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Key indicators

Single-crystal X-ray study T = 298 K Mean σ (C–C) = 0.007 Å R factor = 0.032 wR factor = 0.083 Data-to-parameter ratio = 12.7

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

Bis(μ -N-acetyl-N-phenylglycinato- $\kappa^2 O:O'$)bis[triaqua(1,10-phenanthroline- $\kappa^2 N,N'$)lanthanum(III)] bis(N-acetyl-N-phenylglycinate) dinitrate dihydrate

In the title complex, $[La_2(C_{10}H_{10}NO_3)_2(C_{12}H_8N_2)_4(H_2O)_6]$ -($C_{10}H_{10}NO_3)_2(NO_3)_2 \cdot 2H_2O$, each La^{III} ion is nine-coordinated by four N atoms from two bidentate 1,10-phenanthroline ligands and by five O atoms (two from *N*-acetyl-*N*-phenylglycinate ligands and three from water molecules). The La^{III} cations, which exhibit distorted tricapped trigonal prismatic coordination, are bridged by two *N*-acetyl-*N*-phenylglycinate ligands into a dimeric structure, generated by inversion symmetry. The crystal structure is stabilized by a threedimensional hydrogen-bond network.

Comment

The formula unit of the title compound, (I) (Fig. 1), consists of an $[La_2(C_{10}H_{10}NO_3)_2(C_{12}H_8N_2)_4(H_2O)_6]^{4+}$ cation, two $C_{10}H_{10}O_3N^-$ anions, two NO_3^- anions and two uncoordinated water molecules. Each La^{III} ion is nine-coordinated by four N atoms (N2, N3, N4 and N5) from two 1,10-phenanthroline (L_1) ligands (Table 1), atom O1 from the carboxylate group of an *N*-acetyl-*N*-phenylglycinate (L_2) ligand, atom O3ⁱ (see Table 1 for symmetry code) from the acetyl group of another L_2 ligand and atoms O4, O5 and O6 from three water molecules. The coordination sphere around La is distorted tricapped trigonal prismatic, with the capping positions occupied by atom N3 of L_1 , N4 of another L_1 and O5 (water). The coordinated L_2 ligand bonds to one La via a carboxylate group O atom and to another La atom via an acetyl O atom, thus acting as a bridge. The overall complex cation has inversion symmetry.



The La–O bond lengths in (I) are in the range 2.415 (2)– 2.553 (2) Å, with a carboxylate O atom making the shortest bond. The average La–N bond length in (I) of 2.766 Å is longer than that seen (2.666 Å) in bis[tris(*N*-phenyl-*N*acetylglycine)(1,10-phenanthroline)lanthanum] (Fu *et al.*, 2004)

The crystal packing in (I) is stabilized by $O-H\cdots O$ hydrogen bonds (Table 2). Notable among these are the O4-

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Figure 1 The structure of (I), showing 50% probability displacement ellipsoids and the atom-numbering scheme. H atoms have been omitted for clarity.

H2...O7 and O5-H3...O8 bonds from coordinated water molecules to uncoordinated L_2 molecules. Overall, a threedimensional network results.

Crystal data

Experimental

La(NO₃)₃·nH₂O (1 mmol) and L₁ (2 mmol) were dissolved in distilled water (20 ml). To this solution, an aqueous mixture (30 ml) of HL₂ (1 mmol) and NaOH (1 mmol) was added dropwise at 313 K. The resulting mixture was stirred for 6 h and part of the solvent was evaporated in a rotary vacuum evaporator at the same temperature. The resulting solution was filtered and the filtrate left in air for about six weeks, after which large yellow block-shaped crystals of (I) were obtained. Elemental analysis found: C 51.93, H 4.36, N 9.64%; calculated for $C_{88}H_{88}La_2N_{14}O_{26}\!\!:C$ 51.88, H 4.29, N 9.55%.



Figure 2

m1338

The crystal packing of (I), showing the the $O \cdots O$ hydrogen-bonded interactions as dashed lines (H atoms have been omitted for clarity).

 $[La_2(C_{10}H_{10}NO_3)_2(C_{12}H_8N_2)_4-$ (H2O)6](C10H10NO3)2-(NO₃)₂·2H₂O $M_r = 2035.54$ Triclinic, P1 a = 11.4722 (19) Å b = 14.271(2) Å c = 14.986 (2) Å $\alpha = 66.966 \ (2)^{\circ}$ $\beta = 86.448 (2)^{\circ}$ $\gamma = 79.303 (2)^{\circ}$

V = 2218.6 (6) Å³ Z = 1 $D_{\rm r} = 1.524 {\rm Mg m}^{-3}$ Mo $K\alpha$ radiation Cell parameters from 6354 reflections $\theta = 2.3 - 27.8^{\circ}$ $\mu = 1.04 \text{ mm}^{-1}$ T = 298 (2) KBlock, yellow $0.45\times0.37\times0.19~\text{mm}$

 $w = 1/[\sigma^2(F_o^2) + (0.0434P)^2]$

+ 1.4707P] where $P = (F_o^2 + 2F_c^2)/3$

 $\Delta \rho_{\rm max} = 0.82 \ {\rm e} \ {\rm \AA}^{-3}$

 $\Delta \rho_{\rm min} = -0.45 \text{ e} \text{ Å}^{-3}$

 $(\Delta/\sigma)_{\rm max} = 0.001$

Data collection

Bruker SMART CCD area-detector 7742 independent reflections 6642 reflections with $I > 2\sigma(I)$ diffractometer φ and ω scans $R_{\rm int} = 0.017$ $\theta_{\rm max} = 25.0^\circ$ Absorption correction: multi-scan (SADABS; Bruker, 1997) $h = -13 \rightarrow 13$ $T_{\min} = 0.653, T_{\max} = 0.828$ $k=-16\rightarrow 16$ 11765 measured reflections $l = -14 \rightarrow 17$

Refinement

Refinement on F^2 $R[F^2 > 2\sigma(F^2)] = 0.032$ $wR(F^2) = 0.083$ S = 1.017742 reflections 610 parameters H atoms treated by a mixture of independent and constrained refinement

Table 1

Selected bond distances (Å).

La1-O1	2.415 (2)	La1-N2	2.726 (3)
La1-O5	2.483 (2)	La1-N4	2.745 (3)
La1-O3 ⁱ	2.503 (2)	La1-N3	2.755 (3)
La1-O4	2.542 (2)	La1-N5	2.838 (3)
La1-O6	2.553 (2)		. ,

Symmetry code: (i) 2 - x, -y, -z.

 Table 2

 Hydrogen-bonding geometry (Å, °).

$D - H \cdots A$	D-H	$H \cdots A$	$D \cdot \cdot \cdot A$	$D - \mathbf{H} \cdots A$
O4−H1···O2	0.893 (10)	2.002 (15)	2.855 (3)	159 (3)
$O4-H2 \cdot \cdot \cdot O7$	0.898 (10)	1.720 (11)	2.616 (3)	175 (4)
O5-H3···O8	0.903 (10)	1.706 (14)	2.598 (4)	169 (4)
$O5-H4\cdots O10^{i}$	0.896 (10)	1.888 (16)	2.760 (4)	164 (3)
$O6-H5\cdots O11^{i}$	0.897 (10)	1.879 (17)	2.744 (4)	161 (4)
$O6-H14\cdots O9^{ii}$	0.896 (10)	1.843 (15)	2.719 (3)	165 (4)
$O13-H15\cdots O12^{i}$	0.902 (10)	2.015 (12)	2.910 (5)	172 (3)
O13-H16···O2 ⁱⁱⁱ	0.901 (10)	1.948 (15)	2.825 (4)	164 (4)

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

Water H atoms were found in difference maps and the O–H distances were restrained to 0.90 (1) Å; the $U_{iso}(H)$ values were allowed to refine. All other H atoms were placed in idealized posi-

tions and constrained to ride on their parent atoms, with C–H distances of 0.93–0.97 Å, depending on hybridization, and with $U_{iso}(H) = 1.2U_{ca}(C)$.

Data collection: *SMART* (Bruker, 1997); cell refinement: *SAINT* (Bruker, 1997); data reduction: *SAINT*; program(s) used to solve structure: *SHELXS*97 (Sheldrick, 1997a); program(s) used to refine structure: *SHELXL*97 (Sheldrick, 1997a); molecular graphics: *SHELXTL* (Sheldrick, 1997b); software used to prepare material for publication: *SHELXTL*.

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