

2-[4-(Dimethylamino)phenyl]-6-methoxy-1,3-benzothiazole

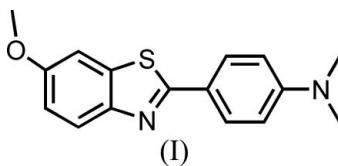
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Key indicators

Single-crystal X-ray study
 $T = 293$ K
Mean $\sigma(\text{C}-\text{C}) = 0.002$ Å
 R factor = 0.033
 wR factor = 0.095
Data-to-parameter ratio = 13.1For details of how these key indicators were
automatically derived from the article, see
<http://journals.iucr.org/e>.In the title compound, $\text{C}_{16}\text{H}_{16}\text{N}_2\text{OS}$, the benzothiazole ring system makes a dihedral angle of 8.64 (5°) with the dimethylaminophenyl group.Received 12 December 2006
Accepted 30 December 2006

Comment

Benzothiazole aniline (BTA) analogues bind to β -amyloid plaques with high affinity (Klunk *et al.*, 2001). Their structures are very important for understanding the interaction between the ligand and the β -amyloid plaques. In the title compound, (I), Fig. 1, the benzothiazole ring system makes a dihedral angle of 8.64 (5°) with the dimethylaminophenyl group. Within the benzothiazole unit, the six-membered ring makes a dihedral angle of 2.29 (7°) with the five-membered ring.

Experimental

The title compound, (I), was prepared according to the literature procedure of Mathis *et al.* (2003). Single crystals suitable for X-ray diffraction studies were obtained by slow evaporation of a tetrahydrofuran solution over a period of two days.

Crystal data

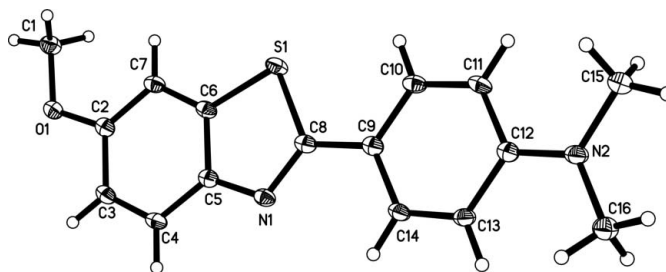
 $\text{C}_{16}\text{H}_{16}\text{N}_2\text{OS}$
 $M_r = 284.37$
Monoclinic, $P2_1/n$
 $a = 14.997$ (3) Å
 $b = 5.9717$ (12) Å
 $c = 15.617$ (3) Å
 $\beta = 101.24$ (3°)
 $V = 1371.8$ (5) Å³ $Z = 4$
 $D_x = 1.377$ Mg m⁻³
Mo $K\alpha$ radiation
 $\mu = 0.23$ mm⁻¹
 $T = 293$ (2) K
Prism, colorless
 $0.24 \times 0.20 \times 0.18$ mm

Figure 1

The molecular structure of (I), showing displacement ellipsoids drawn at the 30% probability level.

Data collection

Bruker P4 area-detector diffractometer	7871 measured reflections
ω scans	2405 independent reflections
Absorption correction: multi-scan (<i>SADABS</i> ; Sheldrick, 1996)	2153 reflections with $I > 2\sigma(I)$
$T_{\min} = 0.946$, $T_{\max} = 0.959$	$R_{\text{int}} = 0.025$
	$\theta_{\text{max}} = 25.0^\circ$

Refinement

Refinement on F^2	$w = 1/[\sigma^2(F_o^2) + (0.055P)^2 + 0.283P]$
$R[F^2 > 2\sigma(F^2)] = 0.033$	where $P = (F_o^2 + 2F_c^2)/3$
$wR(F^2) = 0.095$	$(\Delta/\sigma)_{\text{max}} = 0.001$
$S = 1.10$	$\Delta\rho_{\text{max}} = 0.23 \text{ e } \text{\AA}^{-3}$
2405 reflections	$\Delta\rho_{\text{min}} = -0.24 \text{ e } \text{\AA}^{-3}$
184 parameters	
H-atom parameters constrained	

All H atoms were positioned geometrically and refined as riding atoms, with C–H = 0.93–0.96 Å and $U_{\text{iso}}(\text{H}) = 1.2U_{\text{eq}}(\text{C})$ or $1.5U_{\text{eq}}(\text{methyl C})$.

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

This work was supported by the National Natural Science Foundation of China (NSFC 20471011).

References

- Bruker (1997). *SMART*, *SAINTE* and *SHELXTL*. Bruker AXS Inc., Madison, Wisconsin, USA.
- Klunk, W. E., Wang, Y., Huang, G. F., Debnath, M. L., Holt, D. P. & Mathis, C. A. (2001). *Life Sci.* **69**, 1471–1484.
- Mathis, C. A., Wang, Y., Holt, D. P., Huang, G. F., Debnath, M. L. & Klunk, W. E. (2003). *J. Med. Chem.* **46**, 2740–2754.
- Sheldrick, G. M. (1996). *SADABS*. University of Göttingen, Germany.
- Sheldrick, G. M. (1997). *SHELXS97* and *SHELXL97*. University of Göttingen, Germany.