Table 3. *Hydrogen-bonding geometry (Å, °)*

D—H···*A*	*D*—H	H···*A*	*D*···*A*	*D*—H···*A*
O1*A*—H1*A*···N21*B*^{i}	0.92 (2)	1.88 (2)	2.795 (2)	173 (2)
O1*B*—H1*B*···N21*A*	0.91 (2)	1.90 (2)	2.798 (2)	172 (2)

Symmetry code: (i) $x, \frac{1}{2}-y, \frac{1}{2}+z$.

Data collection: CAD-4*F*. Cell refinement: CAD-4*F*. Data reduction: *ENPROC* (Rettig, 1978). Program(s) used to solve structure: *SHELXS*86 (Sheldrick, 1990). Program(s) used to refine structure: *SHELXL*93 (Sheldrick, 1993). Molecular graphics: Stereochemical Workstation (Siemens, 1989). Software used to prepare material for publication: *SHELXL*93.

Lists of structure factors, anisotropic displacement parameters, H-atom coordinates and complete geometry have been deposited with the IUCr (Reference: MU1277). Copies may be obtained through The Managing Editor, International Union of Crystallography, 5 Abbey Square, Chester CH1 2HU, England.

References

Abrahams, S. C. & Keve, E. T. (1971). *Acta Cryst.* A**27**, 157–161.

Baughman, R. G., Virant, M. S. & Jacobson, R. A. (1981). *J. Agric. Food Chem.* **29**, 989–991.

Domenicano, A. & Murray-Rust, P. (1979). *Tetrahedron Lett.* **20**, 2283–2286.

Higashi, T. & Osaki, K. (1977). *Acta Cryst.* B**33**, 607–609.

Rettig, S. (1978). *ENPROC. Data Reduction Program for Enraf–Nonius CAD-4F Diffractometer.* University of British Columbia, Vancouver BC, Canada.

Sheldrick, G. M. (1990). *Acta Cryst.* A**46**, 467–473.

Sheldrick, G. M. (1993). *SHELXL*93. *Program for the Refinement of Crystal Structures.* University of Göttingen, Germany.

Siemens (1989). *Stereochemical Workstation Operation Manual.* Release 3.4. Siemens Analytical X-ray Instruments Inc., Madison, Wisconsin, USA.

Acta Cryst. (1996). C**52**, 3173–3177

2′,3′-Dideoxy-3′-nitrothymidine and 2′-Propoxy-3′-nitrothymidine

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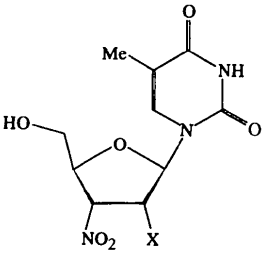
Abstract

The crystal structures of 2′,3′-dideoxy-3′-nitrothymidine, $C_{10}H_{13}N_3O_6$ and 2′-propoxy-3′-nitrothymidine, $C_{13}H_{19}N_3O_7$, are reported. Both compounds are analogous to the anti-HIV nucleoside 3′-azido-2′,3′-dideoxythymidine (AZT). The replacement of the azido group in AZT by the nitro group in these two compounds has resulted in a sugar pucker preference of C2′-*endo* type, as observed in both structures, AZT itself and several of its derivatives.

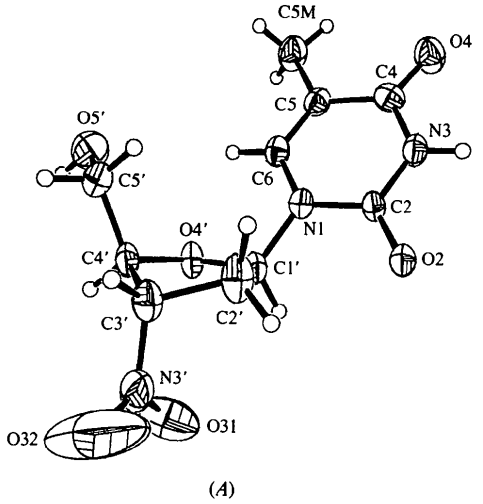
Comment

A number of modified nucleosides have established antiviral and/or anticancer activity arising from their mis-incorporation into DNA or RNA during replication or transcription. In particular, nucleosides lacking a hydroxyl group at the 3′ position can have activity against human immunodeficiency virus (HIV) by acting as inhibitors of the viral reverse transcriptase enzyme which transcribes viral RNA into DNA. AZT, 3′-azido-2′,3′-dideoxythymidine, is an effective inhibitor which is in current clinical use with HIV patients. The title compounds, 2′,3′-dideoxy-, (I) and 2′-propoxy-3′-nitrothymidine, (II), were synthesised (Hossain, Papchikhin, Garg, Fedorov, & Chattopadhyaya, 1993) as part of an attempt to develop new and more effective reverse transcriptase inhibitors. In this paper, we examine their conformational features, and compare them with those of AZT itself.

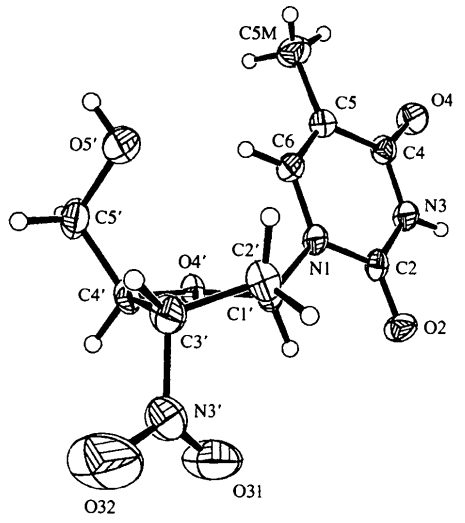


(I) X = H
(II) $X = OCH_2CH_2CH_3$

Compound (I) is the 3′-nitro analogue of AZT. It has two molecules in the asymmetric unit (Fig. 1). These have distinct conformations about the glycosidic bond with glycosidic angles [O4′—C1′—N1—C2 (χ)] of −172.4 (4)° and −127.1 (4)° for molecules *A* and *B*, respectively. The values for the exocyclic torsion angle [C3′—C4′—C5′—O5′ (γ)] are dissimilar with molecule *A* having a *trans* conformation [174.4 (4)°] and molecule *B* being *gauche*(+) with a torsion angle of 53.0 (6)°. The deoxyribose sugar rings have similar puckers, molecules *A* and *B* having phase angles of pseudorotation *P* (Neidle, 1994) of 202.5 (6)° and 169.6 (6)°, respectively. These correspond to C3′-*exo* and C2′-*endo* sugar puckers, respectively. Compound (II), the 2′-propoxy derivative of (I), has the propyl group in an extended conformation, oriented on the *endo* side of the sugar. Other conformational features of compound (II) include a glycosidic torsion angle of −121.1 (4)°, a pseudorotation phase angle of 140.9 (4)° for the ribose ring (C1′-*exo*/C2′-*endo* pucker) and a C4′—C5′ exocyclic torsion angle of 50.6 (5)°, *i.e* in the *gauche*(+) range.



(*A*)



(*B*)

Fig. 1. Plots of the two independent molecules in the crystal structure of 2′,3′-dideoxy-3′-nitrothymidine. Displacement ellipsoids are shown at 50% probability levels. H atoms are drawn as small circles of arbitrary radius.

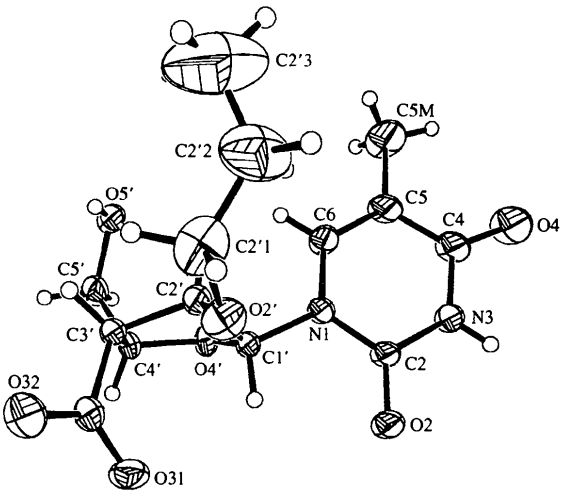


Fig. 2. Plot of the structure of 2′-propoxy-3′-nitrothymidine. Displacement ellipsoids are shown at 50% probability levels. H atoms are drawn as small circles of arbitrary radius.

We have examined the conformational preferences of compound (I) by means of molecular-mechanics calculations (*HYPERCHEM*; Hypercube Inc., 1994) using the *MM+* force field. Structures for 2′,3′-dideoxy-3′-nitrothymidine were generated with either C2′-*endo* or C3′-*endo* sugar puckers and were subjected to molecular mechanics minimizations. The final structures had energies of 14.63 and 11.54 kcal mole^{-1}, respectively. The former lower-energy structure was intermediate in conformation between the two crystallographic structures for compound (I), (molecules *A* and *B*), with a glycosidic angle of $-150(3)°$.

The nitro group has equivalent geometry for all three molecules in the two present structures, within experimental error. The nitro groups are oriented with respect to the ribose sugar rings so that in all three molecules they are approximately parallel to the C3′—H3′ vector. The nitro group orientation with respect to the ribose ring can be defined by the C2′—C3′—N3′—O32 torsion angle. This corresponds to the C2′—C3′—N3′*A*—N3′*B* torsion angle in AZT itself. For compound (I), molecules *A* and *B* have values for this torsion angle of 119(2) and 143.2(7)°, respectively. Compound (II) has a value of 105.7(5)° for this angle, indicating that the nitro group has considerable flexibility with respect to the ribose ring. Crystallographic studies of AZT itself and various 3′-azido-3′-deoxythymidine analogs (Birnbaum, Giziewicz, Gabe, Lin & Prusoff, 1987; Camerman, Mastropaolo & Camerman, 1987; Van Roey *et al.*, 1988) have shown that the 3′-azido group prefers to adopt a *trans* conformation with respect to the C2′—C3′ bond. For example, the C2′—C3′—N3′*A*—N3′*B* torsion angle in the two independent molecules in the crystal structure of AZT itself has values of 178 and 176°.

The crystal structures of AZT itself (Birnbaum, Giziewicz, Gabe, Lin & Prusoff, 1987; Camerman, Mastropaolo & Camerman, 1987; Van Roey *et al.*, 1988) show that the deoxyribose sugar pucker preference is in the C2′-*endo* or the closely related C3′-*exo* domain, which have pseudorotation phase angles in the range 170–220°. Similar puckers have been observed in other nucleoside analogues with *anti*-HIV activity, leading to the hypothesis (Van Roey, Salerno, Chu & Schinazi, 1989; Taylor, Van Roey, Schinazi & Chu, 1990) that C2′-*endo*/ C3′-*exo* types of sugar conformational preference are important for antiviral activity. An NMR study of AZT bound to HIV-1 reverse transcriptase (Painter, Aulabaugh & Andrews, 1993), however, suggests that

the sugar pucker of the drug is predominantly C4′-*exo*, with a *P* angle of 60°, *i.e* close to the puckers observed here for the 3′-nitro compounds. Neither nitrothymidine examined in this study was active against HIV specific reverse transcriptase. This suggests that sugar pucker of the stand-alone nucleoside in the crystal lattice or in solution is not by itself a major criterion of activity. Of greater relevance are the conformational preferences of the sugar moiety when the nucleoside in its 5′-triphosphate form is bound to viral reverse transcriptase.

The two independent molecules in the structure of compound (I) form a hydrogen-bonded symmetric dimer with distances O2*A*···N3*B* of 2.815 (6) Å and N3*A*···O2*B* of 2.877 (6) Å, corresponding to thymine···thymine base pairing. The molecules link into an infinite two-dimensional network, perpendicular to **c**, which involves the O5′ atoms.

Experimental

Crystals were obtained from aqueous ethanol by slow evaporation at room temperature. The compounds were prepared as described (Hossain, Papchikhin, Garg, Fedorov & Chattopadhyaya, 1993).

Compound (I)

Crystal data

$C_{10}H_{13}N_3O_6$
M_r = 271.23
Monoclinic
$P2_1$
a = 5.5880 (10) Å
b = 11.6450 (10) Å
c = 18.561 (2) Å
β = 97.560 (10)°
V = 1197.3 (3) Å^3
Z = 4
D_x = 1.505 Mg m^{-3}
D_m not measured

Cu $K\alpha$ radiation
λ = 1.54178 Å
Cell parameters from 25 reflections
θ = 10.–22.°
μ = 1.086 mm^{-1}
T = 293 (2) K
Plate
0.4 × 0.3 × 0.08 mm
Colorless

Data collection

Enraf–Nonius CAD-4*T* diffractometer
$\omega/2\theta$ scans
Absorption correction: refined from ΔF (*DIFABS*; Walker & Stuart, 1983)
T_{min} = 0.73, T_{max} = 0.98
2077 measured reflections
2077 independent reflections

1893 observed reflections [$I > 2\sigma(I)$]
θ_{max} = 65°
$h = 0 \rightarrow 6$
$k = 0 \rightarrow 13$
$l = -21 \rightarrow 21$
3 standard reflections monitored every 250 reflections
frequency: 60 min
intensity decay: none

Refinement

Refinement on F^2
$R[F^2 > 2\sigma(F^2)]$ = 0.0551
$wR(F^2)$ = 0.1722
S = 0.894
2077 reflections
343 parameters
H atoms: riding model with U_{iso} values refined
$w = 1/[\sigma^2(F_o^2) + (0.1558P)^2 + 0.5423P]$ where $P = (F_o^2 + 2F_c^2)/3$
$(\Delta/\sigma)_{max}$ = 0.024
$\Delta\rho_{max}$ = 0.442 e Å^{-3}
$\Delta\rho_{min}$ = −0.392 e Å^{-3}
Extinction correction: none
Atomic scattering factors from *International Tables for Crystallography* (1992, Vol. C, Tables 4.2.6.8 and 6.1.1.4)

Table 1. *Fractional atomic coordinates and equivalent isotropic displacement parameters (Å^2) for (I)*

$U_{eq} = (1/3)\sum_i\sum_j U_{ij} a_i^* a_j^* \mathbf{a}_i.\mathbf{a}_j$.

	x	y	z	U_{eq}
C1′*A*	−0.1445 (8)	0.3349 (5)	0.9421 (2)	0.0343 (10)
C2′*A*	0.0995 (9)	0.3658 (7)	0.9859 (3)	0.0506 (14)
C3′*A*	0.0377 (10)	0.3835 (6)	1.0625 (3)	0.0466 (13)
N3′*A*	0.0588 (14)	0.2737 (7)	1.1043 (3)	0.079 (2)
O31*A*	−0.0593 (13)	0.1906 (7)	1.0837 (4)	0.108 (2)
O32*A*	0.190 (4)	0.2683 (9)	1.1547 (8)	0.320 (13)
C4′*A*	−0.2231 (10)	0.4231 (5)	1.0493 (3)	0.0404 (12)
O4′*A*	−0.3254 (6)	0.3683 (4)	0.9829 (2)	0.0401 (8)
C5′*A*	−0.2388 (12)	0.5515 (5)	1.0436 (3)	0.0517 (14)
O5′*A*	−0.4751 (10)	0.5891 (5)	1.0248 (3)	0.0758 (14)
N1*A*	−0.1840 (8)	0.3927 (4)	0.8701 (2)	0.0386 (9)
C2*A*	−0.0365 (8)	0.3570 (4)	0.8210 (2)	0.0341 (10)
O2*A*	0.1244 (7)	0.2851 (3)	0.8369 (2)	0.0443 (9)
N3*A*	−0.0807 (8)	0.4054 (4)	0.7531 (2)	0.0410 (10)
C4*A*	−0.2552 (9)	0.4873 (5)	0.7301 (3)	0.0404 (11)
O4*A*	−0.2683 (8)	0.5243 (4)	0.6684 (2)	0.0563 (11)
C5*A*	−0.4046 (9)	0.5200 (4)	0.7843 (3)	0.0399 (12)
C5*MA*	−0.5960 (11)	0.6070 (6)	0.7640 (3)	0.056 (2)
C6*A*	−0.3617 (9)	0.4722 (5)	0.8514 (3)	0.0378 (11)
C1′*B*	0.5267 (8)	0.2474 (4)	0.5550 (2)	0.0333 (10)
C2′*B*	0.7216 (9)	0.3244 (5)	0.5316 (3)	0.0383 (11)
C3′*B*	0.7236 (9)	0.2905 (5)	0.4526 (3)	0.0399 (11)
N3′*B*	0.5411 (9)	0.3591 (5)	0.4034 (2)	0.0523 (12)
O31*B*	0.3389 (9)	0.3701 (6)	0.4204 (3)	0.084 (2)
O32*B*	0.5884 (13)	0.3884 (8)	0.3456 (4)	0.121 (3)
C4′*B*	0.6465 (9)	0.1646 (5)	0.4485 (2)	0.0350 (10)
O4′*B*	0.5198 (6)	0.1468 (3)	0.5104 (2)	0.0337 (7)
C5′*B*	0.8548 (9)	0.0811 (6)	0.4509 (3)	0.0472 (13)
O5′*B*	1.0294 (7)	0.1032 (5)	0.5122 (2)	0.0575 (12)
N1*B*	0.5687 (7)	0.2114 (4)	0.6312 (2)	0.0338 (9)
C2*B*	0.4115 (8)	0.2496 (4)	0.6779 (2)	0.0316 (10)
O2*B*	0.2471 (6)	0.3174 (4)	0.6593 (2)	0.0443 (9)
N3*B*	0.4569 (7)	0.2068 (4)	0.7464 (2)	0.0366 (9)
C4*B*	0.6327 (9)	0.1277 (4)	0.7728 (3)	0.0351 (11)
O4*B*	0.6462 (7)	0.0939 (4)	0.8363 (2)	0.0497 (10)
C5*B*	0.7908 (8)	0.0922 (5)	0.7210 (3)	0.0368 (11)
C5*MB*	0.9844 (11)	0.0048 (6)	0.7435 (3)	0.054 (2)
C6*B*	0.7525 (8)	0.1355 (5)	0.6543 (3)	0.0370 (11)

Table 2. *Selected geometric parameters (Å, °) for (I)*

C2′*A*—C3′*A*	1.521 (7)	N3′*A*—O31*A*	1.205 (10)
C3′*A*—N3′*A*	1.492 (10)	C2′*B*—C3′*B*	1.520 (7)
C3′*A*—C4′*A*	1.518 (8)	C3′*B*—N3′*B*	1.505 (7)
N3′*A*—O32*A*	1.112 (9)	C3′*B*—C4′*B*	1.528 (8)
N3′*A*—C3′*A*—C4′*A*	110.7 (5)	N3′*B*—C3′*B*—C4′*B*	108.3 (4)
N3′*A*—C3′*A*—C2′*A*	111.0 (5)	N3′*B*—C3′*B*—C2′*B*	110.9 (5)
C4′*A*—C3′*A*—C2′*A*	102.8 (4)	C4′*B*—C3′*B*—C2′*B*	105.0 (4)
O32*A*—N3′*A*—O31*A*	119.6 (10)	O32*B*—N3′*B*—O31*B*	121.8 (6)
O32*A*—N3′*A*—C3′*A*	119.0 (10)	O32*B*—N3′*B*—C3′*B*	119.1 (5)
O31*A*—N3′*A*—C3′*A*	121.4 (5)	O31*B*—N3′*B*—C3′*B*	118.4 (5)
O4′*A*—C1′*A*—C2′*A*—C3′*A*		17.3 (7)	
C1′*A*—C2′*A*—C3′*A*—C4′*A*		−28.6 (6)	
C2′*A*—C3′*A*—N3′*A*—O31*A*		−59.0 (10)	
C2′*A*—C3′*A*—C4′*A*—O4′*A*		30.7 (6)	
C2′*A*—C1′*A*—O4′*A*—C4′*A*		2.2 (6)	
C3′*A*—C4′*A*—O4′*A*—C1′*A*		−21.0 (6)	
C3′*A*—C4′*A*—C5′*A*—O5′*A*		174.4 (4)	
O4′*A*—C1′*A*—N1*A*—C2*A*		−172.4 (4)	
O4′*B*—C1′*B*—C2′*B*—C3′*B*		27.6 (5)	
C1′*B*—C2′*B*—C3′*B*—C4′*B*		−29.7 (5)	

C2′B—C3′B—N3′B—O31B	−45.9 (8)
C2′B—C3′B—C4′B—O4′B	21.6 (5)
C2′B—C1′B—O4′B—C4′B	−15.0 (5)
C3′B—C4′B—O4′B—C1′B	−4.2 (5)
C3′B—C4′B—C5′B—O5′B	53.0 (6)
O4′B—C1′B—N1B—C2B	−127.1 (4)

Compound (II)

Crystal data

$C_{13}H_{19}N_3O_7$
M_r = 329.31
Monoclinic
$C2$
a = 15.746 (2) Å
b = 9.3730 (10) Å
c = 11.304 (2) Å
β = 100.190 (10)°
V = 1642.0 (4) Å^3
Z = 4
D_x = 1.332 Mg m^{-3}
D_m not measured

Cu $K\alpha$ radiation
λ = 1.54178 Å
Cell parameters from 25 reflections
θ = 1.5–22.5°
μ = 0.933 mm^{-1}
T = 293 (2) K
Elongated prism
0.4 × 0.25 × 0.15 mm
Pale yellow

Data collection

Enraf–Nonius CAD-4T diffractometer
$\omega/2\theta$ scans
Absorption correction: refined from ΔF (*DIFABS*; Walker & Stuart, 1983)
T_{min} = 0.83, T_{max} = 0.98
1416 measured reflections
1369 independent reflections
1338 observed reflections [$I > 2\sigma(I)$]

R_{int} = 0.0387
θ_{max} = 65°
$h = 0 \rightarrow 18$
$k = 0 \rightarrow 10$
$l = -13 \rightarrow 12$
3 standard reflections monitored every 250 reflections
frequency: 60 min
intensity decay: none

Refinement

Refinement on F^2
$R[F^2 > 2\sigma(F^2)]$ = 0.0640
$wR(F^2)$ = 0.1748
S = 1.192
1368 reflections
208 parameters
H atoms: riding model with U_{iso} values refined
$w = 1/[\sigma^2(F_o^2) + (0.1198P)^2 + 1.0598P]$ where $P = (F_o^2 + 2F_c^2)/3$

$(\Delta/\sigma)_{max}$ = −0.001
$\Delta\rho_{max}$ = 0.375 e Å^{-3}
$\Delta\rho_{min}$ = −0.333 e Å^{-3}
Extinction correction: none
Atomic scattering factors from *International Tables for Crystallography* (1992, Vol. C, Tables 4.2.6.8 and 6.1.1.4)

Table 3. *Fractional atomic coordinates and equivalent isotropic displacement parameters (Å^2) for (II)*

$U_{eq} = (1/3)\sum_i\sum_j U_{ij} a_i^* a_j^* \mathbf{a}_i.\mathbf{a}_j$.

	x	y	z	U_{eq}
C1′	0.2588 (3)	0.8400 (5)	0.1512 (4)	0.0340 (10)
C2′	0.3485 (3)	0.8927 (5)	0.1404 (4)	0.0338 (10)
O2′	0.3427 (2)	1.0289 (4)	0.0870 (3)	0.0507 (10)
C2′1	0.4176 (4)	1.1134 (7)	0.1134 (7)	0.066 (2)
C2′2	0.4385 (7)	1.1605 (8)	0.2389 (10)	0.096 (3)
C2′3	0.5145 (11)	1.151 (2)	0.3075 (18)	0.176 (9)
C3′	0.3792 (3)	0.7728 (5)	0.0649 (4)	0.0313 (9)
N3′	0.3511 (2)	0.8065 (4)	−0.0668 (3)	0.0387 (9)
O31′	0.2756 (2)	0.7966 (5)	−0.1094 (3)	0.0524 (10)
O32′	0.4075 (3)	0.8476 (6)	−0.1216 (3)	0.0634 (12)
C4′	0.3328 (3)	0.6399 (5)	0.1025 (4)	0.0321 (9)
O4′	0.2690 (2)	0.6911 (4)	0.1699 (3)	0.0376 (8)
C5′	0.3933 (3)	0.5408 (5)	0.1810 (4)	0.0404 (10)
O5′	0.4438 (2)	0.6153 (4)	0.2789 (3)	0.0447 (9)
N1	0.2232 (2)	0.9007 (5)	0.2506 (3)	0.0386 (9)
C2	0.1462 (3)	0.9715 (5)	0.2252 (4)	0.0368 (10)
O2	0.1043 (2)	0.9885 (5)	0.1218 (3)	0.0502 (10)
N3	0.1168 (3)	1.0267 (5)	0.3235 (3)	0.0437 (10)
C4	0.1569 (4)	1.0158 (7)	0.4423 (4)	0.0516 (13)
O4	0.1225 (3)	1.0716 (7)	0.5197 (4)	0.082 (2)
C5	0.2349 (3)	0.9333 (7)	0.4636 (4)	0.0523 (14)
C5M	0.2802 (5)	0.9099 (12)	0.5920 (5)	0.084 (3)
C6	0.2646 (3)	0.8804 (6)	0.3678 (4)	0.0461 (12)

Table 4. *Selected geometric parameters (Å, °) for (II)*

C2′—C3′	1.540 (6)	N3′—O31′	1.204 (5)
C3′—N3′	1.509 (5)	N3′—O32′	1.231 (5)
C3′—C4′	1.541 (6)		
N3′—C3′—C2′	109.1 (3)	O31′—N3′—O32′	124.8 (4)
N3′—C3′—C4′	111.7 (3)	O31′—N3′—C3′	118.4 (3)
C2′—C3′—C4′	103.1 (3)	O32′—N3′—C3′	116.8 (4)
O4′—C1′—C2′—C3′	40.3 (4)	C2′—C1′—O4′—C4′	−34.5 (4)
C1′—C2′—C3′—C4′	−30.8 (4)	C3′—C4′—O4′—C1′	14.0 (4)
C2′—C3′—N3′—O31′	−71.7 (5)	C3′—C4′—C5′—O5′	50.6 (5)
N3′—C3′—C4′—O4′	−105.3 (4)	O4′—C1′—N1—C2	−121.1 (4)
C2′—C3′—C4′—O4′	11.8 (4)		

Both structures were solved by direct methods and refined by full-matrix least-squares. H atoms were calculated geometrically except for those attached to the O5′ atoms which were located in difference Fourier maps. Empirical absorption corrections were applied on account of the non-isotropic shape of the crystals.

High thermal motion was found for the O atoms of the nitro groups, especially for molecule A in (I). There was no evidence of disorder for these groups but the motion is likely to have contributed to the relatively high R factors.

The absolute configuration was assigned to agree with the known absolute stereochemistry of β-nucleosides.

Structure (II) contains a small void at (0.00, 0.370, 0.500), close to O4 and O5′. No residual density was found in that area.

For both compounds, data collection: *CAD-4 Operations Manual* (Enraf–Nonius, 1977); cell refinement: *CAD-4 Operations Manual*; data reduction: *MolEN* (Fair, 1990); program(s) used to solve structures: *SHELXS86* (Sheldrick, 1990); program(s) used to refine structures: *SHELXL93* (Sheldrick, 1993); molecular graphics: *ORTEX* (McArdle, 1993).

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Lists of structure factors, anisotropic displacement parameters, H-atom coordinates and complete geometry have been deposited with the IUCr (Reference: SK1024). Copies may be obtained through The Managing Editor, International Union of Crystallography, 5 Abbey Square, Chester CH1 2HU, England.

References

Birnbaum, G. I., Giziewicz, J., Gabe, E. J., Lin, T.-S. & Prusoff, W. H. (1987). *Can. J. Chem.* **65**, 2135–2139.

Camerman, A., Mastropaolo, D. & Camerman, N. (1987). *Proc. Natl Acad. Sci. USA*, **84**, 8239–8242.
Enraf–Nonius (1977). *CAD-4 Operations Manual*. Enraf–Nonius, Delft, The Netherlands.
Fair, C. K. (1990). *MolEN. An Interactive Intelligent System for Crystal Structure Analysis*. Enraf–Nonius, Delft, The Netherlands.
Hossain, N., Papchikhin, A., Garg, N., Fedorov, I. & Chattopadhyaya, J. (1993). *Nucleosides & Nucleotides*, **12**, 499–528.
Hypercube Inc. (1994). *HYPERCHEM*. Version 4. Hypercube Inc., 419 Phillip Street, Waterloo, Ontario, N2L 3X2, Canada.
McArdle, P. (1993). *J. Appl. Cryst.* **26**, 752.
Neidle, S. (1994). In *DNA Structure and Recognition*. Oxford University Press.
Painter, G. R., Aulabaugh A. E. & Andrews, C. W. (1993). *Biochem. Biophys. Res. Commun.* **191**, 1166–1171.
Sheldrick, G. M. (1990). *Acta Cryst.* A**46**, 467–473.
Sheldrick, G. M. (1993). *SHELXL93. Program for the Refinement of Crystal Structures*. University of Göttingen, Germany.
Taylor, E. W., Van Roey, P., Schinazi, R. F. & Chu, C. K. (1990). *Antiviral Chem. Chemother.* **1**, 163–173.
Van Roey, P., Salerno, J. M., Chu, C. K., & Schinazi, R. F. (1989). *Proc. Natl Acad. Sci. USA*, **86**, 3929–3933.
Van Roey, P., Salerno, J. M., Duax, W. L., Chu, C. K., Ahn, M. K. & Schinazi, R. F. (1988). *J. Am. Chem. Soc.* **110**, 2277–2282.
Walker, N. & Stuart, D. (1983). *Acta Cryst.* A**39**, 158–166.

Acta Cryst. (1996). C**52**, 3177–3179

1-Methyl-2-phenyldecahydroquinolin-4-one Oxime

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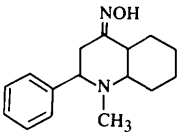
Abstract

The piperidine and cyclohexane rings in the title compound, $C_{16}H_{22}N_2O$, adopt a chair–chair conformation. The methyl group at N1 and the phenyl ring at C2 are oriented equatorially while the rest of the molecule is planar. The molecules are well stacked and the packing in the unit cell is stabilized by O—H···N hydrogen-bonded chains and weaker C—H···O and C—H···N bonds.

Comment

An *ORTEP*II (Johnson, 1976) diagram of the title compound, (I), with the atom-numbering scheme is shown in Fig. 1. The torsion angle H9—C9—C10—H10 [179 (2)°] confirms the *trans* fusion of the piperidine and cyclohexane rings in the molecule. It is evident from the ring torsion angles that the piperidine and cyclohexane rings are in a chair–chair conformation.



(I)

The angles C2—N1—C11 = 109.8 (2), C2—N1—C9 = 109.4 (1) and C9—N1—C11 = 110.7 (1)° indicate tetrahedral geometry at the N atom. The methyl group at N1 [C3—C2—N1—C11 = −173.9 (2)°] and the phenyl ring at C2 [C4—C3—C2—C14 = 178.7 (2)°] are equatorially oriented. The torsion angle C3—C4—N12—O13 [−2.1 (3)°] indicates that the oxime moiety has a planar conformation.

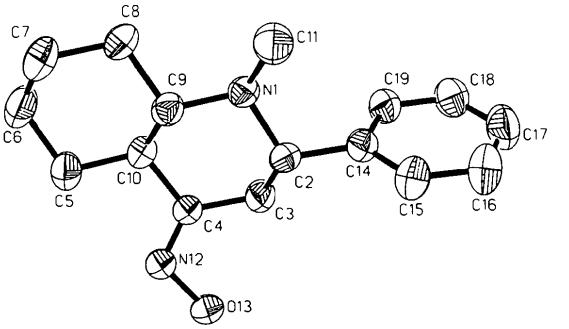


Fig. 1. *ORTEP*II (Johnson, 1976) diagram of the molecule with 50% probability ellipsoids.

From the stereoview of the packing (Fig. 2), it is clear that the phenyl ring of one molecule stacks well with the piperidine ring of the other molecule. It is found that there is an intermolecular O—H···N hydrogen bond (Table 3) which leads to a chain-like arrangement of the molecules (Fig. 2). In addition, an intramolecular C—H···O hydrogen bond and intermolecular C—H···O bonds are also found (Table 3).

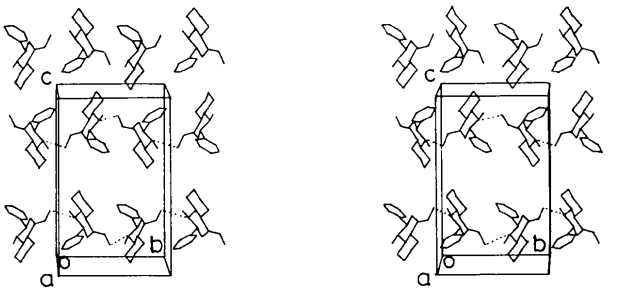


Fig. 2. Stereoview of the molecular packing (down the *a* axis) showing the chain-like arrangement of the molecules formed by intermolecular O—H···N hydrogen bonds.