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4-Methyl-7-[3-(4-*o*-tolylpiperazin-1-yl)propoxy]-2*H*-chromen-2-one

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The title compound, $C_{24}H_{28}N_2O_3$, is an α_1-adrenoceptor antagonist. The piperazine ring adopts an almost perfect chair conformation. Intermolecular π–π interactions and C—H···O hydrogen bonds stabilize the crystal packing.

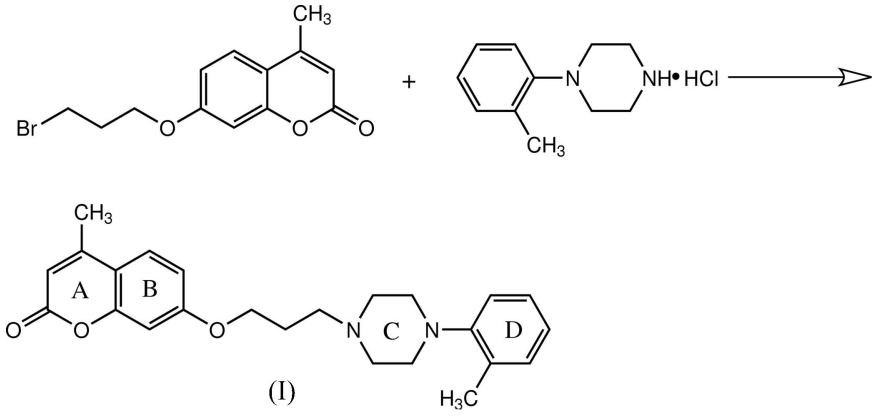
Key indicators

Single-crystal X-ray study
T = 298 K
Mean σ(C–C) = 0.004 Å
R factor = 0.048
wR factor = 0.131
Data-to-parameter ratio = 13.9

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

Comment

A series of coumarin derivatives has been designed and synthesized based on the pharmacophore model of α_1-adrenoceptor antagonists (Fang *et al.*, 2003). The structure elucidation of these compounds is important for the understanding of their biological activities, and the crystal structures of these compounds are especially important for the evaluation of their structure–activity relationships. However, reports of the crystal structures of this kind of compound are scarce (Estrada *et al.*, 2000). In this context, the crystal structure of the title compound, (I), is reported here.



(I)

The molecular structure of (I) is shown in Fig. 1. The piperazine ring *C* (N1/N2/C14–C17) adopts an almost perfect chair conformation. The equatorially substituted atom N1 meets the requirements for the bioactive conformation of an α_1-adrenoceptor antagonist (Kuipers *et al.*, 1997).

The crystal packing of (I) shows an intermolecular π–π interaction and a C—H···O hydrogen bond. Ring *B* stacks with a symmetry-equivalent ring at $(2-x, 1-y, -z)$, with an interplanar distance of 3.48 (2) Å and an centroid-to-centroid distance of 3.79 (2) Å. A C—H···O hydrogen bond links the molecules into a chain running along the *b* axis (Table 2).

Experimental

The synthesis of (I) was performed according to the method of Jain *et al.* (1967). A mixture of 7-bromopropyl-4-methylcoumarin (594 mg, 2 mmol), 1-(2-methylphenyl)piperazine hydrochloric salt (425 mg,

2 mmol) and anhydrous K_2CO_3 (276 mg, 2 mmol) was stirred at reflux in acetone (5 ml) and anhydrous ethanol (5 ml) for 48 h. The precipitate was filtered off and washed with fresh chloroform. The solvent was evaporated under reduced pressure from the combined filtrate and washings. The residue was chromatographed on a silica-gel column by eluting with a cyclohexane–acetone mixture (8:1 *v*/*v*) to give a colourless solid (170 mg, 21%; m.p. 511 K). ^{1}H NMR (500 MHz, $CDCl_3$, δ, p.p.m.): 7.49 (*d*, 1H, H5, J = 8.75 Hz), 6.84 (*d*, 1H, H8, J = 2.46 Hz), 6.87 (*dd*, 1H, H6, J = 8.74 Hz, 2.48 Hz), 6.84–7.20 (*m*, 4H, Ph), 6.13 (*s*, 1H, H3), 4.12 (*t*, 2H, CH_2O, J = 6.3 Hz), 2.96 [*m*, 4H, $N_4(CH_2)_2$], 2.64 [*m*, 6H, $(CH_2)_3N_1$], 2.39 (*s*, 3H, 4-CH_3), 2.31 (*s*, 3H, CH_3), 2.06 (*m*, 2H, CH_2). Single crystals suitable for diffraction analysis were obtained by slow evaporation of a solution of (I) in a mixture of ethanol and ethyl acetate (1:1 *v*/*v*) at room temperature.

Crystal data

$C_{24}H_{28}N_2O_3$	V = 1053.1 (8) Å^3
M_r = 392.48	Z = 2
Triclinic, $P\overline{1}$	D_x = 1.238 Mg m^{-3}
a = 7.099 (3) Å	Mo $K\alpha$ radiation
b = 9.659 (4) Å	μ = 0.08 mm^{-1}
c = 16.195 (7) Å	T = 298 (2) K
α = 76.822 (5)°	Prism, colourless
β = 77.420 (6)°	0.42 × 0.30 × 0.11 mm
γ = 83.658 (5)°	

Data collection

Bruker SMART-1000 CCD area-detector diffractometer	5495 measured reflections
φ and ω scans	3663 independent reflections
Absorption correction: multi-scan (*SADABS*; Bruker, 2000)	1980 reflections with $I > 2\sigma(I)$
T_{min} = 0.971, T_{max} = 0.991	R_{int} = 0.020
	θ_{max} = 25.0°

Refinement

Refinement on F^2	$w = 1/[\sigma^2(F_o^2) + (0.0711P)^2 + 0.4P]$ where $P = (F_o^2 + 2F_c^2)/3$
$R[F^2 > 2\sigma(F^2)]$ = 0.048	$(\Delta/\sigma)_{max} < 0.001$
$wR(F^2)$ = 0.131	$\Delta\rho_{max}$ = 0.14 e Å^{-3}
S = 1.01	$\Delta\rho_{min}$ = −0.21 e Å^{-3}
3663 reflections	
264 parameters	
H-atom parameters constrained	

Table 1
Selected torsion angles (°).

N1—C14—C15—N2	−59.1 (3)	N2—C16—C17—N1	58.0 (3)

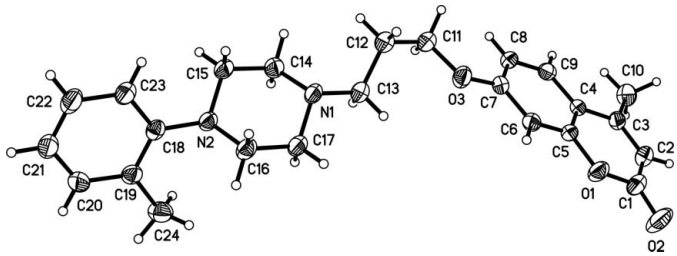


Figure 1
The molecular structure of (I), showing the atom-labelling scheme. Displacement ellipsoids are drawn at the 30% probability level and H atoms are shown as spheres of arbitrary radii.

Table 2
Hydrogen-bond geometry (Å, °).

D—H···A	D—H	H···A	D···A	D—H···A
C8—H8···O2^{i}	0.93	2.59	3.514 (3)	174

Symmetry code: (i) $x, y+1, z$.

H atoms were found in a difference map, but they were refined using a riding model with C—H = 0.93 Å for $C_{aromatic}$ and 0.97 Å for $C_{methylene}$ and C_{methyl}, and with $U_{iso}(H) = 1.2U_{eq}(C)$ or $1.5U_{eq}(C_{methyl})$. The methyl groups were allowed to rotate but not to tip.

Data collection: *SMART* (Bruker, 2000); cell refinement: *SAINT* (Bruker, 2000); data reduction: *SAINT*; program(s) used to solve structure: *SHELXS97* (Sheldrick, 1997); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *SHELXTL* (Bruker, 2000); software used to prepare material for publication: *SHELXTL* and *PLATON* (Spek, 2003).

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