

2,4,5-Trimethoxybenzaldehyde monohydrate

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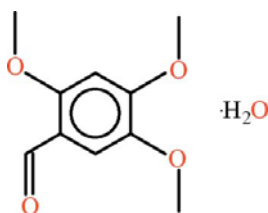
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Key indicators: single-crystal X-ray study; $T = 296$ K; mean $\sigma(\text{C}-\text{C}) = 0.005$ Å; R factor = 0.060; wR factor = 0.212; data-to-parameter ratio = 12.9.

In the title compound, $\text{C}_{10}\text{H}_{12}\text{O}_4 \cdot \text{H}_2\text{O}$, the 2,4,5-trimethoxybenzaldehyde molecule is almost planar (rms deviation = 0.0183 Å). There is an $R_2^2(5)$ ring motif due to $\text{O}-\text{H} \cdots \text{O}$ hydrogen bonding. In the crystal, the molecules are stabilized in the form of one-dimensional polymeric chains extending along [010] due to $\text{O}-\text{H} \cdots \text{O}$ hydrogen bonding with adjacent water molecules. The H atoms involved in intermolecular hydrogen bonding are disordered over two sets of sites of equal occupancy.

Related literature

For related background and related structures, see: Asiri *et al.* (2010*a,b*), Hussain *et al.* (2010). For graph-set notation, see: Bernstein *et al.* (1995).



Experimental

Crystal data

$\text{C}_{10}\text{H}_{12}\text{O}_4 \cdot \text{H}_2\text{O}$

$M_r = 214.21$

Monoclinic, $P2_1/c$

$a = 18.084$ (5) Å

$b = 4.2456$ (10) Å

$c = 14.600$ (4) Å

$\beta = 108.290$ (9)°

$V = 1064.3$ (5) Å³

$Z = 4$

Mo $K\alpha$ radiation

$\mu = 0.11$ mm⁻¹

$T = 296$ K

$0.22 \times 0.10 \times 0.08$ mm

Data collection

Bruker Kappa APEXII CCD diffractometer

Absorption correction: multi-scan (SADABS; Bruker, 2005)

$T_{\min} = 0.992$, $T_{\max} = 0.995$

8287 measured reflections

1915 independent reflections

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

$R_{\text{int}} = 0.066$

Refinement

$R[F^2 > 2\sigma(F^2)] = 0.060$

$wR(F^2) = 0.212$

$S = 1.05$

1915 reflections

148 parameters

3 restraints

H atoms treated by a mixture of independent and constrained refinement

$\Delta\rho_{\text{max}} = 0.18$ e Å⁻³

$\Delta\rho_{\text{min}} = -0.22$ e Å⁻³

Table 1

Hydrogen-bond geometry (Å, °).

$D-\text{H} \cdots A$	$D-\text{H}$	$\text{H} \cdots A$	$D \cdots A$	$D-\text{H} \cdots A$
$\text{O5}-\text{H51} \cdots \text{O2}$	0.85 (4)	2.54 (5)	3.181 (5)	133 (4)
$\text{O5}-\text{H51} \cdots \text{O3}$	0.85 (4)	2.19 (4)	3.006 (5)	160 (4)
$\text{O5}-\text{H52} \cdots \text{O5}^{\text{i}}$	0.83 (10)	1.89 (10)	2.710 (6)	174 (19)
$\text{O5}-\text{H53} \cdots \text{O5}^{\text{ii}}$	0.86 (10)	1.86 (10)	2.714 (6)	169 (7)

Symmetry codes: (i) $-x + 1, -y, -z + 1$; (ii) $-x + 1, -y + 1, -z + 1$.

Data collection: *APEX2* (Bruker, 2009); cell refinement: *SAINT* (Bruker, 2009); data reduction: *SAINT*; program(s) used to solve structure: *SHELXS97* (Sheldrick, 2008); program(s) used to refine structure: *SHELXL97* (Sheldrick, 2008); molecular graphics: *ORTEP-3 for Windows* (Farrugia, 1997) and *Mercury* (Bruno *et al.*, 2002); software used to prepare material for publication: *WinGX* (Farrugia, 1999) and *PLATON* (Spek, 2009).

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Supplementary data and figures for this paper are available from the IUCr electronic archives (Reference: DN2621).

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