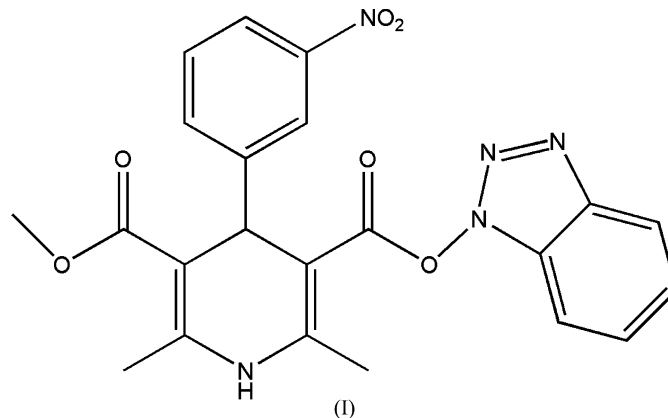


3-Benzotriazol-1-yl 5-methyl 2,6-dimethyl-4-(3-nitrophenyl)-1,4-dihydropyridine-3,5-dicarboxylateLi-Qin Jiang^{a*} and Feng-Xia Sun^b^aCollege of Pharmaceuticals & Biotechnology, Tianjin University, Tianjin 300072, People's Republic of China, and ^bCollege of Chemical and Pharmaceutical Engineering, Hebei University of Science and Technology, Shijiazhuang 050018, People's Republic of ChinaCorrespondence e-mail:
sunfengxia_1999@sohu.com**Key indicators**Single-crystal X-ray study
 $T = 294$ K
Mean $\sigma(\text{C}-\text{C}) = 0.004$ Å
Disorder in main residue
 R factor = 0.052
 wR factor = 0.146
Data-to-parameter ratio = 13.4For details of how these key indicators were automatically derived from the article, see <http://journals.iucr.org/e>.

The title compound, $\text{C}_{22}\text{H}_{19}\text{N}_5\text{O}_6$, is an important intermediate in the synthesis of nefidipine-type pharmaceuticals. The dihydropyridine ring has a flattened boat conformation. Molecules are linked by $\text{N}-\text{H}\cdots\text{N}$ hydrogen bonds.

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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 is a key intermediate for their preparation. Fig. 1 shows its molecular structure. The dihydropyridine ring has a flattened boat conformation. This compares well with the structure of 3-benzotriazol-1-yl-5-*tert*-butyl-2,6-dimethyl-4-(3-nitrophenyl)-1,4-dihydropyridine-3,5-dicarboxylate and nefidipine (Liu *et al.*, 2006; Hofmann & Cimiraglia, 1990; Ramusino & Vari, 1999). The nitro group is found to be disordered.



Intermolecular hydrogen bonds link the molecules in a chain (Table 1 and Fig. 2); the acceptor is a triazole N atom.

Experimental

2,6-Dimethyl-4-(*m*-nitrophenyl)-1,4-dihydropyridine-3,5-dicarboxylic acid monomethyl ester (332 mg, 1 mmol) was dissolved in 25 ml CH_2Cl_2 , and a solution of dicyclohexylcarbodiimide (206 mg, 1 mmol) and benzotriazol-1-ol (135 mg, 1 mmol) in 10 ml CH_2Cl_2 was added dropwise at 278 K. The reaction mixture was stirred at 276–279 K for 8 h. The solvent was removed by vacuum evaporation at 293 K. The product was purified by chromatography on a silica gel column (eluted with ethyl acetate and petroleum ether, 1:5) at room temperature (yield 450 mg). Crystals were obtained by slow evaporation of the solution.

Crystal data

C₂₂H₁₉N₅O₆
M_r = 449.42
 Monoclinic, *P*₂₁/*c*
a = 8.113 (3) Å
b = 17.934 (5) Å
c = 14.723 (4) Å
 β = 98.008 (6)°
V = 2121.2 (11) Å³
Z = 4

D_x = 1.407 Mg m⁻³
 Mo Kα radiation
 Cell parameters from 2365 reflections
 θ = 2.5–22.6°
 μ = 0.11 mm⁻¹
T = 294 (2) K
 Block, colourless
 0.26 × 0.22 × 0.20 mm

Data collection

Bruker SMART CCD area detector diffractometer
 φ and ω scans
 Absorption correction: multi-scan (SADABS; Sheldrick, 1996)
T_{min} = 0.973, *T_{max}* = 0.979
 11847 measured reflections

4343 independent reflections
 2397 reflections with *I* > 2σ(*I*)
R_{int} = 0.046
 θ_{max} = 26.5°
h = -9 → 10
k = -20 → 22
l = -14 → 18

Refinement

Refinement on *F*²
R [*F*² > 2σ(*F*²)] = 0.052
wR (*F*²) = 0.146
S = 1.00
 4343 reflections
 324 parameters
 H atoms treated by a mixture of independent and constrained refinement

$w = 1/[\sigma^2(F_o^2) + (0.063P)^2 + 0.4855P]$
 where $P = (F_o^2 + 2F_c^2)/3$
 (Δσ)_{max} < 0.001
 Δρ_{max} = 0.46 e Å⁻³
 Δρ_{min} = -0.33 e Å⁻³

Table 1

Hydrogen-bond geometry (Å, °).

<i>D</i> —H... <i>A</i>	<i>D</i> —H	H... <i>A</i>	<i>D</i> ... <i>A</i>	<i>D</i> —H... <i>A</i>
N4—H4A...N1 ⁱ	0.83 (2)	2.28 (3)	3.079 (3)	163 (2)

Symmetry code: (i) -*x* + 1, *y* + ½, -*z* + ½.

The H atom bonded to N4 was located in a difference map and refined freely. All other H atoms were positioned geometrically and refined using a riding model, with C—H = 0.97 Å and *U*_{iso}(H) = 1.2*U*_{eq}(C). The nitro group is disordered; each O atom was refined on two alternative sites with equal occupancy, and restraints were applied for geometrical similarity, planarity, and approximately isotropic displacement parameters.

Data collection: SMART (Bruker, 1997); cell refinement: SAINT (Bruker, 1997); 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, 1997); software used to prepare material for publication: SHELXTL.

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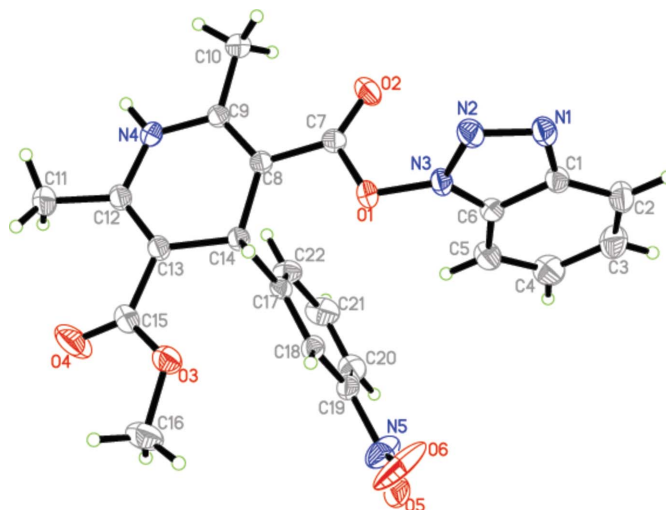


Figure 1

Molecular structure of the title compound. Displacement ellipsoids are drawn at the 30% probability level and H atoms are shown as small spheres of arbitrary radii.

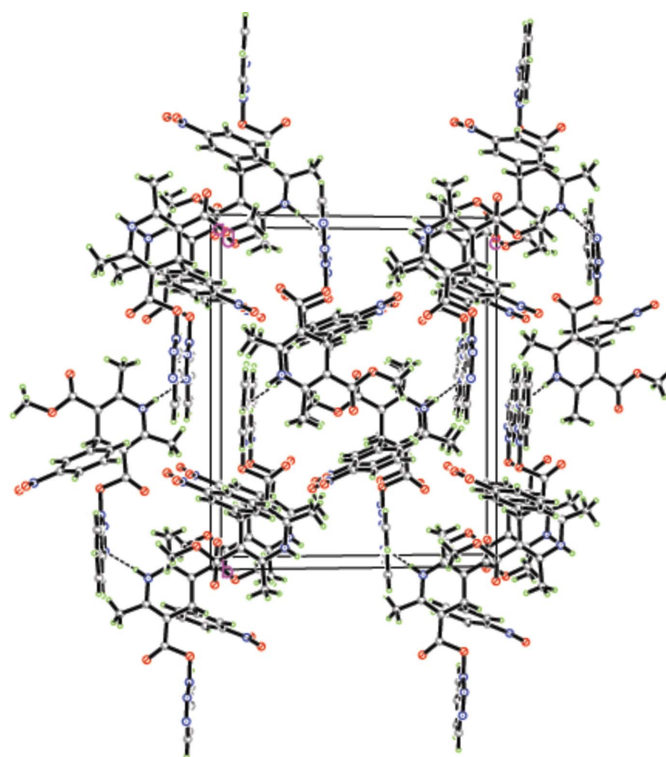


Figure 2

A packing diagram of (I). Dashed lines indicate hydrogen bonds.

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