metal-organic papers

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Key indicators

Single-crystal X-ray study T = 298 KMean $\sigma(\text{C}-\text{C}) = 0.008 \text{ Å}$ R factor = 0.033 wR factor = 0.084 Data-to-parameter ratio = 20.2

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

Dipotassium ethane-1,1-diylbis(diazeniumdiolate) monohydrate

The ethane-1,1-bis(diazeniumdiolate) anion in the title compound, $2K^+ \cdot C_2H_4N_4O_4^{2-} \cdot H_2O$, acts as a complex bridging ligand. Both the N and the O atoms of the diazeniumdiolate substituents are coordinated to the K^+ cations, revealing the delocalization of a negative charge over the four-atom groups.

Comment

Thermally explosive diazeniumdiolate-substituted products are synthesized by the reaction of nitric oxide gas with ketones and with alcohols in the presence of alkali alcoholates. Our interest in these compounds stems from their exothermic decomposition and NO-donor properties (Arulsamy & Bohle, 2001, 2005*b*; Arulsamy *et al.*, 2003). The title compound, (I), can be synthesized either from 2-butanone or from 1-propanol (Arulsamy & Bohle, 2005*b*).



The ethane-1,1-bis(diazeniumdiolate) anion contains two planar diazeniumdiolate groups. The dihedral angle between these two groups is $81.88 (10)^{\circ}$ (Fig. 1). Geometric parameters (Table 1) associated with the substituents are consistent with those in other diazeniumdiolate compounds (Arulsamy & Bohle, 2001, 2005a; Klebe et al., 1996). The anion interacts with the two K⁺ cations in a complex manner, as shown in Fig. 2. Firstly, each of the two pairs of the diazeniumdiolate O atoms is coordinated to each of the two cations with the anion acting as a bridging dinucleating ligand. Secondly, the diazeniumdiolate O atoms interact with two different cations and act as single atom bridges. Thirdly, the terminal N and O atoms together bind a single cation, forming three-membered chelate rings. These interactions suggest that the negative charge of the anionic substituent is delocalized over the four-atom groups.

The water molecule is coordinated to both cations (Table 1), and is also involved in a moderately strong hydrogen-bonding interaction with the anion (Table 2). Significantly, the tertiary C-H group is not associated with any of the electronegative groups or with the water molecule through hydrogen bonding.

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Figure 1

Drawing of the asymmetric unit, with the atom-numbering scheme. Displacement ellipsoids are drawn at the 50% probability level.



Figure 2

Coordination environment of the $K^{\scriptscriptstyle +}$ cations. H atoms have been omitted and some atoms are unlabeled for clarity.

Experimental

The title compound was synthesized and recrystallized as described elsewhere (Arulsamy & Bohle, 2005b).

Crystal data

Crystat aata	
$2K^+ \cdot C_2H_4N_4O_4^- \cdot H_2O$	Mo $K\alpha$ radiation
$M_r = 244.31$	Cell parameters from 73
Rhombohedral, R3	reflections
a = 14.2510 (12) Å	$\theta = 4.6 - 12.5^{\circ}$
$\alpha = 116.402 \ (7)^{\circ}$	$\mu = 1.02 \text{ mm}^{-1}$
$V = 1390.9 (8) \text{ Å}^3$	T = 298 (2) K
Z = 6	Block, colorless
$D_x = 1.750 \text{ Mg m}^{-3}$	$0.42 \times 0.36 \times 0.32 \text{ mm}$

Data collection

Bruker P4 diffractometer ω scans Absorption correction: ψ scan (*SHELXS97*; Sheldrick, 1997) $T_{min} = 0.667$, $T_{max} = 0.721$ 3377 measured reflections 2631 independent reflections 2106 reflections with $I > 2\sigma(I)$

Refinement

Refinement on F^2 $R[F^2 > 2\sigma(F^2)] = 0.033$ $wR(F^2) = 0.084$ S = 1.032631 reflections 130 parameters H atoms treated by a mixture of independent and constrained refinement

Table 1

Selected geometric parameters (Å, °).

$k = -19 \rightarrow 4$
$l = -10 \rightarrow 20$
3 standard reflections
every 97 reflections
intensity decay: 1%

 $\begin{aligned} R_{\rm int} &= 0.026\\ \theta_{\rm max} &= 30.0^\circ\\ h &= -10 \rightarrow 20 \end{aligned}$

$$\begin{split} &w = 1/[\sigma^2(F_o^2) + (0.0342P)^2 \\ &+ 0.3737P] \\ &where \ P = (F_o^2 + 2F_c^2)/3 \\ (\Delta/\sigma)_{max} = 0.002 \\ \Delta\rho_{max} = 0.37 \ e^{-3} \\ \Delta\rho_{min} = -0.31 \ e^{-3} \end{split}$$

$K1 - O2^i$	2.6436 (13)	K2-O1	2.8507 (18)
$K1 - O3^{ii}$	2.6748 (13)	K2-O4	3.006 (2)
K1-O1	2.7933 (18)	K2-N4	3.117 (2)
$K1-O4^{ii}$	2.8420 (16)	$K2-N2^{vi}$	3.168 (2)
K1-N2 ⁱⁱⁱ	2.889 (2)	K2-N3	3.188 (3)
$K1 - O4^{iv}$	2.9374 (15)	K2-O3	3.236 (3)
K1 - O1W	2.9506 (18)	O1-N1	1.292 (2)
K1-O2	2.969 (3)	N1-N2	1.2841 (19)
$K1 - O2^{iii}$	3.173 (3)	N1-C1	1.465 (2)
$K1-K2^{iv}$	3.7814 (7)	N2-O2	1.290 (2)
$K1-K1^{v}$	3.8632 (19)	O3-N3	1.3038 (19)
K2 - O1W	2.722 (3)	N3-N4	1.283 (2)
$K2-O3^{ii}$	2.7248 (14)	N3-C1	1.475 (2)
$K2-O2^{vi}$	2.7944 (16)	N4-O4	1.291 (2)
N2-N1-O1	125.46 (14)	N4-N3-O3	124.88 (14)
N2-N1-C1	115.81 (15)	N4-N3-C1	119.06 (14)
O1-N1-C1	118.67 (14)	O3-N3-C1	115.93 (13)
N1-N2-O2	113.61 (15)	N3-N4-O4	113.20 (14)
O1-N1-N2-O2	-1.5(2)	O1-N1-C1-C2	62.7 (2)
O2-N2-N1-C1	-178.69(14)	O1-N1-C1-N3	-61.3(2)
N2 - N1 - C1 - C2	-119.95 (19)	O3-N3-C1-N1	-54.37(19)
N2-N1-C1-N3	116.04 (16)	O3-N3-C1-C2	-176.51 (18)
N1-C1-N3-O3	-54.37 (19)	O3-N3-N4-O4	-0.6(2)
C1-N3-N4-O4	-176.22 (14)		. ,

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

Table 2Hydrogen-bond geometry (Å, °).

D-H	$H \cdot \cdot \cdot A$	$D \cdot \cdot \cdot A$	$D - \mathbf{H} \cdot \cdot \cdot A$
0.85 (3) 0.81 (4)	1.95 (3) 2.10 (4)	2.773 (2) 2.908 (4)	163 (3) 175 (3)
	<i>D</i> -H 0.85 (3) 0.81 (4)	$\begin{array}{c ccc} D-H & H \cdots A \\ \hline 0.85 (3) & 1.95 (3) \\ 0.81 (4) & 2.10 (4) \end{array}$	$\begin{array}{c ccccccccccccccccccccccccccccccccccc$

Symmetry codes: (iv) -y + 1, -z + 1, -x + 1; (vii) x + 1, y + 1, z + 1.

The methyl H atoms were positioned geometrically at distances of 0.96 Å from the parent C atom, and a riding model was used during the refinement process $[U_{iso}(H) = 1.5U_{eq}(C)]$. The remaining H atoms were located in a difference synthesis and were refined isotropically [C-H = 1.02 (2) Å and O-H = 0.81 (4) and 0.85 (3) Å].

Data collection: *XSCANS* (Bruker, 1996); cell refinement: *XSCANS*; data reduction: *SHELXTL* (Bruker, 1996); program(s) used to solve structure: *SHELXS97* (Sheldrick, 1997); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular

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graphics: *SHELXTL*; software used to prepare material for publication: *SHELXTL*.

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