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Key indicators

Single-crystal X-ray study T = 294 K Mean σ (C–C) = 0.005 Å R factor = 0.054 wR factor = 0.111 Data-to-parameter ratio = 14.5

For details of how these key indicators were automatically derived from the article, see http://journals.iucr.org/e.

N-(4,6-Dichloro-1,3,5-triazin-2-yl)aniline

The synthesis of the title compound, $C_9H_6Cl_2N_4$, and its crystal structure are reported in this paper. The crystal structure is stabilized by N-H···Cl and N-H···N hydrogen-bonding interactions.

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Comment

The amine derivatives of 2,4,6-trichloro[1,3,5]triazine possess valuable properties, as they are widely used as starting materials for many products, including drugs and light stabilizers (Mathias & Simanek, 1994; Manasek & Hrdlovik, 1990). The title compound, $C_9H_6Cl_2N_4$, (I), has been synthesized from 2,4,6-trichloro-1,3,5-triazine and aniline. The bond lengths and angles are within normal ranges and selected values are given in Table 1. The crystal structure is stabilized by N-H···Cl hydrogen bonds and a weak N-H···N interaction (Fig.2).



Experimental

2,4,6-Trichloro-1,3,5-triazine (4.61 g, 0.025 mol) and aniline (2.33 g, 0.025 mol) were added to acetone (30 ml), and stirred at 273 K for 2 h. A solution of Na₂CO₃ (1.38 g, 0.013 mol) in water (10 ml) was then added dropwise for 1 h. The reaction mixture was stirred at 273–278 K for a further 3 h. The precipitate was filtered off, and the acetone was evaporated under reduced pressure. The title compound (5.54 g) was obtained in a yield of 92.3%. Suitable crystals (m.p. 407–409 K) were obtained by slow evaporation of a solution in a mixture of dichloromethane and ethyl acetate (6:1 ν/ν).



Figure 1

A view of the molecule of (I). Displacement ellipsoids are drawn at the 30% probability level and H atoms are shown as small spheres of arbitrary radii.

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Crystal data

 $C_9H_6Cl_2N_4$ $M_r = 241.08$ Orthorhombic, *Pbca* a = 14.114 (3) Å b = 5.5098 (10) Å c = 25.621 (5) Å V = 1992.4 (6) Å³ Z = 8 $D_x = 1.607$ Mg m⁻³

Data collection

Bruker SMART 1000 CCD areadetector diffractometer φ and ω scans Absorption correction: multi-scan (*SADABS*; Sheldrick, 1996) $T_{min} = 0.800, T_{max} = 0.884$ 10293 measured reflections

Refinement

Refinement on F^2 $R[F^2 > 2\sigma(F^2)] = 0.054$ $wR(F^2) = 0.111$ S = 1.132033 reflections 140 parameters H atoms treated by a mixture of independent and constrained refinement

Table 1

Selected geometric parameters (Å, $^{\circ}$).

Cl1-C4	1.725 (4)	N2-C11	1.413 (4)
N5-C6 N2-C2	1.323 (5) 1.346 (4)	N2-H2	0.94 (3)
C6-N5-C4 C2-N2-C11 C2-N2-H2	110.9 (3) 131.6 (3) 110 (2)	C11-N2-H2 N3-C4-Cl1	118 (2) 116.0 (3)
C2-N3-C4-N5 C2-N3-C4-Cl1	0.8 (5) 178.7 (2)	C11-N2-C2-N3 C2-N2-C11-C12	174.8(3) -1.4(6)

Table 2

Hydrogen-bond geometry (Å, °).

$D - H \cdots A$	D-H	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - \mathbf{H} \cdots \mathbf{A}$
$\begin{array}{c} N2 - H2 \cdots N3^{i} \\ N2 - H2 \cdots Cl1^{i} \end{array}$	0.94 (3)	2.72 (4)	3.615 (4)	160 (3)
	0.94 (3)	2.80 (3)	3.465 (3)	129 (3)

Symmetry codes: (i) -x + 1, $y + \frac{1}{2}$, $-z + \frac{3}{2}$.

Mo $K\alpha$ radiation Cell parameters from 2959 reflections $\theta = 3.2-25.9^{\circ}$ $\mu = 0.62 \text{ mm}^{-1}$ T = 294 (2) K Block, colourless $0.34 \times 0.22 \times 0.20 \text{ mm}$

2033 independent reflections 1427 reflections with $I > 2\sigma(I)$ $R_{int} = 0.039$ $\theta_{max} = 26.4^{\circ}$ $h = -17 \rightarrow 15$ $k = -6 \rightarrow 6$ $l = -32 \rightarrow 31$

$$\begin{split} &w = 1/[\sigma^2(F_o^2) + (0.0096P)^2 \\ &+ 3.9817P] \\ &where \ P = (F_o^2 + 2F_c^2)/3 \\ (\Delta/\sigma)_{max} < 0.001 \\ \Delta\rho_{max} = 0.24 \ e \ \text{\AA}^{-3} \\ \Delta\rho_{min} = -0.31 \ e \ \text{\AA}^{-3} \end{split}$$





The H atom of the NH group was initially located in a difference Fourier map and was refined with an N-H distance restraint of 0.94 (3) Å. All other H atoms were positioned geometrically and refined using a riding model, with C-H = 0.93 Å and $U_{\rm iso}({\rm H}) =$ $1.2U_{\rm eq}({\rm C})$. In the absence of significant anomalous dispersion effects, Friedel-pair reflections were merged prior to refinement.

Data collection: *SMART* (Bruker, 1997); cell refinement: *SMART*; data reduction: *SAINT* (Bruker, 1997); program(s) used to solve structure: *SHELXS97* (Sheldrick, 1997); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *SHELXTL* (Bruker, 1997); software used to prepare material for publication: *SHELXTL*.

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