metal-organic papers

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Key indicators

Single-crystal X-ray study T = 298 K Mean σ (C–C) = 0.006 Å R factor = 0.025 wR factor = 0.070 Data-to-parameter ratio = 13.4

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

Tetrakis(μ -N-acetyl-N-phenylglycinato)bis[(N-acetyl-N-phenylglycinato)(1,10phenanthroline- $\kappa^2 N, N'$)lanthanum(III)] dihydrate

In the title complex, $[La_2(C_{10}H_{10}NO_3)_6(C_{12}H_8N_2)_2]\cdot 2H_2O$, the La^{III} atoms are bridged by two terdentate and two bidentate carboxylate groups with an inversion centre between the two La^{III} ions. Each La atom is nine-coordinated by two N atoms of 1,10-phenanthroline and seven O atoms belonging to *N*-acetyl-*N*-phenylglycine molecules, and exhibits distorted tricapped trigonal prismatic geometry. The crystal structure is stabilized by intermolecular $O-H\cdots O$ hydrogen bonds.

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Comment

The title complex, (I) (Fig. 1), contains one dinuclear lanthanum/phenanthroline/*N*-acetyl-*N*-phenylglycinate complex and two uncoordinated water molecules. Each lanthanum ion is coordinated by one 1,10-phenanthroline (L_1) ligand *via* atoms N4 and N5 (Table 1), one chelating bidentate carboxylate group of an *N*-phenyl-*N*-acetylglycine (L_2) ligand *via* O7 and O8, two bridging bidentate carboxylate groups of L_2 via O5ⁱ (see Table 1 for symmetry code) and O4, and one bridging terdentate carboxylate group of L_2 via O1ⁱ and chelating terdentate carboxytate groups of L_2 via O1 and O2.



Overall, the coordination geometry around La is that of a distorted tricapped trigonal prism, with the capping positions occupied by atoms N5 of L_1 and O1 and O7 of two L_2 ligands. The two La ions are connected by four L_2 ligands via two bidentate and two terdentate carboxylate bridges with an inversion centre between the two La ions. The average of the bridging bidentate La-O bonds (2.452 Å) is slightly shorter than that of the bridging terdentate La-O bonds (2.467 Å), which in turn is shorter than the average of the chelating terdentate La-O bonds (2.584 Å).

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7083 independent reflections 6303 reflections with $I > 2\sigma(I)$

 $w = 1/[\sigma^2(F_o^2) + (0.0402P)^2]$

where $P = (F_0^2 + 2F_c^2)/3$

+ 1.0763P]

 $\Delta \rho_{\rm max} = 1.15 \ {\rm e} \ {\rm \AA}^{-3}$

 $\Delta \rho_{\rm min} = -0.57 \ {\rm e} \ {\rm \AA}^{-3}$

 $(\Delta/\sigma)_{\rm max} = 0.004$

 $R_{\rm int} = 0.014$ $\theta_{\rm max} = 25.0^{\circ}$

 $h = -11 \rightarrow 14$

 $k = -15 \rightarrow 16$

 $l = -13 \rightarrow 16$





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



Figure 2

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

The La–O bonds in (I) are shorter than the equivalent bonds in the related compound bis(1,10-phenanthroline)tris(trans-2,3-dimethylacrylato)lanthanum(III) (Lu et al., 2001), where the corresponding La-O bridging bidentate, La-O bridging terdentate, and La-O chelating terdentate distances are 2.473, 2.474 and 2.661 Å, respectively. The other bond lengths and angles in (I) are unexceptional.

The water O atom in (I) does not coordinate to La but participates in intermolecular O-H···O hydrogen bonds (Table 2) which stabilize the crystal packing of (I) (Fig. 2).

Experimental

La(NO₃)₃·nH₂O (1 mmol) and L₁ (1 mmol) were dissolved in anhydrous ethanol (20 ml). To this solution, an aqueous mixture (30 ml) of L₂ (2 mmol) and NaOH (2 mmol) was added dropwise at 313 K. The mixture was stirred for 4 h and about half of the solvent was evaporated in a rotary vacuum evaporator at the same temperature. The resulting solution was filtered and left to stand in air for about 20 d. Large yellow block-shaped crystals of (I) were obtained (m.p. 531.5 K). Elemental analysis found: C 55.13, H 4.32, N 7.52%; calculated for $C_{84}H_{80}La_2N_{10}O_{20}$: C 55.21, H 4.41, N 7.66%.

Crystal data

$[La_2(C_{10}H_{10}NO_3)_6(C_{12}H_8N_2)_2]$	Z = 1
$2H_2O$	$D_x = 1.496 \text{ Mg m}^{-3}$
$M_r = 1827.40$	Mo $K\alpha$ radiation
Triclinic, P1	Cell parameters from 7895
a = 11.777 (3) Å	reflections
b = 13.574(3) Å	$\theta = 2.3 - 28.3^{\circ}$
c = 14.114 (3) Å	$\mu = 1.12 \text{ mm}^{-1}$
$\alpha = 65.372 \ (2)^{\circ}$	T = 298 (2) K
$\beta = 86.194 \ (3)^{\circ}$	Block, yellow
$\gamma = 81.600 \ (3)^{\circ}$	$0.45 \times 0.32 \times 0.18 \text{ mm}$
$V = 20290(8) \text{ Å}^3$	

Data collection

Bruker SMART CCD area-detector diffractometer φ and ω scans Absorption correction: multi-scan (SADABS; Bruker, 1999) $T_{\min} = 0.633, T_{\max} = 0.824$ 10710 measured reflections

Refinement

Refinement on F^2 $R[F^2 > 2\sigma(F^2)] = 0.025$ $wR(F^2) = 0.070$ S = 1.007083 reflections 529 parameters H atoms treated by a mixture of independent and constrained

refinement

Table 1

Selected bond distances (Å).

La1-O4	2.431 (2)	La1-O1	2.5762 (19)
La1-O1 ⁱ	2.4672 (19)	La1-N4	2.658 (2)
La1–O5 ⁱ	2.474 (2)	La1-N5	2.674 (2)
La1-O8	2.513 (2)	La1-O2	2.675 (2)
La1-O7	2.573 (2)	La1···La1 ⁱ	4.0167 (9)

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

Table 2

Hydrogen-bonding geometry (Å, °).

$D - H \cdot \cdot \cdot A$	D-H	$H \cdot \cdot \cdot A$	$D \cdot \cdot \cdot A$	$D - H \cdot \cdot \cdot A$
$010-H1\cdots03^{ii}$ $010-H2\cdots09^{iii}$	0.912 (10) 0.910 (10)	1.960 (14) 1.927 (12)	2.858 (5) 2.836 (5)	168 (3) 178 (4)

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

The water H atoms were located in a difference map 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 positions and constrained to ride on their parent atoms, with C–H distances of 0.93–0.97 Å and $U_{\rm iso}({\rm H}) = 1.2 U_{\rm eq}({\rm C})$. The highest peak in the difference map is 1.57 Å from atom C35.

Data collection: *SMART* (Bruker, 1999); cell refinement: *SAINT-Plus* (Bruker, 1999); data reduction: *SAINT-Plus*; program(s) used to solve structure: *SHELXS*97 (Sheldrick, 1997*a*); program(s) used to refine structure: *SHELXL*97 (Sheldrick, 1997*a*); molecular graphics: *SHELXTL* (Sheldrick, 1997*b*); software used to prepare material for publication: *SHELXTL*.

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