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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 $=0.041$
$w R$ factor $=0.138$
Data-to-parameter ratio $=13.0$

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

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## 5-[3-(Quinolin-8-yloxy)propyl]-1,3,4-oxadiazole-2(3H)-thione

The title compound, $\mathrm{C}_{14} \mathrm{H}_{13} \mathrm{~N}_{3} \mathrm{O}_{2} \mathrm{~S}$, crystallizes as a thione tautomer. There are two molecules in the asymmetric unit which differ in conformation. The molecules are connected via intermolecular $\mathrm{N}-\mathrm{H} \cdots \mathrm{N}$ and $\mathrm{N}-\mathrm{H} \cdots \mathrm{O}$ hydrogen bonds into a one-dimensional helical structure.

## Comment

In the course of our studies on 1,3,4-oxadiazole-2-thione derivatives the title compound, (I), was synthesized and its crystal structure determined. 1,3,4-Oxadiazole-2-thiones are known to possess a broad spectrum of biological activities (Ram \& Vlietinck, 1988; Boschelli et al., 1993; Bahadur \& Pandy, 1980).

(I)

The asymmetric unit of (I) contains two molecules in the usual thione tautomeric form (Du et al., 2004; Thamotharan et al., 2005) (Table 1). The two molecules differ in conformation. In one molecule, the conformation along the O3-C24$\mathrm{C} 25-\mathrm{C} 26-\mathrm{C} 27-\mathrm{O} 4$ bond sequence is trans-trans-trans, whereas in the second molecule the conformation is (+)gauche-trans-(-)gauche along the corresponding O1$\mathrm{C} 10-\mathrm{C} 11-\mathrm{C} 12-\mathrm{C} 13-\mathrm{O} 2$ bond sequence (Table 1). Despite these differences, the dihedral angles between the mean planes of the 1,3,4-oxadiazole and the quinoline rings are not very different $\left[11.3(2)\right.$ and $22.6(1)^{\circ}$ for the molecules containing atoms O 3 and O 1 , respectively]. The molecules are connected via intermolecular $\mathrm{N}-\mathrm{H} \cdots \mathrm{N}$ and $\mathrm{N}-\mathrm{H} \cdots \mathrm{O}$ hydrogen bonds into a one-dimensional helical structure (Table 2 and Fig. 2).

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## Experimental

To a solution of 4-(quinolin-8-yloxy)butanohydrazide ( 0.01 mol ) in ethanol $(30 \mathrm{ml})$, potassium hydroxide $(0.0125 \mathrm{~mol})$ and carbon disulfide were added ( 0.014 mol ). The solution was refluxed for 9 h and the solvent was evaporated under reduced pressure. The residue was dissolved in water and acidified with dilute HCl . The solid (I) which precipitated was filtered off and recrystallized from a mixture of dimethylformamide and ethanol (5:1) (m.p. 505-506 K). Analysis calculated for $\mathrm{C}_{14} \mathrm{H}_{13} \mathrm{~N}_{3} \mathrm{O}_{2} \mathrm{~S}$ : C 58.52 , H 4.56 , $\mathrm{N} 14.62 \%$; found: C 58.50 , H 4.58, N $14.61 \%$. Crystals of (I) suitable for single-crystal X-ray analysis were selected directly from the sample after recrystallization.

## Crystal data

$\mathrm{C}_{14} \mathrm{H}_{13} \mathrm{~N}_{3} \mathrm{O}_{2} \mathrm{~S}$
$M_{r}=287.33$
Triclinic, $P \overline{1}$
$a=7.3208$ (5) A
$b=11.5523$ (7) A
$c=16.7934$ (10) $\AA$
$\alpha=84.271$ (3) ${ }^{\circ}$
$\beta=89.326(4)^{\circ}$
$\gamma=75.357(2)^{\circ}$

## Data collection

Bruker SMART diffractometer $\varphi$ and $\omega$ scans
Absorption correction: multi-scan (SADABS; Sheldrick, 1996)
$T_{\text {min }}=0.901, T_{\text {max }}=0.965$

## Refinement

Refinement on $F^{2}$
$R\left[F^{2}>2 \sigma\left(F^{2}\right)\right]=0.041$
$w R\left(F^{2}\right)=0.138$
$S=1.00$
4781 reflections
369 parameters
H atoms treated by a mixture of independent and constrained refinement

$$
\begin{aligned}
& V=1367.13(15) \AA^{3} \\
& Z=4 \\
& D_{x}=1.396 \mathrm{Mg} \mathrm{~m}^{-3} \\
& \text { Mo } K \alpha \text { radiation } \\
& \mu=0.24 \mathrm{~mm}^{-1} \\
& T=293(2) \mathrm{K} \\
& \text { Block, colourless } \\
& 0.44 \times 0.26 \times 0.15 \mathrm{~mm}
\end{aligned}
$$

7016 measured reflections
4781 independent reflections
4241 reflections with $I>2 \sigma(I)$
$R_{\text {int }}=0.015$
$\theta_{\text {max }}=25.0^{\circ}$

$$
\begin{aligned}
& w=1 /\left[\sigma^{2}\left(F_{\mathrm{o}}^{2}\right)+(0.1 P)^{2}\right. \\
& \quad+0.33 P] \\
& \text { where } P=\left(F_{\mathrm{o}}^{2}+2 F_{\mathrm{c}}^{2}\right) / 3 \\
& (\Delta / \sigma)_{\max }=0.001 \\
& \Delta \rho_{\max }=0.46 \mathrm{e} \AA^{-3} \\
& \Delta \rho_{\min }=-0.32 \mathrm{e}^{-3}
\end{aligned}
$$

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

| S1-C14 | $1.6467(19)$ | $\mathrm{N} 3-\mathrm{N} 2$ | $1.388(2)$ |
| :--- | :---: | :--- | ---: |
| S2-C28 | $1.6543(19)$ | $\mathrm{N} 6-\mathrm{N} 5$ | $1.392(2)$ |
|  |  |  |  |
| O2-C13-C12-C11 | $-71.7(2)$ | $\mathrm{C} 25-\mathrm{C} 26-\mathrm{C} 27-\mathrm{O} 4$ | $-168.98(17)$ |
| C13-C12-C11-C10 | $-171.58(16)$ | C27-C26-C25-C24 | $173.48(17)$ |
| O1-C10-C11-C12 | $72.6(2)$ | $\mathrm{O} 3-\mathrm{C} 24-\mathrm{C} 25-\mathrm{C} 26$ | $-176.73(17)$ |

Table 2
Hydrogen-bond geometry $\left(\AA^{\circ},{ }^{\circ}\right)$.

| $D-\mathrm{H} \cdots A$ | $D-\mathrm{H}$ | $\mathrm{H} \cdots A$ | $D \cdots A$ | $D-\mathrm{H} \cdots A$ |
| :--- | :--- | :--- | :--- | :--- |
| N3-H1 $\cdots \mathrm{N} 4$ | $0.93(2)$ | $1.84(2)$ | $2.770(2)$ | $174(2)$ |
| N3-H1 3 O3 | $0.93(2)$ | $2.54(2)$ | $3.036(2)$ | $113.6(17)$ |
| N6-H29 ${ }^{\mathrm{i}}$ | $0.91(2)$ | $1.89(2)$ | $2.782(2)$ | $165(2)$ |

Symmetry code: (i) $x-1, y, z$.


Figure 1
The asymmetric unit of (I) showing the atom labelling and displacement ellipsoids drawn at the $50 \%$ probability level. H atoms have been omitted for clarity. The dashed lines indicate hydrogen bonds.


Figure 2
The helical structure formed by hydrogen bonds (dashed lines) in (I). H atoms have been omitted for clarity.

All H atoms were initially located in a difference Fourier map. The methylene H atoms were constrained to an ideal geometry, with $\mathrm{C}-$ $\mathrm{H}=0.97 \AA$ and $U_{\text {iso }}(\mathrm{H})=1.5 U_{\text {eq }}(\mathrm{C})$. The positions of the amine H atoms were refined freely along with isotropic displacement parameters. All quinoline H atoms were placed in geometrically idealized positions, with $\mathrm{C}-\mathrm{H}=0.93 \AA$ and $U_{\text {iso }}(\mathrm{H})=1.2 U_{\text {eq }}(\mathrm{C})$.

Data collection: SMART (Siemens, 1996); cell refinement: SAINT (Siemens, 1996); data reduction: SAINT; program(s) used to solve structure: SHELXS97 (Sheldrick, 1997a); program(s) used to refine structure: SHELXL97 (Sheldrick, 1997a); molecular graphics: SHELXTL (Sheldrick, 1997b); software used to prepare material for publication: SHELXTL.

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