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4-Chloro-*N*-cyclohexylbenzene-sulfonamideShahzad Sharif,^a Shumaila Younas Mughal,^a Islam Ullah Khan,^a Mehmet Akkurt^{b*} and Muneeb Hayat Khan^c

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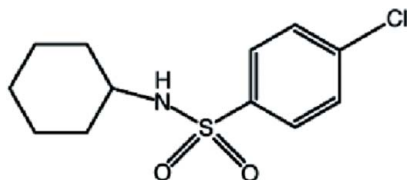
Received 13 January 2012; accepted 16 January 2012

Key indicators: single-crystal X-ray study; $T = 296$ K; mean $\sigma(\text{C}-\text{C}) = 0.005$ Å; R factor = 0.053; wR factor = 0.150; data-to-parameter ratio = 21.4.

The title compound, $\text{C}_{12}\text{H}_{16}\text{ClNO}_2\text{S}$, adopts an L-shaped conformation, with the central C—S—N—C torsion angle being $-78.0(2)^\circ$. The cyclohexyl ring adopts a chair conformation. In the crystal, adjacent molecules are connected by pairs of N—H \cdots O hydrogen bonds around an inversion centre, forming cyclic dimers [graph set $R_2^2(8)$].

Related literature

For background to the pharmacological uses of sulfonamides, see: Korolkovas (1988); Mandell & Sande (1992). For related structures, see: Sharif *et al.* (2011); Khan *et al.* (2010); John *et al.* (2010). For ring conformational analysis, see: Cremer & Pople (1975).



Experimental

Crystal data

$\text{C}_{12}\text{H}_{16}\text{ClNO}_2\text{S}$
 $M_r = 273.78$
 Monoclinic, $P2_1/c$
 $a = 11.1226(5)$ Å
 $b = 6.2490(2)$ Å
 $c = 19.8635(9)$ Å
 $\beta = 96.505(2)^\circ$

$V = 1371.73(10)$ Å³
 $Z = 4$
 Mo $K\alpha$ radiation
 $\mu = 0.42$ mm⁻¹
 $T = 296$ K
 $0.29 \times 0.15 \times 0.11$ mm

Data collection

Bruker APEXII CCD
 diffractometer
 12714 measured reflections

3365 independent reflections
 2075 reflections with $I > 2\sigma(I)$
 $R_{\text{int}} = 0.030$

Refinement

$R[F^2 > 2\sigma(F^2)] = 0.053$
 $wR(F^2) = 0.150$
 $S = 1.03$
 3365 reflections
 157 parameters
 1 restraint

H atoms treated by a mixture of independent and constrained refinement
 $\Delta\rho_{\text{max}} = 0.39$ e Å⁻³
 $\Delta\rho_{\text{min}} = -0.25$ e Å⁻³

Table 1

Hydrogen-bond geometry (Å, °).

$D-H\cdots A$	$D-H$	$H\cdots A$	$D\cdots A$	$D-H\cdots A$
$\text{N1}-\text{H1N}\cdots\text{O1}^i$	0.85 (4)	2.05 (4)	2.891 (4)	170 (3)

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

Data collection: APEX2 (Bruker, 2007); cell refinement: SAINT (Bruker, 2007); data reduction: SAINT; program(s) used to solve structure: SIR97 (Altomare *et al.*, 1999); program(s) used to refine structure: SHELXL97 (Sheldrick, 2008); molecular graphics: ORTEP-3 for Windows (Farrugia, 1997); software used to prepare material for publication: WinGX (Farrugia, 1999) and PLATON (Spek, 2009).

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Supplementary data and figures for this paper are available from the IUCr electronic archives (Reference: HG5164).

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supporting information

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4-Chloro-*N*-cyclohexylbenzenesulfonamide

Shahzad Sharif, Shumaila Younas Mughal, Islam Ullah Khan, Mehmet Akkurt and Muneeb Hayat Khan

S1. Comment

Sulfonamide group containing drugs are extensively used for the treatment of certain infections caused by Gram-positive and Gram-negative microorganisms (Korolkovas, 1988; Mandell & Sande, 1992). In continuation of our on going structural studies of cyclohexylamine and sulfonamides synthesis (John *et al.*, 2010; Khan *et al.*, 2010; Sharif *et al.*, 2011), herein the crystal structure of title compound (I) is described.

In (I), (Fig. 1), the S atom has a distorted tetrahedral geometry within a CNO₂ donor set [maximum deviation: O—S—O = 119.45 (12)°]. The central C6—S1—N1—C7 torsion angle is -78.0 (2)°. The C7—C12 cyclohexyl ring adopts a chair conformation, with puckering parameters (Cremer & Pople, 1975) Q = 0.536 (4) Å, θ = 180.0 (4) °, φ = 196 (16) °.

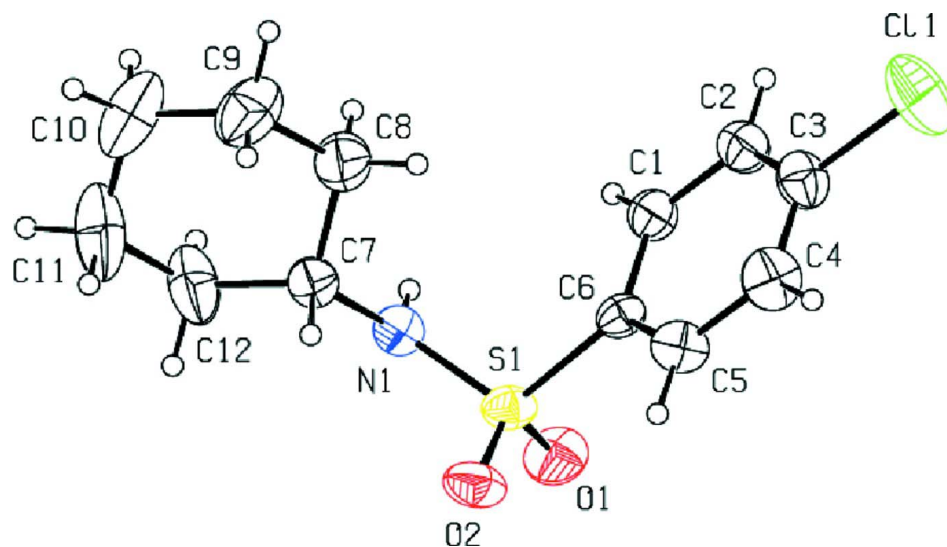
In the crystal, two adjacent molecules are linked by a pair of N—H···O hydrogen bonds, forming an inversion dimer with an R₂²(8) ring motif (Table 1, Fig. 2).

S2. Experimental

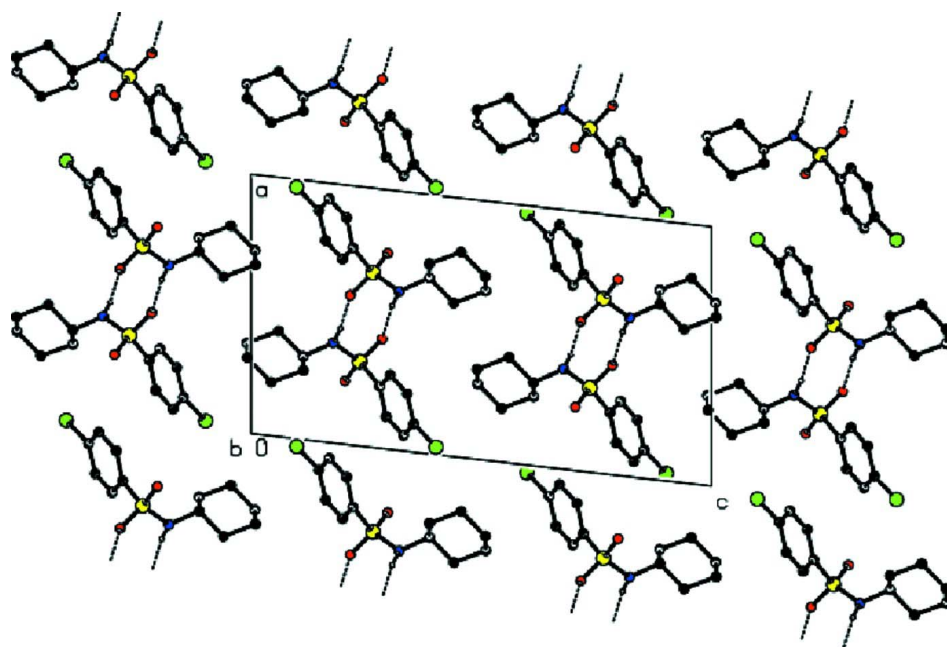
To 115 μ l (1 mmol) of cyclohexylamine in 10 ml distilled water, was added 211 mg (1 mmol) of 4-chlorobenzenesulfonyl chloride while maintaining the pH of reaction mixture at 8 by using 3% sodium carbonate solution. Consumption of the reactants was confirmed by TLC. The pH of reaction mixture was adjusted by 3 N HCl at 3. Precipitates formed, washed with water and crystallized from methanol.

S3. Refinement

The NH H-atom was located in a difference Fourier map and isotropically refined with a distance restraint: N—H = 0.86 (2) Å. C-bound H atoms were placed in calculated positions with C—H distances in the range 0.93–0.98 Å and were refined using a riding model with $U_{\text{iso}}(\text{H}) = 1.2U_{\text{eq}}(\text{C})$. In the final refinement two low angle reflections evidently effected by the beam stop were omitted, *i.e.* 0 0 2 and 1 0 0.

**Figure 1**

The title molecule, showing the atom numbering scheme. Displacement ellipsoids for non-H atoms are drawn at the 30% probability level.

**Figure 2**

The crystal packing of (I) down *b* axis, showing the molecules are linked into dimers by pairs of N—H...O hydrogen bonds, forming $R_2^2(8)$ graph-set motif. Hydrogen atoms not involved in hydrogen bonding have been omitted for clarity.

4-Chloro-*N*-cyclohexylbenzenesulfonamide

Crystal data

$C_{12}H_{16}ClNO_2S$

$M_r = 273.78$

Monoclinic, $P2_1/c$

Hall symbol: $-P 2_1/c$

$a = 11.1226 (5) \text{ \AA}$

$b = 6.2490 (2) \text{ \AA}$

$c = 19.8635 (9) \text{ \AA}$
 $\beta = 96.505 (2)^\circ$
 $V = 1371.73 (10) \text{ \AA}^3$
 $Z = 4$
 $F(000) = 576$
 $D_x = 1.326 \text{ Mg m}^{-3}$
 Mo $K\alpha$ radiation, $\lambda = 0.71069 \text{ \AA}$

Cell parameters from 3062 reflections

$\theta = 2.6\text{--}21.6^\circ$
 $\mu = 0.42 \text{ mm}^{-1}$
 $T = 296 \text{ K}$
 Needle, light brown
 $0.29 \times 0.15 \times 0.11 \text{ mm}$

Data collection

Bruker APEXII CCD
 diffractometer
 Radiation source: sealed tube
 Graphite monochromator
 φ and ω scans
 12714 measured reflections
 3365 independent reflections

2075 reflections with $I > 2\sigma(I)$

$R_{\text{int}} = 0.030$
 $\theta_{\text{max}} = 28.3^\circ$, $\theta_{\text{min}} = 3.4^\circ$
 $h = -14 \rightarrow 14$
 $k = -6 \rightarrow 8$
 $l = -26 \rightarrow 26$

Refinement

Refinement on F^2
 Least-squares matrix: full
 $R[F^2 > 2\sigma(F^2)] = 0.053$
 $wR(F^2) = 0.150$
 $S = 1.03$
 3365 reflections
 157 parameters
 1 restraint
 Primary atom site location: structure-invariant
 direct methods

Secondary atom site location: difference Fourier
 map

Hydrogen site location: inferred from
 neighbouring sites
 H atoms treated by a mixture of independent
 and constrained refinement

$w = 1/[\sigma^2(F_o^2) + (0.0613P)^2 + 0.526P]$

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

$(\Delta/\sigma)_{\text{max}} < 0.001$

$\Delta\rho_{\text{max}} = 0.39 \text{ e \AA}^{-3}$

$\Delta\rho_{\text{min}} = -0.25 \text{ e \AA}^{-3}$

Special details

Geometry. Bond distances, angles *etc.* have been calculated using the rounded fractional coordinates. All su's are estimated from the variances of the (full) variance-covariance matrix. The cell e.s.d.'s are taken into account in the estimation of distances, angles and torsion angles

Refinement. Refinement on F^2 for ALL reflections except those flagged by the user for potential systematic errors. Weighted R -factors wR and all goodnesses of fit S are based on F^2 , conventional R -factors R are based on F , with F set to zero for negative F^2 . The observed criterion of $F^2 > \sigma(F^2)$ is used only for calculating $-R$ -factor-obs *etc.* and is not relevant to the choice of reflections for refinement. R -factors based on F^2 are statistically about twice as large as those based on F , and R -factors based on ALL data will be even larger.

Fractional atomic coordinates and isotropic or equivalent isotropic displacement parameters (\AA^2)

	x	y	z	$U_{\text{iso}}^*/U_{\text{eq}}$
Cl1	0.97047 (9)	0.63719 (19)	0.09885 (6)	0.1159 (5)
S1	0.67445 (5)	0.02579 (10)	0.26455 (3)	0.0538 (2)
O1	0.57744 (18)	-0.0412 (3)	0.21563 (11)	0.0788 (8)
O2	0.75531 (17)	-0.1301 (3)	0.29647 (11)	0.0710 (7)
N1	0.61305 (18)	0.1518 (3)	0.32146 (11)	0.0527 (7)
C1	0.7127 (2)	0.3981 (4)	0.19816 (13)	0.0581 (9)
C2	0.7777 (3)	0.5312 (4)	0.16141 (14)	0.0650 (9)
C3	0.8901 (3)	0.4698 (5)	0.14686 (14)	0.0654 (10)
C4	0.9396 (2)	0.2788 (5)	0.16961 (16)	0.0733 (11)
C5	0.8750 (2)	0.1454 (4)	0.20712 (14)	0.0606 (9)

C6	0.7611 (2)	0.2037 (4)	0.22098 (12)	0.0465 (7)
C7	0.6789 (2)	0.2145 (4)	0.38711 (12)	0.0541 (8)
C8	0.7329 (3)	0.4325 (5)	0.38666 (16)	0.0829 (11)
C9	0.7924 (4)	0.4979 (7)	0.45609 (18)	0.1069 (17)
C10	0.7084 (4)	0.4802 (9)	0.5084 (2)	0.117 (2)
C11	0.6528 (5)	0.2674 (10)	0.50951 (18)	0.135 (2)
C12	0.5920 (4)	0.1970 (7)	0.44002 (17)	0.1033 (16)
H1	0.63600	0.43810	0.20780	0.0700*
H1N	0.555 (3)	0.234 (6)	0.3060 (19)	0.1390*
H2	0.74580	0.66260	0.14640	0.0780*
H4	1.01630	0.23970	0.15970	0.0880*
H5	0.90830	0.01600	0.22310	0.0730*
H7	0.74450	0.11150	0.39850	0.0650*
H8A	0.67010	0.53500	0.37150	0.0990*
H8B	0.79270	0.43550	0.35470	0.0990*
H9A	0.86230	0.40740	0.46850	0.1280*
H9B	0.82060	0.64450	0.45420	0.1280*
H10A	0.75200	0.51000	0.55240	0.1410*
H10B	0.64520	0.58700	0.49970	0.1410*
H11A	0.59300	0.26840	0.54140	0.1620*
H11B	0.71460	0.16380	0.52540	0.1620*
H12A	0.56470	0.05020	0.44260	0.1240*
H12B	0.52180	0.28630	0.42710	0.1240*

Atomic displacement parameters (Å²)

	U^{11}	U^{22}	U^{33}	U^{12}	U^{13}	U^{23}
C11	0.0867 (7)	0.1367 (9)	0.1293 (9)	−0.0197 (6)	0.0339 (6)	0.0505 (7)
S1	0.0456 (4)	0.0438 (3)	0.0725 (4)	−0.0069 (3)	0.0087 (3)	−0.0065 (3)
O1	0.0634 (12)	0.0815 (13)	0.0904 (14)	−0.0310 (10)	0.0034 (11)	−0.0211 (11)
O2	0.0691 (12)	0.0436 (9)	0.1030 (15)	0.0083 (9)	0.0210 (11)	0.0082 (9)
N1	0.0393 (11)	0.0562 (12)	0.0629 (13)	0.0041 (9)	0.0071 (10)	0.0035 (10)
C1	0.0540 (15)	0.0589 (15)	0.0637 (16)	0.0058 (13)	0.0169 (13)	0.0006 (12)
C2	0.0704 (18)	0.0594 (15)	0.0664 (16)	0.0034 (14)	0.0132 (15)	0.0056 (13)
C3	0.0553 (16)	0.0765 (18)	0.0646 (16)	−0.0132 (15)	0.0076 (13)	0.0050 (14)
C4	0.0398 (14)	0.091 (2)	0.090 (2)	−0.0036 (15)	0.0118 (15)	0.0011 (18)
C5	0.0418 (14)	0.0602 (15)	0.0793 (18)	0.0021 (12)	0.0048 (13)	0.0025 (13)
C6	0.0410 (12)	0.0461 (12)	0.0514 (13)	−0.0033 (10)	0.0015 (10)	−0.0093 (10)
C7	0.0463 (14)	0.0565 (14)	0.0597 (15)	0.0112 (12)	0.0063 (12)	0.0059 (12)
C8	0.095 (2)	0.082 (2)	0.0727 (19)	−0.0204 (19)	0.0134 (18)	−0.0077 (16)
C9	0.106 (3)	0.119 (3)	0.095 (3)	−0.014 (2)	0.009 (2)	−0.038 (2)
C10	0.092 (3)	0.178 (5)	0.082 (2)	0.019 (3)	0.009 (2)	−0.049 (3)
C11	0.132 (4)	0.216 (6)	0.059 (2)	−0.014 (4)	0.018 (2)	0.022 (3)
C12	0.100 (3)	0.141 (3)	0.072 (2)	−0.027 (2)	0.023 (2)	0.021 (2)

Geometric parameters (Å, °)

C11—C3	1.731 (4)	C10—C11	1.468 (8)
S1—O1	1.431 (2)	C11—C12	1.531 (6)
S1—O2	1.425 (2)	C1—H1	0.9300
S1—N1	1.594 (2)	C2—H2	0.9300
S1—C6	1.762 (3)	C4—H4	0.9300
N1—C7	1.475 (3)	C5—H5	0.9300
N1—H1N	0.85 (4)	C7—H7	0.9800
C1—C2	1.366 (4)	C8—H8A	0.9700
C1—C6	1.384 (4)	C8—H8B	0.9700
C2—C3	1.370 (5)	C9—H9A	0.9700
C3—C4	1.370 (4)	C9—H9B	0.9700
C4—C5	1.374 (4)	C10—H10A	0.9700
C5—C6	1.376 (3)	C10—H10B	0.9700
C7—C12	1.510 (5)	C11—H11A	0.9700
C7—C8	1.489 (4)	C11—H11B	0.9700
C8—C9	1.517 (5)	C12—H12A	0.9700
C9—C10	1.478 (6)	C12—H12B	0.9700
O1—S1—O2	119.45 (12)	C5—C4—H4	120.00
O1—S1—N1	106.00 (12)	C4—C5—H5	120.00
O1—S1—C6	105.28 (12)	C6—C5—H5	120.00
O2—S1—N1	108.77 (12)	N1—C7—H7	108.00
O2—S1—C6	107.29 (11)	C8—C7—H7	108.00
N1—S1—C6	109.82 (11)	C12—C7—H7	108.00
S1—N1—C7	123.29 (16)	C7—C8—H8A	109.00
S1—N1—H1N	114 (3)	C7—C8—H8B	109.00
C7—N1—H1N	116 (3)	C9—C8—H8A	109.00
C2—C1—C6	120.0 (2)	C9—C8—H8B	109.00
C1—C2—C3	119.6 (3)	H8A—C8—H8B	108.00
C11—C3—C2	119.2 (2)	C8—C9—H9A	109.00
C2—C3—C4	121.1 (3)	C8—C9—H9B	109.00
C11—C3—C4	119.7 (2)	C10—C9—H9A	109.00
C3—C4—C5	119.5 (2)	C10—C9—H9B	109.00
C4—C5—C6	119.9 (2)	H9A—C9—H9B	108.00
S1—C6—C1	120.05 (17)	C9—C10—H10A	109.00
S1—C6—C5	119.92 (19)	C9—C10—H10B	109.00
C1—C6—C5	120.0 (2)	C11—C10—H10A	109.00
N1—C7—C8	113.5 (2)	C11—C10—H10B	109.00
C8—C7—C12	111.2 (3)	H10A—C10—H10B	108.00
N1—C7—C12	107.7 (2)	C10—C11—H11A	109.00
C7—C8—C9	112.1 (3)	C10—C11—H11B	109.00
C8—C9—C10	111.9 (4)	C12—C11—H11A	109.00
C9—C10—C11	112.3 (4)	C12—C11—H11B	109.00
C10—C11—C12	113.0 (4)	H11A—C11—H11B	108.00
C7—C12—C11	110.8 (4)	C7—C12—H12A	110.00
C2—C1—H1	120.00	C7—C12—H12B	109.00

C6—C1—H1	120.00	C11—C12—H12A	109.00
C1—C2—H2	120.00	C11—C12—H12B	109.00
C3—C2—H2	120.00	H12A—C12—H12B	108.00
C3—C4—H4	120.00		
O1—S1—N1—C7	168.78 (18)	C1—C2—C3—C11	178.7 (2)
O2—S1—N1—C7	39.2 (2)	C11—C3—C4—C5	-179.3 (2)
C6—S1—N1—C7	-78.0 (2)	C2—C3—C4—C5	0.6 (5)
N1—S1—C6—C5	135.6 (2)	C3—C4—C5—C6	0.6 (4)
O2—S1—C6—C1	-165.3 (2)	C4—C5—C6—S1	176.1 (2)
N1—S1—C6—C1	-47.2 (2)	C4—C5—C6—C1	-1.1 (4)
O1—S1—C6—C1	66.5 (2)	N1—C7—C8—C9	176.1 (3)
O2—S1—C6—C5	17.5 (2)	C12—C7—C8—C9	54.6 (4)
O1—S1—C6—C5	-110.7 (2)	N1—C7—C12—C11	-178.0 (3)
S1—N1—C7—C12	-144.8 (2)	C8—C7—C12—C11	-53.2 (4)
S1—N1—C7—C8	91.8 (2)	C7—C8—C9—C10	-54.4 (4)
C6—C1—C2—C3	0.7 (4)	C8—C9—C10—C11	53.3 (5)
C2—C1—C6—S1	-176.7 (2)	C9—C10—C11—C12	-53.2 (6)
C2—C1—C6—C5	0.5 (4)	C10—C11—C12—C7	53.0 (5)
C1—C2—C3—C4	-1.3 (4)		

Hydrogen-bond geometry (\AA , $^\circ$)

$D-H\cdots A$	$D-H$	$H\cdots A$	$D\cdots A$	$D-H\cdots A$
N1—H1N \cdots O1 ⁱ	0.85 (4)	2.05 (4)	2.891 (4)	170 (3)

Symmetry code: (i) $-x+1, y+1/2, -z+1/2$.