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Key indicators

Single-crystal X-ray study
T = 100 K
Mean $\sigma(\text{C}-\text{C}) = 0.002 \text{ \AA}$
R factor = 0.030
wR factor = 0.080
Data-to-parameter ratio = 23.0

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

2-(4-Chlorophenyl)-5-(phenylsulfonyl)perhydro-1,3-thiazolo[3,4-a]pyrrolo[4,5-c]pyrrole

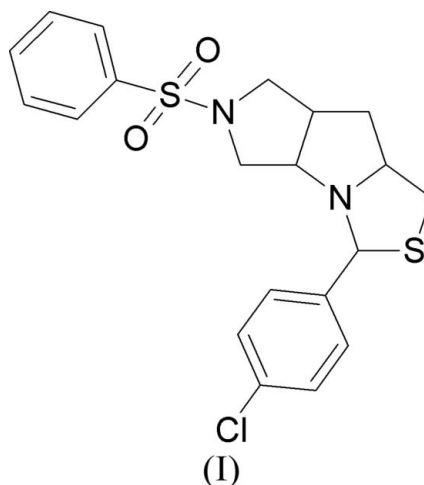
The thiazolidine ring and the two pyrrolidine rings in the title compound, $\text{C}_{20}\text{H}_{21}\text{ClN}_2\text{O}_2\text{S}_2$, adopt twisted conformations. In the crystal structure, the molecules translated by a unit cell along the *a* axis are linked by intermolecular $\text{C}-\text{H}\cdots\text{O}$ hydrogen bonds into a chain and inversion-related molecules in adjacent chains are interconnected *via* $\text{C}-\text{H}\cdots\pi$ interactions to form a double-stranded chain.

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Comment

Some pyrrolo[1,2-*c*]thiazole derivatives are used as platelet-activating factor (PAF) antagonists (Weissman *et al.*, 1993; Le Naour *et al.*, 1994). They also inhibit cytokine-dependent induction of human immunodeficiency virus (HIV) expression in chronically infected promonocytic cells (Weissman *et al.*, 1993). 5-Oxo-hexahydropyrrolo[3,2-*b*]pyrroles have been found to act as inhibitors of human cytomegalovirus protease (Borthwick *et al.*, 2000). Since the title compound, (I), also contains a pyrrolopyrrole and a pyrrolothiazole unit it may also exhibit some biological activity.



The molecular structure of (I) is illustrated in Fig. 1. Bond lengths and angles in (I) agree with those observed in a similar structure, 2-(4-bromophenyl)-5-(phenylsulfonyl)perhydrothiazolo[3,4-*a*]pyrrolo [4,5-*c*]pyrrole, (II) (Kumar *et al.*, 2006). The configuration around atom N1 is nearly planar, whereas atom N2 exhibits a pyramidal geometry. The thiazolidine ring and the two pyrrolidine rings (N1/C1–C4 and N2/C3/C2/C5/C6) adopt twisted conformations. The Cremer & Pople (1975) puckering parameters q_2 and φ are, respectively: 0.397 (1) Å and 124.9 (2) ° for the thiazolidine ring, 0.363 (1) Å and 60.7 (2) ° for the pyrrolidine ring (N1/C1–C4), and 0.419 (1) Å and 198.1 (2) ° for the pyrrolidine ring (N2/C3/C2/C5/C6).

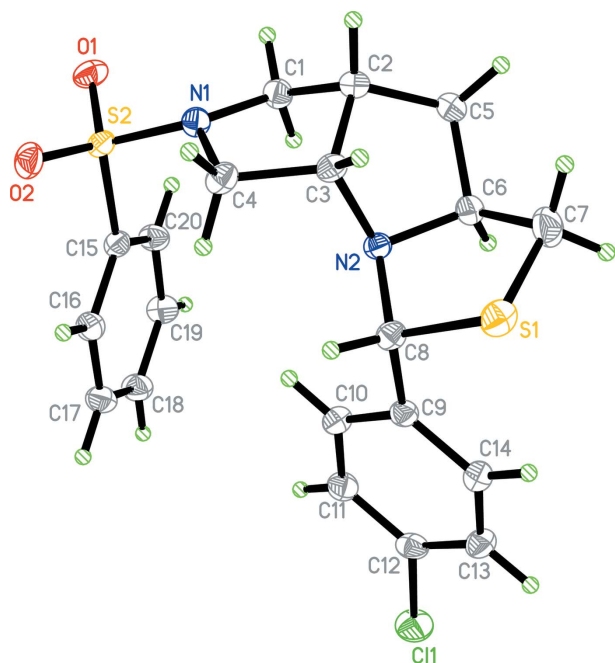


Figure 1
The structure of (I), showing 60% probability displacement ellipsoids and the atomic numbering scheme.

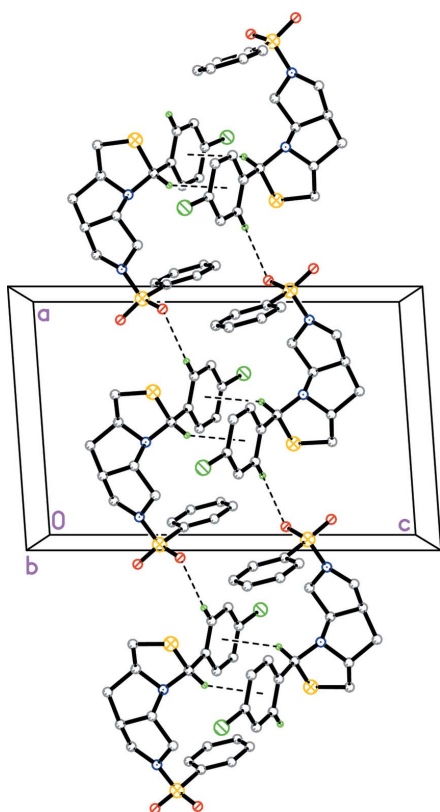


Figure 2
A view of a hydrogen-bonded (dashed lines) double-stranded chain in (I). Only the H atoms involved in hydrogen bonding are shown.

The crystal packing of (I) reveals that molecules translated by a unit cell along the *a* axis are linked by intermolecular C—

H···O hydrogen bonds (Table 1) into chains. Inversion-related molecules in adjacent chains are interconnected *via* C—H··· π interactions, involving the C9–C14 benzene rings (centroid *Cg*1), to form double-stranded chains along the *a* axis (Fig. 2).

A superimposed fit of the non-H atoms of (I) and the corresponding atoms in (II) (Kumar *et al.*, 2006) gives an r.m.s. deviation of 0.038 Å. This indicates that the conformation of (I) is not significantly altered by replacing the Br atom in (II) by a Cl atom. The pattern of intermolecular C—H··· π hydrogen bonding is identical in the crystal structures of (I) and (II).

Experimental

A solution of *N*-allyl-*N*-(2-oxoethyl)benzenesulfonamide (1 mmol) and 2-(*p*-chlorophenyl)thiazolidine-4-carboxylic acid (1.2 mmol) in dry toluene (30 ml) was refluxed for 4 h. After completion of the reaction, the solvent was evaporated off vacuum and the residue was chromatographed (SiO₂) using a hexane–ethyl acetate (9:1) mixture, to yield the title compound. Compound (I) was recrystallized from ethyl acetate.

Crystal data

C ₂₀ H ₂₁ ClN ₂ O ₂ S ₂	<i>Z</i> = 4
<i>M_r</i> = 420.96	<i>D_x</i> = 1.446 Mg m ^{−3}
Monoclinic, <i>P</i> 2 ₁ / <i>c</i>	Mo <i>K</i> α radiation
<i>a</i> = 10.4869 (2) Å	μ = 0.43 mm ^{−1}
<i>b</i> = 11.2536 (2) Å	<i>T</i> = 100 (2) K
<i>c</i> = 16.4220 (2) Å	Block, colourless
β = 94.052 (1)°	0.56 × 0.33 × 0.32 mm
<i>V</i> = 1933.20 (6) Å ³	

Data collection

Bruker SMART APEXII CCD area-detector diffractometer	25474 measured reflections
ω scans	5600 independent reflections
Absorption correction: multi-scan (<i>SADABS</i> ; Bruker, 2005)	5046 reflections with <i>I</i> > 2σ(<i>I</i>)
<i>T</i> _{min} = 0.795, <i>T</i> _{max} = 0.874	<i>R</i> _{int} = 0.026
	θ _{max} = 30.0°

Refinement

Refinement on <i>F</i> ²	$w = 1/[\sigma^2(F_o^2) + (0.0399P)^2 + 0.9249P]$
$R[F^2 > 2\sigma(F^2)] = 0.030$	where $P = (F_o^2 + 2F_c^2)/3$
$wR(F^2) = 0.080$	(Δ/σ) _{max} = 0.001
<i>S</i> = 1.03	$\Delta\rho$ _{max} = 0.48 e Å ^{−3}
5600 reflections	$\Delta\rho$ _{min} = −0.33 e Å ^{−3}
244 parameters	
H-atom parameters constrained	

Table 1

Hydrogen-bond geometry (Å, °).

*Cg*1 is the centroid of the ring C9–C14.

<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>
C3—H3···S1	1.00	2.83	3.2274 (11)	104
C14—H14···S1	0.95	2.66	3.1103 (13)	110
C14—H14···O2 ⁱ	0.95	2.51	3.3863 (14)	153
C16—H16···O2	0.95	2.57	2.9246 (15)	102
C8—H8··· <i>Cg</i> 1 ⁱⁱ	1.00	2.61	3.4999 (12)	148

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

The H atoms were positioned geometrically and were treated as riding on their parent C atoms, with C–H = 0.95–1.00 Å and $U_{\text{iso}}(\text{H}) = 1.2U_{\text{eq}}(\text{C})$.

Data collection: *APEX2* (Bruker, 2005); cell refinement: *APEX2*; data reduction: *SAINT* (Bruker, 2005); program(s) used to solve structure: *SHELXTL* (Sheldrick, 1998); program(s) used to refine structure: *SHELXTL*; molecular graphics: *SHELXTL*; software used to prepare material for publication: *SHELXTL* and *PLATON* (Spek, 2003).

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