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N,*N*,*N*′,*N*′-Tetrakis(carboxymethyl)-2,2′-(ethylenedioxy)dianilinium dichloride dihydrate

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Key indicators

Single-crystal X-ray study
T = 119 K
Mean σ(C–C) = 0.002 Å
R factor = 0.034
wR factor = 0.097
Data-to-parameter ratio = 15.9

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

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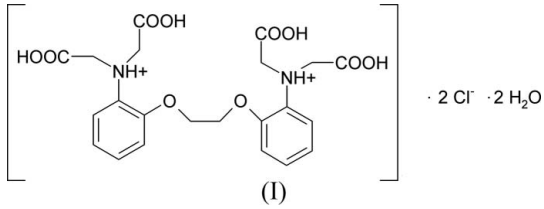
In the title compound, $C_{22}H_{26}N_2O_{10}^{2+}\cdot 2Cl^-\cdot 2H_2O$, the asymmetric unit contains one-half cation, one chloride ion and one water molecule. The cation is located on a center of inversion. The system containing both benzene rings and the linker between them is almost planar, while the acid side-chains are oriented nearly perpendicular to that plane. The crystal structure is stabilized by several hydrogen bonds and also by ionic interactions.

Comment

In the early 1980s Tsien (1980) introduced new calcium chelators and buffers, BAPTA [1,2-bis(2-aminophenoxy)-ethane-*N*,*N*,*N*′,*N*′-tetraacetic acid] and its derivatives. BAPTA is related in structure and function to EDTA (ethylenediaminetetraacetic acid) and EGTA (ethylene glycol tetraacetic acid), all three compounds having four acetic acid groups attached to N atoms. BAPTA has a high affinity not only for Ca^{2+}, but also for Fe^{2+} and Fe^{3+} (Britigan *et al.*, 1998). BAPTA can also induce cytoskeleton disassembly (Saoudi *et al.*, 2004) and affect Ca^{2+}-activated K^+ currents (Lancaster & Batchelor, 2000). The usage of BAPTA-type Ca^{2+} buffers allows control of cytosolic calcium level (Pethig *et al.*, 1989).

At this time there is no reported crystal structure of BAPTA, although structures of similar molecules and a complex of FBAPTA (5,5′-difluoro-1,2-bis(2-aminophenoxy)ethane-*N*,*N*,*N*′,*N*′-tetraacetic acid) with Ca^{2+} have been reported (Gerig *et al.*, 1987). Similar structures include tetramethyl 1,2-bis(2-aminophenoxy)ethane-*N*,*N*,*N*′,*N*′-tetraacetate (Rademeyer *et al.*, 2004) and 1,2-bis(2-aminophenoxy)ethane (Rademeyer *et al.*, 2005). In this paper we report the crystal structure of 1,2-bis(2-aminophenoxy)ethane-*N*,*N*,*N*′,*N*′-tetraacetic acid dihydrochloride dihydrate, (I).



(I)

The asymmetric unit of (I) contains one half-cation of diprotonated BAPTA as well as one chloride ion and one water molecule (Fig. 1). The BAPTA cation is located on a center of inversion. The structure of (I) is stabilized mainly by ionic interactions and hydrogen bonding (Table 1, Fig. 2). Two of the O atoms (O1 and O2) are not involved in hydrogen

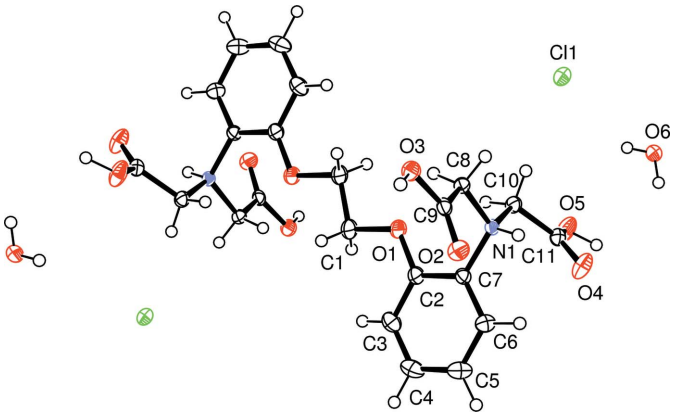


Figure 1
The molecular structure and atom-labeling scheme for (I), with displacement ellipsoids drawn at the 50% probability level. H atoms are drawn as spheres of arbitrary radius. Only atoms in the asymmetric unit are labeled [unlabeled atoms are generated by symmetry code $(2-x,1-y,1-z)$].

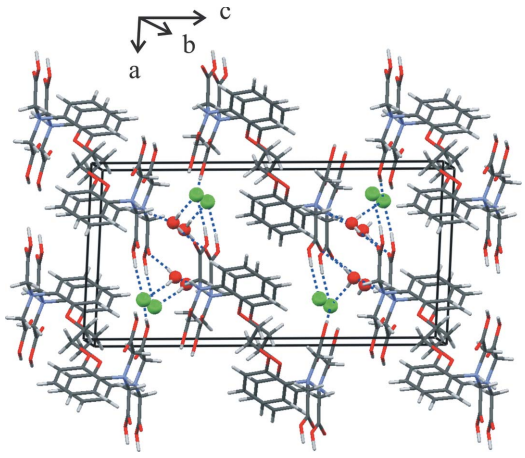


Figure 2
The crystal packing of (I) with the chloride ion and O atom of the water molecule shown as spheres. Hydrogen bonds are drawn as dashed lines.

bonds. The water molecule participates in three hydrogen bonds – as a donor for two and an acceptor in one. The Cl atom is an acceptor for three O—H···Cl^- hydrogen bonds.

The system containing both benzene rings and the linker between them is almost planar, with the torsion angle for C1—O1—C2—C3 being the largest variant at 6.2 (2)°. This is very similar to the conformation found in one of the molecules in the structure of tetramethyl 1,2-bis(2-aminophenoxy)ethane-*N*,*N*,*N*′,*N*′-tetraacetate (Rademeyer *et al.*, 2004). The torsion angles C7—N1—C8—C9 and C7—N1—C10—C11 are 59.2 (1) and −72.1 (1)°, respectively. The corresponding angles in the structure of FBAPTA with Ca^{2+} (Gerig *et al.*, 1987) are completely different, indicating that the BAPTA molecule has significant conformational flexibility.

Experimental

BAPTA-AM [1,2-bis(2-aminophenoxy)ethane-*N*,*N*,*N*′,*N*′-tetraacetic acid tetrakis(acetoxymethyl ester)] was purchased from Sigma. Crystallization was performed at room temperature from a solution in 1 *M* HCl. The 1 *M* HCl hydrolyzed the ester bonds, removing the acetoxymethyl ester group from the end of each of the four chains, resulting in crystals of BAPTA [1,2-bis(2-aminophenoxy)ethane-*N*,*N*,*N*′,*N*′-tetraacetic acid] dihydrochloride dihydrate, which were used for X-ray diffraction experiments.

Crystal data

$C_{22}H_{26}N_2O_{10}^{2+}\cdot 2Cl^-\cdot 2H_2O$
M_r = 585.38
Monoclinic, $P2_1/c$
a = 10.358 (1) Å
b = 6.183 (1) Å
c = 20.726 (1) Å
β = 92.48 (1)°
V = 1326.1 (3) Å^3
Z = 2
D_x = 1.466 Mg m^{-3}
Mo $K\alpha$ radiation
μ = 0.31 mm^{-1}
T = 119 (2) K
Needle, colorless
0.48 × 0.06 × 0.05 mm

Data collection

Rigaku R-AXIS RAPID diffractometer
ω scans
Absorption correction: multi-scan (Otwinowski *et al.*, 2003)
T_{min} = 0.98, T_{max} = 0.99
104679 measured reflections
3680 independent reflections
3028 reflections with $I > 2\sigma(I)$
R_{int} = 0.045
θ_{max} = 29.6°

Refinement

Refinement on F^2
$R[F^2 > 2\sigma(F^2)]$ = 0.034
$wR(F^2)$ = 0.098
S = 1.07
3680 reflections
232 parameters
All H-atom parameters refined
$w = 1/[\sigma^2(F_o^2) + (0.055P)^2 + 0.2141P]$ where $P = (F_o^2 + 2F_c^2)/3$
$(\Delta/\sigma)_{max}$ = 0.001
$\Delta\rho_{max}$ = 0.39 e Å^{-3}
$\Delta\rho_{min}$ = −0.20 e Å^{-3}

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

D—H···A	D—H	H···A	D···A	D—H···A
O3—HO3···Cl1^{i}	0.91 (2)	2.09 (2)	2.9968 (11)	171 (2)
N1—HN1···O6^{ii}	0.89 (2)	1.84 (2)	2.7146 (14)	165 (2)
O6—HO6*A*···Cl1^{iii}	0.81 (2)	2.43 (2)	3.2378 (12)	170 (2)
O6—HO6*B*···O4^{iv}	0.79 (3)	2.10 (3)	2.8761 (15)	166 (3)
O5—HO5···Cl1^{iii}	0.98 (3)	2.01 (3)	2.9862 (11)	174 (2)

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

Refined C—H distances are in the range 0.90 (2)–1.010 (18) Å.

Data collection: *HKL-2000* (Otwinowski & Minor, 1997); cell refinement: *HKL-2000*; data reduction: *HKL-2000*; program(s) used to solve structure: *HKL-3000SM* (Minor *et al.*, 2006) and *SHELXS97* (Sheldrick, 1997); program(s) used to refine structure: *HKL-3000SM* and *SHELXL97* (Sheldrick, 1997); molecular graphics: *HKL-3000SM*, *ORTEPIII* (Burnett & Johnson, 1996), *ORTEP-3* (Farrugia, 1997) and *Mercury* (Macrae *et al.*, 2006); software used to prepare material for publication: *HKL-3000SM*.

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