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3-Benzotriazol-1-yl 5-*tert*-butyl 2,6-dimethyl-4-(3-nitrophenyl)-1,4-dihydropyridine-3,5-dicarboxylate

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Key indicators

Single-crystal X-ray study
T = 293 K
Mean σ(C–C) = 0.003 Å
R factor = 0.048
wR factor = 0.155
Data-to-parameter ratio = 14.2

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

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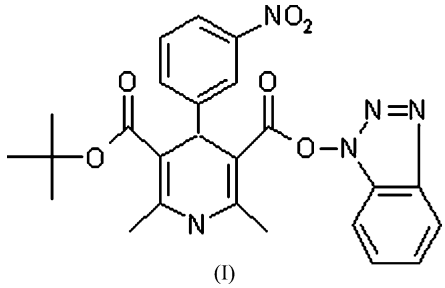
The title compound, $C_{25}H_{25}N_5O_6$, is an important intermediate in the synthesis of nefidipine-type pharmaceuticals. The crystal packing is stabilized by intermolecular N—H···O hydrogen bonds.

Comment

4-Aryl-1,4-dihydropyridine-3,5-dicarboxylic diesters of the nefidipine type have become almost indispensable for the treatment of cardiovascular diseases since they first appeared on the market in 1975 (Yiu & Knaus, 1999; Goldmann & Stoltefuss, 1991). The title compound, (I), is a key intermediate for their preparation.



(I)

Fig. 1 shows the structure of the title compound. The molecule contains an aromatic ring, *R*1 (C13—C18), a dihydropyridine ring, *R*2, and a benzotriazole ring system, *R*3. The dihedral angles for *R*1/*R*2, *R*1/*R*3 and *R*2/*R*3 are 88.3 (2), 43.4 (2) and 92.3 (2)°, respectively. This compares well with

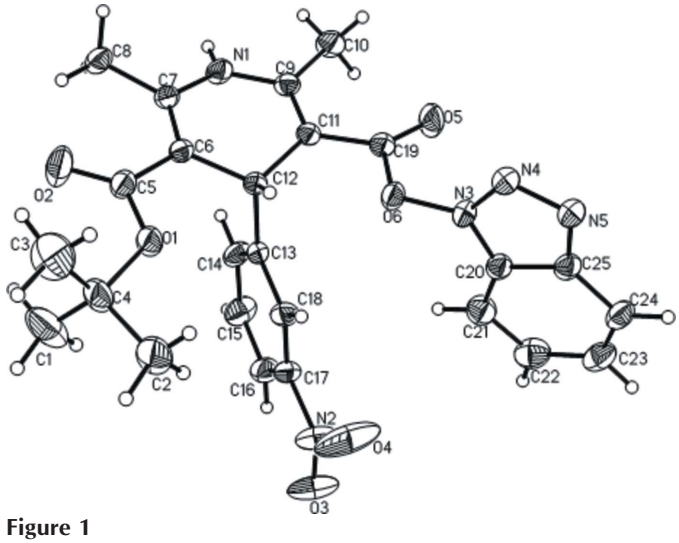


Figure 1
A view of the title compound. Displacement ellipsoids are drawn at the 30% probability level.

the values for nefidipine (Hofmann & Cimiraglia, 1990; Ramusino & Varí, 1999).

An intermolecular N—H···O hydrogen bond links the molecules into infinite chains (Table 1).

Experimental

2,6-Dimethyl-4-(3-nitro-phenyl)-1,4-dihydropyridine-3,5-dicarboxylic acid mono-*tert*-butyl ester (491 mg, 1 mmol) was dissolved in CH_2Cl_2 (30 ml); dicyclohexylcarbodiimide (206 mg, 1 mmol) and benzotriazol-1-ol (135 mg, 1 mmol) in CH_2Cl_2 (10 ml) were added to the solution at 278 K. The reaction mixture was stirred at 276–279 K for a further 10 h. The solvent CH_2Cl_2 was removed by vacuum evaporation at 293 K. The product was purified by chromatography on a silica gel column (eluted by ethyl acetate and petroleum ether, 1:5) at room temperature with a yield of 92% (450 mg). Suitable crystals were obtained by slow evaporation of a solution in methanol.

Crystal data

$C_{25}H_{25}N_5O_6$
M_r = 491.50
Monoclinic, $P2_1/n$
a = 10.332 (2) Å
b = 15.163 (3) Å
c = 16.010 (3) Å
β = 90.96 (3)°
V = 2507.6 (9) Å^3
Z = 4
D_x = 1.302 Mg m^{-3}
Mo $K\alpha$ radiation
Cell parameters from 19215 reflections
θ = 3.3–25.5°
μ = 0.10 mm^{-1}
T = 293 (2) K
Rod, yellow
0.38 × 0.25 × 0.11 mm

Data collection

Rigaku R-AXIS RAPID IP area-detector diffractometer
oscillation scans
Absorption correction: multi-scan (*ABSCOR*; Higashi, 1995)
T_{min} = 0.965, T_{max} = 0.989
23558 measured reflections
4620 independent reflections
3165 reflections with $I > 2\sigma(I)$
R_{int} = 0.050
θ_{max} = 25.5°
$h = -12 \rightarrow 12$
$k = -18 \rightarrow 18$
$l = -19 \rightarrow 19$

Refinement

Refinement on F^2
$R[F^2 > 2\sigma(F^2)]$ = 0.048
$wR(F^2)$ = 0.155
S = 1.01
4620 reflections
325 parameters
H-atom parameters constrained
$w = 1/[\sigma^2(F_o^2) + (0.1P)^2]$ where $P = (F_o^2 + 2F_c^2)/3$
$(\Delta/\sigma)_{max} < 0.001$
$\Delta\rho_{max}$ = 0.34 e Å^{-3}
$\Delta\rho_{min}$ = −0.23 e Å^{-3}

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

D—H···A	D—H	H···A	D···A	D—H···A
N1—H1D···O4^{i}	0.86	2.49	3.265 (3)	151

Symmetry code: (i) $x-1, y, z$.

H atoms were placed in calculated positions and constrained to ride on their parent atoms, with C—H = 0.93–0.98 Å, N—H = 0.86 Å and U_{iso}(H) = 1.2U_{eq}(C,N) and 1.5U_{eq}(methyl C).

Data collection: *RAPID-AUTO* (Rigaku, 2004); cell refinement: *RAPID-AUTO*; data reduction: *RAPID-AUTO*; 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*.

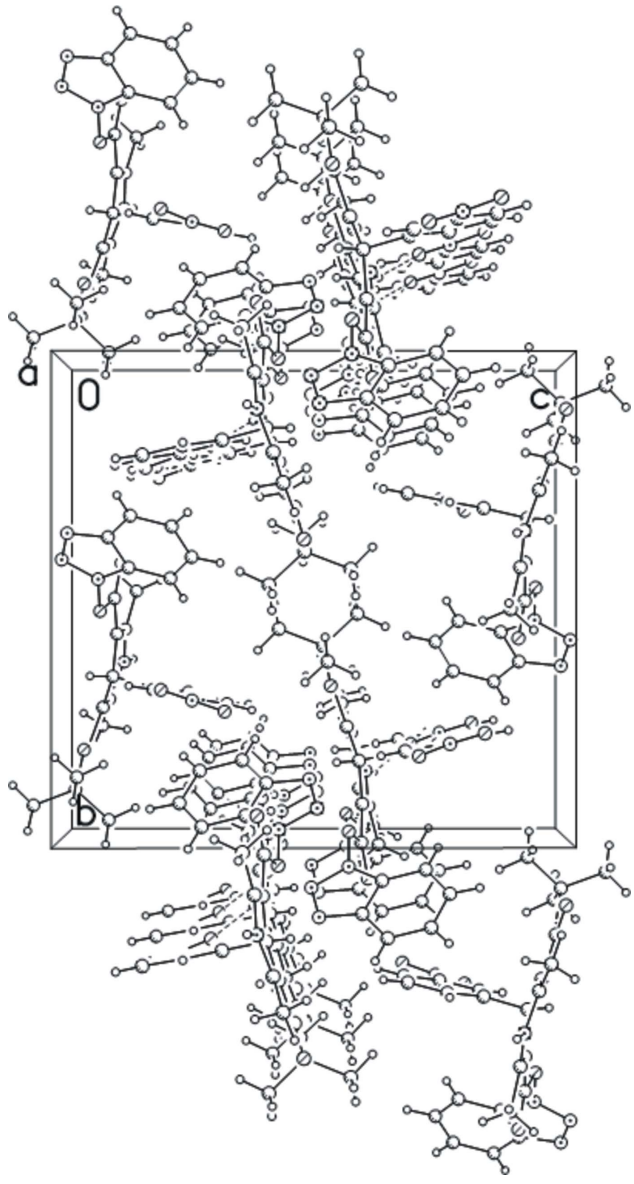


Figure 2
The packing of (I).

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References

Bruker (1997). *SHELXTL*. Bruker AXS Inc., Madison, Wisconsin, USA.
Goldmann, S. & Stoltefuss, J. (1991). *Angew. Chem. Int. Ed. Engl.* **30**, 1559–1578.
Higashi, T. (1995). *ABSCOR*. Rigaku Corporation, Tokyo, Japan.
Hofmann, H. J. & Cimiraglia, R. (1990). *J. Mol. Struct.* (*THEOCHEM*), **205**, 1–11.
Ramusino, M. C. & Varí, M. R. (1999). *J. Mol. Struct.* (*THEOCHEM*), **492**, 257–268.
Rigaku (2004). *RAPID-AUTO*. Rigaku/MSC Inc., 9009 New Trails Drive, The Woodlands, TX 77381, USA.
Sheldrick, G. M. (1997). *SHELXS97* and *SHELXL97*. University of Göttingen, Germany.
Yiu, S. H. & Knaus, E. E. (1999). *Drug Dev. Res.* **48**, 26–37.