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N,*N*′-{[Ethane-1,2-diylbis(oxy)]bis(ethane-2,1-diyl)}bis(4-methylbenzenesulfonamide)

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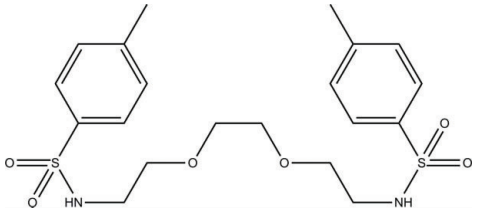
Key indicators: single-crystal X-ray study; T = 296 K; mean σ(C–C) = 0.004 Å; R factor = 0.053; wR factor = 0.150; data-to-parameter ratio = 14.2.

The asymmetric unit of the title compound, $C_{20}H_{28}N_2O_6S_2$, contains one half-molecule, related to the other half by a twofold rotation axis. The two aromatic rings of the molecule make a dihedral angle of 50.91 (7)°. The O—CH_2—CH_2—O and N—CH_2—CH_2—O fragments both adopt *gauche* conformations, with torsion angles of 76.0 (4) and 70.4 (3)°, respectively. In the crystal, adjacent molecules are linked through N—H···O hydrogen bonds into chains along the *a*-axis direction. The chains are further connected *via* C—H···O interactions into a two-dimensional supramolecular network in the *ac* plane.

Related literature

For similar structures, see: Polyakova *et al.* (1990); Ding *et al.* (2003).



Experimental

Crystal data

$C_{20}H_{28}N_2O_6S_2$
M_r = 456.56
Monoclinic, $C2/c$
a = 11.135 (7) Å
b = 9.220 (6) Å
c = 21.452 (15) Å
β = 93.680 (12)°
V = 2198 (3) Å^3
Z = 4
Mo $K\alpha$ radiation
μ = 0.28 mm^{-1}
T = 296 K
0.23 × 0.14 × 0.04 mm

Data collection

Bruker APEXII CCD diffractometer
Absorption correction: multi-scan (*SADABS*; Sheldrick, 1996)
T_{min} = 0.938, T_{max} = 0.989
5135 measured reflections
1983 independent reflections
1558 reflections with $I > 2\sigma(I)$
R_{int} = 0.055

Refinement

$R[F^2 > 2\sigma(F^2)]$ = 0.053
$wR(F^2)$ = 0.150
S = 1.03
1983 reflections
140 parameters
1 restraint
H atoms treated by a mixture of independent and constrained refinement
$\Delta\rho_{max}$ = 0.32 e Å^{-3}
$\Delta\rho_{min}$ = −0.36 e Å^{-3}

Table 1
Hydrogen-bond geometry (Å, °).

D—H···A	D—H	H···A	D···A	D—H···A
N1—H1···O2^{i}	0.82 (2)	2.14 (2)	2.944 (3)	171 (3)
C6—H6···O1^{ii}	0.93	2.56	3.311 (4)	138

Symmetry codes: (i) $-x+1, y, -z+\frac{3}{2}$; (ii) $-x+1, -y, -z+1$.

Data collection: *APEX2* (Bruker, 2007); cell refinement: *SAINT* (Bruker, 2007); data reduction: *SAINT*; program(s) used to solve structure: *SHELXS97* (Sheldrick, 2008); program(s) used to refine structure: *SHELXL97* (Sheldrick, 2008); molecular graphics: *X-SEED* (Barbour, 2001); software used to prepare material for publication: *SHELXL97* and *publCIF* (Westrip, 2010).

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Supplementary data and figures for this paper are available from the IUCr electronic archives (Reference: PV2551).

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