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## Structure Reports

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## Key indicators

Single-crystal X-ray study
$T=293 \mathrm{~K}$
Mean $\sigma(\mathrm{C}-\mathrm{C})=0.003 \AA$
$R$ factor $=0.030$
$w R$ factor $=0.076$
Data-to-parameter ratio $=8.5$
For details of how these key indicators were automatically derived from the article, see http://journals.iucr.org/e.
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## 1-(4-Hydroxyphenyl)-3-(1H-1,2,4-triazol-1-yl)-propan-1-one

In the title compound, $\mathrm{C}_{11} \mathrm{H}_{11} \mathrm{~N}_{3} \mathrm{O}_{2}$, the dihedral angles made by the planes of the triazole and benzene rings with the plane through the $\mathrm{OC}_{3}$ atoms of the ketone group are 72.87 (4) and $7.10(3)^{\circ}$, respectively. There are some intermolecular interactions in the crystal structure, which contribute to the stability.

## Comment

Triazole rings appear frequently in the structures of various natural products and biologically active compounds, notably thiamine (vitamin B), penicillins and antibiotics, such as micrococcin (James \& Watson, 1966). Triazole derivatives have also attracted considerable attention in industry and agriculture because of their significant biological activities (Zhang et al., 2002). In this paper, we report the structure of the title compound (I).

(I)

In the title compound (Fig. 1), the bond lengths and angles are generally normal in the benzene and triazole rings (Ji et al., 2002). The $\mathrm{C}=\mathrm{O}$ bond length is close to the typical $\mathrm{C}=\mathrm{O}$ double-bond length (Table 1). Atom C3 lies in the plane of the triazole ring, and atoms O1, C1, C2 and C6 are coplanar (plane $p 1)$. The dihedral angles formed by the triazole and C6-C11 rings with $p 1$ are 72.87 (4) and $7.10(3)^{\circ}$, respectively. The $\mathrm{C} 2-\mathrm{C} 3-\mathrm{N} 1-\mathrm{N} 2, \mathrm{O} 1-\mathrm{C} 1-\mathrm{C} 2-\mathrm{C} 3, \mathrm{C} 7-\mathrm{C} 6-\mathrm{C} 1-\mathrm{O} 1$ and $\mathrm{C} 5-\mathrm{N} 1-\mathrm{C} 3-\mathrm{C} 2$ torsion angles are 68.2 (2), 4.1 (3), 172.0 (2) and $112.7(2)^{\circ}$, respectively. The most interesting structural features of the title compound are $\mathrm{O}-\mathrm{H} \cdots \mathrm{N}$ intermolecular


Figure 1
The structure of the title compound, showing $35 \%$ probability displacement ellipsoids and the atom-numbering scheme.

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hydrogen bonds and weak $(\mathrm{C}-\mathrm{H} \cdots Y$ hydrogen bonds; $Y=\mathrm{O}$ and N ) intermolecular interactions (see Table 2). These interactions stabilize the crystal structure.

## Experimental

The title compound was prepared according to the method reported by Ogata et al. (1987). Single crystals of the title compound suitable for X-ray measurements were obtained by recrystallization from methanol at room temperature.

## Crystal data

$\mathrm{C}_{11} \mathrm{H}_{11} \mathrm{~N}_{3} \mathrm{O}_{2}$
$M_{r}=217.23$
Monoclinic, $C c$
$a=22.759(4) \AA$
$b=5.5729(9) \AA$
$c=8.3902(14) \AA$
$\beta=90.929(2)^{\circ}$
$V=1064.0(3) \AA^{3}$
$Z=4$

$$
D_{x}=1.356 \mathrm{Mg} \mathrm{~m}^{-3}
$$

Mo $K \alpha$ radiation
Cell parameters from 1098 reflections
$\theta=3.6-26.7^{\circ}$
$\mu=0.10 \mathrm{~mm}^{-1}$
$T=293$ (2) K
Block, colourless
$0.28 \times 0.22 \times 0.20 \mathrm{~mm}$

## Data collection

Bruker SMART CCD area-detector diffractometer
$\varphi$ and $\omega$ scans
Absorption correction: multi-scan (SADABS; Sheldrick, 1996) $T_{\text {min }}=0.958, T_{\text {max }}=0.981$
3413 measured reflections
1271 independent reflections 1006 reflections with $I>2 \sigma(I)$
$R_{\text {int }}=0.018$
$\theta_{\text {max }}=27.9^{\circ}$
$h=-29 \rightarrow 21$
$k=-7 \rightarrow 7$
$l=-9 \rightarrow 11$

## Refinement

Refinement on $F^{2}$

$$
\begin{aligned}
& w=1 / {\left[\sigma^{2}\left(F_{\mathrm{o}}{ }^{2}\right)+(0.0423 P)^{2}\right.} \\
&+0.0744 P] \\
& \text { where } P=\left(F_{\mathrm{o}}{ }^{2}+2 F_{\mathrm{c}}^{2}\right) / 3 \\
&(\Delta / \sigma)_{\max }=0.001 \\
& \Delta \rho_{\max }=0.12 \mathrm{e} \AA^{-3} \\
& \Delta \rho_{\min }=-0.13 \mathrm{e} \AA^{-3}
\end{aligned}
$$

$w R\left(F^{2}\right)=0.076$
$S=1.03$
1271 reflections
149 parameters
H atoms treated by a mixture of independent and constrained refinement

Table 1
Selected geometric parameters ( $\left({ }^{\circ},{ }^{\circ}\right)$.

| $\mathrm{N} 1-\mathrm{C} 3$ | $1.459(3)$ | $\mathrm{C} 1-\mathrm{C} 6$ | $1.476(3)$ |
| :--- | ---: | :--- | ---: |
| $\mathrm{O} 1-\mathrm{C} 1$ | $1.218(2)$ | $\mathrm{C} 1-\mathrm{C} 2$ | $1.513(3)$ |
| $\mathrm{O} 2-\mathrm{C} 9$ | $1.347(2)$ |  |  |
| $\mathrm{O} 1-\mathrm{C} 1-\mathrm{C} 2-\mathrm{C} 3$ | $4.1(3)$ | $\mathrm{N} 2-\mathrm{N} 1-\mathrm{C} 3-\mathrm{C} 2$ | $-68.2(2)$ |
| $\mathrm{C} 5-\mathrm{N} 1-\mathrm{C} 3-\mathrm{C} 2$ | $112.7(2)$ | $\mathrm{O} 1-\mathrm{C} 1-\mathrm{C} 6-\mathrm{C} 7$ | $-172.0(2)$ |

Table 2
Hydrogen-bond geometry ( $\mathrm{A},{ }^{\circ}$ ).

| $D-\mathrm{H} \cdots A$ | D-H | $\mathrm{H} \cdots A$ | $D \cdots A$ | $D-\mathrm{H} \cdots A$ |
| :---: | :---: | :---: | :---: | :---: |
| $\mathrm{O} 2-\mathrm{H} 2 \cdots \mathrm{~N} 3{ }^{\mathrm{i}}$ | 0.857 (10) | 1.834 (11) | 2.685 (2) | 172 (3) |
| $\mathrm{C} 3-\mathrm{H} 3 A \cdots \mathrm{O} 1^{\text {ii }}$ | 0.97 | 2.55 | 3.162 (3) | 120 |
| $\mathrm{C} 3-\mathrm{H} 3 \mathrm{~B} \cdots \mathrm{~N} 2^{\text {iii }}$ | 0.97 | 2.59 | 3.534 (3) | 163 |
| $\mathrm{C} 4-\mathrm{H} 4 \cdots \mathrm{O} 2^{\text {iv }}$ | 0.93 | 2.43 | 3.327 (3) | 162 |
| C5-H5 $\cdots \mathrm{N} 2^{\text {v }}$ | 0.93 | 2.51 | 3.389 (5) | 157 |

Symmetry codes: (i) $x-\frac{1}{2}, y-\frac{1}{2}, z$; (ii) $x,-y+1, z+\frac{1}{2} ;$ (iii) $x,-y, z+\frac{1}{2}$; (iv) $x+\frac{1}{2}, y-\frac{1}{2}, z ;$ (v) $x, y+1, z$.

H atoms on O atoms were located in a difference Fourier map and refined freely. All other H atoms were placed in calculated positions, with $\mathrm{C}-\mathrm{H}=0.93$ or $0.97 \AA$, and included in the final cycles of refinement using a riding model, with $U_{\text {iso }}(\mathrm{H})=1.2 U_{\text {eq }}(\mathrm{C})$. In the absence of significant anomalous scattering, Friedel pairs were merged.

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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