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(+)-(*Z*)-(1*S*,2*S*,3*S*,4*R*,1′*S*,2′*S*,3′*S*,4′*R*,5′*R*)-2,3,4-Trihydroxy-5-(hydroxymethyl)-*N*-[2′,3′,4′-trihydroxy-5′-(hydroxymethyl)cyclohex-1′-yl]-cyclohex-5-en-1-aminium chloride dihydrate

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Key indicators

Single-crystal X-ray study
T = 295 K
Mean σ(C–C) = 0.002 Å
Disorder in main residue
R factor = 0.038
wR factor = 0.093
Data-to-parameter ratio = 12.8

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

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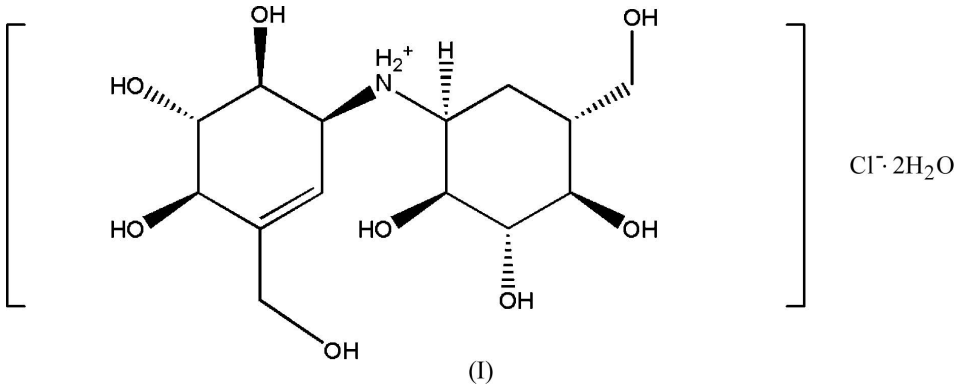
In the crystal structure of the title compound, $C_{14}H_{26}NO_8^+\cdot Cl^-\cdot 2H_2O$, both the cation and anion lie on special positions of site symmetry 2. The cation and anion, along with the water molecules of crystallization, are linked into a three-dimensional network by extensive hydrogen bonds.

Comment

The hydrochloride salt of the pseudo-amino sugar validamine (Kameda *et al.*, 1985) was obtained by treating the primary compound with hydrogen chloride. We have previously reported the crystal structure (Chang *et al.*, 2004) and noted that it features extensive hydrogen bonding arising from interactions amongst the ammonium and hydroxy groups. We have also characterized *N*-dihydroxypropylvalidamine as the picrate salt (Zhu *et al.*, 2005). The present report details the crystal struture of *N*-[2,3,4-trihydroxy-5-(hydroxymethyl)cyclohex-5-en-1-yl]validamine, (I), which has been isolated as the dihydrated hydrochloride (Fig. 1).



(I)

Compound (I), or validoxylamine as it is called, was obtained from validamcycin A, the most active of the validamycin compounds (Asano *et al.*, 1991). The presence of the C═C double bond in the hydrochloride salt is indicated by the solution ^{1}H NMR signal at 5.98 p.p.m. and also by the solution ^{13}C NMR signals at 114.21 and 147.34 p.p.m.

The cation and anion both lie on special positions of site symmetry 2. This symmetry element relates the trihydroxy(hydroxymethyl)cyclohexyl group to the trihydroxy(hydroxymethyl)cyclohexenyl group. The cyclohexyl ring adopts a chair conformation and the cyclohexenyl ring adopts a half-chair conformation. The bulky substituents increase the C—N—C angle somewhat [116.4 (2)°].

In the crystal structure, the cation interacts with the chloride anion and the water molecules through extensive hydrogen bonds (Table 1), giving rise to a network motif.

Experimental

Validoxylamine was synthesized by hydrolysis of validamycin A (Asano *et al.*, 1991). A solution of validoxylamine hydrate (1 g, 2.83 mmol) in water (5 ml) was treated with 2 *N* hydrochloric acid to a pH of 3.0. The solution was evaporated to dryness to yield a colorless compound that was recrystallized from 80% aqueous ethanol (yield 0.8 g; m.p. 385–386 K). ^{1}H NMR (300 MHz, D_2O): δ 1.75–1.88 (*m*, 2H), 2.27 (*d*, 1H, J = 15 Hz), 3.43 (*t*, 1H, J = 9 Hz), 3.65 (*t*, 1H, J = 9 Hz), 3.72–3.83 (*m*, 2H), 3.88–3.93 (*m*, 3H), 4.10–4.21 (*m*, 2H), 4.31 (*m*, 3H), 5.98 (*s*, 1H). ^{13}C NMR (75 MHz, D_2O): δ 25.00, 38.86, 58.02, 59.27, 61.78, 62.01, 66.83, 70.85, 70.90, 72.30, 72.36, 74.39, 114.21, 147.34 p.p.m.. ESI–MS *m*/*z*: 336 (M^+ + 1).

Crystal data

$C_{14}H_{26}NO_8^+\cdot Cl^-\cdot 2H_2O$
M_r = 407.84
Tetragonal, $P4_32_12$
a = 7.9421 (3) Å
c = 29.028 (1) Å
V = 1831.00 (7) Å^3
Z = 4
D_x = 1.479 Mg m^{-3}
Mo $K\alpha$ radiation
Cell parameters from 7629 reflections
θ = 2.6–27.0°
μ = 0.26 mm^{-1}
T = 295 (2) K
Block, colorless
0.47 × 0.38 × 0.34 mm

Data collection

Bruker AXS SMART 1000 CCD diffractometer
φ and ω scans
Absorption correction: multi-scan (*SADABS*; Sheldrick, 1996)
T_{min} = 0.887, T_{max} = 0.916
10894 measured reflections
2006 independent reflections
1894 reflections with $I > 2\sigma(I)$
R_{int} = 0.064
θ_{max} = 27.0°
$h = -10 \rightarrow 9$
$k = -9 \rightarrow 10$
$l = -32 \rightarrow 37$

Refinement

Refinement on F^2
$R[F^2 > 2\sigma(F^2)]$ = 0.038
$wR(F^2)$ = 0.093
S = 1.10
2006 reflections
157 parameters
H atoms treated by a mixture of independent and constrained refinement
$w = 1/[\sigma^2(F_o^2) + (0.044P)^2 + 0.4597P]$ where $P = (F_o^2 + 2F_c^2)/3$
$(\Delta/\sigma)_{max} < 0.001$
$\Delta\rho_{max}$ = 0.18 e Å^{-3}
$\Delta\rho_{min}$ = −0.28 e Å^{-3}
Absolute structure: Flack (1983), 746 Friedel pairs
Flack parameter: 0.16 (9)

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

D—H···A	D—H	H···A	D···A	D—H···A
O1—H1*O*···O1*W*	0.85 (1)	1.89 (1)	2.715 (2)	168 (3)
O2—H2*O*···O1*W*^{i}	0.85 (1)	1.96 (1)	2.781 (2)	162 (3)
O3—H3*O*···O2^{ii}	0.85 (1)	1.91 (1)	2.750 (2)	173 (3)
O4—H4*O*···Cl1	0.85 (1)	2.29 (1)	3.137 (1)	176 (3)
N1—H1*N*···O1	0.85 (1)	2.19 (3)	2.699 (2)	118 (3)
N1—H1*N*···Cl1^{iii}	0.85 (1)	2.69 (1)	3.111 (2)	112 (1)
O1*W*—H1*W*1···O3^{iv}	0.85 (1)	1.97 (1)	2.799 (2)	166 (2)
O1*W*—H1*W*2···O4^{v}	0.85 (1)	1.87 (1)	2.726 (2)	175 (3)

Symmetry codes: (i) $x-\frac{1}{2}, -y+\frac{1}{2}, -z+\frac{5}{4}$; (ii) $y, x, -z+1$; (iii) $y+\frac{1}{2}, -x+\frac{1}{2}, z+\frac{1}{4}$; (iv) $y+1, x, -z+1$; (v) $y+\frac{1}{2}, -x+\frac{3}{2}, z+\frac{1}{4}$.

The Flack (1983) refinement indicates the possibility of some inversion twinning. The cation lies on a twofold axis; as this symmetry element relates the trihydroxy(hydroxymethyl)cyclohexyl group to the trihydroxy(hydroxymethyl)cyclohexenyl group, the cation is disordered with respect to the four atoms, *i.e.* C1/C5/C6/C7 and C1′/C5′/C6′/C7′. The —C1—C5═C6—C7— set of atoms has the double bond in a *trans* configuration; the unprimed atoms belong to the cyclohexenyl ring, whereas the primed C atoms belong to the cyclohexyl ring. The anisotropic displacement parameters of the primed atoms were set equal to those of the unprimed atoms; additionally, the C1—C6 distance was restrained to within 0.01 Å of the C1′–C6′ distance. The C4–C5 and C5–C7 distances were similarly restrained. The carbon-bound H atoms were placed at calculated positions [methine C—H = 0.98 Å, methylene C—H = 0.97 Å, double bond C—H = 0.93 Å; U_{iso}(H) = 1.2U_{eq}(C)] and were included in the refinement in the riding-model approximation. The hydroxy, water and ammonium H atoms were located in difference Fourier maps and were refined with distance restraints of O—H = N—H = 0.85 (1) Å and H···H = 1.39 (1) Å.

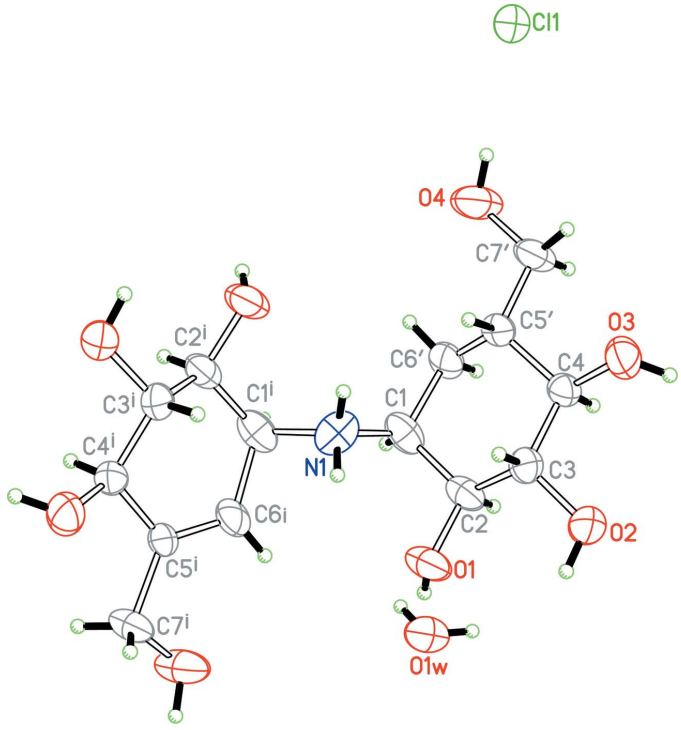


Figure 1
An *ORTEPII* plot (Johnson, 1976) of compound (I), showing the atom-numbering scheme. Displacement ellipsoids are drawn at the 50% probability level and H atoms as spheres of arbitrary radii [symmetry code: (i) $1+y, x-1, 1-z$].

Data collection: *SMART* (Bruker, 2003); cell refinement: *SAINT* (Bruker, 2003); 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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