

N-(4-Chlorobenzylidene)-3,4-dimethyl-isoxazol-5-amine

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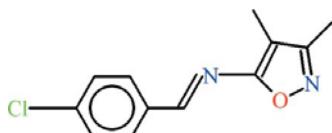
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Key indicators: single-crystal X-ray study; $T = 296\text{ K}$; mean $\sigma(\text{C}-\text{C}) = 0.003\text{ \AA}$; R factor = 0.044; wR factor = 0.120; data-to-parameter ratio = 14.4.

The molecule of the title compound, $\text{C}_{12}\text{H}_{11}\text{ClN}_2\text{O}$, has *E* configuration at the azomethine double bond and is virtually planar with a dihedral angle of $1.25(13)^\circ$ between the benzene and isoxazole rings. $\text{C}-\text{H}\cdots\pi$ interactions stabilize the crystal structure.

Related literature

For related structures, see: Asiri *et al.* (2010*a,b*); Fun *et al.* (2010*a,b*); Shad *et al.* (2008); Tahir *et al.* (2008). For graph-set notation, see: Bernstein *et al.* (1995).



Experimental

Crystal data

$\text{C}_{12}\text{H}_{11}\text{ClN}_2\text{O}$

$M_r = 234.68$

Monoclinic, $P2_1/n$

$a = 5.0877(2)\text{ \AA}$

$b = 24.5197(9)\text{ \AA}$

$c = 9.4673(4)\text{ \AA}$

$\beta = 94.871(2)^\circ$

$V = 1176.77(8)\text{ \AA}^3$

$Z = 4$

Mo $K\alpha$ radiation

$\mu = 0.30\text{ mm}^{-1}$

$T = 296\text{ K}$

$0.30 \times 0.16 \times 0.14\text{ mm}$

Data collection

Bruker Kappa APEXII CCD

diffractometer

Absorption correction: multi-scan

(*SADABS*; Bruker, 2005)

$T_{\min} = 0.868$, $T_{\max} = 0.965$

9016 measured reflections

2112 independent reflections

1539 reflections with $I > 2\sigma(I)$

$R_{\text{int}} = 0.030$

Refinement

$R[F^2 > 2\sigma(F^2)] = 0.044$

$wR(F^2) = 0.120$

$S = 1.07$

2112 reflections

147 parameters

H-atom parameters constrained

$\Delta\rho_{\max} = 0.15\text{ e \AA}^{-3}$

$\Delta\rho_{\min} = -0.14\text{ e \AA}^{-3}$

Table 1

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

$Cg1$ is the centroid of the O1/N2/C10/C9/C8 ring.

$D-\text{H}\cdots A$	$D-\text{H}$	$\text{H}\cdots A$	$D\cdots A$	$D-\text{H}\cdots A$
C11—H11C \cdots Cg1 ⁱ	0.96	2.91	3.644 (2)	134

Symmetry code: (i) $x + 1, y, z$.

Data collection: *APEX2* (Bruker, 2009); cell refinement: *SAINT* (Bruker, 2009); data reduction: *SAINT*; program(s) used to solve structure: *SHELXS97* (Sheldrick, 2008); program(s) used to refine structure: *SHELXL97* (Sheldrick, 2008); molecular graphics: *ORTEP-3 for Windows* (Farrugia, 1997) and *PLATON* (Spek, 2009); software used to prepare material for publication: *WinGX* (Farrugia, 1999) and *PLATON*.

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Supplementary data and figures for this paper are available from the IUCr electronic archives (Reference: GK2296).

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