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Key indicators

Single-crystal X-ray study T = 298 K Mean σ (C–C) = 0.003 Å R factor = 0.051 wR factor = 0.139 Data-to-parameter ratio = 17.2

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

A monoclinic modification of *N*-(3,4-dibenzoyl-2,5-dimethylpyrrol-1-yl)-4-methoxybenzamide

The molecule of the title compound, $C_{28}H_{24}N_2O_4$, in the monoclinic modification shows no significant differences in bond dimensions from those in the reported orthorhombic modification [Gao *et al.* (2004). *Acta Cryst.* E**60**, o1733–o1735]. Two molecules are linked across a center of inversion by a pair of amide–carbonyl hydrogen bonds [2.867 (2) Å].

Comment

N-(Dibenzoyldimethylpyrrol-1-yl)-4-methoxybenzamide represents a pyrrole that is severely crowded owing to substituents on all atoms of the five-membered ring. A previous study had documented the compound belonging to the orthorhombic crystal system (Gao *et al.*, 2004). The synthesis, albeit in a slightly different solvent, afforded the monoclinic modification, (I) (Fig. 1). It is not clear whether the two modifications were obtained in the same reaction, or whether the solvent itself governed the crystallization. The principal bond dimensions are not significantly different in the two modifications; the monoclinic modification is marginally denser ($D_x = 1.263 \text{ Mg m}^{-3}$) than the orthorhombic modification ($D_x = 1.250 \text{ Mg m}^{-3}$).



Experimental

Glacial acetic acid (3 ml) was added to an ethanol solution (3 ml) of benzoylacetone (21.1 g, 0.13 mol) and 4-methoxybenzoylhydrazine (16.2 g, 0.10 mol) in the condensation for the α , β -diketone with the hydrazine. The mixture was refluxed for 3 h. The pale yellow title compound was isolated as crystals when the filtered solution was set aside for several days. Analysis calculated for C₂₈H₂₄N₂O₄: C 74.32, H 5.35, N 6.19%; found: C 74.60, H 5.30, N 6.11%. In the previously reported synthesis (Gao *et al.*, 2004), methanol was used as solvent.

Crystal data	
$C_{28}H_{24}N_2O_4$	$D_x = 1.263 \text{ Mg m}^{-3}$
$M_r = 452.49$	Mo $K\alpha$ radiation
Monoclinic, $P2_1/c$	Cell parameters from 20917
a = 15.643 (3) Å	reflections
b = 10.258 (2) Å	$\theta = 3.1-27.5^{\circ}$
c = 16.563 (3) Å	$\mu = 0.09 \text{ mm}^{-1}$
$\beta = 116.49 \ (3)^{\circ}$	T = 298 (2) K
$V = 2378.7 (8) \text{ Å}^3$	Prism, yellow
Z = 4	$0.40 \times 0.27 \times 0.21 \text{ mm}$

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organic papers

Data collection

Rigaku R-AXIS RAPID diffractometer ω scans Absorption correction: multi-scan (*ABSCOR*; Higashi, 1995) $T_{min} = 0.660, T_{max} = 0.982$ 22118 measured reflections

Refinement

Refinement on F^2 $R[F^2 > 2\sigma(F^2)] = 0.051$ $wR(F^2) = 0.139$ S = 1.035414 reflections 314 parameters H atoms treated by a mixture of independent and constrained refinement

Table 1Selected geometric parameters (Å, °).

-			
N1-N2	1.386 (2)	C2-C7	1.468 (2)
N1-C1	1.374 (2)	C3-C4	1.376 (2)
N1-C4	1.376 (2)	C3-C14	1.478 (2)
C2-C3	1.441 (2)	C4-C6	1.486 (2)
C1-N1-C4	112.2 (1)	C3-C2-C7	124.6 (1)
C1-N1-N2	124.7 (1)	C4-C3-C2	107.6 (1)
C4-N1-N2	123.1 (1)	C4-C3-C14	123.9 (1)
N1-C1-C2	106.0(1)	C2-C3-C14	128.5 (1)
N1-C1-C5	120.2 (1)	C3-C4-N1	106.3 (1)
C2-C1-C5	133.3 (1)	C3-C4-C6	132.6 (1)
C1-C2-C3	107.9(1)	N1-C4-C6	121.0 (1)
C1-C2-C7	125.9 (1)		

5414 independent reflections

 $w = 1/[\sigma^2(F_o^2) + (0.0708P)^2]$

+ 0.5812P] where $P = (F_o^2 + 2F_c^2)/3$

 $\Delta \rho_{\rm max} = 0.32 \ {\rm e} \ {\rm \AA}^{-3}$

 $\Delta \rho_{\rm min} = -0.19 \ {\rm e} \ {\rm \AA}^{-3}$

 $(\Delta/\sigma)_{\rm max} = 0.001$

 $R_{\rm int}=0.032$

 $\theta_{\rm max} = 27.5^{\circ}$

 $h = -20 \rightarrow 20$

 $k = -13 \rightarrow 13$

 $l = -20 \rightarrow 21$

4210 reflections with $I > 2\sigma(I)$

H atoms bonded to C atoms were placed in calculated positions $[C-H = 0.93 \text{ Å} \text{ and } U_{iso}(H) = 1.2U_{eq}(C)$ for aromatic H atoms, and C-H = 0.96 Å and $U_{iso}(H) = 1.5U_{eq}(C)$ for methyl H atoms, which were rotated to fit the electron density] and included in the refinement in the riding-model approximation. The amide H atom was refined isotropically.





Data collection: *RAPID-AUTO* (Rigaku, 1998); cell refinement: *RAPID-AUTO*; data reduction: *CrystalStructure* (Rigaku/MSC, 2002); program(s) used to solve structure: *SHELXS*97 (Sheldrick, 1997); program(s) used to refine structure: *SHELXL*97 (Sheldrick, 1997); molecular graphics: *ORTEP*II (Johnson, 1976); software used to prepare material for publication: *SHELXL*97.

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