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Bis(di- μ -acetato-aqua{2-[*N*-ethyl-*N*-(2-hydroxy-4-methylbenzyl)aminomethyl]-1-methylbenzimidazole}nickel)nickel(II) tetrahydrate

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Bis(di- μ -acetato-aqua{2-[*N*-ethyl-*N*-(2-hydroxy-4-methylbenzyl)amino-methyl]-1-methylbenzimidazole}-nickel)nickel(II) tetrahydrate

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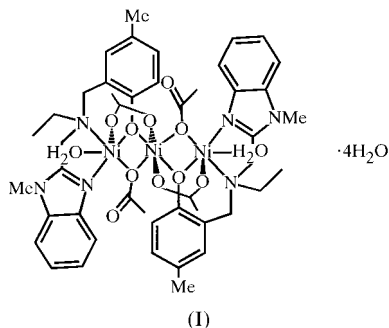
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The previously unknown title compound, tetra- μ -acetato-1:2 κ^2 O;1:2 κ^2 O':2:3 κ^2 O;2:3 κ^2 O':*O*'-diaqua-1 κ O,3 κ O-bis(μ -2-[[*N*-ethyl-*N*-(2-hydroxy-5-methylbenzyl)amino]methyl]-1-methyl-1*H*-benzimidazole)-1 κ^3 N³,*N*,*O*:2 κ O;3 κ^3 N³,*N*,*O*:2 κ O-trinickel(II) tetrahydrate, [Ni₃(C₁₈H₂₂N₃O)₂(C₂H₃O₂)₄(H₂O)₂].4H₂O, (I), is a centrosymmetric linear trinuclear nickel(II) complex, where the Ni atoms are in an octahedral coordination and the ligand heteroatoms act so as to model amino acid residues.



Experimental

2-[[*N*-Ethyl-*N*-(2-hydroxy-5-methylbenzyl)amino]methyl]-1-methyl-1*H*-benzimidazole (*L*; 0.224 g, 0.725 mmol) dissolved in methanol (7 ml) was added slowly to a suspension of NiBr₂ (0.231 g, 0.966 mmol) in refluxing methanol. Heating was continued until dissolution of the nickel salt was complete, affording a clear green

solution. Sodium acetate (0.277 g, 0.203 mmol) dissolved in methanol (5 ml) was added to the green solution. The solvent was removed under vacuum, resulting in a crude green product. This material was dissolved in acetonitrile and the solution filtered and evaporated to dryness. Recrystallization from methanol/2-propanol resulted in crystals of suitable quality for X-ray structure determination.

Crystal data

[Ni ₃ (C ₁₈ H ₂₂ N ₃ O) ₂ (C ₂ H ₃ O ₂) ₄ (H ₂ O) ₂].4H ₂ O	<i>Z</i> = 1
<i>M_r</i> = 1137.15	<i>D_x</i> = 1.419 Mg m ⁻³
Triclinic, <i>P</i> $\bar{1}$	Cu <i>K</i> α radiation
<i>a</i> = 11.130 (2) Å	Cell parameters from 25 reflections
<i>b</i> = 11.732 (2) Å	θ = 17.2–26.1°
<i>c</i> = 12.258 (2) Å	μ = 1.831 mm ⁻¹
α = 99.66 (2)°	<i>T</i> = 193 (2) K
β = 110.34 (1)°	Plate, colourless
γ = 110.23 (1)°	0.12 × 0.12 × 0.02 mm
<i>V</i> = 1330.6 (5) Å ³	

Data collection

Rigaku AFC-6R diffractometer	<i>R</i> _{int} = 0.031
ω -2 θ scans	θ _{max} = 60.04°
Absorption correction: ψ scan (North <i>et al.</i> , 1968)	<i>h</i> = -11 → 12
<i>T</i> _{min} = 0.873, <i>T</i> _{max} = 0.965	<i>k</i> = -12 → 13
4152 measured reflections	<i>l</i> = -13 → 0
3940 independent reflections	3 standard reflections
2872 reflections with <i>F</i> > 2.5 σ (<i>F</i> _o)	every 150 reflections
	intensity decay: 0.82%

Refinement

Refinement on <i>F</i>	H-atom parameters not refined
<i>R</i> = 0.058	<i>w</i> = 1/ σ^2 (<i>F</i> _o)
<i>wR</i> = 0.047	(Δ / σ) _{max} < 0.001
<i>S</i> = 1.750	$\Delta\rho$ _{max} = 0.64 e Å ⁻³
2865 reflections	$\Delta\rho$ _{min} = -0.68 e Å ⁻³
322 parameters	

The coordinates of the two H atoms of the O8 water molecule could not be reliably located and were not included in the refinement.

Data collection: *MSC/AFC Diffractometer Control Software* (Molecular Structure Corporation, 1994); cell refinement: *MSC/AFC Diffractometer Control Software*; data reduction: *TEXSAN* (Molecular Structure Corporation, 1992–1997); program(s) used to solve structure: *SIR92* (Altomare *et al.*, 1994); program(s) used to refine structure: *Xtal3.4 CRYLSQ* (Hall *et al.*, 1995); software used to prepare material for publication: *Xtal3.4 BONDLA CIFIO*.

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