

## (2E)-3-[4-(Dimethylamino)phenyl]-1-(2,5-dimethyl-3-thienyl)prop-2-en-1-one

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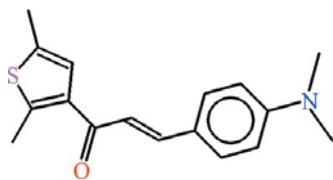
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Key indicators: single-crystal X-ray study;  $T = 296$  K; mean  $\sigma(C-C) = 0.003$  Å; disorder in main residue;  $R$  factor = 0.049;  $wR$  factor = 0.156; data-to-parameter ratio = 14.8.

The asymmetric unit of the title compound,  $C_{17}H_{19}NOS$ , contains two independent molecules which differ in the dihedral angles between the five- and six-membered rings [12.52 (10) and 4.63 (11) $^\circ$ ]. Weak intermolecular C–H···O hydrogen bonds link the two independent molecules into pseudocentrosymmetric dimers. In one molecule, the O atom of the carbonyl group is disordered over two positions in a 0.699 (4):0.301 (4) ratio.

### Related literature

For background and related crystal structures, see: Asiri *et al.* (2010a,b,c). For graph-set notation, see: Bernstein *et al.* (1995).



### Experimental

#### Crystal data

$C_{17}H_{19}NOS$   
 $M_r = 285.40$   
Triclinic,  $P\bar{1}$   
 $a = 7.7665$  (2) Å  
 $b = 12.8624$  (4) Å  
 $c = 16.0318$  (4) Å  
 $\alpha = 79.917$  (1) $^\circ$   
 $\beta = 80.029$  (2) $^\circ$

$\gamma = 79.300$  (1) $^\circ$   
 $V = 1532.90$  (7) Å<sup>3</sup>  
 $Z = 4$   
Mo  $K\alpha$  radiation

$\mu = 0.21$  mm<sup>-1</sup>  
 $T = 296$  K  
 $0.32 \times 0.23 \times 0.20$  mm

#### Data collection

Bruker Kappa APEXII CCD diffractometer  
Absorption correction: multi-scan (*SADABS*; Bruker, 2005)  
 $T_{\min} = 0.947$ ,  $T_{\max} = 0.962$

22632 measured reflections  
5536 independent reflections  
3543 reflections with  $I > 2\sigma(I)$   
 $R_{\text{int}} = 0.039$

#### Refinement

$R[F^2 > 2\sigma(F^2)] = 0.049$   
 $wR(F^2) = 0.156$   
 $S = 1.02$   
5536 reflections

373 parameters  
H-atom parameters constrained  
 $\Delta\rho_{\max} = 0.19$  e Å<sup>-3</sup>  
 $\Delta\rho_{\min} = -0.23$  e Å<sup>-3</sup>

**Table 1**  
Hydrogen-bond geometry (Å,  $^\circ$ ).

D–H···A	D–H	H···A	D···A	D–H···A
C6–H6···O2	0.93	2.48	3.275 (3)	143
C19–H19···O1A	0.93	2.52	3.317 (9)	144
C19–H19···O1B	0.93	2.48	3.264 (3)	142

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 for Windows* (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: CV2751).

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