organic compounds

L-Asparagine

Kazuhiko Yamada,[a,b]* **Daisuke Hashizume,**[c] **Tadashi Shimizu**[a] **and Shigeyuki Yokoyama**[b]

[a]National Institute for Materials Science, 3-13, Sakura, Tsukuba 305-0003, Japan, [b]Protein Research Group, Genomic Sciences Center, Yokohama Institute, RIKEN, 1-7-22, Suehiro, Tsurumi, Yokohama, Kanagawa 230-0045, Japan, and [c]Molecular Characterization Team, RIKEN, 2-1, Hirosawa, Wako, Saitama 351-0198, Japan
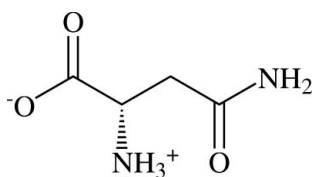Correspondence e-mail: yamada.kazuhiko@nims.go.jp

Crystals of anhydrous L-aspargine, $C_4H_8N_2O_3$, were obtained from a saturated aqueous solution. The molecules are in their zwitterionic form. Although the carboxyl group is deprotonated, the distances of the two C⋯O bonds are significantly different [1.2407 (19) and 1.262 (2) Å], due to different hydrogen-bond environments. The conformation of the side chain is *trans*, which distinguishes it significantly from that of L-asparagine monohydrate.

Related literature

For related literature on single-crystal diffraction studies of L-asparagine monohydrate, see: Arnold *et al.* (2000); Chandrasekhar *et al.* (2003); Flaig *et al.* (2002); Kartha & de Vries (1961); Ramanadham *et al.* (1972); Smirnova *et al.* (1990); Verbist *et al.* (1972); Wang *et al.* (1985); Weisinger-Lewin *et al.* (1989). The unit cell and space group of the title compound were previously determined by powder X-ray diffraction (PDF: 37-1659). For the sample preparation of the title compound, see Yamada *et al.* (2007). For related literature on crystal structures of L-aspartic acid and its monohydrate, see: Derissen *et al.* (1968); Umadevi *et al.* (2003).

Experimental

Crystal data

$C_4H_8N_2O_3$	b = 6.7001 (5) Å
M_r = 132.12	c = 8.0543 (5) Å
Monoclinic, $P2_1$	β = 91.706 (5)°
a = 5.0622 (4) Å	V = 273.06 (3) Å^3

Z = 2	T = 90 K
Mo $K\alpha$ radiation	$0.65 \times 0.36 \times 0.08$ mm
μ = 0.14 mm^{-1}	

Data collection

Rigaku AFC-8 with Saturn70 CCD diffractometer	865 independent reflections
Absorption correction: none	815 reflections with $I > 2\sigma(I)$
3379 measured reflections	R_{int} = 0.045

Refinement

$R[F^2 > 2\sigma(F^2)]$ = 0.032	1 restraint
$wR(F^2)$ = 0.085	All H-atom parameters refined
S = 1.08	$\Delta\rho_{max}$ = 0.22 e Å^{-3}
865 reflections	$\Delta\rho_{min}$ = −0.29 e Å^{-3}
114 parameters	

Table 1
Selected geometric parameters (Å, °).

O1—C2	1.2407 (19)	O3—C4	1.240 (2)
O2—C2	1.262 (2)		
C2—C1—C3—C4	170.64 (14)		

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

D—H⋯A	D—H	H⋯A	D⋯A	D—H⋯A
N1—H1NA⋯O2^i	0.92 (4)	1.83 (4)	2.741 (2)	167 (3)
N1—H1NB⋯O3^{ii}	1.01 (3)	1.94 (3)	2.908 (2)	159 (3)
N1—H1NC⋯O2^{iii}	1.00 (3)	1.82 (3)	2.807 (2)	169 (3)
N2—H2NA⋯O1^{iv}	0.94 (3)	1.91 (3)	2.8456 (19)	174 (3)
N2—H2NB⋯O3^v	0.92 (3)	2.03 (3)	2.921 (2)	163 (2)

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

Data collection: *CrystalClear SM* (Rigaku/MSC Inc., 2005); cell refinement: *CrystalClear SM*; data reduction: *HKL-2000* (Otwinowski & Minor, 1997); program(s) used to solve structure: *SIR2004* (Burla *et al.*, 2005); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *ORTEP-3 for Windows* (Farrugia, 1997); software used to prepare material for publication: *SHELXL97*.

References

Arnold, W. D., Sanders, L. K., McMahon, M. T., Volkov, A. V., Wu, G., Coppens, P., Wilson, S. R., Godbout, N. & Oldfield, E. (2000). *J. Am. Chem. Soc.* **122**, 4708–4717.
Burla, M. C., Caliandro, R., Camalli, M., Carrozzini, B., Cascarano, G. L., De Caro, L., Giacovazzo, C., Polidori, G. & Spagna, R. (2005). *J. Appl. Cryst.* **38**, 381–388.
Chandrasekhar, S., Hota, R., Choudhury, A. R. & Row, T. N. G. (2003). Private communication.
Derissen, J. L., Endeman, H. J. & Peerdeman, A. F. (1968). *Acta Cryst.* B**24**, 1349–1354.
Farrugia, L. J. (1997). *J. Appl. Cryst.* **30**, 565.
Flaig, R., Koritsanszky, T., Dittrich, B., Wagner, A. & Luger, P. (2002). *J. Am. Chem. Soc.* **124**, 3407–3417.
Kartha, G. & de Vries, A. (1961). *Nature (London)*, **192**, 862–863.
Otwinowski, Z. & Minor, W. (1997). *Methods Enzymol.* **276**, 307–326.

doi:10.1107/S1600536807039505

Ramanadham, M., Sikka, S. K. & Chidambaram, R. (1972). *Acta Cryst.* B**28**, 3000–3005.

Rigaku/MSC Inc. (2005). *CrystalClear SM*. Version 1.3.6. Rigaku/MSC Inc., The Woodlands, Texas, USA.

Sheldrick, G. M. (1997). *SHELXL97*. University of Göttingen, Germany.

Smirnova, V. I., Sorokina, N. I., Safonov, A. A., Verin, I. A. & Tischenko, G. N. (1990). *Kristallografiya*, **35**, 50–53.

Umadevi, K., Anitha, K., Sridhar, B., Srinivasan, N. & Rajaram, R. K. (2003). *Acta Cryst.* E**59**, o1073–o1075.

Verbist, J. J., Lehmann, M. S., Koetzle, T. F. & Hamilton, W. C. (1972). *Acta Cryst.* B**28**, 3006–3013.

Wang, J. L., Berkovitch-Yellin, Z. & Leiserowitz, L. (1985). *Acta Cryst.* B**41**, 341–348.

Weisinger-Lewin, Y., Frolow, F., McMullan, R. K., Koetzle, T. F., Lahav, M. & Leiserowitz, L. (1989). *J. Am. Chem. Soc.* **111**, 1035–1040.

Yamada, K., Yamazaki, T., Asanuma, M., Hirota, H., Yamamoto, N. & Kajihara, Y. (2007). *Chem. Lett.* **36**, 192–193.

supplementary materials

L-Asparagine

K. Yamada, D. Hashizume, T. Shimizu and S. Yokoyama

Comment

L-Asparagine is one of the fundamental natural amino acid residues in proteins. It has been believed that it plays an important role in the formation of the secondary structures in proteins due to the fact that the side chain can form efficient hydrogen bonds with the peptide backbone. In general, amino acids very often have polymorphs. The crystal structures of *L*-asparagine monohydrate (Kartha & de Vries, 1961; Verbist *et al.*, 1972; Ramanadham *et al.*, 1972; Wang *et al.*, 1985; Weisinger-Lewin *et al.*, 1989; Smirnova *et al.*, 1990; Arnold *et al.*, 2000; Flaig *et al.*, 2002; Chandrasekhar *et al.*, 2003) and D-asparagine monohydrate (Chandrasekhar *et al.*, 2003) have been reported so far. A powder X-ray diffraction study (PDF:37–1659) has been also reported for anhydrous *L*-asparagine. In the present study, a single-crystal structure determination of anhydrous *L*-asparagine, (I), is reported.

The single-crystal diffraction analysis confirms the space group and the unit-cell dimensions previously proposed by the powder diffraction study, and shows that, as expected, the title molecule exists as a zwitter ion in the crystal (Fig. 1). The distances of the C⋯O bonds in the carboxylate group are significantly different although the group is deprotonated. The corresponding distances are 1.2407 (19) and 1.262 (2) Å for C2—O1 and C2—O2, respectively. The discrepancy is attributed to the number and kind of the intermolecular hydrogen bonds each O atom of the carboxylate participates in. The O2 atom forms two strong hydrogen bonds with neighboring cationic ammonium groups. O1, on the other hand, forms only one relatively weak hydrogen bond with the neutral amide group (Table 2 and Fig. 2). Owing to the formation of two strong hydrogen bonds, the C1—O2 bond is strongly polarized, and the distance of the C1—O2 bond is elongated accordingly. The carbonyl oxygen in the side chain, O3, also forms two hydrogen bonds with each one ammonium and amide group of neighboring molecules.

It is of interest to compare the present structure with that of *L*-asparagine monohydrate (Ramanadham *et al.*, 1972). In the *L*-asparagine monohydrate crystal, the C⋯O bonds in the ionized carboxyl group are 1.243 and 1.257 Å, which is in good agreement with those in (I), but with a slightly less pronounced difference in C—O bond lengths. Both oxygen atoms in the monohydrate exhibit each one relatively weak N—H⋯O hydrogen bond to an amide group, but the oxygen atom with the longer C—O distance forms two additional strong H bonds with solvate water molecules. The oxygen atom with the shorter C—O bond, on the other hand, forms only one strong hydrogen bond, in this case to the ammonium group. As the difference in the hydrogen bonding environment is thus less pronouced for the monohydrate than in the anhydrous structure this may also explain the more pronounced difference in the C—O distances found in the structure of the title compound.

The conformation of the backbone of (I) is quite different from that of the monohydrate. In (I), the torsion angle of C2—C1—C3—C4 is 170.64 (14)°, while, in the monohydrate, the corresponding angle is −53.08°. As mentioned, there are significant differences between the crystal structures and the side-chain conformations of anhydrous and monohydrate asparagines, which can be attributed most likely to the different hydrogen bonding environment induced by the presence of the water molecules. Similar differences are also found in the crystal structures of *L*-aspartic acid (Derissen *et al.*, 1968) and *L*-aspartic acid monohydrate (Umadevi *et al.*, 2003). The corresponding torsion angles of the side-chains, for example, are 178.2° and 52.8°, for *L*-aspartic acid and its monohydrate, respectively.

supplementary materials

Experimental

The title compound, asparagine oxygen-17 isotope enriched at the carboxyl group, was synthesized with the aim to perform solid-state ^{17}O NMR experiments. *L*-Asparagine was obtained by deprotection of both the N-terminus and side-chain groups from ^{17}O-enriched N-α-Fmoc-N-β-trityl-*L*-asparagine. Detailed procedures have been described elsewhere (Yamada *et al.*, 2007).

Colorless crystals of *L*-asparagine monohydrate can be obtained by slow cooling of an aqueous solution (Verbist *et al.*, 1972; Ramanadham *et al.*, 1972). Colorless platelike crystals of anhydrous *L*-asparagine used in the present study, on the other hand, were obtained from a saturated aqueous solution after it was left standing at room temperature for a few months.

Refinement

All H atoms were found in difference density Fourier maps. Their positions and isotropic displacement parameters were freely refined. The refined C—H and N—H bond lengths are in the expected range: 1.00 (3) Å and 107.6 (18)–109.8 (15)° for the methyne C—H distance and the C/N—C—H angle, respectively; 1.01 (3)–1.03 (3) Å, 107.3 (15)–110.9 (18)° and 110 (2)° for the methylene C—H, C—C—H and H—C—H values, respectively; 0.92 (4)–1.01 (3) Å, 109 (2)–114.5 (18)° and 105 (2)–112 (3)° for the ammonium N—H, C—N—H and H—N—H values, respectively; 0.92 (3)–0.94 (3) Å, 118.6 (15)–120.2 (16)° and 121 (2)° for the amide N—H, C—N—H and H—N—H values, respectively. The range of the U_{iso} values for the H atoms is 0.020 (7)–0.044 (9) Å^{2}.
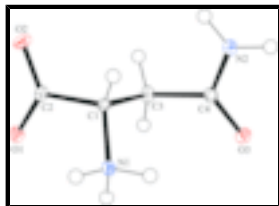
Figures

Fig. 1. A view of the molecular structure of (I), showing the atom-labelling scheme. Displacement ellipsoids are drawn at the 50% probability level.
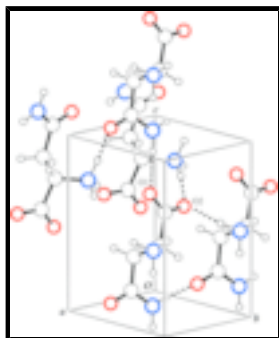

Fig. 2. A packing diagram of (I). Broken lines indicate the hydrogen bonds.

L-Asparagine

Crystal data

$C_4H_8N_2O_3$	$F_{000} = 140$
$M_r = 132.12$	$D_x = 1.607$ Mg m^{-3}
Monoclinic, $P2_1$	Mo $K\alpha$ radiation $\lambda = 0.71073$ Å
Hall symbol: P 2yb	Cell parameters from 1254 reflections
$a = 5.0622$ (4) Å	$\theta = 2.5$–$32.2°$
$b = 6.7001$ (5) Å	$\mu = 0.14$ mm^{-1}
$c = 8.0543$ (5) Å	$T = 90$ K
$\beta = 91.706$ (5)°	Plate, colourless
$V = 273.06$ (3) Å^3	$0.65 \times 0.36 \times 0.08$ mm
$Z = 2$	

Data collection

AFC-8 with Saturn70 CCD diffractometer	865 independent reflections
Radiation source: fine-focus rotating anode	815 reflections with $I > 2\sigma(I)$
Monochromator: confocal	$R_{int} = 0.045$
Detector resolution: 28.5714 pixels mm^{-1}	$\theta_{max} = 30.1°$
$T = 90$ K	$\theta_{min} = 2.5°$
ω scans	$h = -7 \rightarrow 7$
Absorption correction: none	$k = -9 \rightarrow 9$
3379 measured reflections	$l = -11 \rightarrow 11$

Refinement

Refinement on F^2	Hydrogen site location: difference Fourier map
Least-squares matrix: full	All H-atom parameters refined
$R[F^2 > 2\sigma(F^2)] = 0.032$	$w = 1/[\sigma^2(F_o^2) + (0.0469P)^2 + 0.0383P]$ where $P = (F_o^2 + 2F_c^2)/3$
$wR(F^2) = 0.085$	$(\Delta/\sigma)_{max} < 0.001$
$S = 1.08$	$\Delta\rho_{max} = 0.22$ e Å^{-3}
865 reflections	$\Delta\rho_{min} = -0.29$ e Å^{-3}
114 parameters	Extinction correction: none
1 restraint	
Primary atom site location: structure-invariant direct methods	
Secondary atom site location: difference Fourier map	

Special details

Experimental. All Friedel pairs were merged, and all f"s of containing atoms were set to zero.

supplementary materials

Geometry. All e.s.d.'s (except the e.s.d. in the dihedral angle between two l.s. planes) are estimated using the full covariance matrix. The cell e.s.d.'s are taken into account individually in the estimation of e.s.d.'s in distances, angles and torsion angles; correlations between e.s.d.'s in cell parameters are only used when they are defined by crystal symmetry. An approximate (isotropic) treatment of cell e.s.d.'s is used for estimating e.s.d.'s involving l.s. planes.

Refinement. Refinement of F^2 against ALL reflections. The weighted R-factor wR and goodness of fit S are based on F^2, conventional R-factors R are based on F, with F set to zero for negative F^2. The threshold expression of $F^2 > 2\sigma(F^2)$ is used only for calculating R-factors(gt) *etc*. and is not relevant to the choice of reflections for refinement. R-factors based on F^2 are statistically about twice as large as those based on F, and R– factors based on ALL data will be even larger.

Fractional atomic coordinates and isotropic or equivalent isotropic displacement parameters ($Å^2$)

	x	y	z	U_{iso}*/U_{eq}
O1	0.2240 (2)	0.1487 (2)	0.59976 (15)	0.0152 (3)
O2	−0.1823 (2)	0.1359 (2)	0.48234 (15)	0.0146 (3)
O3	0.5526 (2)	0.0384 (3)	−0.00341 (16)	0.0159 (3)
N1	0.4009 (3)	0.3459 (2)	0.32483 (18)	0.0113 (3)
H1NA	0.353 (6)	0.451 (6)	0.391 (4)	0.044 (9)*
H1NB	0.458 (5)	0.393 (5)	0.212 (4)	0.031 (8)*
H1NC	0.563 (5)	0.287 (5)	0.380 (3)	0.024 (7)*
N2	0.1172 (3)	0.0801 (2)	−0.06008 (19)	0.0137 (3)
H2NA	0.151 (5)	0.112 (5)	−0.171 (3)	0.028 (7)*
H2NB	−0.051 (5)	0.079 (5)	−0.022 (3)	0.020 (7)*
C1	0.1734 (3)	0.2065 (3)	0.3083 (2)	0.0097 (3)
H1	0.034 (5)	0.273 (5)	0.237 (3)	0.019 (6)*
C2	0.0645 (3)	0.1617 (3)	0.48026 (19)	0.0097 (3)
C3	0.2553 (4)	0.0114 (3)	0.2244 (2)	0.0126 (3)
H3A	0.420 (6)	−0.049 (5)	0.283 (3)	0.025 (7)*
H3B	0.102 (5)	−0.084 (4)	0.231 (3)	0.021 (7)*
C4	0.3218 (3)	0.0440 (3)	0.04381 (19)	0.0108 (3)

Atomic displacement parameters ($Å^2$)

	U^{11}	U^{22}	U^{33}	U^{12}	U^{13}	U^{23}
O1	0.0139 (6)	0.0228 (7)	0.0088 (5)	0.0022 (6)	0.0002 (4)	0.0018 (5)
O2	0.0096 (6)	0.0183 (6)	0.0160 (6)	−0.0017 (6)	0.0020 (4)	0.0045 (5)
O3	0.0106 (7)	0.0229 (7)	0.0143 (5)	0.0015 (5)	0.0016 (4)	−0.0015 (5)
N1	0.0128 (7)	0.0115 (7)	0.0097 (6)	−0.0022 (6)	0.0017 (5)	−0.0008 (5)
N2	0.0127 (7)	0.0190 (8)	0.0096 (6)	−0.0011 (6)	0.0013 (5)	−0.0007 (5)
C1	0.0090 (7)	0.0120 (7)	0.0081 (6)	−0.0011 (6)	0.0013 (5)	0.0016 (5)
C2	0.0116 (8)	0.0076 (8)	0.0099 (7)	0.0007 (6)	0.0024 (5)	0.0007 (5)
C3	0.0166 (8)	0.0123 (8)	0.0091 (6)	0.0016 (7)	0.0028 (5)	0.0004 (6)
C4	0.0129 (8)	0.0094 (8)	0.0103 (7)	−0.0010 (6)	0.0018 (5)	−0.0011 (6)

Geometric parameters ($Å$, °)

O1—C2	1.2407 (19)	N2—H2NA	0.94 (3)
O2—C2	1.262 (2)	N2—H2NB	0.92 (3)

O3—C4	1.240 (2)	C1—C3	1.535 (3)
N1—C1	1.485 (2)	C1—C2	1.536 (2)
N1—H1NA	0.92 (4)	C1—H1	1.00 (3)
N1—H1NB	1.01 (3)	C3—C4	1.518 (2)
N1—H1NC	1.00 (3)	C3—H3A	1.03 (3)
N2—C4	1.334 (2)	C3—H3B	1.01 (3)
C1—N1—H1NA	109 (2)	C2—C1—H1	109.8 (15)
C1—N1—H1NB	111.0 (18)	O1—C2—O2	126.99 (15)
H1NA—N1—H1NB	112 (3)	O1—C2—C1	118.07 (14)
C1—N1—H1NC	114.5 (18)	O2—C2—C1	114.90 (13)
H1NA—N1—H1NC	106 (3)	C4—C3—C1	111.70 (14)
H1NB—N1—H1NC	105 (2)	C4—C3—H3A	107.3 (15)
C4—N2—H2NA	118.6 (15)	C1—C3—H3A	110.9 (18)
C4—N2—H2NB	120.2 (16)	C4—C3—H3B	109.5 (15)
H2NA—N2—H2NB	121 (2)	C1—C3—H3B	107.4 (15)
N1—C1—C3	110.86 (14)	H3A—C3—H3B	110 (2)
N1—C1—C2	109.90 (14)	O3—C4—N2	122.28 (15)
C3—C1—C2	109.84 (14)	O3—C4—C3	121.80 (14)
N1—C1—H1	107.6 (18)	N2—C4—C3	115.92 (15)
C3—C1—H1	108.8 (17)		
N1—C1—C2—O1	−36.1 (2)	N1—C1—C3—C4	−67.71 (17)
C3—C1—C2—O1	86.1 (2)	C2—C1—C3—C4	170.64 (14)
N1—C1—C2—O2	145.97 (16)	C1—C3—C4—O3	107.35 (19)
C3—C1—C2—O2	−91.81 (18)	C1—C3—C4—N2	−72.2 (2)

Hydrogen-bond geometry (Å, °)

D—H⋯A	D—H	H⋯A	D⋯A	D—H⋯A
N1—H1NA⋯O2[i]	0.92 (4)	1.83 (4)	2.741 (2)	167 (3)
N1—H1NB⋯O3[ii]	1.01 (3)	1.94 (3)	2.908 (2)	159 (3)
N1—H1NC⋯O2[iii]	1.00 (3)	1.82 (3)	2.807 (2)	169 (3)
N2—H2NA⋯O1[iv]	0.94 (3)	1.91 (3)	2.8456 (19)	174 (3)
N2—H2NB⋯O3[v]	0.92 (3)	2.03 (3)	2.921 (2)	163 (2)

Symmetry codes: (i) −*x*, *y*+1/2, −*z*+1; (ii) −*x*+1, *y*+1/2, −*z*; (iii) *x*+1, *y*, *z*; (iv) *x*, *y*, *z*−1; (v) *x*−1, *y*, *z*.

Fig. 1

Fig. 2