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Key indicators

Single-crystal X-ray study T = 296 KMean $\sigma(\text{C}-\text{C}) = 0.003 \text{ Å}$ R factor = 0.041 wR factor = 0.103 Data-to-parameter ratio = 14.5

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

2-(1*H*-1,2,3-Benzotriazol-1-yl)-1-benzoylethyl 2,4-dichlorobenzoate

In the crystal structure of the title compound, $C_{22}H_{15}Cl_2N_3O_3$, molecules are linked into dimers by $C-H\cdots O$ intermolecular hydrogen bonds. The packing is further stabilized by $\pi-\pi$ interactions.

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Comment

We have recently reported the structure of 2-(1H-1,2,3-benzotriazol-1-ylmethyl)-1-benzoylethyl 4-ethylbenzoate, (II) (Wan, Peng*et al.*, 2005). As part of our ongoing studies, the title compound, (I), was synthesized and its structure is presented here.



The bond lengths and angles (Table 1) in (I) are within normal ranges (Allen *et al.*, 1987) and are comparable with the corresponding ones in (II).



© 2006 International Union of Crystallography All rights reserved The molecular structure of (I), with the atom-numbering scheme. Displacement ellipsoids are drawn at the 50% probalitity level.

organic papers

In (I), the benzotriazole system is almost planar, with a dihedral angle of 1.52 (8)° between triazole ring *A* (N1–N3/C10/C15) and benzene ring *B* (C10–C15). The dihedral angles between the mean planes of the benzotriazole system and rings *C* (C1–C6) and *D* (C17–C22) are 43.82 (8) and 6.47 (8)°, respectively. The dihedral angle between rings *C* and *D* is 38.96 (9)°.

In the crystal structure, molecules of (I) are linked into dimers by C-H···O hydrogen bonds (Table 2 and Fig. 2). The packing is further stabilized by π - π interactions between ring D at (x, y, z) and ring D at (-x, -y, 1-z), with a distance of 3.721 (2) Å between the centroids of the two rings.

Experimental

The title compound was prepared according to the literature method of Wan, Li *et al.* (2005). Single crystals suitable for X-ray measurements were obtained by slow evaporation of an acetone/petroleum ether (1:1) (yield 4.0 g, 46%; m.p. 443.5–444.3 K).

Crystal data

C ₂₂ H ₁₅ Cl ₂ N ₃ O ₃	$D_{\rm r} = 1.460 {\rm Mg} {\rm m}^{-3}$
$M_r = 440.27$	Mo $K\alpha$ radiation
Monoclinic, $P2_1/c$	Cell parameters from 3057
$a = 9.1235 (12) \text{\AA}$	reflections
b = 9.4228 (12) Å	$\theta = 2.2-23.6^{\circ}$
c = 23.307 (3) Å	$\mu = 0.35 \text{ mm}^{-1}$
$\beta = 90.916 \ (2)^{\circ}$	T = 296 (2) K
V = 2003.4 (4) Å ³	Block, colorless
Z = 4	$0.33 \times 0.17 \times 0.12 \text{ mm}$
Data collection	

Siemens SMART 1000 CCD area-	3943 independent reflections
detector diffractometer	2846 reflections with $I > 2\sigma(I)$
ω scans	$R_{\rm int} = 0.024$
Absorption correction: multi-scan	$\theta_{\rm max} = 26.0^{\circ}$
(SADABS; Sheldrick, 1996)	$h = -10 \rightarrow 11$
$T_{\min} = 0.892, T_{\max} = 0.959$	$k = -11 \rightarrow 7$
11397 measured reflections	$l = -27 \rightarrow 28$

Refinement

Refinement on F^2	$w = 1/[\sigma^2(F_0^2) + (0.0449P)^2]$
$R[F^2 > 2\sigma(F^2)] = 0.041$	+ 0.3548P]
$wR(F^2) = 0.103$	where $P = (F_0^2 + 2F_c^2)/3$
S = 1.02	$(\Delta/\sigma)_{\rm max} = 0.001$
3943 reflections	$\Delta \rho_{\rm max} = 0.20 \text{ e} \text{ Å}^{-3}$
271 parameters	$\Delta \rho_{\rm min} = -0.21 \text{ e } \text{\AA}^{-3}$
H-atom parameters constrained	

Table 1

Selected geometric parameters (Å, °).

Cl1-C18	1.729 (2)	O2-C16	1.351 (2)
Cl2-C20	1.739 (2)	O2-C8	1.435 (2)
O1-C7	1.212 (2)	O3-C16	1.193 (2)
02-C8-C9	107.04 (14)	C9-C8-C7	112.38 (16)
O2-C8-C7	109.34 (15)		





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

$D - H \cdots A$	D-H	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - H \cdots A$
$C21-H21A\cdotsO1^{i}$	0.93	2.46	3.371 (2)	166
Symmetry code: (i) $-x$,	-y - 1, -z +	1.		

H atoms were positioned geometrically, with C-H = 0.93, 0.97 and 0.98 Å for aromatic, methylene and methine H atoms, respectively, and constrained to ride on their parent atoms, with $U_{\rm iso}({\rm H}) = 1.2U_{\rm eq}({\rm C})$.

Data collection: *SMART* (Siemens, 1996); cell refinement: *SAINT* (Siemens, 1996); data reduction: *SAINT*; program(s) used to solve structure: *SHELXTL* (Sheldrick, 1997); program(s) used to refine structure: *SHELXTL*; molecular graphics: *SHELXTL*; software used to prepare material for publication: *SHELXTL*, *PARST* (Nardelli, 1995) and *PLATON* (Spek, 2003).

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