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4-{3-[(4-Fluorobenzylidene)amino]-2-oxo-1,3-oxazolidin-5-ylmethyl}morpholine

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Key indicators

Single-crystal X-ray study
T = 291 K
Mean σ(C–C) = 0.004 Å
Disorder in main residue
R factor = 0.075
wR factor = 0.177
Data-to-parameter ratio = 12.0

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

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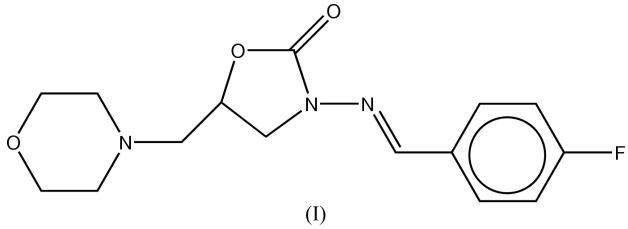
A series of derivatives of 3-amino-2-oxazolidinone have been prepared. The 5-morpholinomethyl-3-(4-chlorobenzylideneamino)-2-oxazolidinone derivative is a potential psychotropic drug. Preliminary clinical data showed that the compound exhibits antidepressive activity in humans. The molecular geometry of the title compound, $C_{15}H_{18}FN_3O_3$, is similar to 5-morpholinomethyl-3-(4-chlorobenzylideneamino)-2-oxazolidinone. Two atoms of the title compound are disordered so that two different conformations of the oxazolidinone ring were found; one is a twist and the other is an envelope conformation. The crystal structure of title compound is formed by weak intermolecular C—H···O hydrogen bonds resulting in a two-dimensional infinite hydrogen-bond network.

Comment

In the Pharmaceutical Research Institute in Warsaw, a series of derivatives of 3-amino-2-oxazolidinone have been prepared (Chilmonczyk *et al.*, 1997). It has been found that the oxazolidinone derivative 5-morpholinomethyl-3-(4-chlorobenzylideneamino)-2-oxazolidinone, (II), is a potential psychotropic drug (Chilmonczyk, 1995). Preliminary clinical data show that the compound exhibits antidepressive activity in humans (Rybakowski & Araszkiewicz, 1999). It can be supposed that other derivatives of this class can also exhibit biological activity. It is generally accepted that a specific energetically preferred conformation of a compound (so-called bioactive conformation) determines the nature of interactions with its molecular target or pharmacological receptor. Therefore, it is of basic importance to get an insight into such molecular parameters as charge distribution, the most preferred conformation or distances between specified points within a molecule (Krzywda *et al.*, 2000).



(I)

A perspective view of the title compound, (I), together with the atom-numbering scheme are shown in Fig. 1. All interatomic distances are normal. The molecular geometry of (I) is similar to that of the chloride monohydrate of (II) (Bartczak *et al.*, 2001). The weighted r.m.s. deviation for all atoms of (I) and the inverted molecule of (II) is 0.218 (2) Å. A superposition of (I) and (II) is depicted in Fig. 2. Bartczak *et al.* (2001) found

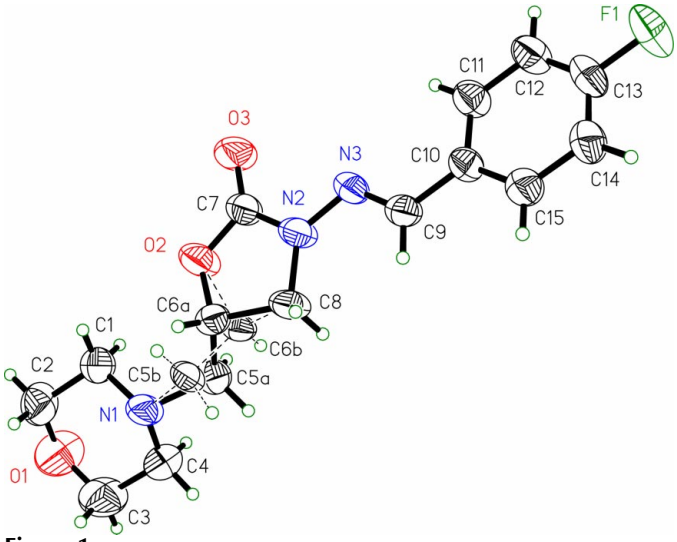


Figure 1
The molecular structure of (I). Displacement ellipsoids are drawn at the 50% probability level. The disordered part is indicated by dashed lines.

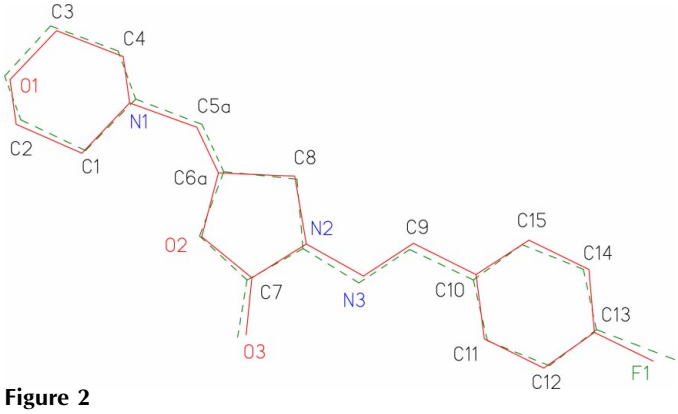


Figure 2
Superposition of inverted (II) and (I). The structure of (II) is indicated by dashed lines. The disordered atoms have been omitted for clarity.

that the primary location of molecular interaction with an acid residue within a putative receptor site is at N1. Thus, we can suppose that for (I) proton transfer also occurs from the acid residue, and (I) will be interacting *via* the same N1 atom. The oxazolidinone ring exists in a twist and an envelope conformation, as shown by the asymmetry parameters; ΔC_2 = 2.77 (5) and ΔC_s = 4.62 (5), and ΔC_2 = 13.66 (8) and ΔC_s = 2.90 (6), respectively (Duax & Norton, 1975). According to the asymmetry parameters, the morpholine ring exists in an almost ideal chair conformation. The structure of (I) is assembled by intermolecular weak C—H···O hydrogen bonds into a two-dimensional infinite hydrogen bond network (Fig. 3 and Table 2). The absence of an intermolecular hydrogen bond linking C1 and O2 in (I), which creates a fused three-membered ring system in (II), could be one of the reasons for the disorder observed in (I).

The decreased number of hydrogen bonds and their weakening in (I) does not change the molecular geometry, which suggests that inserting hydrochloric acid into the structure, even if it increases the number of hydrogen bonds, does not change its geometry and can eliminate disorder.

Experimental

The title compound was prepared according to the method of Chilmonczyk *et al.* (1997).

Crystal data

$C_{15}H_{18}FN_3O_3$
M_r = 307.32
Triclinic, $P\overline{1}$
a = 6.4808 (7) Å
b = 9.9636 (9) Å
c = 12.2753 (11) Å
α = 91.600 (9)°
β = 101.048 (10)°
γ = 106.114 (12)°
V = 744.62 (12) Å^3
Z = 2
D_x = 1.371 Mg m^{-3}
Mo $K\alpha$ radiation
Cell parameters from 1319 reflections
θ = 5–22°
μ = 0.11 mm^{-1}
T = 291 (1) K
Plate, colourless
0.30 × 0.11 × 0.08 mm

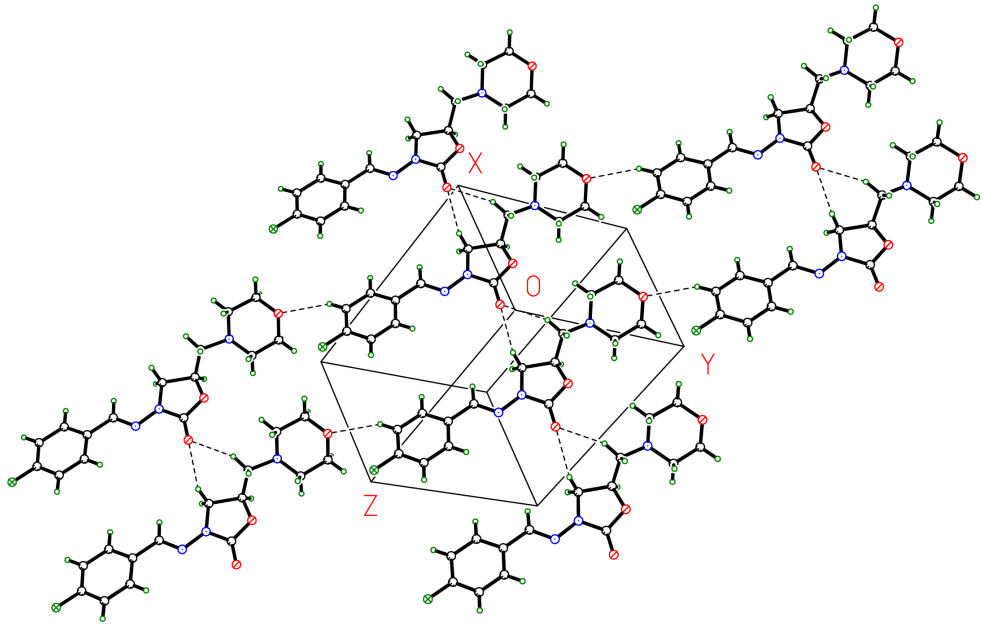


Figure 3
Packing diagram of (I) showing intermolecular hydrogen bonds creating a two-dimensional net structure. Hydrogen bonds are indicated by dashed lines.

Data collection

Kuma KM4–CCD diffractometer
ω scans
Absorption correction: numerical (*X-RED*; Stoe &Cie, 1999)
T_{min} = 0.969, T_{max} = 0.992
2638 measured reflections
2638 independent reflections
2090 reflections with $I > 2\sigma(I)$
θ_{max} = 25.1°
$h = -7 \rightarrow 7$
$k = -11 \rightarrow 11$
$l = 0 \rightarrow 14$
2 standard reflections
every 50 reflections
intensity decay: 1.2%

Refinement

Refinement on F^2
$R[F^2 > 2\sigma(F^2)]$ = 0.075
$wR(F^2)$ = 0.177
S = 1.20
2638 reflections
219 parameters
H-atom parameters constrained
$w = 1/[\sigma^2(F_o^2) + (0.0691P)^2 + 0.2292P]$ where $P = (F_o^2 + 2F_c^2)/3$
$(\Delta/\sigma)_{max} < 0.001$
$\Delta\rho_{max}$ = 0.20 e Å^{-3}
$\Delta\rho_{min}$ = −0.17 e Å^{-3}
Extinction correction: *SHELXL*97
Extinction coefficient: 0.020 (5)

Table 1
Selected torsion angles (°).

O2—C7—N2—C8	−2.9 (4)	N1—C5*A*—C6*A*—C8	156.2 (4)
C7—N2—C8—C6*A*	−6.8 (5)	C1—N1—C5*B*—C6*B*	−71.8 (7)
N2—C8—C6*A*—O2	12.9 (5)	N1—C5*B*—C6*B*—O2	85.4 (7)
C8—C6*A*—O2—C7	−15.9 (6)	N1—C5*B*—C6*B*—C8	−171.1 (4)
C6*A*—O2—C7—N2	12.6 (5)	C1—C2—O1—C3	58.1 (4)
C7—N2—C8—C6*B*	24.1 (6)	C2—O1—C3—C4	−56.6 (4)
N2—C8—C6*B*—O2	−32.0 (6)	O1—C3—C4—N1	56.1 (4)
C8—C6*B*—O2—C7	32.9 (6)	C3—C4—N1—C1	−55.9 (4)
C6*B*—O2—C7—N2	−20.1 (5)	C4—N1—C1—C2	56.7 (4)
C1—N1—C5*A*—C6*A*	70.5 (5)	N1—C1—C2—O1	−58.3 (4)
N1—C5*A*—C6*A*—O2	−95.2 (6)	N2—N3—C9—C10	178.2 (2)

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

D—H···*A*	*D*—H	H···*A*	*D*···*A*	*D*—H···*A*
C5*A*—H5*A*1···O3^{i}	0.97	2.40	3.314 (5)	157
C8—H8*B*···O3^{i}	0.97	2.47	3.143 (3)	126
C14—H14···O1^{ii}	0.93	2.54	3.375 (4)	150

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

Data collection: *CrysAlis CCD* (UNIL IC & Kuma, 2000); cell refinement: *CrysAlis RED* (UNIL IC & Kuma, 2000); data reduction: *CrysAlis RED*; program(s) used to solve structure: *SHELXS*97 (Sheldrick, 1990*a*); program(s) used to refine structure: *SHELXL*97 (Sheldrick, 1997); molecular graphics: *XP* in *SHELXTL*/*PC* (Sheldrick, 1990*b*) *ORTEP*-3 (Farrugia, 1997); software used to prepare material for publication: *SHELXL*97.

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