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N-[4-Cyano-3-(trifluoromethyl)phenyl]-3-(4-fluorophenylsulfonyl)-2-hydroxy-2-methylpropionamide

Xiu-Rong Hu* and Jian-Ming Gu

Centre of Analysis and Measurement, Zhejiang University, Hangzhou, Zhejiang 310028, People's Republic of China

Correspondence e-mail: huxiurong@yahoo.com.cn

Key indicators

Single-crystal X-ray study
T = 296 K
Mean σ(C–C) = 0.003 Å
R factor = 0.040
wR factor = 0.098
Data-to-parameter ratio = 16.1

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

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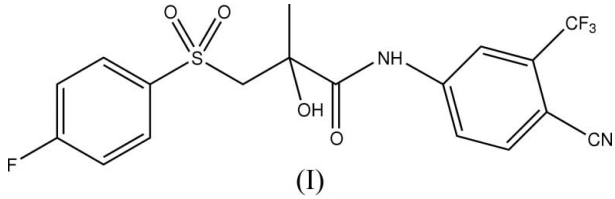
The structure of the title compound, $C_{18}H_{14}F_4N_2O_2S$, consists of molecules that pack in a linear hydrogen-bonded chain along the *c* axis. This hydrogen-bonding arrangement involves the hydroxy group and one of the sulfonyl O atoms.

Comment

The title compound, (I), also known as bicalutamide, belongs to a class of drugs called anti-androgens. It is thought to prevent the growth of prostate cancer by blocking the effects of androgens on the cancer cells (Bohl *et al.*, 2005; Tucker *et al.*, 1988). Two polymorphs of bicalutamide have been reported previously (Tetsuya *et al.*, 2003; Westheim & Raymond, 2004), but their crystal structures were not studied. We report here the crystal structure of the title compound, (I).



(I)

In the crystal structure of (I), the hydroxy group and one of the sulfonyl O atoms are involved in a hydrogen-bonded network (Table 2). The crystal packing is influenced by this intermolecular hydrogen-bond interaction, which links the molecules into a chain propagating along the *c* axis. The cyano group deviates slightly from the plane of the benzene ring (C5–C10) and the deviations of atoms C11 and N32 are 0.106 (3) and 0.196 (4) Å, respectively. The CN group is not conjugated with the benzene ring, resulting in a longer bond length for C8—C11 (Table 1) compared to a Csp^2—Csp^2 bond. The two benzene rings in (I) form a dihedral angle of 40.35 (7)°.

Experimental

N-(4-Cyano-3-trifluoromethylphenyl)-3-(4-fluorophenylsulfanyl)-2-hydroxy-2-methylpropionamide (25.0 g, 63 mmol), CH_2Cl_2 (600 ml) and 85% *m*-chloroperoxybenzoic acid (22.0 g, 123 mmol) were mixed in a three-necked bottle and stirred at room temperature for 24 h. Na_2SO_4 (500 ml, 10%) was then added to the solution and it was stirred for 15 min. The organic part was extracted and washed with Na_2CO_3 (saturated, 3 × 200 ml) and NaCl (saturated, 2 × 150 ml) and dried using anhydrous $MgSO_4$; the CH_2Cl_2 was recovered by vacuum distillation. The final product was recrystallized from an ethanol solution and a crystalline product (21.5 g, yield 83%) was obtained (Sepp-Lorenzino & Slovin, 2000; Thurlow, 1998). This was recrystallized from chloroform, giving colourless crystals of (I) suitable for X-ray diffraction.

Crystal data

$C_{18}H_{14}F_4N_2O_4S$
M_r = 430.37
Monoclinic, $P2_1/c$
a = 14.882 (5) Å
b = 12.213 (3) Å
c = 10.461 (3) Å
β = 104.680 (13)°
V = 1839.3 (9) Å^3
Z = 4
D_x = 1.554 Mg m^{-3}
Mo $K\alpha$ radiation
Cell parameters from 14876 reflections
θ = 3.0–27.5°
μ = 0.24 mm^{-1}
T = 296 (1) K
Block, colourless
0.29 × 0.25 × 0.17 mm

Data collection

Rigaku R-AXIS RAPID diffractometer
ω scans
Absorption correction: multi-scan (*ABSCOR*; Higashi, 1995)
T_{min} = 0.881, T_{max} = 0.959
17686 measured reflections
4206 independent reflections
2973 reflections with $F^2 > 2\sigma(F^2)$
R_{int} = 0.027
θ_{max} = 27.5°
$h = -19 \rightarrow 19$
$k = -15 \rightarrow 15$
$l = -13 \rightarrow 11$

Refinement

Refinement on F^2
$R[F^2 > 2\sigma(F^2)]$ = 0.040
$wR(F^2)$ = 0.098
S = 1.00
4206 reflections
262 parameters
H-atom parameters constrained
$w = 1/[0.0006F_o^2 + 1.16\sigma(F_o^2)]/(4F_o^2)$
$(\Delta/\sigma)_{max} < 0.001$
$\Delta\rho_{max}$ = 0.29 e Å^{-3}
$\Delta\rho_{min}$ = −0.39 e Å^{-3}

Table 1
Selected bond lengths (Å).

O21—C2	1.416 (2)	N31—C5	1.401 (2)
O22—C4	1.215 (2)	N32—C11	1.135 (2)
N31—C4	1.355 (2)	C8—C11	1.446 (2)

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

D—H···A	D—H	H···A	D···A	D—H···A
O21—H211···O23^{i}	0.91	2.47	2.856 (2)	106

Symmetry code: (i) $+x, -y+\frac{1}{2}, +z-\frac{1}{2}$.

The H atoms of the hydroxy and amido groups were located in difference Fourier maps and included in the refinement based on the as-found O—H and N—H bond lengths, but their isotropic displacement paramenters were initially refined and then fixed in the final stage. The other H atoms were placed in calculated positions, with C—H = 0.93–0.97 Å, and included in the refinement in the riding model, with U_{iso}(H) = 1.2U_{eq} ($C_{methylene}$ and $C_{aromatic}$) or 1.5U_{eq}(C_{methyl}).

Data collection: *PROCESS-AUTO* (Rigaku, 1998); cell refinement: *PROCESS-AUTO*; data reduction: *CrystalStructure* (Rigaku/MSC, 2004); program(s) used to solve structure: *SHELXS97* (Sheldrick, 1997); program(s) used to refine structure: *CRYSTALS* (Betteridge *et al.*, 2003); molecular graphics: *ORTEP-3 for Windows* (Farrugia, 1997); software used to prepare material for publication: *CrystalStructure*.

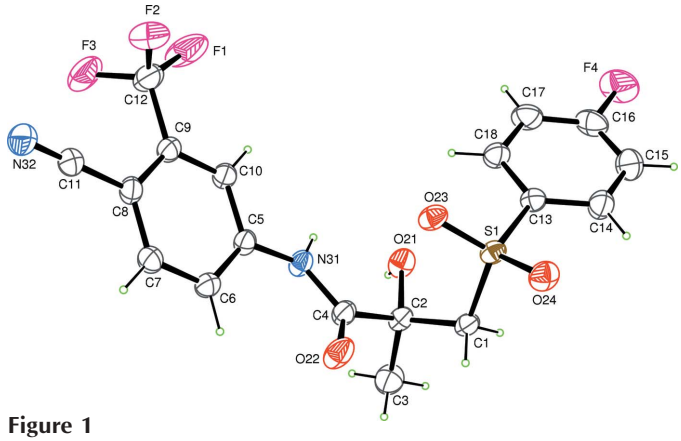


Figure 1
A view of (I). Displacement ellipsoids are drawn at the 30% probability level and H atoms are shown as small circles of arbitary radii.

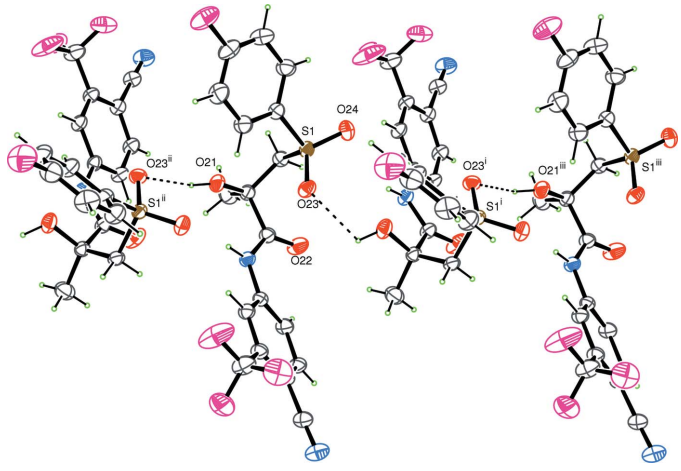


Figure 2
A chain of molecules in (I). Displcement ellipsoids are drawn at the 30% probability level and hydrogen bonds are shown as dashed lines. [Symmetry code: (i) $x, \frac{1}{2}-y, \frac{1}{2}+z$; (ii) $x, \frac{1}{2}-y, -\frac{1}{2}+z$; (iii) $x, y, 1+z$.]

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