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2-[(*E*)-(4-Chlorophenyl)methyleneamino]-*N*-(*X*-methylphenyl)-4,5,6,7tetrahydro-1-benzothiophene-3-carboxamide, where *X* = 2 and 3

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The title compounds, both $C_{23}H_{21}CIN_2OS$, are isomeric, with (I) and (II) being the *N*-3-methylphenyl and *N*-2-methylphenyl derivatives, respectively. The dihedral angle between the 4-chlorophenyl group and the thiophene ring in (II) [38.1 (1)°] is larger than that in (I) [7.1 (1)°], indicating steric repulsion between the chlorophenyl and *o*-toluidine groups in (II). In both compounds, an intramolecular N-H···N hydrogen bond forms a pseudo-six-membered ring, thus locking the molecular conformation. In the crystal structures, molecules are connected *via* N-H···O hydrogen bonds, forming chains along the *b* axis in (I) and along the *c* axis in (II). Intermolecular C-H···O/S and π - π interactions are also observed in (II), but not in (I).

Comment

The design and synthesis of compounds which possess important pharmacological properties, such as antibacterial, anticancer, anti-inflamatory and antitoxic properties, is an area of research with widespread potential application in medicine (Pellis & West, 1968; Cohen et al., 1977; Csaszar & Morvay, 1983; Lakshmi et al., 1985), and in this regard we have selected thiophene derivatives (El-Maghraby et al., 1984; Dzhurayev et al., 1992; Gewald et al., 1966), which have been found to exhibit these activities. In this context, S-containing Schiff bases are most effective. We have already reported the crystal structures of biologically active thiophene-3-carboxamide derivatives (Vasu et al., 2003, 2004). In this paper, structure analyses are presented for the two title compounds, (I) and (II), which show antibacterial and antifungal activities (Mohan & Saravanan, 2002, 2003). The compounds are isomers of each other, differing only in the position of attachment of the methyl at the meta and ortho positions.

Compounds (I) (Fig. 1 and Table 1) and (II) (Fig. 2 and Table 3) contain three different structural moieties and these will be discussed separately. The thiophene ring is essentially planar. The six-membered cyclohexene ring adopts a half-chair conformation, with atoms C6 and C7 deviating from the C5/C3/C4/C8 plane by -0.246 (7) and 0.218 (7) Å, respectively, in (I), and by -0.249 (5) and 0.320 (1) Å, respectively, in (II). The puckering parameters (Cremer & Pople, 1975) generated by *PLATON* (Spek, 1990) for the cyclohexene ring are $q_2 = 0.138$ (4) Å, $\varphi_2 = -151$. (2)° and $\tau = 25$ (1)° in (I), with corresponding values of 0.126 (3) Å, -131 (2)° and 26 (1)° in (II).



The bond angles in the toluidine ring, C20-C21-C22 in (I) [118.6 (1)°] and C17-C22-C21 in (II) [117.6 (2)°], deviate significantly from the ideal value of 120°. This deviation is due to the electron-donating inductive effect of the methyl group (Vasu *et al.*, 2003, 2004). The angle between the mean planes of the *m*-toluidine and thiophene rings is 18.4 (1)° in (I), whereas that between the *o*-toluidine and thiophene rings is 12.9 (1)° in (II). The C16-N2-C17-C18 torsion angle is 11.4 (5)° in (I) and 27.4 (4)° in (II), indicating that the presence of a methyl group in the *ortho* position in (II) causes rotation about the N2-C17 bond to minimize steric repulsion with the amino H atom. An intramolecular N-H···N hydrogen bond (Tables 2 and 4) in each structure locks the molecule into a rigid pseudo-six-membered ring conformation and removes the conformational flexibility.



Figure 1

The molecular structure of (I), showing the atom-numbering scheme. Displacement ellipsoids are drawn at the 50% probability level and H atoms not involved in hydrogen bonding have been omitted for clarity. The broken lines show the $N-H\cdots N$ intramolecular hydrogen bond.

The amino H atom is also involved in an intermolecular N-H...O hydrogen bond, and molecular chains are formed. In (I), these chains are along the b axis, related by a b-glide plane $(\frac{1}{2} - x, \frac{1}{2} + y, z)$ orthogonal to the *a* axis (Fig. 3). In (II), the chains are along the *b* axis, related by a *c*-glide plane $(x, \frac{1}{2} - y, \frac{1}{2} - y)$ $z + \frac{1}{2}$) orthogonal to the b axis (Fig. 4). There are no inter-



Figure 2

The molecular structure of (II), showing the atom-numbering scheme. Displacement ellipsoids are drawn at the 50% probability level and H atoms not involved in hydrogen bonding have been omitted for clarity. The broken lines show the $N-H\cdots N$ intramolecular hydrogen bond.



Figure 3

A packing diagram for (I). The dotted lines show the formation of N-H...O hydrogen-bonded chains.



Figure 4

A packing diagram for (II). The dotted lines show $N-H \cdots O$ hydrogen bonds, and C-H···O, C-H···S and π - π interactions.

molecular C-H···O/S or π - π interactions in (I). On the other hand, in (II), the chlorophenyl rings are oriented in a manner that facilitates intermolecular $\pi - \pi$ interactions, the centre-tocentre distance between the chlorophenyl rings being 3.863 Å. In (II), there are also intermolecular $C-H \cdot \cdot \cdot O/S$ interactions (Fig. 4 and Table 4).

Experimental

The title compounds were synthesized using the Gewald reaction (Gewald et al., 1966). For compound (I), m-cyanotoluidine was refluxed with cyclohexanone in the presence of sulfur, dimethylamine and ethanol at 313-323 K for 1 h. The resulting product was then treated with 4-chlorobenzaldehyde in an equimolar ratio in the presence of ethanol, which yielded (I). This was then recrystallized from a mixture of dichloromethane and ethyl acetate (1:2) by slow evaporation. Yellow crystals of (I) were obtained after four weeks and used for single-crystal data collection. For compound (II), a similar procedure was followed using o-cyanotoluidine, and later 4-chlorobenzaldehyde was added. The compound was purified and crystallized using the same procedure as for (I).

Compound (I)

Crystal data

Mo $K\alpha$ radiation
Cell parameters from 650
reflections
$\theta = 1.6-26.4^{\circ}$
$\mu = 0.31 \text{ mm}^{-1}$
T = 293 (2) K
Block, yellow
$0.30 \times 0.25 \times 0.15 \text{ mm}$

Data collection

Bruker SMART APEX CCD area- detector diffractometer	4113 independent reflections 2436 reflections with $I > 2\sigma(I)$
φ and ω scans	$R_{\rm int} = 0.069$
Absorption correction: multi-scan	$\theta_{\rm max} = 26.4^{\circ}$
(SADABS; Sheldrick, 1996)	$h = -16 \rightarrow 15$
$T_{\min} = 0.908, \ T_{\max} = 0.956$	$k = -10 \rightarrow 10$
29 534 measured reflections	$l = -42 \rightarrow 42$
Refinement	
Refinement on F^2	$w = 1/[\sigma^2(F_o^2) + (0.0454P)^2$

R

R R(F) = 0.060 $wR(F^2) = 0.136$ S = 1.024113 reflections 262 parameters H atoms treated by a mixture of independent and constrained refinement

Table 1

Selected geometric parameters (Å, °) for (I).

N2-C16	1.350 (4)	N1-C9	1.274 (3)
N2-C17	1.411 (4)	N1-C1	1.382 (4)
C21-C22-C17	121.5 (3)	C22-C21-C20	118.6 (3)
C9-N1-C1-S1	-11.1 (4)	C16-N2-C17-C18	11.4 (5)
C1-C2-C16-N2	-28.7 (4)	C11-C10-C9-N1	4.4 (4)

+2.7373P]

 $(\Delta/\sigma)_{\rm max} < 0.001$ $\Delta \rho_{\rm max} = 0.29 \text{ e} \text{ Å}^{-3}$

 $\Delta \rho_{\rm min} = -0.23 \ {\rm e} \ {\rm \AA}^{-3}$

where $P = (F_o^2 + 2F_c^2)/3$

Table 2

Hydrogen-bonding geometry (Å,	°)	for ((I).
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$D - H \cdot \cdot \cdot A$	D-H	$H \cdot \cdot \cdot A$	$D{\cdots}A$	$D - \mathrm{H} \cdots A$
$\begin{array}{c} N2 {-} HN2 {\cdots} N1 \\ N2 {-} HN2 {\cdots} O1^i \end{array}$	0.85 (3)	2.32 (3)	2.887 (4)	125 (3)
	0.85 (3)	2.26 (3)	3.009 (4)	147 (3)

Symmetry code: (i) $\frac{3}{2} - x, \frac{1}{2} + y, z$.

Compound (II)

Crystal data

$C_{23}H_{21}CIN_2OS$ $M_r = 408.94$ Monoclinia P2 (a)	Mo $K\alpha$ radiation Cell parameters from 725
a = 17511(4) Å	$\theta = 1.7 - 25.4^{\circ}$
b = 12.519 (3) Å	$\mu = 0.31 \text{ mm}^{-1}$
c = 9.232 (2) Å	T = 293 (2) K
$\beta = 97.406 \ (4)^{\circ}$	Block, yellow
$V = 2006.9 (8) \text{ Å}^3$	$0.30 \times 0.15 \times 0.10 \text{ mm}$
Z = 4	
$D_x = 1.354 \text{ Mg m}^{-3}$ Data collection	
Bruker SMART APEX CCD area- detector diffractometer	3307 reflections with $I > 2\sigma(I)$ $R_{\text{int}} = 0.018$
φ and ω scans	$\theta_{\rm max} = 26.4^{\circ}$
Absorption correction: multi-scan	$h = -21 \rightarrow 21$
(SADABS; Sheldrick, 1996)	$k = -15 \rightarrow 15$
$T_{\min} = 0.921, \ T_{\max} = 0.970$	$l = -11 \rightarrow 11$
15 187 measured reflections	
3994 independent reflections	

Refinement

Refinement on F^2	$w = 1/[\sigma^2(F_o^2) + (0.1224P)^2$
R(F) = 0.048	+ 0.6875P]
$wR(F^2) = 0.157$	where $P = (F_o^2 + 2F_c^2)/3$
S = 0.91	$(\Delta/\sigma)_{\rm max} = 0.001$
3994 reflections	$\Delta \rho_{\rm max} = 0.43 \ {\rm e} \ {\rm \AA}^{-3}$
262 parameters	$\Delta \rho_{\rm min} = -0.42 \text{ e } \text{\AA}^{-3}$
H atoms treated by a mixture of	
independent and constrained	
refinement	

Table 3

Selected geometric parameters (Å, °) for (II).

N2-C16	1.336 (3)	N1-C9	1.281 (2)
N2-C17	1.421 (3)	N1-C1	1.389 (3)
C17-C22-C21	117.6 (2)	C20-C21-C22	122.3 (2)
N2-C16-C2-C1	-38.2 (3)	C16-N2-C17-C18	27.4 (4)
C9-N1-C1-S1	-25.1 (2)	C11-C10-C9-N1	-11.1 (3)

Table 4

Hydrogen-bonding geometry (Å, $^{\circ}$) for (II).

$D - H \cdot \cdot \cdot A$	D-H	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - H \cdots A$
N2−H2N···N1	0.77 (3)	2.52 (3)	2.985 (3)	121 (2)
$N2-H2N\cdots O1^{i}$	0.77 (3)	2.52 (3)	3.250 (3)	159 (3)
$C11 - H11 \cdot \cdot \cdot S1^{ii}$	0.93	2.84	3.747 (2)	166
$C23-H23C\cdots O1^{i}$	0.96	2.48	3.406 (3)	163

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

For both compounds, amino atom H2N and atom H9 (bonded to C9) were located from difference Fourier maps and were refined isotropically. All other H atoms were constrained to ride on their parent atoms, with C-H = 0.93-0.97 Å and $U_{iso}(H) = 1.2U_{eq}(C)$ or $1.5U_{eq}(C_{methyl})$. The methyl groups were allowed to rotate freely about their C–C bond. In both compounds, the C6–C7 bond length is shorter than the expected value. These C atoms of the cyclohexene moiety have a large vibrational degree of freedom and this is reflected in the large atomic displacement parameters, resulting in the short C–C bond length.

For both compounds, data collection: *SMART* (Bruker, 1998); cell refinement: *SMART*; data reduction: *SAINT* (Bruker, 1998); program(s) used to solve structure: *SIR*92 (Altomare *et al.*, 1993); program(s) used to refine structure: *SHELXL*97 (Sheldrick, 1997); molecular graphics: *ORTEP-3 for Windows* (Farrugia, 1997) and *CAMERON* (Watkin *et al.*, 1993); software used to prepare material for publication: *PLATON* (Spek, 2003).

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Supplementary data for this paper are available from the IUCr electronic archives (Reference: OB1203). Services for accessing these data are described at the back of the journal.

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