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Key indicators

Single-crystal X-ray study
 T = 292 K
 Mean $\sigma(\text{C}-\text{C}) = 0.003 \text{ \AA}$
 R factor = 0.052
 wR factor = 0.135
 Data-to-parameter ratio = 19.6

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

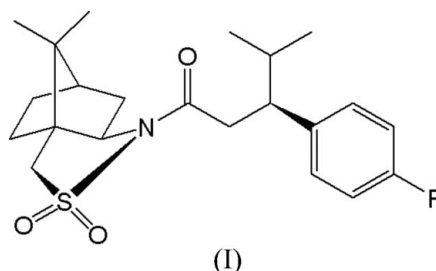
**(-)-N-[(3S)-3-(4-Fluorophenyl-4-methyl)-
 hexanoyl]bornane-10,2-sultam**

In the title compound, $\text{C}_{22}\text{H}_{30}\text{FNO}_3\text{S}$, molecules are linked *via*
 C—H···O interactions.

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Comment

The readily available enantiomers of bornane-10,2-sultam
 serve as efficient, versatile and practical chiral auxiliaries
 (Oppolzer, 1990), and we have focused our attention on this
 field. In this paper, we present the X-ray crystallographic
 analysis of the title compound, (I).



In (I), the six-membered ring of sultam shows a boat form
 (Fig. 1). The C7/C6/C5/C4 and C4/C9/C8/C7 planes form a
 dihedral angle of 92.6 (3)°. The C4/C3/C7 plane forms dihe-
 dral angles to the aforementioned planes of 123.6 (1) and
 125.8 (4)°, respectively. The molecules are linked *via* C—
 H···O interactions (Table 2).

Experimental

For the prepreparation of compound (I), *N*-[3-(4-fluorophenyl)propen-
 oyl]bornane-10,2-sultam (2.908 g, 8.0 mmol) was reacted with *i*-
 PrMgCl (16.0 mmol) in anhydrous THF (60 ml) at 193 K (yield
 2.184 g, 67%); $[\alpha]_D^{31} = -84.2^\circ$ (c 1.05, CHCl_3) (Huang *et al.*, 1999).
 Crystals appropriate for X-ray data collection were obtained by slow
 evaporation of a dichloromethane solution at 293 K.

Crystal data

$\text{C}_{22}\text{H}_{30}\text{FNO}_3\text{S}$	$Z = 4$
$M_r = 407.53$	$D_x = 1.282 \text{ Mg m}^{-3}$
Orthorhombic, $P2_12_12_1$	Mo $K\alpha$ radiation
$a = 11.3245$ (11) \AA	$\mu = 0.18 \text{ mm}^{-1}$
$b = 12.7667$ (12) \AA	$T = 292$ (2) K
$c = 14.6079$ (14) \AA	Block, colorless
$V = 2112.0$ (3) \AA^3	0.30 × 0.20 × 0.20 mm

Data collection

Bruker SMART CCD area-detector diffractometer	5040 independent reflections
φ and ω scans	4546 reflections with $I > 2\sigma(I)$
Absorption correction: none	$R_{\text{int}} = 0.088$
20597 measured reflections	$\theta_{\text{max}} = 28.2^\circ$

Refinement

Refinement on F^2
 $R[F^2 > 2\sigma(F^2)] = 0.052$
 $wR(F^2) = 0.135$
 $S = 1.03$
 5040 reflections
 257 parameters
 H-atom parameters constrained

$w = 1/[\sigma^2(F_o^2) + (0.0809P)^2 + 0.1599P]$
 where $P = (F_o^2 + 2F_c^2)/3$
 $(\Delta/\sigma)_{\max} = 0.001$
 $\Delta\rho_{\max} = 0.46 \text{ e } \text{\AA}^{-3}$
 $\Delta\rho_{\min} = -0.21 \text{ e } \text{\AA}^{-3}$
 Absolute structure: Flack (1983),
 1860 Friedel pairs
 Flack parameter: 0.00 (8)

Table 1

Selected geometric parameters (\AA , $^\circ$).

C9–N1	1.475 (2)	C22–F1	1.360 (3)
C10–S1	1.789 (2)	N1–S1	1.6878 (16)
C11–O3	1.199 (3)	O1–S1	1.425 (2)
C11–N1	1.394 (3)	O2–S1	1.427 (2)
C4–C10–S1	106.61 (14)	N1–S1–C10	95.63 (10)
C4–C5–C6–C7	−4.3 (2)	C12–C13–C17–C18	−56.1 (2)
C7–C8–C9–C4	−9.9 (2)	C4–C9–N1–S1	18.55 (18)
C10–C4–C9–N1	−30.1 (2)	C9–N1–S1–C10	−1.72 (16)
C9–C4–C10–S1	28.4 (2)	C4–C10–S1–N1	−15.94 (19)
C11–C12–C13–C14	166.99 (18)		

Table 2

Hydrogen-bond geometry (\AA , $^\circ$).

$D-H\cdots A$	$D-H$	$H\cdots A$	$D\cdots A$	$D-H\cdots A$
C1–H1B \cdots N1	0.96	2.58	3.226 (3)	125
C12–H12A \cdots O2	0.97	2.43	3.158 (3)	131
C10–H10A \cdots O3 ⁱ	0.97	2.36	3.236 (3)	150
C8–H8A \cdots O2 ⁱⁱ	0.97	2.60	3.458 (3)	148
C6–H6A \cdots O2 ⁱⁱ	0.97	2.56	3.477 (3)	157

Symmetry codes: (i) $x - \frac{1}{2}, -y + \frac{1}{2}, -z + 2$; (ii) $x + \frac{1}{2}, -y + \frac{1}{2}, -z + 2$.

All H atoms were constrained to an ideal geometry with C–H distances of 0.93–0.98 \AA , and with $U_{\text{iso}}(\text{H}) = 1.2U_{\text{eq}}(\text{C})$ or $1.5U_{\text{eq}}(\text{C}_{\text{methyl}})$. The absolute configuration of (I) based on the Flack (1983) parameter is consistent with the known absolute configuration of (−)-2,10-sultam (Boiadjev & Lightner, 2001).

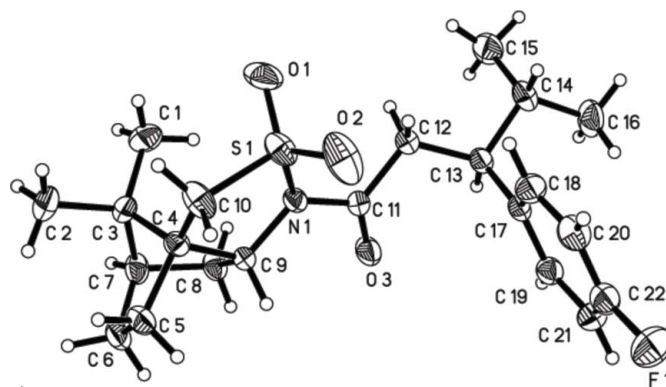


Figure 1

The molecular structure of (I), showing the atom-labeling scheme. Displacement ellipsoids are drawn at the 30% probability level.

Data collection: *SMART* (Bruker, 2001); cell refinement: *SAINTE-Plus* (Bruker, 2001); data reduction: *SAINTE-Plus*; program(s) used to solve structure: *SHELXS97* (Sheldrick, 1997); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *SHELXTL* (Bruker, 2001); software used to prepare material for publication: *SHELXTL*.

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