

**1,4,8,11-Tetrakis(carboxymethyl)-5,5,7,12,12,14-hexamethyl-1,4,8,11-tetraazoniacyclotetradecane tetrachloride octahydrate**Shi-Fan Wang,<sup>a</sup> Huan-Qiu Li,<sup>a</sup>  
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The crystal structure of the centrosymmetric title compound, C<sub>24</sub>H<sub>48</sub>N<sub>4</sub>O<sub>8</sub><sup>4+</sup>·4Cl<sup>-</sup>·8H<sub>2</sub>O, consists of a 14-membered methyl-substituted C<sub>10</sub>N<sub>4</sub> cationic ring which interacts with the chloride ions and water molecules of crystallization to give a three-dimensional hydrogen-bonded network structure.

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**Comment**The title compound, (I), a hydrochloride salt of an edta type of amino acid whose four amine N atoms belong to a 14-membered C<sub>10</sub>N<sub>4</sub> macrocyclic ring (Fig. 1), is the methyl-substituted derivative of 1,4,8,11-tetraazacyclotetradecane-1,4,8,11-tetraacetic acid hexahydrate.**Key indicators**

Single-crystal X-ray study

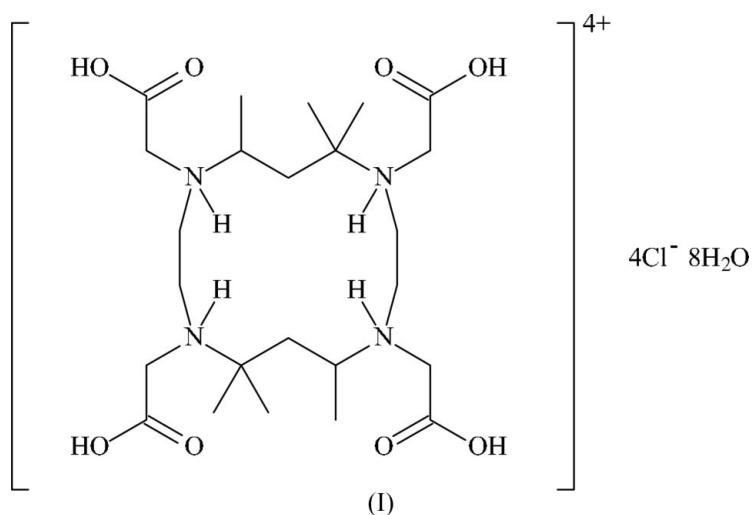
T = 295 K

Mean  $\sigma(\text{C}-\text{C}) = 0.002 \text{ \AA}$ 

R factor = 0.044

wR factor = 0.121

Data-to-parameter ratio = 16.4

For details of how these key indicators were automatically derived from the article, see <http://journals.iucr.org/e>.The unsubstituted parent compound exists in the zwitterionic form as two out of the four amine N atoms are protonated (Maurya *et al.*, 1991; Spirlet *et al.*, 1991). In the synthesis of such compounds, hydrochloric acid is usually added to precipitate the amino acid, but hydrochloric acid can be incorporated into the crystal structure, as was found in the present study.The 14-membered macrocycle in (I) lies on a center of inversion; each N atom is linked to a carboxymethyl group, but the macrocycle carries four positive charges arising from the protonation of the N atoms. The net charge is balanced by four chloride ions; the cation and anions interact with each other and with the water molecules of crystallization to furnish a hydrogen-bonded (Table 1) network structure. Another homolog, namely 1,4,7,10-tetrakis(*N*-carboxymethyl)-1,4,7,10-tetraazacyclododecane, crystallizes as a dihydrochloride pentahydrate; two of the four amine units of the 12-membered C<sub>8</sub>N<sub>4</sub> ring are protonated (Aime *et al.*, 1999).

Experimental

The tetraazamacrocycle  $\gamma$ -C-meso-5,5,7,12,12,14-hexamethyl-1,4,8,11-tetraazacyclotetradecane was synthesized according to the literature method of Hay *et al.* (1975). The macrocycle (0.28 g, 1 mmol) and five molar equivalents of ethyl bromoacetate (0.85 g, 5 mmol) were refluxed in 1 M sodium hydroxide for an hour. After the solution was cooled, 1 M hydrochloric acid was added to lower the pH to about unity. The solution was left in a refrigerator. Large colorless crystals separated and were collected and washed with water.

Crystal data

$C_{24}H_{48}N_4O_8^{4+} \cdot 4Cl^- \cdot 8H_2O$   
 $M_r = 806.59$   
 Triclinic,  $P\bar{1}$   
 $a = 8.6283$  (3) Å  
 $b = 10.6995$  (4) Å  
 $c = 11.0065$  (4) Å  
 $\alpha = 100.161$  (1)°  
 $\beta = 94.482$  (1)°  
 $\gamma = 103.168$  (1)°  
 $V = 966.42$  (6) Å<sup>3</sup>

$Z = 1$   
 $D_x = 1.386$  Mg m<sup>-3</sup>  
 Mo  $K\alpha$  radiation  
 Cell parameters from 8332 reflections  
 $\theta = 2.4$ – $28.3$ °  
 $\mu = 0.38$  mm<sup>-1</sup>  
 $T = 295$  (2) K  
 Block, colorless  
 $0.35 \times 0.22 \times 0.18$  mm

Data collection

Bruker APEX area-detector diffractometer  
 $\varphi$  and  $\omega$  scans  
 Absorption correction: none  
 11066 measured reflections  
 4351 independent reflections

4153 reflections with  $I > 2\sigma(I)$   
 $R_{int} = 0.017$   
 $\theta_{max} = 27.5$ °  
 $h = -11 \rightarrow 11$   
 $k = -13 \rightarrow 13$   
 $l = -14 \rightarrow 14$

Refinement

Refinement on  $F^2$   
 $R[F^2 > 2\sigma(F^2)] = 0.044$   
 $wR(F^2) = 0.121$   
 $S = 1.05$   
 4351 reflections  
 265 parameters  
 H atoms treated by a mixture of independent and constrained refinement

$w = 1/[\sigma^2(F_o^2) + (0.0657P)^2 + 0.404P]$   
 where  $P = (F_o^2 + 2F_c^2)/3$   
 $(\Delta/\sigma)_{max} = 0.001$   
 $\Delta\rho_{max} = 0.37$  e Å<sup>-3</sup>  
 $\Delta\rho_{min} = -0.34$  e Å<sup>-3</sup>

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

$D-H \cdots A$	$D-H$	$H \cdots A$	$D \cdots A$	$D-H \cdots A$
$O1-H1o \cdots O1w$	0.85 (1)	1.67 (1)	2.514 (2)	171 (3)
$O3-H3o \cdots O2w^i$	0.85 (1)	1.69 (1)	2.541 (2)	173 (3)
$O1w-H1w1 \cdots O4^{ii}$	0.85 (1)	2.17 (3)	2.889 (2)	143 (4)
$O1w-H1w2 \cdots Cl1$	0.85 (1)	2.40 (1)	3.221 (2)	163 (3)
$O2w-H2w1 \cdots O2^{iii}$	0.84 (1)	2.00 (2)	2.767 (2)	152 (3)
$O2w-H2w2 \cdots Cl1^{iv}$	0.84 (1)	2.25 (1)	3.087 (2)	179 (2)
$O3w-H3w1 \cdots Cl1$	0.85 (1)	2.41 (2)	3.198 (2)	156 (3)
$O3w-H3w2 \cdots Cl2$	0.85 (1)	2.40 (1)	3.216 (2)	163 (3)
$O4w-H4w1 \cdots Cl1^v$	0.85 (1)	2.47 (1)	3.313 (2)	170 (3)
$O4w-H4w2 \cdots Cl2^v$	0.85 (1)	2.38 (2)	3.172 (2)	157 (3)
$N1-H1n \cdots O4w$	0.86 (1)	2.02 (1)	2.869 (2)	174 (2)
$N2-H2n \cdots Cl2^{vi}$	0.86 (1)	2.32 (1)	3.173 (2)	170 (2)

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

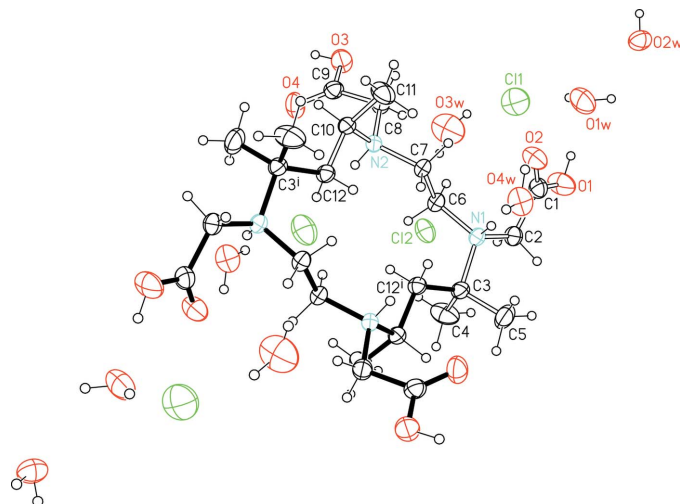


Figure 1  
 ORTEPII plot (Johnson, 1976) of (I), showing the atom-numbering scheme. Displacement ellipsoids are drawn at the 50% probability level and H atoms are drawn as spheres of arbitrary radii. [Symmetry code: (i)  $2 - x, 1 - y, 1 - z$ .]

The carbon-bound H atoms were positioned geometrically [ $C-H = 0.96$ – $0.98$  Å and  $U_{iso} = 1.2U_{eq}(C)$ , or  $1.5U_{eq}(C)$  for methyl H atoms] and were included in the refinement in the riding-model approximation. The water, acid and amino H atoms were located in difference Fourier maps, and were refined with distance restraints of  $O-H = N-H = 0.85$  (1) Å.

Data collection: SMART (Bruker, 2002); cell refinement: SAINT (Bruker, 2002); data reduction: SAINT; program(s) used to solve structure: SHELXS97 (Sheldrick, 1997); program(s) used to refine structure: SHELXL97 (Sheldrick, 1997); molecular graphics: ORTEPII (Johnson, 1976); software used to prepare material for publication: SHELXL97.

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References

Aime, S., Barge, A., Bruce, J. I., Botta, M., Howard, J. A. K., Moloney, J. M., Parker, D., de Sousa, A. S. & Woods, M. (1999). *J. Am. Chem. Soc.* **121**, 5762–5771.  
 Bruker (2002). SAINT and SMART. Bruker AXS Inc., Madison, Wisconsin, USA.  
 Hay, R. W., Lawrence, G. A. & Curtis, N. F. (1975). *J. Chem. Soc. Perkin Trans. 1*, pp. 591–593.  
 Johnson, C. K. (1976). ORTEPII. Report ORNL-5138. Oak Ridge National Laboratory, Tennessee, USA.  
 Maurya, M. R., Zaluzec, E. J., Pavkovic, S. F. & Herlinger, A. W. (1991). *Inorg. Chem.* **30**, 3657–3662.  
 Sheldrick, G. M. (1997). SHELXS97 and SHELXL97. University of Göttingen, Germany.  
 Spirlet, M. R., Rebizant, J., Barthelemy, P. P. & Desreux, J. F. (1991). *J. Chem. Soc. Dalton Trans.* pp. 2477–2481.