2,4-Dimethoxybenzoic acid and 2,5-dimethoxybenzoic acid

Dewey H. Barich,[a] Mark T. Zell,[b] Douglas R. Powell[c] and Eric J. Munson[a]*

[a]Department of Pharmaceutical Chemistry, University of Kansas, 2095 Constant Ave., Lawrence, KS 66047, USA, [b]Pfizer Global Research and Development, Ann Arbor Laboratories, 2800 Plymouth Road, Ann Arbor, Michigan 48105, USA, and [c]University of Kansas, Rm 2010 Malott Hall, 1251 Wescoe Hall Drive, Lawrence, KS 66045, USA

Correspondence e-mail: munson@ku.edu

The title compounds (both $C_9H_{10}O_4$) have nearly planar structures, and the methyl and/or carboxylic acid groups lie out of the molecular plane, as dictated by steric interactions. 2,5-Dimethoxybenzoic acid (2,5-DMBA) forms an unusual intramolecular hydrogen bond between the carboxylic acid group and the O atom of the methoxy group in the 2-position [O···O = 2.547 (2) Å and O—H···O = 154 (3)°]. 2,4-DMBA forms a typical hydrogen-bond dimer with a neighboring molecule.

Comment

The crystal structures of only four of the six isomers of dimethoxybenzoic acid (DMBA) have been determined previously. These four isomers exhibit considerable conformational differences. For example, the plane defined by the carboxylic acid group lies nearly parallel to the aromatic ring plane in 3,4-DMBA (3.4°; Pinkus et al., 2002) and 3,5-DMBA (1.4°; Lynch et al., 1994), but is 36.5 and 56.2° out of the plane in 2,3-DMBA (Swaminathan et al., 1977; Bryan & White, 1982a) and 2,6-DMBA (Swaminathan et al., 1976; Bryan & White, 1982b), respectively. For the title compounds, viz. 2,4-DMBA, (I), and 2,5-DMBA, (II), this angle is 6.3 (2) and 2.3 (3)°, respectively.
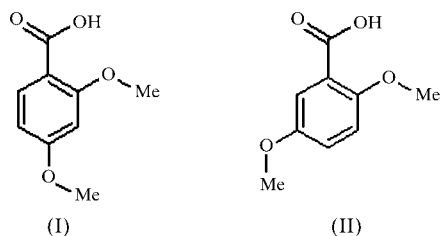
The 2,4-DMBA isomer (Fig. 1) exhibits a relatively common intermolecular pair of hydrogen bonds between the carboxylic
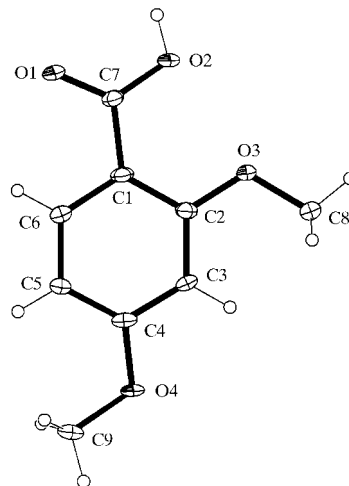

Figure 1
A molecular structure diagram of 2,4-DMBA, showing 50% probability displacement ellipsoids and the atom-numbering scheme.

acid O atoms of two molecules (Table 1). This hydrogen-bonding arrangement is also found in 2,3-DMBA (Swaminathan et al., 1977; Bryan & White, 1982a), 3,4-DMBA (Pinkus et al., 2002) and 3,5-DMBA (Lynch et al., 1994), as well as in 2-methoxybenzoic acid (Parvez, 1987) and 4-methoxybenzoic acid (Etter et al., 1988), the two monomethoxybenzoic acids with determined crystal structures.
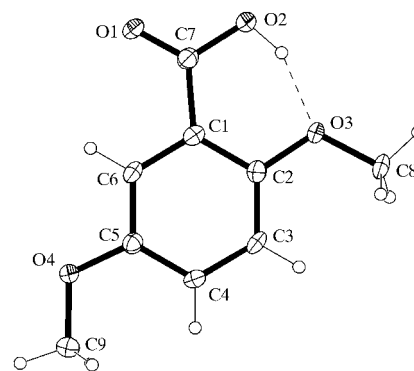

Figure 2
A molecular structure diagram of 2,5-DMBA, showing 50% probability displacement ellipsoids and the atom-numbering scheme. Also shown is the intramolecular hydrogen bond (dashed line).

The hydrogen-bonding arrangement in 2,5-DMBA (Fig. 2) is unusual in that, unlike most of the DMBA isomers, the carboxylic acid group does not hydrogen bond with the carboxylic acid group of a neighboring molecule but instead forms an intramolecular hydrogen bond with the methoxy O atom bonded to C2 (Table 2).

Experimental

2,4-DMBA and 2,5-DMBA were obtained from Aldrich and used without further purification. Samples of both compounds were recrystallized from methanol.

Compound (I)

Crystal data

$C_9H_{10}O_4$
$M_r = 182.17$
Triclinic, $P\bar{1}$
$a = 6.7602\ (13)$ Å
$b = 7.7124\ (15)$ Å
$c = 8.0237\ (15)$ Å
$\alpha = 94.995\ (4)°$
$\beta = 95.894\ (4)°$
$\gamma = 96.759\ (4)°$
$V = 411.14\ (14)$ Å^3
$Z = 2$
$D_x = 1.472$ Mg m^{-3}

Mo $K\alpha$ radiation
Cell parameters from 1306
  reflections
$\theta = 2.6–26.0°$
$\mu = 0.12$ mm^{-1}
$T = 100\ (2)$ K
Block, colorless
$0.22 \times 0.17 \times 0.04$ mm

Data collection

Bruker SMART APEX
  diffractometer
ω scans
Absorption correction: multi-scan
  (SADABS; Sheldrick, 2000)
  $T_{min} = 0.975$, $T_{max} = 0.995$
2584 measured reflections
1563 independent reflections

1298 reflections with $I > 2\sigma(I)$
$R_{int} = 0.012$
$\theta_{max} = 26.0°$
$h = -7 \rightarrow 8$
$k = -9 \rightarrow 9$
$l = -9 \rightarrow 7$

Refinement

Refinement on F^2
$R[F^2 > 2\sigma(F^2)] = 0.047$
$wR(F^2) = 0.136$
$S = 1.04$
1563 reflections
121 parameters
H atoms treated by a mixture of
  independent and constrained
  refinement

$w = 1/[\sigma^2(F_o^2) + (0.1P)^2]$
  where $P = (F_o^2 + 2F_c^2)/3$
$(\Delta/\sigma)_{max} = 0.001$
$\Delta\rho_{max} = 0.37$ e Å^{-3}
$\Delta\rho_{min} = -0.43$ e Å^{-3}

Table 1
Hydrogen-bonding geometry (Å, °) for (I).

$D-H\cdots A$	$D-H$	$H\cdots A$	$D\cdots A$	$D-H\cdots A$
O2—H2$\cdots$O1^i	0.91 (2)	1.71 (2)	2.6192 (15)	172.7 (18)

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

Compound (II)

Crystal data

$C_9H_{10}O_4$
$M_r = 182.17$
Monoclinic, $P2_1/c$
$a = 10.0810\ (17)$ Å
$b = 12.534\ (2)$ Å
$c = 6.6408\ (11)$ Å
$\beta = 92.729\ (4)°$
$V = 838.1\ (2)$ Å^3
$Z = 4$
$D_x = 1.444$ Mg m^{-3}

Mo $K\alpha$ radiation
Cell parameters from 2576
  reflections
$\theta = 2.6–26.0°$
$\mu = 0.11$ mm^{-1}
$T = 100\ (2)$ K
Block, colorless
$0.33 \times 0.17 \times 0.06$ mm

Data collection

Bruker SMART APEX
  diffractometer
ω scans
Absorption correction: multi-scan
  (SADABS; Sheldrick, 2000)
  $T_{min} = 0.963$, $T_{max} = 0.993$
5021 measured reflections
1633 independent reflections

1421 reflections with $I > 2\sigma(I)$
$R_{int} = 0.023$
$\theta_{max} = 26.0°$
$h = -12 \rightarrow 11$
$k = -15 \rightarrow 15$
$l = -8 \rightarrow 8$

Refinement

Refinement on F^2
$R[F^2 > 2\sigma(F^2)] = 0.060$
$wR(F^2) = 0.168$
$S = 1.01$
1633 reflections
122 parameters
H atoms treated by a mixture of
  independent and constrained
  refinement

$w = 1/[\sigma^2(F_o^2) + (0.086P)^2$
  $+ 1.5P]$
  where $P = (F_o^2 + 2F_c^2)/3$
$(\Delta/\sigma)_{max} = 0.007$
$\Delta\rho_{max} = 0.51$ e Å^{-3}
$\Delta\rho_{min} = -0.34$ e Å^{-3}

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

$D-H\cdots A$	$D-H$	$H\cdots A$	$D\cdots A$	$D-H\cdots A$
O2—H2$\cdots$O3	0.88 (4)	1.72 (4)	2.547 (2)	154 (3)

The positions of the H atoms on the carboxylic acid groups were found from difference maps and refined independently. The positions of all other H atoms were determined geometrically (aromatic H—C = 0.95 Å and methyl H—C = 0.98 Å) and refined with a riding model. The $U_{iso}(H)$ parameters were assigned values of $1.2U_{eq}$ ($1.5U_{eq}$ for methyl groups) of the carrier atom.

For both compounds, data collection: SMART (Bruker, 1998); cell refinement: SMART; data reduction: SAINT (Bruker, 1998); program(s) used to solve structure: SHELXS97 (Sheldrick, 1990); program(s) used to refine structure: SHELXL97 (Sheldrick, 1997a); molecular graphics: SHELXTL (Sheldrick, 1997b); software used to prepare material for publication: SHELXTL.

References

Bruker (1998). SMART and SAINT. Bruker AXS Inc., Madison, Wisconsin, USA.
Bryan, R. F. & White, D. H. (1982a). Acta Cryst. B**38**, 1012–1014.
Bryan, R. F. & White, D. H. (1982b). Acta Cryst. B**38**, 1014–1016.
Etter, M. C., Urbanczyk-Lipkowska, Z., Fish, P. A., Panunto, T. W., Baures, P. W. & Frye, J. S. (1988). J. Crystallogr. Spectrosc. Res. **18**, 311–325.
Lynch, D. E., Smith, G., Byriel, K. A. & Kennard, C. H. L. (1994). Acta Cryst. C**50**, 1259–1262.
Parvez, M. (1987). Acta Cryst. C**43**, 2243–2245.
Pinkus, A. G., Kautz, J. A. & Ahobila-Vajjula, P. (2002). J. Chem. Crystallogr. **32**, 149–152.
Sheldrick, G. M. (1990). Acta Cryst. A**46**, 467–473.
Sheldrick, G. M. (1997a). SHELXL97. University of Göttingen, Germany.
Sheldrick, G. M. (1997b). SHELXTL. Bruker AXS Inc., Madison, Wisconsin, USA.
Sheldrick, G. M. (2000). SADABS. University of Göttingen, Germany.
Swaminathan, S., Sarangapani, K. & Lessinger, L. (1977). Cryst. Struct. Commun. **6**, 369–371.
Swaminathan, S., Vimala, T. M. & Lotter, H. (1976). Acta Cryst. B**32**, 1897–1900.