

4-Vinylbenzyl analogs of adenine
and uracil: reactive monomers for
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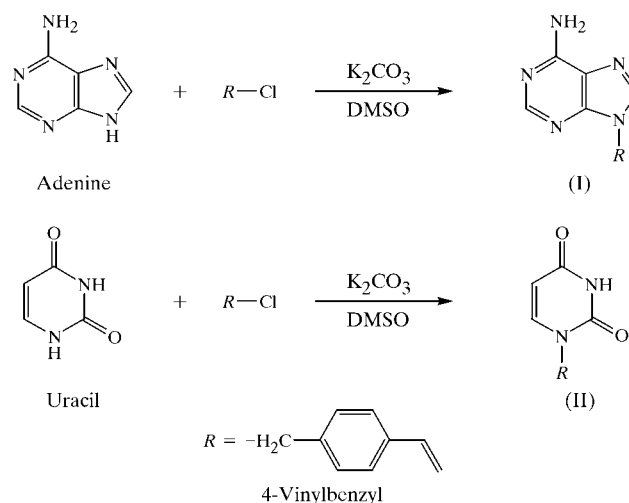
The crystal structures of 9-(4-vinylbenzyl)adenine, C₁₄H₁₃N₅, and 1-(4-vinylbenzyl)uracil, C₁₃H₁₂N₂O₂, are composed of zigzag ribbon-like structures that are stabilized by conventional (N—H···N-type) hydrogen bonds for the former and conventional (N—H···O-type) and non-conventional (C—H···O-type) hydrogen bonds for the latter; the hydrogen-bonding patterns are represented by graph-sets R₂²(9) and R₂²(8), respectively. The adenine and uracil moieties in these alkylated derivatives are planar and are inclined at angles of 84.44 (4) and 79.07 (7)°, respectively, with respect to the phenyl rings.

Comment

Our current research efforts are focused towards developing metallated nucleobase polymeric resins possessing catalytic activity towards phosphate ester hydrolysis (Srivatsan & Verma, 2000, 2001; Madhavaiah *et al.*, 2002). These resins are generally prepared by AIBN-initiated (AIBN is 2,2'-azobisisobutyronitrile) free-radical polymerization of functional monomers, such as 9-allyl adenine, followed by metallation by a copper salt. We have performed extensive kinetic analyses of phosphate ester hydrolysis using copper-metallated nucleobase resins as catalysts and have found significant rate acceleration of hydrolytic reactions over the uncatalyzed rate, using model substrates. We report here two new reactive nucleobase monomers, namely 9-(4-vinylbenzyl)adenine, (I), and 1-(4-vinylbenzyl)uracil, (II), for incorporation in polymeric resins used to design multiple usage catalysts for phosphate ester hydrolysis. X-ray crystallographic studies were performed to establish unequivocally the site of alkylation in each case. The structures of (I) and (II) are presented in this paper.

Compound (I), the vinylated adenine monomer wherein a vinylbenzyl group is substituted at the N9 position of adenine (Fig. 1 and Table 1), utilizes both Watson–Crick and Hoogsteen hydrogen-bonding faces (Saenger, 1984), with the

participation of two exocyclic amino H atoms, with inequivalent H···N distances of 2.11 and 2.20 Å, and almost linear N—H···N angles, resulting in a zigzag chain structure that is stabilized by conventional hydrogen bonds (Fig. 2 and Table 2). The hydrogen-bonding pattern in the polymeric motif can be best described by graph-set R₂²(9) (Etter *et al.*, 1990). The molecular dimensions in (I) are normal and lie within expected ranges for corresponding bond distances and angles (Orpen *et al.*, 1994). The adenine moiety is almost planar [maximum deviation of 0.0260 (10) Å for N19] and is inclined at an angle 84.44 (4)° to the mean plane of the phenyl ring. The vinyl group is almost coplanar with the phenyl ring; the mean planes of the two groups are inclined at an angle of 6.8 (3)° with respect to one another.



In compound (II), wherein alkylation has taken place at the expected N1 position of uracil (Fig. 3 and Table 3), the H atom attached to C5 in the pyrimidine ring acts as a donor, forming a weak hydrogen bond with a carbonyl (O1) acceptor. This O atom behaves as a double acceptor, forming a hydrogen bond with an N—H donor as well, thus aiding in the formation of an extended ribbon-like structure that derives stability from both conventional and non-conventional hydrogen bonds (Fig. 4 and Table 4). The hydrogen-bonding pattern in the polymeric motif of (II) can also be described by graph-set R₂²(8) (Etter *et al.*, 1990). A similar structure has been reported for uracil (Stewart & Jensen, 1967), based on a similar hydrogen-

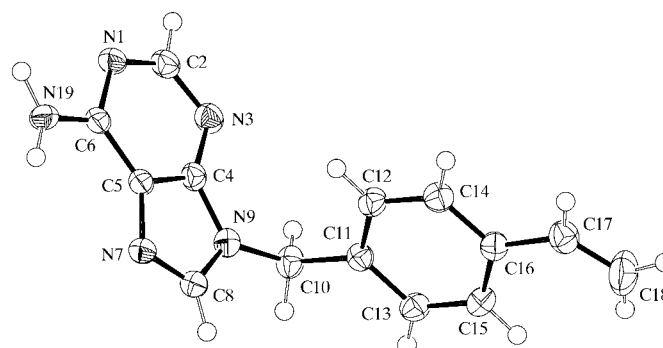


Figure 1
ORTEP (Johnson, 1976) drawing of (I), with displacement ellipsoids plotted at the 50% probability level.

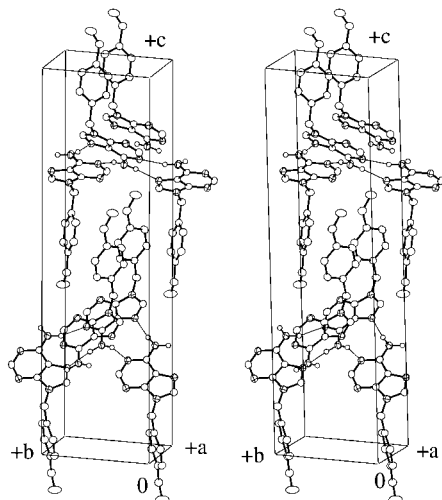


Figure 2
Stereoview of the unit cell of (I) showing the hydrogen-bonded polymeric chains. H atoms attached to C atoms have been omitted for clarity.

bonding pattern. The molecular dimensions in (II) are also normal and lie within expected ranges. The uracil moiety in (II) is essentially planar [maximum deviation of 0.0085 (12) Å] and is oriented at an angle of 79.07 (7)° with respect to the phenyl ring. However, the vinyl group in (II) is not coplanar with the phenyl ring; the mean planes of the two groups are inclined at an angle of 15.4 (3)° with respect to one another.

The formation and co-operativity of hydrogen bonds dictate the structural stability of biological macromolecules such as nucleic acids and proteins (Saenger, 1984). These interactions are responsible for ensuring precise biomolecular recognition and are utilized extensively for the stabilization of protein and ribonucleic acid folding events (Rose & Wolfenden, 1993; Moore, 1999). In recent years, non-conventional hydrogen-bonding interactions have received significant recognition owing to their occurrence in and contribution to the overall stability of biological systems (Wahl & Sundaralingam, 1997; Desiraju & Steiner, 1999). The two reactive nucleobase monomers reported in this paper display both conventional and non-conventional hydrogen bonds in their crystal structures, and these interactions have been invoked to stabilize an extended array of modified nucleobases. We intend to harness

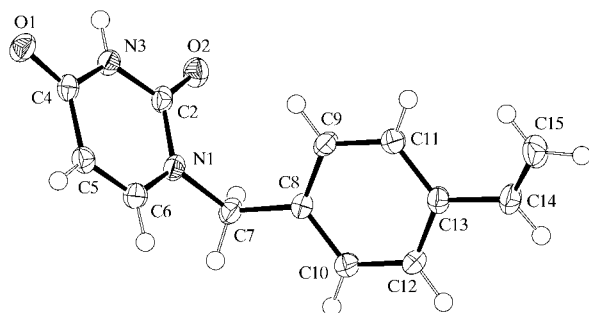


Figure 3
ORTEPII (Johnson, 1976) drawing of (II), with displacement ellipsoids plotted at the 50% probability level.

the observed hydrogen-bonding interactions in (I) and (II) to engineer specificity in our polymeric constructs for enhancing substrate–catalyst recognition.

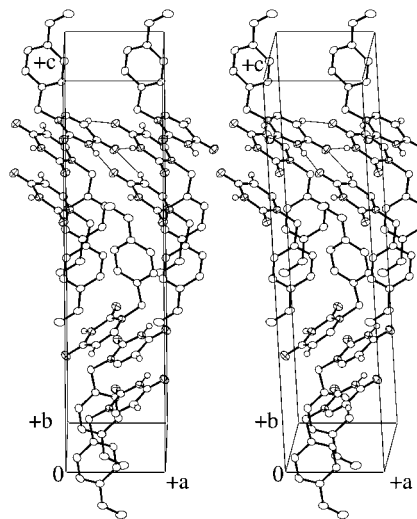


Figure 4
Stereoview of the unit cell of (II) showing the hydrogen-bonding pattern. H atoms not involved in hydrogen bonds have been omitted for clarity.

Experimental

Compounds (I) and (II) were prepared by alkylation of adenine and uracil, respectively, with 4-vinylbenzyl chloride, using anhydrous carbonate in dimethyl sulfoxide (DMSO). These analogs were thoroughly characterized by the usual spectroscopic techniques (Srivatsan & Verma, 2002). Compound (I) was recrystallized from methanol/chloroform (1:1) and compound (II) was recrystallized from methanol. Details of the syntheses and characterization of these derivatives will be reported elsewhere.

Compound (I)

Crystal data

$C_{14}H_{13}N_5$
 $M_r = 251.29$
Orthorhombic, $P2_12_12_1$
 $a = 5.2885$ (1) Å
 $b = 8.1643$ (2) Å
 $c = 28.8446$ (5) Å
 $V = 1245.42$ (4) Å³
 $Z = 4$
 $D_x = 1.340$ Mg m⁻³

Mo $K\alpha$ radiation
Cell parameters from 9411 reflections
 $\theta = 1.0$ – 30.5°
 $\mu = 0.09$ mm⁻¹
 $T = 170$ (2) K
Block, colourless
 $0.25 \times 0.22 \times 0.20$ mm

Data collection

Nonius KappaCCD diffractometer
 ω and φ scans
Absorption correction: multi-scan (SORTAV; Blessing, 1995, 1997)
 $T_{\min} = 0.979$, $T_{\max} = 0.983$
9411 measured reflections
2201 independent reflections

1988 reflections with $I > 2\sigma(I)$
 $R_{\text{int}} = 0.052$
 $\theta_{\text{max}} = 30.5^\circ$
 $h = -6 \rightarrow 7$
 $k = -11 \rightarrow 11$
 $l = -40 \rightarrow 41$
Intensity decay: <0.1%

Refinement

Refinement on F^2
 $R[F^2 > 2\sigma(F^2)] = 0.039$
 $wR(F^2) = 0.111$
 $S = 1.04$
2201 reflections
178 parameters
H-atom parameters constrained

$w = 1/[\sigma^2(F_o^2) + (0.0774P)^2 + 0.0463P]$
where $P = (F_o^2 + 2F_c^2)/3$
 $(\Delta/\sigma)_{\text{max}} < 0.001$
 $\Delta\rho_{\text{max}} = 0.27$ e Å⁻³
 $\Delta\rho_{\text{min}} = -0.22$ e Å⁻³

Table 1
Selected geometric parameters (Å, °) for (I).

N1—C2	1.343 (2)	C5—N7	1.3909 (18)
N1—C6	1.3550 (17)	C6—N19	1.330 (2)
C2—N3	1.327 (2)	C8—N9	1.3648 (19)
N3—C4	1.3494 (18)	N9—C10	1.4608 (19)
C4—N9	1.3720 (19)	C17—C18	1.304 (3)
C2—N1—C6	119.13 (13)	C8—N9—C4	106.02 (12)
C2—N3—C4	110.13 (13)	C8—N9—C10	127.31 (13)
C8—N7—C5	103.86 (13)	C4—N9—C10	126.38 (13)

Table 2
Hydrogen-bonding geometry (Å, °) for (I).

<i>D</i> —H... <i>A</i>	<i>D</i> —H	H... <i>A</i>	<i>D</i> ... <i>A</i>	<i>D</i> —H... <i>A</i>
N19—H19 <i>A</i> ...N7 ⁱ	0.97 (2)	2.07 (2)	3.0351 (19)	174 (2)
N19—H19 <i>B</i> ...N1 ⁱⁱ	0.96 (2)	2.01 (2)	2.9242 (19)	159 (2)

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

Compound (II)

Crystal data

$C_{13}H_{12}N_2O_2$
 $M_r = 228.25$
 Orthorhombic, $P2_12_12_1$
 $a = 5.9603$ (2) Å
 $b = 7.0132$ (2) Å
 $c = 25.9571$ (9) Å
 $V = 1085.03$ (6) Å³
 $Z = 4$
 $D_x = 1.395$ Mg m⁻³

Mo $K\alpha$ radiation
 Cell parameters from 6507 reflections
 $\theta = 1.0$ – 30.6°
 $\mu = 0.10$ mm⁻¹
 $T = 170$ (2) K
 Prism, colourless
 $0.18 \times 0.15 \times 0.14$ mm

Data collection

Nonius KappaCCD diffractometer
 ω and φ scans
 Absorption correction: multi-scan (SORTAV; Blessing, 1995, 1997)
 $T_{\min} = 0.983$, $T_{\max} = 0.986$
 6507 measured reflections
 1901 independent reflections
 1525 reflections with $I > 2\sigma(I)$
 $R_{\text{int}} = 0.098$
 $\theta_{\text{max}} = 30.6^\circ$
 $h = -8 \rightarrow 8$
 $k = -5 \rightarrow 10$
 $l = -35 \rightarrow 37$
 Intensity decay: $<0.1\%$

Refinement

Refinement on F^2
 $R[F^2 > 2\sigma(F^2)] = 0.054$
 $wR(F^2) = 0.135$
 $S = 1.00$
 1901 reflections
 154 parameters
 H-atom parameters constrained
 $w = 1/[\sigma^2(F_o^2) + (0.0658P)^2 + 0.3792P]$
 where $P = (F_o^2 + 2F_c^2)/3$
 $(\Delta/\sigma)_{\text{max}} < 0.001$
 $\Delta\rho_{\text{max}} = 0.31$ e Å⁻³
 $\Delta\rho_{\text{min}} = -0.32$ e Å⁻³

Table 3
Selected geometric parameters (Å, °) for (II).

O1—C4	1.243 (3)	N1—C7	1.472 (3)
O2—C2	1.218 (3)	N3—C4	1.381 (3)
N1—C6	1.377 (3)	C14—C15	1.324 (4)
N1—C2	1.382 (3)		
C6—N1—C2	121.47 (19)	C2—N1—C7	118.9 (2)
C6—N1—C7	119.7 (2)	C4—N3—C2	126.7 (2)

Table 4
Hydrogen-bonding geometry (Å, °) for (II).

<i>D</i> —H... <i>A</i>	<i>D</i> —H	H... <i>A</i>	<i>D</i> ... <i>A</i>	<i>D</i> —H... <i>A</i>
N3—H3...O1 ⁱ	0.88	1.91	2.788 (3)	178
C5—H5...O1 ⁱⁱ	0.95	2.44	3.296 (3)	150

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

In (I) and (II), most of the H atoms were visible in difference Fourier syntheses and all were included in the refinements at geometrically idealized positions, with C—H distances in the range 0.95–0.99 Å and N—H distances of 0.88 Å, utilizing riding models; H atoms attached to N19 in (I) were allowed to refine. H atoms were given U_{iso} values 1.2 times the equivalent isotropic displacement parameters of the atoms to which they were bonded. The absolute structures could not be determined in this analysis.

For both compounds, data collection: COLLECT (Hooft, 1998); cell refinement: HKL DENZO (Otwinowski & Minor, 1997); data reduction: SCALEPACK (Otwinowski & Minor, 1997); program(s) used to solve structure: SAPI91 (Fan, 1991); 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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Supplementary data for this paper are available from the IUCr electronic archives (Reference: FR1366). Services for accessing these data are described at the back of the journal.

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