Acta Crystallographica Section E Structure Reports Online

ISSN 1600-5368

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Key indicators

Single-crystal X-ray study T = 298 KMean σ (C–C) = 0.003 Å R factor = 0.058 wR factor = 0.088 Data-to-parameter ratio = 11.9

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

© 2003 International Union of Crystallography Printed in Great Britain – all rights reserved 5-[5-(4-Methoxyphenyl)-3-trifluoromethyl-1*H*-pyrazol-1-yl]-2-sulfamoylbenzyl propionate: a novel 1,5-diraylpyrazole class of COX-2 inhibitor

The title compound, $C_{21}H_{20}F_3N_3O_5S$, has been made during our research program on COX-2 inhibitors. The molecules are held together by intermolecular hydrogen bonds involving the amide N atom with the unsubstituted N atom of the pyrazole ring and with an O atom of the sulfanamide group, across centers of symmetry.

Comment

With a view to identifying novel COX-2 inhibitors, we have carried out extensive chemical modification of celecoxib. The title compound, (I), emerged as one of the potent molecules from an SAR (structure–activity relationship) study. The molecular structure of (I) is shown in Fig. 1. The bond lengths and angles are normal (Allen *et al.*, 1987) and the five-membered ring is planar.



Weak intramolecular interactions, particularly C3– H1...O3, C6–H3...O1 and C7–H4...O2, influence the observed conformation of the molecule. In the crystal structure, the molecules are held together by hydrogen-bonding and C–H...O interactions. Both H atoms of the sulfonamide group are involved in intermolecular hydrogen bonds, connecting molecules across centers of symmetry. The N1– H20...N3ⁱⁱ hydrogen bond results in the formation of hydrogen-bonded dimers (all symmetry codes in Table 1). These dimers are linked into a chain along the *a* axis by the hydrogen bond N1–H19...O1ⁱ, which is supported by the weak interaction C20–H18...O1^{iv}. The weak interactions C12–H11...O4ⁱⁱⁱ and C18–H14...O2ⁱⁱⁱ connect molecules along the *bc* diagonal.

Experimental

The title compound was synthesized (Singh *et al.*, 2003) by chemoselective acylation of the intermediate 2-hydroxymethyl-4-[5-(4methoxyphenyl)-3-trifluoromethyl-1*H*-1-pyrazolyl]-1-benzenesulfonamide (Lohray *et al.*, 2000). Crystals suitable for X-ray diffraction analysis were grown from methanol. Received 1 October 2003 Accepted 9 October 2003 Online 23 October 2003

DRL publication No. 253-A.





The structure of (I), showing 50% probability displacement ellipsoids and the atom-numbering scheme.



Figure 2

Packing of the molecules, viewed approximately down the c axis. Hydrogen bonds are indicated by thin lines.

Crystal data

$C_{21}H_{20}F_{3}N_{3}O_{5}S$	Z = 2
$M_r = 483.46$	$D_x = 1.493 \text{ Mg m}^{-3}$
Triclinic, $P\overline{1}$	Cu Ka radiation
a = 10.4490 (8) Å	Cell parameters from 25
b = 12.0126 (8) Å	reflections
c = 9.2196(9) Å	$\theta = 22.7 - 24.6^{\circ}$
$\alpha = 111.068 \ (6)^{\circ}$	$\mu = 1.94 \text{ mm}^{-1}$
$\beta = 94.851 \ (7)^{\circ}$	T = 298.1 K
$\gamma = 86.328 \ (6)^{\circ}$	Block, colorless
V = 1075.3 (2) Å ³	$0.50\times0.50\times0.40$ mm
Data collection	
Digalay AEC 78 diffractomator	P = 0.051

Rigaku AFC-7S diffractometer ω -2 θ scans Absorption correction: ψ scan (North et al., 1968) $T_{\min} = 0.346, T_{\max} = 0.461$ 4902 measured reflections 3926 independent reflections 3801 reflections with $F^2 > 2\sigma(F^2)$

 $R_{int} = 0.051$ $\theta_{\rm max} = 68.0^\circ$ $h = -12 \rightarrow 12$ $k = -13 \rightarrow 14$ $l = -11 \rightarrow 4$ 3 standard reflections every 150 reflections intensity decay: 2.6% Refinement

Weighting by Chebychev poly-
nomial with 3 parameters
(Carruthers & Watkin, 1979):
232.809, 288.588, 57.8579
$(\Delta/\sigma)_{\rm max} = 0.010$
$\Delta \rho_{\rm max} = 0.41 \text{ e } \text{\AA}^{-3}$
$\Delta \rho_{\rm min} = -0.35 \text{ e } \text{\AA}^{-3}$
Extinction correction: Larson
(1970) (equation 22)
Extinction coefficient: 416 (22)

lable l			
Hydrogen-bonding	geometry	(Å,	°).

$D - H \cdot \cdot \cdot A$	D-H	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - \mathbf{H} \cdot \cdot \cdot A$
$N1 - H19 \cdots O1^{i}$	0.85 (4)	2.25 (4)	3.057 (4)	159 (4)
$N1 - H20 \cdot \cdot \cdot N3^{ii}$	0.85 (4)	2.26 (4)	3.103 (4)	169 (3)
C3-H1···O3	0.95	2.31	2.678 (3)	103
C6-H3···O1	0.95	2.47	2.852 (3)	104
$C7-H4 \cdot \cdot \cdot O2$	0.95	2.45	2.769 (3)	100
C12-H11···O4 ⁱⁱⁱ	0.95	2.52	3.433 (4)	163
C18−H14···O2 ⁱⁱⁱ	0.95	2.47	3.379 (3)	160
$C20-H18\cdots O1^{iv}$	0.95	2.47	3.273 (3)	142

Symmetry codes: (i) -x, 1-y, 1-z; (ii) 1-x, 1-y, 1-z; (iii) x, y-1, z-1; (iv) -x, -y, 1-z.

H atoms bonded to nitrogen were located in a difference map and were freely refined with individual U_{iso} values. Other H atoms were positioned geometrically and refined as riding, with C-H = 0.95 Å and $U_{iso}(H) = 1.2U_{eq}(C)$.

Data collection: MSC/AFC Diffractometer Control Software (Molecular Structure Corporation, 1994); cell refinement: MSC/AFC Diffractometer Control Software; data reduction: CRYSTALS (Watkin et al., 1996); program(s) used to solve structure: SIR92 (Altomare et al., 1993); program(s) used to refine structure: CRYS-TALS; molecular graphics: CrystalStructure (Rigaku/MSC and Rigaku, 2003); software used to prepare material for publication: CrystalStructure.

The authors thank Dr A. Venkateswarlu and Dr K. Anji Reddy for their interest and encouragement in this work.

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