

In both compounds the puckering parameters (Cremer & Pople, 1975) for the pyrimidine ring [$Q = 0.464$ (3) (I), 0.455 (2) Å (II); $\theta = 49.1$ (4) (I), 44.0 (2)° (II); $\varphi = 313.5$ (5) (I), 320.2 (3)° (II)], the six-membered C5...C10 ring [$Q = 0.557$ (4) (I), 0.569 (2) Å (II); $\theta = 5.4$ (4) (I), 2.7 (2)° (II)] and the spirocyclohexane C2—C12...C16 ring [$Q = 0.562$ (3) (I), 0.569 (2) Å (II); $\theta = 0.4$ (3) (I), 1.5 (2)° (II)] indicate a half-chair conformation for the hetero ring and chair conformations for the two carbocyclic rings, with 1H_6 , 1C_4 and 1C_4 conformational forms, respectively (Boeyens, 1978). The out-of-plane amplitudes (Å) for atoms N1 and C6, with respect to the least-squares planes of ring atoms C2, N3, C4, C5, are 0.178 (2) and -0.513 (3) for (I) and 0.254 (1) and -0.430 (1) for (II). In our previous study (Ribár, Kapor, Kálmán, Argay, Fülöp & Bernáth, 1989), we plotted the out-of-plane distances for C6 atom against the puckering parameter φ for a series of related compounds. Here, we reproduce this diagram (Fig. 2), with the points for the C6 and N1 atoms from this study added. (It is important to note that here the N1 atom has taken the role of O1 atom in the previously studied compounds.) One can see that the new values are in good agreement with plotted curves, indicating a similar conclusion, *i.e.* the pyrimidin-4-one moiety, like the 1,3-oxazin-4-one moiety (Ribár *et al.*, 1989), adopts a 1H_6 (Boeyens, 1978) half-chair conformation in both compounds.

The molecules of the compounds are connected through hydrogen bonds of N—H...O type to form dimers. The corresponding bond lengths and angles are $H3\cdots O11 = 2.056$ (32) (I), 1.979 (24) Å (II),

$N3\cdots O11 = 2.868$ (3) (I), 2.861 (2) Å (II), $\angle N3\cdots H3\cdots O11 = 165.0$ (31) (I), 173.3 (21)° (II). The molecular packing in the crystal is shown in Fig. 3.

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Structure of 3',5'-Di-O-acetyl-N⁴-methoxycytosine

BY L. VAN MEERVELT

Laboratorium voor Macromoleculaire Structuurchemie, KU Leuven, Celestijnenlaan 200F, B-3001 Leuven, Belgium

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Abstract. $C_{14}H_{19}N_3O_7$, $M_r = 341.32$, orthorhombic, $P2_12_12_1$, $a = 11.219$ (8), $b = 12.136$ (7), $c = 12.324$ (7) Å, $V = 1678$ (3) Å³, $Z = 4$, $D_x = 1.35$, $D_m = 1.34$ (2) g cm⁻³, $\lambda(\text{Mo } K\alpha) = 0.71069$ Å, $\mu = 1.18$ cm⁻¹, $F(000) = 720$, $T = 292$ K, $R = 0.075$ for 1096 unique observed diffractometer data [$I \geq 2.0\sigma(I)$]. The modified base N⁴-methoxycytosine is present in the imino tautomeric form, with the methoxy group in the *syn* configuration.

Introduction. The base analogue N⁴-methoxycytosine (mo⁴C) is ambivalent in its hydrogen-bonding potential, since it forms stable base pairs with both adenine and guanine in oligonucleotide duplexes (Anand, Brown & Salisbury, 1987). Watson–Crick base pairing would only be compatible with mo⁴C in the *anti* amino form, while no such constraints would be required for wobble pairing. The structure determination of the left-handed double helix

d(CGCGmo⁴CG)₂ shows that the mo⁴C.G base pair is of the wobble type with mo⁴C in the imino form, and the methoxy group in the *syn* configuration (Van Meervelt, Moore, Kong Thoo Lin, Brown & Kennard, 1990). In this tautomer mo⁴C mimics thymine. The crystal structure analysis of a 3',5'-protected N⁴-methoxycytosine was undertaken to determine the stereochemistry of the methoxy group and in which tautomer (amino-imino) the free-base analogue occurs.

Experimental. The compound was prepared by Dr P. Kong Thoo Lin (Kong Thoo Lin & Brown, 1989) and crystallized by evaporation from ethanol/water. Data were collected on an Enraf-Nonius CAD-4 diffractometer for a colourless crystal (0.21 × 0.16 × 0.16 mm). The density was obtained by flotation in aqueous cadmium chloride. The cell parameters were calculated by least squares from the 2θ values of 19 reflections with 6.3 < θ < 16.4°. 2584 reflections were scanned [*h* 0:12, *k* -13:13, *l* 0:13; (sin θ/λ)_{max} = 0.55; ω/2θ-scan mode; graphite-monochromatized Mo Kα radiation]. Three standard reflections ($\bar{8}0\bar{4}$, $0\bar{8}4$, $\bar{7}60$) showed fluctuations of 4%. The data were corrected for Lp but not for absorption, and merged, resulting in the unique set of 1358 reflections, of which 262 reflections were considered as unobserved [*I* < 2σ(*I*)]. All non-H atoms were found by direct methods (*GENSIN*, *GENTAN*; Hall & Stewart, 1989). H atoms were placed at calculated distances (C—H, N—H = 1.04 Å). The structure was refined on *F* by full-matrix least-squares procedures using anisotropic temperature factors for non-H atoms. H atoms were allowed to ride on their carrier atoms with an isotropic temperature factor 10% greater than those of the carrier atom. Final convergence was reached at *R* = 0.075 [*wR* = 0.029, *w* = 1/σ(*F*); *S* = 1.439; (Δσ)_{max} = 0.030; number of refined parameters = 217]. Maximum and minimum heights in final difference Fourier synthesis: 0.68 and -0.66 e Å⁻³. Scattering factors from Cromer & Mann (1968) for C, N and O, and from Stewart, Davidson & Simpson (1965) for H. The final atomic coordinates and equivalent isotropic temperature factors are listed in Table 1. The program package *XTAL2.6* (Hall & Stewart, 1989) was used for all calculations.

Discussion. The molecular structure with labelling is depicted in Fig. 1. Bond distances and bond angles are listed in Table 2* and some conformational

* Lists of structure factors, anisotropic thermal parameters, H-atom parameters, least-squares planes, and bond distances and angles involving H atoms have been deposited with the British Library Document Supply Centre as Supplementary Publication No. SUP 54359 (20 pp.). Copies may be obtained through The Technical Editor, International Union of Crystallography, 5 Abbey Square, Chester CH1 2HU, England.

Table 1. Final coordinates and equivalent isotropic thermal parameters with their *e.s.d.*'s in parentheses

$$U_{eq} = \frac{1}{3} \sum_i \sum_j U_{ij} a_i^* a_j^* a_i \cdot a_j$$

	<i>x</i>	<i>y</i>	<i>z</i>	<i>U</i> _{eq} (Å ²)
N(1)	0.8988 (4)	0.8173 (4)	-0.0503 (4)	0.043 (3)
C(2)	0.9584 (5)	0.7662 (5)	-0.1319 (5)	0.043 (4)
N(3)	0.8890 (4)	0.7373 (4)	-0.2207 (4)	0.046 (3)
C(4)	0.7669 (5)	0.7565 (5)	-0.2315 (5)	0.043 (4)
C(5)	0.7104 (5)	0.8030 (5)	-0.1385 (4)	0.046 (4)
C(6)	0.7741 (5)	0.8293 (5)	-0.0528 (4)	0.044 (4)
O(2)	1.0649 (3)	0.7474 (3)	-0.1312 (3)	0.060 (3)
N(4)	0.7088 (4)	0.7398 (4)	-0.3226 (4)	0.056 (3)
O(4)	0.7885 (3)	0.6998 (4)	-0.4030 (3)	0.065 (3)
C(1')	0.9655 (5)	0.8612 (5)	0.0413 (5)	0.044 (4)
C(2')	0.9551 (5)	0.9837 (5)	0.0563 (4)	0.045 (4)
C(3')	0.9659 (5)	0.9980 (5)	0.1800 (4)	0.043 (4)
C(4')	0.9196 (5)	0.8894 (5)	0.2242 (4)	0.042 (4)
O(4')	0.9183 (3)	0.8119 (3)	0.1363 (3)	0.047 (3)
O(3')	1.0916 (3)	1.0137 (3)	0.2043 (3)	0.049 (2)
C(31)	1.1144 (5)	1.0380 (5)	0.3110 (6)	0.051 (4)
C(32)	1.2434 (5)	1.0615 (5)	0.3286 (4)	0.067 (5)
C(5')	0.7957 (4)	0.8968 (5)	0.2752 (4)	0.055 (4)
O(5')	0.7239 (3)	0.9572 (3)	0.1950 (3)	0.048 (3)
C(51)	0.6071 (5)	0.9712 (6)	0.2215 (6)	0.059 (5)
O(51)	0.5680 (3)	0.9420 (4)	0.3086 (4)	0.074 (3)
C(52)	0.5414 (5)	1.0279 (5)	0.1321 (5)	0.065 (4)
O(31)	1.0385 (3)	1.0394 (4)	0.3787 (3)	0.059 (3)
C(41)	0.7237 (6)	0.6913 (8)	-0.5012 (4)	0.092 (6)

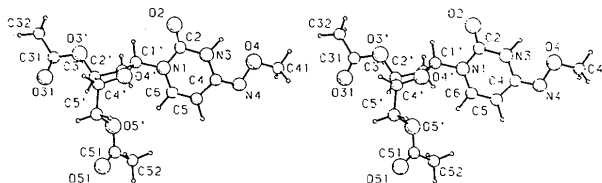


Fig. 1. Stereoscopic view of the molecule (program *PLUTO*; Motherwell & Clegg, 1978).

details and comparisons are given in Table 3. The overall shape of the molecule is determined by the torsion angle χ about the glycosidic bond C(1')—N(1) which is in the usual range for pyrimidine nucleosides (Saenger, 1984). Owing to this *anti* orientation the bulk of the pyrimidine base points away from the sugar. The base analogue N⁴-methoxycytosine is in the imino tautomeric form, with the methoxy group in the *syn* configuration leading to a short van der Waals contact O(4)⋯H(3) (2.16 Å). In the imino form mo⁴C mimics thymine or uracil more than cytosine; bond lengths and angles of the base are in the normal range for thymine or uracil derivatives (Taylor & Kennard, 1982). The plane of the base [six atoms, N(1)—C(6)] makes an angle of 11.5° with the plane through the =N—O—CH₃ moiety. The orientation about C(4')—C(5'), described by γ , is +synclinal [γ = 48.6 (3)°].

Table 3 allows comparison of the free N⁴-methoxycytosine with the base analogue incorporated in the double helical Z-DNA fragment

Table 2. Bond distances (Å) and bond angles (°) with their e.s.d.'s in parentheses

N(1)—C(2)	1.358 (7)	C(2')—C(3')	1.539 (7)
N(1)—C(6)	1.407 (7)	C(3')—C(4')	1.517 (8)
N(1)—C(1')	1.455 (7)	C(3')—O(3')	1.455 (6)
C(2)—N(3)	1.388 (8)	C(4')—O(4')	1.435 (7)
C(2)—O(2)	1.217 (7)	C(4')—C(5')	1.528 (8)
N(3)—C(4)	1.396 (7)	O(3')—C(31)	1.371 (8)
C(4)—C(5)	1.426 (8)	C(31)—C(32)	1.491 (8)
C(4)—N(4)	1.315 (8)	C(31)—O(31)	1.193 (7)
C(5)—C(6)	1.314 (8)	C(5')—O(5')	1.471 (7)
N(4)—O(4)	1.420 (6)	O(5')—C(51)	1.361 (7)
O(4)—C(41)	1.416 (7)	C(51)—O(51)	1.213 (8)
C(1')—C(2')	1.503 (9)	C(51)—C(52)	1.493 (9)
C(1')—O(4')	1.417 (7)		
C(2)—N(1)—C(6)	121.4 (5)	C(2')—C(1')—O(4')	106.7 (4)
C(2)—N(1)—C(1')	119.3 (4)	C(1')—C(2')—C(3')	103.1 (5)
C(6)—N(1)—C(1')	119.4 (4)	C(2')—C(3')—C(4')	103.3 (5)
N(1)—C(2)—N(3)	115.0 (5)	C(2')—C(3')—O(3')	107.1 (4)
N(1)—C(2)—O(2)	124.3 (5)	C(4')—C(3')—O(3')	111.8 (4)
N(3)—C(2)—O(2)	120.6 (5)	C(3')—C(4')—O(4')	107.6 (4)
C(2)—N(3)—C(4)	125.7 (5)	C(3')—C(4')—C(5')	114.0 (5)
N(3)—C(4)—C(5)	115.2 (5)	O(4')—C(4')—C(5')	109.9 (4)
N(3)—C(4)—N(4)	122.8 (5)	C(1')—O(4')—C(4')	110.1 (4)
C(5)—C(4)—N(4)	121.8 (5)	C(3')—O(3')—C(31)	114.0 (4)
C(4)—C(5)—C(6)	120.1 (5)	O(3')—C(31)—C(32)	111.2 (5)
N(1)—C(6)—C(5)	122.2 (5)	O(3')—C(31)—O(31)	122.7 (4)
C(4)—N(4)—O(4)	109.6 (4)	C(32)—C(31)—O(31)	126.0 (6)
N(4)—O(4)—C(41)	107.3 (4)	C(4')—C(5')—O(5')	104.5 (4)
N(1)—C(1')—C(2')	114.7 (5)	C(5')—O(5')—C(51)	115.4 (4)
N(1)—C(1')—O(4')	107.1 (4)	O(5')—C(51)—O(51)	121.6 (6)
O(51)—C(51)—C(52)	127.5 (5)	O(5')—C(51)—C(52)	110.9 (5)

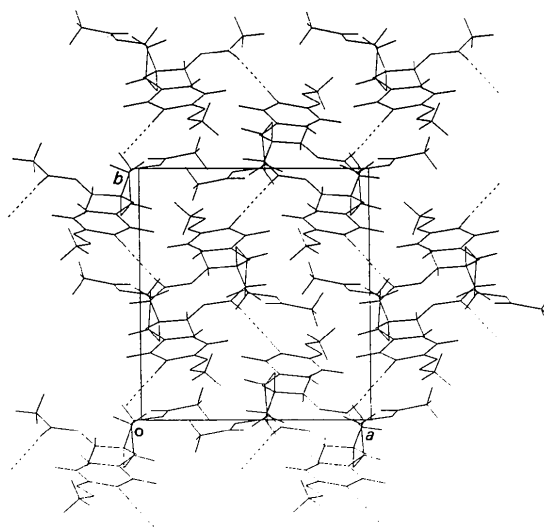
Table 3. Some parameters for *N*⁴-methoxycytosine (a) as free base (this structure), and (b) and (c) in strands 1 and 2 of *d*(CGCGmo⁴CG)₂ (Van Meervelt et al., 1990)

The thermal parameter *U* is averaged for the atoms of the base. Torsion angle τ is defined as C(4)—N(4)—O(4)—C(41), χ as O(4')—C(1')—N(1)—C(2). Phase angle as defined in Saenger (1984).

	(a)	(b)	(c)
C(4)=N(4) (Å)	1.315 (8)	1.28	1.32
τ (°)	-175.7 (6)	-178	-179
χ (°)	-123.4 (5)	-147	-161
Puckering mode	C(2')-endo	C(1')-exo	C(2')-endo
Phase angle (°)	155.5	135	150
<i>U</i> (Å ²)	0.054 (4)	0.23	0.11

d(CGCGmo⁴CG)₂ whose structure was determined at 1.7 Å resolution (Van Meervelt, Moore, Kong Thoo Lin, Brown & Kennard, 1990). One of the two crystallographically independent mo⁴C.G pairs has more efficient hydration and better stacking (also reflected in the lower thermal vibration) and the parameters for this base analogue are closer to the values for the free mo⁴C.

The hydrogen bonding and molecular packing are illustrated in Fig. 2. The cytosine nitrogen N(3) is hydrogen bonded to the carbonyl oxygen O(51) in a molecule generated by a screw axis in the *a* direction

Fig. 2. Molecular packing and hydrogen bonding in 3',5'-di-O-acetyl-*N*⁴-methoxycytosine as seen in projection down *c*. Hydrogen bonds are marked with broken lines (program *PLUTO*; Motherwell & Clegg, 1978).

[N(3)⋯O(51) 3.152 (7), N(3)—H(3) 1.068 (6), H(3)⋯O(51) 2.272 (6) Å, N(3)—H(3)⋯O(51) 138.6 (3)°].

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