

Modified Components of RNA. The Molecular and Crystal Structure of 5-Carboxymethylaminomethyl-2-thiouridine (s^2cmnm^5U)

Michał W. Wieczorek* and Grzegorz D. Bujacz

Institute of Technical Biochemistry, Technical University of Łódź, Stefanowskiego 4/10, 90-924 Łódź, Poland

Dorota A. Adamiak

Institute of Bioorganic Chemistry, Polish Academy of Sciences, Noskowskiego 12/14, 61-704 Poznań, Poland

Andrzej Małkiewicz and Barbara Nawrot

Institute of Organic Chemistry, Technical University of Łódź, Żwirki 36, 90-924 Łódź, Poland

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ABSTRACT

The structure of the title compound **1** has been determined by X-ray analysis. The following crystal data were found: orthorhombic, $P2_12_12_1$, $a = 5.243(2)$, $b = 24.864(4)$, and $c = 37.083(6)$ Å. Three molecules of the compound with four molecules of water are present in the independent part of the unit cell. The sugar ring puckering is 3E for the molecules A and C and 3T_2 for the molecule B. The conformation of the hydroxymethylene group is g^+ and g^- for B and A, C, respectively. The torsion angles χ for all molecules are in the range of the anti conformation. In the crystal lattice of **1** both the intra- and intermolecular hydrogen bonding systems occur.

INTRODUCTION

5-Carboxymethylaminomethyl-2-thiouridine (**1**) (s^2cmnm^5U) (Figure 1) has been discovered in sev-

eral sequences of tRNAs from *B. subtilis* [1], and it is a by-product of the biosynthesis pathway of 5-methylaminomethyl-2-thiouridine (s^2mnm^5U) in *E. coli* strains [2]. Both modified nucleosides are located in the first position of tRNAs anticodon (U_{34}^* , "wobble position"), and both distinctively influence decoding capacity of the biopolymer [3–5]. The function of U_{34}^* as an identity element, by which tRNAs recognize their cognate aminoacyl tRNA synthetase (RS), has been recently experimentally confirmed [6,7]. Moreover, the status of the post-transcriptional modification of U_{34} in tRNA $_{(mnm^5s^2U)}^{Glu}$ from *E. coli* and tRNA $_{(U_{34}^*)}^{Glu}$ from *B. subtilis* seems to be essential also for the mentioned tRNAs recognition/binding with glutamyl tRNA reductase (GluRT), the key step of chlorophyll bio-synthesis via the lately discovered C_5 pathway [8].

To correlate structural features of U_{34}^* with its biological function, the conformation and III-D structure dynamics of variously 5-, 2-substituted uridines [9–12], as well as oligoribonucleosides with these units as components [12–14], have been determined by NMR and CD spectroscopy. Recently, striking progress in the cocrystallization of tRNAs with aminoacyl tRNA synthetases has been

*To whom correspondence should be addressed.

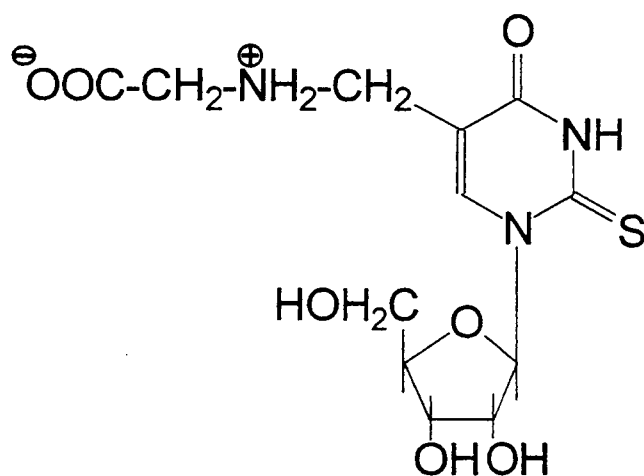


FIGURE 1 5-carboxymethylaminomethyl-2-thiouridine (1).

TABLE 1 Crystal Data and Experimental Details

Molecular formula	$3C_{12}H_{17}N_3O_7S \cdot 4H_2O$
Formula weight	347.34
Crystallization solvent	methanol-isopropanol-water
Space group	$P2_12_12_1$
a (Å)	5.243(2)
b (Å)	24.864(4)
c (Å)	37.083(5)
Z	4
V (Å ³)	4834(2)
μ (cm ⁻¹)	22.1
D_c (g/cm ³)	1.531
Crystal dimensions (mm)	0.04, 0.05, 0.3
Maximum 2θ (°)	130
Radiation, λ (Å)	Cu K_{α} , 1.54178
Scan mode	$\omega/2\theta$
Scan width (°)	$0.70 + 0.14 \tan \theta$
hkl ranges:	$h = 0\ 6$ $k = 0\ 29$ $l = 0\ 43$
No. of reflections measured:	
total	4789
independent	3762
$I \geq 2\sigma(I)$	2829

achieved, and the molecular structures of several such complexes (tRNA-RS) were successfully refined [15].

In this context, comparison of the conformation in the solid state and in the solution of a representative series of wobble uridines should be valuable [21]. In connection with our previous work on the X-ray structure of $cmnm^5U$ [16], we present here the molecular and crystal structure of its 2-thioanalogue 1.

RESULTS AND DISCUSSION

The studied nucleoside crystallizes as a zwitterion. Neither of the oxygen atoms of the carboxyl func-

tion is protonated, and the similar lengths of bonds within the carboxyl function indicate delocalization of a negative charge between both oxygen atoms. The nitrogen atom is bound to four atoms and has a positive charge. It is noteworthy that the "decarboxylated" analog of 1, 5-methylaminomethyl-2-thiouridine (s^2mnm^5U) [18b], and also 5-aminomethyluridine (nm^5U) [19] crystallize as betaines, which are formed by proton transfer from the N_3H imine to the amine function.

Nonhydrogen atom coordinates and equivalent temperature parameters are presented in Table 2. Table 3 includes coordinates of hydrogen atoms. A general view of the refined independent part of the unit cell of compound 1, with its atom numbering scheme, is shown in Figure 2. The three molecules of 1 with solvent are also presented separately to show intra- and intermolecular hydrogen bonding (Figure 3a–c).

The nucleoside crystallizes in the space group $P2_12_12_1$ with three molecules of the compound and four molecules of water in the asymmetric part of the unit cell. In this context, 1 exhibits a more complex crystal structure than its 2-oxo-analog, which crystallized in space group $P2_1$, with one water molecule in the asymmetric part of the unit cell [16].

The thermal vibrations of the oxygen atoms O1w and O2w are evidently weaker in comparison with analogous data for O3w and O4w, reflecting stronger binding of the first two water molecules with their nucleoside counterparts.

The complex H-bonding system distinctively influences the crystal structure of nucleoside 1. Table 4 lists selected hydrogen contacts. All hydrogen contacts not greater than 3.00 Å are given in the supplementary material.

Tables 5–7 contain bond lengths, bond angles, and selected torsion angles, respectively. The torsion angles χ_{CN} ($O1'-C1'-N1-C2$) are $-160(1)$, $-159(1)$, and $-163(1)^\circ$ for the molecules A, B, and C, respectively and fall in the range of the *anti* conformation. Generally, these values are only slightly different from the respective data obtained for the 2-oxo-analog of 1 [16] and speak for relative freedom of the conformation around the *N*-glycosidic bond [16].

The sugar ring puckering is 3E for the molecules A and C (for C, this is slightly deformed toward 3T_2) and 3T_2 for the molecule B. In terms of pseudorotation [25], the ribofuranose ring conformation is characterized by the parameters $P = 19(1)$, $10(1)$, $15(1)^\circ$ and $\tau_m = 42(1)$, $37(1)$, $42(1)$ [26] for molecules A, B, and C, respectively. Figures 3a–c present separately the molecules of the asymmetric unit to show the view of the ribofuranose rings with the hydrogen bonding scheme of the respective molecules A, B, and C.

5-Methylaminomethyl-2-thiouridine [18b], as well as methoxy-2-thiouridine [20] and 2-thiouri-

TABLE 2 Atomic Coordinates ($\times 10^4$) and Equivalent Isotropic Displacement Coefficients ($\text{\AA}^2 \times 10^3$)

	<i>x</i>	<i>y</i>	<i>z</i>	<i>U(eq)</i>		<i>x</i>	<i>y</i>	<i>z</i>	<i>U(eq)</i>
S2A	4841(9)	784(1)	892(1)	58(1)	S2B	2471(9)	-2267(1)	1450(1)	69(1)
O1'A	763(15)	-435(3)	286(2)	34(2)	O1'B	-1277(15)	-3783(3)	1681(2)	41(2)
O2'A	2047(19)	648(3)	-69(2)	49(2)	O2'B	181(19)	-3614(3)	898(2)	52(2)
O3'A	3986(16)	-97(3)	-552(2)	40(2)	O3'B	2418(17)	-4597(3)	1060(2)	48(2)
O5'A	-1686(15)	-1271(3)	-103(2)	36(2)	O5'B	584(23)	-4680(4)	2056(2)	78(3)
O4A	9631(26)	-776(4)	1339(3)	108(4)	O4B	7934(19)	-2788(4)	2458(2)	66(3)
O14A	12148(17)	-2820(3)	484(2)	46(2)	O14B	11014(19)	-4578(4)	3263(2)	69(3)
O15A	12131(17)	-1932(3)	432(2)	49(2)	O15B	10907(17)	-3768(4)	3021(3)	60(3)
N1A	4259(17)	-228(3)	669(2)	27(2)	N1B	2164(19)	-3203(3)	1808(2)	34(2)
N3A	7234(21)	-99(4)	1121(2)	45(2)	N3B	5174(23)	-2594(4)	2008(2)	49(3)
N11A	7093(19)	-1829(3)	544(2)	37(2)	N11B	5819(17)	-3781(4)	2917(2)	29(2)
C1'A	2316(22)	-11(4)	403(2)	26(2)	C1'B	292(26)	-3387(4)	1529(3)	42(3)
C2'A	3610(24)	239(4)	71(2)	34(3)	C2'B	1712(24)	-3637(4)	1209(2)	34(3)
C3'A	3538(23)	-232(4)	-180(3)	30(2)	C3'B	1790(22)	-4233(4)	1324(3)	36(3)
C4'A	966(21)	-480(4)	-108(3)	26(2)	C4'B	-765(25)	-4300(4)	1504(3)	41(3)
C5'A	750(25)	-1060(4)	-216(3)	38(3)	C5'B	-1158(30)	-4754(5)	1767(3)	60(4)
C2A	5389(23)	134(4)	897(3)	36(3)	C2B	3275(27)	-2711(5)	1763(3)	49(3)
C4A	7977(31)	-623(5)	1131(3)	55(4)	C4B	6224(28)	-2927(5)	2267(3)	45(3)
C5A	6712(22)	-970(4)	888(3)	31(2)	C5B	4942(24)	-3450(4)	2293(3)	37(3)
C6A	4893(22)	-767(4)	675(3)	29(2)	C6B	3019(24)	-3562(4)	2067(2)	33(3)
C10A	7522(28)	-1551(4)	894(3)	44(3)	C10B	6091(23)	-3884(5)	2525(3)	43(3)
C12A	8170(23)	-2374(4)	539(4)	44(3)	C12B	7024(25)	-4221(5)	3135(3)	42(3)
C13A	11083(25)	-2380(4)	472(3)	37(3)	C13B	9952(25)	-4185(5)	3136(3)	42(3)
S2C	12912(9)	-1693(1)	2705(1)	65(1)	O1w	7934(27)	-1613(4)	2035(3)	109(4)
O1'C	17242(15)	-1686(3)	3714(2)	33(2)	O2w	4620(50)	-5421(6)	2420(3)	244(10)
O2'C	16200(17)	-626(3)	3320(2)	51(2)	O3w	787(61)	-5419(8)	2785(7)	350(16)
O3'C	14250(16)	-445(3)	4014(2)	41(2)	O4w	13253(50)	-865(8)	1876(6)	293(11)
O5'C	19734(16)	-1686(3)	4396(2)	40(2)					
O4C	7487(17)	-2948(3)	3363(2)	51(2)					
O14C	5888(17)	-3368(3)	4902(2)	42(2)					
O15C	5949(14)	-2735(3)	4483(2)	42(2)					
N1C	13615(18)	-1995(3)	3396(2)	31(2)					
N3C	10337(19)	-2403(4)	3083(2)	40(2)					
N11C	10903(18)	-2804(3)	4347(2)	33(2)					
C1'C	15605(22)	-1578(4)	3409(3)	33(2)					
C2'C	14547(26)	-1018(4)	3469(3)	38(3)					
C3'C	14549(21)	-975(4)	3880(3)	28(2)					
C4'C	17118(21)	-1235(4)	3969(3)	28(2)					
C5'C	17282(24)	-1447(4)	4346(3)	35(3)					
C2C	12298(23)	-2049(4)	3075(3)	31(3)					
C4C	9520(22)	-2701(5)	3373(3)	38(3)					
C5C	11157(21)	-2688(4)	3687(2)	24(2)					
C6C	13123(22)	-2332(4)	3681(3)	31(2)					
C10C	10511(25)	-3058(4)	3986(3)	40(3)					
C12C	9811(23)	-3136(5)	4647(3)	46(3)					
C13C	6973(23)	-3075(4)	4679(3)	30(2)					

Equivalent isotropic *U* is defined as one-third of the trace of the orthogonalized U_{ij} tensor.

TABLE 3 Hydrogen Atom Coordinates ($\times 10^3$)

	x	y	z		x	y	z
H2oA	304(4)	98(1)	0(1)	HO1C	1150(5)	-337(1)	397(1)
H3oA	263(4)	2(1)	-66(1)	HO2C	858(5)	-318(1)	396(1)
H5oA	-190(3)	-164(1)	-18(1)	H21C	1039(5)	-354(2)	464(1)
H3nA	810(4)	15(1)	129(1)	H22C	1061(5)	-293(2)	487(1)
H11A	520(4)	-183(1)	47(1)	H2oB	-167(4)	-379(1)	92(1)
H12A	813(4)	-164(1)	36(1)	H3oB	96(3)	-464(1)	90(1)
H1'A	125(4)	26(1)	52(1)	H5oB	122(4)	-495(1)	220(1)
H2'A	540(5)	37(1)	12(1)	H3nB	571(4)	-225(1)	199(1)
H3'A	480(5)	-48(1)	-11(1)	H11B	404(3)	-376(1)	298(1)
H4'A	-47(4)	-23(1)	-18(1)	H12B	661(3)	-345(1)	298(1)
H5'A	192(5)	-122(1)	-7(1)	H1'B	-52(5)	-305(1)	145(1)
H5'A	110(5)	-117(1)	-47(1)	H2'B	341(5)	-348(1)	116(1)
H6A	372(4)	-98(1)	49(1)	H3'B	322(4)	-426(1)	152(1)
HO1A	646(6)	-176(1)	110(1)	H4'B	-217(5)	-435(1)	129(1)
HO2A	934(6)	-157(1)	95(1)	H5'B	-283(6)	-478(1)	186(1)
H21A	755(5)	-258(1)	77(1)	H5'B	-53(6)	-511(2)	166(1)
H22A	737(5)	-257(1)	32(1)	H6B	201(5)	-392(1)	208(1)
H2oC	1628(3)	-24(1)	337(1)	HO1B	520(5)	-425(1)	246(1)
H3oC	1481(3)	-22(1)	389(1)	HO2B	793(5)	-392(2)	246(1)
H5oC	2037(3)	-184(1)	461(1)	H21B	590(5)	-420(1)	339(1)
H3nC	946(4)	-243(1)	284(1)	H22B	654(5)	-459(1)	301(1)
H11C	1276(4)	-269(1)	438(1)	H11w	879(5)	-147(1)	181(1)
H12C	974(4)	-250(1)	434(1)	H12w	666(5)	-146(1)	212(1)
H1'C	1662(4)	-158(1)	318(1)	H21w	588(10)	-523(2)	234(1)
H2'C	1268(5)	-103(1)	338(1)	H22w	437(10)	-532(1)	265(1)
H3'C	1319(4)	-120(1)	398(1)	H31w	-82(12)	-542(2)	272(2)
H4'C	1865(4)	-94(1)	393(1)	H32w	110(12)	-512(2)	288(2)
H5'C	1614(5)	-177(1)	434(1)	H41w	1448(10)	-61(2)	174(1)
H5'C	1632(5)	-121(1)	452(1)	H42w	1431(10)	-118(2)	197(1)
H6C	1476(4)	-237(1)	385(1)				

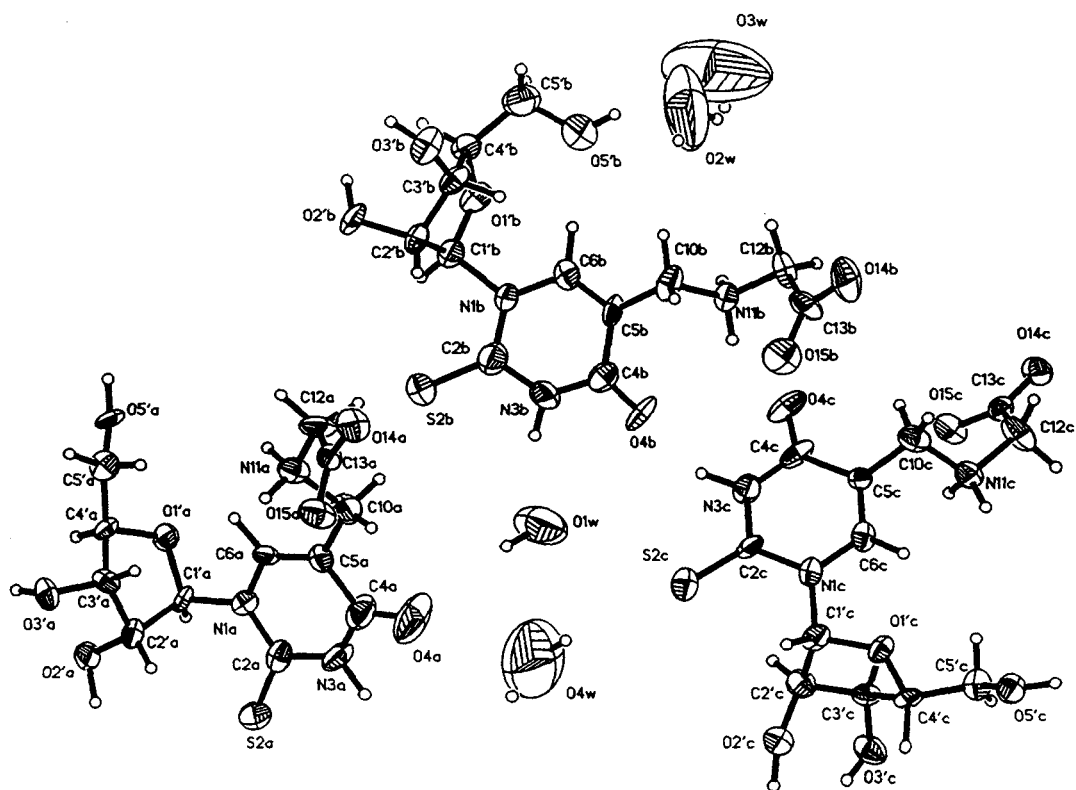


FIGURE 2 Thermal ellipsoidal view and atom numbering scheme of the asymmetric part of the unit cell of 1.

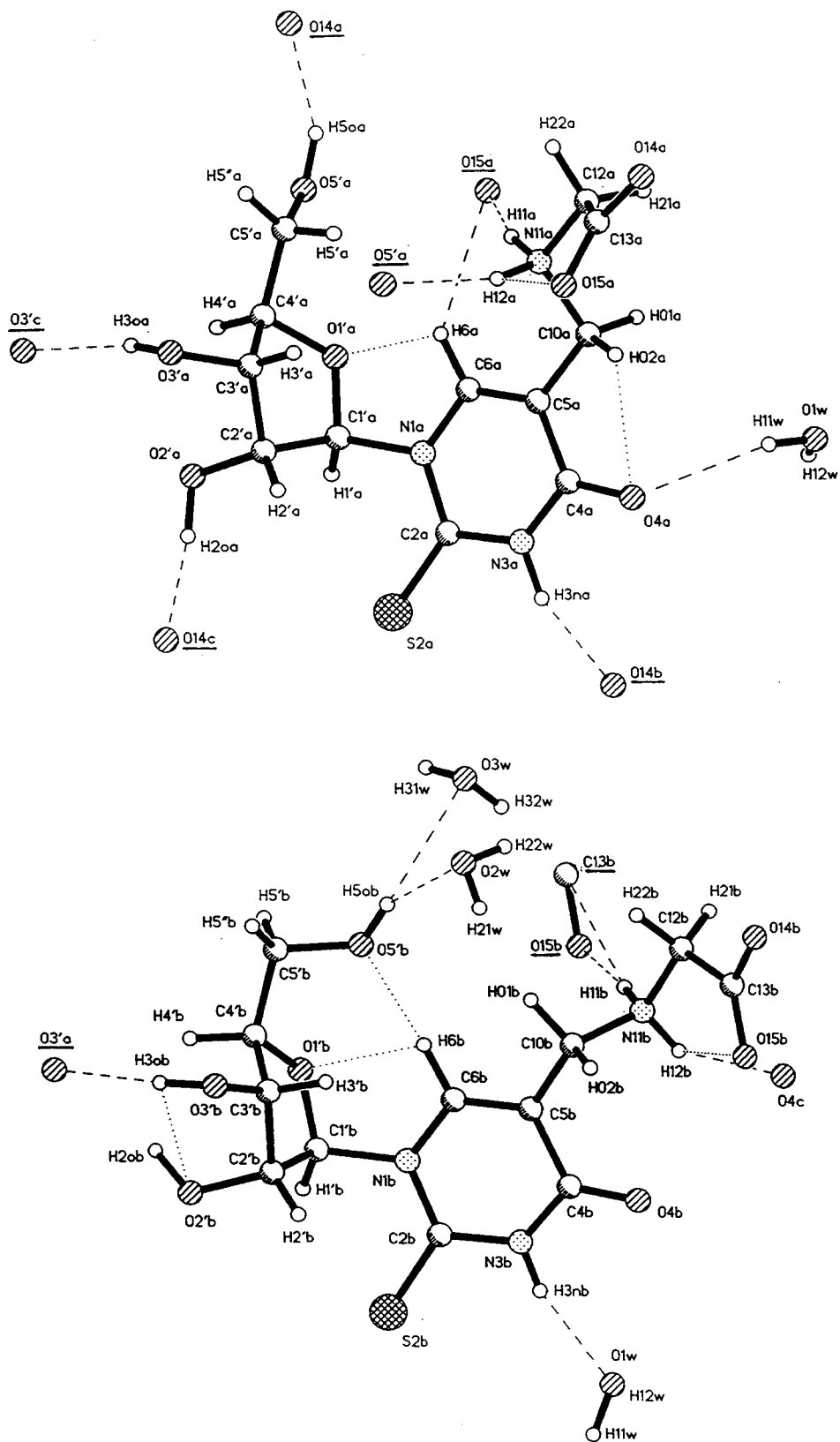


FIGURE 3 The individual hydrogen bonding schemes of each molecule of the asymmetric unit of **1** with atom numbering; the intramolecular bonds are marked by dotted lines, and the intermolecular ones are denoted by dashed lines. Atoms with underlined names are from symmetrical molecules (Table 4).

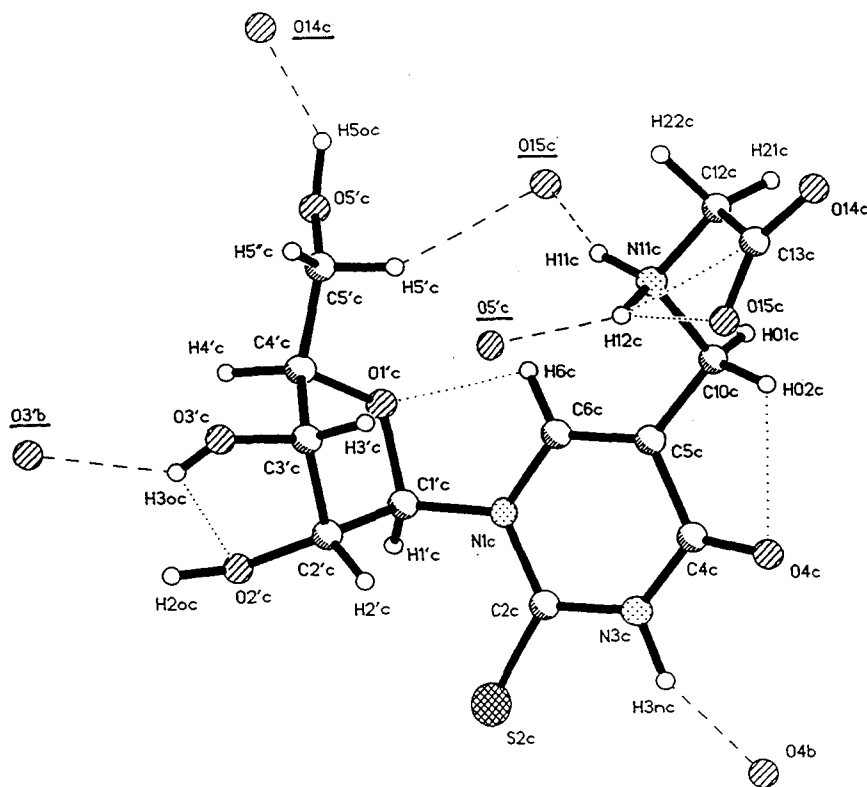


FIGURE 3 Continued

dine-oxycetic acid methyl ester [20], the 2-thioanalog of two wobble position uridines bearing 5-substituents coplanar with the heterobase ring, exhibit also the 3E conformation in the solid state.

One should also notice that all 2-thiouridines hitherto studied exist in solution predominantly as 3E conformers [5,10–12]. The accumulated results strongly suggest that the 2-thio substituent shifts the conformation of uridines toward the biologically important 3E conformation [5,10–12], either in solution or in the solid state. The torsion angles $O5'-C5'-C4'-O4'$ are 60(1), 61(1), and 65(1) $^\circ$, and those of $O5'-C5'-C4'-C3'$ (γ) are 174(1), 61(1), and 179(1) $^\circ$ for molecules *A*, *B*, and *C*, respectively. Thus, the hydroxymethylene group prefers the g^+ conformation in molecule *B*, but g^- for *A* and *C* [21]. The torsion angle $N11-C10-C5-C6$, which describes the spatial relation between the 5-substituent and the heterobase ring, is 27(2) and 38(2) $^\circ$ for molecules *A* and *C*, respectively. The analogous angle for the *B* molecule is equal to $-118(1)^\circ$ and corresponds to that determined for the 2-oxoanalog of **1** [16]. The bond lengths (Table 5) do not differ from those registered for other wobble 2-thiouridines studied so far [18–20].

Three almost flat fragments are present in the molecule of nucleoside **1** (Table 8). The first is formed by the atoms of the heterobase ring (plane

1), the second is formed by four atoms of the sugar moiety (plane 2), and the third is the carboxyl group of the amino acid residue (plane 3). The spatial structure of the nucleoside **1** can be represented by means of the angles between these planes. Least-squares planes, standard deviations of atoms, and dihedral angles between planes are listed in Table 8. Dihedral angles between planes 1 and 2 are 69.6(4) and 70.0(4) $^\circ$, respectively, for molecules *A* and *C*. The analogous angle for molecule *B* is distinctively higher (81.2(4) $^\circ$) and indicates an almost perpendicular arrangement of the mentioned fragments.

The "skew" conformation of the 5-substituent is characterized also by three different values of the torsion angle between planes 1 and 3, which are 55.2(5), 39.3(4), and 48.9(4) $^\circ$ for conformers *A*, *B*, and *C*, respectively.

In conclusion, the presence of the three conformers (*A*, *B*, and *C*) in the independent part reflects relative flexibility of the nucleoside **1** structure, although the sugar moiety seems to be more rigid than its other fragments.

The role of post-transcriptional modification of U_{34} can be discussed in terms of an influence of its 2- and 5-substituents on the geometry and dynamics of the tRNA anticodon arm [13], either via interaction of skew 5-substituents with the sugar-

TABLE 4 Selected Hydrogen Contacts

X	H	Y	X-H(Å)	H...Y(Å)	X...Y(Å)	(X-H...Y)(°)	Symmetry
O2'A	H2oA	O14C	1.02(3)	1.74(2)	2.75(1)	168(2)	1-X, 0.5+Y, 0.5-Z
O3'A	H3oA	O3'C	0.87(3)	1.88(2)	2.70(1)	156(2)	1.5-X, -Y, Z-0.5
O5'A	H5oA	O14A	0.95(3)	1.84(2)	2.74(1)	155(2)	X-1.5, -0.5-Y, -Z
N3A	H3nA	O14B	0.98(4)	1.86(2)	2.78(1)	156(2)	2-X, 0.5+Y, 0.5-Z
N11A	H11A	O15A	1.03(4)	1.63(3)	2.65(1)	167(2)	X-1, Y, Z
N11A	H12A	O5'A	1.00(3)	1.94(2)	2.84(1)	149(2)	1+X, Y, Z
N11A	H12A	O15A	1.00(3)	2.24(3)	2.69(1)	105(2)	
C6A	H6A	O1'A	1.06(5)	2.19(3)	2.73(1)	109(2)	
C6A	H6A	O15A	1.06(5)	2.52(3)	3.36(1)	136(2)	X-1, Y, Z
C10A	HO2A	O4A	0.98(6)	2.45(4)	2.77(2)	98(2)	
O3'B	H3oB	O3'A	0.97(3)	1.78(2)	2.71(1)	160(2)	X-0.5, -0.5-Y, -Z
O3'B	H3oB	O2'B	0.97(3)	2.59(2)	2.78(1)	91(2)	
O5'B	H5oB	O2w	0.92(3)	2.28(6)	3.11(2)	149(2)	
O5'B	H5oB	O3w	0.92(3)	2.46(6)	3.27(3)	146(3)	
N3B	H3nB	O1w	0.91(4)	1.97(6)	2.84(2)	159(3)	
N11B	H11B	O15B	0.96(3)	1.65(3)	2.60(1)	171(2)	X-1, Y, Z
N11B	H11B	C13B	0.96(3)	2.47(5)	3.34(2)	151(2)	X-1, Y, Z
N11B	H12B	O15B	0.94(4)	2.39(3)	2.70(1)	98(2)	
N11B	H12B	O4C	0.94(4)	1.97(2)	2.79(1)	146(2)	
C6B	H6B	O1'B	1.05(4)	2.31(3)	2.72(1)	102(2)	
C6B	H6B	O5'B	1.05(4)	2.03(4)	3.06(2)	169(3)	
O3'C	H3oC	O3'B	0.78(3)	2.12(2)	2.75(1)	137(2)	2-X, 0.5+Y, 0.5-Z
O3'C	H3oC	O2'C	0.78(3)	2.47(2)	2.81(1)	108(2)	
O5'C	H5oC	O14C	0.94(3)	1.91(2)	2.68(1)	137(2)	1.5+X, -0.5-Y, 1-Z
N3C	H3nC	O4B	1.02(3)	1.86(3)	2.81(1)	154(2)	
N11C	H11C	O15C	1.02(3)	1.72(3)	2.70(1)	160(2)	1+X, Y, Z
N11C	H12C	O5'C	0.98(3)	2.02(2)	2.85(1)	141(2)	X-1, Y, Z
N11C	H12C	O15C	0.98(3)	2.14(2)	2.65(1)	111(2)	
C5'C	H5'C	O15C	1.00(5)	2.46(2)	3.32(1)	143(2)	1+X, Y, Z
C6C	H6C	O1'C	1.06(5)	2.20(3)	2.69(1)	106(2)	
O1w	H11w	O4A	1.00(4)	2.51(5)	3.43(2)	154(3)	
O1w	H12w	O4w	0.83(5)	2.48(6)	3.14(3)	137(3)	X-1, Y, Z
O2w	H22w	O3w	0.88(5)	1.96(7)	2.42(4)	111(4)	
O2w	H22w	O4w	0.88(5)	2.55(6)	3.05(3)	116(4)	2-X, Y-0.5, 0.5-Z
O3w	H31w	O4w	0.88(9)	2.26(9)	2.70(4)	111(4)	1-X, Y-0.5, 0.5-Z
O3w	H32w	O14B	0.86(8)	1.94(7)	2.74(2)	156(4)	X-1, Y, Z
O4w	H42w	O1w	1.02(8)	2.20(7)	3.14(3)	152(3)	1+X, Y, Z

TABLE 5 Bond Lengths (Å)

		Molecules			Molecules				
		A	B	C			A	B	C
S2	C2	1.64(1)	1.66(1)	1.66(1)	N3	C2	1.40(2)	1.38(2)	1.35(2)
O1'	C1'	1.40(1)	1.40(1)	1.45(1)	N3	C4	1.36(2)	1.38(2)	1.37(1)
O1'	C4'	1.47(1)	1.47(1)	1.47(1)	N11	C10	1.49(1)	1.48(1)	1.49(1)
O2'	C2'	1.41(1)	1.41(1)	1.42(1)	N11	C12	1.47(1)	1.50(2)	1.50(1)
O3'	C3'	1.44(1)	1.37(1)	1.42(1)	C1'	C2'	1.54(1)	1.53(2)	1.52(2)
O5'	C5'	1.44(2)	1.42(2)	1.43(2)	C2'	C3'	1.50(1)	1.54(1)	1.53(2)
O4	C4	1.22(2)	1.19(2)	1.23(2)	C3'	C4'	1.51(2)	1.51(2)	1.53(2)
O14	C13	1.23(1)	1.22(2)	1.24(1)	C4'	C5'	1.50(1)	1.51(2)	1.50(2)
O15	C13	1.25(1)	1.23(2)	1.24(1)	C4	C5	1.41(2)	1.47(2)	1.45(1)
N1	C1'	1.52(1)	1.50(2)	1.47(1)	C5	C6	1.34(2)	1.34(2)	1.36(2)
N1	C2	1.37(1)	1.36(2)	1.38(1)	C5	C10	1.51(1)	1.51(2)	1.48(1)
N1	C6	1.38(1)	1.39(1)	1.37(1)	C12	C13	1.55(2)	1.54(2)	1.50(2)

TABLE 6 Bond Angles (°)

			Molecules		
			A	B	C
C1'	O1'	C4'	108.9(8)	109.2(8)	109.6(8)
C1'	N1	C2	117.3(8)	118.0(9)	116.8(8)
C1'	N1	C6	121.1(8)	119.6(8)	122.5(8)
C2	N1	C6	121.6(9)	121.6(9)	120.6(9)
C2	N3	C4	127.6(10)	128.2(11)	127.2(10)
C10	N11	C12	112.4(9)	111.2(9)	112.3(8)
O1'	C1'	N1	108.9(8)	108.8(9)	108.4(8)
O1'	C1'	C2'	108.2(8)	108.2(9)	105.9(9)
N1	C1'	C2'	111.6(8)	109.9(9)	113.1(9)
O2'	C2'	C1'	109.3(8)	110.0(9)	110.6(9)
O2'	C2'	C3'	108.8(9)	106.3(8)	109.9(9)
C1'	C2'	C3'	99.8(8)	100.9(8)	102.2(9)
O3'	C3'	C2'	114.2(9)	116.3(9)	114.5(9)
O3'	C3'	C4'	114.3(9)	117.2(9)	114.5(9)
C2'	C3'	C4'	103.5(9)	101.8(9)	100.7(9)
O1'	C4'	C3'	102.1(8)	105.3(9)	102.9(8)
O1'	C4'	C5'	109.5(9)	110.0(9)	109.3(9)
C3'	C4'	C5'	114.4(9)	119.5(10)	113.6(9)
O5'	C5'	C4'	109.8(9)	107.7(10)	108.6(9)
S2	C2	N1	124.4(8)	125.1(9)	124.2(8)
S2	C2	N3	122.3(8)	120.3(9)	120.7(8)
N1	C2	N3	113.2(9)	114.6(10)	115.1(9)
O4	C4	N3	121.3(12)	122.5(12)	121.0(10)
O4	C4	C5	123.1(13)	124.2(12)	123.3(10)
N3	C4	C5	115.7(11)	113.2(11)	115.6(10)
C4	C5	C6	118.8(11)	119.2(10)	116.8(9)
C4	C5	C10	116.4(10)	119.3(10)	117.0(9)
C6	C5	C10	124.9(10)	120.6(10)	126.2(9)
N1	C6	C5	123.2(10)	122.9(10)	123.5(10)
N11	C10	C5	113.0(9)	113.4(9)	112.1(9)
N11	C12	C13	113.0(10)	112.3(10)	112.5(9)
O14	C13	O15	126.7(11)	128.7(12)	126.4(10)
O14	C13	C12	116.8(10)	114.2(11)	116.6(10)
O15	C13	C12	116.4(10)	117.1(11)	116.9(10)

phosphate backbone [18] or the contribution of the 2-thio group to the restriction of the local conformation (²E) [5,10–12] and enhancement of the stacking forces [10–12].

In this context, the presented results of the studies on the conformation and crystal structure of nucleoside **1** do not contradict these statements.

EXPERIMENTAL

5-Carboxymethylaminomethyl-2-thiouridine **1** was synthesized according to the previously reported procedure [17]. The crystallization of sample **1** was achieved by a slow evaporation of the more volatile solvent from an isopropanol-methanol and water mixture (pH 5). Although this procedure was found as optimal, the nucleoside crystallized in the form of thin needles, and it somewhat conditioned the process of the data collection and methodology of the structure refinement.

The crystal data and experimental details are

TABLE 7 Torsional Angles Including Hydrogen Atoms of Hydroxyl Groups (°)

				Molecules		
				A	B	C
S2	C2	N1	C1'	-2(1)	8(2)	3(1)
S2	C2	N1	C6	177(1)	177(1)	-175(1)
S2	C2	N3	C4	-175(1)	-174(1)	-176(1)
O1'	C1'	N1	C2	-160(1)	-159(1)	-163(1)
O1'	C1'	N1	C6	22(1)	32(1)	15(1)
O1'	C1'	C2'	O2'	89(1)	85(1)	88(1)
O1'	C1'	C2'	C3'	-25(1)	-27(1)	-29(1)
O1'	C4'	C3'	O3'	-165(1)	-163(1)	-163(1)
O1'	C4'	C3'	C2'	-40(1)	-35(1)	-40(1)
O1'	C4'	C5'	O5'	60(1)	-61(1)	65(1)
O2'	C2'	C1'	N1	-151(1)	-157(1)	-153(1)
O2'	C2'	C3'	O3'	50(1)	51(1)	48(1)
O2'	C2'	C3'	C4'	-75(1)	-78(1)	-76(1)
O3'	C3'	C2'	C1'	164(1)	165(1)	165(1)
O3'	C3'	C4'	C5'	77(1)	73(1)	79(1)
O5'	C5'	C4'	C3'	174(1)	61(1)	179(1)
O4	C4	N3	C2	180(1)	177(1)	169(1)
O4	C4	C5	C6	179(1)	179(1)	-170(1)
O4	C4	C5	C10	0(2)	-12(2)	10(2)
O14	C13	C12	N11	176(1)	-169(1)	174(1)
O15	C13	C12	N11	0(2)	12(2)	-6(1)
N1	C1'	O1'	C4'	-121(1)	-113(1)	-118(1)
N1	C1'	C2'	C3'	95(1)	91(1)	90(1)
N1	C2	N3	C4	0(2)	6(2)	1(2)
N1	C6	C5	C4	3(2)	0(2)	0(2)
N1	C6	C5	C10	-178(1)	-170(1)	-179(1)
N3	C2	N1	C1'	-177(1)	-173(1)	-174(1)
N3	C2	N1	C6	1(1)	-4(2)	8(1)
N3	C4	C5	C6	-1(2)	2(2)	8(2)
N3	C4	C5	C10	180(1)	172(1)	-172(1)
N11	C10	C5	C4	-153(1)	73(1)	-141(1)
N11	C10	C5	C6	27(2)	-118(1)	38(2)
C1'	O1'	C4'	C3'	25(1)	18(1)	23(1)
C1'	O1'	C4'	C5'	146(1)	148(1)	144(1)
C1'	N1	C6	C5	176(1)	170(1)	174(1)
C1'	C2'	C3'	C4'	39(1)	37(1)	42(1)
C2'	C1'	O1'	C4'	0(1)	6(1)	4(1)
C2'	C1'	N1	C2	81(1)	83(1)	80(1)
C2'	C1'	N1	C6	-98(1)	-86(1)	-102(1)
C2'	C3'	C4'	C5'	-158(1)	-159(1)	-158(1)
C2	N1	C6	C5	-3(2)	1(2)	-8(2)
C2	N3	C4	C5	-1(2)	-6(2)	-9(2)
C5	C10	N11	C12	173(1)	-179(1)	170(1)
C10	N11	C12	C13	-80(1)	75(1)	-79(1)
H2o	O2'	C2'	C1'	108(2)	-55(2)	-162(2)
H2o	O2'	C2'	H2'	-18(2)	177(2)	75(3)
H2o	O2'	C2'	C3'	-144(2)	53(2)	-50(3)
H3o	O3'	C3'	C2'	-81(2)	-75(2)	-31(3)
H3o	O3'	C3'	H3'	158(2)	168(2)	-154(2)
H3o	O3'	C3'	C4'	38(2)	46(2)	85(2)
H5o	O5'	C5'	C4'	178(2)	-155(2)	178(2)
H5o	O5'	C5'	H5'	-73(3)	81(3)	-74(3)
H5o	O5'	C5'	H5''	44(3)	-38(3)	41(3)

TABLE 8 Least-Squares Planes^a

Plane	Atom	Deviation (Esd) (Å)			
		Molecule A	Molecule B	Molecule C	
1	N1	0.007(8)	-0.004(8)	-0.042(8)	
	C2	-0.001(11)	0.029(12)	0.038(10)	
	N3	-0.005(9)	-0.022(10)	0.025(9)	
	C4	0.005(13)	0.019(12)	-0.077(11)	
	C5	0.010(11)	0.003(11)	0.027(10)	
	C6	-0.018(11)	-0.005(10)	0.035(10)	
	M1=	0.6985(30)	0.6557(33)	0.6126(34)	
	M2=	0.1810(47)	-0.3747(43)	-0.7125(29)	
	M3=	-0.6923(30)	-0.6555(33)	-0.3422(38)	
	D=	-0.2676(193)	-0.6636(486)	3.6390(593)	
2	C1'	-0.001(10)	-0.046(12)	-0.023(11)	
	C2'	0.001(11)	0.020(10)	0.018(12)	
	C4'	0.000(10)	-0.027(12)	-0.014(10)	
	O1'	0.000(7)	0.018(7)	0.011(7)	
	M1=	-0.7667(37)	-0.7497(36)	0.7822(36)	
	M2=	0.6336(43)	0.2004(76)	0.4149(58)	
	M3=	-0.1037(69)	-0.6308(48)	-0.4648(53)	
	D=	-1.1024(62)	-5.3321(645)	-0.0815(963)	
	3	C12	-0.011(14)	-0.003(11)	-0.001(11)
		C13	0.023(11)	0.011(11)	0.003(10)
O14		-0.004(7)	-0.002(7)	-0.001(7)	
O15		-0.004(7)	-0.004(10)	-0.001(7)	
M1=		-0.1393(74)	0.0350(65)	-0.1303(61)	
M2=		-0.0867(48)	-0.4067(53)	-0.6952(36)	
M3=		-0.9865(11)	-0.9129(23)	-0.7069(35)	
D=		-2.0461(536)	-6.2126(866)	-7.4300(886)	
Dihedral angles between planes (°)					
Plane 1/Plane 2		69.6(4)	81.2(4)	70.0(4)	
Plane 2/Plane 3	55.2(5)	39.3(4)	48.9(4)		
Plane 1/Plane 3	81.1(6)	62.1(5)	86.5(4)		

^aEquation of the plane: $M_1x + M_2y + M_3z - D = 0$.

shown in Table 1. The intensity data were collected using a CAD4 diffractometer with graphite monochromatized Cu K_α radiation. The lattice constants were refined by a least-squares fit of 25 reflections in the θ range 9.9–20.1°. A small decline in intensities of three standard reflections (1, -2, -4; 1, 1, -4; 1, 3, 2) was observed: 4.5% during 113.3 hours of exposure time. For that reason, the data file was corrected by use of the DECAY program [27].

The structure was solved by use of the SHELXS-86 program [22]; 2829 reflections with $I \geq 2\sigma(I)$ were used to refine it by full-matrix least-squares using F^2 's (SHELXTL program [28]). All hydrogen atoms were found in a difference Fourier map and set as riding with fixed isotropic thermal parameters (all $U = 0.08 \text{ \AA}^2$). Anisotropic thermal parameters were applied for all nonhydrogen atoms. The refinement converged to $R = 0.0755$ and $R_w = 0.0707$ with the weight $w = 1/[\sigma^2(F) + 0.001521F^2]$ for 660 refined parameters. The largest residual peak in the final difference Fourier map was 0.54 e\AA^{-3} .

Scattering factors were taken from the International Tables for X-ray Crystallography [23]. Hydrogen bonds, torsion angles, and least-squares planes were calculated by the CSU program [24]. Values of $F_{\text{obs}}/F_{\text{calc}}$, anisotropic displacement coefficients, and full data including hydrogen atoms are deposited at the Cambridge Crystallographic Data Centre [29].

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