

supporting information

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N-[(2,4-Dimethylphenyl)carbamothioyl]-2-methylbenzamide

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S1. Comment

The title compound, (I), is isomeric to the previously reported 1-(2,3-dimethylphenyl)-3-(2-methylbenzoyl)thiourea (II), (Khawar Rauf *et al.*, 2007) with the difference that the 2,3-dimethylphenyl ring is replaced by 2,4-dimethylphenyl (Fig.1). The bond lengths and angles are in normal range (Allen *et al.*, 1987) and in agreement with those in (II). The central thiourea moiety (S1/N1/N2/C9), 2-methylbenzoyl (C1—C8), and 2,3-dimethylphenyl (C10—C15) rings are each planar with a maximum deviation of 0.040 (2) Å for C8 atom from the least square plane. The dihedral angles between the thiourea moiety and the 2-methylbenzoyl and 2,3-dimethylphenyl rings are 52.96 (11) and 70.34 (12)°, respectively. The *trans-cis* geometry of the thiourea moiety is stabilized by N2—H2···O1 and C17—H17B···S1 intramolecular hydrogen bonds. In the crystal structure, the molecules are linked to form dimers by the N1—H1···S1 intermolecular hydrogen bond (symmetry codes as in Table 2) and arranged parallel to *c* axis (Fig.2).

S2. Experimental

The mixture of 2-methylbenzoyl chloride (9.720 g, 0.025 mol) with the equimolar amount of ammonium thiocyanate (1.903 g, 0.025 mol) and 2,3-dimethyl aniline (3.025 g, 0.025 mol) in 40 ml dry acetone was refluxed with stirring for 4 h. The solution was filtered and left to evaporate at room temperature. The colourless crystals obtained after a few days, was found suitable for X-ray investigations. The yield was 85% with melting point 413.2–415.7 K.

S3. Refinement

H atoms on the C and N parent atoms were positioned geometrically, with C—H = 0.96, 0.93 and N—H = 0.86 Å and constrained to ride on their parent atoms with $U_{\text{iso}}(\text{H}) = 1.2U_{\text{eq}}(\text{CH and NH})$ and $1.5U_{\text{eq}}(\text{CH}_3)$.

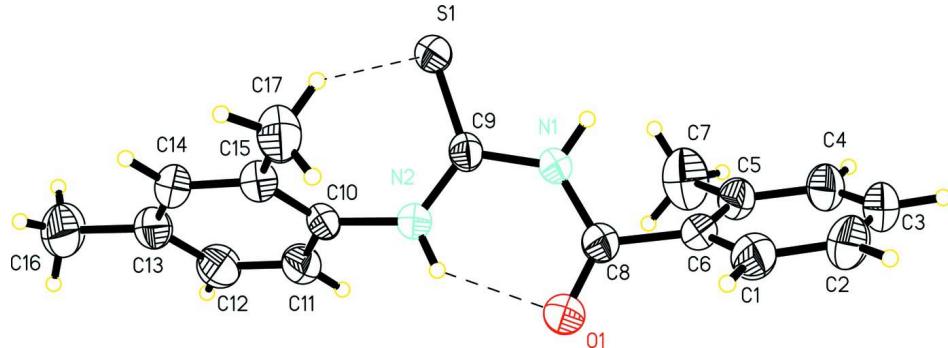
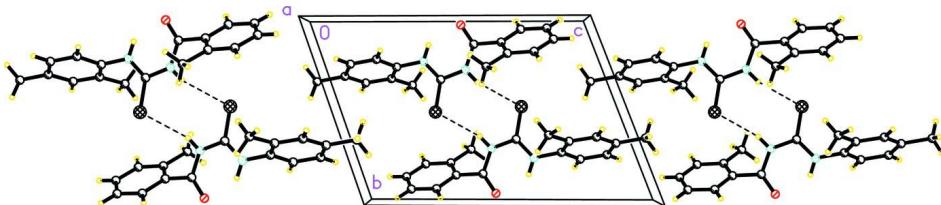


Figure 1

The molecular structure of (I) with displacement ellipsoids drawn at 50% probability level. The dashed lines indicate the intramolecular hydrogen bonds.

**Figure 2**

A packing diagram of (I). Hydrogen bonds are shown by dashed lines.

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Crystal data

$C_{17}H_{18}N_2OS$
 $M_r = 298.39$
Triclinic, $P\bar{1}$
Hall symbol: -P 1
 $a = 6.2569 (15)$ Å
 $b = 9.862 (2)$ Å
 $c = 13.986 (3)$ Å
 $\alpha = 69.461 (4)^\circ$
 $\beta = 86.199 (4)^\circ$
 $\gamma = 75.206 (4)^\circ$
 $V = 781.1 (3)$ Å³

$Z = 2$
 $F(000) = 316$
 $D_x = 1.269 \text{ Mg m}^{-3}$
Mo $K\alpha$ radiation, $\lambda = 0.71073$ Å
Cell parameters from 1377 reflections
 $\theta = 1.5\text{--}25.5^\circ$
 $\mu = 0.21 \text{ mm}^{-1}$
 $T = 298 \text{ K}$
Slab, colourless
 $0.27 \times 0.18 \times 0.09$ mm

Data collection

Bruker SMART APEX CCD area-detector diffractometer
Radiation source: fine-focus sealed tube
Graphite monochromator
Detector resolution: 83.66 pixels mm⁻¹
 ω scans
Absorption correction: multi-scan (*SADABS*; Bruker, 2000)
 $T_{\min} = 0.946$, $T_{\max} = 0.982$

7817 measured reflections
2904 independent reflections
2069 reflections with $I > 2\sigma(I)$
 $R_{\text{int}} = 0.034$
 $\theta_{\max} = 25.5^\circ$, $\theta_{\min} = 1.5^\circ$
 $h = -7 \rightarrow 7$
 $k = -11 \rightarrow 11$
 $l = -16 \rightarrow 16$

Refinement

Refinement on F^2
Least-squares matrix: full
 $R[F^2 > 2\sigma(F^2)] = 0.047$
 $wR(F^2) = 0.119$
 $S = 1.02$
2904 reflections
193 parameters
0 restraints
Primary atom site location: structure-invariant direct methods

Secondary atom site location: difference Fourier map
Hydrogen site location: inferred from neighbouring sites
H-atom parameters constrained
 $w = 1/[\sigma^2(F_o^2) + (0.0567P)^2 + 0.1084P]$
where $P = (F_o^2 + 2F_c^2)/3$
 $(\Delta/\sigma)_{\max} = 0.001$
 $\Delta\rho_{\max} = 0.23 \text{ e } \text{\AA}^{-3}$
 $\Delta\rho_{\min} = -0.17 \text{ e } \text{\AA}^{-3}$

Special details

Geometry. All e.s.d.'s (except the e.s.d. in the dihedral angle between two l.s. planes) are estimated using the full covariance matrix. The cell e.s.d.'s are taken into account individually in the estimation of e.s.d.'s in distances, angles and torsion angles; correlations between e.s.d.'s in cell parameters are only used when they are defined by crystal symmetry. An approximate (isotropic) treatment of cell e.s.d.'s is used for estimating e.s.d.'s involving l.s. planes.

C5—C6—C8—O1	123.3 (3)	C11—C10—C15—C14	−1.9 (3)
C1—C6—C8—N1	120.3 (2)	N2—C10—C15—C14	−179.21 (19)
C5—C6—C8—N1	−58.6 (3)	C11—C10—C15—C17	175.5 (2)
C10—N2—C9—N1	−174.81 (18)	N2—C10—C15—C17	−1.8 (3)

Hydrogen-bond geometry (Å, °)

D—H···A	D—H	H···A	D···A	D—H···A
N2—H2···O1	0.86	2.03	2.706	135
C17—H17B···S1	0.96	2.80	3.496	130
N1—H1···S1 ⁱ	0.86	2.57	3.372	155

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