Data collection

Siemens SMART CCD	2522 independent reflections
System diffractometer	1964 reflections with
ω scans (1271 frames, 0.30°,	$I > 2\sigma(I)$
10 s, detector distance	$R_{\rm int} = 0.060$
5.5 cm, detector angle	$\theta_{\rm max} = 26.60^{\circ}$
23.0°)	$h = -17 \rightarrow 18$
Absorption correction: none	$k = -6 \rightarrow 8$
6368 measured reflections	$l = -15 \rightarrow 16$

Refinement

Refinement on F^2	$w = 1/[\sigma^2(F_o^2) + (0.0629P)^2]$
$R[F^2 > 2\sigma(F^2)] = 0.051$	+ 0.452 <i>P</i>]
$wR(F^2) = 0.154$	where $P = (F_o^2 + 2F_c^2)/3$
S = 1.063	$(\Delta/\sigma)_{\rm max} = 0.033$
2522 reflections	$\Delta \rho_{\rm max} = 0.376 \ {\rm e} \ {\rm \AA}^{-3}$
125 parameters	$\Delta \rho_{\rm min}$ = -0.171 e Å ⁻³
H atoms treated by a	Extinction correction: none
mixture of independent	Scattering factors from
and constrained refinement	International Tables for
	Crystallography (Vol. C)

Table 1. Selected geometric parameters (Å, °)

Sil—Ol	1.6485 (16)	01—C3	1.437 (3)
Sil—C6	1.852 (3)	C1-C2	1.168 (5)
Si1—C7	1.855 (3)	C2—C3	1.474 (5)
Sil—C8	1.874 (3)	C3C5	1.527 (4)
01—Si1—C6	111.92 (11)	C1—C2—C3	176.4 (3)
01—Si1—C7	110.45 (12)	C2—C3—C4	110.2 (2)
01—Si1—C8	103.73 (10)	C5-C3-C4	109.5 (2)
C3-01Si1	132.28 (18)	C4 ⁱ —C4—C3	113.8 (2)
C8_Si1_O1_C3	168.9 (2)	C1-C2-C3-C5	66 (6)
Si1-01-C3-C2	-18.2(3)	C1-C2-C3-C4	-55 (6)
Sil-01-C3-C5	103.2 (3)	01-C3-C4-C4	61.5 (4)
Sil—Ol—C3—C4	-139.06 (19)	C2-C3-C4-C4 ⁱ	-60.7(4)
C1-C2-C3-01	-174 (6)	C5-C3-C4-C4 ⁱ	178.5 (3)
• • · · · •			

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

H-atom positions were calculated from idealized geometries and refined as riding on the corresponding C atoms.

Data collection: *SMART* (Siemens 1996a). Cell refinement: *SAINT* (Siemens 1996a). Data reduction: *SAINT*. Program(s) used to solve structure: *SHELXS*90 (Sheldrick, 1990). Program(s) used to refine structure: *SHELXL*97 (Sheldrick, 1997). Molecular graphics: *SHELXTL* (Siemens, 1996b). Software used to prepare material for publication: *SHELXL*97.

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Supplementary data for this paper are available from the IUCr electronic archives (Reference: SK1151). Services for accessing these data are described at the back of the journal.

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Ammonium Hydrogen Tartronate

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Abstract

The title compound, ammonium hydrogen hydroxypropanedioate, $NH_4^+.C_3H_3O_5^-$, has a very short noncentrosymmetric O—H···O hydrogen bond [2.443 (2) Å] between the carboxyl and carboxylate groups. The hydroxyl group attached to C1 forms a bifurcated hydrogen bond with intra- and intermolecular O atoms. The NH₄⁺ cation forms six N—H···O hydrogen bonds including two bifurcated hydrogen bonds, by which a layer composed of the cations and anions is formed.

Comment

It has been found that acid salts of carboxylic acids form very short O—H···O hydrogen bonds (Macdonald *et al.*, 1972; Videnova *et al.*, 1980; Kroon & Kanters, 1982; Hermansson & Tellgren, 1983; Misaki *et al.*, 1986). The structure of ammonium hydrogen tartronate, (I), is expected to be suitable for a detailed investigation of the bonding behavior of the H atom, because the molecule contains only a few light atoms with low atomic numbers.



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The molecular structure and crystal packing are shown in Fig. 1. The hydrogen-bond geometries are summarized in Table 1. The short O5—H5 \cdots O3 bond lies in a general position and, thus, it is not centrosymmetric. An elongated peak around the center of the O5 \cdots O3 bond was observed in a difference Fourier map drawn by omitting atom H5, and the least-squares refinement resulted in a long O5—H5 bond. The hydroxyl group, O1—H1O, links the layers formed by the cations and anions.



Fig. 1. Projection of the crystal structure viewed down the a axis with the numbering of atoms of the asymmetric unit. Hydrogen bonds are shown as thin solid lines.

The NH^{\ddagger} ion donates hydrogen bonds to six O atoms, while the K⁺ ion in potassium hydrogen tartronate, (II), in the same space group as (I) is coordinated by eight O atoms (Kroon & Kanters, 1982). This means that the hydrogen bonds govern the coordination around NH^{\ddagger} more than the electrostatic interaction. This fact is reflected in the differences in the crystal structures and lattice constants between (I) and (II).

Experimental

Crystals were grown by slow evaporation from an aqueous solution containing equimolar amounts of tartronic acid (SIGMA T-0657) and ammonia. A rather long crystal was used for diffraction measurement, because the crystals of (I) tended to grow as thin needles and crack when cut.

Mo $K\alpha$ radiation

Cell parameters from 25

 $0.75 \times 0.12 \times 0.10 \text{ mm}$

 $\lambda = 0.71073 \text{ Å}$

reflections

 $\mu = 0.158 \text{ mm}^{-1}$

 $\theta = 9.5 - 11.0^{\circ}$

T = 295 K

Prismatic

Colorless

 $\theta_{\rm max} = 27.5^{\circ}$

 $h = 0 \rightarrow 5$

 $k = 0 \rightarrow 11$ $l = -18 \rightarrow 18$

3 standard reflections

every 97 reflections

intensity decay: none

Crystal data

NH₄⁴.C₃H₃O₅ $M_r = 137.09$ Monoclinic $P2_1/c$ a = 4.3226 (6) Å b = 9.073 (2) Å c = 14.284 (2) Å $\beta = 91.73 (1)^\circ$ $V = 560.0 (2) Å^3$ Z = 4 $D_x = 1.626 \text{ Mg m}^{-3}$ D_m not measured

Data collection

Rigaku AFC-5*R* diffractometer $\omega/2\theta$ scans Absorption correction: none 1456 measured reflections 1293 independent reflections 1110 reflections with $I > 0.5\sigma(I)$ $R_{int} = 0.012$

Refinement

Refinement on F	$\Delta q_{\rm max} = 0.27 {\rm e} {\rm \AA}^{-3}$
R = 0.066	$\Delta \rho_{\rm min} = -0.30 \text{ e} \text{ Å}^{-3}$
wR = 0.055	Extinction correction:
S = 1.22	$I_{\rm corr} = I_o(1 + gI_c)$
1110 reflections	Extinction coefficient:
111 parameters	0.328×10^{-5}
All H atoms refined	Scattering factors from Inter-
$w = 1/\sigma^2(F)$	national Tables for X-ray
$(\Delta/\sigma)_{\rm max} = 0.05$	Crystallography (Vol. IV)

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

D—H···A	D—H	H <i>A</i>	$D \cdots A$	D—H···A
O5H5···O3 ⁱ	1.18(3)	1.26 (3)	2.443 (2)	178 (3)
O1—H1O· · · O2 ^{ⁱⁱ}	0.90 (3)	2.06 (3)	2.775 (2)	136(3)
O1—H1O· · · O2	0.90 (3)	2.17 (3)	2.654 (2)	113 (3)
N1—H1N···O2 ⁱ	0.95 (4)	2.10 (5)	3.044 (3)	169 (4)
N1—H2N···O3	0.88 (3)	2.21 (3)	2.892 (3)	135 (3)
N1H2N···O5	0.88 (3)	2.24 (4)	2.910 (3)	133 (3)
N1—H3N···O4 ⁱⁱⁱ	1.08 (6)	1.82 (6)	2.901 (3)	177 (5)
N1—H4N···O4 ^{iv}	0.85 (4)	2.21 (4)	2.903 (3)	139 (3)
N1—H4N···O1 [™]	0.85 (4)	2.40 (4)	3.129 (3)	145 (3)
Symmetry codes: (i) $-1 - x, y - \frac{1}{2}, \frac{1}{2} - z$; (ii) $-x, 1 - y, -z$; (iii)				
$-1 - x, \frac{1}{2} + y, \frac{1}{2} - z;$ (iv) $x, \frac{1}{2} - y, \frac{1}{2} + z.$				

Data collection and cell refinement were carried out with RASAII software (Rigaku Corporation, 1990). The structure was solved by direct methods using *MITHRIL* (Gilmore, 1984) and refined by full-matrix least-squares techniques using *TEXSAN* (Molecular Structure Corporation, 1985). H atoms were located from a difference Fourier map and refined isotropically. The displacement ellipsoids were drawn using *ORTEPII* (Johnson, 1976). Calculations were performed on a VAX 3100 computer using *TEXSAN* at the X-ray Laboratory of Okayama University, Japan.

Supplementary data for this paper are available from the IUCr electronic archives (Reference: AB1514). Services for accessing these data are described at the back of the journal.

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1H-Indole-3-propionic Acid

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(Received 18 July 1997; accepted 10 November 1997)

Abstract

The title compound, $C_{11}H_{11}NO_2$, has a fully extended propionic acid side chain. The molecules are held together as dimers by centrosymmetric pairs of intermolecular hydrogen bonds between the carboxyl groups. The O···O distance is 2.649 (2) Å.

Comment

The title compound, (I), has antibacterial activity against *Pseudomonas solanacearum* which causes a serious disease of many crop plants belonging to the family Solanaceae (Toyoda *et al.*, 1991; Matsuda *et al.*, 1993). It is also known as a hormone-type plant growth regulator like indole-3-acetic acid (Fargasova, 1994). Until now, its functional mechanism was unclear. Therefore, it is important to clarify its structure and conformation in order to investigate its function. Accordingly, the precise crystal structure of the title compound has been redetermined; its original structure determination was reported from film data, with an *R* value of 0.16 (Lahiri *et al.*, 1978). The non-

standard space group $P2_1/a$ was chosen to agree with the original determination, which had unit-cell dimensions a = 12.38, b = 5.25, c = 14.39 Å and $\beta = 95^{\circ}$.



The molecular structure of the title compound with the atomic labeling is shown in Fig. 1. The indole ring and the carboxyl group are in an *anti* conformation. The torsion angles, O(1)—C(12)—C(11)—C(10) –179.1 (1) and C(9)—C(3)—C(10)—C(11) –178.1 (2)°, indicate that the molecule has a nearly planar fully extended conformation. It may be important to take the planar conformation of indole-3-propionic acid into consideration for investigating the mechanism of the antibacterial or plant growth regulatory action. No stacking interactions between indole rings are observed. The crystal structure is stabilized by van der Waals interactions and hydrogen bonds between carboxyl groups, O(1)— $H(3) \cdots O(2)(1 - x, -y, -z) 2.649 (2)$ Å.



Fig. 1. ORTEPII (Johnson, 1976) drawing of the title compound with the atomic numbering scheme. Ellipsoids for non-H atoms correspond to 50% probability.

Experimental

The colorless pillar-shaped crystal used for analysis was obtained by the slow evaporation of a 90% ethanol solution of the title compound at room temperature.

Crystal data

$C_{11}H_{11}NO_{2}$ $M_{r} = 189.21$ Monoclinic $P2_{1}/a$ $a = 12.346 (3) \text{ Å}$ $b = 5.244 (3) \text{ Å}$ $c = 14.362 (2) \text{ Å}$ $\beta = 94.77 (2)^{\circ}$ $V = 926.6 (5) \text{ Å}^{3}$ $Z = 4$	Mo $K\alpha$ radiation $\lambda = 0.71069$ Å Cell parameters from 25 reflections $\theta = 20.89-24.11^{\circ}$ $\mu = 0.088 \text{ mm}^{-1}$ T = 296 K Pillar $0.4 \times 0.3 \times 0.2 \text{ mm}$ Colorless
$V = 926.6 (5) A^{2}$ Z = 4 $D_{x} = 1.356 \text{ Mg m}^{-3}$ D_{m} not measured	Colorless