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Key indicators

Single-crystal X-ray study T = 294 KMean σ (C–C) = 0.003 Å R factor = 0.039 wR factor = 0.103 Data-to-parameter ratio = 12.9

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

N-(1-Cyanocyclohexyl)-1,2,3-benzothiadiazole-7-carboxamide

The title compound, $C_{14}H_{14}N_4OS$, is a derivative of acibenzolar-S-methyl or BTH, a plant elicitor. The asymmetric unit contains two independent molecules in each of which the benzothiadiazole ring system is planar and the cyclohexane ring adopts a chair conformation. In the crystal structure, molecules are linked by $N-H\cdots N$ and $C-H\cdots N$ hydrogen bonds.

Comment

Acibenzolar-S-methyl (also called BTH) is a leading plant activator, a kind of environmentally benign agrochemical developed in recent years with a new mode of action (Gozzo, 2003). Many studies have been carried out on the structural modification of this compound (Bao, Liu et al., 2005; Kunz et al., 1997). In order to find more powerful plant activators that can be applied to prevent and cure diseases caused by viruses, and to understand the quantitative structure-activity relationship (QSAR) of this new kind of pesticide, the title compound, (I), was synthesized. A search of the Cambridge Structural Database (Version 5.26 with updates to August 2005; Allen, 2002), revealed only seven structures containing the benzothiadiazole group. Recently, we have reported the structures of N-phenyl-N'-(1,3-thiazol-2-yl)-1,2,3-benzothiadiazole-7-carboxamidine (Bao, Fan et al., 2005) and N-(1-cyano-1-methylbutyl)-1,2,3-benzothiadiazole-7-carboxamide (Ai et al., 2005). We now report here the crystal structure of N-(1-cyanocyclohexyl)-1,2,3-benzothiadiazole-7carboxamide, (I).



The asymmetric unit of (I) contains two crystallographically independent molecules (Fig. 1). Bond lengths and angles in (I) are normal, and values for the two independent molecules agree well with each other (Table 1). In both independent molecules, the benzothiadiazole ring system is essentially planar and the cyclohexane ring adopts a chair conformation. In one of the molecules, the amide plane and benzothiadiazole ring system are coplanar, whereas in the other (containing atom S2), they are twisted by 14.3 (1)°. The crystal structure is

© 2005 International Union of Crystallography Printed in Great Britain – all rights reserved Received 26 September 2005 Accepted 2 November 2005 Online 10 November 2005 stabilized by $N-H\cdots N$ and $C-H\cdots N$ hydrogen bonds (Table 2).

Experimental

Compound (I) was prepared according to the reported procedure of Fan *et al.* (2005). Single crystals suitable for X-ray diffraction were obtained by recrystallization from a mixture of petroleum ether and ethyl acetate (2:1 v/v).

Z = 4

 $D_x = 1.401 \text{ Mg m}^{-3}$

Cell parameters from 956 reflections

4777 independent reflections

3527 reflections with $I > 2\sigma(I)$

Mo $K\alpha$ radiation

 $\theta = 3.4-26.2^{\circ}$ $\mu = 0.24 \text{ mm}^{-1}$

T = 294 (2) K

 $R_{\rm int} = 0.025$

 $\begin{array}{l} \theta_{\max} = 25.0^{\circ} \\ h = -13 \rightarrow 11 \\ k = -13 \rightarrow 14 \end{array}$

 $l = -14 \rightarrow 13$

Block, colourless $0.30 \times 0.24 \times 0.14 \text{ mm}$

Crystal data

$C_{14}H_{14}N_4OS$
$M_r = 286.35$
Triclinic, $P\overline{1}$
a = 11.0871 (17) Å
b = 11.8713 (19) Å
c = 12.0846 (19) Å
$\alpha = 117.308 \ (4)^{\circ}$
$\beta = 96.217 \ (6)^{\circ}$
$\gamma = 100.195 \ (5)^{\circ}$
V = 1357.9 (4) Å ³

Data collection

Bruker SMART CCD area-detector
diffractometer
φ and ω scans
Absorption correction: multi-scan
(SADABS; Sheldrick, 1996)
$T_{\min} = 0.920, \ T_{\max} = 0.967$
7142 measured reflections

Refinement

P efinement on F^2	$w = 1/[\sigma^2(F^2) + (0.0462P)^2]$
	$W = 1/[0 (T_0) + (0.04021)]$
$R[F^2 > 2\sigma(F^2)] = 0.039$	+ 0.3245P
$wR(F^2) = 0.103$	where $P = (F_0^2 + 2F_c^2)/3$
S = 1.02	$(\Delta/\sigma)_{\rm max} = 0.001$
4777 reflections	$\Delta \rho_{\rm max} = 0.22 \ {\rm e} \ {\rm \AA}^{-3}$
370 parameters	$\Delta \rho_{\rm min} = -0.20 \text{ e } \text{\AA}^{-3}$
H atoms treated by a mixture of	Extinction correction: SHELXL97
independent and constrained	Extinction coefficient: 0.028 (2)
refinement	

Table 1

Selected bond lengths (Å).

S1-C1	1.704 (2)	N3-C7	1.351 (3)
S1-N1	1.707 (2)	N3-C8	1.460 (3)
S2-C15	1.704 (2)	N4-C14	1.140 (3)
S2-N5	1.713 (2)	N5-N6	1.273 (3)
O1-C7	1.230 (2)	N6-C16	1.393 (3)
O2-C21	1.227 (2)	N7-C21	1.343 (3)
N1-N2	1.282 (3)	N7-C22	1.466 (3)
N2-C2	1.386 (3)	N8-C28	1.129 (3)

Table 2

Hydrogen-bond geometry (Å, °).

$D - H \cdots A$	D-H	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - \mathbf{H} \cdot \cdot \cdot A$
$\begin{array}{c} N3 - H3A \cdots N8^{i} \\ C10 - H10B \cdots N5^{ii} \end{array}$	0.84 (2)	2.33 (2)	3.135 (3)	163 (2)
	0.97	2.53	3.384 (4)	147

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

The amine H atoms were located in a difference Fourier map and refined isotropically [N-H = 0.78 (2) and 0.84 (2) Å]. H atoms





attached to C atoms were placed in idealized positions and constrained to ride on their parent atoms, with C–H = 0.93–0.97 Å and $U_{\rm iso}({\rm H}) = 1.2-1.5U_{\rm eq}({\rm C})$.

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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