

supporting information

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N-(4-Chlorobenzylidene)-3,4-dimethylisoxazol-5-amine

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S1. Comment

The title compound (Fig. 1) has been prepared in continuation of our work on the synthesis of Schiff bases of 3,4-dimethylisoxazol-5-amine. We have recently reported the crystal structure of N-(4-bromobenzylidene)-3,4-dimethylisoxazol-5-amine (Asiri *et al.*, 2010a), which is isostructural with the title compound.

The crystal structures of 4-chloro-2-[(*E*)-{4-[*N*-(3,4-dimethylisoxazol-5-yl)sulfamoyl]phenyl}iminio]methyl]-phenolate (Shad *et al.*, 2008), 4-bromo-2-((*E*)-{4-[3,4-dimethylisoxazol-5-yl)sulfamoyl]phenyl} iminomethyl)phenolate (Tahir *et al.*, 2008), 2-[(*E*)-(3,4-dimethylisoxazol-5-yl)iminomethyl]phenol (Fun *et al.*, 2010a), 1-[(*E*)-(3,4-dimethylisoxazol-5-yl)iminomethyl]-2-naphthol (Fun *et al.*, 2010b) and *N*-[4-(dimethylamino)benzylidene]-3,4-dimethylisoxazol-5-amine (Asiri *et al.*, 2010b) have also been published previously, which contain the 5-amino-3,4-dimethylisoxazole moiety.

In the title compound, the 4-chlorobenzylidene moiety A (C1—C7/CL1) and 5-amino-3,4-dimethylisoxazole moiety B (N1/C8—C12/N2/O1) are planar with r. m. s. deviation of 0.0042 and 0.0076 Å, respectively. The dihedral angle between A/B is 1.10 (11)°. R. m. s. deviation from the plane of all non-hydrogen atoms in the molecule is 0.0200 Å, with the largest deviation of the CL1 atom [0.0534 (11) Å]. Weak intramolecular H-bonding of C—H···O type (Table 1, Fig. 1) exists and complete an S(5) ring motif (Bernstein *et al.*, 1995). There exists no π···π interaction. The C—H···π interaction (Table 1) play an important role in stabilizing the molecules.

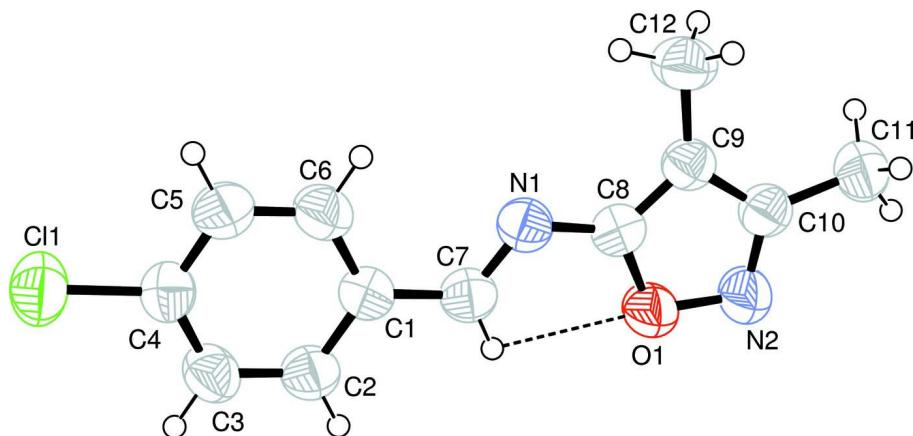
S2. Experimental

A mixture of 4-chlorobenzaldehyde (0.30 g, 2.2 mmol) and 5-amino-3,4-dimethylisoxazole (0.24 g, 2.2 mmol) in ethanol (15 ml) was refluxed for 5 h with stirring to give a light brown precipitate. This material was filtered off and washed with ethanol to give the pure Schiff base (m.p. 397 K; yield: 78.5%).

¹H-NMR (CDCl_3) δ: 9.97 (s, 1H, $\text{CH}_{\text{olefinic}}$), 7.79 (d, H3, $\text{CH}_{\text{aromatic}}$, $J = 5.4$ Hz), 7.75 (dd, H4, $\text{CH}_{\text{aromatic}}$, $J = 8.4$ Hz), 7.69 (dd, H5, $\text{CH}_{\text{aromatic}}$, $J = 8.4$ Hz), 7.61 (d, H6 $\text{CH}_{\text{aromatic}}$, $J = 4.8$ Hz), 2.25 (s, N—CH₃), 1.76 (s, -CH₃).

S3. Refinement

The H-atoms were positioned geometrically (C—H = 0.93–0.96 Å) and refined as riding with $U_{\text{iso}}(\text{H}) = xU_{\text{eq}}(\text{C})$, where x = 1.5 for methyl and x = 1.2 for other H-atoms.

**Figure 1**

View of the title compound with the atom numbering scheme. The displacement ellipsoids are drawn at the 50% probability level. H-atoms are shown as small spheres of arbitrary radii. The dotted line indicates the intramolecular hydrogen H-bond.

N-(4-Chlorobenzylidene)-3,4-dimethylisoxazol-5-amine

Crystal data

$C_{12}H_{11}ClN_2O$
 $M_r = 234.68$
Monoclinic, $P2_1/n$
Hall symbol: -P 2yn
 $a = 5.0877 (2)$ Å
 $b = 24.5197 (9)$ Å
 $c = 9.4673 (4)$ Å
 $\beta = 94.871 (2)^\circ$
 $V = 1176.77 (8)$ Å³
 $Z = 4$

$F(000) = 488$
 $D_x = 1.325$ Mg m⁻³
Mo $K\alpha$ radiation, $\lambda = 0.71073$ Å
Cell parameters from 1539 reflections
 $\theta = 2.3-25.3^\circ$
 $\mu = 0.30$ mm⁻¹
 $T = 296$ K
Needle, light brown
 $0.30 \times 0.16 \times 0.14$ mm

Data collection

Bruker KAPPA APEXII CCD
diffractometer
Radiation source: fine-focus sealed tube
Graphite monochromator
Detector resolution: 8.10 pixels mm⁻¹
 ω scans
Absorption correction: multi-scan
(SADABS; Bruker, 2005)
 $T_{\min} = 0.868$, $T_{\max} = 0.965$

9016 measured reflections
2112 independent reflections
1539 reflections with $I > 2\sigma(I)$
 $R_{\text{int}} = 0.030$
 $\theta_{\max} = 25.3^\circ$, $\theta_{\min} = 2.3^\circ$
 $h = -6 \rightarrow 6$
 $k = -29 \rightarrow 29$
 $l = -11 \rightarrow 11$

Refinement

Refinement on F^2
Least-squares matrix: full
 $R[F^2 > 2\sigma(F^2)] = 0.044$
 $wR(F^2) = 0.120$
 $S = 1.07$
2112 reflections
147 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

