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Key indicators

Single-crystal X-ray study T = 293 K Mean σ (C–C) = 0.005 Å R factor = 0.049 wR factor = 0.145 Data-to-parameter ratio = 13.6

For details of how these key indicators were automatically derived from the article, see http://journals.iucr.org/e. The metabolism of all-*trans*-retinoic acid is mediated by a cytochrome dependent P-450 system. The title compound, $C_{21}H_{23}N_5S$, is an inhibitor of the P-450 system. Two planar rings connected *via* a central CH group form a dihedral angle of 80.2 (1)°; the planar systems connected through an NH group form a dihedral angle of 37.12 (8)°. The N-H···N hydrogen bonds link the molecules of the title compound into infinite chains stretching along the *c* direction.

1-yl)propyl]phenyl}-2-benzothiazolamine

(+)-*N*-{4-[(1*S*,2*S*)-2-(Dimethylamino)-1-(1*H*-imidazol-

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Comment

All-*trans*-retinoic acid (ATRA) is a metabolite of retinol (Vitamin A) which is involved in growth and epithelial differentiation in mammals. However the potency of ATRA is strongly attenuated by its rapid metabolism involving the stage of hydroxylation, mediated by a cytochrome dependent P-450 system (Leo *et al.*, 1989). The P-450 system is inhibited by the title compound, which leads to increased plasma levels of ATRA.

All four rings in the molecule of the title compound (I) (Fig. 1) are essentially planar. The imidazolyl ring is almost perpendicular to the phenylene ring [dihedral angle 80.2 (1)°]; the phenylene ring and the benzothiazolyl ring are twisted with a dihedral angle of 37.12 (8)°. The secondary amine group is almost coplanar with the benzothiazolyl moiety [dihedral angle 4.3 (2)°] but is twisted with respect to the phenylene ring [dihedral angle 37.3 (3)°]. The degree of coplanarity and conjugation with the π -electron systems of the aromatic rings is reflected in the C–N bond lengths. The C19–N18 bond [1.357 (4) Å] is significantly shorter than the C15–N18 bond [1.411 (4) Å].



The N18—H18···N9 hydrogen bond [H18···N9ⁱ 2.07 Å, N18···N9ⁱ 2.884 (4) Å, N18—H18···N9ⁱ 158° (D—H distance not normalized); symmetry code (i): $\frac{1}{2} - x$, 1 - y, $z - \frac{1}{2}$] links two molecules related by the 2_1 screw axis parallel to *c*, thus giving rise to infinite one-dimensional chains stretching along the *c* axis of the crystal.

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Figure 1

Perspective view of a molecule of the title compound with atomic numbering scheme. Displacement ellipsoids are drawn at the 50% probability level.

Experimental

The title compound was obtained from the Janssen Research Foundation, Beerse, Belgium. The synthesis has been described by Venet et al. (1997). Single crystals were grown by slow evaporation from a solution in ethanol.

Crystal data

 $C_{21}H_{23}N_5S$ $M_r = 377.51$ Orthorhombic, $P2_12_12_1$ a = 9.4442 (9) Åb = 13.725(1) Å c = 15.703(1) Å $V = 2035.4 (3) \text{ Å}^3$ Z = 4 $D_x = 1.232 \text{ Mg m}^{-3}$

Data collection

Siemens P4 four-circle diffractometer $\omega/2\theta$ scans Absorption correction: ψ scan XEMP (Siemens, 1989) $T_{\rm min}=0.625,\ T_{\rm max}=0.886$ 3908 measured reflections 3370 independent reflections 2912 reflections with $I > 2\sigma(I)$

Cu $K\alpha$ radiation Cell parameters from 37 reflections $\theta = 5.6 - 26.6^{\circ}$ $\mu = 1.52 \text{ mm}^{-1}$ T = 293 KPrism, colourless $0.30 \times 0.24 \times 0.08 \text{ mm}$

$R_{\rm int} = 0.023$
$\theta_{\rm max} = 69.2^{\circ}$
$h = -9 \rightarrow 9$
$k = -16 \rightarrow 16$
$l = -19 \rightarrow 19$
3 standard reflections
every 100 reflections
intensity decay: none

Refinement

Refinement on F^2	$(\Delta/\sigma)_{\rm max} = 0.001$
$R[F^2 > 2\sigma(F^2)] = 0.049$	$\Delta \rho_{\rm max} = 0.17 \ {\rm e} \ {\rm \AA}^{-3}$
$wR(F^2) = 0.145$	$\Delta \rho_{\rm min} = -0.18 {\rm e} {\rm \AA}^{-3}$
S = 1.07	Extinction correction: SHELXL9
3370 reflections	(Sheldrick, 1997)
248 parameters	Extinction coefficient: 0.0023 (4)
H-atom parameters constrained	Absolute structure: Flack (1983).
$w = 1/[\sigma^2(F_o^2) + (0.0806P)^2]$	847 Friedel pairs.
+ 0.5545P]	Flack parameter $= 0.01$ (3)
where $P = (F_o^2 + 2F_c^2)/3$	

Table 1

Hydrogen-bonding geometry (Å, °).

$D - H \cdot \cdot \cdot A$	D-H	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - \mathbf{H} \cdots A$
$N18 - H18 \cdot \cdot \cdot N9^{i}$	0.86	2.07	2.884 (4)	158
C22-H22···N9 ⁱⁱ	0.93	2.72	3.503 (5)	142
$C23-H23\cdots N1^{ii}$	0.93	2.74	3.614 (5)	157

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

After checking their presence in the difference map, H atoms were placed at their geometrically calculated positions (the NH group has a planar environment), except for those of the methyl groups. The latter were found from a circular difference Fourier synthesis. All H atoms were allowed to ride on their parent atom and, for the methyl groups, to rotate around their local threefold axis. The isotropic displacement factors were fixed at 1.25 $U_{\rm eq}$ of their parent atoms.

Data collection: XSCANS (Siemens, 1996); cell refinement: XSCANS; data reduction: XSCANS; program(s) used to solve structure: SIR92 (Altomare et al., 1994); program(s) used to refine structure: SHELXL97 (Sheldrick, 1997); molecular graphics: DIAMOND (Bergerhoff, 1996); software used to prepare material for publication: PARST (Nardelli, 1983).

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