	16(1)	−14(7)	1(4)	1(3)
1C2′	7961(7)	−4063(4)	141(3)	94(7)	25(3)	14(1)	23(8)	0(6)	−7(3)
1O2′	9487(5)	−3706(3)	111(2)	93(6)	35(2)	25(1)	12(6)	0(5)	−17(3)
1C3′	6857(8)	−3609(5)	−354(3)	110(9)	31(3)	19(2)	−12(9)	−1(6)	−13(4)
1O3′	7065(6)	−2574(4)	−364(3)	143(8)	37(3)	34(2)	−17(8)	1(6)	−28(3)
1C4′	5254(8)	−3899(5)	−64(3)	97(8)	42(3)	17(1)	−17(9)	15(6)	7(4)
1C5′	4593(9)	−4831(5)	−329(3)	130(10)	44(4)	19(2)	−25(11)	−7(7)	7(4)
1O5	5604(7)	−5664(3)	−259(2)	175(8)	35(2)	20(1)	13(8)	−14(6)	9(3)
2S	−403(2)	−6728(1)	−19(1)	127(2)	46(1)	15(1)	−6(2)	−9(2)	−1(1)
2N1	1198(7)	−7638(4)	920(3)	142(9)	28(2)	18(1)	−6(8)	−2(6)	10(3)
2C2	2132(9)	−7753(5)	1448(3)	170(12)	30(3)	17(1)	−7(10)	1(8)	−2(4)
2N3	2771(8)	−7019(4)	1773(3)	160(9)	31(3)	16(1)	3(9)	−13(6)	−14(3)
2C4	2442(7)	−6131(4)	1502(3)	94(8)	34(3)	13(1)	−25(9)	2(5)	0(3)
2C5	1520(8)	−5959(4)	957(3)	110(8)	30(3)	12(1)	−12(9)	2(6)	3(3)
2C6	820(7)	−6774(5)	617(3)	104(8)	36(3)	12(1)	−1(9)	22(5)	5(3)
2N7	1427(6)	−4963(4)	821(2)	106(7)	37(3)	13(1)	−14(8)	0(5)	−5(3)
2C8	2283(9)	−4558(5)	1286(3)	132(10)	33(3)	17(1)	5(10)	10(6)	−1(3)
2N9	2919(6)	−5225(4)	1719(2)	101(7)	35(3)	13(1)	−10(7)	0(5)	−2(3)
2C1′	3681(7)	−4957(4)	2340(3)	84(8)	29(3)	20(2)	17(8)	−9(6)	5(3)
2O1′	4938(6)	−5601(4)	2442(2)	91(6)	54(3)	21(1)	−11(7)	5(4)	−11(3)
2C2′	2648(8)	−5063(5)	2937(3)	102(8)	35(3)	17(1)	15(9)	9(6)	8(4)
2O2′	1600(6)	−4285(3)	3019(2)	127(7)	38(2)	25(1)	−36(7)	−11(5)	24(3)
2C3′	3861(8)	−5147(5)	3476(3)	113(9)	50(4)	16(2)	−2(11)	−24(6)	4(4)
2O3′	4413(7)	−4179(4)	3625(3)	196(10)	50(3)	24(1)	−1(10)	−50(6)	18(3)
2C4′	5127(8)	−5739(5)	3144(3)	84(8)	39(3)	23(2)	13(9)	−10(6)	10(4)
2C5′	5103(9)	−6846(6)	3292(4)	152(11)	44(4)	23(2)	−2(12)	−19(8)	−9(5)
2O5′	3682(7)	−7280(4)	3125(2)	169(9)	49(3)	22(1)	38(9)	−12(6)	−20(3)

[a] Temperature factors in the form; exp = $(b_{11}h^2 + b_{22}k^2 + b_{33}l^2 + b_{12}hk + b_{13}hl + b_{23}kl)$.

The cell dimensions and the subsequent intensity measurements were carried out at 22 ± 4°, with Ni filtered Cu Kα radiation.

The intensities were measured by the stationary crystal-stationary counter technique using balanced Ni-Co filters. A General Electric XRD-6 diffractometer was utilized for this purpose. In the range of measurement (0 to 150° in 2 Θ), 2,729 unique reflections out of a possible number of 2,799 had intensities significantly greater than their background counts. These data were corrected for Lorentz and polarization factors and $\alpha_1 - \alpha_2$ splitting. An adjustment for the anisotropy of transmission of X-rays as a function of the angle ϕ was made as a means of correcting for absorption. The crystal used to collect the data was approximately 0.5 mm. along a (which in turn was parallel to the ϕ axis) and approximately 0.1 mm. in diameter. The structure factors were put on an absolute scale by a Wilson plot (2).

A three-dimensional Patterson synthesis calculated with only the $|F_0^2|$ terms having a value of $\sin \Theta/\lambda$ greater than 0.5 enabled the positions of the two unique sulfurs to be found. The coordinates of the 36 other nonhydrogen atoms were located in subsequent electron density Fourier syntheses. The positional and isotropic thermal parameters of these atoms were refined by least squares using a block diagonal approximation to the normal equations. A modified version of ACA program No. 317 of Gantzel, Sparks, and Trueblood (unpublished) was used for this purpose. Anisotropic temperature factors were introduced after the R value ($\Sigma||F_0| - |F_0||/\Sigma|F_0|$) was less than 0.2. After two cycles of least squares, a difference electron density map was calculated and 18 of the 24 hydrogens were easily located. The least squares was continued, including these atoms with isotropic temperature factors, until the shifts were less than $^1/_3$ of their estimated standard deviations (*SD*'s). A final difference map was then calculated and the positions of the four other hydrogens were obtained. The weighting scheme utilized in the final cycles of refinement was $W^{-1} = [(|F_0| - 15)/10]^2 + 1$, such that $\langle W\Delta^2 \rangle$ was constant throughout the range of $|F_0|$ (16). The unobserved data were given zero weight. The final R value for the observed data is 0.067.[1]

Throughout the above calculations, the atomic form factors utilized were those of Cromer and Waber (3) with the exception of hydrogen for which those in the International Tables of Crystallography (4) were used.

A listing of the fractional coordinates and temperature factors for the various atoms may be found in Tables I and II. Since the absolute configuration

[1] A list of the observed and calculated structure factors has been deposited in the Health Sciences Library, State University of New York at Buffalo, under the title of this publication.

TABLE II—POSITIONAL ($\times 10^4$) AND THERMAL PARAMETERS OF HYDROGENS AND THEIR RESPECTIVE ESTIMATED *SD*'S IN PARENTHESES

Name	Atom to Which it is Attached	x/a	y/b	z/c	B_{iso} (A^2)[b]
H1	1N1	780(7)	−786(7)	201(4)	2.3(2.9)
H2	1C2	616(8)	−745(5)	99(3)	0.1(1.3)
H3	1C8	881(7)	−330(4)	192(3)	−0.7(1.0)
H4	1C1′	740(6)	−309(4)	92(2)	−1.5(0.9)
H5	1C2′	795(9)	−478(6)	15(4)	0.9(1.6)
H6	1O2′	1054	−404	18	[a]
H7	1C3′	702(7)	−379(4)	−80(3)	−0.5(1.1)
H8	1O3′	619	−210	−21	[a]
H9	1C4′	459(9)	−328(6)	−32(4)	1.2(1.5)
H10	1C5′	351(11)	−499(6)	−6(4)	2.7(1.8)
H11	1C5′	436(8)	−486(5)	−84(3)	0.3(1.3)
H12	1O5′	578(11)	−564(7)	15(4)	1.9(1.8)
H13	2N1	88(11)	−816(9)	68(4)	2.4(2.0)
H14	2C2	222(8)	−841(5)	160(3)	−0.1(1.2)
H15	2C8	236(9)	−388(5)	124(3)	0.7(1.4)
H16	2C1′	397(8)	−412(5)	221(3)	−0.6(1.1)
H17	2C2′	202(8)	−565(5)	285(3)	0.4(1.3)
H18	2O2′	66	−424	273	[a]
H19	2C3′	353(8)	−543(5)	391(3)	−0.2(1.2)
H20	2O3′	466(11)	−422(7)	412(4)	3.1(1.9)
H21	2C4′	613(10)	−540(6)	325(4)	1.6(1.7)
H22	2C5′	588	−730	293	[a]
H23	2C5′	541(12)	−696(7)	376(5)	4.1(2.2)
H24	2O5′	338(12)	−717(7)	259(5)	2.8(2.3)

[a] The use of the scattering curve for the free hydrogen atom usually results in anomalously low values for *B* [Jensen, L. H., and Sundaralingham, M., *Science*, **145**, 1185(1964)]. [b] These were found in the final difference electron density synthesis.

was not determined, the positional parameters were set so that they adhere to the usual convention for D-ribosides. The prefix number on each atom denotes to which of the two unique molecules the atom belongs. The estimated *SD*'s in these tables were calculated from the inverses of the full normal equation blocks. The estimated *SD*'s in the positional parameters of the nonhydrogen atoms, except for the sulfurs, are approximately 0.006 Å. and for the sulfurs 0.002 Å. These *SD*'s correspond to an uncertainty of about 0.009 Å. and 0.4° in bond lengths and angles involving the C, N, and O atoms and in the case of the C—S bonds, 0.006 Å. The errors in the hydrogen positions are at least ten times as great as those for the atoms to which they are attached, *i.e.*, average bond length error of 0.09 Å.

The intramolecular bond distances and angles for the compound are shown in Figs. 1 and 2. The angles involving the hydrogens are not presented in these figures, and only those relevant to the discussion will be presented because of their estimated *SD*'s. They are, however, in good agreement with their expected values. In general, the bond distances and angles in the two unique purine moieties are considered to be similar, *i.e.*, using the levels of significance suggested by Cruickshank and Robertson (6), the comparative differences are not highly significant.

DISCUSSION

The bond distances of both purine residues together with the placement of a hydrogen on each of

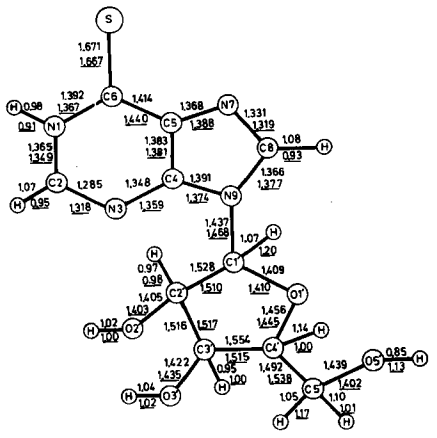

Fig. 1—Schematic drawing of molecule showing bond lengths. The distances for molecule 2 are underlined.

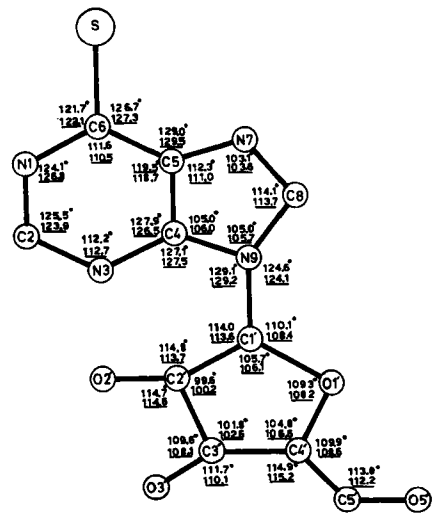

Fig. 2—Bond angles. Those obtained for molecule 2 are underlined.

TABLE III—LEAST-SQUARES PLANES[a]

Atoms Comprising L.S. Plane	Displacement (Å.) Molecule 1	Displacement (Å.) Molecule 2	Other Atoms	Displacement (Å.) Molecule 1	Displacement (Å.) Molecule 2
N1	−0.021	0.014	S	0.109	0.091
C2	0.002	−0.013	C1′	−0.211	0.250
N3	0.019	0.003	H(N1)	0.04	−0.10
C4	−0.006	−0.007	H(C2)	0.11	0.04
C5	−0.003	−0.002	H(C8)	−0.05	−0.04
C6	0.014	−0.002		—	—
N7	0.007	−0.003		—	—
C8	0.000	−0.001		—	—
N9	−0.011	0.010		—	—
C1′	—	—	C2′	0.612	0.632
O1′	—	—	C3′	−0.055	0.032
C4′	—	—	C5′	1.191	1.179

[a] Calculated by the method of Schomaker, V., Waser, J., Marsh, R. E., and Bergman, G., *Acta Cryst.*, **12**, 600(1959).

the N(1) atoms, indicate that at least in the solid state the molecule exists in the thiolactam form rather than the mercapto form. This configuration has also been observed in the crystal structures of 6-mercaptopurine (5) and 2,4-dithiouracil (17). The C—S bond length in each of the two unique nucleoside molecules agrees well with the corresponding distance in the former structure; 1.673 ± 0.003 Å. Based on the compilation of structural data of sulfur compounds by Abrahams (13), the 1.67-Å. length corresponds to approximately 20% single bond character. It thus appears that though the thione configuration, (—NH—C(=S)—), is the predominant valence state, the zwitterionic amidic form, (—+NH = C(—S⁻)—), makes a substantial contribution to the overall resonance.

With the exception of the imidazole portion of the purine residue, the bond lengths and angles are in quite good agreement with those found for 6-mercaptopurine. The disparity observed between the imidazole rings of the two structures is expected as the free base is protonated at N7 rather than at N9.

The least-squares planes calculated through the purine residues (see Table III) show that the atoms comprising the two rings are essentially coplanar. Both C1′ and S are significantly displaced from these least-squares planes. In molecule 1, they are displaced on opposite sides while in molecule 2, they are on the same side of the plane. It is not uncommon in nucleoside structures to find exocyclic atoms significantly out of the base plane. The equations of the least-squares planes are as follows:

$$\text{purine 1}(-0.8208X + 0.1171Y + 0.5591Z = 4.5373 \text{ Å.})$$

$$\text{purine 2}(-0.8044X + 0.0714Y + 0.5898Z = 0.4884 \text{ Å.})$$

X, Y, and Z are the coordinates measured in Å. along a, b, and c, respectively.

The torsion angles (ϕ_{CN}) about the glycosidic bonds (7, 8) in molecules 1 and 2 are +135° and +144°, respectively. The *syn* conformations in the two molecules are stabilized by 05′-H...N3 intramolecular hydrogen bonds. Though the majority of X-ray structural analyses on purine nucleosides show a preference for the *anti* conformation in the solid state, there have been three other nucleosidic compounds reported in the *syn* configuration; formycin, an antibiotic (18), adenosine 3′-5′-cyclic phosphate (19), and deoxyguanosine in the hydrogen bonded complex with 5-bromodeoxycytidine (14).

TABLE IV—CONFORMATIONAL ANGLES

Angle	Molecule 1	Molecule 2	Deoxyquanosine
$\phi C_1' \rightarrow C_2'$	39.3	41.2	30.61
$\phi C_2' \rightarrow C_3'$	−40.6	−36.9	−30.9
$\phi C_3' \rightarrow C_4'$	27.8	23.3	20.2
$\phi C_4' \rightarrow O_1'$	−2.1	1.3	−2.1
$\phi O_1' \rightarrow C_1'$	−24.6	−25.8	−17.6
ϕ_{0c}	55.4	56.7	42.8
ϕ_{00}	62.5	62.7	70.7

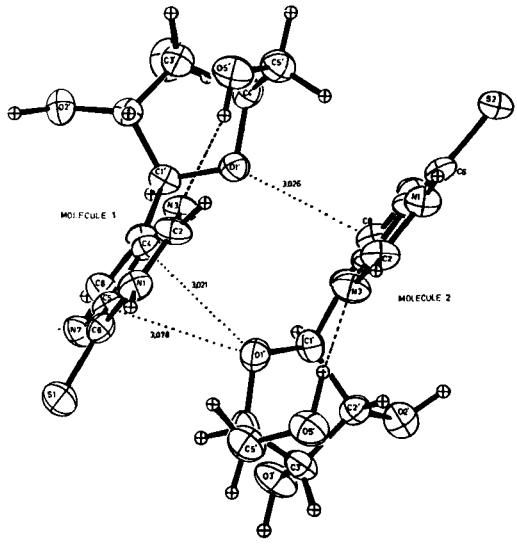

Fig. 3—View of the two unique molecules as seen down the b *axis. The thermal ellipsoids enclose a probability density of 0.50 for the nonhydrogen atoms (15).*

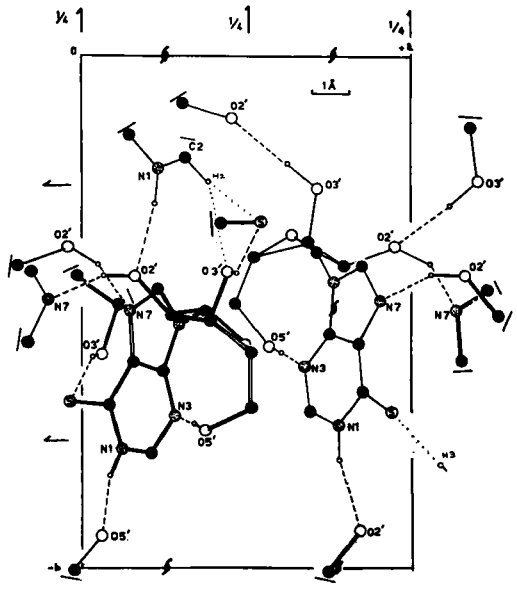

Fig. 4—Hydrogen bonding scheme about the two unique molecules as viewed down the c *axis. Dashed lines represent proposed hydrogen bonding scheme, while dotted lines are short contacts of the C-H variety. Key:* ●, *carbon;* ⊛, *nitrogen;* ○, *oxygen;* —, *molecule 1;* =, *molecule 2.*

The former two have chemical features not typical of the natural nucleosides and -tides and, therefore, a comparison with these will not be offered. The latter compound exhibits a similar intramolecular hydrogen bond. It has been shown (7, 9) using molecular models that purine nucleosides have very little restriction to rotation about the glycosidic bond, in contrast to pyrimidine nucleosides.

Although the glycosidic bond lengths fall within the usual range for nucleosidic compounds, they do appear to be significantly different (at 95% confidence level) from each other. This may be the result of the variation in the rotation angles about the glycosidic bonds and the adjacent furanose bonds. It has been shown that rotation about single bonds involving hetero-atoms having unshared pairs of electrons can influence neighboring bond lengths and angles (10).

The puckering of the furanose rings is such that C2′ is displaced on the same side of the five-member rings as C5′. *Endo* puckering of C2′ was also observed in the *syn* structure of deoxyguanosine (14). Since the usual sugar distortion in nucleotides and -sides involves C2′ and/or C3′, it can be described as a twist about the C2′—C3′ bond relative to the plane of the other three ring atoms (8). In these terms, molecule 1 shows a C2′ (*endo*)—C3′ (*exo*) conformation, while the other has a C2′ (*endo*)—C3′ (*endo*) conformation (*cf.* Table III). The overall configuration of the sugar residues can best be described in terms of torsional angles about each of the ring bonds. These twist angles, as defined by Brown and Levy (11) and Sundaralingam (10) are given in Table IV, for the two unique riboses with those for the furanose moiety in deoxyguanosine. The agreement of these angles among the three sugars is excellent. These angles probably reflect the most stable sugar configuration for the *syn* conformer.

The orientation of the exocyclic C5′-05′ bond with reference to furanose ring is usually described by its projected angle down C4′-C5′ with respect to 01′ and C3′ (12). These angles are referred to as ϕ_{00} and ϕ_{0c}, respectively. The intramolecular 05′-H... N3 interactions constrain the values of these angles to be in the vicinity of 60° (*i.e.*, gauche).

Distortions from tetrahedral symmetry of the ribose carbons are commonly found in the crystal structures of nucleosides and -tides. These deformations are possibly the result of intermolecular associations and the nonbonding interactions within the ribose structure. These reasons may also be re-

TABLE V—SHORT INTERMOLECULAR CONTACTS

Hydrogen Bonds		Pertinent Distances and Angles	
Acceptor	Donor[a]		
1O2′	1O3′-H8 (1)	1O3′...1O2′	2.871 Å.
		H8...1O2′	1.85 Å.
		1O3′-H8...1O2′	168°
1O5′	2N1-H13 (2)	2N1...1O5′	2.722 Å.
		H13...1O5′	1.83 Å.
		2N1-H13...1O5′	168°
1N3	1O5′-H12	1O5′...1N3	2.882 Å.
		H12...1N3	2.08 Å.
		1O5′-H12...1N3	158°
1N7	2O2′-H18 (3)	2O2 ...1N7	2.828 Å.
		H18...1N7	1.89 Å.
		2O2′-H18...1N7	155°
2S	2O3′-H20 (4)	2O3′...2S	3.133 Å.
		H20...2S	2.27 Å.
		2O3′-H20...2S	142°
		2C3′-2O3′-H	103°
2O2′	1N1-H1 (5)	1N1...2O2′	2.902 Å.
		H1...2O2′	2.00 Å.
		1N1-H....2O2′	151°
2N3	2O5′-H24	2O5′...2N3	2.871 Å.
		H24...2N3	1.74 Å.
		2O5′-H24...2N3	175°
2N7	1O2′-H6 (6)	1O2′...2N7	2.793 Å.
		H6...2N7	2.02 Å.
		1O2′-H6...2N7	131°
Other Short Contacts			
		1S...H3 (10)	2.47 Å.
		1O1′...2C8	3.026
		1O3′...H6 (7)	2.60
		2S...H(2) (8)	2.64
		2O5′...1C8 (9)	3.030
		2O5′...H3 (9)	2.56
		2O5′...H4 (9)	2.41
		2O1′...1C4	3.021
		2O1′...1C5	3.078
		2O3′...H(2) (5)	2.53
		2S...H(2)-1C2 (8)	162°
		1S...H3-1C8 (10)	155°

[a] The value in parentheses following the donor atom name denotes its equivalent position in fractional coordinates, as follows: (1) $^1/_2 + x, ^1/_2 - y, -z$, (2) $^1/_2 + x, ^3/_2 - y, -z$, (3) $1 + x, y, z$, (4) $^1/_2 - x, 1 - y, z - ^1/_2$, (5) $1 - x, y - ^1/_2, ^1/_2 - z$, (6) $x - 1, y, z$, (7) $x - ^1/_2, ^1/_2 - y, -z$, (8) $x - ^1/_2, ^3/_2 - y, -z$, (9) $1 - x, ^1/_2 + y, ^1/_2 - z$, (10) $2 - y - ^1/_2, ^1/_2 - z$.

sponsible for the differences in the bond lengths and angles between the two unique sugars. The two ribose moieties have bond lengths and angles which closely resemble those found in other nucleosidic structures.

The two unique molecules in the asymmetric unit (as shown in Fig. 3) appear to be approximately related by a noncrystallographic twofold axis nearly parallel to the *b* axis. The only short contacts between the two molecules shown in Fig. 3 are those involving 1O1′...2C8, 2O1′...1C4 and 2O1′...1C5, which have distances of 3.026 Å., 3.021 Å., and 3.078 Å., respectively. These are slightly less than the sum of the van der Waals radii of the respective atoms (3.1 Å.).

The arrangement of the hydrogen bonds around the two unique nucleosides are shown in Fig. 4. The pertinent distances and angles associated with the various hydrogen bridges are given in Table V. An interesting facet of the proposed intermolecular bonding scheme is the presence of a 2O3′-H...2S hydrogen interaction. The 2O3′ proton is considerably displaced from the plane of the purine nucleus and the C6-S...H angle also deviates considerably from linearity (116°). These distortions may possibly result from the valence state of the sulfur. The O3′-H...S distance of 3.133 Å. is much shorter than the O-H...S length reported in the structure of 6-mercaptopurine hydrate (3.374 Å.). There is also a very short contact between the 1C2 hydrogen (H2) and 2S, which is suggestive of a C-H...S interaction (20). The other sulfur (1S) appears to be only participating in a C-H type interaction and by virtue of its length (H3...1S 2.47 Å.) is a relatively strong hydrogen bond.

There are two N1-H...O hydrogen bonds. The 2N1-H...1O5′ length is 2.722 Å., while the 1N1-H...2O2′ interaction is 2.902 Å. The difference in the strengths of these two hydrogen bonds appears to be attributable to differences about N1 in the two unique residues. The N1-C6 bond length of molecule 2 is 0.025 Å. shorter than the same bond in molecule 1, and the C6-N1-C2 angle 2.7° greater than in molecule 1. Though these differences are only significant at the 95% confidence level, they are consistent with the marked inequality of the hydrogen bond lengths, *i.e.*, the proton on 2N1 is more acidic in character than the one on 1N1.

Each of the O2′ atoms is participating in the hydrogen bonding scheme as both a donor and acceptor, while the O3′ atoms only appear to be acting as donors. The other short intermolecular contacts are listed in Table V. Although some of these H contacts are slightly shorter than normal van der Waals contacts, only two are felt to be of a significant nature (mentioned above).

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Keyphrases

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Heavy atom technique—structure
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