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## Key indicators

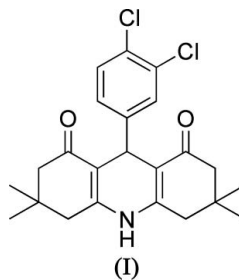
Single-crystal X-ray study  
 $T = 298$  K  
Mean  $\sigma(C-C) = 0.009$  Å  
 $R$  factor = 0.069  
 $wR$  factor = 0.186  
Data-to-parameter ratio = 14.8For details of how these key indicators were  
automatically derived from the article, see  
<http://journals.iucr.org/e>.9-(3,4-Dichlorophenyl)-3,3,6,6-tetramethyl-  
1,2,3,4,5,6,7,8,9,10-decahydroacridine-1,8-dione

The title compound,  $C_{23}H_{25}Cl_2NO_2$ , was synthesized by the reaction of 5,5-dimethylcyclohexane-1,3-dione with 3,4-dichlorobenzaldehyde and ammonium acetate under solvent-free conditions at 353 K. X-ray analysis reveals that the dihydropyridine and cyclohexene rings adopt envelope conformations.

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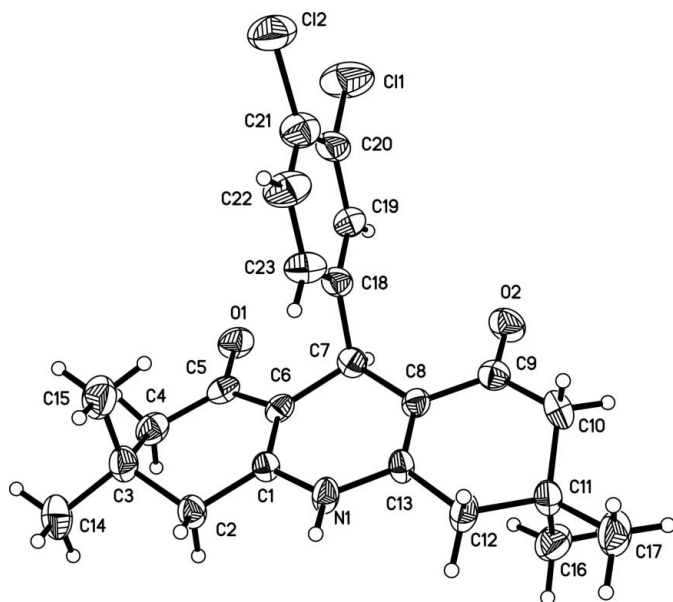
## Comment

The solvent-free reaction has attracted great attention in recent years (Tanaka & Toda, 2000) and has proved to have many advantages: reduced pollution, low costs, and simplicity in process and handling. 1,4-Dihydropyridines are well known compounds, as a consequence of their pharmacological profile as calcium channel modulators (Janis *et al.*, 1987), which have become almost indispensable for the treatment of cardiovascular diseases such as hypertension, cardiac arrhythmia and angina. The discovery of acridines as antimalarial and anti-tumor agents has attracted the attention of organic chemists and thus led to intensive interest in the synthesis of several drugs based on acridine (Khurana *et al.*, 1990; Matsumoto *et al.*, 1983). We report here the crystal structure of the title compound, (I), which was synthesized by the solvent-free reaction of 5,5-dimethylcyclohexane-1,3-dione and 3,4-dichlorobenzaldehyde and ammonium acetate at 353 K.

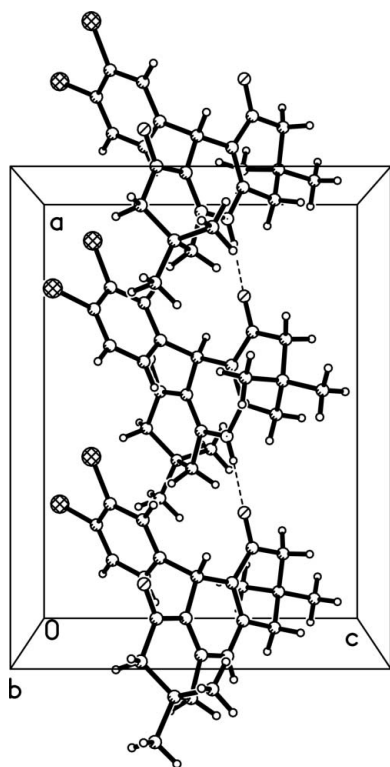


In (I) (Fig. 1), the dihydropyridine ring is in an envelope conformation, with atom C7 deviating from the C1/C6/C8/C13/N1 plane by 0.189 (8) Å. Both cyclohexene rings adopt envelope conformations: atom C3 deviates from the C1/C2/C4–C6 plane by 0.659 (9) Å and atom C11 deviates from the C8–C10/C12/C13 plane by 0.602 (9) Å. The dihedral angle between the C1/C6/C8/C13/N1 and C1/C2/C4–C6 planes is 6.8 (4)°, and that between the C1/C6/C8/C13/N1 and C8–C10/C12/C13 planes is 3.5 (4)°. The dichlorophenyl group is twisted away from the C1/C6/C8/C13/N1 plane by 83.2 (1)°.

The crystal packing shows that intermolecular N–H...O hydrogen bonds (Table 1) link the molecules into a chain along the *a* axis (Fig. 2).



**Figure 1**  
The structure of (I), showing 40% probability displacement ellipsoids and the atom-numbering scheme.



**Figure 2**  
A view of the N—H...O hydrogen-bonded (dashed lines) chain in (I).

## Experimental

Compound (I) was prepared by the reaction of 5,5-dimethylcyclohexane-1,3-dione (4 mmol, 0.560 g) with 3,4-dichlorobenzaldehyde (2 mmol, 0.350 g) and  $\text{NH}_4\text{OAc}$  (3 mmol, 0.231 g) under solvent-free conditions. Single crystals suitable for X-ray diffraction were obtained by slow evaporation of an ethanol solution.

## Crystal data

$\text{C}_{23}\text{H}_{25}\text{Cl}_2\text{NO}_2$   
 $M_r = 418.34$   
 Orthorhombic,  $Pna2_1$   
 $a = 14.155 (3) \text{ \AA}$   
 $b = 14.352 (3) \text{ \AA}$   
 $c = 10.704 (3) \text{ \AA}$   
 $V = 2174.6 (9) \text{ \AA}^3$   
 $Z = 4$   
 $D_x = 1.278 \text{ Mg m}^{-3}$

Mo  $K\alpha$  radiation  
 Cell parameters from 1556 reflections  
 $\theta = 2.4\text{--}18.8^\circ$   
 $\mu = 0.32 \text{ mm}^{-1}$   
 $T = 298 (2) \text{ K}$   
 Block, colourless  
 $0.43 \times 0.40 \times 0.38 \text{ mm}$

## Data collection

Bruker SMART CCD area-detector diffractometer  
 $\varphi$  and  $\omega$  scans  
 Absorption correction: multi-scan (SADABS; Sheldrick, 1996)  
 $T_{\min} = 0.876$ ,  $T_{\max} = 0.889$   
 10745 measured reflections

3745 independent reflections  
 1776 reflections with  $I > 2\sigma(I)$   
 $R_{\text{int}} = 0.081$   
 $\theta_{\max} = 25.0^\circ$   
 $h = -12 \rightarrow 16$   
 $k = -17 \rightarrow 14$   
 $l = -12 \rightarrow 12$

## Refinement

Refinement on  $F^2$   
 $R[F^2 > 2\sigma(F^2)] = 0.069$   
 $wR(F^2) = 0.186$   
 $S = 1.01$   
 3745 reflections  
 253 parameters  
 H-atom parameters constrained

$w = 1/[\sigma^2(F_o^2) + (0.0795P)^2]$   
 where  $P = (F_o^2 + 2F_c^2)/3$   
 $(\Delta/\sigma)_{\max} = 0.001$   
 $\Delta\rho_{\max} = 0.74 \text{ e \AA}^{-3}$   
 $\Delta\rho_{\min} = -0.34 \text{ e \AA}^{-3}$   
 Absolute structure: Flack (1983),  
 1745 Friedel pairs  
 Flack parameter: 0.09 (14)

**Table 1**

Hydrogen-bond geometry ( $\text{\AA}$ ,  $^\circ$ ).

$D\text{---}H\cdots A$	$D\text{---}H$	$H\cdots A$	$D\cdots A$	$D\text{---}H\cdots A$
$\text{N1---H1}\cdots\text{O1}^i$	0.86	1.85	2.708 (6)	174

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

H atoms were placed in geometrically idealized positions ( $\text{N---H} = 0.86 \text{ \AA}$  and  $\text{C---H} = 0.93\text{--}0.98 \text{ \AA}$ ) and allowed to ride on their parent atoms, with  $U_{\text{iso}}(\text{H}) = 1.2U_{\text{eq}}(\text{C}, \text{N})$  or  $1.5U_{\text{eq}}(\text{methyl C})$ .

Data collection: SMART (Bruker, 1998); cell refinement: SAINT (Bruker, 1999); 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, 1999); software used to prepare material for publication: SHELXTL.

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