

organic compounds

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(2E)-1-(2,5-Dimethyl-3-thienyl)-3-(2-methoxyphenyl)prop-2-en-1-one

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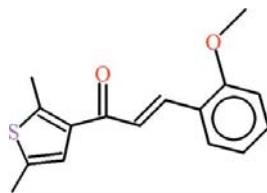
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Key indicators: single-crystal X-ray study; $T = 296\text{ K}$; mean $\sigma(\text{C}-\text{C}) = 0.002\text{ \AA}$; R factor = 0.036; wR factor = 0.102; data-to-parameter ratio = 14.4.

In the title compound, $C_{16}H_{16}O_2S$, the central propenone group is almost planar (r.m.s. deviation = 0.009 Å) and subtends dihedral angles of 8.55 (8) and 16.22 (8)° to the 2-methoxyphenyl and 2,5-dimethylthiophene residues, respectively. The dihedral angle between the ring systems is 23.47 (5)°. In the crystal, molecules are linked by weak C–H···π interactions and aromatic π–π stacking [phenyl ring centroid–centroid separation = 3.6418 (11) Å; thiophene–thiophene ring separation = 3.8727 (9) Å].

Related literature

For background to chalcone derivatives and related crystal structures, see: Asiri *et al.* (2010a,b,c).



Experimental

Crystal data

$C_{16}H_{16}O_2S$
 $M_r = 272.35$

Monoclinic, $C2/c$
 $a = 26.2978 (6)\text{ \AA}$

$b = 7.5018 (2)\text{ \AA}$
 $c = 14.7242 (3)\text{ \AA}$
 $\beta = 105.771 (1)^\circ$
 $V = 2795.45 (11)\text{ \AA}^3$
 $Z = 8$

Mo $K\alpha$ radiation
 $\mu = 0.23\text{ mm}^{-1}$
 $T = 296\text{ K}$
 $0.32 \times 0.24 \times 0.22\text{ mm}$

Data collection

Bruker Kappa APEXII CCD diffractometer
Absorption correction: multi-scan (*SADABS*; Bruker, 2005)
 $T_{\min} = 0.937$, $T_{\max} = 0.942$

10569 measured reflections
2516 independent reflections
2150 reflections with $I > 2\sigma(I)$
 $R_{\text{int}} = 0.023$

Refinement

$R[F^2 > 2\sigma(F^2)] = 0.036$
 $wR(F^2) = 0.102$
 $S = 1.04$
2516 reflections

175 parameters
H-atom parameters constrained
 $\Delta\rho_{\max} = 0.22\text{ e \AA}^{-3}$
 $\Delta\rho_{\min} = -0.21\text{ e \AA}^{-3}$

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

$Cg2$ is the centroid of C1–C6 ring.

$D-\text{H}\cdots A$	$D-\text{H}$	$\text{H}\cdots A$	$D\cdots A$	$D-\text{H}\cdots A$
$C7-\text{H7A}\cdots Cg2^i$	0.96	2.89	3.768 (2)	153

Symmetry code: (i) $-x, -y + 1, -z + 1$.

Data collection: *APEX2* (Bruker, 2009); cell refinement: *SAINT* (Bruker, 2009); data reduction: *SAINT*; program(s) used to solve structure: *SHELXS97* (Sheldrick, 2008); program(s) used to refine structure: *SHELXL97* (Sheldrick, 2008); molecular graphics: *ORTEP-3* (Farrugia, 1997) and *PLATON* (Spek, 2009); software used to prepare material for publication: *WinGX* (Farrugia, 1999) and *PLATON*.

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Supplementary data and figures for this paper are available from the IUCr electronic archives (Reference: HB5609).

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