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2,4-Dichloro-*N*-(3-chlorophenyl)-benzenesulfonamideB. Thimme Gowda,^{a*} Sabine Foro,^b P. G. Nirmala^a and Hartmut Fuess^b

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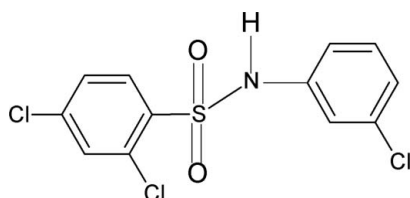
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Key indicators: single-crystal X-ray study; $T = 299$ K; mean $\sigma(\text{C}-\text{C}) = 0.003$ Å; R factor = 0.036; wR factor = 0.100; data-to-parameter ratio = 16.6.

In the title compound, $\text{C}_{12}\text{H}_8\text{Cl}_3\text{NO}_2\text{S}$, the conformation of the $\text{N}-\text{H}$ bond in the $\text{C}-\text{SO}_2-\text{NH}-\text{C}$ segment is *anti* to the *meta*-Cl in the aniline ring. The molecule is twisted at the S atom, the $\text{C}-\text{SO}_2-\text{NH}-\text{C}$ torsion angle being $62.3(2)^\circ$. The dihedral angle between the two benzene rings is $69.3(1)^\circ$. The crystal structure features inversion dimers linked by pairs of $\text{N}-\text{H}\cdots\text{O}$ hydrogen bonds.

Related literature

For the preparation of the title compound, see: Savitha & Gowda (2006). For our studies of the effect of substituents on the structures of *N*-(aryl)arylsulfonamides, see: Gowda *et al.* (2008, 2010); Nirmala *et al.* (2010). For related structures, see: Gelbrich *et al.* (2007); Perlovich *et al.* (2006).



Experimental

Crystal data

$\text{C}_{12}\text{H}_8\text{Cl}_3\text{NO}_2\text{S}$
 $M_r = 336.60$

Monoclinic, $P2_1/c$
 $a = 7.9414(5)$ Å

$b = 14.483(1)$ Å
 $c = 12.593(1)$ Å
 $\beta = 99.880(7)^\circ$
 $V = 1426.91(17)$ Å³
 $Z = 4$

Mo $K\alpha$ radiation
 $\mu = 0.78$ mm⁻¹
 $T = 299$ K
 $0.32 \times 0.24 \times 0.22$ mm

Data collection

Oxford Diffraction Xcalibur diffractometer with a Sapphire CCD detector
Absorption correction: multi-scan (*CrysAlis RED*; Oxford)

Diffraction, 2009
 $T_{\min} = 0.788$, $T_{\max} = 0.847$
5551 measured reflections
2897 independent reflections
2364 reflections with $I > 2\sigma(I)$
 $R_{\text{int}} = 0.011$

Refinement

$R[F^2 > 2\sigma(F^2)] = 0.036$
 $wR(F^2) = 0.100$
 $S = 1.04$
2897 reflections
175 parameters
1 restraint

H atoms treated by a mixture of independent and constrained refinement
 $\Delta\rho_{\text{max}} = 0.36$ e Å⁻³
 $\Delta\rho_{\text{min}} = -0.45$ e Å⁻³

Table 1

Hydrogen-bond geometry (Å, °).

$D-\text{H}\cdots A$	$D-\text{H}$	$\text{H}\cdots A$	$D\cdots A$	$D-\text{H}\cdots A$
$\text{N1}-\text{H1N}\cdots\text{O2}^i$	0.85 (1)	2.16 (2)	2.932 (2)	152 (2)

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

Data collection: *CrysAlis CCD* (Oxford Diffraction, 2009); cell refinement: *CrysAlis RED* (Oxford Diffraction, 2009); data reduction: *CrysAlis RED*; program(s) used to solve structure: *SHELXS97* (Sheldrick, 2008); program(s) used to refine structure: *SHELXL97* (Sheldrick, 2008); molecular graphics: *PLATON* (Spek, 2009); software used to prepare material for publication: *SHELXL97*.

Supplementary data and figures for this paper are available from the IUCr electronic archives (Reference: BQ2217).

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supporting information

Acta Cryst. (2010). E66, o1552 [doi:10.1107/S1600536810020349]

2,4-Dichloro-*N*-(3-chlorophenyl)benzenesulfonamide

B. Thimme Gowda, Sabine Foro, P. G. Nirmala and Hartmut Fuess

S1. Comment

In the present work, as a part of studying the substituent effects on the structures of *N*-(aryl)arylsulfonamides (Gowda *et al.*, 2008, 2010; Nirmala *et al.*, 2010), the structure of 2,4-dichloro-*N*-(3-chlorophenyl)-benzenesulfonamide (I) has been determined. The conformations of the N—H bond in the C—SO₂—NH—C segment is *anti* to the *meta*-Cl in the aniline ring (Fig. 1).

The molecule is twisted at the S atom with the C1—SO₂—NH—C7 torsion angle of 62.3 (2)°, compared to the values of 67.8 (2)° in 2,4-dichloro-*N*-(4-chlorophenyl)benzenesulfonamide (II) (Nirmala *et al.*, 2010), 55.1 (3)° (molecule 1) and -48.3 (3)° (molecule 2) in 2,4-dichloro-*N*-(phenyl)-benzenesulfonamide (III) (Gowda *et al.*, 2010) and -60.1 (2)° in *N*-(3-chlorophenyl)-benzenesulfonamide (IV) (Gowda *et al.*, 2008).

The sulfonyl benzene and the aniline benzene rings in (I) are tilted relative to each other by 69.3 (1)°, compared to the values of 65.0 (1)° in (II), 80.5 (2)° in the molecule 1 and 64.9 (1)° in molecule 2 of (III), and 65.4 (1)° in (IV). The other bond parameters in (I) are similar to those observed in (II), (III), (IV) and other aryl sulfonamides (Perlovich *et al.*, 2006; Gelbrich *et al.*, 2007).

In the crystal structure, the pairs of intermolecular N—H···O hydrogen bonds (Table 1) link the molecules *via* inversion-related dimers into infinite zigzag sequences running parallel to the *c*-axis (Fig. 2.).

S2. Experimental

The solution of 1,3-dichlorobenzene (10 cc) in chloroform (40 cc) was treated dropwise with chlorosulfonic acid (25 cc) at 0 ° C. After the initial evolution of hydrogen chloride subsided, the reaction mixture was brought to room temperature and poured into crushed ice in a beaker. The chloroform layer was separated, washed with cold water and allowed to evaporate slowly. The residual 2,4-dichlorobenzenesulfonylchloride was treated with 3-chloroaniline in the stoichiometric ratio and boiled for ten minutes. The reaction mixture was then cooled to room temperature and added to ice cold water (100 cc). The resultant solid 2,4-dichloro-*N*-(3-chlorophenyl)benzenesulfonamide was filtered under suction and washed thoroughly with cold water. It was then recrystallized to constant melting point from dilute ethanol. The purity of the compound was checked and characterized by recording its infrared and NMR spectra (Savitha & Gowda, 2006).

Prism like colorless single crystals used in X-ray diffraction studies were grown in ethanolic solution by slow evaporation at room temperature.

S3. Refinement

The H atom of the NH group was located in a difference map and later restrained to N—H = 0.86 (1)Å. The other H atoms were positioned with idealized geometry using a riding model with C—H = 0.93Å. All H atoms were refined with isotropic displacement parameters (set to 1.2 times of the U_{eq} of the parent atom).

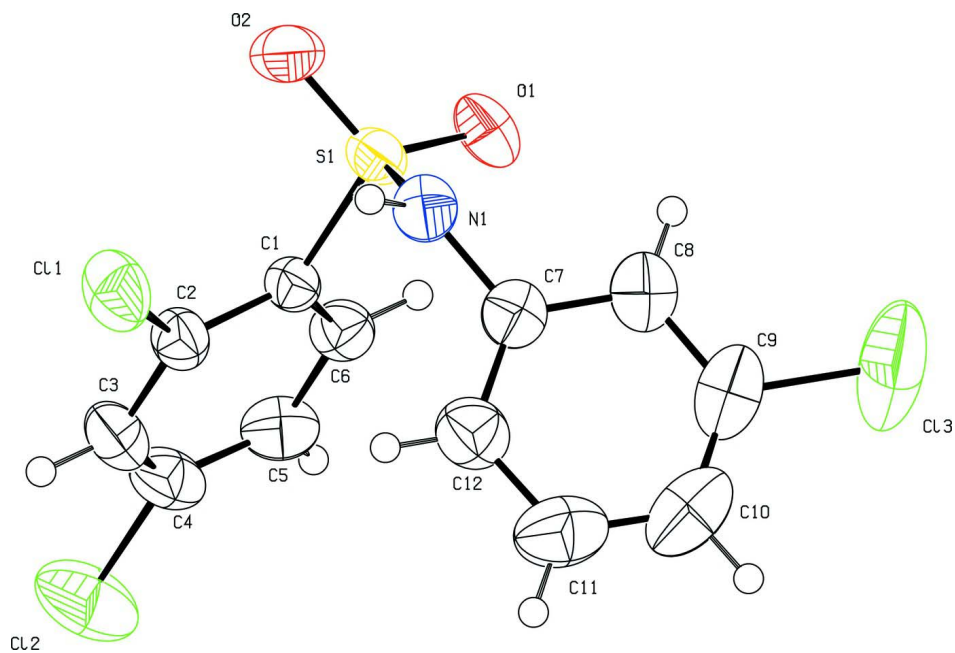
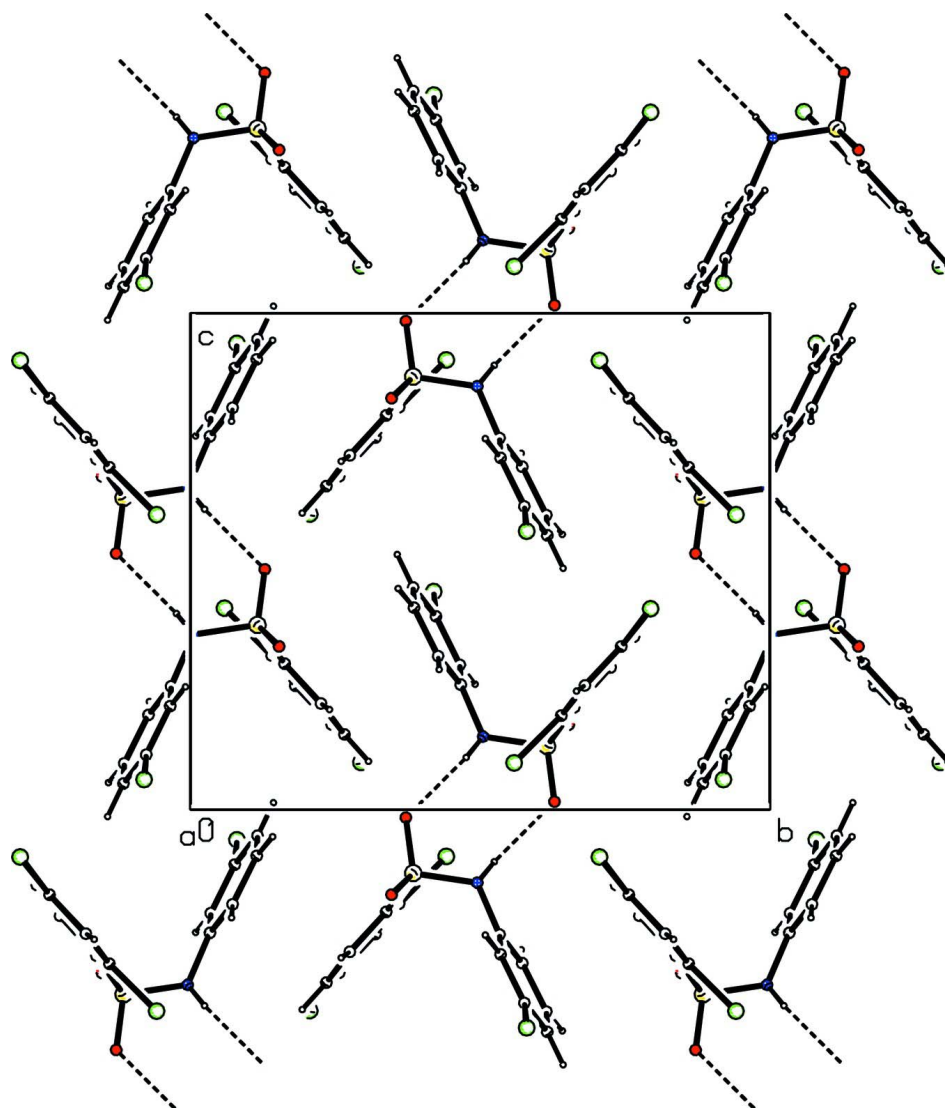


Figure 1

Molecular structure of (I), showing the atom labelling scheme and displacement ellipsoids are drawn at the 50% probability level.

**Figure 2**

Molecular packing of (I) with hydrogen bonding shown as dashed lines.

2,4-Dichloro-N-(3-chlorophenyl)benzenesulfonamide

Crystal data

$C_{12}H_8Cl_3NO_2S$

$M_r = 336.60$

Monoclinic, $P2_1/c$

Hall symbol: $-P 2_1/c$

$a = 7.9414 (5) \text{ \AA}$

$b = 14.483 (1) \text{ \AA}$

$c = 12.593 (1) \text{ \AA}$

$\beta = 99.880 (7)^\circ$

$V = 1426.91 (17) \text{ \AA}^3$

$Z = 4$

$F(000) = 680$

$D_x = 1.567 \text{ Mg m}^{-3}$

Mo $K\alpha$ radiation, $\lambda = 0.71073 \text{ \AA}$

Cell parameters from 3499 reflections

$\theta = 2.6\text{--}27.8^\circ$

$\mu = 0.78 \text{ mm}^{-1}$

$T = 299 \text{ K}$

Prism, colorless

$0.32 \times 0.24 \times 0.22 \text{ mm}$

Data collection

Oxford Diffraction Xcalibur
 diffractometer with a Sapphire CCD detector
 Radiation source: fine-focus sealed tube
 Graphite monochromator
 Rotation method data acquisition using ω and
 phi scans
 Absorption correction: multi-scan
 (*CrysAlis RED*; Oxford Diffraction, 2009)
 $T_{\min} = 0.788$, $T_{\max} = 0.847$

5551 measured reflections
 2897 independent reflections
 2364 reflections with $I > 2\sigma(I)$
 $R_{\text{int}} = 0.011$
 $\theta_{\max} = 26.4^\circ$, $\theta_{\min} = 2.6^\circ$
 $h = -9 \rightarrow 7$
 $k = -18 \rightarrow 11$
 $l = -15 \rightarrow 15$

Refinement

Refinement on F^2
 Least-squares matrix: full
 $R[F^2 > 2\sigma(F^2)] = 0.036$
 $wR(F^2) = 0.100$
 $S = 1.04$
 2897 reflections
 175 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
 $w = 1/[\sigma^2(F_o^2) + (0.0494P)^2 + 0.6274P]$
 where $P = (F_o^2 + 2F_c^2)/3$
 $(\Delta/\sigma)_{\max} < 0.001$
 $\Delta\rho_{\max} = 0.36 \text{ e } \text{\AA}^{-3}$
 $\Delta\rho_{\min} = -0.45 \text{ e } \text{\AA}^{-3}$

Special details

Experimental. *CrysAlis RED* (Oxford Diffraction, 2009) Empirical absorption correction using spherical harmonics, implemented in SCALE3 ABSPACK scaling algorithm.

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.

Refinement. Refinement of F^2 against ALL reflections. The weighted R -factor wR and goodness 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 threshold expression of $F^2 > \sigma(F^2)$ is used only for calculating R -factors(gt) *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)

	<i>x</i>	<i>y</i>	<i>z</i>	$U_{\text{iso}}^*/U_{\text{eq}}$
C1	0.6496 (2)	0.66240 (13)	0.20597 (15)	0.0362 (4)
C2	0.8135 (2)	0.63993 (14)	0.18941 (17)	0.0425 (4)
C3	0.9548 (3)	0.68078 (16)	0.25032 (19)	0.0533 (5)
H3	1.0643	0.6663	0.2387	0.064*
C4	0.9309 (3)	0.74336 (16)	0.32854 (19)	0.0547 (6)
C5	0.7707 (3)	0.76563 (15)	0.34839 (18)	0.0522 (5)
H5	0.7576	0.8072	0.4026	0.063*
C6	0.6298 (3)	0.72508 (14)	0.28628 (16)	0.0444 (4)
H6	0.5207	0.7399	0.2984	0.053*
C7	0.4639 (3)	0.46645 (14)	0.25186 (17)	0.0463 (5)
C8	0.3117 (3)	0.46491 (17)	0.2915 (2)	0.0573 (6)
H8	0.2131	0.4912	0.2527	0.069*
C9	0.3098 (4)	0.42366 (19)	0.3893 (2)	0.0717 (8)

C10	0.4536 (5)	0.3843 (2)	0.4475 (2)	0.0825 (9)
H10	0.4498	0.3569	0.5139	0.099*
C11	0.6029 (4)	0.3857 (2)	0.4069 (2)	0.0781 (8)
H11	0.7005	0.3584	0.4454	0.094*
C12	0.6094 (3)	0.42742 (17)	0.3092 (2)	0.0601 (6)
H12	0.7114	0.4291	0.2823	0.072*
N1	0.4655 (2)	0.50514 (13)	0.14722 (14)	0.0467 (4)
H1N	0.518 (3)	0.4758 (15)	0.1051 (16)	0.056*
O1	0.32239 (17)	0.65286 (12)	0.17118 (14)	0.0566 (4)
O2	0.46876 (19)	0.62821 (11)	0.01602 (12)	0.0539 (4)
Cl1	0.84810 (7)	0.55858 (5)	0.09422 (5)	0.06238 (19)
Cl2	1.11005 (10)	0.79410 (6)	0.40465 (7)	0.0923 (3)
Cl3	0.11963 (17)	0.41977 (9)	0.43921 (11)	0.1318 (5)
S1	0.46174 (6)	0.61555 (4)	0.12798 (4)	0.04136 (15)

Atomic displacement parameters (Å²)

	U^{11}	U^{22}	U^{33}	U^{12}	U^{13}	U^{23}
C1	0.0324 (9)	0.0372 (9)	0.0386 (9)	0.0013 (7)	0.0047 (7)	0.0034 (8)
C2	0.0368 (10)	0.0445 (11)	0.0470 (11)	0.0029 (8)	0.0097 (8)	0.0012 (9)
C3	0.0345 (10)	0.0564 (13)	0.0678 (14)	-0.0026 (9)	0.0052 (9)	0.0019 (11)
C4	0.0466 (12)	0.0485 (12)	0.0624 (14)	-0.0081 (10)	-0.0088 (10)	0.0017 (11)
C5	0.0625 (14)	0.0427 (11)	0.0479 (12)	0.0016 (10)	-0.0006 (10)	-0.0057 (9)
C6	0.0444 (10)	0.0424 (11)	0.0460 (11)	0.0066 (9)	0.0070 (8)	0.0019 (9)
C7	0.0523 (12)	0.0378 (10)	0.0490 (11)	-0.0065 (9)	0.0093 (9)	-0.0055 (9)
C8	0.0591 (13)	0.0496 (12)	0.0663 (15)	-0.0022 (11)	0.0197 (11)	-0.0032 (11)
C9	0.090 (2)	0.0592 (15)	0.0750 (18)	-0.0069 (14)	0.0411 (16)	-0.0009 (14)
C10	0.125 (3)	0.0673 (18)	0.0601 (16)	-0.0066 (18)	0.0288 (18)	0.0079 (14)
C11	0.094 (2)	0.0657 (17)	0.0681 (17)	0.0031 (15)	-0.0044 (16)	0.0130 (14)
C12	0.0557 (14)	0.0555 (14)	0.0674 (15)	-0.0009 (11)	0.0059 (11)	0.0043 (12)
N1	0.0485 (10)	0.0457 (10)	0.0464 (10)	-0.0029 (8)	0.0096 (7)	-0.0066 (8)
O1	0.0327 (7)	0.0618 (10)	0.0757 (10)	0.0072 (7)	0.0099 (7)	-0.0023 (8)
O2	0.0539 (9)	0.0612 (10)	0.0430 (8)	0.0048 (7)	-0.0022 (6)	0.0057 (7)
Cl1	0.0493 (3)	0.0732 (4)	0.0684 (4)	0.0065 (3)	0.0207 (3)	-0.0179 (3)
Cl2	0.0679 (4)	0.0830 (5)	0.1112 (6)	-0.0200 (4)	-0.0263 (4)	-0.0164 (4)
Cl3	0.1353 (9)	0.1419 (9)	0.1448 (10)	0.0015 (7)	0.0994 (8)	0.0213 (7)
S1	0.0320 (2)	0.0465 (3)	0.0440 (3)	0.00248 (19)	0.00210 (19)	0.0006 (2)

Geometric parameters (Å, °)

C1—C6	1.388 (3)	C7—N1	1.434 (3)
C1—C2	1.392 (3)	C8—C9	1.372 (4)
C1—S1	1.7739 (19)	C8—H8	0.9300
C2—C3	1.379 (3)	C9—C10	1.371 (5)
C2—C11	1.736 (2)	C9—Cl3	1.733 (3)
C3—C4	1.376 (3)	C10—C11	1.370 (5)
C3—H3	0.9300	C10—H10	0.9300
C4—C5	1.376 (3)	C11—C12	1.380 (4)

C4—C12	1.736 (2)	C11—H11	0.9300
C5—C6	1.382 (3)	C12—H12	0.9300
C5—H5	0.9300	N1—S1	1.617 (2)
C6—H6	0.9300	N1—H1N	0.845 (10)
C7—C12	1.375 (3)	O1—S1	1.4210 (15)
C7—C8	1.385 (3)	O2—S1	1.4323 (16)
C6—C1—C2	119.20 (18)	C7—C8—H8	120.8
C6—C1—S1	117.65 (14)	C10—C9—C8	121.7 (3)
C2—C1—S1	123.15 (15)	C10—C9—C13	119.4 (2)
C3—C2—C1	120.61 (19)	C8—C9—C13	118.9 (3)
C3—C2—C11	117.71 (16)	C11—C10—C9	119.3 (3)
C1—C2—C11	121.67 (15)	C11—C10—H10	120.4
C4—C3—C2	118.8 (2)	C9—C10—H10	120.4
C4—C3—H3	120.6	C10—C11—C12	120.5 (3)
C2—C3—H3	120.6	C10—C11—H11	119.8
C3—C4—C5	122.0 (2)	C12—C11—H11	119.8
C3—C4—C12	118.26 (18)	C7—C12—C11	119.4 (3)
C5—C4—C12	119.73 (19)	C7—C12—H12	120.3
C4—C5—C6	118.8 (2)	C11—C12—H12	120.3
C4—C5—H5	120.6	C7—N1—S1	121.42 (14)
C6—C5—H5	120.6	C7—N1—H1N	117.6 (17)
C5—C6—C1	120.57 (19)	S1—N1—H1N	113.7 (17)
C5—C6—H6	119.7	O1—S1—O2	119.51 (10)
C1—C6—H6	119.7	O1—S1—N1	108.32 (10)
C12—C7—C8	120.8 (2)	O2—S1—N1	105.74 (10)
C12—C7—N1	120.2 (2)	O1—S1—C1	106.18 (9)
C8—C7—N1	118.9 (2)	O2—S1—C1	108.96 (9)
C9—C8—C7	118.4 (3)	N1—S1—C1	107.65 (9)
C9—C8—H8	120.8		
C6—C1—C2—C3	-1.4 (3)	C8—C9—C10—C11	-0.3 (5)
S1—C1—C2—C3	177.92 (17)	C13—C9—C10—C11	178.6 (2)
C6—C1—C2—C11	177.31 (15)	C9—C10—C11—C12	0.9 (5)
S1—C1—C2—C11	-3.4 (3)	C8—C7—C12—C11	0.5 (4)
C1—C2—C3—C4	0.7 (3)	N1—C7—C12—C11	-176.2 (2)
C11—C2—C3—C4	-178.03 (18)	C10—C11—C12—C7	-1.0 (4)
C2—C3—C4—C5	0.6 (4)	C12—C7—N1—S1	-107.0 (2)
C2—C3—C4—C12	179.93 (17)	C8—C7—N1—S1	76.3 (2)
C3—C4—C5—C6	-1.3 (4)	C7—N1—S1—O1	-52.11 (19)
C12—C4—C5—C6	179.44 (17)	C7—N1—S1—O2	178.66 (16)
C4—C5—C6—C1	0.6 (3)	C7—N1—S1—C1	62.30 (18)
C2—C1—C6—C5	0.7 (3)	C6—C1—S1—O1	-2.34 (18)
S1—C1—C6—C5	-178.61 (16)	C2—C1—S1—O1	178.34 (17)
C12—C7—C8—C9	0.1 (4)	C6—C1—S1—O2	127.61 (16)
N1—C7—C8—C9	176.8 (2)	C2—C1—S1—O2	-51.71 (19)
C7—C8—C9—C10	-0.2 (4)	C6—C1—S1—N1	-118.17 (16)
C7—C8—C9—C13	-179.12 (19)	C2—C1—S1—N1	62.51 (19)

Hydrogen-bond geometry (Å, °)

<i>D—H···A</i>	<i>D—H</i>	<i>H···A</i>	<i>D···A</i>	<i>D—H···A</i>
N1—H1N···O2 ⁱ	0.85 (1)	2.16 (2)	2.932 (2)	152 (2)

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