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## Structure Reports

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## Peter G. Jones ${ }^{\text {a }}$ and Piotr Kuśb ${ }^{\text {b }}$

${ }^{\mathrm{a}}$ Institut für Anorganische und Analytische Chemie, Technische Universität Braunschweig, Postfach 3329, 38023 Braunschweig, Germany, and ${ }^{\text {b }}$ Department of Chemistry, Silesian University, 9 Szkolna Street, 40-006 Katowice, Poland

Correspondence e-mail: p.jones@tu-bs.de

## Key indicators

Single-crystal X-ray study
$T=133 \mathrm{~K}$
Mean $\sigma(\mathrm{C}-\mathrm{C})=0.003 \AA$
$R$ factor $=0.065$
$w R$ factor $=0.170$
Data-to-parameter ratio $=21.7$
For details of how these key indicators were automatically derived from the article, see http://journals.iucr.org/e.
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## $N$-Cyclohexyl-4-(methoxycarbonyl)benzamide

The title compound, methyl 4-(cyclohexylaminocarbonyl)benzoate, $\mathrm{C}_{15} \mathrm{H}_{19} \mathrm{NO}_{3}$, crystallizes with two independent molecules in the asymmetric unit, which differ in their ring orientations. The molecules are connected by $\mathrm{N}-\mathrm{H} \cdots \mathrm{O}=\mathrm{C}$ hydrogen bonds to form chains parallel to the $a$ axis.

## Comment

Terephthaldiamide derivatives can be synthesized from various amines and dimethyl terephthalate (Horner \& Weissbach, 1972; Jones et al., 2002). We have previously reported several terephthaldiamide structures (Jones et al., 2002); we report here the structure of $N$-cyclohexyl-4(methoxycarbonyl)benzamide, (I), a compound that was first described by Anzeil et al. (1999).

(I)

Compound (I) crystallizes with two independent molecules in the asymmetric unit (Fig. 1). These differ in the relative ring


Figure 1
The two independent molecules of the title compound in the asymmetric unit. Displacement ellipsoids are drawn at the $50 \%$ probability level. The H -atom radii are arbitrary.

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Figure 2
Packing diagram of the title compound, viewed perpendicular to the $a b$ plane in the region $z \simeq \frac{1}{4}$. Hydrogen bonds are indicated by dashed lines. H atoms not involved in hydrogen bonding have been omitted. The independent molecules alternate in the chain, beginning at the left with molecule 1 (unprimed molecule in Fig. 1). A second chain (not shown) at $z \simeq \frac{3}{4}$ is generated by inversion.
orientations about the bonds $\mathrm{C} 1-\mathrm{C} 7$ and $\mathrm{N}-\mathrm{C} 8$ (see torsion angles in Table 1). Bond lengths and angles may be considered normal.

The molecules are connected by two classical hydrogen bonds (Table 2) between the two sets of $\mathrm{N}-\mathrm{H}$ and $\mathrm{O}=\mathrm{C}$ groups to form chains parallel to the $a$ axis. The two independent molecules alternate in these chains, which are generated solely by translation. The inversion operator generates a second such chain in the unit cell.

## Experimental

Compound (I) was prepared according to our literature method (Jones et al., 2002). The resulting white solid was washed several times with methanol and was collected in $30 \%$ yield. [m.p. $336-337 \mathrm{~K}$; literature m.p. (Anzeil et al., 1999) 335-337 K]. Analysis calculated for $\mathrm{C}_{15} \mathrm{H}_{19} \mathrm{NO}_{3}$ : C $68.94, \mathrm{H} 7.32$, N $5.36 \%$; found: $\mathrm{C} 68.56, \mathrm{H} 7.12$, N $4.93 \% .{ }^{1} \mathrm{H}$ NMR $\left(\mathrm{CDCl}_{3}, 500 \mathrm{MHz}\right): \delta 8.04(d, 2 \mathrm{H}, J=8.3 \mathrm{~Hz}), 7.76$ $(d, 2 \mathrm{H}, J=8.3 \mathrm{~Hz}), 5.95(b s, 1 \mathrm{H}, \mathrm{NH}), 3.95(m, 1 \mathrm{H}), 3.93(s, 3 \mathrm{H}$, -OCH3), 2.02 ( $m, 2 \mathrm{H}$ ), 1.60-1.80 ( $m, 3 \mathrm{H}$ ), $1.40(m, 2 \mathrm{H}), 1.20-1.35$ $(m, 3 \mathrm{H})$. Probably the low solubility of monoamide (I) in the reaction mixture leads to the mono-cyclohexyl derivative. The single crystal was obtained by slow evaporation in air of a solution in a water/ acetonitrile mixture.
$\mathrm{C}_{15} \mathrm{H}_{19} \mathrm{NO}_{3}$
$M_{r}=261.31$
Triclinic, $P \overline{1}$
$a=10.107(2) \AA$
$b=11.957(2) \AA$
$c=12.836(2) \AA$
$\alpha=64.832(5)^{\circ}$
$\beta=78.988(5)^{\circ}$
$\gamma=72.857(5)^{\circ}$
Crystal data $^{\circ}$

Tablet, colourless
Data collection
Bruker SMART 1000 CCD diffractometer
$\omega$ scans
Absorption correction: none
15334 measured reflections
7675 independent reflections

## Refinement

Refinement on $F^{2}$
$R\left[F^{2}>2 \sigma\left(F^{2}\right)\right]=0.065$
$w R\left(F^{2}\right)=0.170$
$S=1.04$
7675 reflections
353 parameters
H atoms treated by a mixture of independent and constrained refinement
$0.4 \times 0.2 \times 0.1 \mathrm{~mm}$

5496 reflections with $I>2 \sigma(I)$
$R_{\text {int }}=0.058$
$\theta_{\text {max }}=30.0^{\circ}$
$h=-14 \rightarrow 14$
$k=-16 \rightarrow 16$
$l=-17 \rightarrow 18$

$$
\begin{aligned}
& w=1 /[ \sigma^{2}\left(F_{o}{ }^{2}\right)+(0.0834 P)^{2} \\
&+0.2716 P] \\
& \text { where } P=\left(F_{o}{ }^{2}+2 F_{c}^{2}\right) / 3 \\
&(\Delta / \sigma)_{\max }<0.001 \\
& \Delta \rho_{\max }=0.44 \mathrm{e}^{-3} \AA^{-3} \\
& \Delta \rho_{\min }=-0.30 \mathrm{e}^{-3}
\end{aligned}
$$

Table 1
Selected torsion angles ( ${ }^{\circ}$ ).

| $\mathrm{C} 6-\mathrm{C} 1-\mathrm{C} 7-\mathrm{N}$ | $-17.9(2)$ | $\mathrm{C}^{\prime}-\mathrm{C1}^{\prime}-\mathrm{C}^{\prime}-\mathrm{N}^{\prime}$ | $-45.2(2)$ |
| :--- | :---: | :---: | :---: |
| $\mathrm{C} 9-\mathrm{C} 8-\mathrm{N}-\mathrm{C} 7$ | $93.99(18)$ | $\mathrm{C} 9^{\prime}-\mathrm{C}^{\prime}-\mathrm{N}^{\prime}-\mathrm{C} 7^{\prime}$ | $131.68(16)$ |

Table 2
Hydrogen-bonding geometry ( $\mathrm{A}^{\circ}$ ) .

| $D-\mathrm{H} \cdots A$ | $D-\mathrm{H}$ | $\mathrm{H} \cdots A$ | $D \cdots A$ | $D-\mathrm{H} \cdots A$ |
| :--- | :--- | :--- | :--- | :--- |
| $\mathrm{~N}-\mathrm{H} 01 \cdots \mathrm{O}^{1^{\text {i }}}$ | $0.85(2)$ | $2.06(2)$ | $2.8908(19)$ | $162.8(19)$ |
| N '-H01 $\cdots \mathrm{O} 1$ | $0.84(2)$ | $2.10(2)$ | $2.9158(19)$ | $164.1(19)$ |

Symmetry code: (i) $1+x, y, z$.
The amide H atom was refined freely. Methyl H atoms were refined using a rigid methyl group $\left(\mathrm{C}-\mathrm{H}=0.98 \AA \AA^{\circ}\right.$ and $\mathrm{H}-\mathrm{C}-\mathrm{H}=$ $109.5^{\circ}$ ). Other H atoms were included using a riding model with fixed $\mathrm{C}-\mathrm{H}$ bond lengths ( A ) of 0.95 (aromatic), $0.99\left(s p^{3} \mathrm{CH}\right)$ or 1.00 $\left(\mathrm{CH}_{2}\right) \cdot U_{\text {iso }}(\mathrm{H})$ values were fixed at $1.2 U_{\text {eq }}$ of the parent atom.

Data collection: SMART (Bruker, 1998); cell refinement: SAINT (Bruker, 1998); data reduction: SAINT; program(s) used to solve structure: SHELXS97 (Sheldrick, 1990); program(s) used to refine structure: SHELXL97 (Sheldrick, 1997); molecular graphics: XP (Siemens, 1994); software used to prepare material for publication: SHELXL97.

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