

N-(5-Chloro-1,3-thiazol-2-yl)-2,4-difluorobenzamide

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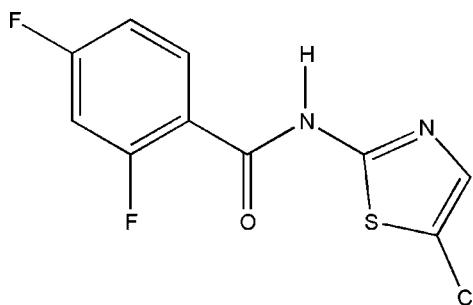
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Key indicators: single-crystal X-ray study; $T = 296\text{ K}$; mean $\sigma(\text{C}-\text{C}) = 0.005\text{ \AA}$; R factor = 0.047; wR factor = 0.136; data-to-parameter ratio = 12.9.

The title compound, $\text{C}_{10}\text{H}_5\text{ClF}_2\text{N}_2\text{OS}$, was obtained by linking an amino heterocycle and a substituted benzoyl chloride. The dihedral angle between the two rings is $41.2(2)^\circ$ and the equalization of the amide C–N bond lengths reveals the existence of conjugation between the benzene ring and the thiazole unit. In the crystal, pairs of N–H \cdots N hydrogen bonds link molecules into inversion dimers. Non-classical C–H \cdots F and C–H \cdots O hydrogen bonds stabilize the crystal structure.

Related literature

For synthesis and the biological activity of thiazolides, see: Ballard *et al.* (2011).

**Experimental***Crystal data*

$M_r = 274.68$

Triclinic, $P\bar{1}$
 $a = 6.929(2)\text{ \AA}$
 $b = 7.330(2)\text{ \AA}$
 $c = 12.179(4)\text{ \AA}$
 $\alpha = 101.669(3)^\circ$
 $\beta = 98.277(3)^\circ$
 $\gamma = 111.796(3)^\circ$

$V = 545.9(3)\text{ \AA}^3$
 $Z = 2$
 $\text{Mo } K\alpha \text{ radiation}$
 $\mu = 0.55\text{ mm}^{-1}$
 $T = 296\text{ K}$
 $0.35 \times 0.33 \times 0.27\text{ mm}$

Data collection

Bruker APEXII CCD
diffractometer
Absorption correction: multi-scan
(*SADABS*; Sheldrick, 1996)
 $T_{\min} = 0.831$, $T_{\max} = 0.866$

3930 measured reflections
1998 independent reflections
1693 reflections with $I > 2\sigma(I)$
 $R_{\text{int}} = 0.028$

Refinement

$R[F^2 > 2\sigma(F^2)] = 0.047$
 $wR(F^2) = 0.136$
 $S = 1.06$
1998 reflections

155 parameters
H-atom parameters constrained
 $\Delta\rho_{\max} = 1.25\text{ e \AA}^{-3}$
 $\Delta\rho_{\min} = -0.33\text{ e \AA}^{-3}$

Table 1
Hydrogen-bond geometry (\AA , $^\circ$).

$D-\text{H}\cdots A$	$D-\text{H}$	$\text{H}\cdots A$	$D\cdots A$	$D-\text{H}\cdots A$
N1–H1 \cdots N2 ⁱ	0.86	2.15	2.988 (3)	166
C4–H4 \cdots F2 ⁱⁱ	0.93	2.38	3.127 (4)	137
C4–H4 \cdots O3 ⁱⁱ	0.93	2.56	3.329 (4)	140

Symmetry codes: (i) $-x + 2$, $-y + 1$, $-z + 1$; (ii) $x + 1$, y , z .

Data collection: *APEX2* (Bruker, 2008); cell refinement: *SAINT* (Bruker, 2008); data reduction: *SAINT*; program(s) used to solve structure: *SHELXS97* (Sheldrick, 2008); program(s) used to refine structure: *SHELXL97* (Sheldrick, 2008); molecular graphics: *SHELXTL* (Sheldrick, 2008); software used to prepare material for publication: *SHELXTL*.

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Supplementary data and figures for this paper are available from the IUCr electronic archives (Reference: RK2350).

References

- Ballard, T. E., Wang, X., Olekhovich, I., Koerner, T., Seymour, C., Salamoun, J., Warthan, M., Hoffman, P. S. & Macdonald, T. L. (2011). *ChemMedChem*, **6**, 362–377.
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supplementary materials

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N-(5-Chloro-1,3-thiazol-2-yl)-2,4-difluorobenzamide

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Comment

Nitazoxanide, (2-acetyloloxy-*N*-(5-nitro-2-thiazolyl)benzamide), belonged to nitrothiazole analogue, was developed as a promising compound to treat both human and animal diseases (Ballard *et al.*, 2011). In this paper, we report the synthesis and structure of the title compound, which is a derivative of nitazoxanide. The conjugation between benzene ring and thiazole moiety confirmed the existance of amide anion, which is considered to directly inhibit the *PFOR* enzyme (key enzyme of central intermediary metabolism in anaerobic organisms). The classical intermolecular hydrogen bonds N1—H1···N2ⁱ forms centrosymmetrical dimers (Table 1). The non-classical intermolecular hydrogen bonds C4—H4···F2ⁱⁱ and C4—H4···O3ⁱⁱ stabilize molecular packing in crystal. Symmetry codes: (i) -*x*+2, -*y*+1, -*z*+1; (ii) *x*+1, *y*, *z*.

Experimental

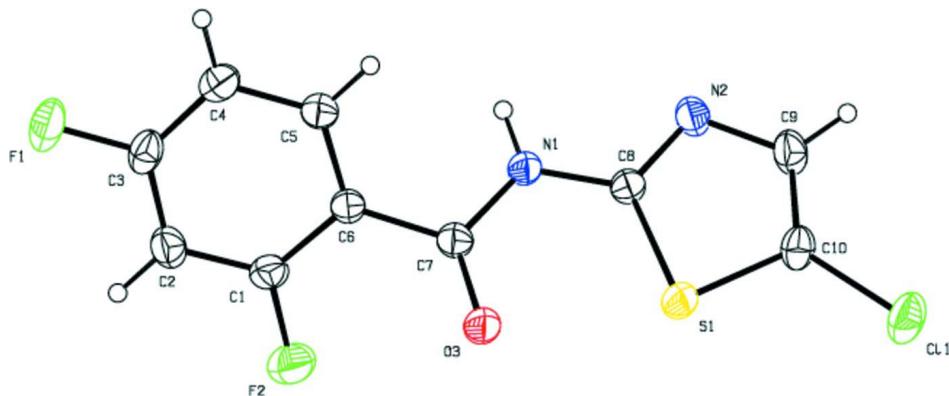
The title compound was obtained according to routine method: to a solution of 5-chlorothiazol-2-amine (1 mmol) in distilled pyridine was added a equimolar amount of 2,4-difluorobenzoyl chloride with stirring. When addition was complete, the reaction mixture was allowed to stand at room temperature and stirred over night. The reaction was judged complete by *TLC* analysis. The crude product then seperated on dilution was filtered out, washed with 10% NaHCO₃ solution, then several times with water. The dry solid was purified by chromatography to give pure compound and the crystals were obtained by recrystallization from CH₃OH.

Refinement

The positions of all H atoms were determined geometrically and refined using a riding model with C—H = 0.93 Å, N—H = 0.86 Å and *U*_{iso}(H) = 1.2*U*_{eq}(C, N).

Computing details

Data collection: *APEX2* (Bruker, 2008); cell refinement: *SAINT* (Bruker, 2008); data reduction: *SAINT* (Bruker, 2008); program(s) used to solve structure: *SHELXS97* (Sheldrick, 2008); program(s) used to refine structure: *SHELXL97* (Sheldrick, 2008); molecular graphics: *SHELXTL* (Sheldrick, 2008); software used to prepare material for publication: *SHELXTL* (Sheldrick, 2008).

**Figure 1**

The molecular structure of title compound with the atom labels. Displacement ellipsoids are drawn at the 30% probability level. H atoms are presented as a small spheres of arbitrary radius.

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Crystal data



$M_r = 274.68$

Triclinic, $P\bar{1}$

Hall symbol: -P 1

$a = 6.929 (2)$ Å

$b = 7.330 (2)$ Å

$c = 12.179 (4)$ Å

$\alpha = 101.669 (3)^\circ$

$\beta = 98.277 (3)^\circ$

$\gamma = 111.796 (3)^\circ$

$V = 545.9 (3)$ Å³

$Z = 2$

$F(000) = 276$

$D_x = 1.671 \text{ Mg m}^{-3}$

Melting point = 428–429 K

Mo $K\alpha$ radiation, $\lambda = 0.71073$ Å

Cell parameters from 2870 reflections

$\theta = 3.1\text{--}28.2^\circ$

$\mu = 0.55 \text{ mm}^{-1}$

$T = 296$ K

Block, colourless

$0.35 \times 0.33 \times 0.27$ mm

Data collection

Bruker APEXII CCD

diffractometer

Radiation source: fine-focus sealed tube

Graphite monochromator

φ - and ω -scans

Absorption correction: multi-scan

(*SADABS*; Sheldrick, 1996)

$T_{\min} = 0.831$, $T_{\max} = 0.866$

3930 measured reflections

1998 independent reflections

1693 reflections with $I > 2\sigma(I)$

$R_{\text{int}} = 0.028$

$\theta_{\max} = 25.5^\circ$, $\theta_{\min} = 3.1^\circ$

$h = -8 \rightarrow 8$

$k = -8 \rightarrow 8$

$l = -14 \rightarrow 14$

Refinement

Refinement on F^2

Least-squares matrix: full

$R[F^2 > 2\sigma(F^2)] = 0.047$

$wR(F^2) = 0.136$

$S = 1.06$

1998 reflections

155 parameters

0 restraints

Primary atom site location: structure-invariant

direct methods

Secondary atom site location: difference Fourier map

Hydrogen site location: inferred from neighbouring sites

H-atom parameters constrained

$w = 1/[\sigma^2(F_o^2) + (0.0689P)^2 + 0.4949P]$
where $P = (F_o^2 + 2F_c^2)/3$

$(\Delta/\sigma)_{\max} < 0.001$

$\Delta\rho_{\max} = 1.25 \text{ e } \text{\AA}^{-3}$

$\Delta\rho_{\min} = -0.33 \text{ e } \text{\AA}^{-3}$

Extinction correction: *SHELXL97* (Sheldrick, 2008), $F_c^* = k F_c [1 + 0.001 x F_c^2 \lambda^3 / \sin(2\theta)]^{-1/4}$

Extinction coefficient: 0.53 (3)

Special details

Geometry. All s.u.'s (except the s.u. in the dihedral angle between two l.s. planes) are estimated using the full covariance matrix. The cell s.u.'s are taken into account individually in the estimation of s.u.'s in distances, angles and torsion angles; correlations between s.u.'s in cell parameters are only used when they are defined by crystal symmetry. An approximate (isotropic) treatment of cell s.u.'s is used for estimating s.u.'s involving l.s. planes.

Refinement. Refinement of F^2 against ALL reflections. The weighted R -factor wR and goodness of fit S are based on F^2 , conventional R -factors R are based on F , with F set to zero for negative F^2 . The threshold expression of $F^2 > \sigma(F^2)$ is used only for calculating R -factors(gt) etc. and is not relevant to the choice of reflections for refinement. R -factors based on F^2 are statistically about twice as large as those based on F , and R -factors based on ALL data will be even larger.

Fractional atomic coordinates and isotropic or equivalent isotropic displacement parameters (\AA^2)

	x	y	z	$U_{\text{iso}}^*/U_{\text{eq}}$
C1	1.0517 (5)	0.7233 (5)	0.9365 (3)	0.0438 (7)
C2	1.2260 (5)	0.8083 (5)	1.0282 (3)	0.0494 (8)
H2	1.2296	0.8968	1.0958	0.059*
C3	1.3958 (5)	0.7579 (5)	1.0168 (3)	0.0467 (8)
C4	1.3945 (5)	0.6268 (5)	0.9182 (3)	0.0464 (7)
H4	1.5116	0.5954	0.9126	0.056*
C5	1.2153 (5)	0.5432 (5)	0.8280 (3)	0.0413 (7)
H5	1.2120	0.4530	0.7612	0.050*
C6	1.0387 (4)	0.5896 (4)	0.8336 (2)	0.0358 (6)
C7	0.8392 (5)	0.4900 (4)	0.7407 (2)	0.0390 (7)
C8	0.6940 (4)	0.3522 (4)	0.5350 (2)	0.0365 (6)
C9	0.5284 (5)	0.2099 (5)	0.3514 (3)	0.0505 (8)
H9	0.5166	0.1733	0.2722	0.061*
C10	0.3587 (5)	0.1551 (4)	0.3969 (3)	0.0447 (7)
Cl1	0.09389 (14)	0.01753 (14)	0.32522 (8)	0.0662 (4)
F1	1.5714 (3)	0.8434 (3)	1.10528 (18)	0.0673 (6)
F2	0.8890 (3)	0.7783 (4)	0.9458 (2)	0.0796 (8)
N1	0.8646 (4)	0.4602 (4)	0.62983 (19)	0.0376 (6)
H1	0.9916	0.5106	0.6191	0.045*
N2	0.7224 (4)	0.3246 (4)	0.4302 (2)	0.0449 (6)
O3	0.6609 (3)	0.4314 (4)	0.75914 (18)	0.0553 (6)
S1	0.43196 (11)	0.24360 (11)	0.54607 (6)	0.0421 (3)

Atomic displacement parameters (\AA^2)

	U^{11}	U^{22}	U^{33}	U^{12}	U^{13}	U^{23}
C1	0.0358 (15)	0.0438 (16)	0.0480 (17)	0.0122 (13)	0.0149 (13)	0.0095 (13)
C2	0.0483 (18)	0.0462 (17)	0.0386 (16)	0.0079 (14)	0.0089 (14)	0.0038 (13)
C3	0.0365 (15)	0.0494 (18)	0.0420 (16)	0.0035 (13)	0.0018 (12)	0.0198 (14)
C4	0.0377 (15)	0.0559 (19)	0.0504 (18)	0.0196 (14)	0.0119 (14)	0.0236 (15)
C5	0.0396 (15)	0.0447 (16)	0.0393 (15)	0.0156 (13)	0.0128 (12)	0.0123 (13)
C6	0.0329 (13)	0.0370 (14)	0.0339 (14)	0.0084 (11)	0.0107 (11)	0.0119 (11)
C7	0.0377 (15)	0.0413 (15)	0.0368 (15)	0.0135 (12)	0.0117 (12)	0.0121 (12)
C8	0.0339 (13)	0.0349 (14)	0.0372 (14)	0.0094 (11)	0.0101 (11)	0.0110 (11)
C9	0.0490 (18)	0.0455 (17)	0.0361 (16)	0.0020 (14)	0.0049 (13)	0.0052 (13)

C10	0.0414 (16)	0.0335 (15)	0.0440 (16)	0.0049 (12)	0.0006 (13)	0.0066 (12)
Cl1	0.0435 (5)	0.0572 (6)	0.0666 (6)	-0.0003 (4)	-0.0052 (4)	0.0058 (4)
F1	0.0444 (11)	0.0784 (14)	0.0528 (12)	0.0031 (10)	-0.0082 (9)	0.0204 (10)
F2	0.0495 (12)	0.0830 (16)	0.0895 (17)	0.0280 (11)	0.0141 (11)	-0.0104 (13)
N1	0.0304 (11)	0.0443 (13)	0.0336 (12)	0.0099 (10)	0.0091 (10)	0.0111 (10)
N2	0.0423 (13)	0.0449 (14)	0.0341 (13)	0.0058 (11)	0.0096 (11)	0.0062 (11)
O3	0.0349 (11)	0.0801 (17)	0.0385 (12)	0.0114 (11)	0.0119 (9)	0.0125 (11)
S1	0.0327 (4)	0.0449 (5)	0.0426 (5)	0.0098 (3)	0.0088 (3)	0.0114 (3)

Geometric parameters (\AA , $^\circ$)

C1—F2	1.343 (4)	C7—O3	1.220 (3)
C1—C2	1.366 (4)	C7—N1	1.371 (4)
C1—C6	1.393 (4)	C8—N2	1.306 (4)
C2—C3	1.374 (5)	C8—N1	1.379 (4)
C2—H2	0.9300	C8—S1	1.729 (3)
C3—F1	1.348 (3)	C9—C10	1.334 (5)
C3—C4	1.374 (5)	C9—N2	1.378 (4)
C4—C5	1.376 (4)	C9—H9	0.9300
C4—H4	0.9300	C10—Cl1	1.719 (3)
C5—C6	1.394 (4)	C10—S1	1.730 (3)
C5—H5	0.9300	N1—H1	0.8600
C6—C7	1.480 (4)		
F2—C1—C2	117.5 (3)	O3—C7—N1	120.7 (3)
F2—C1—C6	119.1 (3)	O3—C7—C6	123.3 (3)
C2—C1—C6	123.4 (3)	N1—C7—C6	116.0 (2)
C1—C2—C3	117.4 (3)	N2—C8—N1	121.3 (2)
C1—C2—H2	121.3	N2—C8—S1	115.8 (2)
C3—C2—H2	121.3	N1—C8—S1	122.9 (2)
F1—C3—C4	119.0 (3)	C10—C9—N2	115.1 (3)
F1—C3—C2	118.5 (3)	C10—C9—H9	122.5
C4—C3—C2	122.5 (3)	N2—C9—H9	122.5
C3—C4—C5	118.3 (3)	C9—C10—Cl1	127.8 (3)
C3—C4—H4	120.9	C9—C10—S1	111.6 (2)
C5—C4—H4	120.9	Cl1—C10—S1	120.56 (19)
C4—C5—C6	122.0 (3)	C7—N1—C8	122.4 (2)
C4—C5—H5	119.0	C7—N1—H1	118.8
C6—C5—H5	119.0	C8—N1—H1	118.8
C1—C6—C5	116.4 (3)	C8—N2—C9	110.0 (3)
C1—C6—C7	120.8 (3)	C8—S1—C10	87.44 (14)
C5—C6—C7	122.6 (3)		
F2—C1—C2—C3	-177.5 (3)	C1—C6—C7—N1	145.0 (3)
C6—C1—C2—C3	0.2 (5)	C5—C6—C7—N1	-40.5 (4)
C1—C2—C3—F1	178.6 (3)	N2—C9—C10—Cl1	178.5 (2)
C1—C2—C3—C4	-0.3 (5)	N2—C9—C10—S1	-0.6 (4)
F1—C3—C4—C5	-179.1 (3)	O3—C7—N1—C8	-4.4 (4)
C2—C3—C4—C5	-0.1 (5)	C6—C7—N1—C8	173.7 (2)
C3—C4—C5—C6	0.8 (4)	N2—C8—N1—C7	-179.6 (3)

F2—C1—C6—C5	178.1 (3)	S1—C8—N1—C7	−0.1 (4)
C2—C1—C6—C5	0.4 (4)	N1—C8—N2—C9	179.1 (3)
F2—C1—C6—C7	−7.1 (4)	S1—C8—N2—C9	−0.4 (3)
C2—C1—C6—C7	175.2 (3)	C10—C9—N2—C8	0.7 (4)
C4—C5—C6—C1	−0.9 (4)	N2—C8—S1—C10	0.1 (2)
C4—C5—C6—C7	−175.6 (3)	N1—C8—S1—C10	−179.4 (3)
C1—C6—C7—O3	−37.0 (4)	C9—C10—S1—C8	0.3 (3)
C5—C6—C7—O3	137.5 (3)	C11—C10—S1—C8	−178.9 (2)

Hydrogen-bond geometry (Å, °)

D—H···A	D—H	H···A	D···A	D—H···A
N1—H1···N2 ⁱ	0.86	2.15	2.988 (3)	166
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