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Key indicators

Single-crystal X-ray study T = 291 K Mean σ (C–C) = 0.003 Å R factor = 0.037 wR factor = 0.099 Data-to-parameter ratio = 14.9

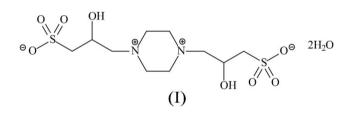
For details of how these key indicators were automatically derived from the article, see http://journals.iucr.org/e.

2,2'-Dihydroxy-3,3'-(piperazinediium-1,4-diyl)bis(propanesulfonate) dihydrate

The buffer reagent piperazine-1,4-diylbis(2-hydroxypropanesulfonic acid) (PBHPS), when crystallized from an aqueous solution, exists as the title centrosymmetric hydrated zwitterion, $C_{10}H_{22}N_2O_8S_2\cdot 2H_2O$. The zwitterion and solvent water molecules are linked by hydrogen bonds into a threedimensional network.

Comment

Piperazine-1,4-diylbis(2-hydroxypropanesulfonic acid), abbreviated PBHPS, is used as a buffer (Mash *et al.*, 2003; Wiedmer *et al.*, 2005), the crystal structure of which has not been reported to date. The compound exists as a centrosymmetric dihydrated piperazinium-1,4-bis(2-hydroxypropylsulfonate) zwitterion, (I) (Fig. 1). The six-membered piperazinium ring adopts the common chair conformation and the two 2-hydroxypropylsulfonate substitutents occupy equatorial positions. The structure is stabilized by extensive hydrogen-bonding interactions which give rise to a threedimensional network (Table 1).



Another piperazine-sulfonate type of buffer, 4-(2hydroxyethyl)-1-piperazineethylsulfonic acid (HEPES), also exists as a zwitterionic molecule that interacts with adjacent zwitterions, but the hydrogen bonds lead to a sheet structure

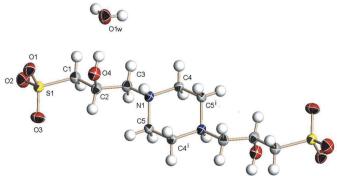


Figure 1

The structure of (I). Displacement ellipsoids are drawn at the 50% probability level, and H atoms are shown as spheres of arbitrary radii. The di-zwitterion lies on a centre of inversion [symmetry code: (i) 1 - x, 1 - y, 1 - z.]

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Received 13 July 2006 Accepted 15 July 2006 (Wouters *et al.*, 1996). A second orthorhombic HEPES polymorph is also known, in which the H atom was found to be bonded to the sulfonate group (Gao *et al.*, 2004).

Experimental

Commerically available piperazine-1,4-diylbis(2-hydroxypropanesulfonic acid) (0.38 g, 1.0 mmol) was dissolved in methanol (15 ml). The pH of the solution was adjusted to about 7.5 by the addition of drops of hydrochloric acid. The clear solution was set aside for a week for crystals of (I) to form.

Crystal data

 $\begin{array}{l} C_{10}H_{22}N_2O_8S_2\cdot 2H_2O\\ M_r = 398.45\\ Monoclinic, \ P2_1/n\\ a = 8.6675 \ (8) \ \mathring{A}\\ b = 7.2050 \ (6) \ \mathring{A}\\ c = 13.198 \ (1) \ \mathring{A}\\ \beta = 96.859 \ (1)^\circ\\ V = 818.31 \ (12) \ \mathring{A}^3 \end{array}$

Data collection

 Bruker APEXII area-detector diffractometer
φ and ω scans
Absorption correction: none
4919 measured reflections

Refinement

Refinement on F^2 $R[F^2 > 2\sigma(F^2)] = 0.037$ $wR(F^2) = 0.099$ S = 1.031865 reflections 125 parameters H atoms treated by a mixture of

independent and constrained refinement

Z = 2 $D_x = 1.617 \text{ Mg m}^{-3}$ Mo K α radiation $\mu = 0.38 \text{ mm}^{-1}$ T = 291 (2) K Block, colourless $0.21 \times 0.14 \times 0.05 \text{ mm}$

1865 independent reflections 1551 reflections with $I > 2\sigma(I)$ $R_{\text{int}} = 0.021$ $\theta_{\text{max}} = 27.5^{\circ}$

$$\begin{split} w &= 1/[\sigma^2(F_o^2) + (0.0464P)^2 \\ &+ 0.5041P] \\ \text{where } P &= (F_o^2 + 2F_c^2)/3 \\ (\Delta/\sigma)_{\text{max}} &= 0.001 \\ \Delta\rho_{\text{max}} &= 0.38 \text{ e} \text{ Å}^{-3} \\ \Delta\rho_{\text{min}} &= -0.24 \text{ e} \text{ Å}^{-3} \end{split}$$

Table 1

Hydrogen-bond geometry (Å, °).

$D - H \cdots A$	D-H	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - \mathbf{H} \cdots A$
O4−H4 <i>O</i> ···O1 <i>W</i>	0.85(1)	1.89(1)	2.732 (3)	174 (2)
$O1W-H1W2\cdots O2^{i}$	0.84(1)	1.90 (2)	2.698 (2)	157 (3)
O1W−H1W1···O4 ⁱⁱ	0.84(1)	2.28 (3)	2.824 (2)	123 (3)
$N1 - H1N \cdots O1^{ii}$	0.85 (1)	2.09 (2)	2.834 (2)	147 (2)

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

Carbon-bound H atoms were positioned geometrically (C–H = 0.97 and 0.98 Å) and were included in the refinement in the ridingmodel approximation, with $U_{iso}(H) = 1.2U_{eq}(C)$. The ammonium and water H atoms were located in a difference Fourier map and were refined with a distance restraint of N–H = O–H = 0.85 (1) Å.

Data collection: *SMART* (Bruker, 2004); cell refinement: *SAINT* (Bruker, 2004); 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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