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Key indicators

Single-crystal X-ray study T = 295 KMean $\sigma(\text{C}-\text{C}) = 0.006 \text{ Å}$ R factor = 0.062 wR factor = 0.151 Data-to-parameter ratio = 13.5

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

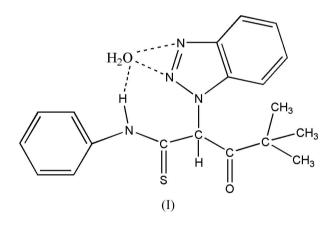
2-(1*H*-Benzo-1,2,3-triazol-1-yl)-4,4-dimethyl-3-oxo-*N*-phenylpentanethioamide monohydrate

The title compound, $C_{19}H_{22}N_4O_2S \cdot H_2O$, was synthesized in order to search for new benzotriazole compounds with high bioactivity. There are some intermolecular hydrogen-bond interactions in the crystal structure, providing stabilization.

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Comment

The triazole motif appears frequently in the structures of various natural products and biologically active compounds, notably thiamine (vitamin B), penicillins, antibiotics such as micrococcin (James & Watson, 1966), and many other metabolic products of fungi and primitive marine animals. Benzo-triazole derivatives also exhibit better pharmacological activity than triazole compounds and have different biological activities (Zhang *et al.*, 2002). In order to search for new benzotriazole compounds with higher bioactivity, we synthesized the title compound, (I), and describe its structure here.



The title compound crystallizes as a monohydrate. Bond lengths and angles in the benzotriazole system are in good agreement with those quoted in a previous report (Xu *et al.*, 2005). The C=S bond length is shorter than the typical C=S bond length [1.68 Å; Allen *et al.*, 1987]. The S1/N1/C1/C2 group is planar and nearly coplanar with the phenyl ring (dihedral angle: $4.4 (1)^{\circ}$). The dihedral angles formed by the benzotriazole ring system with the phenyl ring is 82.6 (2)°.

The most interesting structural feature of the title compound is the presence of intermolecular hydrogen-bond interactions (Table 2), which stabilize the structure.

Experimental

The title compound was prepared by reaction of 1-(1*H*-benzo[1,2,3]triazol-1-yl)-3,3-dimethylbutan-2-one (4.34 g, 0.02 mol),

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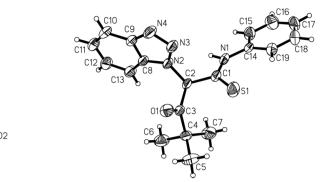


Figure 1

View of the title compound, (I), with displacement ellipsoids drawn at the 40% probability level.

phenyl isothiocyanate (2.24 g, 0.02 mol) and potassium hydroxide (2.24 g, 0.04 mol) in dimethylsulfoxide at room temperature. Single crystals suitable for X-ray measurements were obtained by recrystallization from ethanol-water (v/v = 3:1) at room temperature.

Crystal data

$C_{19}H_{20}N_4OS \cdot H_2O$	Z = 2
$M_r = 370.47$	$D_x = 1.304 \text{ Mg m}^{-3}$
Triclinic, $P\overline{1}$	Mo $K\alpha$ radiation
$a = 5.7572 (14) \text{\AA}$	Cell parameters from 1048
b = 11.545 (3) Å	reflections
c = 14.778 (4) Å	$\theta = 2.3-22.3^{\circ}$
$\alpha = 78.575 \ (4)^{\circ}$	$\mu = 0.19 \text{ mm}^{-1}$
$\beta = 81.022 \ (3)^{\circ}$	T = 295 (2) K
$\gamma = 81.362 \ (4)^{\circ}$	Block, yellow
$V = 943.7 (4) \text{ Å}^3$	$0.26 \times 0.18 \times 0.16 \ \mathrm{mm}$

Data collection

Bruker SMART CCD area-detector
diffractometer
φ and ω scans
Absorption correction: multi-scan
(SADABS; Sheldrick, 1996)
$T_{\min} = 0.943, T_{\max} = 0.970$
5114 measured reflections

Refinement

Refinement on F^2
$$\begin{split} R[F^2 > 2\sigma(F^2)] &= 0.062 \\ wR(F^2) &= 0.151 \end{split}$$
S = 0.803274 reflections 242 parameters

$D_x = 1.304 \text{ Mg m}^{-3}$
Mo $K\alpha$ radiation
Cell parameters from 1048
reflections
$\theta = 2.3 - 22.3^{\circ}$
$\mu = 0.19 \text{ mm}^{-1}$
T = 295 (2) K
Block, yellow
$0.26 \times 0.18 \times 0.16 \text{ mm}$

3274 independent reflections
1
1619 reflections with $I > 2\sigma(I)$
$R_{\rm int} = 0.148$
$\theta_{\rm max} = 25.0^{\circ}$
$h = -6 \rightarrow 6$
$k = -13 \rightarrow 7$
$l = -17 \rightarrow 17$

H atoms treated by a mixture of independent and constrained refinement $w = 1/[\sigma^2(F_o^2) + (0.0587P)^2]$ where $P = (F_o^2 + 2F_c^2)/3$ $(\Delta/\sigma)_{\rm max}=0.001$ $\Delta \rho_{\rm max} = 0.23 \ {\rm e} \ {\rm \mathring{A}}^{-3}$ $\Delta \rho_{\rm min} = -0.30 \text{ e} \text{ Å}^{-3}$

Table 1

Selected geometric parameters (Å, °).

S1-C1	1.632 (3)	N3-N4	1.295 (4)
N1-C1 N1-C14	1.331 (4) 1.407 (4)	O1-C3	1.198 (4)
C1-N1-C14	132.8 (3)	N1-C1-S1	128.3 (3)
N4-N3-N2 N1-C1-C2	108.2 (3) 111.7 (3)	O1-C3-C4	121.6 (3)

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

$D - H \cdot \cdot \cdot A$	D-H	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - \mathbf{H} \cdots A$
$O2-H2B\cdots N4^{i}$	0.85	2.10	2.926 (4)	163
$O2-H2A\cdots N3^{ii}$	0.85	2.02	2.866 (4)	176
$N1 - H1 \cdots O2^{iii}$	0.89 (4)	1.93 (4)	2.766 (4)	155 (3)

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

All H atoms were placed in calculated positions. H atoms bonded to C and O atoms were constrained to ride on their parent atom (C-H = 0.93–0.96 Å and O–H = 0.85 Å), with U_{iso} values of $1.2U_{eq}(C)$ for the aryl and CH H atoms and 1.5 U_{eq} (C,O) for the CH₃ and water H atoms. The position and isotropic displacement parameter of the NH H atom were refined freely. The crystals showed a weak diffracting ability, which could account for the rather high R_{int} and low goodness-of-fit.

Data collection: SMART (Bruker, 1998); cell refinement: SAINT (Bruker, 1999); data reduction: SAINT; program(s) used to solve structure: SHELXS97 (Sheldrick, 1997); program(s) used to refine structure: SHELXL97 (Sheldrick, 1997); molecular graphics: SHELXTL (Bruker, 1999); software used to prepare material for publication: SHELXTL.

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