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Key indicators

Single-crystal X-ray study $T=123~\mathrm{K}$ Mean $\sigma(\mathrm{C-C})=0.003~\mathrm{\mathring{A}}$ R factor = 0.038 wR factor = 0.080 Data-to-parameter ratio = 14.7

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

3,4-Dichloro-1-nitrobenzene-aniline (2/1)

The solvate structure of 3,4-dichloro-1-nitrobenzene with aniline, $2C_6H_3Cl_2NO_2\cdot C_6H_7N$, is reported. Ribbons of 3,4-dichloronitrobenzene, formed by $Cl\cdot\cdot\cdot Cl$ and $N-O\cdot\cdot\cdot Cl$ interactions, are linked together $via\ N-H\cdot\cdot\cdot O$ hydrogen bonds with aniline into an undulating two-dimensional sheet.

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Comment

The title compound, (I), was produced during an automated parallel crystallization polymorph screen on 3,4-dichloronitrobenzene (3,4-DCNB). The sample was identified as a novel form using multi-sample X-ray powder diffraction analysis of all recrystallized samples (Florence *et al.*, 2003). Subsequent manual recrystallization from a saturated aniline solution by slow evaporation at 298 K yielded samples suitable for single-crystal X-ray analysis. The title solvate, (I), crystallizes in the space group $P2_1/n$ with two molecules of 3,4-DCNB and one molecule of aniline in the asymmetric unit (Fig. 1).

The crystal structure of (I) is characterized by ribbons of 3,4-DCNB, which are linked by aniline molecules to form a

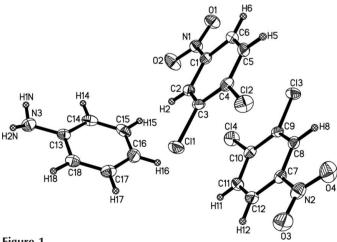


Figure 1

The asymmetric unit of (I), showing the numbering scheme used.

Displacement ellipsoids are drawn at the 50% probability level.

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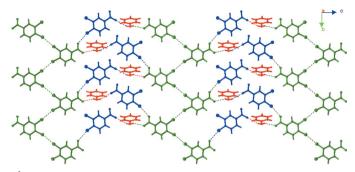


Figure 2
The two-dimensional network formed by (I), showing the intermolecular interactions involved as dashed lines (3,4-DCNB molecule 1: green; 3,4-DCNB molecule 2: blue; aniline: red).

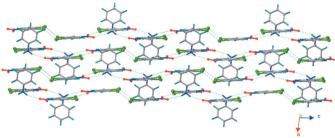


Figure 3
Packing diagram viewed perpendicular to the sheets, illustrating the outof-plane aniline molecules and the stacking arrangement of the sheets.
Intermolecular interactions are shown as dashed lines.

continuous sheet (Fig. 2). Molecules of type 1 (C1–C6) form a zigzag chain via Cl···Cl interactions [Cl1···Cl2ⁱ = 3.399 (1) Å and C3–Cl1···Cl2ⁱ = 149.4 (1)°; symmetry code: (i) $\frac{3}{2} - x$, $\frac{1}{2} + y$, $\frac{3}{2} - z$]. These molecules are then involved in a second contact with molecules of type 2 (C7–Cl2) via N–O···Cl interactions [O2···Cl4ⁱⁱ = 3.056 (2) Å and N1–O2···Cl4ⁱⁱ = 140.1 (1)°; symmetry code: (ii) 1 - x, 1 - y, 1 - z], thus forming 3,4-DCNB ribbons running parallel to the b axis. The aniline solvent molecules, which lie in a perpendicular plane, link these ribbons into an undulating sheet through two N–H···O interactions [N3···O1ⁱⁱⁱ = 2.52 (2) Å and N3–H1N···O1ⁱⁱⁱ = 157 (2)°, and N3···O3ⁱ = 2.64 (2) Å and N3–H2N···O3ⁱ = 147 (2)°; symmetry code: (iii) 2 - x, 1 - y, 1 - z]. These sheets form an interdigitated ABAB stack parallel to the a axis (Fig. 3).

Experimental

A single-crystal sample of the title compound was recrystallized from aniline solution by slow evaporation at $\it ca$ 293 K.

Crystal	data
.rvsiai	aana

$2C_6H_3Cl_2NO_2\cdot C_6H_7N$	$D_x = 1.625 \text{ Mg m}^{-3}$
$M_r = 477.11$	Mo $K\alpha$ radiation
Monoclinic, $P2_1/n$	Cell parameters from 4734
a = 6.9774 (2) Å	reflections
b = 10.1668 (3) Å	$\theta = 1.0 - 27.9^{\circ}$
c = 27.6762 (7) Å	$\mu = 0.64 \text{ mm}^{-1}$
$\beta = 96.495 \ (2)^{\circ}$	T = 123 (2) K
$V = 1950.69 (9) \text{ Å}^3$	Triangle, orange
Z=4	$0.45 \times 0.30 \times 0.15 \text{ mm}$

Data collection

Nonius KappaCCD diffractometer	$R_{\rm int} = 0.058$
ω and φ scans	$\theta_{\rm max} = 27.9^{\circ}$
Absorption correction: none	$h = -9 \rightarrow 9$
22354 measured reflections	$k = -13 \rightarrow 13$
4629 independent reflections	$l = -36 \rightarrow 36$
3314 reflections with $I > 2\sigma(I)$	

Refinement

$w = 1/[\sigma^2(F_0^2) + (0.0275P)^2]$
+ 0.7246P]
where $P = (F_0^2 + 2F_c^2)/3$
$(\Delta/\sigma)_{\rm max} = 0.002$
$\Delta \rho_{\text{max}} = 0.28 \text{ e Å}^{-3}$
$\Delta \rho_{\min} = -0.32 \text{ e Å}^{-3}$

C-H distances are in the range 0.09 (2)–1.00 (2) Å, and N-H distances are 0.86 (2) and 0.87 (2) Å.

Data collection: *COLLECT* (Hooft, 1998) and *DENZO* (Otwinowski & Minor, 1997) and *COLLECT*; cell refinement: *DENZO*; data reduction: *DENZO*; program(s) used to solve structure: *SHELXS97* (Sheldrick, 1997); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *SHELXTL* (Bruker, 2000) and *OLEX* (Dolomanov *et al.*, 2003); software used to prepare material for publication: *SHELXL97* and *PLATON* (Spek, 2003).

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