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#### **Key indicators**

Single-crystal X-ray study T = 293 K Mean  $\sigma$ (C–C) = 0.005 Å R factor = 0.021 wR factor = 0.054 Data-to-parameter ratio = 11.9

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

# Bis(hydrogen 5-nitroisophthalato)(1,10phenanthroline)lead(II) monohydrate

In the title compound,  $[Pb(C_8H_4NO_6)_2(C_{12}H_8N_2)]\cdot H_2O$ , the lead(II) ion lies on a twofold axis and exhibits an approximately tetrahedral configuration. The water molecule also lies on a twofold rotation axis.  $O-H\cdots O$  hydrogen bonds and  $C-H\cdots\pi$  interactions are involved in the formation of two-dimensional network structures which are interlinked by  $C-H\cdots O$  hydrogen bonds.

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# Comment

Bi- or multidentate ligands containing carboxyl groups are often used to coordinate to metal centers to generate interesting coordination polymers (Hu *et al.*, 2004; Sun *et al.*, 2003; Yaghi *et al.*, 1998). The lead(II) ion usually shows a different coordination chemistry, due to the presence of the lone-pair electrons (Foreman, 2000; Yuan *et al.*, 2004). Hence, it is of interest to study the crystal structures of lead(II) carboxylates. We report here the hydrothermal synthesis and crystal structure of a mononuclear compound, namely bis(hydrogen 5nitroisophthalato)(1,10-phenanthroline)lead(II) monohydrate, (I).



In (I), the coordination geometry of the Pb<sup>II</sup> atom is best described as highly distorted tetrahedral, made up of two N atoms of a phenanthroline ligand and two O atoms from two hydrogen 5-nitroisophthalate anions (Fig. 1). The crystal structure analysis shows that a crystallographic twofold symmetry axis passes through the lead(II) ion and bisects the C13-C13<sup>i</sup> and C14-C14<sup>i</sup> bonds [symmetry code: (i)  $\frac{1}{2} - x$ ,  $\frac{3}{2} - y$ , z]. The 1,10-phenanthroline system is almost perpendicular to the benzene ring of the 5-nitroisophthalate anion, the dihedral angle between the planes being 83.80 (2)°. The water molecule also lies on a twofold rotation axis.

O3-H3···O2<sup>ii</sup> and O7-H7A···O4<sup>ii</sup> [symmetry code: (ii) 1 - x, 1 - y, 2 - z] intermolecular hydrogen bonds (Table 2) link the molecules into a two-dimensional network structure. This network structure is further stabilized by  $\pi$ - $\pi$  stacking interactions between the N1-pyridine rings of the 1,10-phenanthroline moieties at (x, y, z) and  $(\frac{1}{2} - x, \frac{1}{2} - y, z)$ 

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Figure 1

The coordination environment of the Pb atom in (I), with the atom numbering, showing displacement ellipsoids at the 50% probability level. Unlabelled atoms are related to labelled atoms by  $\frac{1}{2} - x$ ,  $\frac{3}{2} - y$ , z.



## Figure 2

The three-dimensional network in (I), formed by hydrogen bonds and  $\pi$ - $\pi$  stacking interactions.

[centroid–centroid distance = 3.490(2) Å]. The two-dimensional networks are interlinked by C–H···O interactions, as shown in Fig. 2.

# **Experimental**

The title compound was synthesized by a hydrothermal method from a mixture of 5-nitroisophthalic acid (0.5 mmol),  $Pb(NO_3)_2 \cdot 4H_2O$ (0.5 mmol), 1,10-phenanthroline (1.0 mol) and water (10.0 ml) in a 15 ml Teflon-lined stainless steel reactor. The solution was heated at 403 K for 5 d and then cooled slowly to room temperature; colorless crystals of (I) were collected for X-ray analysis.

## Crystal data

$[Pb(C_8H_4NO_6)_2(C_{12}H_8N_2)]\cdot H_2O$
$M_r = 825.65$
Orthorhombic, Pccn
a = 22.6083 (17)  Å
b = 6.2232(5) Å
c = 20.0394 (15)  Å
V = 2819.5 (4) Å <sup>3</sup>
Z = 4
$D_{\rm r} = 1.945 {\rm Mg} {\rm m}^{-3}$

Mo K $\alpha$  radiation Cell parameters from 853 reflections  $\theta = 2.3-23.2^{\circ}$  $\mu = 6.06 \text{ mm}^{-1}$ T = 293 (2) K Prism, colorless  $0.26 \times 0.13 \times 0.12 \text{ mm}$ 

#### Data collection

Bruker SMART CCD area-detector	
diffractometer	
$\varphi$ and $\omega$ scans	
Absorption correction: multi-scan	
(SADABS; Bruker, 2000)	
$T_{\rm min} = 0.302, \ T_{\rm max} = 0.530$	
13880 measured reflections	

# Refinement

refinement

Pb1

N1-N1-

Refinement on  $F^2$   $R[F^2 > 2\sigma(F^2)] = 0.021$   $wR(F^2) = 0.054$  S = 1.042543 reflections 213 parameters H atoms treated by a mixture of independent and constrained 2543 independent reflections 2003 reflections with  $I > 2\sigma(I)$  $R_{int} = 0.030$  $\theta_{max} = 25.2^{\circ}$  $h = -20 \rightarrow 27$  $k = -7 \rightarrow 7$  $l = -23 \rightarrow 24$ 

# $$\begin{split} &w = 1/[\sigma^2(F_o^2) + (0.0253P)^2 \\ &+ 1.2381P] \\ &where \ P = (F_o^2 + 2F_c^2)/3 \\ (\Delta/\sigma)_{\rm max} = 0.002 \\ \Delta\rho_{\rm max} = 0.64 \ {\rm e} \ {\rm \AA}^{-3} \\ \Delta\rho_{\rm min} = -0.42 \ {\rm e} \ {\rm \AA}^{-3} \end{split}$$

Table 1			
Selected	geometric parameters	(Å,	°).

-N1	2.434 (2)	Pb1-O1	2.554 (2)
$-Pb1-N1^{i}$ $-Pb1-O1^{i}$	68.27 (11) 77.21 (8)	N1-Pb1-O1 O1 <sup>i</sup> -Pb1-O1	74.96 (8) 146.23 (11)

Symmetry code: (i)  $\frac{1}{2} - x, \frac{3}{2} - y, z$ .

Tal	ole	2		
**				

Hydrogen-bonding geometry (Å, °).

$D - H \cdot \cdot \cdot A$	D-H	$H \cdots A$	$D \cdots A$	$D - H \cdots A$
$O7-H7A\cdots O4^{ii}$	0.81 (2)	2.09 (2)	2.860 (3)	157 (4)
O3−H3···O2 <sup>ii</sup>	0.82	1.73	2.506 (3)	156
$C3-H3A\cdots O3$	0.93	2.34	2.676 (4)	101
$C3-H3A\cdots O3^{ii}$	0.93	2.27	3.158 (4)	160
C9−H9···O1 <sup>iii</sup>	0.93	2.45	3.099 (4)	127
C10−H10···O5 <sup>iv</sup>	0.93	2.53	3.292 (4)	140
$C11 - H11 \cdots O4^{v}$	0.93	2.55	3.390 (4)	150
		(***)	4 (1) 4	3 3 ()

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

The water H atom was located and refined with an O–H distance restraint [O-H = 0.82 (2) Å] and with  $U_{iso}(H) = 1.5U_{eq}(O)$ . The other H atoms were placed in calculated positions (C-H = 0.93 Å) and included in the refinement in the riding-model approximation, with  $U_{iso}(H)$  values set at  $1.2U_{eq}(\text{parent atom})$ .

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

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