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Deepak Chopra,^a* T. P. Mohan,^b K. S. Rao^b and T. N. Guru Row^a

^aSolid State and Structural Chemistry Unit, Indian Institute of Science, Bangalore 560 012, Karnataka, India, and ^bRallis India Limited, Peenya Industrial Area, Bangalore 560 078, India

Correspondence e-mail: deepak@sscu.iisc.ernet.in

Key indicators

Single-crystal X-ray study T = 293 K Mean σ (C–C) = 0.003 Å R factor = 0.050 wR factor = 0.149 Data-to-parameter ratio = 15.7

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

Methyl 2(*E*)-methoxyimino-2-[2-(2-methylphenoxymethyl)phenyl]acetate

The title compound (also known as kresoxim-methyl), $C_{18}H_{19}NO_4$, is an active agrochemical exhibiting fungicidal activity. The dihedral angle between the two rings is 65.9 (1)°. The crystal structure is stabilized by weak but highly directional $C-H\cdots O$ and $C-H\cdots \pi$ intermolecular interactions.

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Comment

An important aspect in the rational design of bioactive molecules involves relating chemical structure to biological activity (Lewis *et al.*, 1991). The conformation of the molecule is found to influence the levels of biological activity. Correlation of the results obtained from X-ray crystallography with biological activity has aided in the chemical design of few active agrochemicals. The activity of a series of triazolyl ketone herbicides (Anderson *et al.*, 1983) has been investigated along with the fungicidal activities of *N*-phenylsuccinamides (Zenei *et al.*, 1988). In this paper, we report the structure of the title compound, (I), which possesses fungicidal activity.



In (I), there is an intramolecular C8–H8B···O2 interaction (Fig. 1 and Table 2), forming a pseudo-seven-membered ring [Etter symbol S(7); Bernstein *et al.*, 1995]. Molecules are linked *via* C14–H14···O3ⁱⁱ hydrogen bond (see Table 2 for symmetry code), forming chains along the *b* axis. Furthermore, weak but highly directional C–H·· π interactions form molecular chains parallel to the *c* axis (Fig. 2 and Table 2).

Experimental

Compound (I) was obtained from Rallis India, Bangalore. Single crystals were grown by slow evaporation of an acetone solution at 278 K.

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organic papers

Crystal data

C18H19NO4 $M_r = 313.34$ Monoclinic, C2/c a = 16.843 (16) Åb = 15.480 (14) Åc = 13.728 (13) Å $\beta = 114.337 (14)^{\circ}$ $V = 3261 (5) \text{ Å}^3$ Z = 8

Data collection

Bruker SMART APEX CCD areadetector diffractometer φ and ω scans Absorption correction: multi-scan (SADABS; Sheldrick, 1996) $T_{\min} = 0.933, T_{\max} = 0.982$ 16747 measured reflections

Refinement

Refinement on F^2	$w = 1/[\sigma^2(F_o^2) + (0.0725P)^2]$
$R[F^2 > 2\sigma(F^2)] = 0.050$	+ 1.85P]
$wR(F^2) = 0.149$	where $P = (F_o^2 + 2F_c^2)/3$
S = 1.02	$(\Delta/\sigma)_{\rm max} < 0.001$
3315 reflections	$\Delta \rho_{\rm max} = 0.34 \text{ e } \text{\AA}^{-3}$
211 parameters	$\Delta \rho_{\rm min} = -0.23 \text{ e } \text{\AA}^{-3}$
H-atom parameters constrained	

 $D_x = 1.276 \text{ Mg m}^{-3}$

Cell parameters from 865

Mo $K\alpha$ radiation

reflections $\theta = 1.4-26.4^{\circ}$

 $\mu = 0.09 \text{ mm}^{-1}$

T = 293 (2) K

 $R_{\rm int} = 0.032$

 $\theta_{\rm max} = 26.4^{\circ}$ $h=-21\rightarrow 20$

 $k = -19 \rightarrow 19$

 $l = -17 \rightarrow 16$

Block, colorless

 $0.28 \times 0.25 \times 0.20 \text{ mm}$

3315 independent reflections 2332 reflections with $I > 2\sigma(I)$

Table 1

Selected geometric parameters (Å, °).

01-C5	1.365 (2)	O2-N1	1.379 (2	
01-C8	1.428 (2)	N1-C15	1.287 (2	
C5-O1-C8-C9	179.98 (14)	C9-C10-C15-N1	72.0 (2)	
C10-C9-C8-O1	63.6 (2)	C11-C10-C15-C18	71.6 (2)	
C17-O4-C18-C15	178.73 (17)	C8-O1-C5-C4	2.8 (3)	

Table	2	
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H	lyd	lrogen-	bonding	g geomet	try ((A, °).
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$D - H \cdots A$	D-H	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - H \cdots A$
$\begin{array}{c} \hline C8-H8B\cdots O2\\ C17-H17B\cdots Cg1^{i}\\ C14-H14\cdots O3^{ii} \end{array}$	0.97	2.52	3.191 (3)	126
	0.96	2.81	3.504 (4)	130
	0.93	2.60	3.440 (4)	151

Symmetry codes: (i) $x, -y, \frac{1}{2} + z$; (ii) $\frac{3}{2} - x, y - \frac{1}{2}, \frac{1}{2} - z$. Cg1 is the centroid of the C9–C14 benzene ring

All H atoms were constrained to ideal geometry, with C-H distances in the range 0.93–0.97 Å, and with $U_{iso}(H) = 1.2U_{eq}(C)$ or $1.5U_{eq}(C_{methyl})$. The methyl groups were allowed to rotate freely about the C-C bonds.

Data collection: SMART (Bruker, 2000); cell refinement: SAINT (Bruker, 2000); data reduction: SAINT; program(s) used to solve structure: SIR92 (Altomare et al., 1993); program(s) used to refine structure: SHELXL97 (Sheldrick, 1997); molecular graphics: CAMERON (Watkin et al., 1993); software used to prepare material for publication: PLATON (Spek, 2003).

We thank the Department of Science and Technology, India, for data collection on the CCD facility set up under the



Figure 1

The molecular structure of (I), showing 50% probability ellipsoids. The dotted line indicates the C-H···O intramolecular interaction. Other H atoms have been omitted.





Packing diagram of (I), showing, by dotted lines, the $C-H \cdots O$ hydrogen bond and $C-H\cdots\pi$ intermolecular chains along the b and c axes, respectively.

IRHPA-DST program. D. Chopra thanks the CSIR, India, for a JRF.

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