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3,4-Dihydroxyphenylacetic acid

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Key indicators

Single-crystal X-ray study
T = 296 K
Mean σ(C–C) = 0.008 Å
R factor = 0.051
wR factor = 0.220
Data-to-parameter ratio = 15.7

For details of how these key indicators were automatically derived from the article, see http://journals.iucr.org/e.

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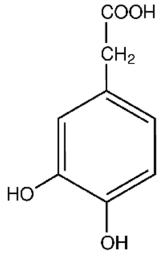
In the title compound, $C_8H_8O_4$, the acetic acid side chain adopts a roughly perpendicular orientation with respect to the phenyl ring. Hydrogen bonding between carboxyl groups results in the formation of a centrosymmetric dimer. An intramolecular hydrogen bond is formed in the catechol part of the molecule. Molecules are linked together through hydrogen bonds between hydroxyl and carboxylic acid O atoms.

Comment

It is important to clarify the detailed structure of the catecholamine metabolites in order to study catecholamine action as well as the metabolic pathway. In this context, the structures of the dopamine metabolites 3-methoxytyramine (Okabe, Mori & Sasaki, 1991; Okabe & Mori, 1992) and homovanillic acid (Okabe, Hatanaka & Sasaki, 1991), the noradrenaline metabolite normetanephrine (Pattanayek *et al.*, 1984) and the adrenaline metabolite 4-hydroxy-3-methoxymandelic acid (Okabe *et al.*, 1995) have been reported. We report here the crystal structure of the title compound, (I).



(I)

This compound is the principal metabolite of dopamine, but its structure could not be determined for a long time because of the difficulty of crystallization. The acetic acid side chain is oriented roughly perpendicular to the catechol ring of the molecule [torsion angle C2—C1—C7—C8 −87.2 (6)°]. This conformational feature of the molecule resembles that observed for dopamine, adrenaline and the corresponding amines (Barlow *et al.*, 1989), as well as the catecholamine metabolites homovanillic acid (Okabe, Hatanaka & Sasaki, 1991), 3-methoxytyramine (Okabe & Mori, 1992) and 4-hydroxy-3-methoxymandelic acid (Okabe *et al.*, 1995). This seems to be one of the important structural requirements for enzymatic recognition through the metabolic pathway. There is an intramolecular hydrogen bond between the two hydroxyl groups of the catechol ring (Table 2). This had not been observed in the crystal structures of the main catechol amine

metabolites, dopamine hydrochloride (Giesecke, 1980), (−)-adrenaline (Andersen, 1975*a*), (−)-noradrenaline (Andersen, 1975*b*) or noradrenaline hydrochloride (Carlström & Bergin, 1967). Two molecules of (I) form a centrosymmetric dimer by hydrogen bonding between the carboxyl groups.

Experimental

The colorless thin plate crystal used for analysis was obtained by slow evaporation from a solution in a mixture of diethyl ether and *n*-hexane (6:1 volume ratio) at room temperature.

Crystal data

$C_8H_8O_4$	Mo Kα radiation
M_r = 168.14	Cell parameters from 18 reflections
Orthorhombic, *Pbca*	θ = 10.1–13.1°
a = 16.181 (2) Å	μ = 0.12 mm^{-1}
b = 11.625 (2) Å	T = 296.2 K
c = 7.938 (3) Å	Thin plate, colorless
V = 1493.2 (6) Å^3	0.35 × 0.20 × 0.02 mm
Z = 8	
D_x = 1.496 Mg m^{-3}	

Data collection

Rigaku AFC-5*R* diffractometer	$h = 0 \rightarrow 21$
ω–2θ scans	$k = 0 \rightarrow 15$
1714 measured reflections	$l = -10 \rightarrow 0$
1714 independent reflections	3 standard reflections
493 reflections with $I > 2\sigma(I)$	every 150 reflections
θ_{max} = 27.5°	intensity decay: 0.2%

Refinement

Refinement on F^2	H-atom parameters not refined
$R[F^2 > 2\sigma(F^2)]$ = 0.051	$w = 1/[\sigma^2(F_o^2) + (0.1P)^2]$ where $P = (F_o^2 + 2F_c^2)/3$
$wR(F^2)$ = 0.220	$(\Delta/\sigma)_{max} < 0.001$
S = 0.84	$\Delta\rho_{max}$ = 0.25 e Å^{-3}
1714 reflections	$\Delta\rho_{min}$ = −0.30 e Å^{-3}
109 parameters	

Table 1
Selected geometric parameters (Å, °).

O1—C8	1.301 (7)	C1—C7	1.520 (7)
O2—C8	1.219 (7)	C2—C3	1.379 (7)
O3—C3	1.368 (6)	C3—C4	1.394 (8)
O4—C4	1.381 (6)	C4—C5	1.367 (8)
C1—C2	1.397 (7)	C5—C6	1.402 (7)
C1—C6	1.381 (8)	C7—C8	1.489 (8)
C2—C1—C6	118.9 (4)	O4—C4—C5	122.1 (5)
C2—C1—C7	121.4 (5)	C3—C4—C5	120.6 (5)
C6—C1—C7	119.7 (5)	C4—C5—C6	119.4 (5)
C1—C2—C3	120.6 (5)	C1—C6—C5	120.8 (5)
O3—C3—C2	118.7 (5)	C1—C7—C8	112.6 (5)
O3—C3—C4	121.6 (4)	O1—C8—O2	122.4 (5)
C2—C3—C4	119.7 (5)	O1—C8—C7	113.0 (5)
O4—C4—C3	117.3 (5)	O2—C8—C7	124.6 (5)
O1—C8—C7—C1	68.1 (6)	C2—C1—C6—C5	−0.4 (8)
O2—C8—C7—C1	−113.5 (6)	C2—C1—C7—C8	−86.2 (6)
O3—C3—C2—C1	179.2 (5)	C2—C3—C4—C5	−1.1 (8)
O3—C3—C4—O4	−1.9 (7)	C3—C2—C1—C6	1.1 (8)
O3—C3—C4—C5	179.3 (5)	C3—C2—C1—C7	−178.5 (5)
O4—C4—C3—C2	177.7 (5)	C3—C4—C5—C6	1.8 (8)
O4—C4—C5—C6	−176.9 (5)	C5—C6—C1—C7	179.3 (5)
C1—C2—C3—C4	−0.4 (8)	C6—C1—C7—C8	94.1 (6)
C1—C6—C5—C4	−1.0 (8)		

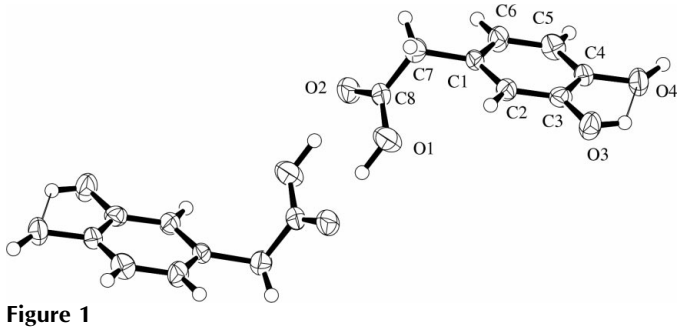


Figure 1
*ORTEP*II (Johnson, 1976) drawing of the title compound with the atomic numbering scheme. Ellipsoids for non-H atoms are shown at the 50% probability level.

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

D—H···A	D—H	H···A	D···A	D—H···A
O1—H9···O2^{i}	1.05	1.67	2.674 (6)	160
O3—H3···O4	0.89	2.25	2.745 (5)	115
O4—H4···O2^{ii}	0.96	2.00	2.843 (6)	146

Symmetry codes: (i) $2-x, -y, 1-z$; (ii) $x-\frac{1}{2}, \frac{1}{2}-y, 1-z$.

All H atoms were located from difference Fourier maps but were not refined.

Data collection and cell refinement: *MSC/AFC Diffractometer Control Software* (Molecular Structure Corporation and Rigaku Corporation, 1999*a*); data reduction: *TEXSAN* (Molecular Structure Corporation and Rigaku Corporation, 1999*b*); program(s) used to solve structure: *SIR*88 (Burla *et al.*, 1989) and *DIRDIF*94 (Beurskens *et al.*, 1994); program(s) used to refine structure: *SHELXL*97 (Sheldrick, 1997); molecular graphics: *ORTEP*II (Johnson, 1976); software used to prepare material for publication: *TEXSAN*.

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