Acta Crystallographica Section C
Crystal Structure Communications
ISSN 0108-2701

7-Deaza-2,8-diazaadenosine

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Received 7 April 2006
Accepted 16 May 2006
Online 15 June 2006

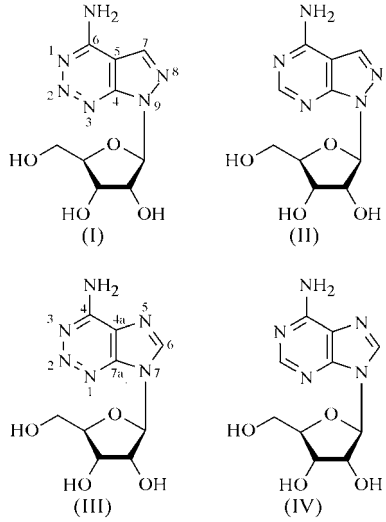
In the title compound [systematic name: 4-amino-7-(β-D-ribofuranosyl)-7*H*-pyrazolo[3,4-*d*][1,2,3]triazine], $C_9H_{12}N_6O_4$, the torsion angle of the N-glycosylic bond is high *anti* [χ = −83.2 (3)°]. The ribofuranose moiety adopts the C2′-*endo*–C1′-*exo* ($^2T_1$) sugar conformation (*S*-type sugar pucker), with P = 152.4° and τ_m = 35.0°. The conformation at the C4′—C5′ bond is +*sc* (*gauche*,*gauche*), with the torsion angle γ = 52.0 (3)°. The compound forms a three-dimensional network that is stabilized by several hydrogen bonds (N—H···O, O—H···N and O—H···O).

Comment

The aza and deaza derivatives of purine nucleosides attract attention because they are valuable tools in chemistry and biology. Many of them show antifungal, antiviral and anticancer activity (Montgomery & Thomas, 1972; Montgomery *et al.*, 1975; Bennett *et al.*, 1976). They also show unusual base-pairing properties when they are constituents of nucleic acids. 7-Deaza-2,8-diaza-2′-deoxyadenosine forms strong base pairs with 2′-deoxyguanosine and weaker ones with 2′-deoxythymidine in duplex DNA (Seela *et al.*, 2004). We now report the single-crystal X-ray structure of the ribonucleoside 7-deaza-2,8-diazaadenosine, (I).

The title nucleoside was synthesized from 8-aza-7-deazaadenosine, (II), *via* its 1,N^6-etheno derivative (Lin *et al.*, 2005) (purine numbering is used throughout this manuscript). The structure of compound (I) is depicted in Fig. 1 and selected geometric parameters are shown in Table 1.

The N-glycosylic bond torsion angle χ (O4′—C1′—N9—C4) of (I), which describes the orientation of the base relative to the sugar moiety, shows a high *anti* conformation [χ = −83.2 (3)°] (IUPAC–IUB Joint Commission on Biochemical Nomenclature, 1983). The glycosylic bond conformation of compound (II) is also high *anti* [χ = −77.6 (3)° for C4—N9—C1′—O4′; 102.4(C8—N9—C1′—O4′)–180°; Sprang *et al.*, 1978]. In contrast, 2-azaadenosine, (III), and adenosine, (IV), adopt the *anti* conformation, with χ = −166.2 and −171.1°, respectively (Singh & Hodgson, 1979; Lai & Marsh, 1972). Thus, the introduction of an additional N atom in the six-membered ring of the purine nucleoside [(IV)→(III)] or in



the corresponding pyrazolo[3,4-*d*]pyrimidine analogue [(II)→(I)] does not lead to significant changes in the conformation of the glycosylic bond. On the other hand, the shift of the imidazole N atom from position 7 to 8 [(III)→(I) or (IV)→(II)] changes the conformation towards *syn*, as is found for related nucleosides (Sprang *et al.*, 1978; Singh & Hodgson, 1979; Lai & Marsh, 1972). The length of the glycosylic bond (C1′—N9) of (I) is 1.444 (3) Å, which is shorter than those of the nucleosides (II) [1.460 (5) Å], (III) [1.470 (4) Å] or (IV) (1.466 Å) (Sprang *et al.*, 1978; Singh & Hodgson, 1979; Lai & Marsh, 1972).

The sugar moiety of (I) shows a pseudorotation phase angle P of 152.4° and an amplitude τ_m of 35.0°, which indicates *S*-conformation ($^2T_1$) (Altona & Sundaralingam, 1972; Rao *et al.*, 1981). This is similar to compound (II) (P = 141.9°, τ_m = −41.9°, $_1T^2$; Sprang *et al.*, 1978). This *S*-conformation is rather uncommon for ribonucleosides. The conformation of the sugar

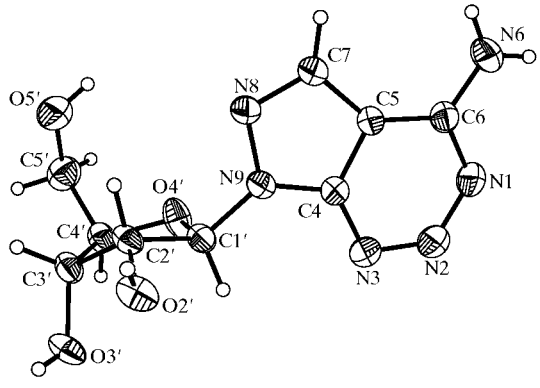


Figure 1
A perspective view of nucleoside (I), showing the atom-numbering scheme. Displacement ellipsoids are drawn at the 50% probability level and H atoms are shown as spheres of small arbitrary size.

 DOI: 10.1107/S010827010601818X

moiety of compounds (III) and (IV) is *N* [$P = 20.8^\circ$, $\tau_m = 39.5^\circ$, $^3T_4$ for (III), and $P = 6.9^\circ$, $\tau_m = 36.8^\circ$, $^3T_2$ for (IV)]. These data are not included in the manuscripts (Singh & Hodgson, 1979; Lai & Marsh, 1972) but are available from the Cambridge Structural Database (CSD, Version 5.27; Allen, 2002). They indicate that the major conformational change results from the alternation of the nitrogen pattern in the five-membered ring (Singh & Hodgson, 1979; Lai & Marsh, 1972). The C3′—C4′—C5′—O5′ torsion angle of compound (I) is 52.0 (3)°, which shows that the exocyclic hydroxyl group prefers a *gauche*,*gauche* (+*sc*) conformation. This is similar to compound (III) ($\gamma = 42.28^\circ$, +*sc*; CSD refcode ZADENH10), but different from compounds (II) ($\gamma = 179.5^\circ$, +*ap*; Sprang *et al.*, 1978) and (IV) ($\gamma = 177.0^\circ$, +*ap*; Lai & Marsh, 1972).

Compound (I) forms a three-dimensional network which is stabilized by several intermolecular hydrogen bonds (listed in Table 2 and shown in Figs. 2 and 3). Whereas hydrogen bonds 1, 2 and 5 (numbers relate to the order of entries in Table 2) lead to double layers perpendicular to the *c* axis (Fig. 2), hydrogen bonds 3 and 4 connect the sugar moieties (O3′—H3′1···O2′) or the sugar moiety with the base (O2′—H2′1···N2) (Fig. 3). The hydrogen-bond acceptor properties of atom N2 have previously been suggested to be involved in the base pairing of 7-deaza-2,8-diaza-2′-deoxyadenosine with 2′-deoxyguanosine within duplex DNA (Seela *et al.*, 2004).

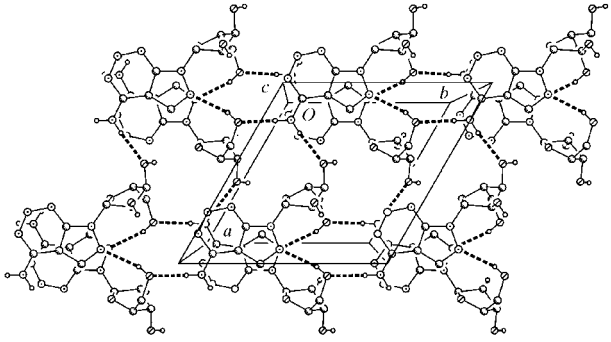


Figure 2
The crystal packing of nucleoside (I), viewed down the *c* axis, showing the layered structure of the crystal. Intermolecular hydrogen bonds 1, 2 and 5 (Table 2) are indicated by dashed lines.

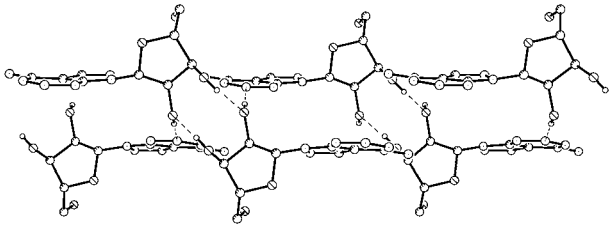


Figure 3
The crystal packing of nucleoside (I), viewed down the *b* axis. Intermolecular hydrogen bonds 3 and 4 (Table 2) are indicated by dashed lines.

Experimental

The title nucleoside was synthesized from 8-aza-7-deazaadenosine, (II), *via* its 1,N^6-etheno derivative (Lin *et al.*, 2005). Compound (I) was recrystallized from water as colourless crystals (m.p. 481–482 K).

Crystal data

$C_9H_{12}N_6O_4$
$M_r = 268.25$
Trigonal, $P3_221$
$a = 9.7859$ (7) Å
$c = 20.3813$ (14) Å
$V = 1690.3$ (2) Å^3
$Z = 6$
$D_x = 1.581$ Mg m^{-3}
Mo $K\alpha$ radiation
$\mu = 0.13$ mm^{-1}
$T = 293$ (2) K
Transparent block, colourless
0.3 × 0.2 × 0.2 mm

Data collection

Siemens *P*4 diffractometer
$2\theta/\omega$ scans
4386 measured reflections
1910 independent reflections
1587 reflections with $I > 2\sigma(I)$
$R_{int} = 0.045$
$\theta_{max} = 30.0^\circ$
3 standard reflections
every 97 reflections
intensity decay: none

Refinement

Refinement on F^2
$R[F^2 > 2\sigma(F^2)] = 0.044$
$wR(F^2) = 0.125$
$S = 1.01$
1910 reflections
175 parameters
H-atom parameters constrained
$w = 1/[\sigma^2(F_o^2) + (0.0781P)^2 + 0.1318P]$ where $P = (F_o^2 + 2F_c^2)/3$
$(\Delta/\sigma)_{max} < 0.001$
$\Delta\rho_{max} = 0.59$ e Å^{-3}
$\Delta\rho_{min} = -0.30$ e Å^{-3}

Table 1
Selected geometric parameters (Å, °).

N1—N2	1.315 (4)	C4—C5	1.387 (3)
N1—C6	1.359 (4)	C6—N6	1.325 (4)
N2—N3	1.323 (3)	C7—N8	1.325 (3)
N3—C4	1.343 (3)	N8—N9	1.374 (3)
C4—N9	1.359 (3)	N9—C1′	1.444 (3)
N2—N1—C6	121.3 (2)	C4—N9—C1′	124.7 (2)
N1—N2—N3	125.2 (2)	N8—N9—C1′	122.7 (2)
N2—N3—C4	114.0 (2)	O4′—C1′—N9	108.42 (18)
N3—C4—N9	125.9 (2)	N9—C1′—C2′	115.19 (19)
C4—N9—N8	110.7 (2)	C1′—O4′—C4′	109.73 (16)
C6—N1—N2—N3	3.8 (4)	N3—C4—N9—C1′	−13.9 (4)
N1—N2—N3—C4	−1.7 (4)	C5—C4—N9—C1′	165.8 (2)
N2—N3—C4—N9	177.0 (2)	C4—N9—C1′—O4′	−83.2 (3)
N2—N3—C4—C5	−2.6 (4)	N8—N9—C1′—O4′	79.6 (3)
N9—C4—C5—C6	−175.3 (2)	O3′—C3′—C4′—O4′	−101.7 (2)
N3—C4—C5—C7	179.3 (2)	C2′—C3′—C4′—C5′	−104.0 (2)
N9—C4—C5—C7	−0.4 (3)	C3′—C4′—C5′—O5′	52.0 (3)
N2—N1—C6—N6	179.8 (3)	N9—C1′—O4′—C4′	−149.78 (19)
C4—C5—C6—N6	176.4 (2)	C2′—C1′—O4′—C4′	−25.6 (2)
C5—C4—N9—N8	1.1 (3)		

Table 2
Hydrogen-bond geometry (Å, °).

D—H···*A*	*D*—H	H···*A*	*D*···*A*	*D*—H···*A*
N6—H6*A*···O5′^{i}	0.86	2.13	2.973 (3)	166
N6—H6*B*···O3′^{ii}	0.86	2.16	2.993 (3)	164
O2′—H2′1···N2^{iii}	0.82	1.91	2.727 (3)	178
O3′—H3′1···O2′^{iv}	0.82	1.99	2.756 (3)	156
O5′—H5′1···N8^{v}	0.82	2.28	3.071 (3)	162

Symmetry codes: (i) $y+1, x+1, -z$; (ii) $x, y+1, z$; (iii) $x-y, -y+1, -z+\frac{1}{3}$; (iv) $x-y, -y, -z+\frac{1}{3}$; (v) $y, x, -z$.

In the absence of suitable anomalous scattering, refinement of the Flack (1983) parameter led to inconclusive values. Therefore, Friedel equivalents were merged before the final refinement. The known configuration of the parent molecule was used to define the enantiomer employed in the refined model. All H atoms were found in a difference Fourier synthesis. In order to maximize the data/parameter ratio, H atoms were placed in geometrically idealized positions (C—H = 0.93–0.98 Å, O—H = 0.82 Å and N—H = 0.86 Å) and constrained to ride on their parent atoms, with U_{iso}(H) = 1.2U_{eq}(C), 1.5U_{eq}(O) or 1.2U_{eq}(N). The OH groups were refined as rigid groups allowed to rotate but not tip.

Data collection: *XSCANS* (Siemens, 1996); cell refinement: *XSCANS*; data reduction: *SHELXTL* (Sheldrick, 1997); program(s) used to solve structure: *SHELXTL*; program(s) used to refine structure: *SHELXTL*; molecular graphics: *SHELXTL*; software used to prepare material for publication: *SHELXTL* and *PLATON* (Spek, 2003).

Supplementary data for this paper are available from the IUCr electronic archives (Reference: JZ3014). Services for accessing these data are described at the back of the journal.

References

Allen, F. H. (2002). *Acta Cryst.* B**58**, 380–388.
Altona, C. & Sundaralingam, M. (1972). *J. Am. Chem. Soc.* **94**, 8205–8212.
Bennett, L. L. J., Allan, P. W., Carpenter, J. W. & Hill, D. L. (1976). *Biochem. Pharmacol.* **25**, 517–521.
Flack, H. D. (1983). *Acta Cryst.* A**39**, 876–881.
IUPAC–IUB Joint Commission on Biochemical Nomenclature (1983). *Eur. J. Biochem.* **131**, 9–15.
Lai, T. F. & Marsh, R. E. (1972). *Acta Cryst.* B**28**, 1982–1989.
Lin, W., Li, H., Ming, X. & Seela, F. (2005). *Org. Biomol. Chem.* **3**, 1714–1718.
Montgomery, J. A., Laseter, A. G., Shortnacy, A. T., Clayton, S. J. & Thomas, H. J. (1975). *J. Med. Chem.* **18**, 564–567.
Montgomery, J. A. & Thomas, H. J. (1972). *J. Med. Chem.* **15**, 182–187.
Rao, S. T., Westhof, E. & Sundaralingam, M. (1981). *Acta Cryst.* A**37**, 421–425.
Seela, F., Lindner, M., Glacon, V. & Lin, W. (2004). *J. Org. Chem.* **69**, 4695–4700.
Sheldrick, G. M. (1997). *SHELXTL*. Release 5.10. Bruker AXS Inc., Madison, Wisconsin, USA.
Siemens (1996). *XSCANS*. Release 2.2. Siemens Analytical X-ray Instruments Inc., Madison, Wisconsin, USA.
Singh, P. & Hodgson, D. J. (1979). *Acta Cryst.* B**35**, 973–976.
Spek, A. L. (2003). *J. Appl. Cryst.* **36**, 7–13.
Sprang, S., Scheller, R., Rohrer, D. & Sundaralingam, M. (1978). *J. Am. Chem. Soc.* **100**, 2867–2872.