

supporting information

Acta Cryst. (2010). E66, o739 [doi:10.1107/S1600536810006641]

Benzene-1,3,5-triyl tris(methanesulfonate)

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S1. Comment

The synthesis of supported organic compounds and dendrimers on Merrifield resin with a mesyl group and a trihydroxybenzene core has been one of our objectives; however the analysis of the supported products on the solid state is only limited to infrared spectroscopy (Grice *et al.*, 2000; Yan *et al.*, 2001). In our previous work we have used mass spectroscopy to characterize intermediates and products (Chavez *et al.*, 2003; Olivas *et al.*, 2008; Madrigal *et al.*, 2006). In this work, and as part of our ongoing research, we have synthesized benzene-1,3,5-triyl trimethanesulfonate using 1,3,5 trihydroxybenzene. The product (I) is an intermediate in the synthesis of complex first, second and third generation dendrimers.

As shown in Fig. 1, the molecule shows two fragments of trimethanesulfonate above and one below the plane of the benzene ring, with angles C5—O3—S2 119.3 (2) $^{\circ}$, C1—O1—S1 121.1 (2) $^{\circ}$ and C3—O2—S3 120.2 (2) $^{\circ}$. This conformation is different from the one shown by the analogue benzene 1,2,5-tris(*p*-toluenesulfonate), where the conformation of the molecule is described as a three-legged table (all fragments of the *p*-toluenesulfonate lay on the top of the benzene ring) stabilized by intramolecular C—H···O and C—H··· π (Vembu *et al.*, 2003).

In the crystal structure of (I), adjacent units are arranged like dimers via intermolecular C3—O2···(O9—S1)ⁱ, (3.035 Å, (i): 2-x, -y, 1-z) oxygen bond interactions (Fig 2). Similar interactions are described in the literature, e.g. the helical structure of sulfate anions formed by non-covalent O···O (2.9413 Å) contacts described in Raghavaiah *et al.* 2006, and it stresses the role of a flip-flop water chain in determining the helical arrangement of sulfate anions in the solid state. These non-covalent O···O interactions are well-established in the literature including their theoretical aspects (Ni *et al.* 2004). In addition, adjacent dimers are linked together *via* intermolecular C—H···O hydrogen bond interactions (table 2).

S2. Experimental

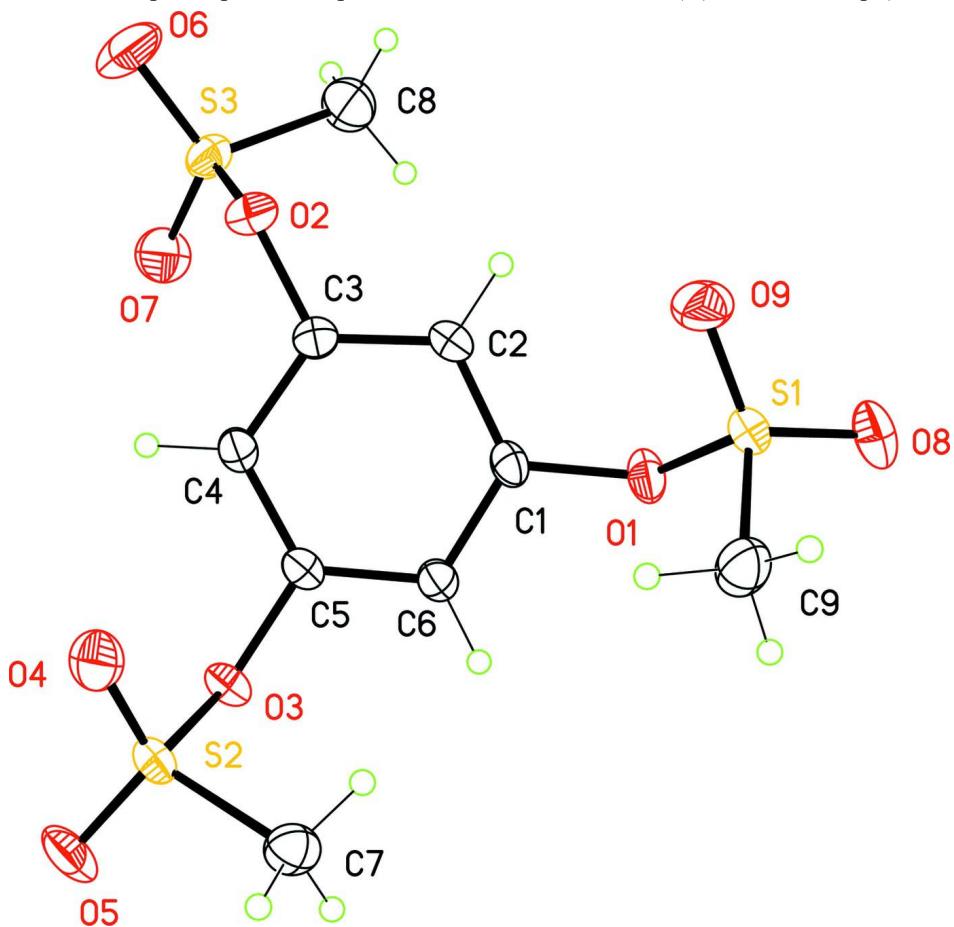
The synthesis of the title compound included reagents and solvents of reagent grade, which were used without further purification. In a round bottom flask of 10 ml provided with a magnetic stirrer, was placed 0.3 g (2.3 mmol) of 1,3,5-trihydroxybenzene and 3 ml of pyridine. The flask was immersed in an ice bath and 0.58 ml (7.6 mmol) of methanesulfonyl chloride was added dropwise. The mixture was stirred for one hour and stored in the refrigerator for 24 hours. The reaction mixture was poured on to cracked ice and the precipitate was washed with a cold solution 20% of HCl (3 x 5 ml) and cold water (3 x 5 ml). The solid obtained was dried under vacuum. The yield was of 49 % of melting point: 142 °C. IR(KBr): 3099, 3027, 1602, 1458, 1367, 1182, 1110 cm⁻¹ (Skoog, *et al.*, 1997). ¹H NMR (CDCl₃): δ 7.51 (s, 3H, CH), 3.49 (s, 9H, CH₃). ¹³C NMR (CDCl₃): δ 149.7(CO), 116.3(CH), 39.1(CH₃).

Crystallization.

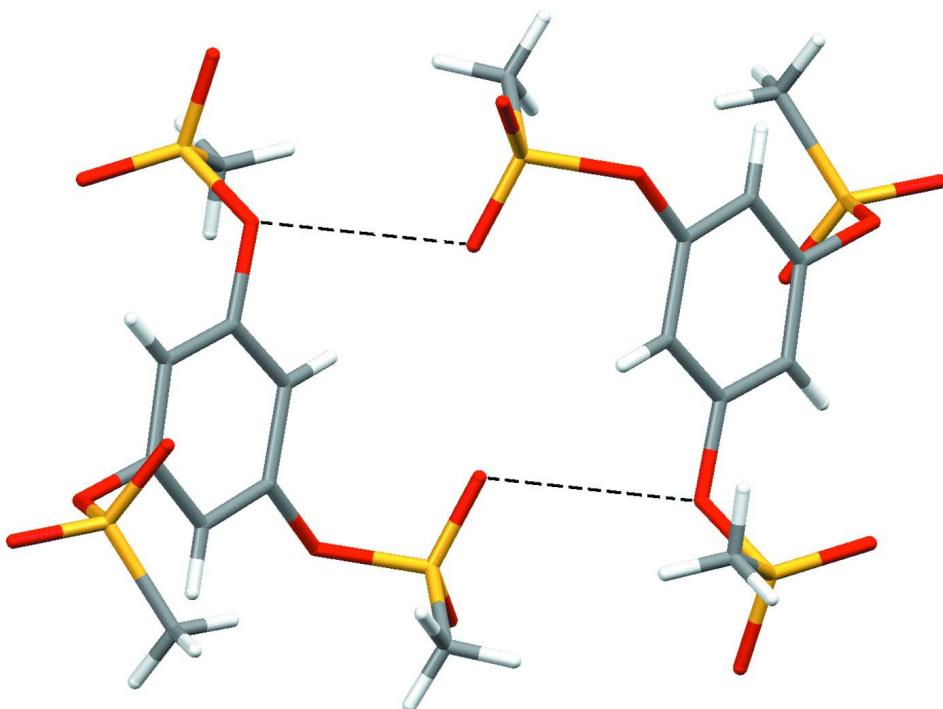
50 mg of benzene-1,3,5-triyl trimethanesulfonate compound was placed in a glass vial and 3 ml of dimethyl sulfoxide was added. The solution was allowed to stand at room temperature for seven days and the crystals formed were separated by filtration.

S3. Refinement

Refinement for H atoms was carried out using a riding model, with distances constrained to: 0.93 Å for aromatic CH, 0.98 Å for methine CH. Isotropic displacement parameters were fixed to $U_{\text{iso}}(\text{H})=1.2/1.5 U_{\text{eq}}(\text{carrier atom})$

**Figure 1**

The title compound (I) with displacement ellipsoids drawn at a 30% probability level.

**Figure 2**

The molecules forming cyclic dimers. O—O bonds are indicated by broken lines.

Benzene-1,3,5-triyl tris(methanesulfonate)

Crystal data

$C_9H_{12}O_9S_3$
 $M_r = 360.37$
Monoclinic, $P2_1/c$
Hall symbol: -P 2ybc
 $a = 8.7810 (5) \text{ \AA}$
 $b = 17.0053 (9) \text{ \AA}$
 $c = 9.7746 (7) \text{ \AA}$
 $\beta = 100.595 (5)^\circ$
 $V = 1434.69 (15) \text{ \AA}^3$
 $Z = 4$

$F(000) = 744$
 $D_x = 1.668 \text{ Mg m}^{-3}$
Mo $K\alpha$ radiation, $\lambda = 0.71073 \text{ \AA}$
Cell parameters from 51 reflections
 $\theta = 4.9\text{--}12.4^\circ$
 $\mu = 0.56 \text{ mm}^{-1}$
 $T = 298 \text{ K}$
Needle, colourless
 $0.40 \times 0.24 \times 0.10 \text{ mm}$

Data collection

Bruker P4
diffractometer
Radiation source: fine-focus sealed tube
Graphite monochromator
 $2\theta/\omega$ scans
Absorption correction: ψ scan
(XSCANS; Siemens, 1996)
 $T_{\min} = 0.258$, $T_{\max} = 0.310$
4418 measured reflections

4176 independent reflections
2333 reflections with $I > 2\sigma(I)$
 $R_{\text{int}} = 0.048$
 $\theta_{\max} = 30.0^\circ$, $\theta_{\min} = 2.4^\circ$
 $h = 0 \rightarrow 12$
 $k = 0 \rightarrow 23$
 $l = -13 \rightarrow 13$
3 standard reflections every 97 reflections
intensity decay: 4.3%

Refinement

Refinement on F^2
 Least-squares matrix: full
 $R[F^2 > 2\sigma(F^2)] = 0.055$
 $wR(F^2) = 0.177$
 $S = 0.92$
 4176 reflections
 190 parameters
 0 restraints
 Primary atom site location: structure-invariant direct methods

Secondary atom site location: difference Fourier map
 Hydrogen site location: inferred from neighbouring sites
 H-atom parameters constrained
 $w = 1/[\sigma^2(F_o^2) + (0.1P)^2]$
 where $P = (F_o^2 + 2F_c^2)/3$
 $(\Delta/\sigma)_{\max} < 0.001$
 $\Delta\rho_{\max} = 0.32 \text{ e } \text{\AA}^{-3}$
 $\Delta\rho_{\min} = -0.33 \text{ e } \text{\AA}^{-3}$

Special details

Geometry. All esds (except the esd in the dihedral angle between two l.s. planes) are estimated using the full covariance matrix. The cell esds are taken into account individually in the estimation of esds in distances, angles and torsion angles; correlations between esds in cell parameters are only used when they are defined by crystal symmetry. An approximate (isotropic) treatment of cell esds is used for estimating esds involving l.s. planes.

Refinement. Refinement of F^2 against ALL reflections. The weighted R -factor wR and goodness of fit S are based on F^2 , conventional R -factors R are based on F , with F set to zero for negative F^2 . The threshold expression of $F^2 > \sigma(F^2)$ is used only for calculating R -factors(gt) etc. and is not relevant to the choice of reflections for refinement. R -factors based on F^2 are statistically about twice as large as those based on F , and R -factors based on ALL data will be even larger.

Fractional atomic coordinates and isotropic or equivalent isotropic displacement parameters (\AA^2)

	<i>x</i>	<i>y</i>	<i>z</i>	$U_{\text{iso}}^*/U_{\text{eq}}$
S1	0.88376 (11)	0.16428 (6)	0.42609 (9)	0.0390 (2)
S2	0.78601 (11)	0.00358 (6)	-0.20344 (8)	0.0376 (2)
S3	0.60481 (12)	-0.19992 (6)	0.32307 (10)	0.0441 (3)
O3	0.6500 (3)	0.00837 (15)	-0.1152 (2)	0.0362 (5)
O2	0.7498 (3)	-0.14794 (15)	0.3008 (3)	0.0414 (6)
O1	0.7281 (3)	0.13465 (16)	0.3276 (2)	0.0431 (6)
C2	0.7397 (4)	-0.0073 (2)	0.3185 (3)	0.0342 (7)
H2A	0.7576	-0.0108	0.4151	0.041*
C6	0.6987 (4)	0.0718 (2)	0.1073 (3)	0.0322 (7)
H6A	0.6893	0.1207	0.0640	0.039*
C4	0.7008 (4)	-0.0705 (2)	0.0917 (3)	0.0322 (7)
H4A	0.6932	-0.1159	0.0380	0.039*
C5	0.6872 (4)	0.0031 (2)	0.0319 (3)	0.0307 (7)
C3	0.7265 (4)	-0.0735 (2)	0.2358 (3)	0.0330 (7)
C1	0.7251 (4)	0.0646 (2)	0.2512 (3)	0.0323 (7)
O5	0.7038 (4)	-0.00487 (19)	-0.3418 (3)	0.0606 (9)
O4	0.8956 (4)	-0.05374 (18)	-0.1437 (3)	0.0564 (8)
C7	0.8698 (5)	0.0967 (2)	-0.1803 (4)	0.0463 (9)
H7A	0.9541	0.1000	-0.2302	0.069*
H7B	0.9079	0.1056	-0.0830	0.069*
H7C	0.7936	0.1359	-0.2148	0.069*
O9	0.9613 (4)	0.09894 (18)	0.4963 (3)	0.0619 (9)
O8	0.8301 (4)	0.22633 (19)	0.5033 (3)	0.0602 (8)
O7	0.4863 (4)	-0.19317 (19)	0.2031 (3)	0.0626 (8)
O6	0.6727 (4)	-0.27378 (18)	0.3633 (4)	0.0759 (10)

C3—C4—C5—O3	−175.6 (3)	S1—O1—C1—C6	−114.3 (3)
S2—O3—C5—C6	98.5 (3)		

Hydrogen-bond geometry (Å, °)

D—H···A	D—H	H···A	D···A	D—H···A
C2—H2A···O5 ⁱ	0.93	2.51	3.392 (4)	159
C9—H9D···O4 ⁱⁱ	0.96	2.32	3.259 (5)	166
C4—H4A···O6 ⁱⁱⁱ	0.93	2.52	3.444 (4)	172
C9—H9C···O8 ^{iv}	0.96	2.55	3.312 (5)	136

Symmetry codes: (i) $x, y, z+1$; (ii) $-x+2, -y, -z$; (iii) $x, -y-1/2, z-1/2$; (iv) $x, -y+1/2, z-1/2$.