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#### **Key indicators**

Single-crystal X-ray study T = 298 KMean  $\sigma$ (C–C) = 0.012 Å R factor = 0.099 wR factor = 0.289 Data-to-parameter ratio = 11.4

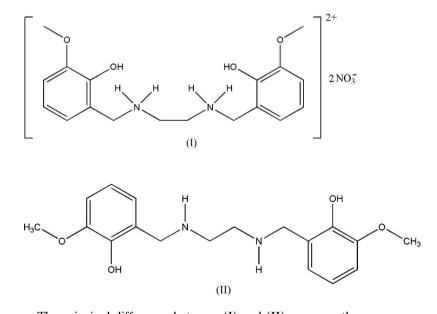
For details of how these key indicators were automatically derived from the article, see http://journals.iucr.org/e.

# 6,6'-Dimethoxy-2,2'-(ethane-1,2-diyldiammoniodimethylene)diphenol dinitrate

In the title compound,  $C_{18}H_{26}N_2O_4^{2+}\cdot 2NO_3^{-}$ , the ions are linked into two chains by  $C-H\cdots O$  hydrogen bonds; these chains are linked into sheets parallel to (001). The asymmetric unit consists of one cation, two half-cations and four anions. Two of the cations have a centre of symmetry at the mid-point of the central C-C bond.

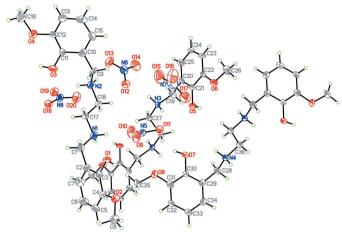
## Comment

*o*-Vanillin diamine derivatives are potentially multidentate ligands. During the course of studies on the coordination chemistry of *o*-vanillin ethylenediamine derivatives, we obtained crystals of the title compound, (I); we report here its crystal structure. The asymmetric unit consists of one cation, two half-cations and four anions. Two of the cations have a centre of symmetry at the mid-point of the central C—C bond (Fig. 1). The bond lengths and angles are normal (Allen *et al.*, 1987) and are in agreement with those in three similar compounds (Xia *et al.*, 2006, 2007*a,b*). The most closely related compound is 6,6'-dimethoxy-2,2'-(ethane-1,2-diyldiimino-dimethylene)diphenol, (II) (Xia *et al.*, 2006).



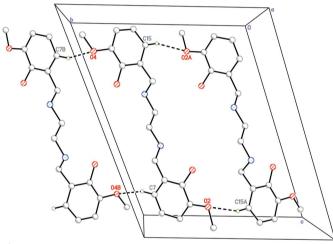
The principal difference between (I) and (II) concerns the intermolecular aggregation. In (I), the ions are linked into two chains of rings by  $C-H\cdots O$  hydrogen bonds. Atoms C7 and C15 in the molecule at (x, y, z) act as hydrogen-bond donors to methoxy atoms O4 in the molecule at (1 - x, 2 - y, 1 - z) and O2 in the molecule at (1 - x, 1 - y, 1 - z), respectively, generating a chain of  $R_2^2(26)$  rings (Bernstein *et al.*, 1995) along the *b*-axis direction (Fig. 2 and Table 1). In addition, atoms C27 and C36 in the molecule at (x, y, z) act as donors to

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### Figure 1

The structure of the independent ions of (I), showing the atom-labelling scheme. Displacement ellipsoids are drawn at the 30% probability level. Unlabelled atoms in the N4 cation are related to labelled atoms by (-x, -y, 1 - z). Unlabelled atoms in the N3 cation are related to labelled atoms by (-x, 1 - y, 1 - z).



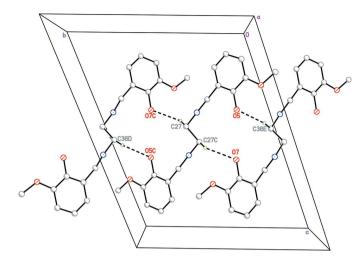
#### Figure 2

A portion of the crystal structure of (I), showing the formation of a hydrogen-bonded sheet built from  $C-H\cdots O$  interactions. For clarity, H atoms not involved in hydrogen bonding have been omitted. Dashed lines indicate hydrogen bonds. [Symmetry codes: (A) 1 - x, 1 - y, 1 - z; (B) 1 - x, 2 - y, 1 - z.]

hydroxy atoms O7 in the molecule at (-x, 1-y, 1-z) and O5 in the molecule at (-x, -y, 1-z), respectively, generating a chain of  $R_2^2(16)$  rings along the *b*-axis direction (Fig. 3 and Table 1). The nitrate anions occupy positions between the two chains, linking the ions into a sheet parallel to the (001) plane. There are no other types of intermolecular hydrogen bonds in the structure of (I) and there are no direction-specific interactions between adjacent sheets. By contrast, in (II), the molecules are linked into sheets by means of  $C-H \cdots O$  and  $O-H \cdots N$  hydrogen bonds; the latter are absent from the structure of (I).

## **Experimental**

To a solution of 6,6'-dimethoxy-2,2'-(ethane-1,2-diyldiiminodimethylene)diphenol (1 mmol) in methanol (20 ml) was added a



#### Figure 3

A portion of the crystal structure of (I), showing the formation of a hydrogen-bonded sheet built from  $C-H \cdots O$  interactions. For clarity, H atoms not involved in hydrogen bonding have been omitted. Dashed lines indicate hydrogen bonds. [Symmetry codes: (C) -x, 1 - y, 1 - z; (D) x, 1 + y, z; (E) -x, -y, 1 - z.]

solution of zinc(II) nitrate (1 mmol) in methanol (10 ml). The mixed solution was stirred for 2 h and then filtered. The solution was allowed to stand, slowly producing crystals of (I).

#### Crystal data

$C_{18}H_{26}N_2O_4^{2+}\cdot 2NO_3^{-}$	V = 2095 (3) Å <sup>3</sup>
$M_r = 458.43$	Z = 4
Triclinic, $P\overline{1}$	$D_x = 1.454 \text{ Mg m}^{-3}$
a = 11.799 (11)  Å	Mo $K\alpha$ radiation
b = 12.417 (11)  Å	$\mu = 0.12 \text{ mm}^{-1}$
c = 16.354 (15)  Å	T = 298 (2) K
$\alpha = 109.127 \ (12)^{\circ}$	Block, colourless
$\beta = 110.774 \ (12)^{\circ}$	$0.38 \times 0.19 \times 0.14 \text{ mm}$
$\gamma = 90.582 \ (13)^{\circ}$	

## Data collection

Siemens SMART 1000 CCD areadetector diffractometer9489 measured reflections $\phi$  and  $\omega$  scans6553 independent reflections $\varphi$  and  $\omega$  scans2443 reflections with  $I > 2\sigma(I)$ Absorption correction: multi-scan<br/>(SADABS; Sheldrick, 1996) $R_{int} = 0.069$  $T_{min} = 0.956, T_{max} = 0.983$  $\theta_{max} = 25.0^{\circ}$ 

## Refinement

Refinement on $F^2$	H-atom parameters constrained
$R[F^2 > 2\sigma(F^2)] = 0.099$	$w = 1/[\sigma^2(F_o^2) + (0.139P)^2]$
$wR(F^2) = 0.289$	where $P = (F_0^2 + 2F_c^2)/3$
S = 0.91	$(\Delta/\sigma)_{\rm max} < 0.001$
6553 reflections	$\Delta \rho_{\rm max} = 0.37 \ {\rm e} \ {\rm \AA}^{-3}$
577 parameters	$\Delta \rho_{\rm min} = -0.34 \ {\rm e} \ {\rm \AA}^{-3}$

## Table 1

Hydrogen-bond geometry (Å, °).

$D - H \cdots A$	D-H	$H \cdots A$	$D \cdots A$	$D - \mathbf{H} \cdots A$
$C36-H36B\cdots O5^{i}$	0.97	2.56	3.477 (9)	158
$C27 - H27A \cdots O7^{ii}$	0.97	2.62	3.473 (9)	147
$C15-H15\cdots O2^{iii}$	0.93	2.62	3.511 (10)	161
$C7-H7A\cdots O4^{iv}$	0.93	2.62	3.480 (11)	155

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

All H atoms were located in difference Fourier maps and then repositioned geometrically. They were refined as riding, with C–H distances of 0.93 (aryl), 0.96 (methyl) or 0.97 Å (methylene), N–H = 0.90 Å and O–H = 0.82 Å.  $U_{iso}$ (H) values were set at  $xU_{eq}$ (carrier atom), where x = 1.5 for methyl and hydroxy, x = 1.2 for the other H atoms.

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

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