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#### **Key indicators**

Single-crystal X-ray study T = 273 K Mean  $\sigma$ (C–C) = 0.003 Å R factor = 0.056 wR factor = 0.150 Data-to-parameter ratio = 18.4

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

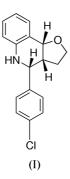
# A diastereoisomer of furo[3,2-c]quinoline

The title compound, 4-(4-chlorophenyl)-2,3,3a,4,5,9bhexahydrofuro[3,2-c]quinoline,  $C_{17}H_{16}CINO$ , was obtained as one of the diastereoisomers from the imino Diels–Alder reaction of an imine and dihydrofuran. The molecule is a *cis* (*endo*) cycloadduct isomer. The tetrahydrofuran ring adopts an envelope conformation, while the *N*-heterocyclic ring is in a sofa conformation. Intermolecular  $N-H\cdots O$  hydrogen bonds lead to chains of molecules running along the *a* axis. Received 13 December 2004 Accepted 17 December 2004 Online 24 December 2004

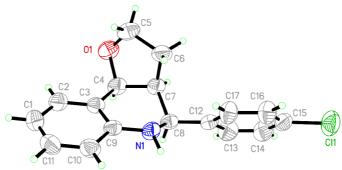
Imine Diels-Alder adducts. Part IV.

### Comment

Diels–Alder adducts from the reaction of imines derived from aromatic amines and aldehydes with dihydrofuran/pyran have been used as a central heterocyclic core for a variety of alkaloids, such as skimmianine and balfouridine (Akhmed Khodzhaeva & Bessonova, 1983; Jurd & Wong, 1981). We have recently reported the pyrano- and furoquinolines synthesized using the imino Diels–Alder reaction with  $ZrCl_4$ as a potential environmentally benign catalyst (Mahesh *et al.*, 2004). The structure of the title compound, (I), is reported here as an early result in our study of this series of compounds.



A perspective view of (I) is shown in Fig. 1. In all essential details, the geometry of the molecule (Table 1), in terms of



#### Figure 1

A view of (I), with the atom-numbering scheme. Displacement ellipsoids are drawn at the 50% probability level and H atoms are shown as small spheres of arbitrary radii.

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interatomic distances and angles, is in good agreement with relevant structures found in the literature (Clegg et al., 1999). The orientations of the junction atoms H7 and H8 differentiate the diastereoisomers for cis or trans configurations. The H7-C7-C8-H8 torsion angle of  $-60.6 (2)^{\circ}$  indicates the cis (endo) arrangement of the ring junction H atoms and is in accordance with the coupling constant J = 8.1 Hz. Similarly, the H4-C4-C7-H7 torsion angle of  $38.3 (2)^{\circ}$  also indicates the cis arrangement of the tetrahydrofuran-ring-junction H atoms.

The substitutions of the quinoline ring produce a considerable twist about the  $C8 \cdot \cdot \cdot C3$  vector. This twist can be seen from the C8-C7-C4-C3 and C8-N1-C9-C3 torsion angles of 39.7 (2) and -22.7 (2)°, respectively. The N-heterocyclic ring of the quinoline moiety is in a sofa conformation [asymmetry parameter  $\Delta C_2(C9-C3) = 0.030(1)$  (Nardelli, 1983)], with atom C8 displaced by 0.600 (2) Å from the N1/C9/C3/C4/C7 basal plane.

The tetrahydrofuran ring adopts an envelope conformation, with an asymmetry parameter  $\Delta C_{\rm s}({\rm C4}) = 0.012$  (1). Atom O1 is displaced by 0.503 (2) Å from the N1/C4/C11/C10 leastsquares plane. The N1-C8-C12-C17 torsion angle between these two rings is  $-32.0(2)^{\circ}$ .

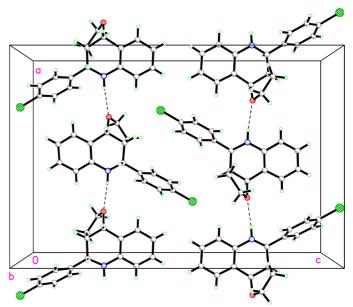
Intermolecular N-H···O hydrogen bonding is observed between the N atom of the quinoline ring system and the O atom of the tetrahydrofuran ring, forming chains along the a axis (Fig. 2). It is interesting to note that the Cl atom present in the structure is not involved in any interactions. A possible intramolecular C-H···N interaction is also observed in the structure (Table 2).

# **Experimental**

To a solution of N-[(1E)-(4-chlorophenyl)methylene]-N-phenylamine (5.5 mmol) in dichloromethane (5 ml) at room temperature were added 2,3-dihydrofuran (5.5 mmol) and ZrCl<sub>4</sub> (10 mol%), and the mixture was stirred for 90 min. The completed reaction was quenched with water and the crude product was purified by column chromatography using 2% ethyl acetate and hexane, to yield the title compound. Crystals of (I) for X-ray study were obtained by recrystallization from a methanol-water (3:1) solution.

Crystal data

C <sub>17</sub> H <sub>16</sub> ClNO	Mo $K\alpha$ radiation
$M_r = 285.76$	Cell parameters from 5262
Orthorhombic, Pbca	reflections
$a = 14.1068 (9) \text{\AA}$	$\theta = 2.4-27.9^{\circ}$
b = 9.5526 (6) Å	$\mu = 0.26 \text{ mm}^{-1}$
c = 21.1298 (13)  Å	T = 273 (2) K
V = 2847.4 (3) Å <sup>3</sup>	Block, colourless
Z = 8	$0.18 \times 0.15 \times 0.13 \text{ mm}$
$D_x = 1.333 \text{ Mg m}^{-3}$	
Data collection	
Bruker SMART APEX CCD area-	3010 reflections with $I > 2\sigma(I)$
detector diffractometer	$R_{\rm int} = 0.023$
$\omega$ scans	$\theta_{\rm max} = 28.0^{\circ}$
Absorption correction: none	$h = -18 \rightarrow 18$
30 760 measured reflections	$k = -12 \rightarrow 12$
3412 independent reflections	$l = -27 \rightarrow 27$





A packing diagram for (I), viewed down the b axis. Dashed lines indicate the N-H···O hydrogen bonds.

Refinement

Refinement on $F^2$
$R[F^2 > 2\sigma(F^2)] = 0.056$
$wR(F^2) = 0.150$
S = 1.14
3412 reflections
185 parameters
H atoms treated by a mixture of
independent and constrained

 $w = 1/[\sigma^2(F_0^2) + (0.0667P)^2]$ + 0.9682P] where  $P = (F_0^2 + 2F_c^2)/3$  $(\Delta/\sigma)_{\rm max} < 0.001$  $\Delta \rho_{\rm max} = 0.44$  e Å<sup>-3</sup>  $\Delta \rho_{\rm min} = -0.24 \text{ e } \text{\AA}^{-3}$ Extinction correction: none

# Table 1

refinement

Selected bond	l lengths (	A).
---------------	-------------	-----

Cl1-C15	1.7450 (19)	N1-C9	1.387 (2)
O1-C5	1.426 (3)	N1-C8	1.452 (2)
O1-C4	1.438 (2)		

Table 2

Hydrogen-bond	geometry	(Å,	°)
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$D - H \cdot \cdot \cdot A$	D-H	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - \mathbf{H} \cdot \cdot \cdot A$
$N1 - H1N \cdots O1^i$ C6 - H6A · · · N1	0.89 (3) 0.97	2.19 (3) 2.60	3.066 (2) 2.988 (2)	168 (2) 105
Symmetry code: (i) x	$+\frac{1}{2}, y, -z + \frac{3}{2}.$			

The H atom on N1 was located in a difference density map and refined freely. All other H atoms were positioned geometrically and treated as riding atoms, with C-H distances in the range 0.93-0.98 Å, and with  $U_{iso}(H) = 1.5U_{eq}(C)$  for methyl H and  $1.2U_{eq}(C)$  for other H.

Data collection: SMART (Bruker, 2001); cell refinement: SAINT (Bruker, 2001); data reduction: SAINT; program(s) used to solve structure: SHELXS97 (Sheldrick, 1997); program(s) used to refine structure: SHELXL97 (Sheldrick, 1997); molecular graphics: SHELXTL/PC (Sheldrick, 1990); software used to prepare material for publication: SHELXL97 and PARST (Nardelli, 1995).

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