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Key indicators

Single-crystal X-ray study T = 291 K Mean σ (C–C) = 0.003 Å R factor = 0.037 wR factor = 0.087 Data-to-parameter ratio = 14.2

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

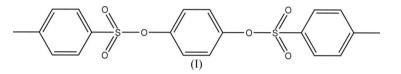
p-Phenylene bis(4-methylbenzenesulfonate)

The molecules of the title compound, $C_{20}H_{18}O_6S_2$, lie across centres of inversion. The dihedral angle between the central and terminal benzene rings is 54.92 (9)°.

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Comment

Sulfonic acid esters exhibit promising efficacy and selectivity against both plasmodium and human skin cancer cells (Betts *et al.*, 2006; Langler *et al.*, 2003). We report here the crystal structure of the title compound, (I).



The molecule of (I) lies across crystallographic inversion centres. Bond lengths and angles in (I) are normal. The dihedral angle between the C1–C6 and C8–C10/C8ⁱ–C10ⁱ planes is 54.92 (9)° [symmetry code: (i) 2 - x, -y, 1 - z]. The C1–S1–O3–C8 torsion angle is 57.79 (16)°.

 $C-H\cdots O$ intermolecular hydrogen bonds (Table 1) link the molecules into a two-dimensional network parallel to the *bc* plane.

Experimental

Compound (I) was prepared according to the literature method of Manivannan *et al.* (2005*a*,*b*). 4-Toluenesulfonyl chloride (1.0 g) in acetone (4 ml) was added dropwise to a solution of 1,4-dihydroxy-benzene (0.26 g) in aqueous NaOH (2.5 ml, 10%), and the mixture was stirred for 10 h. The resulting solid was filtered off and recrys-tallized from acetone.

Crystal data

Data collection

Bruker SMART APEX2 CCD area-	605
detector diffractometer	181
φ and ω scans	112
Absorption correction: multi-scan	$R_{\rm in}$
(SADABS; Bruker, 2005)	$\theta_{\rm ma}$
$T_{\min} = 0.902, \ T_{\max} = 0.942$	

050 measured reflections 819 independent reflections 127 reflections with $I > 2\sigma(I)$ $R_{int} = 0.051$ $P_{max} = 25.5^{\circ}$

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Refinement

Refinement on F^2	H-atom parameters constrained
$R[F^2 > 2\sigma(F^2)] = 0.037$	$w = 1/[\sigma^2(F_o^2) + (0.0406P)^2]$
$wR(F^2) = 0.087$	where $P = (F_o^2 + 2F_c^2)/3$
S = 1.00	$(\Delta/\sigma)_{max} = 0.001$
1819 reflections	$\Delta \rho_{\text{max}} = 0.21 \text{ e } \text{\AA}^{-3}$
128 parameters	$\Delta \rho_{\text{min}} = -0.27 \text{ e } \text{\AA}^{-3}$

Table 1

Hydrogen-bond geometry (Å, °).

$D - H \cdots A$	D-H	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - \mathbf{H} \cdot \cdot \cdot A$
C10-H10···O2 ⁱⁱ	0.93	2.51	3.399 (3)	159
Symmetry code: (ii) r	$-v = \frac{1}{7} = \frac{1}{7}$			

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

H atoms were placed in calculated positions, and refined using a riding model, with C-H = 0.93 or 0.96 Å and $U_{iso}(H) = 1.2U_{eq}(C)$ or $1.5U_{eq}(methyl C)$.

Data collection: *APEX2* (Bruker, 2005); cell refinement: *APEX2*; data reduction: *SAINT* (Bruker, 2005); program(s) used to solve structure: *SHELXS97* (Sheldrick, 1997); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *SHELXTL* (Bruker, 1998); software used to prepare material for publication: *SHELXTL*.

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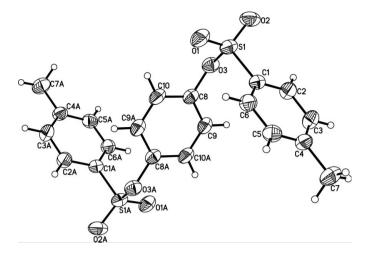


Figure 1

The molecular structure of (I), showing 30% probability displacement ellipsoids and the atomic numbering. Atoms labelled with the suffix A are generated by the symmetry operation (2 - x, -y, 1 - z).

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