

## 5,7-Dichloroquinolin-8-ol

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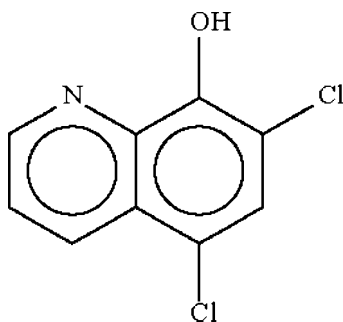
Received 20 April 2009; accepted 21 April 2009

 Key indicators: single-crystal X-ray study;  $T = 123$  K; mean  $\sigma(\text{C}-\text{C}) = 0.003$  Å;  $R$  factor = 0.040;  $wR$  factor = 0.112; data-to-parameter ratio = 15.7.

The molecule of the title compound,  $\text{C}_9\text{H}_5\text{Cl}_2\text{NO}$ , is essentially planar [give maximum or r.m.s. deviation] and the hydroxy group acts as a hydrogen-bond donor to the N atom of a symmetry-related molecule, generating a hydrogen-bonded dimer, which lies on a twofold rotation axis.

### Related literature

Unlike quinolin-8-ol, which yields a large number of metal derivatives, 5,7-dichloroquinolin-8-ol forms only a small number of metal chelates. For their crystal structures, see: García-Granda *et al.* (1987); Artizzu *et al.* (2007, 2008); Day *et al.* (1980); González-Baró *et al.* (1998); Horton & Wendlandt (1963); Miyashita *et al.* (2005); Suganuma *et al.* (2001); Van Deun *et al.* (2004).



### Experimental

#### Crystal data

$\text{C}_9\text{H}_5\text{Cl}_2\text{NO}$   
 $M_r = 214.04$   
 Monoclinic,  $P2_1/c$   
 $a = 15.5726$  (3) Å  
 $b = 3.8062$  (1) Å  
 $c = 16.1269$  (3) Å  
 $\beta = 118.029$  (1)°

$V = 843.76$  (3) Å<sup>3</sup>  
 $Z = 4$   
 Mo  $K\alpha$  radiation  
 $\mu = 0.72$  mm<sup>-1</sup>  
 $T = 123$  K  
 $0.36 \times 0.09 \times 0.02$  mm

#### Data collection

Bruker SMART APEX  
 diffractometer  
 Absorption correction: multi-scan  
 (SADABS; Sheldrick, 1996)  
 $T_{\min} = 0.782$ ,  $T_{\max} = 0.986$

7279 measured reflections  
 1919 independent reflections  
 1644 reflections with  $I > 2\sigma(I)$   
 $R_{\text{int}} = 0.032$

#### Refinement

$R[F^2 > 2\sigma(F^2)] = 0.040$   
 $wR(F^2) = 0.112$   
 $S = 1.05$   
 1919 reflections  
 122 parameters  
 1 restraint

H atoms treated by a mixture of independent and constrained refinement  
 $\Delta\rho_{\text{max}} = 0.55$  e Å<sup>-3</sup>  
 $\Delta\rho_{\text{min}} = -0.36$  e Å<sup>-3</sup>

**Table 1**

Hydrogen-bond geometry (Å, °).

$D-H\cdots A$	$D-H$	$H\cdots A$	$D\cdots A$	$D-H\cdots A$
$\text{O1}-\text{H1}\cdots\text{N1}^i$	0.84 (1)	2.01 (2)	2.761 (2)	150 (3)

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

Data collection: APEX2 (Bruker, 2008); cell refinement: SAINT (Bruker, 2008); data reduction: SAINT; program(s) used to solve structure: SHELXS97 (Sheldrick, 2008); program(s) used to refine structure: SHELXL97 (Sheldrick, 2008); molecular graphics: X-SEED (Barbour, 2001); software used to prepare material for publication: publCIF (Westrip, 2009).

I thank the University of Malaya for supporting this study.

Supplementary data and figures for this paper are available from the IUCr electronic archives (Reference: LH2808).

### References

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## supporting information

*Acta Cryst.* (2009). E65, o1131 [doi:10.1107/S1600536809014846]

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### S1. Comment

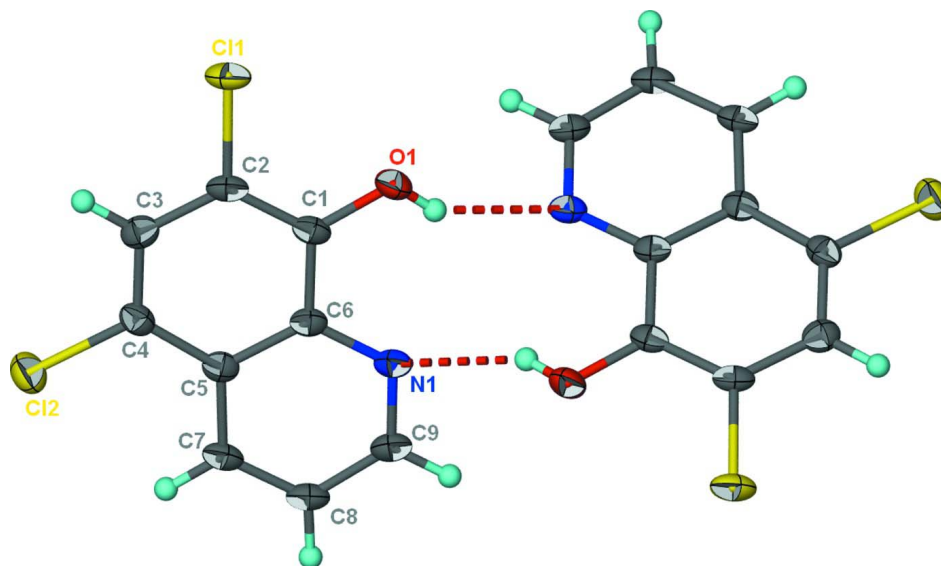
A hydrogen-bonded dimer of the title compound is shown in Fig. 1.

### S2. Experimental

The organic reactant was returned unchanged in an unsuccessful attempt at reacting it with a zinc salt in methanol.

### S3. Refinement

Carbon-bound H-atoms were placed in calculated positions (C–H 0.93 Å) and were included in the refinement in the riding model approximation, with  $U(\text{H})$  set to 1.2  $U(\text{C})$ . The hydroxy hydrogen atom was located in a difference Fourier map, and was refined with a distance restraint of O–H 0.84±0.01 Å; its temperature factor was freely refined.



**Figure 1**

Thermal ellipsoid plot (Barbour, 2001) of a hydrogen-bonded dimer of the title compound; ellipsoids are drawn at the 70% probability level and H atoms of arbitrary radius. The unlabeled molecule is related by the symmetry operator  $-x, y, -z+1/2$

## 5,7-Dichloroquinolin-8-ol

### Crystal data

$\text{C}_9\text{H}_5\text{Cl}_2\text{NO}$   
 $M_r = 214.04$

Monoclinic,  $P2_1/c$   
Hall symbol:  $-P 2_1c$

$a = 15.5726 (3) \text{ \AA}$   
 $b = 3.8062 (1) \text{ \AA}$   
 $c = 16.1269 (3) \text{ \AA}$   
 $\beta = 118.029 (1)^\circ$   
 $V = 843.76 (3) \text{ \AA}^3$   
 $Z = 4$   
 $F(000) = 432$   
 $D_x = 1.685 \text{ Mg m}^{-3}$

Mo  $K\alpha$  radiation,  $\lambda = 0.71073 \text{ \AA}$   
 Cell parameters from 3573 reflections  
 $\theta = 2.5\text{--}28.3^\circ$   
 $\mu = 0.72 \text{ mm}^{-1}$   
 $T = 123 \text{ K}$   
 Plate, colorless  
 $0.36 \times 0.09 \times 0.02 \text{ mm}$

*Data collection*

Bruker SMART APEX  
 diffractometer  
 Radiation source: fine-focus sealed tube  
 Graphite monochromator  
 $\omega$  scans  
 Absorption correction: multi-scan  
 (SADABS; Sheldrick, 1996)  
 $T_{\min} = 0.782$ ,  $T_{\max} = 0.986$

7279 measured reflections  
 1919 independent reflections  
 1644 reflections with  $I > 2\sigma(I)$   
 $R_{\text{int}} = 0.032$   
 $\theta_{\max} = 27.5^\circ$ ,  $\theta_{\min} = 1.5^\circ$   
 $h = -20 \rightarrow 20$   
 $k = -4 \rightarrow 4$   
 $l = -20 \rightarrow 20$

*Refinement*

Refinement on  $F^2$   
 Least-squares matrix: full  
 $R[F^2 > 2\sigma(F^2)] = 0.040$   
 $wR(F^2) = 0.112$   
 $S = 1.05$   
 1919 reflections  
 122 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  
 $w = 1/[\sigma^2(F_o^2) + (0.0684P)^2 + 0.4949P]$   
 where  $P = (F_o^2 + 2F_c^2)/3$   
 $(\Delta/\sigma)_{\max} < 0.001$   
 $\Delta\rho_{\max} = 0.55 \text{ e \AA}^{-3}$   
 $\Delta\rho_{\min} = -0.36 \text{ e \AA}^{-3}$

*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.

*Fractional atomic coordinates and isotropic or equivalent isotropic displacement parameters ( $\text{\AA}^2$ )*

	<i>x</i>	<i>y</i>	<i>z</i>	$U_{\text{iso}}^*/U_{\text{eq}}$
Cl1	0.29367 (4)	0.38966 (13)	0.24587 (3)	0.02310 (17)
Cl2	0.44255 (4)	0.89258 (14)	0.59720 (3)	0.02635 (18)
O1	0.10638 (11)	0.6233 (4)	0.22642 (10)	0.0223 (3)
N1	0.07459 (12)	0.9357 (4)	0.36439 (11)	0.0186 (4)
H1	0.0565 (14)	0.729 (7)	0.220 (2)	0.051 (9)*
C1	0.18119 (14)	0.6852 (5)	0.31223 (13)	0.0176 (4)
C2	0.27416 (15)	0.5885 (5)	0.33230 (13)	0.0184 (4)
C3	0.35486 (14)	0.6504 (5)	0.42003 (14)	0.0193 (4)
H3	0.4180	0.5794	0.4316	0.023*
C4	0.34192 (14)	0.8134 (5)	0.48869 (13)	0.0183 (4)
C5	0.24865 (14)	0.9212 (5)	0.47354 (13)	0.0168 (4)
C6	0.16747 (14)	0.8502 (5)	0.38470 (13)	0.0170 (4)

C7	0.23008 (15)	1.0924 (5)	0.54108 (13)	0.0191 (4)
H7	0.2822	1.1462	0.6013	0.023*
C8	0.13659 (15)	1.1807 (5)	0.51946 (14)	0.0201 (4)
H8	0.1230	1.2970	0.5641	0.024*
C9	0.06103 (15)	1.0957 (5)	0.42978 (14)	0.0204 (4)
H9	-0.0036	1.1574	0.4155	0.024*

*Atomic displacement parameters (Å<sup>2</sup>)*

	$U^{11}$	$U^{22}$	$U^{33}$	$U^{12}$	$U^{13}$	$U^{23}$
Cl1	0.0336 (3)	0.0238 (3)	0.0188 (3)	0.00576 (19)	0.0180 (2)	0.00172 (18)
Cl2	0.0229 (3)	0.0305 (3)	0.0203 (3)	0.0002 (2)	0.0057 (2)	-0.00406 (19)
O1	0.0229 (7)	0.0304 (8)	0.0137 (6)	0.0030 (6)	0.0086 (6)	-0.0021 (5)
N1	0.0230 (8)	0.0202 (9)	0.0157 (7)	0.0008 (6)	0.0117 (6)	0.0020 (6)
C1	0.0242 (10)	0.0166 (9)	0.0139 (8)	-0.0012 (7)	0.0105 (7)	0.0016 (7)
C2	0.0280 (10)	0.0158 (10)	0.0171 (9)	0.0009 (7)	0.0154 (8)	0.0016 (7)
C3	0.0223 (9)	0.0173 (10)	0.0215 (9)	0.0015 (7)	0.0130 (8)	0.0025 (8)
C4	0.0211 (9)	0.0182 (10)	0.0145 (8)	-0.0019 (7)	0.0074 (7)	0.0014 (7)
C5	0.0216 (9)	0.0142 (9)	0.0164 (9)	-0.0012 (7)	0.0104 (7)	0.0021 (7)
C6	0.0220 (9)	0.0161 (9)	0.0162 (9)	-0.0010 (7)	0.0117 (7)	0.0010 (7)
C7	0.0276 (10)	0.0183 (10)	0.0143 (8)	-0.0029 (8)	0.0122 (8)	-0.0001 (7)
C8	0.0297 (10)	0.0187 (10)	0.0181 (9)	-0.0013 (8)	0.0164 (8)	-0.0007 (7)
C9	0.0263 (10)	0.0210 (10)	0.0200 (9)	0.0004 (8)	0.0160 (8)	0.0019 (7)

*Geometric parameters (Å, °)*

Cl1—C2	1.7337 (19)	C3—H3	0.9500
Cl2—C4	1.7412 (19)	C4—C5	1.416 (3)
O1—C1	1.346 (2)	C5—C7	1.411 (3)
O1—H1	0.835 (10)	C5—C6	1.422 (3)
N1—C9	1.318 (2)	C7—C8	1.370 (3)
N1—C6	1.364 (2)	C7—H7	0.9500
C1—C2	1.377 (3)	C8—C9	1.408 (3)
C1—C6	1.428 (3)	C8—H8	0.9500
C2—C3	1.402 (3)	C9—H9	0.9500
C3—C4	1.364 (3)		
C1—O1—H1	111 (2)	C7—C5—C6	117.26 (17)
C9—N1—C6	117.95 (17)	C4—C5—C6	118.24 (17)
O1—C1—C2	120.07 (17)	N1—C6—C5	122.49 (17)
O1—C1—C6	121.87 (17)	N1—C6—C1	117.25 (17)
C2—C1—C6	118.05 (17)	C5—C6—C1	120.26 (17)
C1—C2—C3	122.49 (18)	C8—C7—C5	119.71 (18)
C1—C2—Cl1	119.33 (15)	C8—C7—H7	120.1
C3—C2—Cl1	118.17 (15)	C5—C7—H7	120.1
C4—C3—C2	119.43 (18)	C7—C8—C9	118.71 (17)
C4—C3—H3	120.3	C7—C8—H8	120.6
C2—C3—H3	120.3	C9—C8—H8	120.6

C3—C4—C5	121.50 (18)	N1—C9—C8	123.88 (18)
C3—C4—C12	119.21 (15)	N1—C9—H9	118.1
C5—C4—C12	119.28 (14)	C8—C9—H9	118.1
C7—C5—C4	124.50 (18)		
O1—C1—C2—C3	179.21 (17)	C7—C5—C6—N1	-1.1 (3)
C6—C1—C2—C3	-0.9 (3)	C4—C5—C6—N1	178.25 (17)
O1—C1—C2—C11	0.4 (3)	C7—C5—C6—C1	178.50 (17)
C6—C1—C2—C11	-179.66 (14)	C4—C5—C6—C1	-2.1 (3)
C1—C2—C3—C4	-0.2 (3)	O1—C1—C6—N1	1.6 (3)
C11—C2—C3—C4	178.56 (15)	C2—C1—C6—N1	-178.29 (17)
C2—C3—C4—C5	0.2 (3)	O1—C1—C6—C5	-178.02 (17)
C2—C3—C4—C12	-179.52 (14)	C2—C1—C6—C5	2.1 (3)
C3—C4—C5—C7	-179.67 (18)	C4—C5—C7—C8	-179.00 (19)
C12—C4—C5—C7	0.0 (3)	C6—C5—C7—C8	0.3 (3)
C3—C4—C5—C6	1.0 (3)	C5—C7—C8—C9	0.3 (3)
C12—C4—C5—C6	-179.31 (14)	C6—N1—C9—C8	-0.6 (3)
C9—N1—C6—C5	1.2 (3)	C7—C8—C9—N1	-0.2 (3)
C9—N1—C6—C1	-178.39 (17)		

Hydrogen-bond geometry (Å, °)

<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>
O1—H1...N1 <sup>i</sup>	0.84 (1)	2.01 (2)	2.761 (2)	150 (3)

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