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#### **Key indicators**

Single-crystal X-ray study T = 100 KMean  $\sigma$ (C–C) = 0.003 Å R factor = 0.029 wR factor = 0.078 Data-to-parameter ratio = 15.3

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

(4aSR,7RS,9aRS)-9a-Bromo-7-methyl-5,5dioxo-1,2,4a,6,7,9a-hexahydro-8-oxa-5λ<sup>6</sup>-

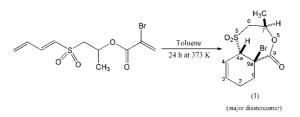
The title compound,  $C_{10}H_{13}BrO_4S$ , crystallizes as a racemic mixture in space group  $P\overline{1}$ . The seven-membered ring exhibits a chair conformation; the methyl group points away from the bromine substituent.

thia-1,4-benzocyclohepten-9-one

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### Comment

As detailed in the first article in this series (Zeller *et al.*, 2004), two of us (NC and PS) have been exploring the potential utility of sulfone-based tethers in intramolecular Diels–Alder cycloaddition reactions. This has resulted in the preparation of a series of bicyclic  $\beta$ -acyloxy sulfone cycloadducts, several of which have been subjected to analysis using single-crystal Xray diffraction. In the present paper, the solid-state structure of the title cycloadduct, (I), as established by single-crystal Xray diffraction methods, is described.



Compound (I) crystallizes as a racemic mixture of both enantiomers. The six-membered ring exhibits the half-chair conformation expected for cyclohexenes, and the angles at the unsaturated C atoms are 123.62 (17)° (for C4–C3–C2) and 124.12 (17)° (for C3–C4–C4A; Fig. 1). The seven-membered ring displays a chair-like conformation. The methyl group on atom C7 is located in the equatorial position, pointing away from the bromine substituent on the bridgehead atom C9A.

### Experimental

Compound (I) was isolated in 58% yield as the major diastereomer from an intramolecular Diels–Alder cycloaddition reaction of 1-[(E)-buta-1,3-dienylsulfonyl]propan-2-yl 2-bromoacrylate in toluene at 373 K. Compound (I) was purified by silica column chromatography (CH<sub>2</sub>Cl<sub>2</sub>/ether, 40:1) and recrystallized from ethyl acetate/hexane (1:1). Crystals suitable for X-ray diffraction analysis were grown *via* slow evaporation of a CH<sub>2</sub>Cl<sub>2</sub> solution.

Crystal data	
$C_{10}H_{13}BrO_4S$	Z = 2
$M_r = 309.17$	$D_x = 1.769 \text{ Mg m}^{-3}$
Triclinic, P1	Mo $K\alpha$ radiation
a = 6.0895 (5)  Å	Cell parameters from 5304
b = 9.1882 (7)  Å	reflections
c = 10.6027 (9)  Å	$\theta = 2.3 - 28.3^{\circ}$
$\alpha = 89.383 (1)^{\circ}$	$\mu = 3.73 \text{ mm}^{-1}$
$\beta = 86.523 \ (1)^{\circ}$	T = 100 (2)  K
$\gamma = 77.697 \ (1)^{\circ}$	Block, colorless
V = 578.55 (8) Å <sup>3</sup>	$0.5 \times 0.5 \times 0.5$ mm

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# organic papers

Data collection

Bruker SMART APEX CCD diffractometer  $\omega$  scans Absorption correction: multi-scan (*SADABS* in *SAINT-Plus*; Bruker, 1997–1999)  $T_{min} = 0.125, T_{max} = 0.159$ 5491 measured reflections

### Refinement

```
Refinement on F^2

R[F^2 > 2\sigma(F^2)] = 0.029

wR(F^2) = 0.078

S = 1.06

2822 reflections

184 parameters

Only coordinates of H atoms

refined
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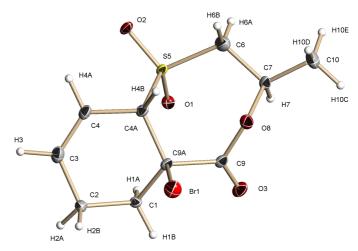
2822 independent reflections 2726 reflections with  $I > 2\sigma(I)$   $R_{int} = 0.030$   $\theta_{max} = 28.3^{\circ}$   $h = -8 \rightarrow 8$   $k = -12 \rightarrow 12$   $l = -14 \rightarrow 14$  $w = 1/[\sigma^2(F_{\alpha}^2) + (0.0552P)^2$ 

 $\begin{array}{l} & \psi = 1/[0^{\circ}(T_{o})^{+}(0.05521)^{\circ} \\ & + 0.2933P] \\ & \text{where } P = (F_{o}^{\circ} + 2F_{c}^{\circ})/3 \\ & (\Delta/\sigma)_{\text{max}} = 0.001 \\ & \Delta\rho_{\text{max}} = 1.12 \text{ e } \text{ Å}^{-3} \\ & \Delta\rho_{\text{min}} = -1.00 \text{ e } \text{ Å}^{-3} \end{array}$ 

All H atoms were positioned geometrically. Their coordinates were then refined freely, and their  $U_{\rm iso}$  values were defined as 1.2 or  $1.5U_{\rm eq}$  of the parent C atom. The s.u. values of the cell parameters are taken from the software, recognizing that the values are unreasonably small (Herbstein, 2000). The maximum and minimum electron-density peaks are located 0.81 and 0.82 Å, respectively, from atom Br1.

Data collection: *SMART* (Bruker, 1997–2000); cell refinement: *SAINT-Plus* (Bruker, 1997–1999); data reduction: *SAINT-Plus*; program(s) used to solve structure: *SHELXS*97 (Sheldrick, 1990); program(s) used to refine structure: *SHELXL*97 (Sheldrick, 1997); molecular graphics: *SHELXTL* (Bruker, 2000); software used to prepare material for publication: *SHELXL*97.

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### Figure 1

The molecular structure, showing 50% probability displacement ellipsoids.

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