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Key indicators

Single-crystal X-ray study T = 173 K Mean σ (C–C) = 0.005 Å Disorder in main residue R factor = 0.048 wR factor = 0.126 Data-to-parameter ratio = 10.6

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

The crystal structure of the title compound, $C_{36}H_{40}N_2O_2$, has been determined at 173 (2) K. The molecule has C_2 symmetry and the asymmetric unit contains one half-molecule. An intramolecular $O-H \cdots N$ hydrogen bond is formed between the phenol OH group and the Schiff base N atom.

(1*R*,2*R*)-(+)-4,4'-Di-tert-butyl-2,2'-[1,2-diphenyl-

ethane-1,2-divlbis(nitrilomethylidyne)]diphenol

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Comment

Manganese-salen complexes are used as catalysts due to their ability for highly stereoselective epoxidization of unfunctionalized alkenes (Lane & Burgess, 2003). The title Schiff base, (I), is one of the precursors to the first [Mn(salen)] type of asymmetric epoxidation catalysts developed by Jacobsen and co-workers (Zhang et al., 1990). We have previously reported the structures of (-)-(1S,2S)-N,N'-bis(salicylidene)-1,2diphenyl-1,2-ethanediamine (Korendovych & Rybak-Akimova, 2003) and its Mn^{III} complex (Korendovych & Rybak-Akimova, 2004). In this paper, we present the results of our study of another derivative of salen. These results were obtained during a course on 'Diffraction Methods in Structure Determination' at Tufts University.



Compound (I) was obtained in the enantiomerically pure (+)-(R,R) form by a Schiff base condensation of 5-*tert*-butyl-2hydroxybenzaldehyde and (1R,2R)-(+)-1,2-diphenyl-1,2ethanediamine. It crystallizes in the non-centrosymmetric space group $P2_12_12$. The molecule lies on a crystallographic twofold axis. Thus, one half-molecule constitutes the asymmetric unit (Fig. 1). The *tert*-butyl group exhibits orientational disorder, which was modelled with two positions.

As in the case of the salicylaldehyde derivative, the structure of (I) is stabilized by the formation of an intramolecular hydrogen bond between the phenol OH group and the Schiff base N atom, forming a six-membered ring. The angle between the planes defined by the rings of the salicylidene fragment and the phenyl substituent in compound (I) is 65.19 (11)°, which is very similar to the value of 63.76 (6)° observed in the non-substituted salicylaldehyde derivative (Korendovych & Rybak-Akimova, 2003). The angles between the planes of

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o1240



Figure 1

A view of the molecular structure of (I), showing the atom-labelling scheme of the asymmetric unit. Unlabelled atoms are related to labelled atoms by the symmetry operator (-x+2, -y+1, z). Displacement ellipsoids are drawn at the 50% probability level. H atoms have been omitted. Both disorder components are shown.





The molecular packing of (I), viewed along the c axis. H atoms have been omitted. Both disorder components are shown.

symmetry-related aromatic rings are $26.79 (9)^{\circ}$ for the phenyl rings and $42.10 (12)^{\circ}$ for the salicylidene benzene rings. These values are also fairly close to those observed for the salicylaldehyde derivative, suggesting a minor influence of the tertbutyl group in the para position on the overall conformation of the molecule. The packing diagram of (I) is presented in Fig. 2.

Experimental

The title compound was prepared according to the general procedure of Zhang et al. (1990). (1R,2R)-(+)-1,2-Diphenyl-1,2-ethanediamine

Mo $K\alpha$ radiation

T = 173 (2) K

Needle, vellow $0.16 \times 0.06 \times 0.04 \text{ mm}$

 $R_{\rm int} = 0.118$ $\theta_{\rm max} = 28.3^{\circ}$

 $h = -13 \rightarrow 13$

 $k = -29 \rightarrow 30$

 $l = -8 \rightarrow 8$

Cell parameters from 1286 reflections $\theta = 2.7 - 26.7^{\circ}$ $\mu = 0.07 \text{ mm}^{-1}$

979 reflections with $I > 2\sigma(I)$

Crystal data
$C_{36}H_{40}N_2O_2$
$M_r = 532.70$
Orthorhombic, P.
a = 10.4213 (16)
h = 22.729(4) Å

. .

c = 6.3769 (10) ÅV = 1510.4 (4) Å³ Z = 2

 $D_{\rm r} = 1.171 {\rm Mg m}^-$

Data collection

Bruker SMART CCD area-detector diffractometer φ and φ scans Absorption correction: none 11737 measured reflections 2142 independent reflections

Refinement

ŀ

S

2

F

Table 3

Refinement on F^2	$w = 1/[\sigma^2(F_0^2) + (0.0572P)^2]$
$R[F^2 > 2\sigma(F^2)] = 0.048$	where $P = (F_0^2 + 2F_c^2)/3$
$\nu R(F^2) = 0.126$	$(\Delta/\sigma)_{\rm max} < 0.001$
C = 0.88	$\Delta \rho_{\rm max} = 0.19 \ {\rm e} \ {\rm \AA}^{-3}$
142 reflections	$\Delta \rho_{\rm min} = -0.16 \text{ e } \text{\AA}^{-3}$
02 parameters	Extinction correction: SHELXL97
I atoms treated by a mixture of	(Sheldrick, 1997)
independent and constrained	Extinction coefficient: 0.031 (3)
refinement	

Table 1 Selected bond lengths (Å).

N1-C11	1.278 (4)	O1-H1	1.05 (4)
N1-C12	1.453 (4)	C6-C11	1.448 (4)
O1-C1	1.348 (4)	$C12 - C12^{i}$	1.559 (6)

Symmetry code: (i) -x + 2, -y + 1, z.

Hydrogen-bond	geometry	(Å,	°).

$D - H \cdots A$	<i>D</i> -H	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - H \cdots A$
O1−H1···N1	1.05 (4)	1.64 (5)	2.578 (4)	147 (4)

Carbon-bound H atoms were placed in idealized positions and refined using a riding model, with C-H = 0.95-1.00 Å and with $U_{\rm iso}({\rm H}) = 1.2 U_{\rm eq}({\rm C})$. The H atom bound to the phenol O atom was found in a difference Fourier map and refined isotropically. In the absence of significant anomalous dispersion effects, Friedel pairs were averaged. The relatively high R_{int} value (0.118) was attributed to small size of the crystal, which resulted in weak diffraction. All attempts to obtain better quality crystals failed.

The tert-butyl group exhibits orientational disorder, which was modelled with two positions. The disordered C atoms were presumed to have the same anisotropic displacement parameters. Furthermore, C-C(methyl) distances in the tert-butyl group were restrained to be

the same for both orientations. The occupancies of the two sites converged at 0.622 (13) and 0.378 (13).

Data collection: *SMART* (Bruker, 1998); cell refinement: *SAINT* (Bruker, 1998); data reduction: *SAINT*; program(s) used to solve structure: *SHELXS97* (Sheldrick, 1997); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *SHELXTL* (Bruker, 2000); software used to prepare material for publication: *XCIF* in *SHELXTL*.

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