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Key indicators

Single-crystal X-ray study T = 290 KMean $\sigma(\text{C-C}) = 0.002 \text{ Å}$ R factor = 0.037 wR factor = 0.105 Data-to-parameter ratio = 16.9

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

Dimethyl 3-(*tert*-butylamino)-5-oxo-7-phenyl-1*H*,5*H*-pyrazolo[1,2-*a*]pyrazole-1,2-dicarboxylate

In the title compound, $C_{20}H_{23}N_3O_5$, the molecule contains two pyrazole rings with an interplanar angle of 34.1 (1)°. The phenyl and pyrazolone rings make a dihedral angle of 35.43 (13)° with one another. There is an intramolecular hydrogen bond between the carbonyl O atom in one of the carboxylate groups and the N atom of the *tert*-butylamine substituent of the pyrazole ring. This is the first structure reported of a polyfunctional pyrazolo[1,2-*a*]pyrazole derivative of potential synthetic and pharmaceutical interest.

Comment

The structure of the title compound has been studied because pyrazolo[1,2-a] pyrazoles have been shown to possess useful biological activities (Radl, 1996). We have recently published a facile synthesis of highly functionalized pyrazolo[1,2-a] pyrazoles *via* a one-pot isocyanide-based three-component reaction (Adib *et al.*, 2005), and we now report the structure of the title compound, (I).



The molecular structure of (I) and the atom-numbering scheme are shown in Fig. 1. The phenyl and pyrazolone rings make a dihedral angle of $35.43 (13)^{\circ}$ with one another. An intramolecular hydrogen bond is formed between the carbonyl O atom of the 2-carboxylate (O2) and the N atom of the *tert*-butylamine (N1), giving rise to a slightly puckered sixmembered chelate ring (Table 2). A noticeable degree of conjugation in this chelate ring makes the 2-carboxylate coplanar with the pyrazole ring.

Experimental

Compound (I) was synthesized according to the literature (Adib *et al.*, 2005). Crystals suitable for crystallographic analysis were obtained (yield 0.27 g, 70%) after recrystallization from 1:1 hexane–ethyl acetate.

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Crystal data

 $\begin{array}{l} C_{20}H_{23}N_3O_5 \\ M_r = 385.41 \\ \text{Monoclinic, } P2_1/n \\ a = 12.1826 \ (8) \text{ Å} \\ b = 9.4017 \ (6) \text{ Å} \\ c = 17.1789 \ (12) \text{ Å} \\ \beta = 91.059 \ (6)^\circ \end{array}$

Data collection

Oxford Xcalibur3 CCD diffractometer Absorption correction: numerical (X-RED; Stoe & Cie, 1997) $T_{\rm min} = 0.976, T_{\rm max} = 0.995$

Refinement

$R[F^2 > 2\sigma(F^2)] = 0.037$	254 parameters
$wR(F^2) = 0.105$	H-atom parameters constrained
S = 1.01	$\Delta \rho_{\rm max} = 0.28 \ {\rm e} \ {\rm \AA}^{-3}$
4282 reflections	$\Delta \rho_{\rm min} = -0.20 \text{ e } \text{\AA}^{-3}$

V = 1967.3 (2) Å³

Mo $K\alpha$ radiation

 $0.5 \times 0.2 \times 0.2$ mm

13972 measured reflections

4282 independent reflections

2751 reflections with $I > 2\sigma(I)$

 $\mu = 0.10 \text{ mm}^{-1}$

T = 290 (2) K

 $R_{\rm int} = 0.026$

Z = 4

Table 1

Selected torsion angles (°).

C14-N2-N3-C11	152.35 (10)	C14-N2-N3-C12	2.23 (13)
C9-N2-N3-C11	14.73 (12)	N2-C14-C15-C20	144.47 (13)

Table 2

Hydrogen-bond geometry (Å, °).

$D - H \cdot \cdot \cdot A$	D-H	$H \cdots A$	$D \cdots A$	$D - \mathbf{H} \cdot \cdot \cdot A$
N1-H1···O2	0.86	2.24	2.7910 (14)	122
C6−H6C···O5	0.96	2.37	3.193 (2)	143
C6−H6C···O5	0.96	2.37	3.193 (2)	143
$C7 - H7A \cdots O2^{i}$	0.96	2.59	3.5461 (19)	175
$C8 - H8B \cdots O5$	0.96	2.41	3.225 (2)	142
$C16-H16\cdots O2^{ii}$	0.93	2.51	3.4422 (18)	178
			. ,	

Symmetry codes: (i) -x + 1, -y, -z; (ii) -x + 1, -y + 1, -z.

All H atoms were positioned at calculated positions and constrained to ride on their parent atoms, with C–H = 0.93–0.98 Å, N–H = 0.86 Å, $U_{\rm iso}({\rm H}) = 1.2U_{\rm eq}({\rm C},{\rm N})$ (for CH and NH groups) and $U_{\rm iso}({\rm H}) = 1.5U_{\rm eq}({\rm C})$ (for CH₃).



Figure 1

Molecular structure of (I), showing the atom numbering scheme, with 50% probability displacement ellipsoids. H atoms are shown as circles of arbitrary radius.

Data collection: *CrysAlis CCD* (Oxford Diffraction, 2003); cell refinement: *CrysAlis RED* (Oxford Diffraction, 2003); data reduction: *CrysAlis RED*; program(s) used to solve structure: *SHELXS97* (Sheldrick, 1997); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *DIAMOND* (Brandenburg, 1999); software used to prepare material for publication: *SHELXL97*.

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