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Key indicators

Single-crystal X-ray study T = 293 K Mean σ (C–C) = 0.003 Å R factor = 0.035 wR factor = 0.091 Data-to-parameter ratio = 13.6

For details of how these key indicators were automatically derived from the article, see http://journals.iucr.org/e. Received 19 April 2006

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5-Chloro-1-(4-chlorophenyl)-4-(2-methoxybenzoylhydrazonomethyl)-3-methyl-1*H*-pyrazole

In the title molecule, $C_{19}H_{16}C_{12}N_4O_2$, all bond lengths and angles show normal values. The two benzene rings make a dihedral angle of 12.55 (2)°. The crystal packing is stabilized by weak intermolecular $C-H\cdots N$ hydrogen bonds and van der Waals forces.

Comment

Arylpyrazoles have a widespread occurrence as substructures in a large variety of compounds with important biological activities and pharmacological properties (Nizar & James, 2002). In the course of our systematic studies aimed at the synthesis of new bioactive compounds, we have synthesized the title compound, (I) (Fig. 1).



The bond lengths and angles (Table 1) in (I) are as expected for this type of compound. The pyrazole ring is planar, the largest deviation from planarity being 0.003 (4) Å for atom C8, and forms a dihedral angle of 50.45 (4)° with the C1–C6 benzene ring. The two benzene rings, C1–C6 and C13–C18, make a dihedral angle of 12.55 (2)°.

The crystal packing (Fig. 2) is stabilized by weak intermolecular $C-H\cdots N$ hydrogen bonds (Table 2) and van der Waals forces.

Experimental

To anhydrous ethanol (15 ml), a mixture of 2-methyloxybenzoylhydrazide (3 mmol, 0.500 g) and 5-chloro-1-(4-chlorophenyl)-3methyl-1*H*-4-pyrazolaldehyde (3 mmol, 0.765 g), synthesized according to Li *et al.* (2004), was added and refluxed for 5 h. The solvent was removed under reduced pressure and the residue was recrystallized from ethanol (m.p. 458 K).



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View of (I), shown with 35% probability displacement ellipsoids.



Figure 2

The packing of the title compound. Hydrogen bonds are shown as dashed lines.

Z = 4

 $D_x = 1.417 \text{ Mg m}^{-3}$

Mo $K\alpha$ radiation

Block, colourless

 $0.28 \times 0.22 \times 0.20$ mm

 $\mu = 0.37 \text{ mm}^{-1}$

T = 293 (2) K

Crystal data

 $\begin{array}{l} C_{19}H_{16}Cl_2N_4O_2\\ M_r = 403.26\\ Monoclinic, P2_1/n\\ a = 9.3332 \ (10) \ {\rm \AA}\\ b = 16.7115 \ (19) \ {\rm \AA}\\ c = 12.3865 \ (14) \ {\rm \AA}\\ \beta = 101.839 \ (2)^\circ\\ V = 1890.8 \ (4) \ {\rm \AA}^3 \end{array}$

Data collection

Bruker APEX-II CCD areadetector diffractometer φ and ω scans Absorption correction: multi-scan (*SADABS*; Sheldrick, 1996) $T_{\rm min} = 0.885, T_{\rm max} = 0.998$ (expected range = 0.824–0.929)

Refinement

Refinement on F^2 $R[F^2 > 2\sigma(F^2)] = 0.035$ $wR(F^2) = 0.091$ S = 1.043338 reflections 246 parameters H-atom parameters constrained 10116 measured reflections 3338 independent reflections 2462 reflections with $I > 2\sigma(I)$ $R_{\text{int}} = 0.020$ $\theta_{\text{max}} = 25.0^{\circ}$

$$\begin{split} &w = 1/[\sigma^2(F_{\rm o}^{~2}) + (0.0403P)^2 \\ &+ 0.4272P] \\ &where \ P = (F_{\rm o}^{~2} + 2F_{\rm c}^{~2})/3 \\ (\Delta/\sigma)_{\rm max} = 0.001 \\ \Delta\rho_{\rm max} = 0.21 \ {\rm e} \ {\rm \AA}^{-3} \\ \Delta\rho_{\rm min} = -0.22 \ {\rm e} \ {\rm \AA}^{-3} \end{split}$$

Table 1

Selected geometric parameters (Å, °).

O1-C12	1.222 (2)	N2-C9	1.316 (3)
O2-C14	1.365 (2)	N3-C11	1.278 (2)
N1-C7	1.354 (2)	C7-C8	1.367 (3)
N1-N2	1.374 (2)	C8-C9	1.418 (3)
C7-N1-N2	109.78 (17)	C7-C8-C9	103.59 (18)
C9-N2-N1	105.69 (15)	N2-C9-C8	111.88 (18)
N1-C7-C8	109.05 (17)		

Table 2 Hydrogen-bond geometry (Å, $^{\circ}$).

Symmetry code: (i) $x + \frac{1}{2}, -y + \frac{1}{2}, z - \frac{1}{2}$.

All H atoms were placed in calculated positions, with C—H = 0.93 or 0.96 Å and N—H = 0.86 Å, and included in the final cycles of refinement using a riding model, with $U_{\rm iso}({\rm H})$ set to $1.2U_{\rm eq}({\rm C,N})$ for CH and NH groups and $1.5U_{\rm eq}({\rm C})$ for methyl groups.

Data collection: *SMART* (Bruker, 1998); cell refinement: *SAINT* (Bruker, 1999); data reduction: *SAINT*; program(s) used to solve structure: *SHELXS97* (Sheldrick, 1997); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *SHELXTL* (Bruker, 1999); software used to prepare material for publication: *SHELXTL*.

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