

N-(2-Bromophenyl)-4-methyl-N-(4-methylphenylsulfonyl)benzenesulfonamide

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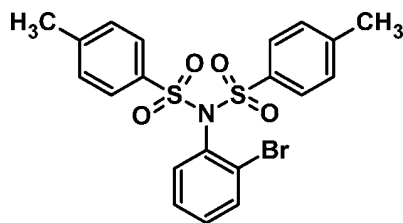
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Key indicators: single-crystal X-ray study; $T = 100$ K; mean $\sigma(\text{C}-\text{C}) = 0.004$ Å; disorder in main residue; R factor = 0.038; wR factor = 0.085; data-to-parameter ratio = 15.9.

In the title compound, $\text{C}_{20}\text{H}_{18}\text{BrNO}_4\text{S}_2$, the mean planes formed by the toluene substituents are inclined at a dihedral angle of 45.34 (8)°. The bromobenzene group is disordered over two positions with an occupancy ratio of 0.74:0.26, resulting in two conformations of the ring; the two rings are oriented at a dihedral angle of 6.6 (6)° with each other. In the crystal structure, weak $\text{C}-\text{H}\cdots\text{O}$ interactions connect the molecules in a zigzag manner along the a axis.

Related literature

For general background, see: Ames & Opalko (1984); Arshad *et al.* (2011). For related structures, see: Zhao *et al.* (2007); Song (2008); Hanson & Hitchcock (2004).



Experimental

Crystal data

$\text{C}_{20}\text{H}_{18}\text{BrNO}_4\text{S}_2$
 $M_r = 480.38$
Monoclinic, $P2_1/c$
 $a = 10.5819$ (15) Å
 $b = 13.1465$ (19) Å
 $c = 14.235$ (2) Å
 $\beta = 95.478$ (2)°
 $V = 1971.2$ (5) Å³
 $Z = 4$
Mo $K\alpha$ radiation
 $\mu = 2.32$ mm⁻¹
 $T = 100$ K
 $0.38 \times 0.33 \times 0.24$ mm

Data collection

Bruker KAPPA APEXII CCD diffractometer
Absorption correction: multi-scan (SADABS; Bruker, 2001)
 $T_{\min} = 0.472$, $T_{\max} = 0.605$
23193 measured reflections
4792 independent reflections
4320 reflections with $I > 2\sigma(I)$
 $R_{\text{int}} = 0.031$

Refinement

$R[F^2 > 2\sigma(F^2)] = 0.038$
 $wR(F^2) = 0.085$
 $S = 1.24$
4792 reflections
301 parameters
H-atom parameters constrained
 $\Delta\rho_{\max} = 0.52$ e Å⁻³
 $\Delta\rho_{\min} = -0.53$ e Å⁻³

Table 1

Hydrogen-bond geometry (Å, °).

$D-H\cdots A$	$D-H$	$H\cdots A$	$D\cdots A$	$D-H\cdots A$
$\text{C5}-\text{H5}\cdots\text{O3}^i$	0.95	2.45	3.199 (3)	135

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

Data collection: APEX2 (Bruker, 2001); cell refinement: SAINT (Bruker, 2001); data reduction: SAINT; program(s) used to solve structure: SHELXS97 (Sheldrick, 2008); program(s) used to refine structure: SHELXL97 (Sheldrick, 2008); molecular graphics: PLATON (Spek, 2009) and X-SEED (Barbour, 2001); software used to prepare material for publication: WinGX (Farrugia, 1999).

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Supplementary data and figures for this paper are available from the IUCr electronic archives (Reference: PV2443).

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