

## Hydrogen-bonding patterns in *cis*-4-ammoniocyclohexanecarboxylate hemihydrate

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In the title compound,  $C_7H_{13}NO_2 \cdot 0.5H_2O$ , *cis*-4-aminocyclohexanecarboxylic acid exists as a zwitterion and co-crystallizes with water molecules in a 2:1 amino acid–water ratio. The cyclohexane ring adopts a chair conformation, with the carboxylate and ammonium groups in axial and equatorial positions, respectively. The basic motif in the crystal structure is a sandwich structure, formed by two amino acid units linked by head-to-tail hydrogen bonds. Hydrogen bonds of the type  $N^+ - H \cdots O - C - O^-$  link these motifs, forming helicoidally extended chains running along the *c* axis. The water molecule lies on a twofold axis and interacts with the chains by means of  $O - H \cdots O$  hydrogen bonds.

### Comment

Amino acids often co-crystallize with water molecules (Görbitz & Hersleth, 2000). In these simple biological systems, the role played by the water molecule is diverse, ranging from just occupying void space in the structure to being involved in co-operative effects associated with the conformation of extended hydrogen-bonding patterns (Jeffrey & Maluszynska, 1982; Dannenberg, 2002). These effects are most relevant in the crystalline solid state, where the periodicity allows the development of interactions between neighboring molecules with redistribution of charge density among functional groups; this process produces effects similar to resonance, in which hydrogen bonds shorten and the energy gain is not additive (Steiner, 2002). We are currently investigating the energetic character and arrangement of hydrogen-bonding patterns in structurally related amino acid hydrates, in which the flexibility of the carbon skeleton and the orientation of the amine and carboxylic acid groups can dictate the way that individual molecules aggregate to form supramolecular structures. In particular, the structures of the isomers 2-, 3- and 4-piperi-

dinecarboxylic acid have been assessed by means of *ab initio* density-functional and semi-empirical calculations (Delgado *et al.*, 2001; Cuervo *et al.*, 2002; Mora *et al.*, 2002). Continuing these studies, we report here the structure of the title compound, (I), which differs from piperidinium-4-carboxylate, (II), in that the ammonium group is positioned outside the six-membered ring, enabling the ammonium group to donate three H atoms for hydrogen bonding.

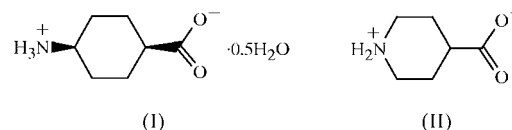
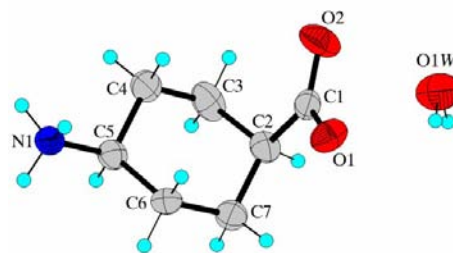
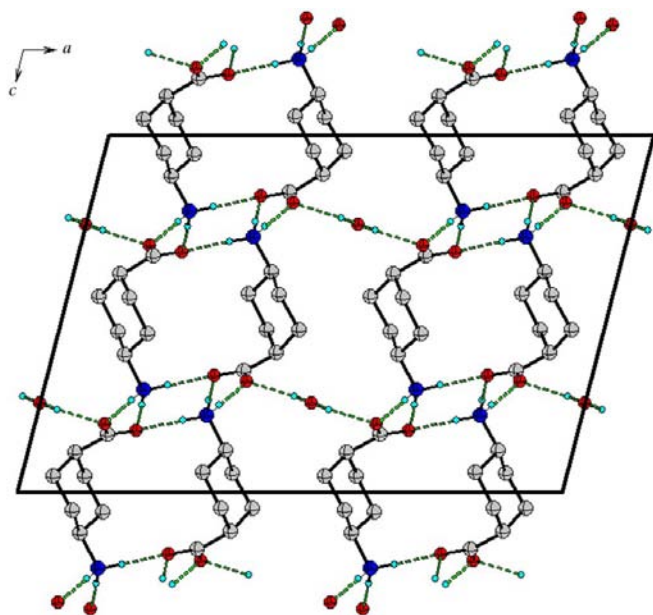


Fig. 1 shows the molecular structure and the atom-labelling scheme. Water atom O1W lies on a twofold axis parallel to the *b* axis. The C1–O1 and C1–O2 distances are equal within  $3\sigma$  (see Table 1), indicating an almost symmetrical carboxylate group. On the other hand, the three H atoms bonded to atom N1 were found in a difference Fourier map, which confirms the zwitterionic nature of the molecule. The asymmetry parameters  $\Delta C_s$  [maximum  $+4.6(2)^\circ$  and minimum  $+0.9(2)^\circ$ ] and  $\Delta C_2$  [maximum  $+6.0(2)^\circ$  and minimum  $+2.3(2)^\circ$ ] (Griffin *et al.*, 1984) and the Cremer & Pople (1975) puckering parameters [ $C_s(C2) = 3.9(2)^\circ$ ,  $C_s(C3) = 4.6(2)^\circ$ ,  $C_s(C4) = 0.9(2)^\circ$ ,  $C_2(C2-C3) = 6.0(2)^\circ$ ,  $C_2(C3-C4) = 3.8(2)^\circ$  and  $C_2(C4-C5) = 2.3(2)^\circ$ ] reveal the presence of three local mirror planes and three local twofold axes, confirming that the cyclohexane ring adopts the more stable chair conformation, as seen in the *trans*- and *cis*- isomers of 4-(aminomethyl)cyclohexanecarboxylic acid (Yamazaki *et al.*, 1981; Groth, 1968) and their hydrohalides (Kadoya *et al.*, 1966). This conformation is also adopted in the liquid state, as revealed by  $^1H$  and  $^{13}C$  NMR spectra taken in  $D_2O$ .

This conformation favors the joining of two amino acid units by head-to-tail hydrogen bonding (Table 2), thus forming a sandwich-like 16-atom macrocycle (Fig. 2). In this sandwich structure, there are three  $N^+ - H \cdots O - C - O^-$  hydrogen bonds, two of which are bifurcated, with atom O1 acting as acceptor. Neighbouring sandwich structures connect *via* their polar ends through hydrogen bonds, giving rise to helicoidally extended chains running along the *c* axis. These chains are held together by intercalated water molecules interacting



**Figure 1**  
The molecular structure of (I), showing displacement ellipsoids at the 50% probability level.



**Figure 2**  
The crystal structure of (I), projected down the *b* axis. Broken lines show hydrogen bonds. H atoms not involved in hydrogen bonding have been omitted for clarity.

through  $O^- - C - O \cdots HW - OW$  hydrogen bonds. This additional hydrogen bond makes carboxylate atom O2 a bifurcated acceptor. The neighbouring chains have intermolecular hydrophobic  $H \cdots H$  contacts that are close to the sum of their van der Waals radii (2.40 Å).

### Experimental

A sample of *cis*-4-aminocyclohexanecarboxylic acid (500 mg, Aldrich, 98%) was dissolved in an ethanol/water mixture (1:8, 2 ml). Crystals of (I) suitable for X-ray diffraction analysis were grown by slow evaporation.  $^{13}C$  NMR (100.6 MHz,  $D_2O$ ):  $\delta$  24.8 (C-3 = C-7), 27.3 (C-4 = C-6), 41.4 (C-7), 49.0 (C-3), 183.6 (C-1);  $^1H$  NMR (400 MHz,  $D_2O$ ):  $\delta$  2.37 (1H, *m*, H-1eq), 1.90 (2H, *m*, H-2eq = H-6eq), 1.61 (2H, *m*, H-2ax = H-6ax), 1.58 (2H, *m*, H-3ax = H-5ax), 1.83 (2H, *dc*, *J* = 10 and 4 Hz, H-3eq = H-5eq), 3.29 (1H, *q*, *J* = 4 Hz, H-4ax).

#### Crystal data

$C_7H_{13}NO_2 \cdot 0.5H_2O$   
 $M_r = 152.19$   
Monoclinic,  $C2/c$   
 $a = 19.871$  (4) Å  
 $b = 6.1614$  (11) Å  
 $c = 13.475$  (2) Å  
 $\beta = 104.452$  (3)°  
 $V = 1597.6$  (5) Å<sup>3</sup>  
 $Z = 8$

$D_x = 1.265$  Mg m<sup>-3</sup>  
Mo  $K\alpha$  radiation  
Cell parameters from 3462 reflections  
 $\theta = 2.1$ – $28.3^\circ$   
 $\mu = 0.10$  mm<sup>-1</sup>  
 $T = 293$  (2) K  
Plate, colourless  
0.30 × 0.30 × 0.20 mm

#### Data collection

Siemens SMART CCD area-detector diffractometer  
 $\varphi$  and  $\omega$  scans  
Absorption correction: multi-scan (*SADABS*; Sheldrick, 1996)  
 $T_{min} = 0.890$ ,  $T_{max} = 0.980$   
7982 measured reflections

1880 independent reflections  
1100 reflections with  $I > 2\sigma(I)$   
 $R_{int} = 0.060$   
 $\theta_{max} = 28.3^\circ$   
 $h = -26 \rightarrow 26$   
 $k = -8 \rightarrow 8$   
 $l = -17 \rightarrow 17$

#### Refinement

Refinement on  $F^2$   
 $R[F^2 > 2\sigma(F^2)] = 0.047$   
 $wR(F^2) = 0.102$   
 $S = 0.97$   
1880 reflections  
118 parameters

H atoms treated by a mixture of independent and constrained refinement  
 $w = 1/[\sigma^2(F_o^2) + (0.0496)^2]$   
where  $P = (F_o^2 + 2F_c^2)/3$   
 $(\Delta/\sigma)_{max} < 0.001$   
 $\Delta\rho_{max} = 0.19$  e Å<sup>-3</sup>  
 $\Delta\rho_{min} = -0.18$  e Å<sup>-3</sup>

**Table 1**  
Selected geometric parameters (Å, °).

C1—O1	1.261 (2)	C2—C3	1.530 (2)
C1—O2	1.245 (2)	C3—C4	1.515 (3)
C5—N1	1.492 (2)	C4—C5	1.513 (2)
C1—C2	1.524 (2)	C5—C6	1.520 (2)
C2—C7	1.529 (2)	C6—C7	1.515 (2)
O2—C1—O1	123.6 (2)	N1—C5—C4	110.6 (1)
O2—C1—C2	118.0 (2)	N1—C5—C6	110.5 (1)
O1—C1—C2	118.4 (2)		

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

<i>D</i> —H $\cdots$ <i>A</i>	<i>D</i> —H	H $\cdots$ <i>A</i>	<i>D</i> $\cdots$ <i>A</i>	<i>D</i> —H $\cdots$ <i>A</i>
N1—H2N $\cdots$ O1 <sup>i</sup>	0.91 (2)	1.84 (2)	2.745 (2)	174 (2)
O1W—H1W $\cdots$ O2 <sup>ii</sup>	0.87 (2)	2.09 (2)	2.942 (2)	169 (2)
N1—H3N $\cdots$ O2 <sup>iii</sup>	0.93 (2)	1.84 (2)	2.763 (2)	171 (2)
N1—H1N $\cdots$ O1 <sup>iv</sup>	0.89 (2)	1.88 (2)	2.769 (2)	171 (2)

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

The H atoms of the  $NH_3^+$  group and of the water molecule were located in difference Fourier maps and refined isotropically. The H atoms of the cyclohexane ring were placed geometrically and their positions were fixed ( $C-H = 0.95$ – $0.98$  Å), with  $U_{iso}(H)$  values of  $1.2U_{eq}(\text{parent})$ .

Data collection: *SMART* (Bruker, 1998); cell refinement: *SAINT* (Bruker, 1998); data reduction: *SAINT*; program(s) used to solve structure: *SHELXS97* (Sheldrick, 1997); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *DIAMOND* (Brandenburg, 1998); software used to prepare material for publication: *SHELXL97* and *PLATON* (Spek, 2003).

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Supplementary data for this paper are available from the IUCr electronic archives (Reference: OB1197). Services for accessing these data are described at the back of the journal.

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