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Key indicators

Single-crystal X-ray study T = 293 K Mean σ (C–C) = 0.004 Å R factor = 0.061 wR factor = 0.173 Data-to-parameter ratio = 12.2

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

© 2003 International Union of Crystallography Printed in Great Britain – all rights reserved In the title compound, $C_4H_7NO_4 \cdot H_2O$, the screw-related aspartic acid molecules are linked along the *a* axis by N-H···O hydrogen bonds to form helical structures. The adjacent helices are inter-linked through $O-H \cdot \cdot \cdot O$ hydrogen bonds and also by the water molecules through $N-H \cdot \cdot \cdot O(W)$ and $O(W)-H \cdot \cdot \cdot O$ hydrogen bonds, to form a three-dimensional network.

L-Aspartic acid monohydrate

Comment

Aspartic acid is a non-essential amino acid, widely distributed in proteins, which plays a major role in the energy cycle of the human body. The crystal structures of L-aspartic acid (Derissen *et al.*, 1968), DL-aspartic acid (Rao, 1973; Sequeira *et al.*, 1989), DL-aspartic acid nitrate monohydrate (Asath Bahadur & Rajaram, 1995), bis(DL-aspartic acid) sulfate (Srinivasan *et al.*, 2001) and L-aspartic acid nitrate–L-aspartic acid (1/1) (Sridhar *et al.*, 2002) have been reported. In the present paper, the crystal structure of L-aspartic acid monohydrate, (I), is reported.



The asymmetric unit of (I) contains one aspartic acid molecule and one water molecule (Fig. 1). The equality of C– O bond distances [1.240 (4) and 1.259 (4) Å] and O–C–C bond angles [118.3 (3) and 115.3 (3)°] (Table 1) characterize the deprotonated carboxylate group. The backbone conformation angle ψ^1 of -10.8 (4)° indicates the *cis* form. The side chain shows a *gauche* II conformation $[\chi^1 =$ -71.8 (3)°]. The branched chain conformation angles χ^{11} and χ^{21} correspond to the *cis* and *trans* forms. The C^{γ} atom is in the *gauche* I [52.7 (3)°] conformation with respect to the C' atom. The molecular structure is stabilized by a weak intramolecular N1–H1B···O3 hydrogen bond.

The screw-related aspartic acid molecules are linked along the *a* axis by N1–H1A···O1ⁱ hydrogen bonds to form a helical structure (Table 2 and Fig. 2). This helical structure is further stabilized by N1–H1C···O3ⁱⁱ hydrogen bonds, which link the molecules translated by one unit along the *a* axis. The adjacent helices are interlinked through O4–H4···O2ⁱⁱⁱ hydrogen bonds and also by the water molecules through N1–H1B···O11^{iv}, O11–H11···O2^v and O11–H12··O2ⁱ Received 16 June 2003 Accepted 23 June 2003 Online 30 June 2003



Figure 1

The asymmetric unit of the title compound, showing 50% probability displacement ellipsoids (Johnson, 1976) and the atom-numbering scheme.



Figure 2

A view of the helical structures formed along the a axis. For clarity, all H atoms except H1A have been omitted.



Figure 3 Hydrogen-bonding network, viewed down the *a* axis.

hydrogen bonds, to form a three-dimensional network. Within the network, the O4—H4···O2ⁱⁱⁱ hydrogen bonds link the screw-related molecules, to form zigzag chains along the *c* axis. A class II hydrogen-bonding pattern is observed in the present structure, having two two-centered hydrogen bonds and one three-centered hydrogen bond (Jeffrey & Saenger, 1991). In the present study, the water molecule shows a planar 1*B*-1/1*D* orientation (Jeffrey & Saenger, 1991). All the symmetry codes are as in Table 2. A view of the molecular packing down the *a* axis is shown in Fig. 3.

Experimental

The title compound was crystallized from an aqueous solution when attempts were made to grow single crystals of a complex of L-aspartic acid with sulfuric acid.

 D_m measured by flotation in a

and xylene

Mo $K\alpha$ radiation

reflections

 $\begin{array}{l} \theta = 8.0\text{--}13.8^{\circ} \\ \mu = 0.14 \ \mathrm{mm}^{-1} \end{array}$

T = 293 (2) K

 $R_{\rm int} = 0.085$

 $\theta_{\rm max} = 24.6^{\circ}$ $h = 0 \rightarrow 6$

 $k = 0 \rightarrow 11$

 $l=-14\rightarrow 14$

3 standard reflections

frequency: 60 min

intensity decay: none

 $w = 1/[\sigma^2(F_o^2) + (0.136P)^2]$

where $P = (F_o^2 + 2F_c^2)/3$

_3

+ 0.3381P]

 $(\Delta/\sigma)_{\rm max} < 0.001$

 $\Delta \rho_{\text{max}} = 0.33 \text{ e } \text{\AA}^{-3}$ $\Delta \rho_{\text{min}} = -0.54 \text{ e } \text{\AA}^{-3}$

Block, colorless $0.3 \times 0.3 \times 0.3$ mm

Cell parameters from 25

mixture of carbon tetrachloride

Crystal data

 $C_{4}H_{7}NO_{4} \cdot H_{2}O$ $M_{r} = 151.12$ Orthorhombic, $P2_{1}2_{1}2_{1}$ a = 5.587 (4) Å b = 9.822 (5) Å c = 11.813 (9) Å $V = 648.2 (8) Å^{3}$ Z = 4 $D_{x} = 1.548 \text{ Mg m}^{-3}$ $D_{m} = 1.54 \text{ Mg m}^{-3}$

Data collection

Enraf–Nonius CAD-4 diffractometer ω –2 θ scans Absorption correction: ψ scan (North *et al.*, 1968) $T_{min} = 0.958, T_{max} = 0.958$ 1318 measured reflections 1132 independent reflections 1132 independent reflections

Refinement

Refinement on F^2 $R[F^2 > 2\sigma(F^2)] = 0.061$ $wR(F^2) = 0.173$ S = 1.061132 reflections 93 parameters H atoms treated by a mixture of independent and constrained refinement

Table 1

Selected geometric parameters (Å, °).

O1-C1	1.240 (4)	C4-O3	1.244 (4)
O2-C1	1.259 (4)	C4-O4	1.322 (4)
O1-C1-O2	126.2 (3)	O2 - C1 - C2	115.3 (3)
O1-C1-C2	118.3 (3)		
01 01 02 11	10.0 (1)		71.0.(2)
OI - CI - C2 - NI	-10.8(4)	N1 - C2 - C3 - C4	-71.9(3)
O2-C1-C2-N1	173.9 (3)	C1-C2-C3-C4	52.8 (3)
O1-C1-C2-C3	-136.2(3)	C2-C3-C4-O3	-2.9(4)
O2-C1-C2-C3	48.5 (3)	C2-C3-C4-O4	177.0 (3)

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

$D - H \cdot \cdot \cdot A$	D-H	$H \cdots A$	$D \cdots A$	$D - H \cdots A$
$N1-H1A\cdotsO1^{i}$	0.89	1.93	2.813 (4)	171
$N1-H1C\cdots O3^{ii}$	0.89	2.02	2.809 (4)	147
O4-H4···O2 ⁱⁱⁱ	0.82	2.15	2.933 (4)	161
$N1 - H1B \cdot \cdot \cdot O11^{iv}$	0.89	2.22	2.854 (4)	128
$O11-H11\cdots O2^{v}$	0.78	2.06	2.837 (4)	170
$O11-H12\cdots O2^i$	0.80	2.05	2.817 (4)	160
$N1-H1B\cdots O3$	0.89	2.55	3.093 (4)	120

Symmetry codes: (i) $x - \frac{1}{2}, \frac{1}{2} - y, -z$; (ii) x - 1, y, z; (iii) $\frac{5}{2} - x, -y, \frac{1}{2} + z$; (iv) $1 - x, y - \frac{1}{2}, \frac{1}{2} - z$; (v) x - 1, 1 + y, z.

The H atoms of the water molecule were located from a difference Fourier map and their isotropic displacement parameters were refined $[U_{iso}(H) = 0.04 (1) \text{ and } 0.07 (2) \text{ Å}^2]$. All other H atoms were placed in geometrically calculated positions and included in the refinement in the riding-model approximation, with U_{iso} equal to $1.2U_{eq}$ of the carrier atom. The data set includes 442 Friedel pairs; however, the lack of any significant anomalous effects precludes the confirmation of the absolute configuration from the diffraction data, and it has been assumed.

Data collection: *CAD-4 Software* (Enraf–Nonius, 1989); cell refinement: *CAD-4 Software*; data reduction: *CAD-4 Software*; program(s) used to solve structure: *SHELXS*97 (Sheldrick, 1997); program(s) used to refine structure: *SHELXL*97 (Sheldrick, 1997); molecular graphics: *PLATON* (Spek, 1999); software used to prepare material for publication: *SHELXL*97.

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