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Key indicators

Single-crystal X-ray study T = 294 KMean σ (C–C) = 0.003 Å R factor = 0.039 wR factor = 0.104 Data-to-parameter ratio = 15.3

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

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

The title compound, $C_{13}H_{14}ClN_5O$, was synthesized from 2,4dichloro-6-morpholino-1,3,5-triazine and aniline. In the crystal structure, there are intermolecular $N-H\cdots O$ hydrogen bonds which propagate infinite chains parallel to the *c* axis. The morpholine ring adopts a chair conformation. Received 23 May 2005 Accepted 24 June 2005 Online 6 July 2005

Comment

1,3,5-Triazine derivatives are of great interest because of their importance as constituents of active dyes and many hindered amine light stabilizers (Goi, 1960; Degussa, 1968; Manasek & Hrdlovik, 1990). The molecular structure of (I) is shown in Fig. 1. In the crystal structure, molecules are linked by N– $H \cdot \cdot \cdot O$ hydrogen bonds parallel to the *c* axis. There is also an intermolecular contact which indicates a weak C– $H \cdot \cdot \cdot Cl$ interaction. The morpholine ring adopts a chair conformation, as expected (see Table 1 and Fig. 2).



Experimental

The title compound was prepared from 2,4-dichloro-6-morpholino-1,3,5-triazine and aniline. 2,4-Dichloro-6-morpholino-1,3,5-triazine was synthesized according to the method described by Dong *et al.* (2005). 2,4-Dichloro-6-morpholino-1,3,5-triazine (23.5 g, 0.1 mol), Na₂CO₃ (5.51 g, 0.051 mol) and aniline (9.3 g, 0.1 mol) were added to toluene (280 ml), which was stirred at 328–333 K for 5 h. The precipitate was filtered off, the solution was washed with water, and the toluene was evaporated under reduced pressure to give compound (I) in 94.3% yield. Crystals suitable for X-ray diffraction were obtained by slow evaporation of a mixed solution in dichloromethane and ethyl acetate (5:1 ν/ν) (m.p. 438–440 K).

Crystal data	
C ₁₃ H ₁₄ ClN ₅ O	D
$M_r = 291.74$	Μ
Monoclinic, $P2_1/c$	C
a = 8.3481 (15) Å	
b = 17.667 (3) Å	θ
c = 9.9401 (18) Å	μ
$\beta = 108.860 \ (3)^{\circ}$	Т
$V = 1387.3 (4) \text{ Å}^3$	B
Z = 4	0.1

 $\begin{array}{l} D_x = 1.397 \ \mathrm{Mg \ m^{-3}} \\ \mathrm{Mo \ } \kappa \alpha \ \mathrm{radiation} \\ \mathrm{Cell \ parameters \ from \ 2305} \\ \mathrm{reflections} \\ \theta = 2.5 - 25.7^{\circ} \\ \mu = 0.28 \ \mathrm{mm^{-1}} \\ T = 294 \ (2) \ \mathrm{K} \\ \mathrm{Block, \ colourless} \\ 0.28 \times 0.22 \times 0.20 \ \mathrm{mm} \end{array}$

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Figure 1

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

Data collection

Bruker SMART CCD area-detector	2831 independent reflections
diffractometer	1842 reflections with $I > 2\sigma(I)$
φ and ω scans	$R_{\rm int} = 0.033$
Absorption correction: multi-scan	$\theta_{\rm max} = 26.4^{\circ}$
(SADABS; Sheldrick, 1996)	$h = -8 \rightarrow 10$
$T_{\min} = 0.920, \ T_{\max} = 0.946$	$k = -16 \rightarrow 22$
7720 measured reflections	$l = -12 \rightarrow 7$
Refinement	

 $w = 1/[\sigma^2(F_0^2) + (0.0414P)^2]$

where $P = (F_o^2 + 2F_c^2)/3$

+ 0.3828P]

 $\Delta \rho_{\rm min} = -0.21 \text{ e } \text{\AA}^{-3}$

 $(\Delta/\sigma)_{\rm max} = 0.001$ $\Delta \rho_{\rm max} = 0.16 \text{ e } \text{\AA}^{-3}$

Refinement on F^2 $R[F^2 > 2\sigma(F^2)] = 0.039$ $wR(F^2) = 0.104$ S = 1.012831 reflections 185 parameters H atoms treated by a mixture of independent and constrained refinement

Table 1

Hydrogen-bond geometry (Å, °).

$D - H \cdot \cdot \cdot A$	D-H	$H \cdots A$	$D \cdots A$	$D - \mathbf{H} \cdot \cdot \cdot A$
$N5-H5\cdotsO1^i$	0.84 (2)	2.08 (2)	2.905 (2)	170 (2)
C				

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

Figure 2

The crystal structure of (I), viewed down the *a* axis. Dashed lines indicate hydrogen-bond interactions.

The N-bound H atom was located in a difference Fourier map and the N-H distance restrained to 0.84 (2) Å. All other H atoms were positioned geometrically and refined using a riding model, with C-H in the range 0.93–0.97 Å and with $U_{iso}(H) = 1.2U_{eq}(C)$.

Data collection: SMART (Bruker, 1997); cell refinement: SAINT (Bruker, 1997); data reduction: SAINT; 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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