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Key indicators

Single-crystal X-ray study
 $T = 173$ K
Mean $\sigma(\text{C}-\text{C}) = 0.002$ Å
 R factor = 0.034
 wR factor = 0.087
Data-to-parameter ratio = 13.9For details of how these key indicators were automatically derived from the article, see <http://journals.iucr.org/e>.

Phthaloyl amlodipine

The title compound [alternatively called 3-ethyl 5-methyl 4-(2-chlorophenyl)-2-(2-phthalamidoethoxymethyl)-6-methyl-1,4-dihydropyridine-3,5-dicarboxylate or ethyl methyl (4*RS*)-4-(2-chlorophenyl)-2-({[2-(1,3-dioxo-1,3-dihydro-2*H*-isoindol-2-yl)ethyl]oxy)methyl)-6-methyl-1,4-dihydropyridine-3,5-dicarboxylate], $\text{C}_{28}\text{H}_{27}\text{ClN}_2\text{O}_7$, is a calcium channel blocker and belongs to the family of anti-anginal and antihypertensive reagents. The dihydropyridine ring adopts an envelope conformation. The molecular conformation is stabilized by an intramolecular $\text{N}-\text{H}\cdots\text{O}$ hydrogen bond.

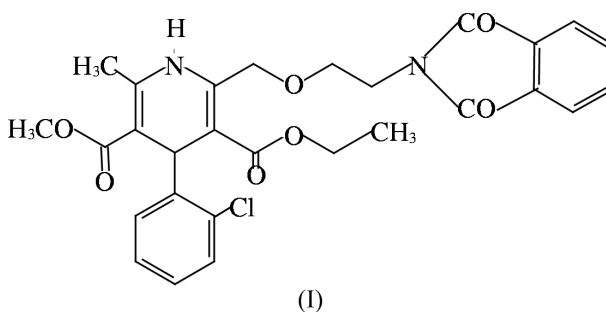
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Comment

The title compound, (I), is a derivative of amlodipine, the latter being anti-anginal and antihypertensive. Amlodipine itself is a calcium channel blocker used for heart medication in the treatment of hypertension (Murdoch & Heel, 1991). In view of the importance of (I), the crystal structure is reported. The dihydropyridine ring exists in an envelope conformation with atoms N1, C2, C3, C5 and C6 in a common plane (r.m.s. deviation = 0.043 Å), whereas atom C4 deviates by 0.372 (2) Å from this plane. The non-H atoms of the ethoxycarbonyl and methoxycarbonyl groups are also almost in the plane of the dihydropyridine ring. The molecular conformation is stabilized by an intramolecular $\text{N}-\text{H}\cdots\text{O}$ hydrogen bond.



The crystal structures of other derivatives of amlodipine have been published by Goldmann *et al.* (1992) and Mereiter & Rollinger (2002).

Experimental

The title compound was obtained as a gift sample from CIPLA Company, Mumbai, India, and was used without further purification. Recrystallization from acetonitrile yielded yellow block-shaped crystals.

Crystal data

$C_{28}H_{27}ClN_2O_7$
 $M_r = 538.97$
 Triclinic, $P\bar{1}$
 $a = 8.0458$ (9) Å
 $b = 10.5193$ (11) Å
 $c = 15.7386$ (17) Å
 $\alpha = 98.073$ (9)°
 $\beta = 90.542$ (9)°
 $\gamma = 103.744$ (8)°
 $V = 1279.8$ (2) Å³

$Z = 2$
 $D_x = 1.399$ Mg m⁻³
 Mo $K\alpha$ radiation
 Cell parameters from 19123 reflections
 $\theta = 3.6$ – 25.7 °
 $\mu = 0.20$ mm⁻¹
 $T = 173$ (2) K
 Block, light yellow
 $0.32 \times 0.28 \times 0.17$ mm

Data collection

Stoe IPDS-II two-circle diffractometer
 ω scans
 Absorption correction: multi-scan (MULABS; Spek, 2003; Blessing, 1995)
 $T_{\min} = 0.919$, $T_{\max} = 0.967$
 23348 measured reflections

4849 independent reflections
 3663 reflections with $I > 2\sigma(I)$
 $R_{\text{int}} = 0.052$
 $\theta_{\text{max}} = 25.8$ °
 $h = -9 \rightarrow 9$
 $k = -12 \rightarrow 12$
 $l = -19 \rightarrow 19$

Refinement

Refinement on F^2
 $R[F^2 > 2\sigma(F^2)] = 0.034$
 $wR(F^2) = 0.088$
 $S = 0.95$
 4849 reflections
 349 parameters

H atoms treated by a mixture of independent and constrained refinement
 $w = 1/[\sigma^2(F_o^2) + (0.0563P)^2]$
 where $P = (F_o^2 + 2F_c^2)/3$
 $(\Delta/\sigma)_{\text{max}} < 0.001$
 $\Delta\rho_{\text{max}} = 0.22$ e Å⁻³
 $\Delta\rho_{\text{min}} = -0.27$ e Å⁻³

Table 1

Hydrogen-bonding geometry (Å, °).

$D-H\cdots A$	$D-H$	$H\cdots A$	$D\cdots A$	$D-H\cdots A$
$N1-H1\cdots O99$	0.87 (2)	2.22 (2)	3.0207 (17)	152.1 (17)

H atoms were located in a difference map. Those bonded to carbon were positioned geometrically and refined with fixed individual displacement parameters [$U_{\text{iso}}(\text{H}) = 1.2U_{\text{eq}}(\text{C})$ or $1.5U_{\text{eq}}(\text{C}_{\text{methyl}})$] using a riding model, with C–H = 1.00, 0.99, 0.98 and 0.95 Å for tertiary CH, secondary CH, methyl CH and aromatic CH groups, respectively. In addition, the methyl groups bonded to the heterocycle and to oxygen were allowed to rotate but not to tip. The H atom bonded to nitrogen was refined isotropically.

Data collection: *X-AREA* (Stoe & Cie, 2001); cell refinement: *X-AREA*; data reduction: *X-AREA*; program(s) used to solve structure: *SHELXS97* (Sheldrick, 1990); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *XP* in *SHELXTL-Plus* (Sheldrick, 1991); software used to prepare material for publication: *SHELXL97* and *PLATON* (Spek, 2003).

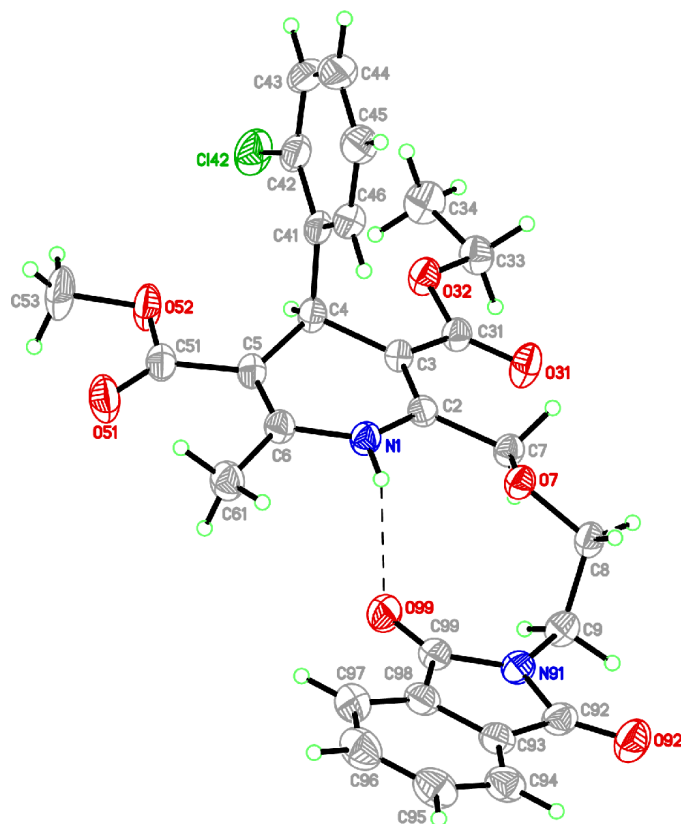


Figure 1

Perspective view of the title compound, with the atom numbering; displacement ellipsoids are drawn at the 50% probability level. The intramolecular hydrogen bond is shown as a dashed line.

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