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Key indicators

Single-crystal X-ray study T = 293 K Mean σ (C–C) = 0.004 Å R factor = 0.026 wR factor = 0.064 Data-to-parameter ratio = 9.3

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

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Ethylenediammonium disodium (1-hydroxyethylidene)diphosphonate tetrahydrate, $[NH_3(CH_2)_2NH_3]Na_2(hedp)\cdot 4H_2O$

The title structure, $C_2H_{10}N_2^{2+}\cdot 2Na^+\cdot C_2H_4O_7P_2^{4-}\cdot 4H_2O$ or $(NH_3CH_2CH_2NH_3)Na_2(hedp)\cdot 4H_2O$ (SDP-2) (hedp = 1-hydroxyethylidenediphosphonate), contains one-dimensional anionic sodium-hedp chains which are connected by N-H···O and O-H···O hydrogen bonds. There are two crystallographically independent P atom environments.

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Comment

Hydroxyethane-1,1-diphosphonic acid (H₄hedp), which has a characteristic P-C-P linkage, finds applications in biomedical areas, water treatment, ion exchange and lipophilic solvent extraction (Francis *et al.*, 1969; Jurisson *et al.*, 1993). Recently, owing to its versatile coordination abilities with metal ions, the compound has been introduced into the field of materials and used as a polydentate ligand to construct novel structures with special properties (Serezhkin *et al.*, 2000; Sergienko, 2000; Nash *et al.*, 1998). Hedp possesses seven active O atoms, so, at most, it can serve as a heptadentate ligand. Furthermore, the CH₃ and OH groups attached to the organic tether of hedp provide not only steric hindrance, but also a possible hydrophobic or hydrophilic environment which may be important in the self-assembly of some metal diphosphonates.



More recently, many efforts have been devoted to synthesizing open-framework metal-hedp compounds. The idea was highlighted by the studies on $Sn_2(hedp)$ (Zapf *et al.*, 1996). Attempting to obtain novel structures, Zheng et al. (2000, 2002), using different organic amines as the template, synthesized several metal-hedp compounds with different structures (see also Song et al., 2001). The authors attributed the structural differences among the compounds to the effect of the templates employed. The smaller size template NH₂CH₂CH₂NH₂ (en) directed the formation of a linear single chain compound, while the larger size templates such as $NH_2(CH_2)_m NH_2$ (m = 4, 5, 6) directed the formation of anionic double chains which were held together by strong hydrogen bonds to form three-dimensional channels. The use of organic amines as templates in the above synthetic process is relatively new; this not only diversifies the members of the family but





The asymmetric unit of SDP-2, with the atomic labeling scheme. Displacement ellipsoids are drawn at the 50% probability level. Dashed lines indicate hydrogen-bonding interactions.

also adds a promising direction for future studies of the compounds.

In the present paper, we describe the synthesis and crystal structure of a new member of the metal-hedp series, $(NH_3CH_2CH_2NH_3)Na_2(hedp)\cdot 4H_2O$ (designated as SDP-2, SDP is sodium diphosphonate), (I).

The fundamental building units of SDP-2 are the extended one-dimensional anionic $[Na_2(hedp)(H_2O)_3]^{2-}$ chains along the b axis; these are charge-balanced by enH_2^{2+} cations and linked together by hydrogen bonds (Figs. 1 and 2). Within a chain, two kinds of Na atom environment are found. The Na1 atom links with the hedp ligand through atoms O1 and O7 from one ligand and $O3^i$, $O4^i$ and $O5^i$ [symmetry code: (i) x, 1 + y, z] from another neighboring ligand. By contrast, there are three bonds from water molecules (O8, O9 and O10) and three bonds from the hedp ligand through O3, O5 and O7 contributing to the coordination of Na2. For the two tetrahedrally coordinated P atoms in the ligand, there are two pendant P=O bonds, namely P1=O2 and P2=O6, with lengths 1.5231 (19) and 1.514 (2) Å, respectively. In comparison with the P=O bond lengths in H₄hedp and other metalhedp compounds, the distance is greater; this can be explained by the fact that there are strong hydrogen bonds between P=O and enH_2^{2+} . Here hedp acts as a pentadentate ligand, bridging the Na atoms through four ionized O(P) atoms of the two diphosphonate groups and the protonated O(C) atom of the hydroxyl group. The torsion angles for O2-P1-C1-P2 and O6-P2-C1-P1 are -166.84 (12) and -166.68 (15)°, respectively. In structural contrast between SDP-2 and another disodium 1-hydroxylidenediphosphonate tetrahydrate (Barnett & Strickland, 1979), the effect of ethylenediamine on tailoring the structure of the sodium 1hydroxylidenediphosphonate is obvious. Between the chains, protonated enH2²⁺ acts as a charge-compensating cation and also bridges the chains through N-H···O hydrogen bonds. Three coordinated water molecules (O8, O9 and O10) and one





SDP-2 structure viewed along [010]. Displacement ellipsoids are drawn at the 60% probability level. Key: C atoms, gray; H atoms, white; N atoms, yellow; P atoms, green; Na atoms, red; O atoms, blue).

luncoordinated water molecule (O11) also contribute to the hydrogen-bonding motif (see Table 2). These strong hydrogen bonds help stabilize the crystal structure.

Experimental

All starting materials were analytically pure and were used without further purification. SDP-2 was prepared by the following method. Na₄C₂H₄O₇P₂, NH₄F (ammonium fluoride), H₂O (deionized water) and C₄H₈O₂ (dioxane), in a 1:0.2:80:2 molar ratio, were stirred at ambient temperature in a plastic container. Ethylenediamine was added dropwise to the mixture until a pH of 10 was achieved. Stirring was continued until a homogeneous white gel formed. The container was covered with a watch glass, and left undisturbed at ambient temperature. After two weeks, transparent colorless crystals began to form. The purity of SDP-2 was verified by elemental analysis: calculated for C₄H₂₂N₂Na₂O₁₁P₂ (wt%): C 12.57, H 5.81, N 7.33, Na 12.03, P 16.21; found: C 11.90, H 4.73, N 7.07, Na 11.85, P 15.30. FT-IR (KBr pellet, v cm⁻¹: 3259, 3103, 2993, 2988, 2130, 1719, 1648, 996, 955, 885, 806, 733. ¹³C CP/MAS NMR (external reference: DSS, δ p.p.m.): 22.8 (CH₃), 36.7 (CH₂CH₂), and 72.1 (=C); ³¹P MAS NMR (external reference: 85% H₃PO₄, δ p.p.m.): 20.1 and 17.9.

Crystal data

$C_2H_{10}N_2^{2+}\cdot 2Na^+\cdot C_2H_4O_7P_2^{4-}\cdot 4H_2O$	Mo $K\alpha$ radiation
$M_r = 382.16$	Cell parameters from 2203
Orthorhombic, Pna2 ₁	reflections
$a = 20.966 (7) \text{ Å}_{1}$	$\theta = 1.9-25.0^{\circ}$
$b = 5.8928 (18) \text{\AA}$	$\mu = 0.41 \text{ mm}^{-1}$
c = 11.871 (4) Å	T = 293 (2) K
$V = 1466.6 (8) \text{ Å}^3$	Block, colorless
Z = 4	$0.20 \times 0.10 \times 0.10 \text{ mm}$
$D_x = 1.731 \text{ Mg m}^{-3}$	
Data collection	
Bruker SMART CCD	2203 independent reflections
diffractometer	2021 reflections with $I > 2\sigma(I)$
ρ and ω scans	$R_{\rm int} = 0.025$
Absorption correction: multi-scan	$\theta_{\rm max} = 25.0^{\circ}$
(SADABS; Sheldrick, 1996)	$h = -24 \rightarrow 22$
$T_{\min} = 0.922, \ T_{\max} = 0.960$	$k = -7 \rightarrow 4$
5700 measured reflections	$l = -12 \rightarrow 14$

Refinement

Refinement on F^2	$w = 1/[\sigma^2(F_o^2) + (0.0395P)^2]$
$R[F^2 > 2\sigma(F^2)] = 0.026$	where $P = (F_o^2 + 2F_c^2)/3$
$wR(F^2) = 0.064$	$(\Delta/\sigma)_{\rm max} = 0.001$
S = 1.06	$\Delta \rho_{\rm max} = 0.27 \ {\rm e} \ {\rm \AA}^{-3}$
2203 reflections	$\Delta \rho_{\rm min} = -0.31 \text{ e} \text{ Å}^{-3}$
236 parameters	Absolute structure: Flack (1983)
H-atom parameters constrained	1217 Friedel pairs
	Flack parameter = $-0.10(10)$

Table 1

Selected geometric parameters (Å, °).

Na1-O1	2.312 (2)	P1-O2	1.5231 (19)
Na1-O7	2.316 (2)	P1-O1	1.5247 (19)
Na1-O5 ⁱ	2.348 (2)	P1-C1	1.855 (3)
Na1-O4 ⁱ	2.414 (3)	C1-O4	1.452 (3)
Na1-O3 ⁱ	2.553 (2)	C1-C2	1.522 (4)
Na2-O10	2.269 (3)	C1-P2	1.862 (3)
Na2-O9	2.351 (2)	P2-O6	1.514 (2)
Na2-O5	2.386 (2)	P2-O7	1.518 (2)
Na2-O8	2.399 (3)	P2-O5	1.5188 (19)
Na2-O3	2.418 (2)	N1-C3	1.477 (4)
Na2-O7	2.706 (3)	N2-C4	1.485 (4)
P1-O3	1.5219 (19)	C3-C4	1.521 (4)
O3-P1-O2	112.43 (11)	O4-C1-P2	102.90 (16)
O3-P1-O1	112.36 (11)	C2-C1-P2	110.51 (19)
O2-P1-O1	110.82 (11)	P1-C1-P2	114.33 (14)
O3-P1-C1	105.93 (11)	O6-P2-O7	113.40 (15)
O2-P1-C1	105.97 (12)	O6-P2-O5	112.44 (13)
O1-P1-C1	108.95 (11)	O7-P2-O5	110.53 (14)
O4-C1-C2	111.7 (2)	O6-P2-C1	105.57 (12)
O4-C1-P1	107.07 (17)	O7-P2-C1	106.62 (11)
C2-C1-P1	110.14 (18)	O5-P2-C1	107.83 (11)

Symmetry code: (i) x, 1 + y, z.

Table 3

Table 2			
Hydrogen-bonding	geometry	(Å,	°).

$D - H \cdots A$	<i>D</i> -H	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - H \cdots A$
N1-H1C···O7	0.92 (3)	1.80 (3)	2.689 (3)	160 (3)
O11−H11B···O1	0.86 (3)	1.99 (3)	2.804 (3)	158 (3)
$N1-H1A\cdots O5^{i}$	0.89 (3)	1.90 (3)	2.768 (3)	163 (3)
$N1 - H1B \cdot \cdot \cdot O6^{ii}$	0.89 (4)	1.98 (4)	2.850 (4)	165 (3)
$N2-H2A\cdots O2^{iii}$	0.91 (4)	1.76 (4)	2.669 (3)	177 (3)
$N2-H2B\cdots O1^{iv}$	0.90 (3)	1.91 (3)	2.781 (3)	163 (3)
$N2-H2C \cdot \cdot \cdot O8^{v}$	0.89 (4)	2.54 (4)	3.199 (4)	131 (3)
O4−H4···O11 ^{vi}	0.86 (4)	1.83 (4)	2.686 (3)	172 (3)
O8−H8A···O9 ^{vii}	0.85 (2)	2.04 (3)	2.869 (3)	165 (3)
$O8-H8B\cdots O6^{viii}$	0.85 (2)	1.83 (2)	2.664 (3)	165 (3)
$O9-H9B\cdots O2^{ix}$	0.86 (3)	1.80 (3)	2.653 (3)	175 (3)
O10−H10A···O6 ^{viii}	0.84 (3)	2.25 (2)	2.957 (4)	143 (3)
$O10-H10B\cdots O6^{ii}$	0.85 (3)	2.31 (2)	3.099 (4)	155 (3)
$O11-H11A\cdots O3^{i}$	0.85 (2)	1.88 (3)	2.668 (3)	154 (3)

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

H atoms of the hydroxy and protonated amino groups were found in difference Fourier maps and were not incorporated in the refinement. H atoms of methyl and methylene groups were placed in geometrically calculated positions and refined with a riding model, with bond distances constrained to 0.96 and 0.97 Å, respectively, and isotropic displacement parameters set at $1.5U_{eq}$ (1.2 for methylene) of the parent atoms. All water H atoms were refined with bond distances restrained to 0.89–0.92 Å, and isotropic displacement parameters set at $1.5U_{eq}$ of the parent atoms.

Data collection: *SMART* (Siemens, 1996); cell refinement: *SMART*; data reduction: *SAINT* (Siemens, 1996) and *SHELXTL* (Sheldrick, 2001); program(s) used to solve structure: *SHELXS97* (Sheldrick, 1997); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *SHELXTL*; software used to prepare material for publication: *SHELXTL*.

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