

3,3,4,4,5,5-Hexafluoro-1,2-bis(3-methylbenzo[*b*]-2-thienyl)cyclopentene

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Key indicators

Single-crystal X-ray study

$T = 293\text{ K}$

Mean $\sigma(\text{C}-\text{C}) = 0.006\text{ \AA}$

R factor = 0.061

wR factor = 0.119

Data-to-parameter ratio = 11.6

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

The title compound, $\text{C}_{23}\text{H}_{14}\text{F}_6\text{S}_2$, was crystallized from a PMMA/chloroform solution (PMMA = polymethylmethacrylate), and its crystal structure was determined. The molecule adopts a photoactive antiparallel conformation. The distance between the two reactive C atoms was determined to be $3.560(7)\text{ \AA}$. The molecule has crystallographic twofold rotation symmetry.

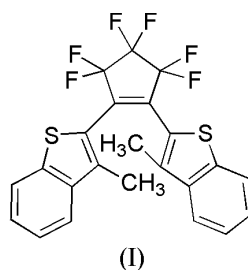
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Comment

As a result of their good thermal stability and high fatigue resistance, photochromic diarylethenes have potential application for opto-electronic devices, such as optical memories and switches (Irie, 2000; Fernandez-Asebes & Lehn, 1999). Diarylethenes usually have one of two conformations in the solid state, parallel or antiparallel (Kobatake *et al.*, 1999; Shibata *et al.*, 2002).



The title compound (BTPF), (I), is a bis(2-thienyl)perfluorocyclopentene derivative. It has attracted our attention due to its interesting non-linear optical properties (Sun *et al.*, 2002). Unlike most diarylethenes recrystallized from organic solution (Pu *et al.*, 2003), the crystals of BTPF were obtained from a PMMA/chloroform solution. The polymer in chloroform causes deposition of BTPF/PMMA films, which act as a membranous substrate that mediates the growth of BTPF crystals. As a result, well-formed yellow block-shaped single crystals were obtained.

The X-ray crystallographic study showed that BTPF is packed in the antiparallel conformation. The general view of a molecule, together with the atom-numbering scheme, is shown in Fig. 1. The distance between the reactive C atoms (C5 and C5ⁱ; symmetry code (i) = $-x, y, \frac{1}{2} - z$) is $3.560(7)\text{ \AA}$, which is close enough for a photocyclization reaction (Ramamurthy & Venkatesan, 1987). The molecule has crystallographic twofold rotation symmetry, the axis passing through C3 and the opposite C=C ring of the cyclopentene ring.

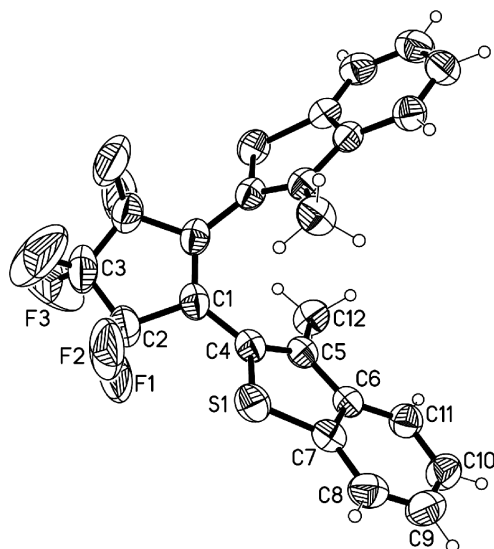


Figure 1
View of the molecule of BTPF, with the atomic numbering scheme. Displacement ellipsoids are drawn at the 35% probability level.

Experimental

The title compound was prepared according to a method described in the literature (Sun *et al.*, 2002). Single crystals were obtained from a PMMA/chloroform solution. The weight ratio of PMMA and BTPF was 5:1.

Crystal data

$C_{23}H_{14}F_6S_2$	$D_x = 1.522 \text{ Mg m}^{-3}$
$M_r = 468.46$	Mo $K\alpha$ radiation
Monoclinic, $C2/c$	Cell parameters from 36 reflections
$a = 18.8350 (18) \text{ \AA}$	$\theta = 3.8\text{--}12.6^\circ$
$b = 9.3507 (9) \text{ \AA}$	$\mu = 0.32 \text{ mm}^{-1}$
$c = 11.643 (2) \text{ \AA}$	$T = 293 (2) \text{ K}$
$\beta = 94.653 (11)^\circ$	Block, yellow
$V = 2043.8 (5) \text{ \AA}^3$	$0.6 \times 0.6 \times 0.2 \text{ mm}$
$Z = 4$	

Data collection

Bruker P4 diffractometer	$\theta_{\text{max}} = 25.0^\circ$
ω scans	$h = -1 \rightarrow 22$
Absorption correction: none	$k = -1 \rightarrow 11$
2244 measured reflections	$l = -13 \rightarrow 13$
1644 independent reflections	3 standard reflections
1198 reflections with $I > 2\sigma(I)$	every 100 reflections
$R_{\text{int}} = 0.024$	intensity decay: none

Refinement

Refinement on F^2	$w = 1/[\sigma^2(F_o^2) + (0.001P)^2 + 7P]$
$R[F^2 > 2\sigma(F^2)] = 0.061$	where $P = (F_o^2 + 2F_c^2)/3$
$wR(F^2) = 0.119$	$(\Delta/\sigma)_{\text{max}} < 0.001$
$S = 1.00$	$\Delta\rho_{\text{max}} = 0.44 \text{ e \AA}^{-3}$
1644 reflections	$\Delta\rho_{\text{min}} = -0.48 \text{ e \AA}^{-3}$
142 parameters	Extinction correction: <i>SHELXTL</i>
H-atom parameters constrained	Extinction coefficient: 0.00043 (17)

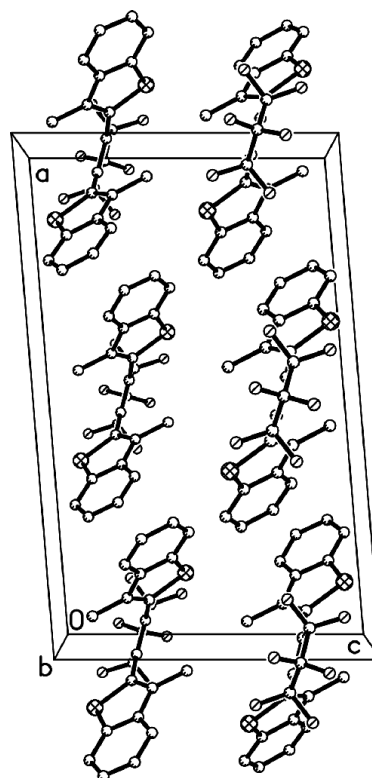


Figure 2
A packing view along the b axis.

H atoms were positioned theoretically and refined using a riding model.

Data collection: *XSCANS* (Bruker, 1997); cell refinement: *XSCANS*; data reduction: *XSCANS*; program(s) used to solve structure: *SHELXTL* (Bruker, 1997); program(s) used to refine structure: *SHELXTL*; molecular graphics: *SHELXTL*; software used to prepare material for publication: *SHELXTL*.

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