

(0.02 mol) and pyridine (0.02 mol) was stirred under reflux in ethanol (40 ml) for 4 h. 2,4-Dichlorobenzaldehyde (0.02 mol) and piperidine (0.02 mol) were added and the mixture was refluxed for 4 h. After cooling and filtration, the title compound was recrystallized from acetic acid. $^1\text{H NMR}$ (p.p.m.): 1.19 (*m*, 3H, CH_3), 2.52 (*s*, 3H, CH_3), 4.12 (*m*, 2H, CH_2), 6.20 (*s*, 1H, CH), 7.27–7.47 (*m*, 8H, ArH), 7.74 (*s*, 1H, CH). M.p. 455–456 K. A portion (20 mg) of (I) was dissolved in dichloromethane (15 ml); the solution was kept at room temperature for 8 d and natural evaporation gave colorless single crystals of (I), suitable for X-ray analysis.

Crystal data

$\text{C}_{23}\text{H}_{18}\text{Cl}_2\text{N}_2\text{O}_3\text{S}\cdot\text{CH}_2\text{Cl}_2$
 $M_r = 558.28$
 Triclinic, $P\bar{1}$
 $a = 9.747$ (4) Å
 $b = 11.291$ (4) Å
 $c = 12.297$ (5) Å
 $\alpha = 84.546$ (7)°
 $\beta = 74.655$ (6)°
 $\gamma = 78.378$ (6)°
 $V = 1277.1$ (9) Å³

$Z = 2$
 $D_x = 1.452$ Mg m⁻³
 Mo $K\alpha$ radiation
 Cell parameters from 1016 reflections
 $\theta = 2.2$ – 26.1 °
 $\mu = 0.58$ mm⁻¹
 $T = 293$ (2) K
 Block, colorless
 $0.22 \times 0.16 \times 0.12$ mm

Data collection

Bruker SMART CCD area-detector diffractometer
 φ and ω scans
 Absorption correction: multi-scan (SADABS; Bruker, 1997)
 $T_{\min} = 0.777$, $T_{\max} = 0.933$
 6583 measured reflections

4478 independent reflections
 2711 reflections with $I > 2\sigma(I)$
 $R_{\text{int}} = 0.032$
 $\theta_{\text{max}} = 25.0$ °
 $h = -11 \rightarrow 11$
 $k = -13 \rightarrow 8$
 $l = -14 \rightarrow 14$

Refinement

Refinement on F^2
 $R[F^2 > 2\sigma(F^2)] = 0.059$
 $wR(F^2) = 0.180$
 $S = 1.05$
 4478 reflections
 309 parameters
 H-atom parameters constrained

$w = 1/[\sigma^2(F_o^2) + (0.0864P)^2 + 0.2487P]$
 where $P = (F_o^2 + 2F_c^2)/3$
 $(\Delta/\sigma)_{\text{max}} < 0.001$
 $\Delta\rho_{\text{max}} = 0.50$ e Å⁻³
 $\Delta\rho_{\text{min}} = -0.46$ e Å⁻³

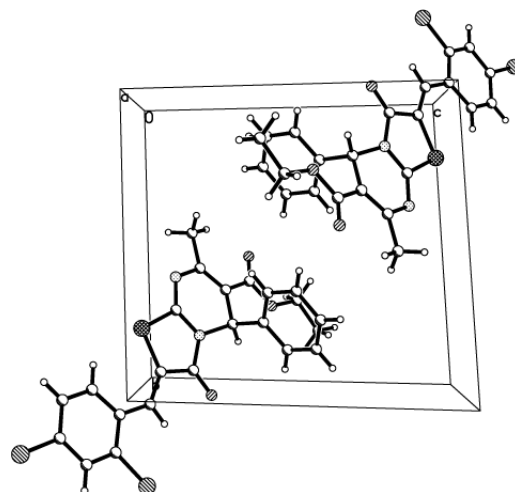


Figure 2

The crystal structure of (I), viewed along the *a* axis.

H atoms were positioned geometrically ($\text{C}-\text{H} = 0.93$ – 0.98 Å) and treated as riding [$U_{\text{iso}}(\text{H}) = 1.2 U_{\text{eq}}(\text{C})$].

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*.

References

- Bruker (1997). *SADABS*, *SMART*, *SAINT* and *SHELXTL*. Versions 5.10. Bruker AXS Inc., Madison, Wisconsin, USA.
 Lu, J., Wang, F.-L., Bai, Y.-J. & Li, W.-H. (2002). *Chin. J. Org. Chem.* **22**, 788–792.
 Sheldrick, G. M. (1997). *SHELXS97* and *SHELXL97*. University of Göttingen, Germany.