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Key indicators

Single-crystal X-ray study
 $T = 273$ K
Mean $\sigma(\text{C}-\text{C}) = 0.004$ Å
 R factor = 0.068
 wR factor = 0.133
Data-to-parameter ratio = 15.4For details of how these key indicators were
automatically derived from the article, see
<http://journals.iucr.org/e>.***N*-(1-Benzylpiperidin-4-yl)-*N'*-(4-methoxybenzoyl)-
thiourea**

In the title compound, $\text{C}_{21}\text{H}_{25}\text{N}_3\text{O}_2\text{S}$, the *p*-anisoyl group is inclined to the central thiourea N_2CS unit by 31.939 (11) $^\circ$ and the piperidine ring adopts a chair conformation. The molecule is stabilized by intra- and intermolecular interactions to form polymeric chains parallel to the *ac* plane.

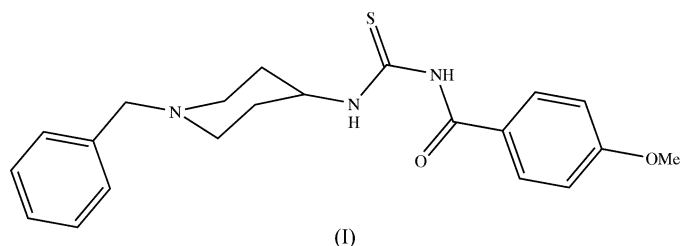
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Comment

Bond lengths and angles in the molecule of the title compound (I) (Fig. 1) are in normal ranges (Allen *et al.*, 1987) and in agreement with those found in *N*-(2-chlorophenyl)-*N'*-(4-methoxybenzoyl)thiourea (Yusof & Yamin, 2004).



The piperidine ring adopts a chair conformation. The methoxybenzoyl and 1-benzyl-1-piperidine fragments are *trans* and *cis*, respectively, with respect to the $\text{C}8=\text{S}1$ thiono group across the $\text{C}8-\text{N}1$ and $\text{C}8-\text{N}2$ bonds. The dihedral angle between the central thiourea unit, $\text{S}1/\text{C}8/\text{N}1/\text{N}2$ [maximum deviation 0.007 (3) Å at $\text{C}8$] and the benzene ring $\text{C}1-\text{C}6/\text{C}7/\text{O}2/\text{C}21$ [maximum deviation 0.017 (3) Å at $\text{C}21$] is 31.93 (11) $^\circ$. The benzyl fragment $\text{C}14-\text{C}20$ [maximum deviation 0.049 (2) Å at $\text{C}14$] is inclined to the central thiourea unit and the $\text{C}1-\text{C}7/\text{O}2/\text{C}21$ ring by 38.17 (12) and 48.40 (11) $^\circ$,

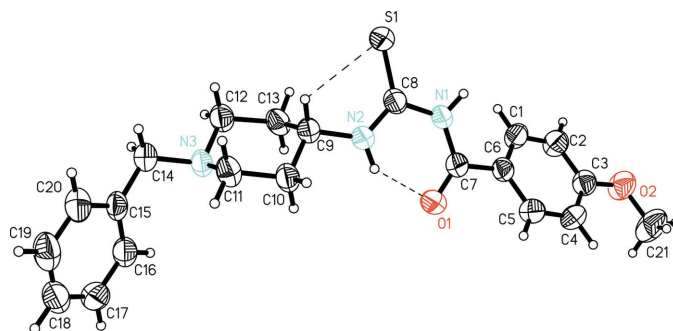


Figure 1

A drawing of the molecule of (I), with the atom-numbering scheme. Displacement ellipsoids are drawn at the 50% probability level. Intramolecular hydrogen bonds are shown as dashed lines.

respectively. There are two intramolecular interactions, *viz.* C9—H9A···S1 and N2—H2A···O1, resulting in the formation of pseudo-five-membered and six-membered rings S1···H2A—C9—N2—C8—S1 and O1···H2A—N2—C8—N1—C7—O1, respectively. In the crystal structure, the molecules are linked by intermolecular interactions, *viz.* N1—H1A···S1ⁱ and C21—H21C···O2ⁱⁱ (symmetry codes as in Table 2), to form polymeric chains parallel to the *ac* plane.

Experimental

A solution of 4-amino-*N*-benzylpiperidine (0.5 g, 1.31 mol) in acetone (50 ml) was added dropwise to an acetone solution (50 ml) containing an equimolar amount of *p*-methoxybenzoyl isothiocyanate. The solution was refluxed for 2 h and then poured into a beaker containing some crushed ice. The white precipitate was washed with cold ethanol and distilled water, then dried in a vacuum (yield 80%). Recrystallization from acetone gave single crystals suitable for X-ray analysis (m.p. 412.2–413.1 K). Analysis calculated: C 65.7, H 6.57, N 10.96, S 8.36, O 8.34%; found: C 66.3, H 6.40, N 10.69, S 7.50, O 9.13%.

Crystal data

C ₂₁ H ₂₅ N ₃ O ₂ S	<i>D_x</i> = 1.261 Mg m ⁻³
<i>M_r</i> = 383.50	Mo Kα radiation
Monoclinic, <i>P</i> 2 ₁ / <i>n</i>	Cell parameters from 1914 reflections
<i>a</i> = 11.775 (2) Å	<i>θ</i> = 1.6–25.5°
<i>b</i> = 7.0646 (14) Å	<i>μ</i> = 0.18 mm ⁻¹
<i>c</i> = 24.362 (5) Å	<i>T</i> = 273 (2) K
<i>β</i> = 94.777 (4)°	Plate, colourless
<i>V</i> = 2019.6 (7) Å ³	0.46 × 0.20 × 0.09 mm
<i>Z</i> = 4	

Data collection

Bruker SMART APEX CCD area-detector diffractometer	3754 independent reflections
<i>ω</i> scans	2953 reflections with <i>I</i> > 2σ(<i>I</i>)
Absorption correction: multi-scan (SADABS; Sheldrick, 1996)	<i>R_{int}</i> = 0.036
<i>T_{min}</i> = 0.921, <i>T_{max}</i> = 0.983	<i>θ_{max}</i> = 25.5°
10172 measured reflections	<i>h</i> = -13 → 14
	<i>k</i> = -8 → 8
	<i>l</i> = -29 → 19

Refinement

Refinement on <i>F</i> ²	$w = 1/[\sigma^2(F_o^2) + (0.0387P)^2 + 0.7201P]$
$R[F^2 > 2\sigma(F^2)] = 0.068$	where $P = (F_o^2 + 2F_c^2)/3$
$wR(F^2) = 0.133$	(Δ/σ) _{max} < 0.001
<i>S</i> = 1.18	$\Delta\rho_{max} = 0.23 \text{ e } \text{Å}^{-3}$
3754 reflections	$\Delta\rho_{min} = -0.16 \text{ e } \text{Å}^{-3}$
244 parameters	
H-atom parameters constrained	

Table 1

Selected bond lengths (Å).

S1—C8	1.667 (3)	N2—C8	1.321 (3)
O1—C7	1.221 (3)	N2—C9	1.465 (3)
O2—C3	1.364 (3)	N3—C11	1.456 (3)
O2—C21	1.409 (4)	N3—C14	1.462 (3)
N1—C7	1.373 (3)	N3—C12	1.463 (3)
N1—C8	1.391 (3)		

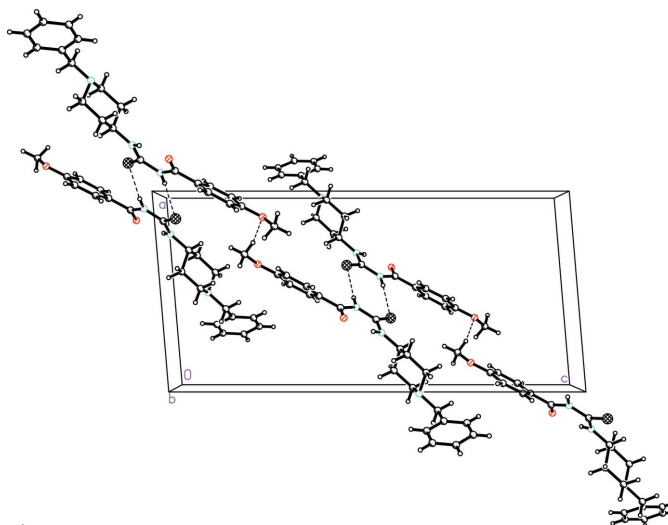


Figure 2

The crystal packing of (I), viewed along the *b* axis. Dashed lines indicate hydrogen bonds.

Table 2

Hydrogen-bond geometry (Å, °).

<i>D</i> —H··· <i>A</i>	<i>D</i> —H	H··· <i>A</i>	<i>D</i> ··· <i>A</i>	<i>D</i> —H··· <i>A</i>
N2—H2A···O1 ⁱ	0.86	1.94	2.627 (3)	136
C9—H9A···S1 ⁱ	0.98	2.80	3.120 (3)	100
N1—H1A···S1 ⁱⁱ	0.86	2.66	3.516 (2)	172
C21—H21C···O2 ⁱⁱⁱ	0.96	2.56	3.438 (4)	152

Symmetry codes: (i) *x*, *y*, *z*; (ii) $-x + 2, -y + 2, -z + 2$; (iii) $-x + \frac{1}{2}, y - \frac{1}{2}, -z + \frac{3}{2}$.

After their location in a difference map, all H atoms were positioned geometrically and allowed to ride on the parent atom with C—H = 0.93–0.96 Å and N—H = 0.86 Å, and *U*_{iso}(H) = 1.2*U*_{eq}(CH₂ and NH) or 1.5*U*_{eq}(CH₃).

Data collection: SMART (Siemens, 1996); cell refinement: SAINT (Siemens, 1996); data reduction: SAINT; program(s) used to solve structure: SHELXTL (Sheldrick, 1997); program(s) used to refine structure: SHELXTL; molecular graphics: SHELXTL; software used to prepare material for publication: SHELXTL, PARST (Nardelli, 1995) and PLATON (Spek, 2003).

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