Acta Crystallographica Section E Structure Reports Online

ISSN 1600-5368

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Key indicators

Single-crystal X-ray study T = 298 KMean σ (C–C) = 0.006 Å R factor = 0.043 wR factor = 0.106 Data-to-parameter ratio = 10.4

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

3-[3-(4-Methoxybenzoyl)thioureido]propionic acid

In the title molecule, $C_{12}H_{14}N_2O_4S$, the methoxybenzoyl group is *trans* to the thiono S atom across the C–N bond. The propionic acid group adopts a *gauche* conformation about the C–C bond, with a C_{COOH} –C–C–N torsion angle of 64.9 (4)°. In the crystal structure, intermolecular O–H···S, N–H···O and C–H···O hydrogen bonds link the molecules into chains parallel to the *c* axis.

Received 29 June 2006 Accepted 11 July 2006

Comment

The title compound, (I), is a carbonoylthiourea derivative of β -alanine analogous to 3-(3-benzoylthiouredo)propionic acid, (II) (Yusof & Yamin, 2003), except that a methoxy group is attached at the *para* position of the benzoyl group (Fig. 1).



The molecule maintains its cis-trans configuration with respect to the positions of the propionic acid and 4methoxybenzoyl groups relative to the S1 atom across the C9-N2 and C9-N1 bonds, respectively. In addition, the molecule adopts a gauche conformation about the C10-C11 bond, with a C12-C11-C10-N2 torsion angle of 64.9 (4) Å; in contrast, compound (II) adopts an anti conformation with a torsion angle of $-179.12 (16)^{\circ}$. The bond lengths and angles are in normal ranges (Allen et al., 1987) and comparable to those in (II). However, the O3-C12 bond length [1.325 (4) Å] is slightly longer than that in (II) [1.296 (2) Å]. The 4methoxyphenyl [C1-C6/O1/C7 (A)] and central carbonylthiourea [S1/O2/N1/N2/C8/C9 (B)] fragments are essentially planar. In the propionic acid fragment [O3/O4/C10/C11/C12 (C)], the maximum deviation from the mean plane is 0.186 (4) Å for atom C10. The dihedral angles A/B and B/Care 10.35 (13) and 62.08 (17)°, respectively. The 4-methoxyphenyl unit is inclined to the propionic acid mean plane with a dihedral angle of 54.29 $(19)^{\circ}$, compared with 22.46 $(13)^{\circ}$ in (II). The intramolecular hydrogen bond N2-H2A···O2

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Figure 1

The molecular structure of (I), shown with 50% probability displacement ellipsoids. The dashed line represents a hydrogen bond.



Figure 2

Packing diagram of the title complex, viewed down the *b* axis. The dashed lines denote intermolecular $N-H\cdots O$, $O-H\cdots S$ and $C-H\cdots O$ hydrogen bonds.

(Table 2) forms a pseudo-six-membered ring (N2/H2A/O2/C8/ N1/C9).

In the crystal structure, molecules are linked by intermolecular $O-H\cdots S$, $N-H\cdots O$ and $C-H\cdots O$ hydrogen bonds (Table 2), forming a one-dimensional chain parallel to the *c* axis, in contrast to a two-dimensional hydrogen-bonded network in (II). The crystal packing (Fig. 2) is further stabilized by van der Waals forces.

Experimental

A solution of 3-aminopropionic acid (0.05 mol, 4.45 g) in 20 ml acetone was added dropwise to a two-necked round-bottomed flask containing an equimolar solution of 4-methoxybenzoylisothiocyanate (0.05 mol, 9.65 g) in 20 ml acetone. The mixture was refluxed for about 5 h and then filtered into a beaker containing ice cubes. The resulting yellow precipitate was washed with cold acetone and distilled water. The product was dried under vaccum and kept in a desiccator (yield 11.99 g, 85%; m.p. 430.3–431.1 K). Recrystallization from ethanol yielded yellow crystals suitable for X-ray analysis.

Crystal data

C.H. N.O.S
$2_{12} 1_{14} 1_{2} 0_{4} 3$
$M_r = 282.31$
Monoclinic, Pc
<i>i</i> = 9.795 (3) Å
b = 4.7790 (13)Å
c = 14.951 (4) Å
$\beta = 108.275 \ (5)^{\circ}$
$V = 664.6 (3) \text{ Å}^3$

Data collection

Bruker SMART APEX CCD areadetector diffractometer ω scans Absorption correction: multi-scan (*SADABS*; Bruker, 2000) $T_{min} = 0.912, T_{max} = 0.979$

Refinement

Refinement on F^2	$w = 1/[\sigma]$
$R[F^2 > 2\sigma(F^2)] = 0.043$	+ 0.0
$wR(F^2) = 0.106$	where
S = 1.15	$(\Delta/\sigma)_{\rm max}$
1792 reflections	$\Delta \rho_{\rm max} =$
172 parameters	$\Delta \rho_{\min} =$
H-atom parameters constrained	Absolute
	628 Fr

Z = 2 $D_x = 1.411 \text{ Mg m}^{-3}$ Mo K α radiation $\mu = 0.26 \text{ mm}^{-1}$ T = 298 (2) K Plate, yellow 0.34 × 0.17 × 0.07 mm

3159 measured reflections 1792 independent reflections 1660 reflections with $I > 2\sigma(I)$ $R_{\text{int}} = 0.019$ $\theta_{\text{max}} = 25.0^{\circ}$

$w = 1/[\sigma^2(F_o^2) + (0.0526P)^2]$
+ 0.0617P]
where $P = (F_o^2 + 2F_c^2)/3$
$(\Delta/\sigma)_{\rm max} < 0.001$
$\Delta \rho_{\rm max} = 0.28 \text{ e } \text{\AA}^{-3}$
$\Delta \rho_{\rm min} = -0.15 \text{ e} \text{ \AA}^{-3}$
Absolute structure: Flack (1983)
628 Friedel pairs
Flack parameter: 0.16 (11)

Table 1 Selected geometric parameters (Å, °).

S1-C9	1.687 (4)	N1-C9	1.375 (4)
O2-C8	1.231 (4)	N1-C8	1.382 (5)
O3-C12	1.325 (4)	N2-C9	1.318 (4)
O4-C12	1.201 (5)	N2-C10	1.463 (5)
C9-N1-C8	128.2 (3)	N2-C9-S1	122.0 (3)
N2-C9-N1	117.7 (3)	N1-C9-S1	120.3 (3)

Table 2

H	lyd	rogen-	bond	geometry	(A, °	') .	
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$D - H \cdots A$	D-H	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - \mathbf{H} \cdot \cdot \cdot A$
$N2-H2A\cdots O2$	0.86	1.94	2.622 (4)	135
$O3-H3 \cdot \cdot \cdot S1^i$	0.82	2.32	3.126 (3)	169
$N1 - H1A \cdots O4^{ii}$	0.86	2.26	3.113 (4)	170
$C1 - H1B \cdots O4^{ii}$	0.93	2.28	3.155 (6)	156

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

All H atoms were positioned geometrically and allowed to ride on their parent atoms, with C–H = 0.93–0.97 Å, N–H = 0.86 Å and O–H = 0.82 Å, with $U_{iso}(H) = 1.2U_{eq}(C,N)$ for CH and NH groups and $1.5U_{eq}(C,O)$ for CH₃ and OH groups.

Data collection: *SMART* (Bruker, 2000); cell refinement: *SAINT* (Bruker, 2000); data reduction: *SAINT*; program(s) used to solve structure: *SHELXS97* (Sheldrick, 1997*a*); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997*a*); molecular graphics: *SHELXTL* (Sheldrick, 1997*b*); software used to prepare material for publication: *SHELXTL*, *PARST* (Nardelli, 1995) and *PLATON* (Spek, 2003).

The authors thank the Malaysian Government and Universiti Kebangsaan Malaysia for research grant IRPA No. 09–02-02-0163.

References

- Allen, F. H., Kennard, O., Watson, D. G., Brammer, L., Orpen, A. G. & Taylor, R. (1987). J. Chem. Soc. Perkin Trans. 2, pp. S1–19.
- Bruker (2000). SADABS (Version 2.01), SMART (Version 5.630) and SAINT (Version 6.36a). Bruker AXS Inc., Madison, Wisconsin, USA.
- Flack, H. D. (1983). Acta Cryst. A39, 876-881.
- Nardelli, M. (1995). J. Appl. Cryst. 28, 659.
- Sheldrick, G. M. (1997a). SHELXS97 and SHELXL97. University of Göttingen, Germany.
- Sheldrick, G. M. (1997b). SHELXTL. Version 5.1. Bruker AXS Inc., Madison, Wisconsin, USA.
- Spek, A. L. (2003). J. Appl. Cryst. 36, 7-13.
- Yusof, M. S. M. & Yamin, B. M. (2003). Acta Cryst. E59, 0828-0829.