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2,3-Dichloropyridine

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Key indicators: single-crystal X-ray study; T = 113 K; mean σ (C–C) = 0.003 Å; disorder in main residue; R factor = 0.025; wR factor = 0.054; data-to-parameter ratio = 15.7

The complete molecule of the title compound, $C_5H_3Cl_2N$, is generated by crystallographic twofold symmetry, which forces the pyridine N atom and the opposite C-H group to be statistically disordered. In the crystal, weak aromatic π - π stacking [centroid-centroid separation = 3.805 (4) Å and slippage = 1.704 Å leads to [100] stacks of molecules. Short $Cl \cdots Cl$ contacts [3.334 (3) Å] are also observed.

Related literature

For the biological activity of related compounds, see: Liu et al. (2011). For related structures, see: Ma et al. (2007), Liu & Liu (2011).



Experimental

Crystal data

C ₅ H ₃ Cl ₂ N	$V = 572.3 (9) \text{ Å}^3$
$M_r = 147.98$	Z = 4
Monoclinic, $C2/c$	Mo $K\alpha$ radiation
a = 3.805 (3) Å	$\mu = 1.00 \text{ mm}^{-1}$
b = 14.196 (12) Å	$T = 113 { m K}$
c = 10.68 (1) Å	$0.36 \times 0.04 \times 0.04$ mm
$\beta = 97.221 \ (14)^{\circ}$	

Data collection

Rigaku Saturn CCD diffractometer Absorption correction: multi-scan (CrystalClear; Rigaku/MSC, 2005) $T_{\min} = 0.714, \ T_{\max} = 0.961$

Refinement

 $R[F^2 > 2\sigma(F^2)] = 0.025$ $wR(F^2) = 0.054$ S = 1.01675 reflections 43 parameters

541 reflections with $I > 2\sigma(I)$ $R_{\rm int} = 0.044$

2936 measured reflections

675 independent reflections

2 restraints All H-atom parameters refined $\Delta \rho_{\rm max} = 0.3 \hat{1} \ {\rm e} \ {\rm \AA}^{-3}$ $\Delta \rho_{\rm min} = -0.19 \text{ e} \text{ Å}^{-3}$

Data collection: CrystalClear (Rigaku/MSC, 2005); cell refinement: CrystalClear; data reduction: CrystalClear; 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: CrystalStructure (Rigaku/MSC, 2005).

Supplementary data and figures for this paper are available from the IUCr electronic archives (Reference: HB5953).

References

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supporting information

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2,3-Dichloropyridine

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S1. Comment

Pyridine derivatives are valuable intermidiates and various biological activities. the structure of 2,3-dichloropyridine was confirmed by X-ray crstallography. For biological activities of related compounds, see: Liu *et al.* (2011). For related structure, see: Ma *et al.* (2007), Liu *et al.* & Liu (2011);

Single-crystal X-ray diffraction analysis reveals that the title compound crystallizes in the monoclinic space group C2/c. As shown in Fig. 1, the pyridine ring is nearly planar [mean deviation = 0.003 Å]. As shown in Fig. 2, the crystal structure is stabilized by van der Waals' interactions.

S2. Experimental

2,3-dichloropyridine is commercially available. Colourless prisms were grown from ethanol.

S3. Refinement

All the H atoms were positioned geometrically (C—H = 0.93Å) and refined as riding with $U_{iso}(H) = 1.2U_{eq}(C)$



Figure 1

The molecular structure of (I). Displacement ellipsoids are drawn at the 30% probability level and H atoms are shown as small spheres of arbitrary radii. Atoms with suffix A are generated by (1-x, y, 3/2-z). Just one orientation of N1 and C3 is shown.



Figure 2

The crystal packing for (I) with short Cl···Cl contacts indicated by dashed lines.

2,3-Dichloropyridine

Crystal data C₅H₃Cl₂N $M_r = 147.98$ Monoclinic, C2/c Hall symbol: -C 2yc a = 3.805 (3) Å b = 14.196 (12) Å c = 10.68 (1) Å $\beta = 97.221$ (14)° V = 572.3 (9) Å³ Z = 4

Data collection

Rigaku Saturn CCD diffractometer Radiation source: rotating anode Multilayer monochromator F(000) = 296 $D_x = 1.717 \text{ Mg m}^{-3}$ Mo $K\alpha$ radiation, $\lambda = 0.71073 \text{ Å}$ Cell parameters from 985 reflections $\theta = 1.9-27.8^{\circ}$ $\mu = 1.00 \text{ mm}^{-1}$ T = 113 KPrism, colorless $0.36 \times 0.04 \times 0.04 \text{ mm}$

Detector resolution: 14.63 pixels mm⁻¹ ω and φ scans Absorption correction: multi-scan (*CrystalClear*; Rigaku/MSC, 2005)

$T_{\min} = 0.714, \ T_{\max} = 0.961$	$\theta_{\rm max} = 27.8^{\circ}, \theta_{\rm min} = 2.9^{\circ}$
2936 measured reflections	$h = -4 \rightarrow 4$
675 independent reflections	$k = -18 \rightarrow 18$
541 reflections with $I > 2\sigma(I)$	$l = -13 \rightarrow 13$
$R_{\rm int} = 0.044$	

Refinement

Refinement on F^2	Secondary atom site location: difference Fourier
Least-squares matrix: full	map
$R[F^2 > 2\sigma(F^2)] = 0.025$	Hydrogen site location: inferred from
$wR(F^2) = 0.054$	neighbouring sites
<i>S</i> = 1.01	All H-atom parameters refined
675 reflections	$w = 1/[\sigma^2(F_o^2) + (0.022P)^2]$
43 parameters	where $P = (F_o^2 + 2F_c^2)/3$
2 restraints	$(\Delta/\sigma)_{\rm max} = 0.001$
Primary atom site location: structure-invariant	$\Delta \rho_{\rm max} = 0.31 \text{ e} \text{ Å}^{-3}$
direct methods	$\Delta \rho_{\rm min} = -0.19 \text{ e } \text{\AA}^{-3}$

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.

	x	У	Ζ	$U_{ m iso}$ */ $U_{ m eq}$	Occ. (<1)
Cl1	0.26918 (10)	0.32961 (3)	0.61537 (4)	0.02346 (14)	
C1	0.3983 (4)	0.43421 (10)	0.69098 (13)	0.0154 (3)	
C2	0.2951 (3)	0.51548 (10)	0.63275 (12)	0.0182 (3)	0.50
H2	0.138 (6)	0.514 (2)	0.5570 (16)	0.022*	0.50
N1	0.2951 (3)	0.51548 (10)	0.63275 (12)	0.0182 (3)	0.50
C3	0.3971 (4)	0.59762 (10)	0.69191 (15)	0.0214 (4)	
Н3	0.312 (4)	0.6559 (8)	0.6561 (15)	0.026*	

Fractional atomic coordinates and isotropic or equivalent isotropic displacement parameters $(Å^2)$

Atomic displacement parameters $(Å^2)$

	U^{11}	U^{22}	U^{33}	U^{12}	U^{13}	U^{23}
C11	0.0279 (3)	0.0201 (2)	0.0216 (2)	-0.00436 (16)	0.00026 (17)	-0.00631 (16)
C1	0.0142 (8)	0.0163 (7)	0.0160 (7)	-0.0009 (6)	0.0031 (6)	-0.0027 (6)
C2	0.0158 (8)	0.0235 (7)	0.0149 (7)	-0.0009 (6)	0.0008 (6)	0.0016 (6)
N1	0.0158 (8)	0.0235 (7)	0.0149 (7)	-0.0009 (6)	0.0008 (6)	0.0016 (6)
C3	0.0184 (9)	0.0185 (8)	0.0269 (9)	0.0015 (6)	0.0012 (7)	0.0073 (7)

Geometric parameters (Å, °)

Cl1—C1	1.7317 (18)	С2—Н2	0.943 (10)
C1—C2	1.346 (2)	C3—C3 ⁱ	1.382 (3)

supporting information

C1—C1 ⁱ C2—C3	1.394 (3) 1.359 (2)	С3—Н3	0.951 (9)	
C2-C1-C1 ⁱ C2-C1-Cl1 C1 ⁱ -C1-Cl1 C1-C2-C3 C1-C2-H2	120.97 (9) 118.07 (12) 120.96 (6) 118.10 (14) 119.2 (18)	C3—C2—H2 C2—C3—C3 ⁱ C2—C3—H3 C3 ⁱ —C3—H3	122.4 (18) 120.92 (9) 119.8 (10) 119.1 (10)	
C1 ⁱ —C1—C2—C3 C11—C1—C2—C3	0.5 (3) -179.84 (12)	C1—C2—C3—C3 ⁱ	0.5 (3)	

Symmetry code: (i) -x+1, y, -z+3/2.