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Key indicators

Single-crystal X-ray study
 T = 113 K
 Mean $\sigma(\text{C}-\text{C}) = 0.003 \text{ \AA}$
 R factor = 0.024
 wR factor = 0.059
 Data-to-parameter ratio = 21.1

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

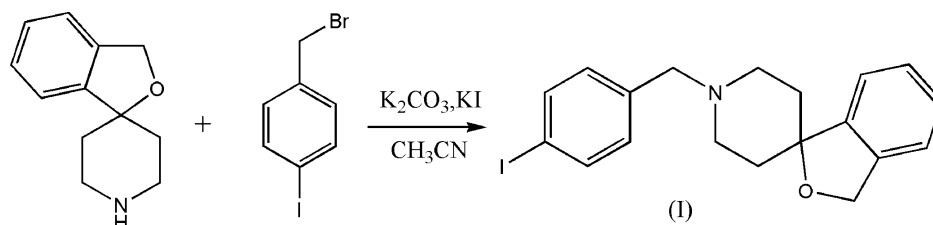
**1'-(4-Iodobenzyl)spiro[isobenzofuran-
 1(3H),4'-piperidine]**

In the title compound, $\text{C}_{19}\text{H}_{20}\text{INO}$, the central piperidine ring
 adopts a chair conformation.

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Comment

Among many different structural classes of sigma-1 receptor
 ligands, the spiro piperidines offer the best potential sigma-1
 receptor affinity and selectivity towards the sigma-2 receptor
 and other brain receptors (Maier & Wuensch, 2002*a,b*). In this
 context, the crystal structures are very important for under-
 standing the interaction between the ligand and the sigma
 receptor.



The molecular structure of the title compound, (I), is shown
 in Fig. 1. The fused benzene ring makes a dihedral angle of
 20.1 (1)° with the plane composed of the three atoms O1, C8
 and C1, the five-membered ring being an envelope with O1 at
 the flap position. The piperidine ring adopts a chair conforma-
 tion.

Experimental

Compound (I) was synthesized according to the literature method of
 Kubota *et al.* (1998) (see scheme). Single crystals suitable for X-ray
 diffraction analysis were obtained by recrystallization from a mixture
 of petroleum ether and diethyl ether (*v:v* 5:1) over a period of 1 d.

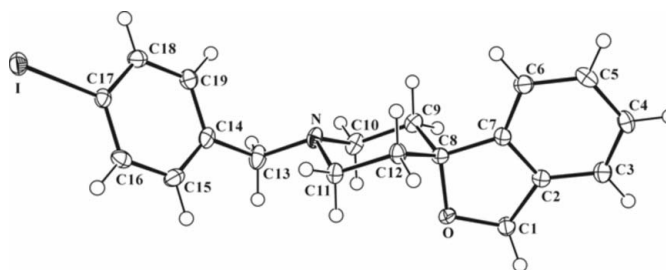


Figure 1
 The molecular structure of (I), with displacement ellipsoids drawn at the
 50% probability level.

Crystal data

$C_{19}H_{20}INO$	$V = 1647.98 (17) \text{ \AA}^3$
$M_r = 405.26$	$Z = 4$
Monoclinic, $P2_1/c$	Mo $K\alpha$ radiation
$a = 10.1099 (6) \text{ \AA}$	$\mu = 1.95 \text{ mm}^{-1}$
$b = 11.8733 (6) \text{ \AA}$	$T = 113 (2) \text{ K}$
$c = 14.262 (1) \text{ \AA}$	$0.24 \times 0.20 \times 0.18 \text{ mm}$
$\beta = 105.722 (3)^\circ$	

Data collection

Rigaku Saturn diffractometer	15887 measured reflections
Absorption correction: multi-scan (Jacobson, 1998)	4225 independent reflections
$T_{\min} = 0.653$, $T_{\max} = 0.721$	3599 reflections with $I > 2\sigma(I)$
	$R_{\text{int}} = 0.035$

Refinement

$R[F^2 > 2\sigma(F^2)] = 0.024$	200 parameters
$wR(F^2) = 0.059$	H-atom parameters constrained
$S = 1.05$	$\Delta\rho_{\max} = 0.45 \text{ e \AA}^{-3}$
4225 reflections	$\Delta\rho_{\min} = -0.81 \text{ e \AA}^{-3}$

All H atoms were positioned geometrically and refined using a riding model, with C—H = 0.95 Å for aromatic H and 0.99 Å for methylene H, and with $U_{\text{iso}}(\text{H}) = 1.2U_{\text{eq}}(\text{C})$.

Data collection: *CrystalClear* (Rigaku/MSC, 2005); cell refinement: *CrystalClear*; data reduction: *CrystalClear*; program(s) used to solve structure: *SHELXS97* (Sheldrick, 1997); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *ORTEP-3* (Farrugia, 1997); software used to prepare material for publication: *CrystalStructure* (Rigaku/MSC, 2005).

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