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Kev indicators

Single-crystal X-ray study T = 173 KMean $\sigma(\text{C-C}) = 0.002 \text{ Å}$ R factor = 0.032 wR factor = 0.077Data-to-parameter ratio = 14.1

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4'-Methylbiphenyl-2-carboxylic acid

The title compound, $C_{14}H_{12}O_2$, is used as an intermediate for the synthesis of various biologically active and pharmaceutical compounds. Bond lengths and angles adopt usual values. The dihedral angles between the two aromatic rings [53.39 (3)°] and between the carboxyl group and adjacent ring [42.37 (10)°] lie in the expected ranges. The crystal structure is characterized by centrosymmetric hydrogen-bonded dimers.

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Comment

The title compound, (I), is used as an intermediate for the synthesis of various biologically active and pharmaceutical compounds (Gillis & Markham, 1997; Markham & Goa, 1997). In view of its importance and in order to determine the conformation of this molecule, a crystal structure determination has been carried out.

A perspective view of (I) is shown in Fig. 1. Bond lengths and angles (Table 1) can be regarded as normal [Cambridge Structural Database (CSD), Version 1.7; *MOGUL* Version 1.0.1; Allen, 2002]. The dihedral angle between the two

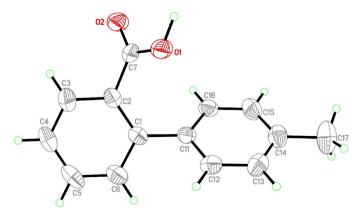


Figure 1
Perspective view of the title compound, with the atom numbering; displacement ellipsoids are drawn at the 50% probability level.

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aromatic rings is 53.39 (3)°. The carboxyl group subtends an angle of 42.37 (10)° with the ring to which it is attached. In seven comparable structures retrieved from the CSD containing the biphenyl-2-carboxylic acid moiety, the dihedral angles between the aromatic rings are in the range 44.9–62.9°, whereas the dihedral angles between the carboxyl group and the adjacent aromatic plane shows a significantly wider range of 32.5–85.9°. The molecules form hydrogen-bonded centrosymmetric dimers in the crystal structure (Table 2).

Experimental

4'-Methylbiphenyl-2-carbonitrile (1.93 g, 10 mmol) was refluxed with methanol (10 ml) and 30% NaOH solution (10 ml) for 3 h to yield the title compound, which was recrystallized from dichloromethane (m.p. 419 K).

Crystal data

$C_{14}H_{12}O_2$	$D_{\rm v} = 1.199 \; {\rm Mg \; m^{-3}}$
$M_r = 212.24$	Mo $K\alpha$ radiation
Monoclinic, $P2_1/c$	Cell parameters from 8476
a = 7.5953 (15) Å	reflections
b = 14.582 (3) Å	$\theta = 3.6 - 25.5^{\circ}$
c = 10.616 (2) Å	$\mu = 0.08 \text{ mm}^{-1}$
$\beta = 90.610 (16)^{\circ}$ $V = 1175.7 (4) \text{ Å}^3$	T = 173 (2) K
$V = 1175.7 (4) \text{ Å}^3$	Block, colourless
Z = 4	$0.30 \times 0.21 \times 0.11 \text{ mm}$

Data collection

Stoe IPDS-II two-circle	$R_{\rm int} = 0.064$
diffractometer	$\theta_{\rm max} = 25.0^{\circ}$
ω scans	$h = -9 \rightarrow 9$
5269 measured reflections	$k = -17 \rightarrow 17$
2073 independent reflections	$l = -10 \rightarrow 12$
1528 reflections with $I > 2\sigma(I)$	

Refinement

Refinement on F^2	H-atom parameters constrained
$R[F^2 > 2\sigma(F^2)] = 0.032$	$w = 1/[\sigma^{2}(F_{o}^{2}) + (0.02P)^{2}]$
$wR(F^2) = 0.077$	where $P = (F_o^2 + 2F_c^2)/3$
S = 0.88	$(\Delta/\sigma)_{\rm max} < 0.001$
2073 reflections	$\Delta \rho_{\text{max}} = 0.13 \text{ e Å}^{-3}$
147 parameters	$\Delta \rho_{\min} = -0.11 \text{ e Å}^{-3}$

Table 1 Selected geometric parameters (Å, °).

C1-C11	1.5011 (18)	C7-O2	1.2287 (15)
C2-C7	1.4920 (17)	C7-O1	1.3225 (14)
O2-C7-O1 O2-C7-C2	122.50 (10) 121.65 (10)	O1-C7-C2	115.78 (11)

Table 2 Hydrogen-bonding geometry (Å, °).

$D-\mathbf{H}\cdot\cdot\cdot A$	D-H	$H \cdot \cdot \cdot A$	$D \cdot \cdot \cdot A$	$D-\mathbf{H}\cdot\cdot\cdot A$
O1-H1···O2 ⁱ	0.84	1.83	2.6604 (13)	170

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

All H atoms were located in a difference map, but were then positioned geometrically and refined with fixed individual displacement parameters (set at 1.2 times $U_{\rm eq}$ of the parent atom, but $1.5U_{\rm eq}$ for hydroxyl and methyl groups) using a riding model, with O-H=0.84 Å and C-H=0.95 and 0.98 Å for aromatic and methyl H atoms, respectively. In addition, the torsion angles of the hydroxyl group and the methyl group were refined.

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: *PLATON* (Spek, 2003); software used to prepare material for publication: *SHELXL97* and *PLATON*.

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