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Key indicators

Single-crystal X-ray study T = 120 KMean $\sigma(\text{C-C}) = 0.003 \text{ Å}$ R factor = 0.042 wR factor = 0.138Data-to-parameter ratio = 15.6

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

3-[4-(Methylsulfonyl)benzoyl]propionic acid

The structure of the title compound, $C_{11}H_{12}O_5S$, (I), comprises a simple molecule that associates *via* carboxylic acid dimers in the solid state. Other associated dimers are formed from $C-H\cdots O$ intermolecular close contacts to the two carbonyl and one sulfonyl O atoms. All three SO_2CH_3 H atoms and one phenyl H atom are also involved in these close-contact associations.

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Experimental

The title compound was obtained from Key Organics Ltd and crystals were grown from an ethanol solution.

Crystal data

 $C_{11}H_{12}O_5S$ $D_x = 1.507 \text{ Mg m}^{-3}$ $M_r = 256.27$ Triclinic, $P\overline{1}$ Mo $K\alpha$ radiation a = 5.1851 (1) ÅCell parameters from 3181 b = 10.5030 (3) Åreflections c = 10.9550 (4) Å $\theta = 2.9 - 27.5^{\circ}$ $\mu = 0.29 \text{ mm}^{-1}$ $\alpha = 96.990 (1)^{\circ}$ $\beta = 101.135 (1)^{\circ}$ T = 120 (2) K $\gamma = 101.786 (3)^{\circ}$ Prism, colourless $V = 564.90 (3) \text{ Å}^3$ $0.40 \times 0.20 \times 0.06 \text{ mm}$

Data collection

Bruker–Nonius KappaCCD areadetector diffractometer 2089 reflections with $I > 2\sigma(I)$ φ and ω scans $R_{\rm int} = 0.032$ Absorption correction: multi-scan (SORTAV; Blessing, 1995) $H_{\rm min} = 0.892, \, T_{\rm max} = 0.983$ $H_{\rm max} = 0.892, \, T_{\rm max} = 0.983$ $H_{\rm max} = 0.892, \, T_{\rm max} = 0.983$ $H_{\rm max} = 0.892, \, T_{\rm max} = 0.983$ $H_{\rm max} = 0.892, \, T_{\rm max} = 0.983$ $H_{\rm max} = 0.983$

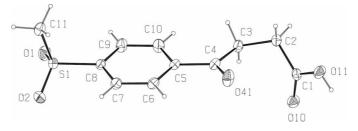


Figure 1
The molecular configuration and atom-numbering scheme for the title compound, showing 50% probability ellipsoids.

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organic papers

Refinement

Refinement on F^2 $R[F^2 > 2\sigma(F^2)] = 0.042$ $wR(F^2) = 0.138$ S = 1.032484 reflections 159 parameters

H atoms treated by a mixture of independent and constrained refinement

 $w = 1/[\sigma^2(F_o^2) + (0.1P)^2]$ where $P = (F_o^2 + 2F_c^2)/3$ $(\Delta/\sigma)_{\text{max}} < 0.001$

 $\Delta \rho_{\text{max}} = 0.47 \text{ e Å}^{-3}$ $\Delta \rho_{\text{min}} = -0.66 \text{ e Å}^{-3}$

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

$D-\mathrm{H}\cdots A$	D-H	$H \cdot \cdot \cdot A$	$D \cdot \cdot \cdot A$	$D-\mathrm{H}\cdots A$
O11—H11···O10 ⁱ	0.79 (3)	1.85 (3)	2.6388 (18)	178 (3)
C6−H6···O41 ⁱⁱ	0.95	2.45	3.346 (2)	157
C9−H9···O1	0.95	2.58	2.942(2)	103
C11-H111···O2 ⁱⁱⁱ	0.98	2.50	3.357 (2)	146
C11−H113···O10 ^{iv}	0.98	2.57	3.483 (2)	155
$C11-H112\cdots O2^{v}$	0.98	2.49	3.423 (2)	160

Symmetry codes: (i) 1-x, 1-y, -z; (ii) 1-x, -y, -z; (iii) x-1, y, z; (iv) x, y-1, z; (v) 1-x, -1-y, 1-z.

All H atoms were included in the refinement, at calculated positions, as riding models, with C-H distances set to 0.95 (Ar-H), 0.98

 (CH_3) and 0.99 Å (CH_2) , except for the carboxylic acid H atom, which was located in a difference synthesis and for which both positional and displacement parameters were refined.

Data collection: *DENZO* (Otwinowski & Minor, 1997) and *COLLECT* (Hooft, 1998); cell refinement: *DENZO* and *COLLECT*; data reduction: *DENZO* and *COLLECT*; program(s) used to solve structure: *SHELXS97* (Sheldrick, 1997); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *PLATON*97 (Spek, 1997); software used to prepare material for publication: *SHELXL*97.

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