Acta Crystallographica Section E Structure Reports Online

ISSN 1600-5368

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Key indicators

Single-crystal X-ray study T = 294 K Mean σ (C–C) = 0.004 Å R factor = 0.053 wR factor = 0.145 Data-to-parameter ratio = 16.4

For details of how these key indicators were automatically derived from the article, see http://journals.iucr.org/e.

tert-Butyl 3-phenylcarbazate

In the molecule of the title compound, $C_{11}H_{16}N_2O_2$, the amide unit has the usual *trans* conformation. In the crystal structure, intermolecular $N-H \cdots O$ hydrogen bonds link the molecules, forming infinite chains. Acylhydrazines are an important synthon used to construct hydrogen-bond networks. Received 14 September 2006 Accepted 21 September 2006

Comment

We report here the molecular structure (Fig. 1) of the title compound, (I). The coordination of atom N2 is almost planar, while that of N1 is markedly pyramidal, similar to that reported by Wardell *et al.* (2006). Atom N1 is at a distance of 0.101 (6)Å from the plane of the phenyl ring, and thus it is nearly coplanar. The four atoms of the carbazate, N2/C7/O1/O2, are essentially coplanar. The C1-N1 [1.399 (4)-Å] and C7-N2 [1.340 (3)-Å] bond lengths are within the ranges of normal C-N single (1.47-1.50-Å) and double (1.34-1.38-Å) bonds (Allen *et al.*, 1987), which indicates that atoms N1 and N2 are conjugated with the aryl plane and carbonyl group, respectively. Based on the relative torsion angles, the amide unit has the usual *trans*-planar conformation (Table 1).



As can be seen from the packing diagram (Fig. 2), intermolecular $N-H\cdots O$ hydrogen bonds (Table 2) link the molecules, forming infinite chains which may be effective in the stabilization of the crystal structure. Dipole–dipole and van der Waals interactions are also effective in the molecular packing.

Experimental

The title compound was prepared from di-*tert*-butyl dicarbonate and phenylhydrazine by the method of Kisseljova *et al.* (2006) (yield 90%, m.p. 362-363 K). Suitable single crystals were grown from an ethyl acetate–*n*-hexane (1:3) solution.

Crystal data

 $C_{11}H_{16}N_2O_2$ $M_r = 208.26$ Monoclinic, $P2_1/c$ a = 10.236 (4) Å b = 13.662 (6) Å c = 8.628 (3) Å $\beta = 101.814$ (7)° V = 1180.9 (8) Å³ Z = 4 $D_x = 1.171 \text{ Mg m}^{-3}$ Mo K\alpha radiation $\mu = 0.08 \text{ mm}^{-1}$ T = 294 (2) KBlock, colourless $0.20 \times 0.14 \times 0.10 \text{ mm}$

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Data collection

Bruker SMART CCD area-detector diffractometer φ and ω scans Absorption correction: multi-scan (*SADABS*; Sheldrick, 1996) $T_{\min} = 0.984$, $T_{\max} = 0.992$

Refinement

Refinement on F^2 $R[F^2 > 2\sigma(F^2)] = 0.053$ $wR(F^2) = 0.145$ S = 1.032400 reflections 146 parameters H atoms treated by a mixture of independent and constrained refinement

Table 1

Selected geometric parameters (Å, $^{\circ}$).

O1-C7	1.204 (3)	N1-N2	1.389 (3
O2-C7	1.343 (3)	N1-C1	1.399 (4
O2-C8	1.471 (3)	N2-C7	1.340 (3
N2-N1-C1	118.4 (3)	O1-C7-N2	125.5 (2)
C7-N2-N1	122.2 (2)	N2-C7-O2	108.9 (2
C1-N1-N2-C7	94.2 (3)	N1-N2-C7-O2	173.2 (3
N1-N2-C7-O1	-6.2 (5)		

6439 measured reflections

 $R_{\rm int} = 0.068$

 $\theta_{\rm max} = 26.5^{\circ}$

2400 independent reflections

 $w = 1/[\sigma^2(F_0^2) + (0.0463P)^2]$

Extinction correction: SHELXL97

Extinction coefficient: 0.011 (2)

+ 0.1989P] where $P = (F_0^2 + 2F_c^2)/3$

 $\Delta \rho_{\rm min} = -0.14 \text{ e } \text{\AA}^{-3}$

 $(\Delta/\sigma)_{\rm max} = 0.004$ $\Delta\rho_{\rm max} = 0.15 \text{ e} \text{ Å}^{-3}$

1102 reflections with $I > 2\sigma(I)$

Table 2

Hydrogen-bond geometry (Å, °).

$D - H \cdots A$	D-H	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - H \cdots A$
$\begin{array}{c} N2 {-} H2 {\cdot} {\cdot} {\cdot} O1^i \\ N1 {-} H1 {\cdot} {\cdot} {\cdot} O2^{ii} \end{array}$	0.85 (3) 0.85 (3)	2.05 (3) 2.40 (3)	2.900 (3) 3.237 (3)	171 (3) 167 (3)
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Symmetry codes: (i) $x, -y + \frac{1}{2}, z + \frac{1}{2}$; (ii) $x, -y + \frac{1}{2}, z - \frac{1}{2}$.

The N-bound H atoms were refined freely, with both N–H = 0.85 (3)Å, while the other H atoms were positioned geometrically, with C–H = 0.93 and 0.96Å for aromatic and methyl H atoms, respectively, and were constrained to ride on their parent atoms, with $U_{iso}(H) = xU_{eq}(C,N)$, where x = 1.5 for methyl and x = 1.2 for all other H atoms.

Data collection: *SMART* (Bruker, 1997); cell refinement: *SAINT* (Bruker, 1997); data reduction: *SAINT*; program(s) used to solve structure: *SHELXS97* (Sheldrick, 1997); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics:



Figure 1

The molecular structure of (I), with the atom-numbering scheme. Displacement ellipsoids are drawn at the 30% probability level.



Figure 2

A packing diagram for (I). Hydrogen bonds are shown as dashed lines.

SHELXTL (Bruker, 1997); software used to prepare material for publication: SHELXTL.

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