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#### **Key indicators**

Single-crystal X-ray study T = 293 K Mean  $\sigma$ (C–C) = 0.002 Å R factor = 0.045 wR factor = 0.137 Data-to-parameter ratio = 19.6

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

# 2-Formylthymol oxime

The structure of the title compound [systematic name: 2-hydroxy-6-methyl-3-(1-methylethyl)benzaldehyde oximel  $C_{11}H_{15}NO_2$ , exhibits intra- as well as intermolecular hydrogen bonding, involving participation of the phenolic OH group in intramolecular hydrogen bonding and the hydroxyl group of the oxime in intermolecular hydrogen bonding. The H atom of the phenolic hydroxyl group forms a strong O-H···N intramolecular hydrogen bond with an O···N distance of 2.5788 (14) Å, which is in the middle of the expected range for such hydrogen bonds. The H atom of the hydroxyl group (in the oxime functionality) forms a weaker hydrogen bond with the phenolic hydroxyl group of a neighboring molecule  $[O \cdots O = 2.8317 (14) \text{ Å}]$ , forming an extended chain, as expected for phenolic aldoximes which have bulky substituents on the aryl ring.

## Comment

Thymol is a naturally occurring phenolic monoterpenoid. It possesses an ecological role and shows a broad spectrum of biological activities (Desai & Shah, 2003). In order to enhance the overall biological activity of thymol, derivatives such as nitroso, amino, azomethine, 4-thiazolidinones, 2-azetidinones and 4-imidazolinones have been prepared (Vashai et al., 1995). On the other hand, derivatization of the hydroxyl group of thymol to ethers and esters has resulted in an increase in biological activities. A structure-activity correlation has also been established in this series of compounds and the overall activity has been found to depend on the nature and position of the functional groups. Thus, thymol was derivatized to 2formyl thymol oxime, (I), to use it for the preparation of metal complexes, as a number of metal-oxime complexes are known to have biological significance (Chakravorty, 1974; Lumme et al., 1984; Jayaraju & Kondapi, 2001). We present the structure of (I) here.



Compound (I) is a member of a general class of phenolic oximes (Smith *et al.*, 2003). These compounds have found

extensive use in industry, mainly as extractants for copper

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A view of the title compound, showing the atom-labeling scheme. Displacement ellipsoids are drawn at the 20% probability level and H atoms are represented by circles of arbitrary size. The dashed line indicates a hydrogen bond.

(Kordosky, 2002), but also as anticorrosives in protective coatings (Thorpe *et al.*, 1999). Another feature of the phenolic oxime ligands is their propensity (Chaudhuri *et al.*, 1993; Bill *et al.*, 1997) to form polynuclear complexes in which both the oxime and phenolate functions can act as bridging units.

Elemental analysis for (I) gave a satisfactory fit to the formula  $C_{11}H_{15}NO_2$ . Table 1 contains selected bond lengths and angles. A view of the molecule and unit-cell contents are shown in Figs. 1 and 2, respectively. The average length of the benzene ring bonds is 1.396 (12) Å, which is in good agreement with generally accepted values.

Hydrogen bonding is a major feature of the structures of phenolic oximes. This results from the high density of hydrogen-bonding donors and acceptors per molecule. Invariably, the phenolic H atom forms an intramolecular hydrogen bond to the N atom of the oxime group, giving a sixmembered ring. Since the phenolic H atom is often not found in Fourier difference maps, this interaction is usually characterized in terms of the phenolic O to oxime N separation. This distance varies little between structures, with a maximum value of 2.65 Å and a minimum of 2.51 Å. However, a general trend is that aldoximes have a greater phenolic O···N distance than the ketoximes (Smith et al., 2003). In all of the free ligand structures, the molecules associate via intermolecular hydrogen bonding. These structures fall into two categories. Dimers result from the interaction of the oxime H atom with an adjacent phenolic O atom to produce a pseudomacrocyclic ligand with a 14-membered inner ring. This structure is seen only for aldoximes with no substituents or only monoatomic substituents on the aromatic ring (Smith et al., 2003).

The introduction of groups which remove planarity in the molecule appears to stop efficient packing of dimeric units in the crystal structure and, instead, a polymeric structure,  $[(H_2sal)_n]$ , is observed. This is true for all phenolic ketoximes



## Figure 2

The molecular packing of the title compound, viewed along the b axis. Dashed lines indicate the hydrogen-bonding interactions.

and for phenolic aldoximes which have bulky substituents on the aryl ring (Smith *et al.*, 2003).

The title compound exhibits intra- as well as intermolecular hydrogen bonding (Table 2), involving participation of the phenolic OH group in intramolecular hydrogen bonding and the hydroxyl group of the oxime in intermolecular hydrogen bonding, as indicated above. The H atom of the phenolic hydroxyl group forms a strong  $O1-H\cdots N1$  intramolecular hydrogen bond with an  $O1\cdots N1$  distance of 2.5788 (14) Å, which is in the middle of the expected range for such hydrogen bonds (Smith *et al.*, 2003).

The H atom of the hydroxyl group (in the oxime functionality) attached to atom N1 forms a weaker hydrogen bond with the phenolic hydroxyl group of a neighboring molecule  $[O2 \cdots O1 = 2.8317 (14) \text{ Å}]$ , forming an extended chain, as expected for phenolic aldoximes which have bulky substituents on the aryl ring (Smith *et al.*, 2003).

## **Experimental**

The title compound was prepared by the condensation of 2-formylthymol (obtained by *ortho*-formylation of thymol) (3.56 g, 20 mmol) with hydroxylamine hydrochloride (1.4 g, 20 mmol) in ethanol (150 ml). Yellow crystals of (I) suitable for X-ray diffraction were obtained upon slow evaporation of the reaction mixture.

## Crystal data

$C_{11}H_{15}NO_2$	$D_x = 1.208 \text{ Mg m}^{-3}$
$M_r = 193.24$	Mo $K\alpha$ radiation
Monoclinic, $P2_1/n$	Cell parameters from 4359
a = 8.8517 (7)  Å	reflections
b = 9.0145 (7)  Å	$\theta = 2.5 - 28.2^{\circ}$
c = 13.5956 (10)  Å	$\mu = 0.08 \text{ mm}^{-1}$
$\beta = 101.698 \ (2)^{\circ}$	T = 293 (2) K
$V = 1062.31 (14) \text{ Å}^3$	Irregular fragment, pale yellow
Z = 4	$0.55 \times 0.45 \times 0.32 \text{ mm}$

Data collection

Bruker SMART 1K CCD area-	2592 independent reflections
detector diffractometer	1897 reflections with $I > 2\sigma(I)$
$\varphi$ and $\omega$ scans	$R_{\rm int} = 0.026$
Absorption correction: multi-scan	$\theta_{\rm max} = 28.3^{\circ}$
(SADABS; Sheldrick, 2002)	$h = -10 \rightarrow 11$
$T_{\min} = 0.716, \ T_{\max} = 0.928$	$k = -10 \rightarrow 11$
8098 measured reflections	$l = -17 \rightarrow 18$

## Refinement

 $\begin{array}{ll} \mbox{Refinement on } F^2 & w = 1/[\sigma^2(F_o^2) + (0.0689P)^2 \\ R[F^2 > 2\sigma(F^2)] = 0.046 & + 0.1206P] \\ wR(F^2) = 0.137 & where \ P = (F_o^2 + 2F_c^2)/3 \\ S = 1.07 & (\Delta/\sigma)_{max} = 0.007 \\ 2592 \ \mbox{reflections} & \Delta\rho_{max} = 0.25 \ \mbox{e} \ \mbox{Å}^{-3} \\ 132 \ \mbox{parameters} & \Delta\rho_{min} = -0.17 \ \mbox{e} \ \mbox{Å}^{-3} \\ \mbox{H-atom parameters constrained} \\ \end{array}$ 

## Table 1

Selected geometric parameters (Å, °).

01-C1 02-N1	1.3710 (14) 1 3982 (14)	N1-C21	1.2743 (16)
C21-N1-O2	112.32 (11)	O1-C1-C2	120.36 (11)
O1-C1-C6	117.15 (11)	N1-C21-C2	121.68 (11)

## Table 2

Hydrogen-bond geometry (Å, °).

$D - \mathbf{H} \cdot \cdot \cdot A$	D-H	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - \mathbf{H} \cdots A$
O1−H1O···N1	0.82	1.85	2.5788 (14)	148
$O2-H2O\cdots O1^i$	0.82	2.02	2.8317 (14)	169

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

H atoms were positioned geometrically and constrained to ride on their parent atoms. For methyl H atoms, C-H = 0.96 Å and  $U_{iso}(H) = 1.5U_{co}(C)$ ; each group was allowed to rotate freely about its C-C bond. For other H atoms, O-H = 0.82 Å, aromatic C-H = 0.93 Å and methine C-H = 0.98 Å, and  $U_{iso}(H) = 1.2U_{eq}(C,O)$ .

Data collection: *SMART* (Bruker, 2001); cell refinement: *SAINT* (Bruker, 2001); data reduction: *SAINT*; program(s) used to solve structure: *SHELXS97* (Sheldrick, 1997); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *SHELXTL* (Sheldrick, 1998); software used to prepare material for publication: *SHELXTL*.

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