

3-Fluoro-4-methylbenzoic acid

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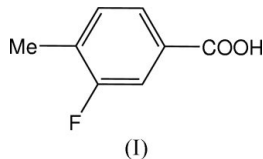
Key indicators

Single-crystal X-ray study
 $T = 120$ K
Mean $\sigma(\text{C}-\text{C}) = 0.002$ Å
 R factor = 0.054
 wR factor = 0.157
Data-to-parameter ratio = 15.9For details of how these key indicators were
automatically derived from the article, see
<http://journals.iucr.org/e>.

The title compound, $\text{C}_8\text{H}_7\text{FO}_2$, shows a nearly planar molecular structure, with a dihedral angle between the benzene ring and the carboxyl group of $6.2(1)^\circ$. Pairs of molecules are linked *via* $\text{O}-\text{H}\cdots\text{O}$ hydrogen bonding into dimers, which are located around centres of inversion.

Comment

The molecule of the title compound, (I), has been determined to provide a reference point for the study of $^{19}\text{F}-^{13}\text{C}-^1\text{H}$ coupling in NMR spectra of solids and liquid crystals (Antonoli, 2004). The molecule is nearly planar (Fig. 1 and Table 1). The dihedral angle between the benzene ring and the carboxyl group of $6.2(1)^\circ$ is somewhat larger than that in the parent 4-methylbenzoic (*p*-toluic) acid, (II), of 2.9° (Takwale & Pant, 1971). In the crystal structure of (I), pairs of molecules are linked into dimers by $\text{O}-\text{H}\cdots\text{O}$ hydrogen bonding, with an $\text{O}\cdots\text{H}$ distance of $1.70(4)$ Å and an $\text{O}\cdots\text{O}$ distance of $2.612(2)$ Å. The $\text{O}-\text{H}\cdots\text{O}$ angle of $176(3)^\circ$ indicates strong hydrogen bonding and the dimers are located around centres of inversion. Dimers are also found in (II) but the crystal packing is completely different from that in (I). In contrast to the structure determination of (II), in the present determination the carboxy H atom was located in a difference map.



Experimental

Compound (I) was commercially available from Acros Organics (Loughborough, England). It was recrystallized from an aqueous solution.

Crystal data

$\text{C}_8\text{H}_7\text{FO}_2$	$D_x = 1.469$ Mg m $^{-3}$
$M_r = 154.14$	Mo $K\alpha$ radiation
Monoclinic, $P2_1/c$	Cell parameters from 979
$a = 3.8132(5)$ Å	reflections
$b = 6.0226(8)$ Å	$\theta = 10.3\text{--}26.0^\circ$
$c = 30.378(4)$ Å	$\mu = 0.12$ mm $^{-1}$
$\beta = 92.50(2)^\circ$	$T = 120(2)$ K
$V = 696.98(16)$ Å 3	Prism, colourless
$Z = 4$	$0.55 \times 0.19 \times 0.16$ mm

Data collection

SMART 6000 CCD area-detector diffractometer	1773 reflections with $I > 2\sigma(I)$
ω scans	$R_{\text{int}} = 0.067$
Absorption correction: none	$\theta_{\text{max}} = 30.0^\circ$
9290 measured reflections	$h = -5 \rightarrow 5$
2036 independent reflections	$k = -8 \rightarrow 8$
	$l = -42 \rightarrow 42$

Refinement

Refinement on F^2
 $R[F^2 > 2\sigma(F^2)] = 0.054$
 $wR(F^2) = 0.157$
 $S = 1.12$
 2036 reflections
 128 parameters
 All H-atom parameters refined

$$w = 1/[\sigma^2(F_o^2) + (0.0713P)^2 + 0.4137P]$$

where $P = (F_o^2 + 2F_c^2)/3$
 $(\Delta/\sigma)_{\max} < 0.001$
 $\Delta\rho_{\max} = 0.49 \text{ e } \text{\AA}^{-3}$
 $\Delta\rho_{\min} = -0.25 \text{ e } \text{\AA}^{-3}$

Table 1

Selected geometric parameters (\AA , $^\circ$).

F—C3	1.3595 (17)	C2—C3	1.379 (2)
O1—C7	1.3076 (18)	C3—C4	1.389 (2)
O2—C7	1.2354 (18)	C4—C5	1.396 (2)
C1—C6	1.389 (2)	C4—C8	1.505 (2)
C1—C2	1.395 (2)	C5—C6	1.393 (2)
C1—C7	1.481 (2)		
C6—C1—C2	120.18 (13)	C3—C4—C5	116.56 (14)
C3—C2—C1	117.86 (14)	C3—C4—C8	121.47 (14)
F—C3—C2	117.88 (14)	C5—C4—C8	121.97 (15)
F—C3—C4	117.96 (13)	C6—C5—C4	121.15 (14)
C2—C3—C4	124.15 (14)	C1—C6—C5	120.10 (14)

Table 2

Hydrogen-bonding geometry (\AA , $^\circ$).

$D-H\cdots A$	$D-H$	$H\cdots A$	$D\cdots A$	$D-H\cdots A$
O1—H01 \cdots O2 ⁱ	0.92 (4)	1.70 (4)	2.6117 (17)	176 (3)

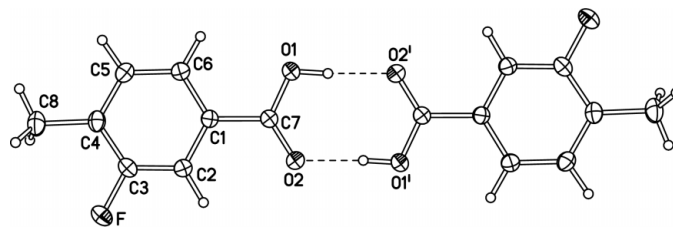
Symmetry code: (i) $-x, 2-y, 1-z$.

Figure 1

The crystal structure of the title compound, showing a hydrogen-bonded dimer with labelling and displacement ellipsoids drawn at the 50% probability level. Hydrogen bonding is indicated by dashed lines. [Symmetry code: (i) $-x, 2-y, 1-z$.]

All H atoms were located in a difference map and were refined freely.

Data collection: *SMART* (Bruker, 2001); cell refinement: *SMART*; data reduction: *SAINT* (Bruker, 2001); program(s) used to solve structure: *SHELXS97* (Sheldrick, 1997); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *SHELXTL* (Bruker, 2001); software used to prepare material for publication: *SHELXTL*.

References

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 Bruker (2001). *SMART* (Version 5.625), *SAINT* (Version 6.02A) and *SHELXTL* (Version 6.12). Bruker AXS Inc., Madison, Wisconsin, USA.
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