Acta Crystallographica Section E

# **Structure Reports Online**

ISSN 1600-5368

# N,N-Bis(2-pyridiniomethyl)glycine diperchlorate

# Anne Nielsen, Andrew D. Bond\* and Christine I. McKenzie

University of Southern Denmark, Department of Chemistry, Campusvej 55, 5230 Odense, Denmark

Correspondence e-mail: adb@chem.sdu.dk

#### **Key indicators**

Single-crystal X-ray study T = 180 KMean  $\sigma(\text{C-C}) = 0.009 \text{ Å}$ Disorder in solvent or counterion R factor = 0.053 wR factor = 0.143 Data-to-parameter ratio = 7.5

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

In the crystal structure of the title compound,  $C_{14}H_{17}$ - $N_3O_2^{2+}$ - $2ClO_4^-$ , at 180 K,  $O-H\cdots O$  hydrogen-bonded dimers are formed across inversion centres.

Received 4 January 2005 Accepted 24 January 2005 Online 5 February 2005

## Comment

The title compound, (I) (Fig. 1), was crystallized in an unsuccessful attempt to prepare an iron complex of N,N-bis(2-pyridylmethyl)glycine. In the crystal structure, the carboxylic acid groups form syn-syn dimers via O $-H\cdots$ O hydrogen bonds across centres of inversion (Fig. 2). The NH groups of the protonated pyridyl rings form  $N-H\cdots$ O hydrogen bonds, bifurcated at the donor, to O atoms of the perchlorate anions.

HO 
$$N+H$$
  $2 \text{ CIO}_4^-$ 

# **Experimental**

N,N-Bis(2-pyridylmethyl)glycine (bpgH; 0.0859 g, 0.334 mmol) in hot acetonitrile (2.75 ml) was added to Fe(ClO<sub>4</sub>)<sub>3</sub>·9H<sub>2</sub>O (0.0861 g, 0.167 mmol) in acetonitrile (0.25 ml). The orange precipitate was dissolved by addition of acetonitrile and water. HClO<sub>4</sub> (70%) in a large excess (HClO<sub>4</sub>:bpgH ca 1000:1) was then added. After 9 d, colourless plate-like crystals precipitated in the yellow solution (yield ca 38%).

### Crystal data

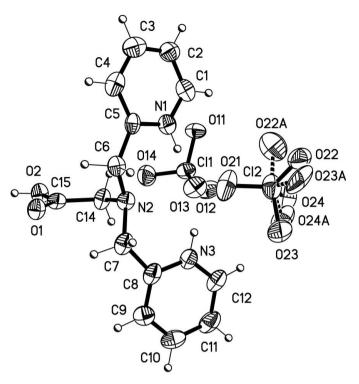
 $C_{14}H_{17}N_3O_2^{2+} \cdot 2ClO_4^{-1}$  $D_x = 1.678 \text{ Mg m}^{-3}$  $M_r = 458.21$ Mo  $K\alpha$  radiation Monoclinic, P2/c Cell parameters from 2492 a = 14.1367 (12) Åreflections b = 7.9021 (8) Å  $\theta = 2.5 - 21.2^{\circ}$ c = 16.8034 (16) Å $\mu = 0.42 \text{ mm}^{-}$  $\beta = 104.907 (3)^{\circ}$ T = 180 (2) K $V = 1813.9 (3) \text{ Å}^3$ Plate, colourless Z = 4 $0.12 \times 0.08 \times 0.01 \text{ mm}$ 

### Data collection

 $\begin{array}{lll} \mbox{Bruker-Nonius X8APEX-II CCD} & 2175 \mbox{ independent reflections} \\ \mbox{diffractometer} & 1542 \mbox{ reflections with } I > 2\sigma(I) \\ \mbox{Thin-slice } \omega \mbox{ and } \varphi \mbox{ scans} & R_{\rm int} = 0.068 \\ \mbox{Absorption correction: multi-scan} & \theta_{\rm max} = 22.0^{\circ} \\ \mbox{ } (SADABS; \mbox{ Sheldrick, 2003)} & h = -14 \rightarrow 14 \\ \mbox{ } T_{\rm min} = 0.665, T_{\rm max} = 0.996 & k = -8 \rightarrow 8 \\ \mbox{15 019 measured reflections} & l = -17 \rightarrow 17 \\ \end{array}$ 

doi:10.1107/S1600536805002503

© 2005 International Union of Crystallography Printed in Great Britain – all rights reserved



**Figure 1**View of the title complex, showing displacement ellipsoids drawn at the 50% probability level for non-H atoms. H atoms are shown as spheres of arbitrary radii. Cl—O bonds in one component of the disordered perchlorate anion are shown as dashed lines.

# Refinement

 $\begin{array}{lll} \text{Refinement on } F^2 & w = 1/[\sigma^2(F_o^2) + (0.0784P)^2 \\ R[F^2 > 2\sigma(F^2)] = 0.053 & + 1.4336P] \\ wR(F^2) = 0.143 & \text{where } P = (F_o^2 + 2F_c^2)/3 \\ S = 1.07 & (\Delta/\sigma)_{\text{max}} < 0.001 \\ 2175 \text{ reflections} & \Delta\rho_{\text{max}} = 0.49 \text{ e Å}^{-3} \\ 290 \text{ parameters} & \Delta\rho_{\text{min}} = -0.40 \text{ e Å}^{-3} \end{array}$ 

 Table 1

 Hydrogen-bonding geometry (Å, °).

$D$ $ H$ $\cdots$ $A$	D-H	$H \cdot \cdot \cdot A$	$D \cdot \cdot \cdot A$	$D-\mathrm{H}\cdots A$
$O2-H2\cdots O1^{i}$	0.85	1.82	2.669 (5)	173
$N1-H1B\cdots O13$	0.88	2.29	3.052 (7)	145
$N1-H1B\cdots O21$	0.88	2.32	2.877 (7)	121
$N3-H3B\cdots O13$	0.88	2.48	3.017 (6)	120
$N3-H3B\cdots O21$	0.88	2.11	2.889 (7)	147

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

Although the best available from the batch, the crystal was relatively small and diffraction was weak. The data were truncated at 0.95  $\mathring{\rm A}$  resolution, and the structure is therefore of relatively low precision. The unusual ratio of apparent transmission factors suggests that the multi-scan correction is treating effects other than absorption by the crystal itself.

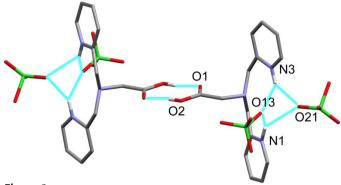


Figure 2
The hydrogen-bonded unit in (I). H atoms not involved in hydrogen bonding have been omitted and only one component of each disordered perchlorate anion is shown; O21, involved in hydrogen bonding, is common to both orientations.

H atoms bound to C atoms were positioned geometrically and allowed to ride during subsequent refinement, with C-H = 0.95 Åand  $U_{iso}(H) = 1.2U_{eq}(C)$  for the H atoms of the pyridyl rings, and C-H = 0.99 Å and  $U_{iso}(H) = 1.2U_{eq}(C)$  for the methylene groups. The H atoms bound to N atoms were evident in Fourier maps, but on account of the relatively low data-to-parameter ratio, they were placed in calculated positions in the final model and allowed to ride, with N-H = 0.88 Å and  $U_{iso}(H) = 1.2U_{eq}(N)$ . The H atom of the carboxyl group was also located in a difference Fourier map, then moved along the O2-H2 bond vector to give O-H = 0.85 Å. It was subsequently allowed to ride on O2 with  $U_{iso}(H) = 1.5U_{eq}(O)$ . One perchlorate anion was modelled as disordered over two orientations. The site-occupancy factors of the O atoms in the two orientations were refined initially with a single isotropic displacement parameter common to all. This gave refined site occupancies of 0.59 (1):0.41 (1), which were subsequently constrained to be 0.60:0.40. Sites Cl2 and O21 (involved in the N-H···O hydrogen bond) are common to both orientations and refined with full site occupancy. The anisotropic displacement parameters of the O atoms of the anion were restrained to be approximately isotropic.

Data collection: *APEX2* (Bruker–Nonius, 2004); cell refinement: *SAINT* (Bruker, 2003); data reduction: *SAINT*; program(s) used to solve structure: *SHELXTL* (Sheldrick, 2000); program(s) used to refine structure: *SHELXTL*; molecular graphics: *SHELXTL*; software used to prepare material for publication: *SHELXTL*.

We are grateful to the Danish Natural Science Research Council (SNF) and Carlsbergfondet for provision of the X-ray equipment.

#### References

Bruker–Nonius (2004). APEX2. Version 1.0-22. Bruker-Nonius BV, Delft, The Netherlands.

Bruker (2003). SAINT. Version 7.06a. Bruker AXS Inc., Madison, Wisconsin, USA.

Sheldrick, G. M. (2000). SHELXTL. Version 6.10. Bruker AXS Inc., Madison, Wisconsin, USA.

Sheldrick, G. M. (2003). SADABS. Version 2.10. Bruker AXS Inc., Madison, Wisconsin, USA.