

4-Amino-3,5-dichlorobenzene-sulfonamide**Xiu-Ying Qin,* Han-Fu Liu and Jia-Xun Lin**College of Pharmacy, Guilin Medical University, Guilin, Guangxi 541004, People's Republic of China
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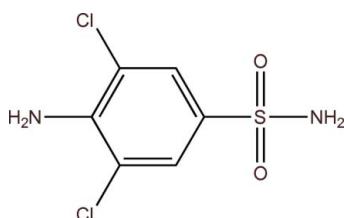
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Key indicators: single-crystal X-ray study; $T = 93\text{ K}$; mean $\sigma(\text{C}-\text{C}) = 0.002\text{ \AA}$; R factor = 0.029; wR factor = 0.074; data-to-parameter ratio = 15.0.

In the title compound, $\text{C}_6\text{H}_6\text{Cl}_2\text{N}_2\text{O}_2\text{S}$, the O atoms of the sulfonamide group lie on one side of the benzene ring and the amino group lies on the opposite side. An intermolecular $\text{N}-\text{H}\cdots\text{Cl}$ interaction occurs. In the crystal, adjacent molecules are linked by $\text{N}-\text{H}\cdots\text{O}$ hydrogen bonds, forming a three-dimensional structure with supporting $\pi-\pi$ stacking interactions [centroid-centroid distance = $3.7903(12)\text{ \AA}$]. A short $\text{Cl}\cdots\text{Cl}$ contact [$3.3177(10)\text{ \AA}$] also occurs.

Related literature

For the preparation, see: Qiu & Lv (2005). For $\text{Cl}\cdots\text{Cl}$ contacts, see: Sakurai *et al.* (1963); Stone *et al.* (1994); Qin *et al.* (2008).

**Experimental***Crystal data* $M_r = 241.09$ Monoclinic, $P2_1/c$ $a = 8.9544(17)\text{ \AA}$ $b = 13.387(3)\text{ \AA}$ $c = 7.5673(15)\text{ \AA}$ $\beta = 95.809(2)^\circ$ $V = 902.4(3)\text{ \AA}^3$

$Z = 4$
Mo $K\alpha$ radiation
 $\mu = 0.92\text{ mm}^{-1}$

$T = 93\text{ K}$
 $0.30 \times 0.27 \times 0.13\text{ mm}$

Data collection

Rigaku SPIDER diffractometer
Absorption correction: multi-scan
(*ABSCOR*; Higashi, 1995)
 $T_{\min} = 0.771$, $T_{\max} = 0.888$

5918 measured reflections
2008 independent reflections
1759 reflections with $I > 2\sigma(I)$
 $R_{\text{int}} = 0.020$

Refinement

$R[F^2 > 2\sigma(F^2)] = 0.029$
 $wR(F^2) = 0.074$
 $S = 1.00$
2008 reflections
134 parameters

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

Table 1
Hydrogen-bond geometry (\AA , $^\circ$).

$D-\text{H}\cdots A$	$D-\text{H}$	$\text{H}\cdots A$	$D\cdots A$	$D-\text{H}\cdots A$
N1—H1A \cdots Cl1 ⁱⁱ	0.80 (2)	2.60 (2)	2.9793 (18)	111 (2)
N1—H1B \cdots O2 ⁱⁱ	0.83 (3)	2.40 (3)	3.199 (2)	160 (2)
N2—H2A \cdots O1 ⁱ	0.81 (2)	2.14 (2)	2.935 (2)	167 (2)
N2—H2B \cdots O2 ⁱⁱⁱ	0.86 (3)	2.08 (3)	2.934 (2)	172 (2)

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

Data collection: *RAPID-AUTO* (Rigaku, 2004); cell refinement: *RAPID-AUTO*; data reduction: *RAPID-AUTO*; program(s) used to solve structure: *SHELXS97* (Sheldrick, 2008); program(s) used to refine structure: *SHELXL97* (Sheldrick, 2008); molecular graphics: *SHELXTL* (Sheldrick, 2008); software used to prepare material for publication: *SHELXL97*.

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Supplementary data and figures for this paper are available from the IUCr electronic archives (Reference: NK2060).

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supporting information

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4-Amino-3,5-dichlorobenzenesulfonamide

Xiu-Ying Qin, Han-Fu Liu and Jia-Xun Lin

S1. Comment

4-Amino-3,5-dichloro-benzenesulfonamide is a primary substance used to synthesize Diclofenac sodium. Although the synthetic methods of the title compound has been reported (Qiu & Lv, 2005), no crystal structure data have been published so far. Our experimental aim was to obtain a Co(II) complex by preparing the potassium salt of 4-amino-3,5-dichloro-benzenesulfonamide modified by salicylaldehyde, and then reacting with $\text{CoCl}_2 \cdot 6\text{H}_2\text{O}$. To our surprise, we obtained yellow crystals which were identified as the title compound. Here, we report the synthesis and crystal structure of the title compound.

In the title compound, $\text{C}_6\text{H}_6\text{Cl}_2\text{N}_2\text{O}_2\text{S}$, the amino and chlorine substituent groups are essentially co-planar (maximum r.m.s. deviation of fitted atoms is -0.0747 \AA) with the benzene ring to which they are bonded. The O atoms of the sulfonamide group lie on one side of the benzene ring and the amino group lies on the opposite side (Scheme I, Fig. 1).

In the crystal, molecules are linked by intermolecular hydrogen bonds $\text{N}—\text{H}\cdots\text{O}$ (Fig. 2., Table 2) and $\pi—\pi$ stacking interactions [3.790 \AA , the distance of the centroids between the two benzene rings, symmetry code as $x, -y + 1/2, z + 1/2$ and $x, -y + 1/2, z - 1/2$], and a short $\text{Cl}\cdots\text{Cl}$ contact [3.318 \AA , symmetry code as $-x, -y - 1, -z$] occurs (Fig. 2). The $\text{Cl}\cdots\text{Cl}$ contact is stronger than that of the $[\text{Zn}(\text{II})(\text{C}_8\text{H}_7\text{O}_4\text{NCl}_2\text{S})(\text{Phen})(\text{H}_2\text{O})]_3$ (Qin *et al.*, 2008).

S2. Experimental

Powdered 4-amino-3,5-dichloro-benzenesulfonamide (2.671 g, 10.08 mmol), KOH(0.504 g, 9.0 mmol) and salicyl-aldehyde (0.53 ml, 5.01 mmol) were mixed in methanol (40 ml). The mixture was stirred at 323 K for 2 h. Then, 1.30 ml solution was taken out from the mixed solution was added into a solution of $\text{CoCl}_2 \cdot 6\text{H}_2\text{O}$ (0.060 g, 0.25 mmol) in methanol (25 ml). This mixture has been stirred at 323 K for 8 h. Subsequently, the reagents were filtrated. The resulting solution was left at room temperature, orange-yellow crystals were obtained after some days.

S3. Refinement

All H atoms were geometrically positioned and refined using a mixed model, with distance restraints of $\text{C}—\text{H} = 0.9500$ and $\text{N}—\text{H} = 0.80(2)–0.86(3) \text{ \AA}$, and with $U_{\text{iso}}(\text{H}) = 1.2U_{\text{eq}}(\text{C})$.

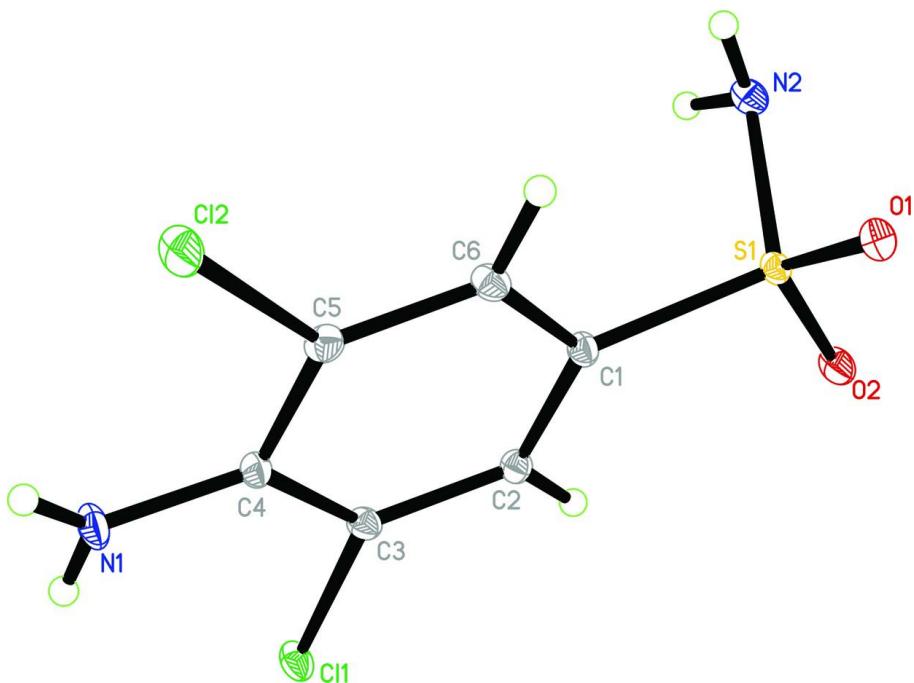
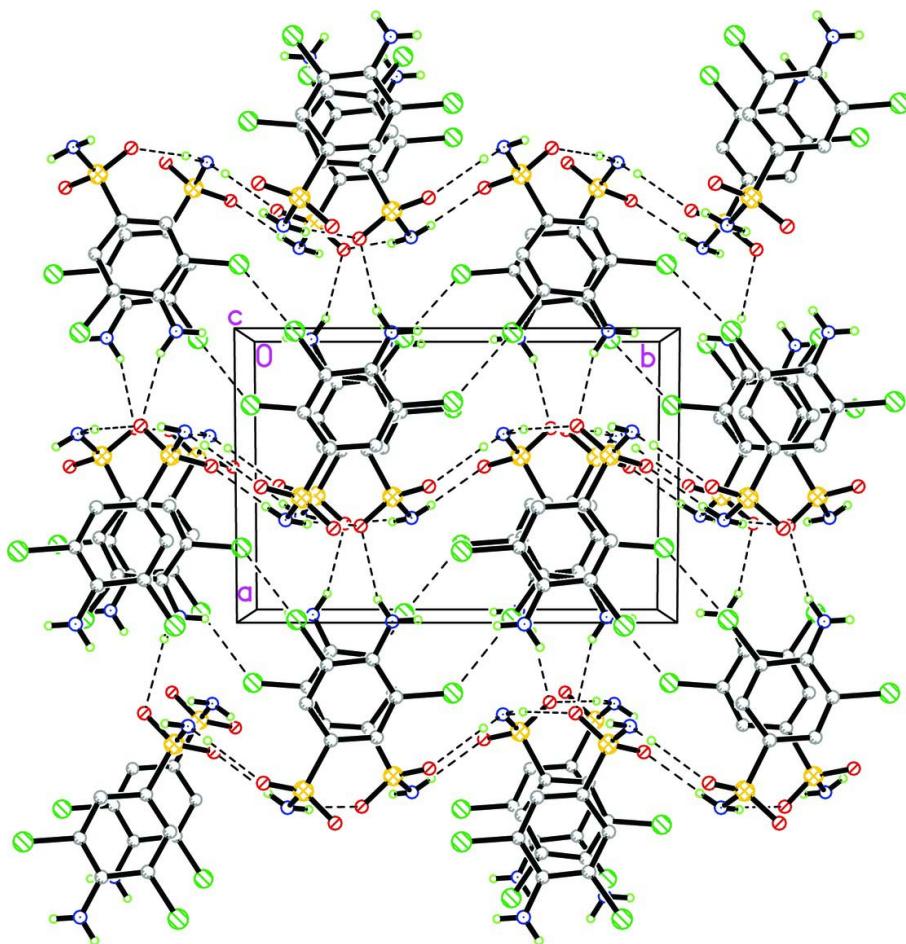


Figure 1

The molecular structure of (I), with atom labels and 30% probability displacement ellipsoids.

**Figure 2**

The packing of (I), viewed down the *c* axis, showing layers of molecules connected by N—H···O hydrogen bonds, Cl···Cl contact and π ··· π stacking interactions.

4-Amino-3,5-dichlorobenzenesulfonamide

Crystal data



$M_r = 241.09$

Monoclinic, $P2_1/c$

Hall symbol: -P 2ybc

$a = 8.9544$ (17) Å

$b = 13.387$ (3) Å

$c = 7.5673$ (15) Å

$\beta = 95.809$ (2)°

$V = 902.4$ (3) Å³

$Z = 4$

$$F(000) = 488$$

$$D_x = 1.774 \text{ Mg m}^{-3}$$

Melting point = 207.2–207.5 K

Mo $K\alpha$ radiation, $\lambda = 0.71073$ Å

Cell parameters from 2008 reflections

$\theta = 3.0\text{--}27.5^\circ$

$\mu = 0.92 \text{ mm}^{-1}$

$T = 93$ K

Block, orange-yellow

0.30 × 0.27 × 0.13 mm

Data collection

Rigaku SPIDER
diffractometer

Radiation source: rotating anode
Graphite monochromator

ω scans

Absorption correction: multi-scan

(*ABSCOR*; Higashi, 1995)

$T_{\min} = 0.771$, $T_{\max} = 0.888$

5918 measured reflections
 2008 independent reflections
 1759 reflections with $I > 2\sigma(I)$
 $R_{\text{int}} = 0.020$

$\theta_{\max} = 27.5^\circ$, $\theta_{\min} = 3.0^\circ$
 $h = -10 \rightarrow 10$
 $k = -17 \rightarrow 10$
 $l = -9 \rightarrow 9$

Refinement

Refinement on F^2
 Least-squares matrix: full
 $R[F^2 > 2\sigma(F^2)] = 0.029$
 $wR(F^2) = 0.074$
 $S = 1.00$
 2008 reflections
 134 parameters
 0 restraints
 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
 $w = 1/[\sigma^2(F_o^2) + (0.0461P)^2 + 0.260P]$
 where $P = (F_o^2 + 2F_c^2)/3$
 $(\Delta/\sigma)_{\max} = 0.001$
 $\Delta\rho_{\max} = 0.45 \text{ e } \text{\AA}^{-3}$
 $\Delta\rho_{\min} = -0.36 \text{ e } \text{\AA}^{-3}$

Special details

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)

	x	y	z	$U_{\text{iso}}^*/U_{\text{eq}}$
C11	0.24595 (5)	0.01031 (3)	0.45203 (6)	0.01881 (13)
Cl2	0.00000 (5)	0.37179 (3)	0.29728 (7)	0.02268 (13)
S1	0.57265 (5)	0.34844 (3)	0.58837 (6)	0.01325 (12)
O1	0.53529 (14)	0.43437 (9)	0.68889 (17)	0.0171 (3)
O2	0.67408 (13)	0.27471 (9)	0.67149 (18)	0.0190 (3)
N1	0.00496 (18)	0.15006 (13)	0.3074 (2)	0.0198 (4)
N2	0.64946 (18)	0.39096 (12)	0.4206 (2)	0.0166 (3)
C1	0.40449 (19)	0.28746 (13)	0.5127 (2)	0.0135 (3)
C2	0.39422 (19)	0.18356 (12)	0.5117 (2)	0.0137 (3)
H2	0.4778	0.1437	0.5551	0.016*
C3	0.26064 (19)	0.13958 (13)	0.4466 (2)	0.0145 (4)
C4	0.13407 (19)	0.19420 (13)	0.3762 (2)	0.0143 (4)
C5	0.15166 (19)	0.29916 (13)	0.3806 (2)	0.0155 (4)
C6	0.28195 (19)	0.34575 (13)	0.4475 (2)	0.0151 (4)
H6	0.2885	0.4166	0.4493	0.018*
H1A	-0.001 (3)	0.0906 (19)	0.305 (3)	0.032 (7)*
H2A	0.604 (3)	0.4378 (17)	0.375 (3)	0.022 (6)*
H1B	-0.071 (3)	0.1841 (18)	0.277 (3)	0.033 (7)*
H2B	0.665 (3)	0.3444 (19)	0.346 (4)	0.039 (7)*

Atomic displacement parameters (\AA^2)

	U^{11}	U^{22}	U^{33}	U^{12}	U^{13}	U^{23}
C11	0.0172 (2)	0.0123 (2)	0.0260 (2)	-0.00223 (16)	-0.00262 (17)	-0.00010 (16)
Cl2	0.0118 (2)	0.0194 (2)	0.0355 (3)	0.00248 (17)	-0.00420 (18)	0.00595 (19)
S1	0.0103 (2)	0.0123 (2)	0.0165 (2)	-0.00140 (15)	-0.00131 (16)	0.00062 (15)
O1	0.0175 (7)	0.0159 (6)	0.0177 (6)	-0.0018 (5)	0.0006 (5)	-0.0024 (5)
O2	0.0132 (7)	0.0156 (6)	0.0267 (7)	-0.0008 (5)	-0.0049 (5)	0.0048 (5)
N1	0.0123 (9)	0.0168 (8)	0.0287 (9)	-0.0024 (7)	-0.0059 (7)	0.0018 (7)
N2	0.0154 (8)	0.0138 (7)	0.0207 (8)	-0.0003 (6)	0.0027 (6)	-0.0002 (6)
C1	0.0112 (9)	0.0153 (8)	0.0137 (8)	-0.0015 (6)	0.0005 (7)	-0.0005 (7)
C2	0.0120 (9)	0.0142 (8)	0.0146 (8)	0.0005 (7)	0.0003 (7)	0.0006 (7)
C3	0.0152 (9)	0.0123 (8)	0.0160 (8)	-0.0006 (7)	0.0017 (7)	0.0008 (6)
C4	0.0113 (9)	0.0174 (8)	0.0140 (8)	-0.0019 (7)	0.0003 (7)	0.0004 (7)
C5	0.0123 (9)	0.0168 (8)	0.0172 (9)	0.0036 (7)	0.0007 (7)	0.0036 (7)
C6	0.0138 (9)	0.0120 (8)	0.0195 (9)	0.0004 (6)	0.0020 (7)	0.0008 (7)

Geometric parameters (\AA , $^\circ$)

C11—C3	1.7363 (18)	N2—H2B	0.86 (3)
Cl2—C5	1.7360 (17)	C1—C2	1.394 (2)
S1—O1	1.4370 (13)	C1—C6	1.395 (2)
S1—O2	1.4419 (13)	C2—C3	1.379 (2)
S1—N2	1.6078 (16)	C2—H2	0.9500
S1—C1	1.7571 (18)	C3—C4	1.407 (2)
N1—C4	1.355 (2)	C4—C5	1.414 (2)
N1—H1A	0.80 (2)	C5—C6	1.374 (2)
N1—H1B	0.83 (3)	C6—H6	0.9500
N2—H2A	0.81 (2)		
O1—S1—O2	119.15 (8)	C3—C2—C1	118.85 (16)
O1—S1—N2	106.00 (8)	C3—C2—H2	120.6
O2—S1—N2	106.61 (8)	C1—C2—H2	120.6
O1—S1—C1	107.86 (8)	C2—C3—C4	123.34 (16)
O2—S1—C1	107.78 (8)	C2—C3—Cl1	118.83 (13)
N2—S1—C1	109.15 (8)	C4—C3—Cl1	117.83 (13)
C4—N1—H1A	119.6 (18)	N1—C4—C3	122.82 (17)
C4—N1—H1B	120.7 (17)	N1—C4—C5	122.09 (16)
H1A—N1—H1B	119 (2)	C3—C4—C5	115.08 (15)
S1—N2—H2A	112.2 (16)	C6—C5—C4	123.25 (16)
S1—N2—H2B	111.9 (17)	C6—C5—Cl2	118.92 (14)
H2A—N2—H2B	113 (2)	C4—C5—Cl2	117.83 (13)
C2—C1—C6	120.47 (16)	C5—C6—C1	118.99 (16)
C2—C1—S1	121.28 (13)	C5—C6—H6	120.5
C6—C1—S1	118.21 (13)	C1—C6—H6	120.5
O1—S1—C1—C2	-140.05 (14)	C11—C3—C4—N1	-2.6 (2)
O2—S1—C1—C2	-10.20 (17)	C2—C3—C4—C5	-1.5 (3)

N2—S1—C1—C2	105.21 (15)	C11—C3—C4—C5	178.10 (13)
O1—S1—C1—C6	42.09 (16)	N1—C4—C5—C6	-179.13 (17)
O2—S1—C1—C6	171.94 (13)	C3—C4—C5—C6	0.2 (3)
N2—S1—C1—C6	-72.65 (16)	N1—C4—C5—Cl2	1.0 (2)
C6—C1—C2—C3	-0.5 (3)	C3—C4—C5—Cl2	-179.65 (13)
S1—C1—C2—C3	-178.35 (13)	C4—C5—C6—C1	0.8 (3)
C1—C2—C3—C4	1.7 (3)	Cl2—C5—C6—C1	-179.29 (13)
C1—C2—C3—Cl1	-177.91 (13)	C2—C1—C6—C5	-0.7 (3)
C2—C3—C4—N1	177.82 (17)	S1—C1—C6—C5	177.19 (13)

Hydrogen-bond geometry (Å, °)

D—H···A	D—H	H···A	D···A	D—H···A
N1—H1A···Cl1	0.80 (2)	2.60 (2)	2.9793 (18)	111 (2)
N2—H2A···O1 ⁱ	0.81 (2)	2.14 (2)	2.935 (2)	167 (2)
N1—H1B···O2 ⁱⁱ	0.83 (3)	2.40 (3)	3.199 (2)	160 (2)
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