

2-(4-Chlorophenyl)-3-cyclohexylthiazolidin-4-one

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Key indicators

Single-crystal X-ray study

$T = 293\text{ K}$

Mean $\sigma(\text{C}-\text{C}) = 0.004\text{ \AA}$

R factor = 0.048

wR factor = 0.119

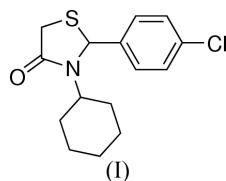
Data-to-parameter ratio = 16.7

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

The thiazolidine ring of the title molecule, $\text{C}_{15}\text{H}_{18}\text{ClNOS}$, is planar within $0.042(3)\text{ \AA}$ and the cyclohexane ring adopts a chair conformation. The molecular structure is stabilized by weak $\text{C}-\text{H}\cdots\text{O}$ and $\text{C}-\text{H}\cdots\pi$ interactions. In the crystal structure, bifurcated $\text{C}-\text{H}\cdots\text{O}$ interactions link symmetry-related molecules to form dimers.

Comment

The therapeutic importance of suitably functionalized thiazolidinone ring systems (Anders *et al.*, 2001; Tanabe *et al.*, 1995; Diurno *et al.*, 1992) has encouraged us to develop an innovative synthesis in which different substituents could be arranged in a pharmacophoric pattern to display diverse pharmacological activities of higher order (Srivastava *et al.*, 2002). Since not much is known about the exact binding site of this class of molecules we thought it appropriate to generate X-ray crystal data of a prototype. Hence the X-ray structure determination of the title compound was undertaken. The data generated, especially 'non-covalent interactions' could be used for structural study and correlation. Non-covalent interactions play a significant role in molecular recognition, stabilization of DNA/RNA structures (Hobza & Sponer, 1999), crystal engineering (Desiraju, 1995) and drug development (Meyer *et al.*, 2003).



In the title molecule, (I) (Fig. 1), the central thiazolidinone ring is planar within $0.042(3)\text{ \AA}$ and its conformation may be described as flattened envelope, with S1 deviating from the C2/N3/C4/C5 plane by $0.139(1)\text{ \AA}$. The cyclohexane ring adopts a chair conformation. The dihedral angle between the C2/N3/C4/C5 plane and the chlorophenyl ring is $83.5(1)^\circ$. The molecular structure is stabilized by $\text{C}-\text{H}\cdots\text{O}$ and $\text{C}-\text{H}\cdots\pi$ interactions (Fig. 1 and Table 1). The crystal packing reveals that a molecule and its inversion equivalent are linked by bifurcated $\text{C}-\text{H}\cdots\text{O}$ interactions to form dimers (Fig. 2). The crystal structure is further stabilized by van der Waals interactions.

Experimental

The title compound was prepared from *p*-chlorobenzaldehyde and mercaptacetic acid, according to a literature procedure (Srivastava

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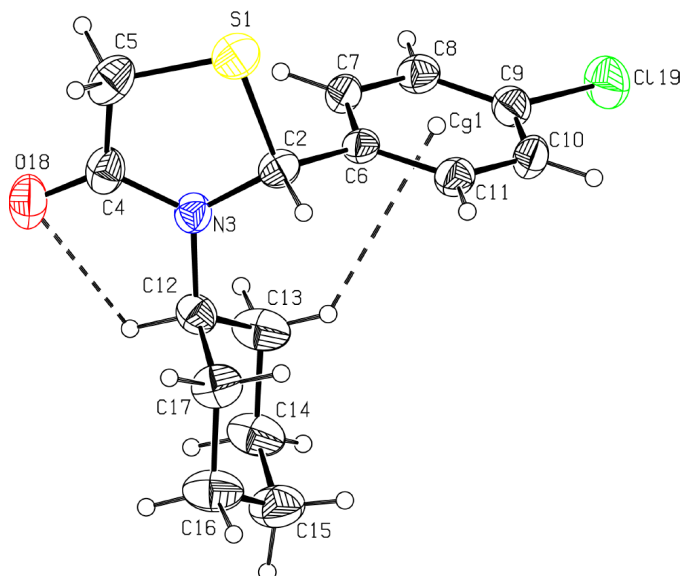


Figure 1
Displacement ellipsoid plot (30% probability), showing the molecular structure and the atom-labelling for the title compound. Non-covalent interactions are shown as dashed lines.

et al., 2002) and diffraction quality crystals were obtained by slow evaporation from a mixture of ethyl acetate and hexane (1:1).

Crystal data

$C_{15}H_{18}ClNO$	$D_x = 1.348 \text{ Mg m}^{-3}$
$M_r = 295.81$	Mo $K\alpha$ radiation
Monoclinic, $C2/c$	Cell parameters from 40 reflections
$a = 17.600 (1) \text{ \AA}$	$\theta = 5.1\text{--}12.5^\circ$
$b = 9.775 (1) \text{ \AA}$	$\mu = 0.40 \text{ mm}^{-1}$
$c = 17.089 (1) \text{ \AA}$	$T = 293 (2) \text{ K}$
$\beta = 97.33 (1)^\circ$	Block, colourless
$V = 2916.0 (4) \text{ \AA}^3$	$0.25 \times 0.20 \times 0.18 \text{ mm}$
$Z = 8$	

Data collection

Bruker P4 diffractometer	$h = -1 \rightarrow 21$
θ - 2θ scans	$k = -1 \rightarrow 12$
Absorption correction: none	$l = -21 \rightarrow 20$
3556 measured reflections	3 standard reflections
2866 independent reflections	every 97 reflections
1731 reflections with $I > 2\sigma(I)$	frequency: 60 min
$R_{\text{int}} = 0.023$	intensity decay: none
$\theta_{\text{max}} = 26.0^\circ$	

Refinement

Refinement on F^2	$w = 1/[\sigma^2(F_o^2) + (0.0439P)^2 + 1.3546P]$
$R[F^2 > 2\sigma(F^2)] = 0.048$	where $P = (F_o^2 + 2F_c^2)/3$
$wR(F^2) = 0.119$	$(\Delta/\sigma)_{\text{max}} < 0.001$
$S = 1.02$	$\Delta\rho_{\text{max}} = 0.21 \text{ e \AA}^{-3}$
2866 reflections	$\Delta\rho_{\text{min}} = -0.21 \text{ e \AA}^{-3}$
172 parameters	
H-atom parameters constrained	

Table 1

Hydrogen-bonding geometry (\AA , $^\circ$).

$D\text{--}H\cdots A$	$D\text{--}H$	$H\cdots A$	$D\cdots A$	$D\text{--}H\cdots A$
$C5\text{--}H5B\cdots O18^i$	0.97	2.56	3.226 (4)	126
$C7\text{--}H7\cdots O18^i$	0.93	2.68	3.601 (3)	169
$C12\text{--}H12\cdots O18$	0.98	2.31	2.785 (3)	109
$C13\text{--}H13A\cdots Cg1$	0.97	2.99	3.717 (3)	133

Symmetry codes: (i) $\frac{1}{2} - x, \frac{1}{2} - y, -z$. Cg1 denotes the centroid of the substituted phenyl ring.

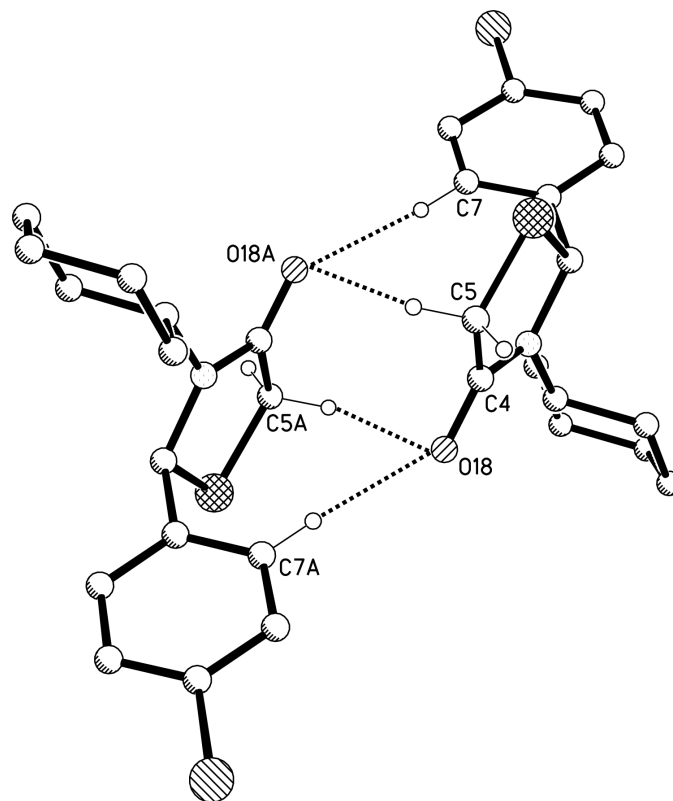


Figure 2

A view of the bifurcated $C\text{--}H\cdots O$ interactions leading to the formation of a dimer. Atoms labelled with the suffix *A* are at the symmetry position $(\frac{1}{2} - x, \frac{1}{2} - y, -z)$, *i.e.* symmetry code (i) in Table 1.

All H atoms were placed in calculated positions and allowed to ride on their parent C atoms, with $C\text{--}H = 0.93\text{--}0.98 \text{ \AA}$ and $U_{\text{iso}}(H) = 1.2U_{\text{eq}}(C)$.

Data collection: *XSCANS* (Siemens, 1996); cell refinement: *XSCANS*; data reduction: *XSCANS*; program(s) used to solve structure: *SHELXTL* (Bruker, 1997); program(s) used to refine structure: *SHELXTL*; molecular graphics: *SHELXTL*; software used to prepare material for publication: *SHELXTL*.

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