

**(*E*)-*N*<sup>2</sup>-{4-[(*E*)-2-(4-Chlorobenzoyl)-ethenyl]-3-methyl-1-phenyl-1*H*-pyrazol-5-yl]-*N*<sup>1</sup>,*N*<sup>1</sup>-dimethylformamidine: polarized molecules within sheets of  $\pi$ -stacked hydrogen-bonded chains**

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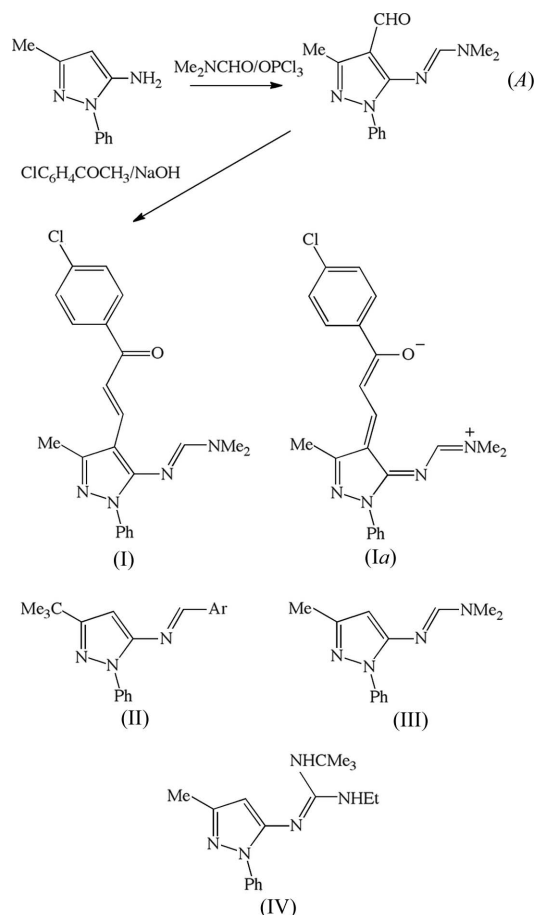
The molecules of the title compound, C<sub>22</sub>H<sub>21</sub>ClN<sub>4</sub>O, are conformationally chiral, and in the space group *P*2<sub>1</sub>2<sub>1</sub>2<sub>1</sub> each crystal contains only one conformational enantiomer. The intramolecular dimensions provide evidence for polarization of the electronic structure. Molecules are linked by a single C—H... $\pi$ (arene) hydrogen bond into chains, which are themselves weakly linked into sheets by an aromatic  $\pi$ – $\pi$  stacking interaction.

## Comment

We are exploring the use of 5-amino-4-formylpyrazoles as building blocks in the synthesis of new heterocyclic compounds containing fused pyrazole ring systems, as such compounds have a wide range of potential applications (Elguero, 1984, 1996). In connection with this synthetic study, we report here the structure of the title compound, (I) (Fig. 1), which forms an interesting structure consisting of  $\pi$ -stacked hydrogen-bonded chains.

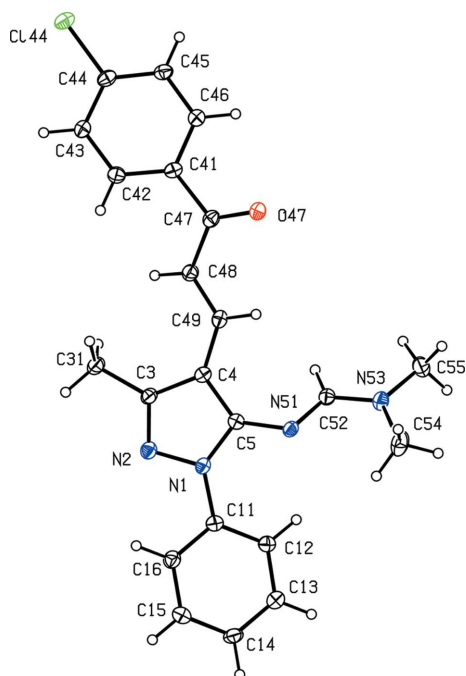
Compound (I) was prepared by base-catalysed condensation of 4'-chloroacetophenone with the intermediate (*E*)-*N*<sup>2</sup>-(4-formyl-3-methyl-1-phenyl-1*H*-pyrazol-5-yl)-*N*<sup>1</sup>,*N*<sup>1</sup>-dimethylformamidine, denoted (A) in the scheme, which itself had been prepared in a single step by reaction of the simple precursor 5-amino-3-methyl-1-phenylpyrazole with an excess of *N,N*-dimethylformamide (DMF) and OPCl<sub>3</sub>, in a process which leads not only to formylation of the pyrazole ring at the hitherto-vacant 4-position, but also to conversion of the

5-amino group to a formamidine function by condensation with DMF.



The molecular conformation of (I) is conveniently considered in terms of the orientations of the various peripheral substituents relative to the central pyrazole ring, as defined by the relevant torsion angles (Table 1). Thus, while the chain between atoms C4 and C41 (Fig. 1) is nearly coplanar with the pyrazole ring, the two benzene rings are both markedly twisted out of this plane: the dihedral angles between the pyrazole ring and the C11–C16 and C41–C46 aryl rings are 25.1 (2)° and 15.7 (2)°, respectively. Similarly, the dimethylaminomethine unit is significantly twisted out of the plane of the pyrazole ring, as shown by the value of the N1–C5–N51–C52 torsion angle (Table 1). Consequently, the molecule of (I) has no internal symmetry and hence it is chiral. In the space group *P*2<sub>1</sub>2<sub>1</sub>2<sub>1</sub>, therefore, each crystal contains only a single conformational enantiomer. However, this has no chemical significance and it may be expected that, in solution, for example, all accessible molecular conformations are populated in a dynamic equilibrium.

The intramolecular dimensions (Table 1) provide evidence for polarization of the electronic structure. The C47–O47 and C48–C49 bonds are both long for their types [mean values (Allen *et al.*, 1987) = 1.222 and 1.340 Å, respectively; upper quartile values = 1.229 and 1.348 Å, respectively], while the C47–C48 and C4–C49 bonds are both short for their types (mean values = 1.464 and 1.455 Å respectively; lower quartile

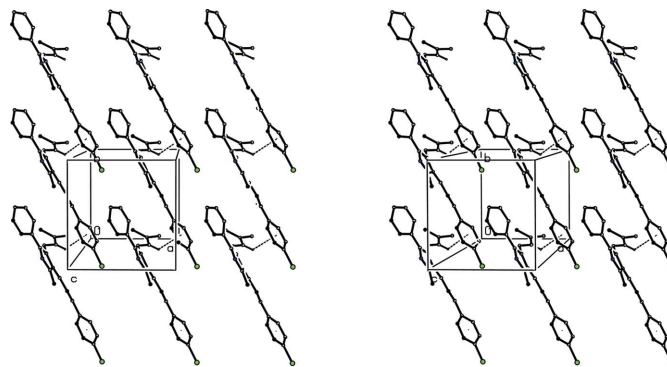


**Figure 1**

The molecular structure of (I), showing the atom-labelling scheme. Displacement ellipsoids are drawn at the 30% probability level and H atoms are shown as small spheres of arbitrary radii.

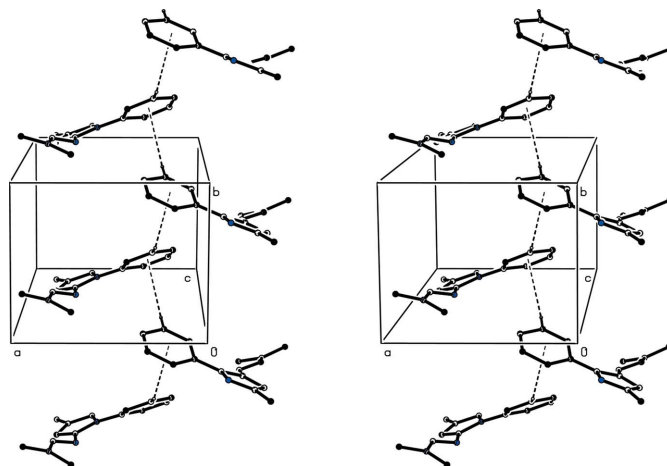
values = 1.453 and 1.447 Å, respectively). In addition, the C52–N53 bond is significantly shorter than the N1–C5 bond. The C5–N51 and N51–C52 distances can be compared with the context-specific examples found in the series of simple Schiff bases, (II) (see scheme), where the substituent Ar represents a range of substituted phenyl, or exceptionally pyridyl, groups (Castillo *et al.*, 2010). For the C5–N51 bond, 15 independent values in the series of compounds (II) range from 1.381 (4) to 1.401 (3) Å, all longer than the comparable bond in (I), while for the N51–C52 bond, the values in the series (II) span the range 1.268 (3)–1.294 (3) Å, all shorter than the corresponding bond in (I). Similarly, in compound (III) [Cambridge Structural Database (CSD; Allen, 2002) refcode CIZQEH; Moreno-Fuquen *et al.*, 1999], the distances corresponding to the C5–N51 and N51–C52 bonds in (I) are 1.383 (2) and 1.289 (2) Å, respectively. The conclusion to be drawn from all of these observations is that the polarized form (Ia) is a significant contributor to the overall electronic structure, in addition to the conventional form (I). Electronic polarization of this type is not possible in series (II), nor in compound (III).

Despite the polarization of the electronic structure in (I), there are no hydrogen bonds involving the O atom as the acceptor. Instead, molecules related by translation are linked by a single C–H... $\pi$ (arene) hydrogen bond (Table 2) into simple chains running parallel to the [010] direction (Fig. 2). These chains are weakly linked into sheets by an aromatic  $\pi$ – $\pi$  stacking interaction. The unsubstituted C11–C16 phenyl ring in the molecule at (x, y, z) makes a dihedral angle of 13.4 (2)° with the substituted C41–C46 ring in the molecule at (–1 + x, 1 + y, z). The ring centroid separation is 3.867 (2) Å and the



**Figure 2**

A stereoview of part of the crystal structure of (I), showing the formation of a sheet parallel to (001) built from the  $\pi$ -stacking of hydrogen-bonded chains parallel to [010]. For the sake of clarity, H atoms not involved in the motif shown have been omitted.

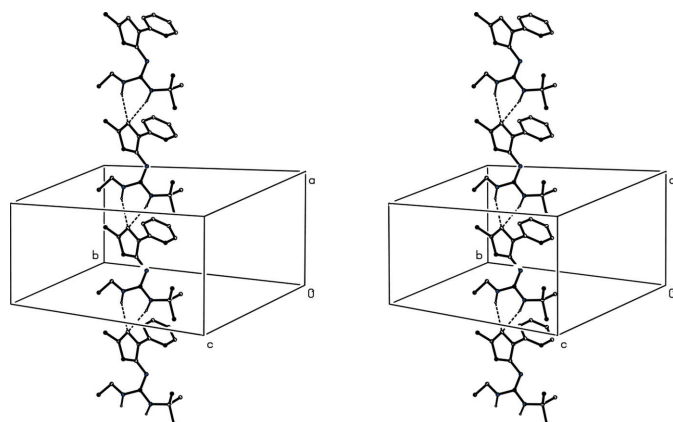


**Figure 3**

A stereoview of part of the crystal structure of (III) (CSD refcode CIZQEH; Moreno-Fuquen *et al.*, 1999), showing the formation of a hydrogen-bonded chain running parallel to the [010] direction. The deposited atomic coordinates have been used and, for the sake of clarity, H atoms not involved in the motif shown have been omitted.

interplanar spacing is *ca* 3.8 Å. The effect of this interaction is to link the hydrogen-bonded chain, albeit weakly, into a sheet parallel to (001) (Fig. 2). Four sheets of this type pass through each unit cell, in the domains  $0 < z < \frac{1}{4}$ ,  $\frac{1}{4} < z < \frac{1}{2}$ ,  $\frac{1}{2} < z < \frac{3}{4}$  and  $\frac{3}{4} < z < 1.0$ , respectively, but there are no direction-specific interactions between adjacent sheets. The only other possible intermolecular contact is a C–H...O contact involving one of the C–H bonds of the methyl group based on atom C55. This bond is likely to be of low acidity and, in addition, the methyl group itself is likely to be undergoing extremely fast rotation about the N53–C55 bond (Riddell & Rogerson, 1996, 1997); hence this contact cannot be regarded as structurally significant.

It is of interest briefly to compare the supramolecular aggregation in (I) with that in the closely related amino-substituted analogues (III) (CSD refcode CIZQEH) and (IV) (CSD refcode YICWUD; Zhang *et al.*, 2007). Neither of the original reports mentioned any intermolecular interactions,

**Figure 4**

A stereoview of part of the crystal structure of (IV) (CSD refcode YICWUD; Zhang *et al.*, 2007), showing the formation of a hydrogen-bonded chain of rings running parallel to the [100] direction. The deposited atomic coordinates have been used and, for the sake of clarity, H atoms not involved in the motif shown have been omitted.

but analysis using the deposited atomic coordinates shows that in (III), molecules related by a  $2_1$  screw axis in the space group  $P2_1/n$  are linked into chains along [010] by a single C—H... $\pi$ (arene) hydrogen bond (Fig. 3), while in compound (IV), molecules related by translation are linked by two independent N—H...N hydrogen bonds into a  $C(7)C(7)$ — $[R_2^1(6)]$  (Bernstein *et al.*, 1995) chain of rings along [100] (Fig. 4).

## Experimental

To a solution containing 1 mmol each of 4'-chloroacetophenone and (*E*)-*N*<sup>2</sup>-(4-formyl-3-methyl-1-phenyl-1*H*-pyrazol-5-yl)-*N*<sup>1</sup>,*N*<sup>1</sup>-dimethylformamide, prepared from 5-amino-3-methyl-1-phenylpyrazole under Vilmaier conditions (Häufel & Breitmaier, 1974), in absolute ethanol (10 ml), a catalytic quantity of sodium hydroxide (0.5 ml of a 30% *w/v* aqueous solution) was added, and the mixture was then stirred at room temperature for 2 h. The resulting solid product was collected by filtration and recrystallized by slow evaporation, at ambient temperature and in air, from a solution in ethanol, yielding crystals of (I) suitable for single-crystal X-ray diffraction. MS (70 eV) *m/z* (%): 392 (*M*<sup>+</sup>, 100), 321 (11), 253 (44), 139 (43), 44 (16); HRMS found: 392.1404;  $C_{22}H_{21}^{35}ClN_4O$  requires: 392.1404.

### Crystal data

$C_{22}H_{21}ClN_4O$	$V = 1970.99$ (11) Å <sup>3</sup>
$M_r = 392.88$	$Z = 4$
Orthorhombic, $P2_12_12_1$	Mo $K\alpha$ radiation
$a = 8.2228$ (3) Å	$\mu = 0.21$ mm <sup>−1</sup>
$b = 8.3506$ (2) Å	$T = 120$ K
$c = 28.7043$ (10) Å	$0.12 \times 0.06 \times 0.06$ mm

### Data collection

Bruker–Nonius KappaCCD area-detector diffractometer	13638 measured reflections
Absorption correction: multi-scan (SADABS; Sheldrick, 2003)	3871 independent reflections
$T_{\min} = 0.978$ , $T_{\max} = 0.987$	2849 reflections with $I > 2\sigma(I)$
	$R_{\text{int}} = 0.082$

**Table 1**

Selected geometric parameters (Å, °).

N1—N2	1.392 (3)	C47—O47	1.236 (4)
N2—C3	1.318 (4)	C47—C48	1.454 (4)
C3—C4	1.434 (4)	C48—C49	1.350 (5)
C4—C5	1.404 (4)	C5—N51	1.379 (4)
N1—C5	1.362 (4)	N51—C52	1.300 (4)
C4—C49	1.427 (4)	C52—N53	1.341 (4)
N2—N1—C11—C12	154.8 (3)	N1—C5—N51—C52	139.7 (3)
C3—C4—C49—C48	−11.8 (6)	C5—N51—C52—N53	179.7 (3)
C4—C49—C48—C47	175.5 (3)	N51—C52—N53—C54	1.9 (5)
C49—C48—C47—C41	−176.9 (3)	N51—C52—N53—C55	177.6 (3)
C48—C47—C41—C42	27.4 (5)		

**Table 2**

Hydrogen-bond geometry (Å, °).

Cg1 is the centroid of the C41–C46 ring.

$D-H\cdots A$	$D-H$	$H\cdots A$	$D\cdots A$	$D-H\cdots A$
C52—H52...Cg1 <sup>i</sup>	0.95	2.83	3.432 (4)	122

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

### Refinement

$$R[F^2 > 2\sigma(F^2)] = 0.056$$

$$wR(F^2) = 0.134$$

$$S = 1.05$$

3871 reflections

256 parameters

H-atom parameters constrained

$$\Delta\rho_{\text{max}} = 0.25 \text{ e Å}^{-3}$$

$$\Delta\rho_{\text{min}} = -0.28 \text{ e Å}^{-3}$$

Absolute structure: Flack (1983), with 1620 Bijvoet pairs

Flack parameter: −0.03 (9)

All H atoms were located in difference maps and then treated as riding atoms in geometrically idealized positions, with C—H = 0.95 (aromatic and alkenyl) or 0.98 Å (methyl), and with  $U_{\text{iso}}(\text{H}) = kU_{\text{eq}}(\text{C})$ , where  $k = 1.5$  for the methyl groups, which were permitted to rotate but not to tilt, and 1.2 for all other H atoms. The correct enantiomorph in the crystal selected for data collection was established by means of the Flack  $x$  parameter (Flack, 1983),  $x = -0.03$  (9), and the Hooft  $y$  parameter (Hooft *et al.*, 2008),  $y = 0.02$  (7), calculated from 1620 Bijvoet pairs, equivalent to 99.1% coverage.

Data collection: *COLLECT* (Nonius, 1999); cell refinement: *DIRAX/LSQ* (Duisenberg *et al.*, 2000); data reduction: *EVALCCD* (Duisenberg *et al.*, 2003); program(s) used to solve structure: *SIR2004* (Burla *et al.*, 2005); program(s) used to refine structure: *SHELXL97* (Sheldrick, 2008); molecular graphics: *PLATON* (Spek, 2009); software used to prepare material for publication: *SHELXL97* and *PLATON*.

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Supplementary data for this paper are available from the IUCr electronic archives (Reference: GG3232). Services for accessing these data are described at the back of the journal.

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