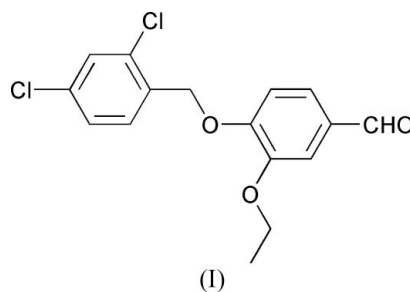
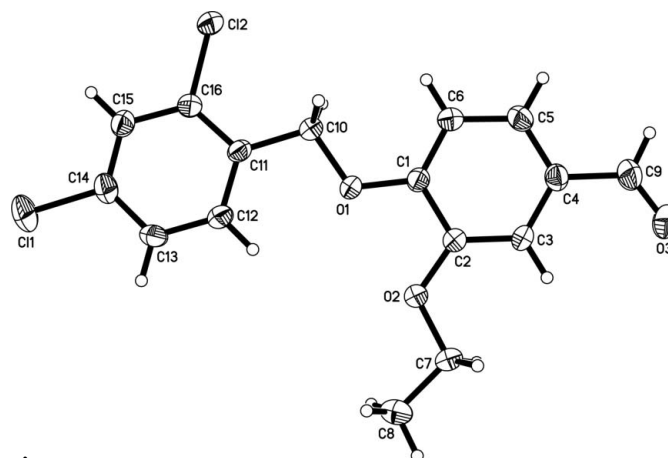


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liu_shouxin@163.comCorrespondence e-mail:
han_jianrong@163.com**Key indicators**Single-crystal X-ray study
 $T = 294$ K
Mean $\sigma(\text{C}-\text{C}) = 0.006$ Å
 R factor = 0.029
 wR factor = 0.083
Data-to-parameter ratio = 8.4For details of how these key indicators were
automatically derived from the article, see
<http://journals.iucr.org/e>.

4-(2,4-Dichlorobenzoyloxy)-3-ethoxybenzaldehyde

In the title compound, $\text{C}_{16}\text{H}_{14}\text{Cl}_2\text{O}_3$, the ethylvanillin group
makes a dihedral angle of $6.15(3)^\circ$ with the dichlorobenzene
ring. Intermolecular $\text{C}-\text{H}\cdots\text{O}$ interactions lead to trimeric
associations of molecules.Received 17 November 2006
Accepted 20 November 2006**Comment**As part of our ongoing studies (Zhen *et al.*, 2006) of the
coordination properties of Schiff bases functioning as ligands,
we have investigated the title compound, (I), which is used as a
precursor in the preparation of Schiff bases.In the molecule of (I) (Fig. 1), the bond lengths and angles
are within their normal ranges (Allen *et al.*, 1987). The
ethylvanillin group (atoms C1–C6/C9/O1/O2) is essentially
planar, with an r.m.s. deviation for the fitted atoms of 0.013 Å.
Its mean plane makes a dihedral angle of $6.15(3)^\circ$ with the
mean plane of the C11–C16 benzene ring.The crystal structure of (I) is stabilized by weak inter-
molecular $\text{C}-\text{H}\cdots\text{O}$ interactions (Table 1 and Fig. 2),
resulting in trimeric associations generated by a crystal-
lographic threefold axis.**Figure 1**The molecular structure of (I), with displacement ellipsoids for non-H
atoms drawn at the 30% probability level.

Experimental

An anhydrous acetonitrile solution (50 ml) of 3-ethoxy-4-hydroxybenzaldehyde (1.66 g, 10 mmol) was added dropwise to a solution (100 ml) of 1-(bromomethyl)-2,4-dichlorobenzene (2.40 g, 10 mmol) and potassium carbonate (1.38 g, 10 mmol) in acetonitrile over a period of 30 min, and the mixture refluxed for 24 h under a nitrogen atmosphere. The solvent was removed and the resultant mixture poured into ice–water (100 ml). The white precipitate was isolated and recrystallized from acetonitrile, and then dried in a vacuum to give the pure compound in 53% yield. Colorless single crystals of (I) suitable for X-ray analysis were obtained by slow evaporation of an acetonitrile solution.

Crystal data

$C_{16}H_{14}Cl_2O_3$
 $M_r = 325.17$
 Trigonal, $R\bar{3}$
 $a = 19.849$ (3) Å
 $c = 10.340$ (2) Å
 $V = 3528.0$ (10) Å³
 $Z = 9$

$D_x = 1.378$ Mg m⁻³
 Mo $K\alpha$ radiation
 $\mu = 0.42$ mm⁻¹
 $T = 294$ (2) K
 Block, colorless
 $0.26 \times 0.24 \times 0.20$ mm

Data collection

Bruker SMART APEX CCD
 diffractometer
 φ and ω scans
 Absorption correction: multi-scan
 (SADABS; Sheldrick, 1996)
 $T_{\min} = 0.878$, $T_{\max} = 0.919$

6567 measured reflections
 1601 independent reflections
 1263 reflections with $I > 2\sigma(I)$
 $R_{\text{int}} = 0.040$
 $\theta_{\text{max}} = 26.4^\circ$

Refinement

Refinement on F^2
 $R[F^2 > 2\sigma(F^2)] = 0.029$
 $wR(F^2) = 0.083$
 $S = 1.02$
 1601 reflections
 191 parameters
 H-atom parameters constrained

$w = 1/[\sigma^2(F_o^2) + (0.0472P)^2 + 0.7953P]$
 where $P = (F_o^2 + 2F_c^2)/3$
 $(\Delta/\sigma)_{\text{max}} < 0.001$
 $\Delta\rho_{\text{max}} = 0.24$ e Å⁻³
 $\Delta\rho_{\text{min}} = -0.18$ e Å⁻³

Table 1

Hydrogen-bond geometry (Å, °).

$D-H\cdots A$	$D-H$	$H\cdots A$	$D\cdots A$	$D-H\cdots A$
$C5-H5\cdots O3^i$	0.93	2.52	3.429 (5)	167

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

Due to insignificant anomalous dispersion effects, Friedel pairs were merged before refinement. The molecule of (I) is achiral, thus

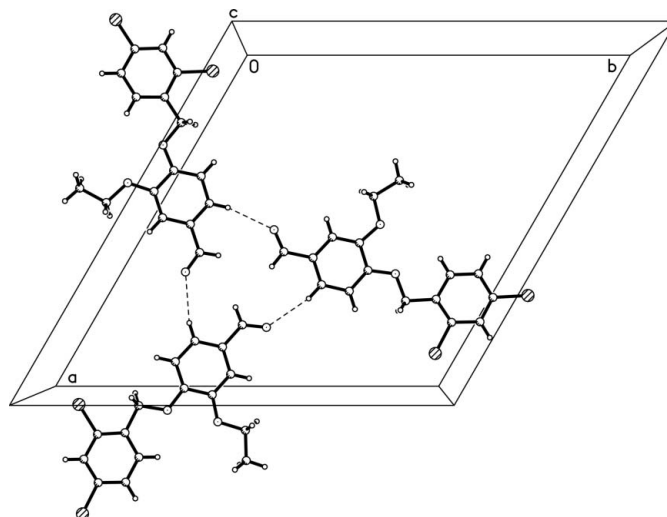


Figure 2

A trimeric association of molecules of (I), with C–H···O interactions shown as dashed lines.

any chirality in an individual crystal must arise from packing effects. The H atoms were included in calculated positions ($C-H = 0.93-0.97$ Å) and refined as riding, with $U_{\text{iso}}(H) = 1.2U_{\text{eq}}(C)$ or $1.5U_{\text{eq}}(\text{methyl C})$.

Data collection: SMART (Bruker, 1999); cell refinement: SAINT (Bruker, 1999); data reduction: SAINT; program(s) used to solve structure: SHELXS97 (Sheldrick, 1997a); program(s) used to refine structure: SHELXL97 (Sheldrick, 1997a); molecular graphics: SHELXTL (Sheldrick, 1997b); software used to prepare material for publication: SHELXTL.

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