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Key indicators

Single-crystal X-ray study

T = 295 K

Mean $\sigma(\text{C}-\text{C}) = 0.006 \text{ \AA}$

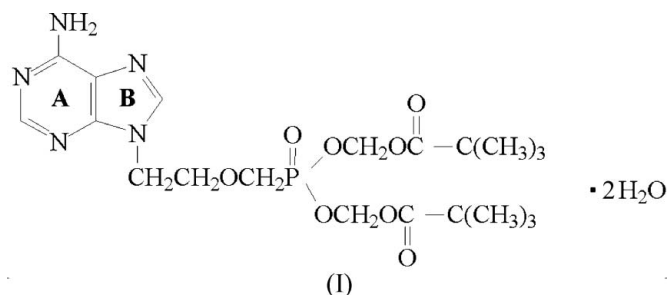
R factor = 0.073

wR factor = 0.146

Data-to-parameter ratio = 14.4

For details of how these key indicators were
automatically derived from the article, see
<http://journals.iucr.org/e>.9-{2-[Bis(pivaloyloxymethoxy)phosphinyl-
methoxy]ethyl}adenine dihydrateIn the title compound, $\text{C}_{20}\text{H}_{32}\text{N}_5\text{O}_8\text{P}\cdot 2\text{H}_2\text{O}$, molecules are
linked to each other *via* intermolecular $\text{N}-\text{H}\cdots\text{O}$, $\text{N}-\text{H}\cdots\text{N}$,
 $\text{O}-\text{H}\cdots\text{O}$ and $\text{O}-\text{H}\cdots\text{N}$ hydrogen bonds with the water
molecules acting as both acceptors and donors.

Comment

9-[2-[Bis(pivaloyloxymethoxy)phosphinylmethoxy]ethyl]ad-
enine (common name adefovir dipivoxil) has been used to
treat adults with chronic hepatitis B (Shepherd *et al.*, 2006).
Recently, we obtained single crystals of the dihydrate of
adefovir dipivoxil, (I), and determined its crystal structure.In (I) (Fig.1), the adenine ring displays the expected planar
conformation. The adefovir dipivoxil molecules are linked by
an intermolecular $\text{N}-\text{H}\cdots\text{N}$ hydrogen bond and by $\text{O}-\text{H}\cdots\text{O}$
and $\text{O}-\text{H}\cdots\text{N}$ hydrogen-bonding interactions involv-
ing the water molecules which act as both acceptors and
donors (Table 1 and Fig. 2).

Experimental

The title compound was synthesized according to Yong *et al.* (2001).
Single crystals of (I) were obtained from an ethanol–chloroform
solution (1:1) after 10 d.

Crystal data

 $\text{C}_{20}\text{H}_{32}\text{N}_5\text{O}_8\text{P}\cdot 2\text{H}_2\text{O}$ $M_r = 537.51$ Triclinic, $P\bar{1}$ $a = 6.0590$ (12) Å $b = 11.221$ (2) Å $c = 20.972$ (4) Å $\alpha = 93.88$ (3) $^\circ$ $\beta = 97.49$ (3) $^\circ$ $\gamma = 102.97$ (3) $^\circ$ $V = 1370.7$ (5) Å^3 $Z = 2$ $D_x = 1.302$ Mg m^{-3} Mo $K\alpha$ radiation $\mu = 0.16$ mm^{-1} $T = 295$ (2) K

Block, colourless

 $0.60 \times 0.40 \times 0.40$ mm

Data collection

MAC DIP 2030K diffractometer

 ω scans

Absorption correction: none

4874 measured reflections

4873 independent reflections

3870 reflections with $I > 2\sigma(I)$ $R_{\text{int}} = 0.048$ $\theta_{\text{max}} = 25.5^\circ$

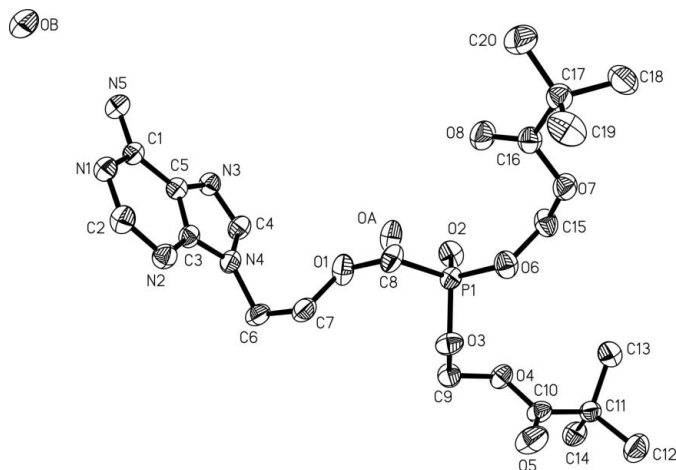


Figure 1
The molecular structure of (I), shown with 30% probability displacement ellipsoids. H atoms have been omitted.

Refinement

Refinement on F^2
 $R[F^2 > 2\sigma(F^2)] = 0.073$
 $wR(F^2) = 0.146$
 $S = 1.01$
 4873 reflections
 338 parameters
 H atoms treated by a mixture of independent and constrained refinement

$w = 1/[\sigma^2(F_o^2) + (0.0129P)^2 + 3.1097P]$
 where $P = (F_o^2 + 2F_c^2)/3$
 $(\Delta/\sigma)_{\max} < 0.001$
 $\Delta\rho_{\max} = 0.26 \text{ e } \text{\AA}^{-3}$
 $\Delta\rho_{\min} = -0.37 \text{ e } \text{\AA}^{-3}$
 Extinction correction: *SHELXL97*
 Extinction coefficient: 0.0088 (10)

Table 1

Hydrogen-bond geometry (\AA , $^\circ$).

$D-H\cdots A$	$D-H$	$H\cdots A$	$D\cdots A$	$D-H\cdots A$
$N5-H5A\cdots OB$	0.86	2.10	2.945 (5)	166
$N5-H5B\cdots N3^i$	0.86	2.18	2.988 (4)	156
$OA-H1A\cdots O2^{ii}$	0.83 (3)	2.008 (19)	2.801 (4)	160 (4)
$OA-H1B\cdots N1$	0.82 (4)	2.12 (3)	2.867 (4)	150 (5)
$OB-H2A\cdots OA^{iii}$	0.83 (3)	2.06 (4)	2.867 (5)	169 (5)
$OB-H2B\cdots OA^{iv}$	0.82 (4)	2.07 (3)	2.882 (5)	174 (6)

Symmetry codes: (i) $-x+2, -y+1, -z+1$; (ii) $x-1, y-1, z$; (iii) $-x+1, -y, -z+1$; (iv) $x+1, y, z$.

The methyl H atoms were placed in calculated positions, with $C-H = 0.96 \text{ \AA}$, allowed to rotate but not tip, and were refined using a riding model, with $U_{\text{iso}}(\text{H}) = 1.5U_{\text{eq}}(\text{C})$. The H atoms on water molecules were placed in idealized positions and their coordinates were refined with $U_{\text{iso}}(\text{H}) = 1.5U_{\text{eq}}(\text{O})$. All other H atoms were placed in geometrically idealized positions, with $C-H = 0.92\text{--}0.98 \text{ \AA}$ and $N-H = 0.86 \text{ \AA}$, and refined in riding mode, with $U_{\text{iso}}(\text{H}) = 1.2U_{\text{eq}}(\text{C}, \text{N})$.

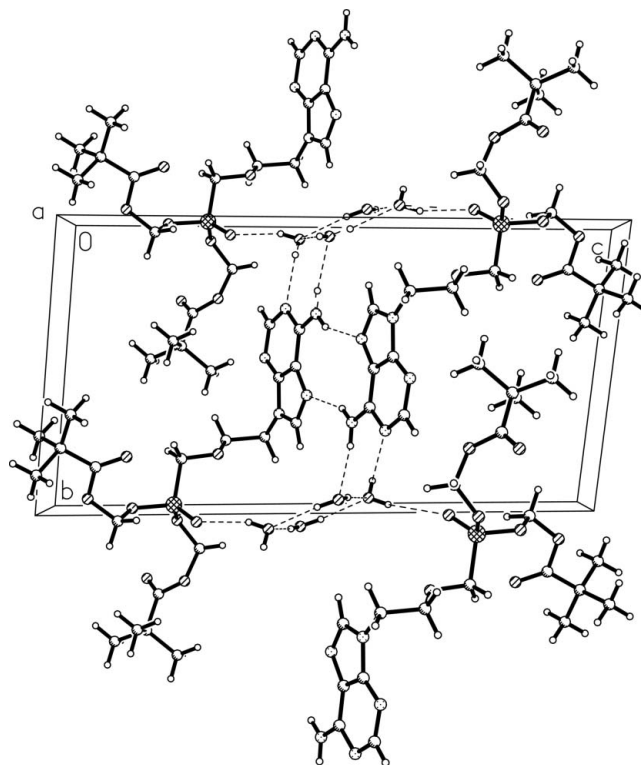


Figure 2
The molecular packing of the title compound, viewed along the b axis. Hydrogen bonds are shown as dashed lines.

Data collection: *DENZO* (Otwinowski & Minor, 1997); cell refinement: *SCALE* (Otwinowski & Minor, 1997); data reduction: *SCALE*; program(s) used to solve structure: *SHELXS97* (Sheldrick, 1997); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *ORTEPII* (Johnson, 1976); software used to prepare material for publication: *SHELXL97*.

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References

- Johnson, C. K. (1976). *ORTEPII*. Report ORNL-5138. Oak Ridge National Laboratory, Tennessee, USA.
- Otwinowski, Z. & Minor, W. (1997). *Methods in Enzymology*, Vol. 276, *Macromolecular Crystallography, Part A*, edited by C. W. Carter Jr & R. M. Sweet, pp. 307–326. New York: Academic Press.
- Sheldrick, G. M. (1997). *SHELXS97* and *SHELXL97*. University of Göttingen, Germany.
- Shepherd, J., Jones, J., Takeda, A., Davidson, P. & Price, A. (2006). *Health Technol. Assess.* **10**, 1–183.
- Yong, Z., Xin, L., Ping, G. & Yu-mei, W. (2001). *J. Shenyang Pharm. Univ.* **18**, 95–97.