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2,2'-(Ethane-1,2-diyl)dibenzimidazolium bis(perchlorate) tetrahydrate

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Key indicators

Single-crystal X-ray study T = 295 KMean $\sigma(\text{C-C}) = 0.005 \text{ Å}$ R factor = 0.069 wR factor = 0.218Data-to-parameter ratio = 14.6

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

The cation, anion and water molecules of the title compound, $C_{16}H_{16}N_4^{\ 2+}\cdot 2ClO_4^{\ -}\cdot 4H_2O$, are linked by hydrogen bonds into a three-dimensional network. The cation lies on a center of inversion, which is located at the mid-point of the $-CH_2CH_2-$ bond.

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Comment

The 2,2'-(ethane-1,2-diyl)dibenzimidazole nitrogen heterocycle, whose synthesis has been described (Dudd *et al.*, 2003), affords crystalline compounds with metal salts; with some, the nitrogen heterocycle binds to the metal atom (Albada *et al.*, 1999, 2000), whereas in others it does not bind, existing instead as a protonated dication (Broughton *et al.*, 1998; Matthews *et al.*, 2003). An attempt to synthesize an erbium perchlorate complex gave 2,2'-(ethane-1,2-diyl)dibenzimidazolium bis-(perchlorate) tetrahydrate, (I) (Fig. 1). The cation lies on a center of inversion, and its four nitrogen-bound H atoms are engaged in hydrogen bonding with the water molecules. The cation, anion and water molecules are linked by hydrogen bonds (Table 1) into a three-dimensional network.

$$\begin{bmatrix} H & H & 1 \\ H & H & 1 \end{bmatrix}^{2+} 2[ClO_4]^{-4}H_2O$$

Experimental

To a hot solution of 2,2'-(ethane-1,2-diyl)dibenzimidazole (0.07 g, 0.30 mmol) in ethanol (5 ml) was added a solution of erbium(III) perchlorate (0.34 g, 0.60 mmol) in acetonitrile (5 ml), giving a clear light-red solution. The solution was filtered and pale-yellow crystals were isolated from the filtrate after 10 d.

Crystal data

 $\begin{array}{lll} \text{C}_{16}\text{H}_{16}\text{N}_{4}^{2+} \cdot 2\text{CIO}_{4}^{-} \cdot 4\text{H}_{2}\text{O} & Z = 2 \\ M_{r} = 535.29 & D_{x} = 1.553 \text{ Mg m}^{-3} \\ \text{Monoclinic, } P2_{1}/n & \text{Mo } K\alpha \text{ radiation} \\ a = 7.0898 \text{ (6) Å} & \mu = 0.35 \text{ mm}^{-1} \\ b = 17.204 \text{ (2) Å} & T = 295 \text{ (2) K} \\ c = 9.9894 \text{ (9) Å} & \text{Block, pale yellow} \\ \beta = 110.072 \text{ (2)}^{\circ} & 0.20 \times 0.16 \times 0.11 \text{ mm} \\ V = 1144.4 \text{ (2) Å}^{3} & \end{array}$

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organic papers

Data collection

Bruker APEX-II area-detector diffractometer φ and ω scans Absorption correction: none 7440 measured reflections

2601 independent reflections 1988 reflections with $I > 2\sigma(I)$ $R_{\rm int} = 0.034$ $\theta_{\rm max} = 27.5^{\circ}$

Refinement

refinement

Refinement on F^2 $R[F^2 > 2\sigma(F^2)] = 0.069$ $wR(F^2) = 0.218$ S = 1.052601 reflections 178 parameters H atoms treated by a mixture of independent and constrained

$$\begin{split} w &= 1/[\sigma^2(F_{\rm o}^2) + (0.1223P)^2 \\ &+ 0.991P] \\ \text{where } P &= (F_{\rm o}^2 + 2F_{\rm c}^2)/3 \\ (\Delta/\sigma)_{\rm max} &= 0.001 \\ \Delta\rho_{\rm max} &= 0.99 \text{ e Å}^{-3} \\ \Delta\rho_{\rm min} &= -0.48 \text{ e Å}^{-3} \end{split}$$

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

$D-\mathbf{H}\cdot\cdot\cdot A$	D-H	$H \cdot \cdot \cdot A$	$D \cdot \cdot \cdot A$	$D-H\cdots A$
$O1w-H1w1\cdots O1$	0.84(1)	2.13 (2)	2.915 (4)	154 (4)
$O1w - H1w2 \cdot \cdot \cdot O2w^{i}$	0.84(1)	2.29(2)	3.083 (4)	158 (4)
$O2w-H2w1\cdots O1^{ii}$	0.85 (1)	2.11 (2)	2.907 (4)	157 (5)
$O2w-H2w2\cdots O1w^{iii}$	0.85(1)	2.13 (4)	2.897 (4)	150 (7)
$N1-H1n\cdots O1w$	0.85 (1)	2.02 (1)	2.853 (4)	169 (4)
$N2-H2n\cdots O2w$	0.85 (1)	1.96 (1)	2.804 (4)	172 (3)
Symmetry codes: (i) $-x + \frac{1}{2}, y - \frac{1}{2}, -z + \frac{1}{2}$.	-x + 1, -y +	1, -z + 1; (ii)	$-x + \frac{3}{2}, y - \frac{1}{2}$	$z_1, -z + \frac{1}{2};$ (iii)

The displacement parameters of the O atoms of the perchlorate were restrained to be nearly isotropic. The carbon-bound H atoms were placed at calculated positions (C-H = 0.93 and 0.97 Å) and were included in the refinement in the riding-model approximation, with $U_{iso}(H)$ set at $1.2U_{eq}(C)$. The water and amino H atoms were located in a difference Fourier map, and were refined with distance restraints of O – H = N – H = 0.85 (1) Å and H · · · H = 1.39 (1) Å; their displacement parameters were freely refined.

Data collection: APEX-2 (Bruker, 2006); cell refinement: SAINT (Bruker, 2006); data reduction: SAINT; program(s) used to solve structure: SHELXS97 (Sheldrick, 1997); program(s) used to refine structure: SHELXL97 (Sheldrick, 1997); molecular graphics: X-

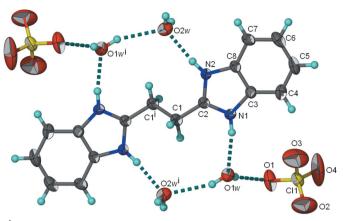


Figure 1

The formula unit of (I), with displacement ellipsoids drawn at the 50% probability level. H atoms are drawn as spheres of arbitrary radius. [Symmetry code: (i) 1 - x, 1 - y, 1 - z.]

SEED (Barbour, 2001); software used to prepare material for publication: SHELXL97.

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