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A Highly Propeller-Twisted Adenine–Adenine Base Pair in 8-*tert*-Butyladenine

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Abstract. $C_9H_{13}N_5$, $M_r = 191{\cdot}24$, monoclinic, $P2_1/c$, $a = 7{\cdot}562\,(1)$, $b = 6{\cdot}825\,(1)$, $c = 20{\cdot}905\,(1)$ Å, $\beta = 104{\cdot}84\,(1)°$, $V = 1042{\cdot}9$ Å^3, $Z = 4$, room temperature, $D_x = 1{\cdot}218$ g cm^{-3}, λ(Cu $K\alpha$) = 1·5418 Å, $\mu = 6{\cdot}6$ cm^{-1}, $F(000) = 408$. The structure was solved by the multisolution technique and refined by the block-diagonal least-squares method to a final R index of 0·045 using 1970 intensities. The adenine bases form three pairs of hydrogen bonds to symmetry-related molecules in the crystal lattice. Two distinct modes of hydrogen bonding are observed. One mode involves a planar interaction between adjacent adenine bases while the second mode is characterized by an unusually high propeller twist angle of 79·3° between the planes through the two participating adenine bases.

Introduction. The crystallographic structure of 8-*tert*-butyladenine was undertaken as part of an ongoing study of nucleic acid constituents. The bulky *tert*-butyl group at the 8 position of the adenine base was expected to interfere with the base stacking normally observed for adenine, thus resulting in new modes of stacking and hydrogen bonding.

Experimental. Crystals were kindly supplied by Dr Norman Kondo. A single crystal of dimensions 0·4 × 0·25 × 0·08 mm was selected for the structure determination. Data were collected on a CAD-4 diffractometer using Ni-filtered Cu $K\alpha$ radiation with $\omega/2\theta$ scans. Lattice parameters determined from 25 centered reflections in the range $30 < 2\theta < 100°$. 3350 reflections were measured with index range $h = 0$ to 9, $k = 0$ to 8, $l = -26$ to 25 up to a maximum 2θ of 154°. 1143 reflections were measured twice and averaged; discrepancy from the mean is 0·013 defined as $\sum|F_1 - F_2|/\sum(F_1 + F_2)$, where F_1 and F_2 are the two observed structure-factor magnitudes for each unique intensity. Out of 2207 independent reflections, 1656 reflections with $I/\sigma(I) > 1{\cdot}5$ were used for the structure analysis. An empirical absorption correction (maximum correction of 20%) was applied as well as corrections for decay, Lorentz and polarization effects. The structure was solved by *MULTAN* (Main, Germain & Woolfson, 1970), with the phase set having the highest figure of merit yielding all non-H atoms. All H atoms were found from difference Fourier maps. The structure was refined using anisotropic temperature factors for the non-H atoms and isotropic temperature factors for the H atoms by block-diagonal least squares to minimize the differences between F_o and F_c. Six low-angle reflections were removed from the final rounds of refinement due to severe secondary extinction. $R = 0{\cdot}045$, $wR = 0{\cdot}070$, $S = 3{\cdot}27$, $\Delta/\sigma = 0{\cdot}08$, $w = 1/[\sigma^2F + (0{\cdot}015F_o)^2]$, and residual electron density between $-0{\cdot}22$ and $0{\cdot}26$ e Å^{-3}. The atomic scattering factors for carbon and nitrogen are from Cromer & Waber (1965) while those for the H atoms are from Stewart, Davidson & Simpson (1965). Calculations were performed on a PDP-11/35 computer using locally developed programs (Rao, Haromy, McAlister & Merritt, unpublished).

Discussion. The atomic coordinates are given in Table 1.† An *ORTEP* (Johnson, 1976) drawing of the structure is given in Fig. 1 showing the atom-numbering scheme and bond lengths for the non-H atoms. Bond angles for non-H atoms are given in Table 2. The molecular geometry agrees well with previously published adenine structures for which the N(1) atom is unprotonated (Taylor & Kennard, 1982). The only significant differences in geometry are found in the vicinity of the substituted C(8) atom. The C(5)—N(7)—C(8) bond angle [104·7 (2)°] is significantly larger than the expected value of 103·9 (2)°, while the N(7)—C(8)—N(9) angle [112·5 (2)°] is significantly smaller than the expected value of 113·8 (2)°.

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† Lists of observed and calculated structure factors and anisotropic thermal parameters for the heavy atoms have been deposited with the British Library Document Supply Centre as Supplementary Publication No. SUP 53428 (9 pp.). Copies may be obtained through The Technical Editor, International Union of Crystallography, 5 Abbey Square, Chester CH1 2HU, England.

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Table 1. *Fractional positional parameters for all atoms of* 8-*tert-butyladenine with e.s.d.'s in parentheses*

$B_{eq} = (4/3)\sum_i\sum_j\beta_{ij}\mathbf{a}_i.\mathbf{a}_j$.

	x	*y*	*z*	B_{eq}/B (Å^2)
N(1)	0·4789 (1)	−0·1526 (2)	0·1493 (1)	3·23 (2)
C(2)	0·3770 (2)	−0·1887 (2)	0·0882 (1)	3·56 (3)
N(3)	0·2257 (2)	−0·0982 (2)	0·0543 (1)	3·31 (2)
C(4)	0·1781 (2)	0·0476 (2)	0·0898 (1)	2·51 (2)
C(5)	0·2738 (2)	0·1056 (2)	0·1528 (1)	2·29 (2)
C(6)	0·4304 (2)	−0·0033 (2)	0·1834 (1)	2·44 (2)
N(6)	0·5324 (2)	−0·0318 (1)	0·2446 (1)	3·16 (2)
N(7)	0·1857 (1)	0·2609 (1)	0·1741 (2)	2·51 (2)
C(8)	0·0404 (2)	0·2932 (2)	0·1252 (1)	2·40 (2)
N(9)	0·0294 (1)	0·1676 (2)	0·0728 (1)	2·75 (2)
C(10)	−0·1084 (2)	0·4407 (2)	0·1252 (1)	2·90 (2)
C(11)	−0·2807 (2)	0·3283 (3)	0·1288 (1)	5·99 (7)
C(12)	−0·1500 (3)	0·5610 (2)	0·0619 (1)	4·55 (4)
C(13)	−0·0472 (3)	0·5760 (3)	0·1849 (1)	6·51 (8)
H(2)	0·416 (2)	−0·298 (2)	0·066 (1)	3·1 (3)
H1(N6)	0·495 (2)	0·129 (2)	0·269 (1)	4·2 (3)
H2(N6)	0·635 (3)	−0·046 (2)	0·265 (1)	5·0 (4)
H(N9)	−0·066 (2)	0·166 (2)	0·036 (1)	4·3 (4)
H1(11)	−0·378 (3)	0·435 (3)	0·131 (1)	5·9 (5)
H2(11)	−0·333 (4)	0·241 (4)	0·087 (1)	10·9 (8)
H3(11)	−0·233 (3)	0·259 (2)	0·178 (1)	6·5 (5)
H1(12)	−0·251 (2)	0·667 (2)	0·065 (1)	4·8 (4)
H2(12)	−0·209 (5)	0·476 (4)	0·014 (1)	11·3 (9)
H3(12)	−0·038 (3)	0·620 (3)	0·053 (1)	6·8 (5)
H1(13)	−0·017 (3)	0·500 (2)	0·228 (1)	7·6 (6)
H2(13)	−0·142 (3)	0·692 (3)	0·183 (1)	7·7 (6)
H3(13)	0·062 (4)	0·646 (4)	0·182 (1)	10·2 (7)

Table 2. *Bond angles* (°) *for* 8-*tert-butyladenine*

The e.s.d. for these angles is 0·2°.

Adenine ring angles		8-*tert*-Butyl-group angles	
N(1)—C(2)—N(3)	129·0	C(10)—C(8)—N(7)	125·9
C(2)—N(3)—C(4)	111·4	C(10)—C(8)—N(9)	121·5
N(3)—C(4)—C(5)	125·9	C(8)—C(10)—C(11)	108·0
N(3)—C(4)—N(9)	128·4	C(8)—C(10)—C(12)	110·4
C(4)—C(5)—C(6)	117·0	C(8)—C(10)—C(13)	109·5
C(5)—C(6)—N(6)	123·6	C(11)—C(10)—C(12)	108·9
C(5)—C(6)—N(1)	118·1	C(11)—C(10)—C(13)	110·3
C(6)—N(1)—C(2)	118·5	C(12)—C(10)—C(13)	109·7
N(1)—C(6)—N(6)	118·3		
C(6)—C(5)—N(7)	132·6		
C(5)—C(4)—N(9)	105·7		
C(4)—C(5)—N(7)	110·3		
C(5)—N(7)—C(8)	104·7		
C(4)—N(9)—C(8)	106·8		
N(7)—C(8)—N(9)	112·5		

The adenine base is nearly planar with an r.m.s deviation of 0·018 Å from a least-squares plane through the nine atoms of the base. There is a small buckle with a dihedral angle of 1·4 (6)° between the least-square planes through the five-membered and through the six-membered rings of the adenine base. The *tert*-butyl group is oriented such that one of the methyl substituents C(13) lies nearly in the plane of the base. This arrangement minimizes the steric contacts between the other two methyl groups and the proton on N(9) of the base.

A packing diagram is shown in Fig. 2. Each *tert*-butyladenine molecule participates in two hydrogen-bonding interactions to each of the three symmetry-related molecules (Table 3, Fig. 3). The strongest hydrogen bonding is between H(N9) and N(3) of symmetry-related pairs of molecules. These hydrogen bonds are symmetric about an inversion center causing both bases to lie on the same plane. The second pair is from H1(N6) to N(1) and N(7) to H2(N6) yielding a hybrid Hoogsteen and Watson–Crick interaction. The two adenine bases in this pair are nearly perpendicular with a dihedral angle of 79·3° (Fig. 4). The third pair of hydrogen bonds is also a hybrid Hoogsteen and Watson–Crick pair, similar to the second, involving a translation-related molecule.

Table 4 lists the propeller twist angles in several published adenine crystal structures showing the hybrid Hoogsten and Watson–Crick self-pairing scheme. The table shows that nonzero propeller twist angles are found for the majority of the adenine self pairs, with *tert*-butyladenine showing a much larger twist than any of the other structures. In addition, *tert*-butyladenine is the only case for which the N(6)—N(1) hydrogen bond is shorter than the N(6)—N(7) bond.

The unusually large propeller twist is encountered because of the steric interactions between the *tert*-butyl group and the adjacent adenine bases (Fig. 2). The *tert*-butyl group stacks over the six-membered ring of the adenine bases as shown in Fig. 5. The closest stacking distance [3·533 (2) Å] is that between the C(11) methyl group and C(6); the C(12) methyl group is stacked over a second adenine with a distance of 3·675 (2) Å; the C(13) methyl group stacks over a third adenine base with a closest distance of 3·600 (2) Å to N(7). The methyl-base-type hydrophobic interactions observed for *tert*-butyladenine may be an important mode of interaction between proteins and nucleic acids.

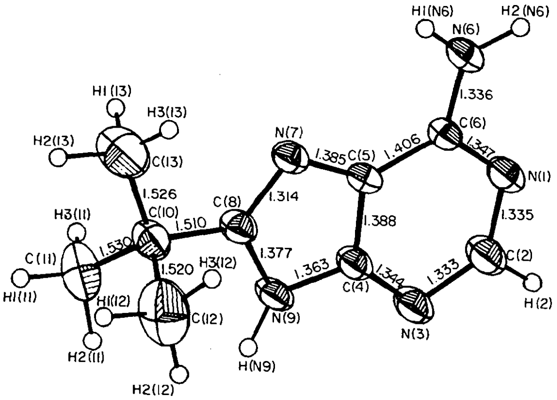

Fig. 1. *ORTEP* plot of 8-*tert*-butyladenine showing 50% probability ellipsoids for the non-H atoms and spheres of arbitrary radius for the H atoms. Atom numbering and bond lengths (Å) for the non-H atoms are shown.

Table 3. *Hydrogen-bonding geometry* (Å, °) *in 8-tert-butyladenine*

A—H···*B*	Symmetry	*A*···*B*	*A*—H	H···*B*	*A*—H···*B*
N(9)—H(N9)···N(3)	$-x, -y, -z$	2·895 (2)	0·91 (2)	2·02 (2)	162 (2)
N(6)—H1(N6)···N(1)	$1-x, 0·5+y, 0·5-z$	3·109 (2)	0·92 (2)	2·24 (2)	157 (2)
N(6)—H2(N6)···N(7)	$1-x, y-0·5, 0·5-z$	2·999 (2)	0·95 (2)	2·08 (2)	164 (2)

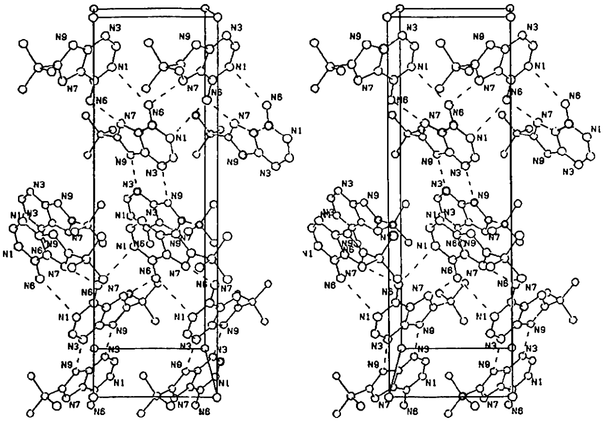

Fig. 2. Stereo packing diagram of 8-*tert*-butyladenine showing base pairing. Hydrogen bonds are indicated by dashed lines.

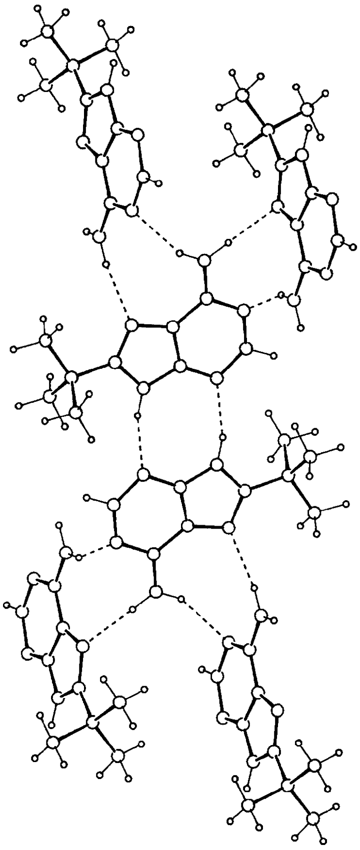

Fig. 3. Hydrogen-bonding scheme. The planar base pair is shown in the center. Two propeller-twisted base pairs are shown at the top and bottom. Note that hydrogen bonds connect each base to three neighbours in the crystal structure.

Table 4. *Propeller twist and hydrogen bonding in hybrid Hoogsteen and Watson–Crick adenine base pairs* (Å, °)

Molecule	N(6)···N(1)	N(6)···N(7)	Propeller twist	Reference
8-*tert*-Butyladenine	3·109 (2)	2·999 (2)	79·3	This work
2′,3′-*O*-Isopropylideneadenosine				Sprang, Roher & Sundaralingam (1978)
Type I	2·864 (8)	3·097 (8)	27·6	
Type II	2·890 (8)	3·046 (8)	27·6	
9-[3-(3-Indolyl)propyl]adenine	2·966 (5)	2·076 (6)	32·8	Bunick & Voet (1982)
9-Methyladenine	2·96 (1)	3·06 (1)	16·2	Stewart & Jensen (1964)
9-Ethyladenine	2·99 (1)	3·01 (1)	25·2	Kaneda & Tanaka (1976)
Deoxyadenosine	2·88 (1)	3·03 (1)	33·1	Watson, Sutor & Tollin (1965)
2-*O*-Methyladenosine				Prusiner & Sundaralingam (1976)
Type I	2·95 (1)	3·00 (1)	0·0	
Type II	2·99 (1)	2·99 (1)	29·9	
Average	2·96 (7)	3·03 (4)	30 (20)	

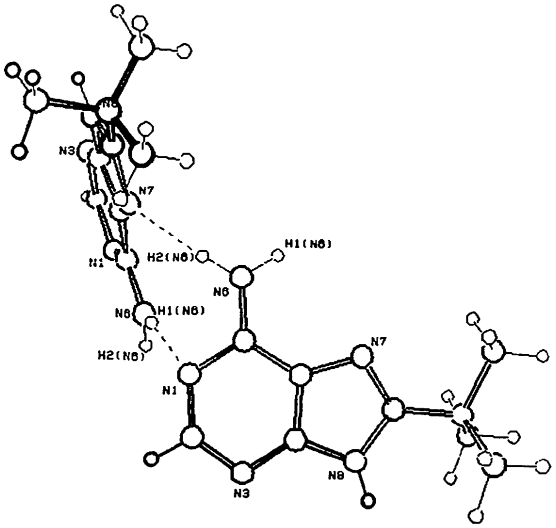

Fig. 4. An isolated propeller-twisted base pair showing the nearly perpendicular propeller twist of 8-*tert*-butyladenine.

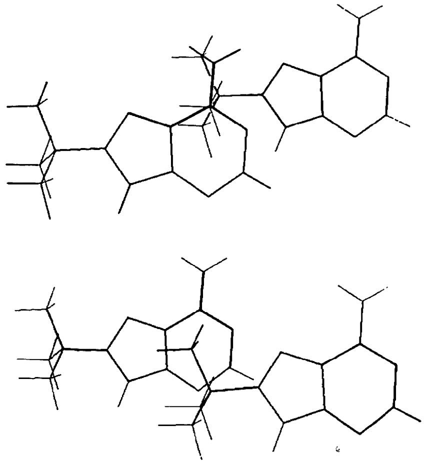

Fig. 5. Stacking interactions between the methyl groups on the *tert*-butyl substituent and symmetry-related adenine bases.

Watson–Crick base pairs have been found with propeller twist angles of up to 25° in double-helical DNA (Drew & Dickerson, 1981), and in tRNA^{phe} (Westhof & Sundaralingam, 1986). The purine–purine G(26)–A(44) base pair in tNRA has been found to exhibit a larger twist angle of about 35°. The present structure, which is an example of a purine–purine self pair, shows a twist angle considerably greater than any previously observed. The weaker hydrogen-bonding interactions inherent to the non-Watson–Crick base pairs probably permit the higher propeller twist angles. Large twist angles may also be encountered for Watson–Crick base pairs when normal stacking interactions are disrupted, for example during transitions between right- and left-handed helices.

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Crystal Studies of Musk Compounds. III. Structures of 6-Acetyl-1,1,2,3,3,5-hexamethylindan (Musk Phantolid) (I) and 6-Acetyl-3-isopropyl-1,1,3,5-tetramethylindan (II)

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Abstract. (I), $C_{17}H_{24}O$, $M_r = 244{\cdot}38$, monoclinic, $P2_1/c$, $a = 10{\cdot}3130\,(7)$, $b = 14{\cdot}292\,(2)$, $c = 10{\cdot}6086\,(8)$ Å, $\beta = 99{\cdot}135\,(7)°$, $V = 1543{\cdot}8\,(3)$ Å^3, $Z = 4$, $D_x = 1{\cdot}05$ Mg m^{-3}, $\lambda(\mathrm{Cu}\ K\alpha) = 1{\cdot}5418$ Å, $\mu = 0{\cdot}451$ mm^{-1}, $F(000) = 536$, room temperature, final $R = 0{\cdot}056$ for 1684 observed reflections. (II), $C_{18}H_{26}O$, $M_r = 258{\cdot}40$, orthorhombic, $Pbca$, $a = 10{\cdot}313\,(1)$, $b = 11{\cdot}049\,(2)$, $c = 28{\cdot}024\,(5)$ Å, $V = 3193{\cdot}3\,(9)$ Å^3, $Z = 8$, $D_x = 1{\cdot}07$ Mg m^{-3}, $\lambda(\mathrm{Cu}\ K\alpha) = 1{\cdot}5418$ Å, $\mu = 0{\cdot}457$ mm^{-1}, $F(000) = 1136$, room temperature, final $R = 0{\cdot}044$ for 2211 observed reflections. The aromatic ring is essentially planar in both compounds, whereas the conformation of the five-membered ring is an almost ideal C(2) envelope in (I) but is a distorted C(2) envelope in (II). The orientation of the acetyl group relative to the aromatic ring is different in (I) and (II). The geometry of the common non-H atoms is compared.

Introduction. This paper is the third in a series dealing with musk compounds [(I) and (II): De Ridder, Goubitz & Schenk (1990*a*,*b*)]. Most known synthetic aromatic musks may be classified by structure into two families according to whether they contain nitro groups (nitromusks) or not. Benzenes, indans and tetralins occur in both families but the non-nitromusks also include hydrindacene and hydrindacenone, naphthindan and naphthindanone, isochroman, coumarin and polycyclic derivatives. During the last few years, the search for new musk

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