

N'-Benzoyl-4*H*-1,2,4-triazole-3-carbohydrazideChang-Hua Ge, Ding-Ben Chen,*
Fu-You Pan, Ling Huang and
Jian-Guo YangDepartment of Chemistry, Taizhou University,
Taizhou 317000, People's Republic of China

Correspondence e-mail: cdb23@163.com

Key indicators

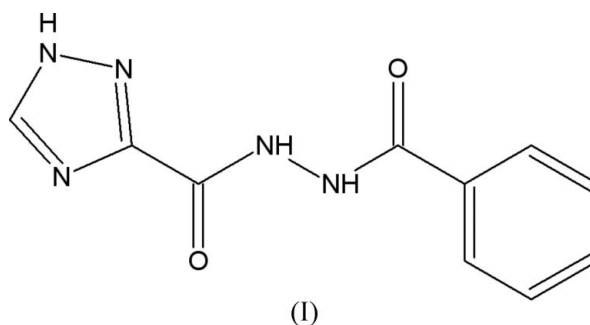
Single-crystal X-ray study
T = 293 K
Mean $\sigma(\text{C}-\text{C}) = 0.003 \text{ \AA}$
R factor = 0.055
wR factor = 0.143
Data-to-parameter ratio = 12.3For details of how these key indicators were
automatically derived from the article, see
<http://journals.iucr.org/e>.

In the crystal structure of the title compound, $\text{C}_{10}\text{H}_9\text{N}_5\text{O}_2$, intermolecular $\text{N}-\text{H}\cdots\text{N}$ [$\text{H}\cdots\text{N} = 2.13(2) \text{ \AA}$] and $\text{N}-\text{H}\cdots\text{O}$ [$\text{H}\cdots\text{O} = 2.016(18)$ and $2.05(2) \text{ \AA}$] hydrogen bonds link molecules into a two-dimensional framework.

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Comment

Recently, compounds containing the 1*H*-1,2,4-triazole group have aroused much interest because of their biological activities, such as fungicidal (Oita & Uchida, 1998), antifungal, antitumoural (Maravalli *et al.*, 2000), antibacterial (Zhou *et al.*, 1998*a*), and plant growth regulating activity (Zhou *et al.*, 1998*b*). In a search for new compounds with bioactivity, we have synthesized triazole compounds derived from 1*H*-1,2,4-triazole-3-carbohydrazide and have recently reported the crystal structures of two such compounds (Chen *et al.*, 2005; Pan & Yang, 2005). We report here the synthesis and crystal structure of *N'*-benzoyl-4*H*-1,2,4-triazole-3-carbohydrazide, (I).



The title compound is shown in Fig. 1 and selected bond lengths and angles are listed in Table 1. The sequence of $\text{C}=\text{O}$, $\text{C}-\text{N}$ and $\text{N}-\text{N}$ bond lengths in the central part of the molecule is consistent with the presence of a conjugated system. The bond distances and angles within the triazole and

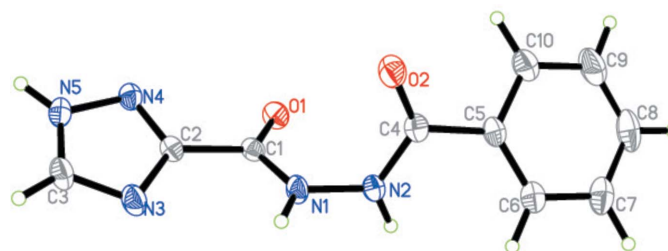


Figure 1
The structure of compound (I), showing 30% probability displacement ellipsoids and the atom-numbering scheme.

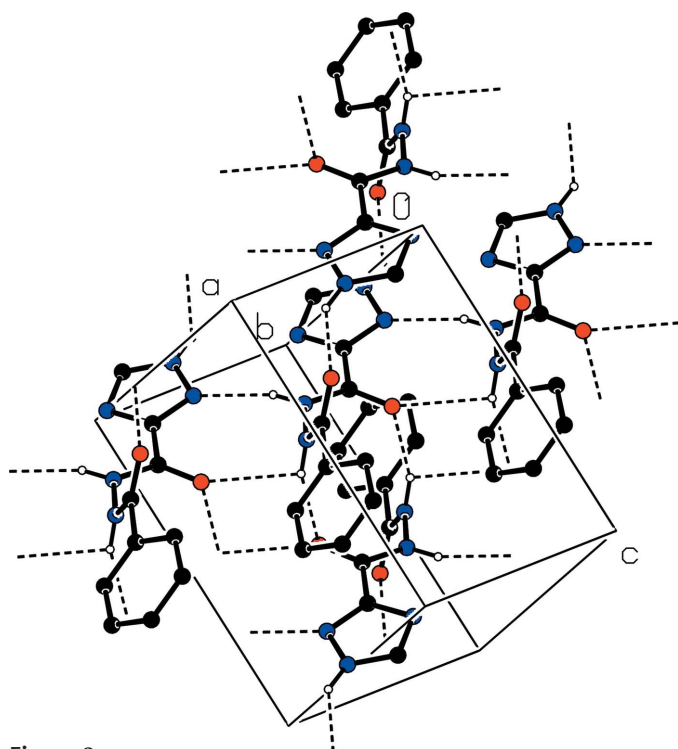


Figure 2
Packing diagram (Spek, 2003) for (I), showing hydrogen bonds as dashed lines. Colour code: red O, blue N and black C. H atoms not involved in hydrogen bonding have been omitted.

phenyl rings are normal and agree with the corresponding values found in 4-phenyl-1-(1*H*-1,2,4-triazole-3-ylcarbonyl)thiosemicarbazide (Chen *et al.*, 2005). The dihedral angle between the triazole and phenyl rings is 29.3 (1)°.

In the crystal structure, intermolecular N—H...N and N—H...O hydrogen bonds link molecules into a two-dimensional framework (Table 2 and Fig. 2).

Experimental

1*H*-1,2,4-Triazole-3-carbohydrazide (0.02 mol, 2.54 g) was dissolved in pyridine (50 ml) and benzoyl chloride (0.02 mol, 2.81 g) was added dropwise to the solution. The mixture was refluxed for 5 h and distilled. A white solid was precipitated by dilution with cold water (100 ml). This product was filtered off, washed with cold water (2 × 30 ml) and recrystallized from ethanol. (yield: 81%; m.p. 521–522 K). IR ν_{\max} (KBr, cm^{-1}): 3310, 3190, 1691.5, 1649.5, 1559.3, 1527.5, 1481.2, 1268.1, 1110.0, 873.7, 722.3, 693.4. ^1H NMR (200 MHz, DMSO): δ 14.62 (1H), 10.40–10.60 (2H), 8.79 (1H), 7.85–7.98 (2H), 7.45–7.70 (3H).

Crystal data

$\text{C}_{10}\text{H}_9\text{N}_5\text{O}_2$
 $M_r = 231.22$
Monoclinic, $P2_1/c$
 $a = 5.3572$ (8) Å
 $b = 21.890$ (3) Å
 $c = 9.2502$ (14) Å
 $\beta = 100.082$ (3)°
 $V = 1068.0$ (3) Å³
 $Z = 4$

$D_x = 1.438$ Mg m⁻³
Mo $K\alpha$ radiation
Cell parameters from 2517 reflections
 $\theta = 5.8$ – 55.9 °
 $\mu = 0.11$ mm⁻¹
 $T = 293$ (2) K
Block, colourless
0.52 × 0.35 × 0.33 mm

Data collection

Siemens SMART CCD area-detector diffractometer
 φ and ω scans
Absorption correction: multi-scan (SADABS; Bruker, 2002)
 $T_{\min} = 0.541$, $T_{\max} = 0.970$
6209 measured reflections

2332 independent reflections
1799 reflections with $I > 2\sigma(I)$
 $R_{\text{int}} = 0.132$
 $\theta_{\max} = 27.0$ °
 $h = -6 \rightarrow 6$
 $k = -23 \rightarrow 27$
 $l = -11 \rightarrow 9$

Refinement

Refinement on F^2
 $R[F^2 > 2\sigma(F^2)] = 0.055$
 $wR(F^2) = 0.143$
 $S = 1.00$
2332 reflections
190 parameters

All H-atom parameters refined
 $w = 1/[\sigma^2(F_o^2) + (0.0736P)^2]$
where $P = (F_o^2 + 2F_c^2)/3$
 $(\Delta/\sigma)_{\max} < 0.001$
 $\Delta\rho_{\max} = 0.34$ e Å⁻³
 $\Delta\rho_{\min} = -0.44$ e Å⁻³

Table 1

Selected geometric parameters (Å, °).

O1—C1	1.2249 (18)	N1—N2	1.3848 (18)
O2—C4	1.2236 (19)	N2—C4	1.346 (2)
N1—C1	1.336 (2)		
C1—N1—N2	118.82 (13)	C4—N2—N1	119.99 (14)

Table 2

Hydrogen-bond geometry (Å, °).

$D-H\cdots A$	$D-H$	$H\cdots A$	$D\cdots A$	$D-H\cdots A$
N5—H5...O2 ⁱ	0.88 (2)	2.02 (2)	2.7681 (18)	142 (2)
N2—H2...O1 ⁱⁱ	0.91 (2)	2.05 (2)	2.9019 (18)	156 (2)
N1—H1...N4 ⁱⁱⁱ	0.87 (2)	2.13 (2)	2.984 (2)	164 (2)

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

All H atoms were refined independently with isotropic displacement parameters. The higher than normal R_{int} value of 0.13 may reflect the poor quality of the data and in turn the lowered precision of the structure.

Data collection: SMART (Bruker, 2002); cell refinement: SAINT (Bruker, 2002); data reduction: SAINT; program(s) used to solve structure: SHELXTL (Bruker, (2002)); program(s) used to refine structure: SHELXTL; molecular graphics: SHELXTL and PLATON (Spek, 2003); software used to prepare material for publication: SHELXTL.

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