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4-[3-(4-Fluorobenzylideneamino)-2-oxo-1,3-oxazolidin-5-ylmethyl]morpholin-4-ium chloride monohydrate

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Key indicators

Single-crystal X-ray study
T = 291 K
Mean σ(C–C) = 0.004 Å
R factor = 0.063
wR factor = 0.201
Data-to-parameter ratio = 16.6

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

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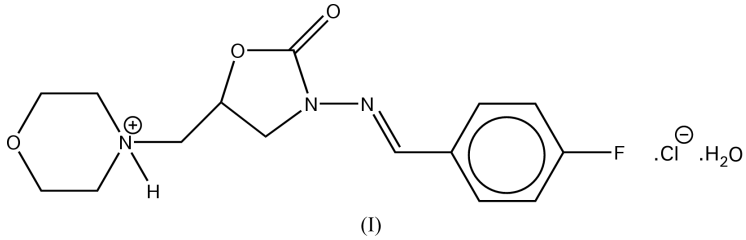
A series of derivatives of 3-amino-2-oxazolidinone have been prepared. The 5-morpholinomethyl-3-(4-chlorobenzylideneamino)-2-oxazolidinone derivative is a potential psychotropic drug. Preliminary clinical data showed that the compound exhibits antidepressive activity in humans. The molecular geometry of the title compound, $C_{15}H_{19}FN_3O_3^+\cdot Cl^-\cdot H_2O$, is similar to that of 5-morpholinomethyl-3-(4-chlorobenzylideneamino)-2-oxazolidinone. The oxazolidinone ring exists in an almost ideal half-chair conformation. The primary location of molecular interaction with an acid residue within a putative receptor site is at the morpholine N atom. The structure of the title compound is built up from strong and weak intermolecular hydrogen bonds forming 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) hereafter, 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 the specific, energetically preferred conformation of a compound (so-called bioactive conformation) determines the nature of interactions with its molecular target, the pharmacological receptor. Therefore, it is of fundamental importance to get an insight into such molecular parameters as charge distribution, most preferred conformation or distances between specified



(I)

points within a molecule (Krzywda *et al.*, 2000). Bartczak *et al.* (2001) have determined the structure of the chloride monohydrate of (II) and found that the primary location of molecular interaction with an acid residue within a putative

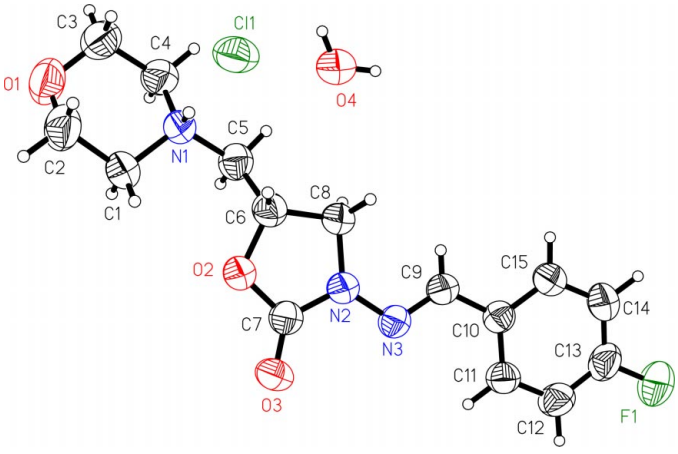


Figure 1
The molecular structure of the title compound (III). Displacement ellipsoids are drawn at the 50% probability level.

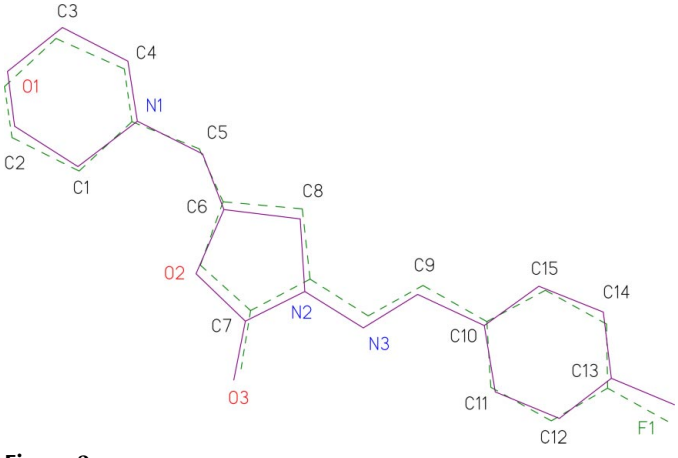


Figure 2
Superposition of two molecules, *i.e.* inverted (III) and (I). Molecule (III) is indicated by dashed lines. The disordered atoms of (III) have been omitted for clarity.

receptor site is at the morpholine N atom. The structure of 5-morpholinomethyl-3-(4-fluorobenzylideneamino)-2-oxazolidinone, (III), has also been previously determined (Kruszynski *et al.*, 2001) but the primary location of molecular interaction with an acid residue within a putative receptor site was only supposed on the basis of similar molecular geometry of (III) and the chloride monohydrate of (II).

The perspective view of the title compound, (I), together with the atom-numbering scheme, is shown in Fig. 1. All interatomic distances are normal. The molecular geometry of (I) is similar to the chloride monohydrate of (II) (Bartczak *et al.*, 2001) and (III). The weighted r.m.s. deviation for all atoms in (I) and inverted molecule (III) is 0.238 (3) Å; for (I) and (III), it is 0.229 (2) Å. The superposition of the two molecules (I) and (III) is shown in Fig. 2. The molecule of (I) shows signs of disorder, as was noticed in (III), but invoking this model did not improve the quality of structure; therefore the model was not applied.

In (I), a proton transfer takes place from hydrochloric acid to the atom N1. This confirms the presumption (Kruszynski *et al.*, 2001) that the molecule interacts with an acid residue within a putative receptor through the atom N1. The oxazolidinone ring of (I) exists in the same almost ideal half-chair conformation as in (II); this can be detected by the asymmetry parameters (Duax & Norton, 1975). Values and positions of the asymmetry parameters for the oxazolidinone ring are shown in Fig. 3. According to the asymmetry parameters the morpholine ring exists in a slightly distorted chair conformation.

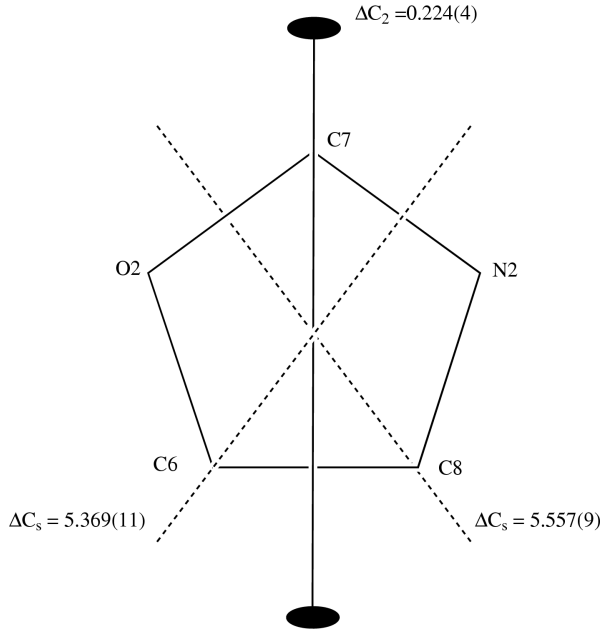


Figure 3
The values and positions of asymmetry parameters for the oxazolidinone ring of the title compound.

The structure of (I) is built up from strong and weak intermolecular hydrogen bonds to form the two-dimensional infinite hydrogen-bond network (Fig. 4 and Table 1). The absence of an intermolecular hydrogen bond linking atoms C1 and O2 in (I) as in (III), which creates a fused three-membered ring system in the chloride monohydrate of (II) (Bartczak *et al.*, 2001), might be one of the reasons for the signs of disorder observed in the molecule.

Experimental

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

Crystal data

$C_{15}H_{19}FN_3O_3^+\cdot Cl^-\cdot H_2O$
M_r = 361.80
Monoclinic, $P2_1/c$
a = 8.9570 (9) Å
b = 27.968 (3) Å
c = 7.1370 (10) Å
β = 104.820 (9)°
V = 1728.4 (4) Å^3
Z = 4
D_x = 1.390 Mg m^{-3}
Cu $K\alpha$ radiation
Cell parameters from 99 reflections
θ = 5–60°
μ = 2.28 mm^{-1}
T = 291 (1) K
Plate, colourless
0.39 × 0.35 × 0.17 mm

Data collection

Kuma KM-4 diffractometer
ω–2θ scans
Absorption correction: numerical (*X-RED*; Stoe & Cie, 1999)
T_{min} = 0.471, T_{max} = 0.698
3674 measured reflections
3674 independent reflections
2689 reflections with $I > 2\sigma(I)$
θ_{max} = 81.5°
$h = -11 \rightarrow 11$
$k = 0 \rightarrow 35$
$l = 0 \rightarrow 9$
3 standard reflections
every 100 reflections
intensity decay: 1.7%

Refinement

Refinement on F^2
$R[F^2 > 2\sigma(F^2)]$ = 0.063
$wR(F^2)$ = 0.201
S = 1.12
3674 reflections
221 parameters
H atoms treated by a mixture of independent and constrained refinement
$w = 1/[\sigma^2(F_o^2) + (0.1136P)^2 + 0.4990P]$ where $P = (F_o^2 + 2F_c^2)/3$
$(\Delta/\sigma)_{max} < 0.001$
$\Delta\rho_{max}$ = 0.87 e Å^{-3}
$\Delta\rho_{min}$ = −0.42 e Å^{-3}

Table 1
Hydrogen-bonding geometry (Å, °).

D—H···A	D—H	H···A	D···A	D—H···A
O4—H41···Cl1^{i}	0.86	2.42	3.225 (3)	157
O4—H42···O3^{ii}	0.85	2.11	2.914 (3)	159
O4—H42···N3^{ii}	0.85	2.88	3.473 (3)	128
N1—H1N···Cl1	0.84 (3)	2.23 (3)	3.051 (3)	165 (3)
C4—H4*A*···O3^{ii}	0.96	2.45	3.390 (4)	165
C5—H5*A*···O4	0.96	2.29	3.243 (4)	173
C5—H5*B*···Cl1^{iii}	0.96	2.81	3.715 (3)	158

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

All H atoms except these of the water molecule and that bonded to atom N1 were placed in calculated positions and were treated as riding on the adjacent C atom. They were refined with individual isotropic displacement parameters equal to 1.2 times the value of the equivalent displacement parameter of the parent C atom for aryl H atoms and equal to 1.5 times for other H atoms. The positional parameters and isotropic displacement parameter of the H atom bonded to atom N1 were free to refine.

Data collection: *KM*-4 *Software* (Kuma, 1993); cell refinement: *KM*-4 *Software*; data reduction: *DATAPROC* (Kuma, 1998); 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*) and *ORTEP*-3 (Farrugia, 1997); software used to prepare material for publication: *SHELXL*97.

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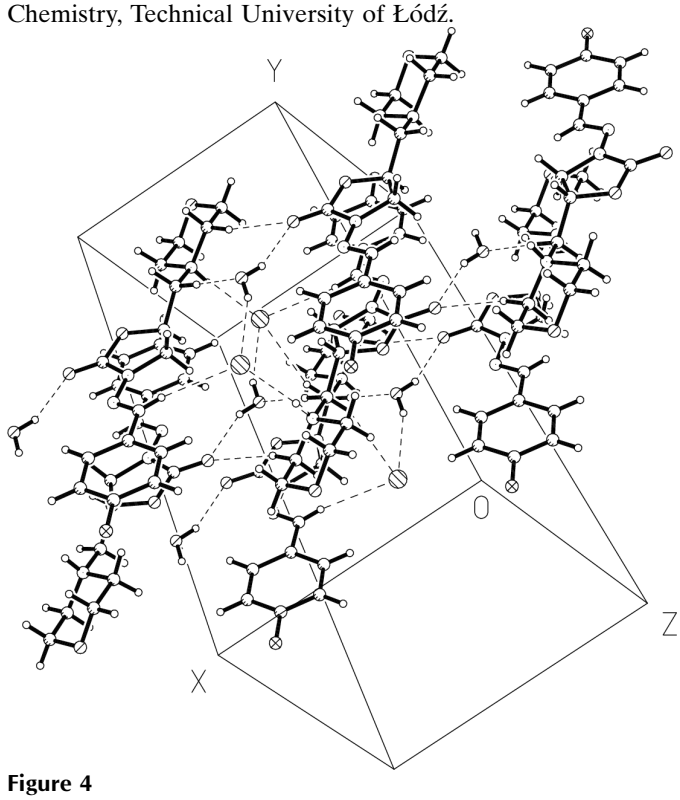

Figure 4
Part of the molecular packing of (I) showing intermolecular hydrogen bonds creating an infinite two-dimensional net structure. Hydrogen bonds are indicated by dashed lines.

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