Acta Crystallographica Section E
**Structure Reports Online**
ISSN 1600-5368

# 3,*t*-6-Dihydroxy-*t*-5-methoxycarbonyl-*c*-6-methyl-*r*-4-phenyl-4,5,6,7-tetrahydro-1*H*-indazole

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**Key indicators**

Single-crystal X-ray study
*T* = 273 K
Mean σ(C–C) = 0.002 Å
*R* factor = 0.042
*wR* factor = 0.113
Data-to-parameter ratio = 12.7

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

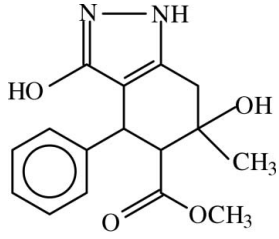


Received 3 January 2006
Accepted 13 January 2006

In the title compound, $C_{16}H_{18}N_2O_4$, the cyclohexene ring adopts a half-chair conformation. In the solid state, intermolecular O—H···N hydrogen bonds link the molecules into dimers. The crystal packing is further stabilized by N—H···O and O—H···O hydrogen bonds and weak C—H···O interactions.

## Comment

1-(2,4-Dichlorobenzyl)-1*H*-indazole-3-carbohydrazide is a potential reversible male contraceptive when administered orally to adult Sprague–Dawley rats (Cheng *et al.*, 2005). Indazole derivatives have been extensively studied as bioactive compounds, exhibiting anti-aggregatory and vasorelaxant activity by NO release, anticancer effects, and antimicrobial and antiparasitic properties (Cerecetto *et al.*, 2005). In view of these important attributes, a crystal structure determination of the title compound, (I), has been undertaken in order to investigate the structure–activity relationships of this class of compounds.




(I)

In (I), the cyclohexene ring adopts a half-chair conformation (Fig. 1), with puckering parameters (Cremer & Pople, 1975) $Q$ = 0.5374 (17) Å, $\theta$ = 129.47 (18)° and $\varphi$= 265.8 (2)°. Atoms C5 and C6 are displaced on opposite sides of the mean plane of atoms C4–C9 of the cyclohexene ring by 0.456 (3) and −0.361 (3) Å, respectively. This plane (C4/C7/C8/C9) makes dihedral angles of 72.85 (6) and 79.26 (9)° with the phenyl ring and methoxycarbonyl group, respectively. The phenyl ring and the methoxycarbonyl group are substituted in the bisectional [C9—C4—C13—C14 = 50.5 (2)°] and β-equatorial orientations [C7—C6—C5—C10 = 163.57 (14)° and C9—C4—C5—C10 = 178.14 (13)°], respectively, relative to the six-membered ring. The methyl and hydroxy groups at C6 are substituted in the α-equatorial [C8—C7—C6—C12 = 167.53 (14)°] and β-axial orientations [C8—C7—C6—O61 = −73.92 (16)°], respectively.

In the crystal structure of (I), atom O31 of the hydroxy group at C3 forms an intermolecular O—H···N hydrogen

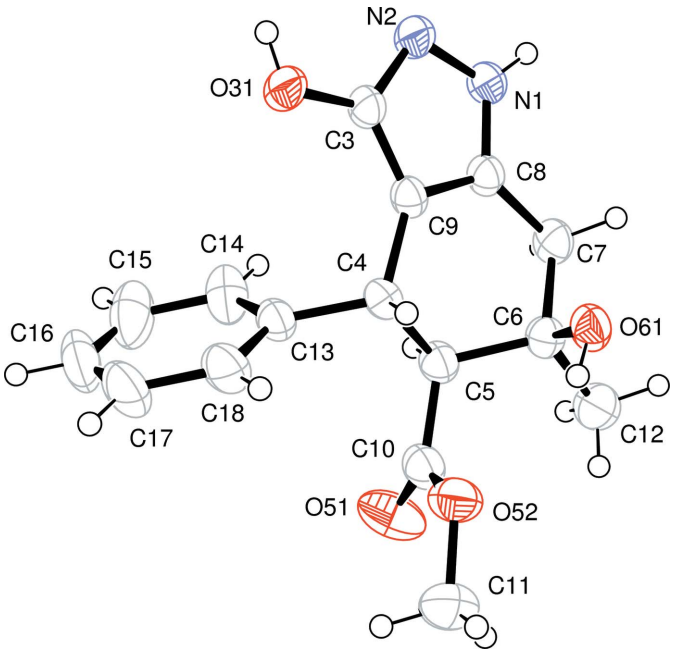



**Figure 1**
A view of (I), showing the atom-labelling scheme and with displacement ellipsoids drawn at the 50% probability level. H atoms are represented by circles of arbitrary radii.

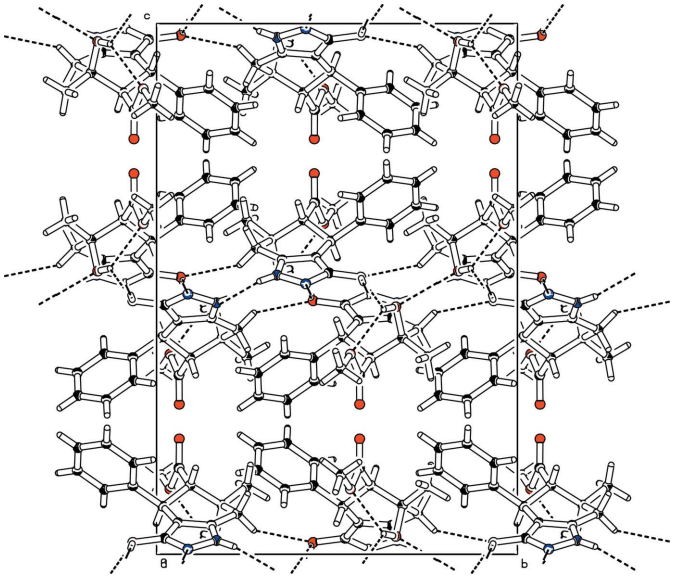


**Figure 2**
The crystal packing of (I), viewed along the *a* axis. Dashed lines indicate O—H···O, O—H···N, N—H···O and C—H···O hydrogen bonds.

bond with atom N2 of an adjacent molecule (Table 1). This interaction links the molecules into a dimer with a graph-set motif of $R_2^2(8)$ (Bernstein *et al.*, 1995). Atom N1 acts as donor for an intermolecular N—H···O interaction (Table 1) with hydroxy atom O61 (*via* atom H1) of a neigbouring molecule, to form a *C*(6) chain motif. Atom O61 acts as donor for a symmetry-related molecule for intermolecular interaction with atom O31 to form a graph-set motif of *C*(8). A weak intermolecular C—H···O interaction (Desiraju, 1997) is also observed (Table 1). Atom C7 acts as a donor for such an interaction with atom O31 of a neigbouring molecule to form a *C*(7) chain motif. These intermolecular hydrogen bonds stabilize the crystal packing (Fig. 2).

## Experimental

A mixture of methyl acetoacetate (100 mmol), benzaldehyde (50 mmol) and methylamine (50 mmol) in ethanol (50 ml) was heated to boiling. The reaction mixture was kept overnight at room temperature. The separated solid was filtered and purified by recrystallization from ethanol. The product was found to be *r*-2,*c*-4-bis(methoxycarbonyl)-*c*-5-hydroxy-*t*-5-methyl-*t*-3-phenylcyclohexanone, (II) (yield 85%, m.p. 444 K). The product, (II) (100 mmol), was dissolved in hot ethanol (25 ml) and, after addition of hydrazine hydrate (150 mmol), the reaction mixture was heated under reflux for 2 h. The hot solution was poured on to ice and the precipitate, (I), was filtered off by suction (yield 70%, m.p. 533 K) and was recrystallized from ethanol.

### *Crystal data*

$C_{16}H_{18}N_2O_4$
$M_r$ = 302.32
Orthorhombic, *Pbca*
*a* = 9.3871 (4) Å
*b* = 14.7295 (6) Å
*c* = 21.6478 (9) Å
*V* = 2993.2 (2) Å$^3$
*Z* = 8
$D_x$ = 1.342 Mg m$^{-3}$
Mo *Kα* radiation
Cell parameters from 9647 reflections
$\theta$ = 2.7–27.7°
$\mu$ = 0.10 mm$^{-1}$
*T* = 273 (2) K
Block, colourless
0.19 × 0.11 × 0.09 mm

### *Data collection*

Bruker SMART APEX CCD area-detector diffractometer
$\omega$ scans
Absorption correction: none
26831 measured reflections
2632 independent reflections
2370 reflections with $I > 2\sigma(I)$
$R_{int}$ = 0.024
$\theta_{max}$ = 25.0°
*h* = −11 → 11
*k* = −17 → 17
*l* = −25 → 25

### *Refinement*

Refinement on $F^2$
$R[F^2 > 2\sigma(F^2)]$ = 0.042
$wR(F^2)$ = 0.113
*S* = 1.05
2632 reflections
207 parameters
H atoms treated by a mixture of independent and constrained refinement
$w = 1/[\sigma^2(F_o^2) + (0.0535P)^2 + 1.343P]$ where $P = (F_o^2 + 2F_c^2)/3$
$(\Delta/\sigma)_{max} < 0.001$
$\Delta\rho_{max}$ = 0.22 e Å$^{-3}$
$\Delta\rho_{min}$ = −0.15 e Å$^{-3}$

**Table 1**
Hydrogen-bond geometry (Å, °).

| *D*—H···*A* | *D*—H | H···*A* | *D*···*A* | *D*—H···*A* |
|---|---|---|---|---|
| N1—H1···O61$^{i}$ | 0.82 (2) | 2.11 (2) | 2.9025 (18) | 164.3 (18) |
| O31—H31···N2$^{ii}$ | 0.82 | 1.85 | 2.6728 (18) | 178 |
| O61—H61···O31$^{iii}$ | 0.82 | 2.23 | 2.8758 (16) | 136 |
| C7—H7*A*···O31$^{iv}$ | 0.97 | 2.57 | 3.3679 (19) | 140 |
| O61—H61···O52 | 0.82 | 2.39 | 3.0065 (16) | 132 |

Symmetry codes: (i) $x+\frac{1}{2}, -y+\frac{1}{2}, -z$; (ii) $-x+1, -y, -z$; (iii) $-x, -y, -z$; (iv) $-x+\frac{1}{2}, y+\frac{1}{2}, z$.

The methyl H atoms were constrained to an ideal geometry, with C—H = 0.96 Å, and with $U_{iso}$(H) = 1.5$U_{eq}$(C), but were allowed to rotate freely about the C—C bond. The hydroxy H atoms were constrained as riding, with O—H = 0.82 Å and $U_{iso}$(H) = 1.5$U_{eq}$(O). Atom H1 was located in a difference Fourier map and its position was

refined freely along with an isotropic displacement parameter. All remaining H atoms were placed in idealized positions, with C—H = 0.93–0.98 Å, and constrained to ride on their parent atoms, with $U_{iso}(H) = 1.2U_{eq}(C)$.

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: *WinGX* (Version 1.64.05; Farrugia, 1999); software used to prepare material for publication: *SHELXL97*.

RH thanks the UGC, India, for the award of an FIP fellowship (2005–2007). RH also gratefully acknowledges the help rendered by K. Murugavel in the synthesis of the compound.

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