

Graphene-like nets of hydrogen-bonded water molecules in the dihydrate of 2-[(2-ammonioethyl)-amino]acetate and the structure of its anhydrous hydroiodide salt

Tove Wiklund, Christine J. McKenzie and Anders Lennartson*

Department of Physics and Chemistry, University of Southern Denmark, Campusvej 55, 5230 Odense M, Denmark

Correspondence e-mail: lennartson@ifk.sdu.dk

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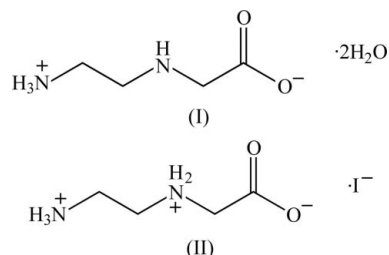
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2-[(2-Ammonioethyl)amino]acetate dihydrate, better known as *N*-(2-aminoethyl)glycine dihydrate, $C_4H_{10}N_2O_2 \cdot 2H_2O$, (I), crystallizes as a three-dimensional hydrogen-bonded network. Amino acid molecules form layers in the *ac* plane separated by layers of water molecules, which form a hydrogen-bonded two-dimensional net composed of fused six-membered rings having boat conformations. The crystal structure of the corresponding hydroiodide salt, namely 2-[(2-ammonioethyl)-ammonio]acetate iodide, $C_4H_{11}N_2O_2^+ \cdot I^-$, (II), has also been determined. The structure of (II) does not accommodate any solvent water molecules, and displays stacks of amino acid molecules parallel to the *a* axis, with iodide ions located in channels, resulting in an overall three-dimensional hydrogen-bonded network structure. *N*-(2-Aminoethyl)glycine is a molecule of considerable biological interest, since its polyamide derivative forms the backbone in the DNA mimic peptide nucleic acid (PNA).

Comment

Slow addition of chloroacetic acid to a large excess of 1,2-diaminoethane at 273 K gives rise to an oily reaction product, from which 2-[(2-ammonioethyl)amino]acetate dihydrate, (I), can be isolated after trituration with dimethyl sulfoxide (DMSO). The amino acid of compound (I) is better known as *N*-(2-aminoethyl)glycine or *N*-(β -aminoethyl)glycine and has attracted considerable interest over the last 20 years. A polypeptide built from *N*-(2-aminoethyl)glycine molecules forms the backbone in peptide nucleic acid (PNA), a synthetic nucleic acid analogue (Nielsen *et al.*, 1991). PNA forms DNA-like double helices and is able to hybridize with DNA (Egholm *et al.*, 1993; Wittung *et al.*, 1994). PNA is resistant to nucleases and proteases; the absence of the phosphate groups

found in DNA and RNA renders PNA uncharged, and the absence of saccharide residues makes PNA achiral. It has even been argued that simple molecules such as PNA may have been the first genetic molecules, preceding RNA and DNA in the evolution of life (Nelson *et al.*, 2000). In this paper, we describe the crystal structures of (I) and its hydroiodide salt, namely 2-[(2-ammonioethyl)ammonio]acetate iodide, (II).



Crystallized under similar conditions, from water and ethanol in the case of (I) or water and propan-2-ol in the case

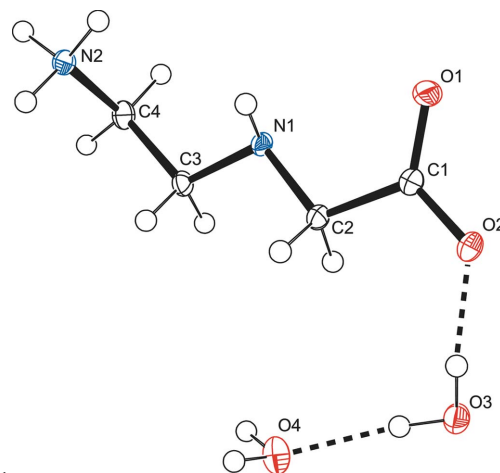


Figure 1

The molecular structure of (I), showing the atom-numbering scheme. Displacement ellipsoids are drawn at the 50% probability level and H atoms are shown as small spheres of arbitrary radii. Dashed lines indicate hydrogen bonds.

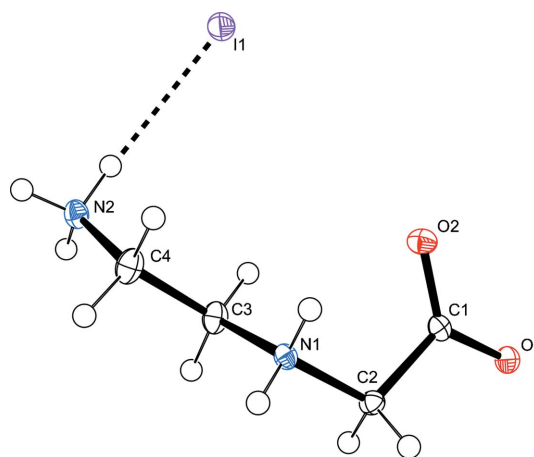
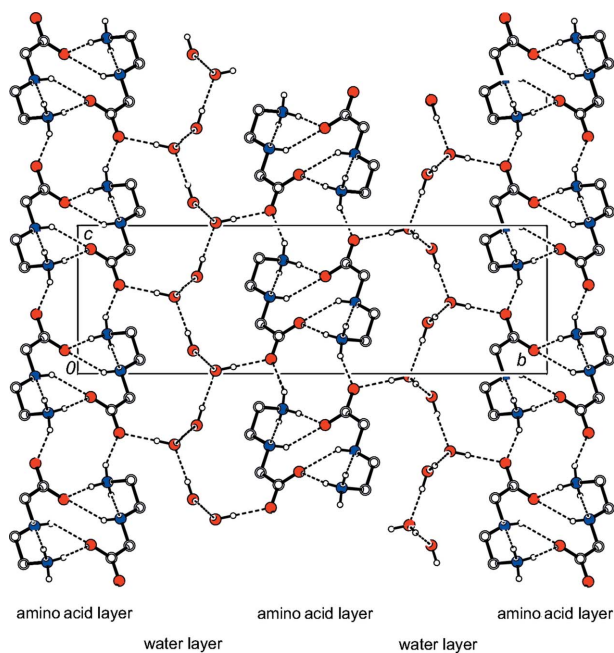


Figure 2

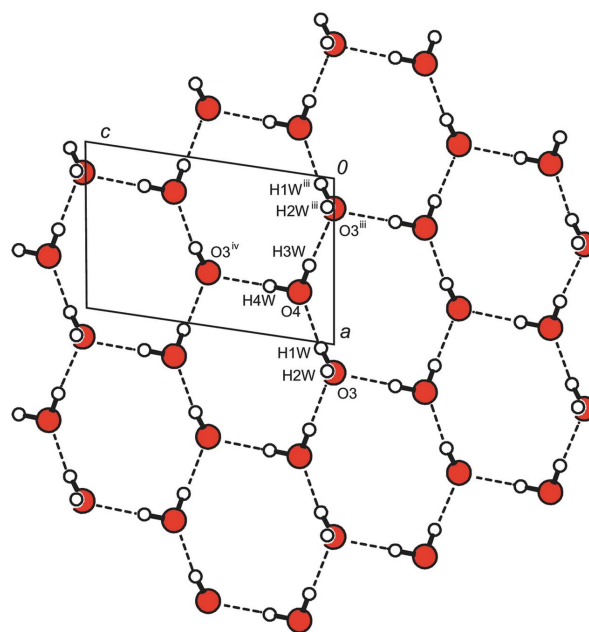
The molecular structure of (II), showing the atom-numbering scheme. Displacement ellipsoids are drawn at the 50% probability level and H atoms are shown as small spheres of arbitrary radii. The dashed line indicates the hydrogen bond.

**Figure 3**

Compound (I) forms a layered structure, here viewed along the *a* axis. Layers of amino acid molecules alternating with layers of water molecules are shown running vertically. Dashed lines indicate hydrogen bonds. H atoms not involved in intermolecular interactions have been omitted for clarity.

of (II), (I) forms a dihydrate while (II) forms an anhydrous product. In the crystalline state, the conformations of the amino acid backbone in (I) and (II) are different. In (I), all non-H atoms lie approximately in one plane [the largest deviation from the plane formed by C1, C2, C3, C4, O1, O2 and N1 in (I) is $-0.0478(9)$ Å for atom C2], except the terminal amino group which is bent out of this plane (Fig. 1); the N1–C3–C4–N2 torsion angle is $-73.96(11)^\circ$. In (II), atoms C2, N1, C3, C4 and N2 lie approximately in one plane [the largest deviation from the plane formed by these five atoms in (II) is $0.1211(17)$ Å for atom C3] (Fig. 2) and, in this structure, it is the carboxylate group that is bent out of the plane; the C3–N1–C2–C1 torsion angle is $76.09(21)^\circ$.

In the crystal structure of (I), the amino acid molecules form stacks parallel to the crystallographic *a* axis, and the molecules in these stacks are directly connected through H3N \cdots N1ⁱⁱⁱ interactions. Adjacent stacks interdigitate, with both atoms H1N and H4N forming hydrogen bonds to atom O1ⁱ. These interactions connect two stacks into a double stack, since atoms H1Nⁱ and H4Nⁱ form hydrogen bonds to atom O1. These double stacks interact with adjacent double stacks through two sets of interactions, one of classical N–H \cdots O interactions and the other of C–H \cdots O interactions; atom H2N forms a hydrogen bond with atom O2ⁱⁱ and atom H4A forms a hydrogen bond with atom O2^v. The H2N \cdots O2ⁱⁱ interactions give rise to chains extending parallel to the [10 $\bar{1}$] direction, while the H4A \cdots O2^v interactions give rise to chains extending parallel to the *c* axis. As a result, the amino acid molecules form hydrogen-bonded layers in the *ac* plane (Fig. 3).

**Figure 4**

The water molecules in the crystal structure of (I) give rise to a hydrogen-bonded two-dimensional graphene-like net. (Symmetry codes are as in Table 1.)

Compound (I) crystallizes with two molecules of water in the asymmetric unit. One of these, corresponding to atom O3, forms a hydrogen bond to the carboxylate group through an H2W \cdots O2 hydrogen bond. The other water molecule, corresponding to atom O4, does not form a hydrogen bond to the amino acid molecules, but only to other water molecules in the crystal structure. In addition to the hydrogen bond to atom O2, the O3 water molecule forms hydrogen bonds to three different O4 water molecules: atom H1W forms a hydrogen bond to atom O4, and atom O3 forms two hydrogen bonds to atoms H3W^{viii} and H4W^{ix} [symmetry codes: (viii) $-1 + x, y, z$; (ix) $-\frac{1}{2} + x, \frac{3}{2} - y, \frac{1}{2} + z$]. The O4 water molecule forms hydrogen bonds to three other water molecules. Apart from accepting a hydrogen bond from atom H1W, it acts as a donor for two additional hydrogen bonds: atom H3W forms a hydrogen bond to atom O3ⁱⁱⁱ and atom H4W forms a hydrogen bond to atom O3^{iv}. The water molecules give rise to layers in the *ac* plane, built from fused six-membered rings in a honeycomb-like fashion, with each ring adopting a boat conformation (Fig. 4). Using the graph-set notation introduced by Etter (Etter, 1990; Etter *et al.*, 1990), these rings may be described as $R_6^0(12)$. Atoms O3 and O4 form the nodes and atom O3 forms hydrogen bonds to the adjacent layers of amino acid molecules situated on either side of the layer, resulting in an overall three-dimensional hydrogen-bonded network structure. Extended hydrogen-bonded water motifs have attracted attention (Mascal *et al.*, 2006; Infantes *et al.*, 2003). There are similar motifs in DL-2-amino-2-thiazoline-4-carboxylic acid trihydrate (Xuan *et al.*, 2003) and in 6-methyl-2-pyridone pentahydrate, in which two similar layers are separated by layers of pyridone molecules (Clegg & Nichol, 2004).

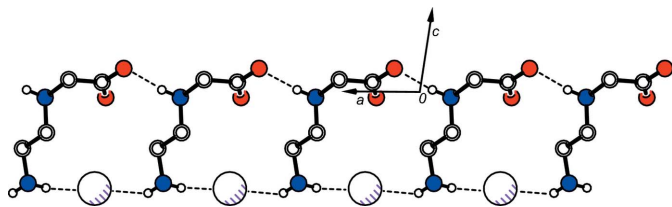


Figure 5

The hydrogen-bonded chain in the structure of (II), running parallel to the crystallographic *a* axis. Dashed lines indicate hydrogen bonds. H atoms not involved in intermolecular interactions have been omitted for clarity.

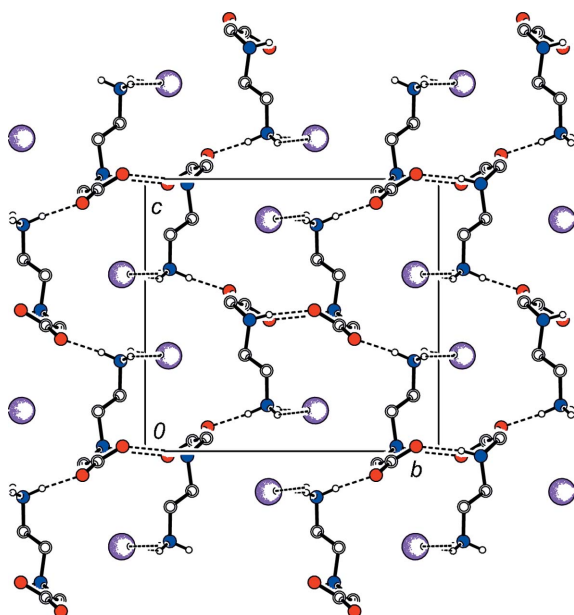


Figure 6

The crystal structure of (II), viewed along the *a* axis. Both amino acid molecules and iodide anions are stacked along the *a* axis. Dashed lines indicate hydrogen bonds. H atoms not involved in intermolecular interactions have been omitted for clarity.

The amino acid molecules in (II) form stacks parallel to the crystallographic *a* axis (Fig. 5), the molecules in these stacks being directly connected through one set of hydrogen bonds *viz.* H1Nⁱⁱⁱ··O1ⁱⁱⁱ. The molecules in the stacks are further linked through iodide ions. Atom H3N forms a hydrogen bond to atom I1, and atom I1 forms a hydrogen bond to atom H5N^{viii} in the next molecule in the stack. As a result, the iodide anions also form stacks parallel to the *a* axis and are aligned in channels (Fig. 6). The stacks in (II) form hydrogen bonds to three adjacent stacks through two sets of hydrogen bonds. Atom H4N forms a hydrogen bond to atom O1^{vii}, and atom O1 forms a hydrogen bond to atom H4N^x [symmetry code: (x) $-\frac{1}{2} + x, \frac{1}{2} - y, \frac{1}{2} + z$], which generates connections to two different stacks. Atom H2N forms a hydrogen bond to atom O2^{vi}, but since atom H2N^{vi} forms a hydrogen bond to atom O2, this set of interactions only connects two adjacent stacks. As a result, (II) forms a three-dimensional hydrogen-bonded network structure.

The structures of (I) and (II) can be compared with that of *N*-(2-ammonioethyl)carbamate, which differs from (I) and (II)

by only one methylene group. Three different polymorphs, (III)–(V), of anhydrous *N*-(2-ammonioethyl)carbamate have been described. Polymorph (III) crystallizes in the space group *Pna*2₁ (Garbaskas *et al.*, 1983) and its molecular conformation resembles that of (II). Polymorphs (IV) (Garbaskas *et al.*, 1983) and (V) (Antsyshkina *et al.*, 2007) were refined in the space groups *P*2₁/*a* and *P*2₁/*c*, respectively, and have molecular conformations resembling the conformation of (I). Polymorph (III) forms a hydrogen-bonded network structure, quite dissimilar from either (I) or (II). In polymorph (IV), the molecules form layers, where all hydrogen bonds occur within the layers. The two surfaces of the layers are dominated by the hydrophobic methylene groups, and the layers appear to be largely held together by dispersion forces. Polymorph (V) forms another hydrogen-bonded network structure. It may be expected that a more detailed study of (I) and (II) would reveal similar cases of polymorphism, or phases displaying different cocrystallized solvents. For example, the crystal structure of (I) displays single graphene-like water layers, while additional water in the crystal structure could give rise to graphite-like assemblies of layers (Clegg & Nichol, 2004).

Experimental

2-[(2-Ammonioethyl)amino]acetate dihydrate, (I), was prepared according to a published procedure (Heimer *et al.*, 1984), with modifications. Chloroacetic acid (28 g, 0.3 mol) was added to stirred 1,2-diaminoethane (200 ml, 3 mol) in small portions at 273 K. The mixture was stirred at ambient temperature overnight, and the excess 1,2-diaminoethane was removed on a rotary evaporator at 333 K. The oily residue was dissolved in a small amount of DMSO and triturated with acetonitrile. This procedure was repeated until the thick residue was insoluble in DMSO. Trituration was continued with small portions of DMSO until the residue crystallized. The crystals were washed with DMSO and diethyl ether (yield 29 g, 63%). The raw product was recrystallized from hot 96% laboratory grade ethanol, washed with ethanol and allowed to dry in air (yield 15.2 g, 33%). Large crystals of (I) suitable for X-ray diffraction were obtained from a second recrystallization and grew slowly overnight from a nearly saturated solution in hot *ca* 70% aqueous ethanol.

2-[(2-Ammonioethyl)ammonio]acetate iodide, (II), was obtained in an attempt to methylate (I). 2-[(2-Ammonioethyl)amino]acetate dihydrate (0.15 g, 1 mmol) was dissolved in boiling ethanol (10 ml). Iodomethane (0.2 ml, 3 mmol) was added, and the reaction mixture was allowed to stand at ambient temperature overnight. The ethanol was evaporated, and the residue was dissolved in water (0.5 ml) and layered with propan-2-ol (1.5 ml). Crystals of (II) were isolated after approximately one week.

Compound (I)

Crystal data

C₄H₁₀N₂O₂·2H₂O
M_r = 154.17
 Monoclinic, *P*2₁/*n*
a = 4.7106 (4) Å
b = 22.8634 (19) Å
c = 7.2804 (6) Å
 β = 98.154 (3)°

V = 776.17 (11) Å³
Z = 4
 Mo *K*α radiation
 μ = 0.12 mm⁻¹
T = 120 K
 0.22 × 0.22 × 0.18 mm

Table 1

Hydrogen-bond geometry (Å, °) for (I).

<i>D</i> —H... <i>A</i>	<i>D</i> —H	H... <i>A</i>	<i>D</i> ... <i>A</i>	<i>D</i> —H... <i>A</i>
N2—H1N...O1 ⁱ	0.929 (17)	1.843 (17)	2.7557 (13)	166.7 (13)
O3—H1W...O4	0.852 (19)	1.893 (19)	2.7413 (13)	174.2 (15)
N2—H2N...O2 ⁱⁱ	0.932 (15)	1.891 (16)	2.7614 (13)	154.5 (13)
O3—H2W...O2	0.88 (2)	1.88 (2)	2.7541 (13)	173.9 (15)
N2—H3N...N1 ⁱⁱⁱ	0.958 (15)	1.946 (15)	2.9018 (13)	176.0 (12)
O4—H3W...O3 ⁱⁱⁱ	0.884 (19)	1.927 (19)	2.8102 (13)	177.3 (15)
N1—H4N...O1 ⁱ	0.875 (14)	2.256 (14)	3.0179 (13)	145.4 (11)
O4—H4W...O3 ^{iv}	0.91 (2)	1.93 (2)	2.8345 (14)	177.1 (17)
C4—H4A...O2 ^v	0.99	2.48	3.4598 (13)	171

Symmetry codes: (i) $-x, -y + 1, -z + 1$; (ii) $x + 1, y, z - 1$; (iii) $x + 1, y, z$; (iv) $x + \frac{1}{2}, -y + \frac{3}{2}, z - \frac{1}{2}$; (v) $x, y, z - 1$.

Table 2

Hydrogen-bond geometry (Å, °) for (II).

<i>D</i> —H... <i>A</i>	<i>D</i> —H	H... <i>A</i>	<i>D</i> ... <i>A</i>	<i>D</i> —H... <i>A</i>
N1—H1N...O1 ⁱⁱⁱ	0.87 (3)	1.95 (3)	2.819 (2)	171 (2)
N1—H1N...O2 ⁱⁱⁱ	0.87 (3)	2.61 (2)	3.260 (2)	132.3 (19)
N1—H2N...O2 ^{vi}	0.87 (3)	1.93 (3)	2.780 (2)	168 (2)
N2—H3N...I1	0.89 (3)	2.60 (3)	3.4753 (19)	166 (2)
N2—H4N...O1 ^{vii}	0.89 (3)	1.82 (3)	2.704 (2)	174 (2)
N2—H5N...I1 ⁱⁱⁱ	0.87 (3)	2.78 (3)	3.552 (2)	148 (2)

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

Data collection

Bruker X8 APEXII CCD area-detector diffractometer
Absorption correction: multi-scan (SADABS; Sheldrick, 2003)
 $T_{\min} = 0.877, T_{\max} = 0.982$

13219 measured reflections
1521 independent reflections
1246 reflections with $I > 2\sigma(I)$
 $R_{\text{int}} = 0.033$

Refinement

$R[F^2 > 2\sigma(F^2)] = 0.029$
 $wR(F^2) = 0.088$
 $S = 1.02$
1521 reflections
123 parameters

H atoms treated by a mixture of independent and constrained refinement
 $\Delta\rho_{\max} = 0.23 \text{ e } \text{Å}^{-3}$
 $\Delta\rho_{\min} = -0.22 \text{ e } \text{Å}^{-3}$

Compound (II)**Crystal data**

$\text{C}_4\text{H}_{11}\text{N}_2\text{O}_2^+\text{I}^-$
 $M_r = 246.05$
Monoclinic, $P2_1/n$
 $a = 5.7129 (3) \text{ Å}$
 $b = 12.4269 (7) \text{ Å}$
 $c = 11.6560 (7) \text{ Å}$
 $\beta = 98.542 (2)^\circ$

$V = 818.32 (8) \text{ Å}^3$
 $Z = 4$
Mo $K\alpha$ radiation
 $\mu = 3.86 \text{ mm}^{-1}$
 $T = 120 \text{ K}$
 $0.22 \times 0.12 \times 0.12 \text{ mm}$

Data collection

Bruker X8 APEXII CCD area-detector diffractometer
Absorption correction: multi-scan (SADABS; Sheldrick, 2003)
 $T_{\min} = 0.350, T_{\max} = 0.655$

14193 measured reflections
1591 independent reflections
1493 reflections with $I > 2\sigma(I)$
 $R_{\text{int}} = 0.025$

Refinement

$R[F^2 > 2\sigma(F^2)] = 0.014$
 $wR(F^2) = 0.032$
 $S = 0.90$
1591 reflections
102 parameters

H atoms treated by a mixture of independent and constrained refinement
 $\Delta\rho_{\max} = 0.68 \text{ e } \text{Å}^{-3}$
 $\Delta\rho_{\min} = -0.64 \text{ e } \text{Å}^{-3}$

C-bound H atoms were positioned geometrically and treated as riding, with $\text{C—H} = 0.99 \text{ Å}$ and $U_{\text{iso}}(\text{H}) = 1.2U_{\text{eq}}(\text{C})$. O- and N-bound H atoms were located in difference Fourier maps and refined freely.

For both compounds, data collection: APEX2 (Bruker, 2004); cell refinement: SAINT (Bruker, 2004); data reduction: SAINT; program(s) used to solve structure: SIR92 (Altomare *et al.*, 1993); program(s) used to refine structure: SHELXL97 (Sheldrick, 2008); molecular graphics: ORTEP-3 (Farrugia, 1997) and PLUTON (Spek, 2009); software used to prepare material for publication: SHELXL97.

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Supplementary data for this paper are available from the IUCr electronic archives (Reference: DN3147). Services for accessing these data are described at the back of the journal.

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