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(*E*)-*N*-{[6-Chloro-4-(4-chlorophenyl)-3-methyl-1-phenyl-1*H*-pyrazolo[3,4-*b*]-pyridin-5-yl]methylene}benzene-1,2-diamine: a three-dimensional framework structure built from only two hydrogen bonds

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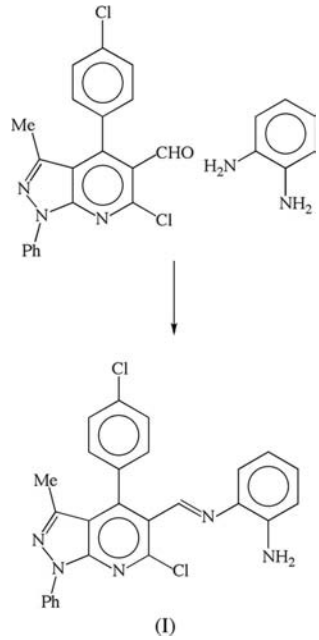
The molecules of the title compound, $C_{26}H_{19}Cl_2N_5$, are conformationally chiral, with none of the aryl groups coplanar with the pyrazolo[3,4-*b*]pyridine core of the molecule. A single unique N—H···N hydrogen bond links the molecules into two symmetry-related sets of *C*(11) chains running parallel to the [011] and [01$\bar{1}$] directions, respectively, and these two sets of chains are linked into a continuous three-dimensional framework structure by a single unique C—H···N hydrogen bond which forms a chain parallel to the [100] direction.

Comment

Simple nitrogen heterocycles, such as pyridines, pyrazoles, pyrimidines or pyrroles, are of interest in chemical biology or medicinal chemistry, and also for the preparation of new fused pyrazolo heterocyclic derivatives. We are currently exploring the use of 6-chloro-4-(4-chlorophenyl)-3-methyl-1-phenyl-1*H*-pyrazolo[3,4-*b*]pyridine-5-carbaldehyde, itself readily prepared under Vilsmeier–Haack formylation conditions from 4-(4-chlorophenyl)-3-methyl-1-phenyl-4,5-dihydro-1*H*-pyrazolo[3,4-*b*]pyridin-6(7*H*)-one, as a building block for the synthesis of polyannellated heterocyclic systems (Verdecía *et al.*, 1996; Girreser *et al.*, 2004; Quiroga *et al.*, 1998, 2005). It was hoped that the reaction of this carbaldehyde with benzene-1,2-diamine would lead to a cyclization, forming a dihydropyrazolo[4′,3′:5,6]pyrido[2,3-*b*][1,5]benzodiazepine system, but instead this reaction led to the formation and isolation of the intermediate title compound, (I) (Fig. 1). In the formation of (I), condensation has occurred between the aldehyde function and one of the amino groups in the benzenediamine reactant (see reaction scheme below), but the cyclization step, involving nucleophilic displacement of the 6-chloro atom on the pyridine ring by the second amino group, has not occurred. We report here the structure of (I), which proves to be of interest as the molecules are linked into a single three-dimensional framework structure by the action of just two symmetry-independent hydrogen bonds.



(I)

The molecular conformation of (I) can be readily defined in terms of five torsion angles (Fig. 1 and Table 1), which show that while the Schiff base-type spacer unit comprising atoms C57, N57 and C51 is almost coplanar with the pyrazolopyridine unit, the three pendent aryl rings are all markedly rotated

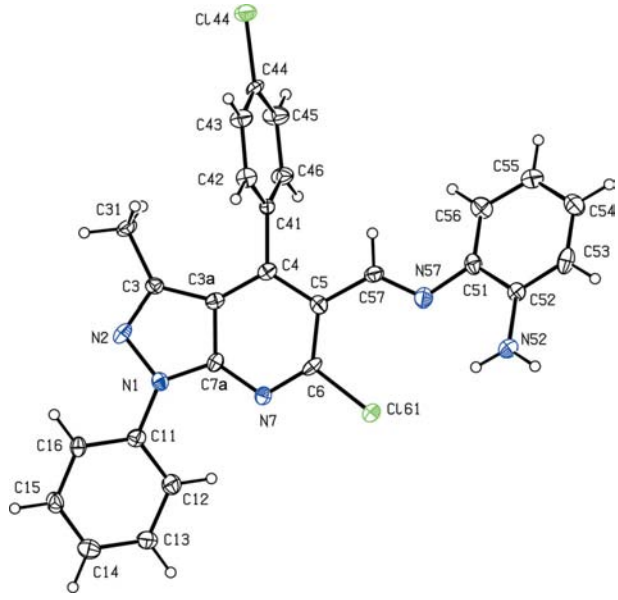


Figure 1
The molecular structure of (I), showing the atom-labelling scheme. Displacement ellipsoids are drawn at the 30% probability level and H atoms are shown as small spheres of arbitrary radii.

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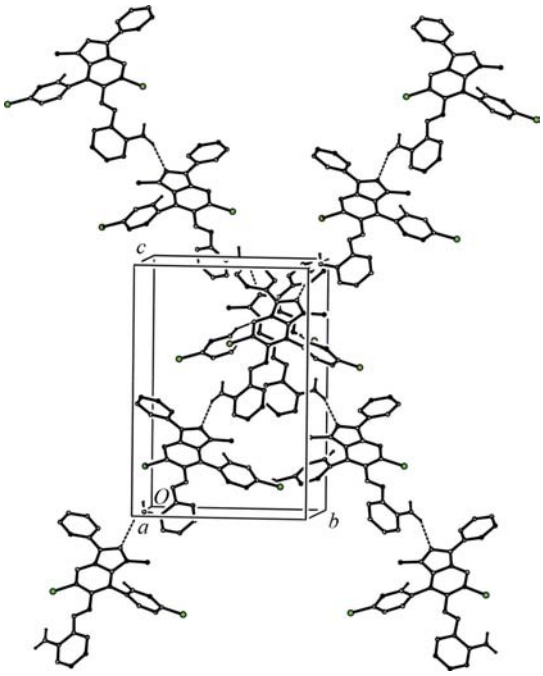


Figure 2
Part of the crystal structure of (I), showing symmetry-related hydrogen-bonded $C(11)$ chains running parallel to the [011] and [01$\bar{1}$] directions, and linked by the C—H···N hydrogen bond. For the sake of clarity, H atoms bonded to C atoms not involved in the motifs shown have been omitted.

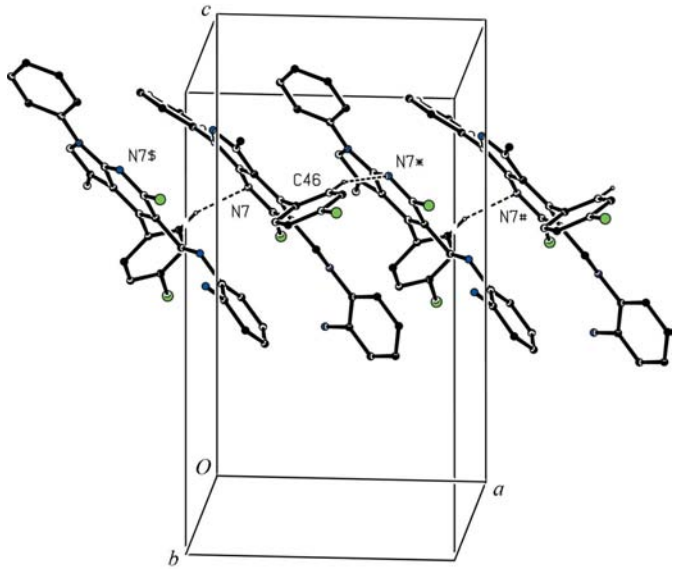


Figure 3
Part of the crystal structure of (I), showing a hydrogen-bonded $C(7)$ chain running parallel to the [100] direction, in which alternate molecules lie in $C(11)$ chains along [011] and [01$\bar{1}$]. Hydrogen bonds are shown as dashed lines. For the sake of clarity, H atoms not involved in the motif shown have been omitted. Atoms marked with an asterisk (*), a hash (#) or a dollar sign ($) are at the symmetry positions $(\frac{1}{2}+x, \frac{3}{2}-y, z)$, $(1+x, y, z)$ and $(-\frac{1}{2}+x, \frac{3}{2}-y, z)$, respectively.

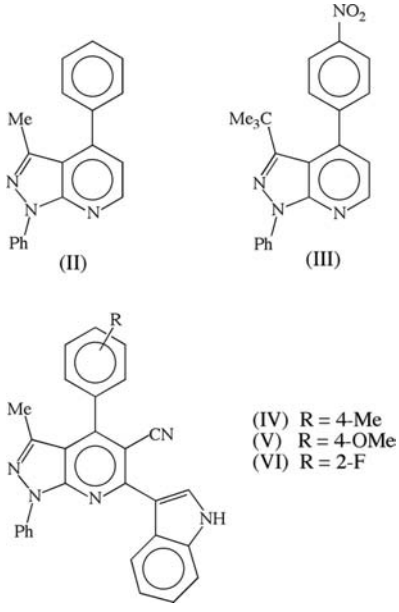
out of this plane. The dihedral angles made between the plane of the pyrazolopyridine unit and the planes of the C11–C16, C41–C46 and C51–C56 aryl rings are 21.4 (2), 75.3 (2) and 29.9 (2)°, respectively. It is reasonable to associate the much larger dihedral angle involving ring C41–C46 with the greater steric congestion in the vicinity of this ring. In particular, a small dihedral angle between this ring and the heterocyclic unit is almost certainly prevented by the presence of both the methyl group containing atom C31 and the C—H bond at atom C57 (Fig. 1). Consistent with this idea, the smallest dihedral angle is found for ring C11–C16, where the intramolecular steric constraints are the least for any of the rings. This conformation means that the molecule of (I) exhibits no internal symmetry and so is conformationally chiral. However, the space group accommodates equal numbers of the two conformational enantiomers, and the choice of the selected asymmetric unit has no chemical significance. The bond distances (Table 1) in the heterocyclic fragment of the molecule, which show the same pattern as found in similar pyrazolo[3,4-*b*]pyridines (Low *et al.*, 2002, 2007; Abonia *et al.*, 2005; Quiroga *et al.*, 2009), having due regard to the differences between the peripheral substituents, are consistent with the occurrence of aromatic-type electronic delocalization within the pyridine ring and strong bond fixation in the pyrazole ring. Likewise, there is strong bond fixation, as expected, in the spacer unit between the pyridine and the aminophenyl rings.

The molecules of (I) are linked into a continuous three-dimensional framework structure by just two symmetry-independent hydrogen bonds, one each of the N—H···N and C—H···N types (Table 2), and the formation of the framework structure is readily analysed in terms of two simple one-dimensional substructures, each of which depends on only one type of hydrogen bond. The N—H···N hydrogen bond links molecules related by an *n*-glide plane. Amino atom N52 in the molecule at (x, y, z) acts as hydrogen-bond donor to pyrazole atom N2 in the molecule at $(\frac{1}{2}-x, \frac{1}{2}+y, -\frac{1}{2}+z)$, so linking molecules related by the *n*-glide plane at $x=\frac{1}{4}$ into a $C(11)$ [see Bernstein *et al.* (1995) for graph-set notation] chain running parallel to the [01$\bar{1}$] direction (Fig. 2). A similar chain is formed by molecules related by the *n*-glide plane at $x=\frac{3}{4}$, and this second chain is related to the first by the action of the 2_1 screw axes parallel to [001]. Hence, the chain based on the *n*-glide plane at $x=\frac{3}{4}$ runs parallel to [011] (Fig. 2), so that the structure consists of alternating layers of $C(11)$ chains along [011] and [01$\bar{1}$], stacked in the [100] direction. Within each layer, the chains are related to one another by unit translations along [010] or [001].

The second substructure is simpler and consists of just a simple chain. Aryl atom C46 in the molecule at (x, y, z) acts as hydrogen-bond donor to pyridine atom N7 in the molecule at $(\frac{1}{2}+x, \frac{3}{2}-y, z)$, so forming a $C(7)$ chain running parallel to the [100] direction and containing molecules related by the *a*-glide plane at $y=\frac{3}{4}$ (Fig. 3). Within this chain, adjacent molecules, for example those at (x, y, z) and $(\frac{1}{2}+x, \frac{3}{2}-y, z)$, are components of $C(11)$ chains along [01$\bar{1}$] and [011], respectively. Hence, the overall action of all the chains parallel to [100] is to link each chain along [01$\bar{1}$] to each chain along [011], so linking all of the molecules into a single three-dimensional framework. There are neither C—H···π(arene)

nor C—H···π(pyridine) hydrogen bonds nor any π–π stacking interactions in the structure of (I).

It is of interest briefly to compare the crystal structure of (I) reported here with those of some close analogues, compounds (II)–(VI) (see scheme below). The crystallization characteristics of (II)-(VI) differ markedly from those of (I). Firstly, (IV) and (V) both crystallize as stoichiometric monosolvates with dimethylformamide (Low *et al.*, 2007). Secondly, unlike (I), which crystallizes in the Sohnke space group $Pna2_1$, compounds (II)–(VI) all crystallize in the centrosymmetric space groups $P\overline{1}$ [for (II) (Low *et al.*, 2002), (III) (Abonia *et al.*, 2005) and (IV) (Low *et al.*, 2007)] or $C2/c$ [for (V) (Low *et al.*, 2007) and (VI) (Quiroga *et al.*, 2009)]. In addition, the crystal structures of (II)–(VI) all contain C—H···π(arene) hydrogen bonds, whereas such interactions are absent from the structure of (I).



In the structure of (II), there are two independent C—H···π(arene) hydrogen bonds, each using a different arene ring as acceptor, and their action is to link the molecules into chains of centrosymmetric rings. These chains are linked into sheets by a π–π stacking interaction between pairs of pyridine rings, giving a two-dimensional supramolecular structure. In (III), the supramolecular structure is one-dimensional and consists of two types of centrosymmetric ring built alternately from pairs of C—H···π(arene) hydrogen bonds and pairs of C—H···O hydrogen bonds. Symmetry-related pairs of C—H···π(arene) hydrogen bonds in the structure of (IV) link pairs of molecules into centrosymmetric dimers, *i.e.* a finite zero-dimensional hydrogen-bonded structure, while in (V), C—H···π(arene) and C—H···N hydrogen bonds once again generate a chain in which two types of centrosymmetric ring alternate. Finally, in the structure of (VI), the molecules are linked into rather complex double chains by a combination of N—H···N, C—H···N and C—H···π(arene) hydrogen bonds. Thus, overall, the supramolecular structures generated by direction-specific interactions are zero-dimensional in (IV), one-dimensional in (III), (V) and (VI), two-dimensional in (II) and three-dimensional in (I). However, in terms just of hydrogen bonds, as opposed to π–π stacking interactions, the hydrogen-bonded structures in (II), (III), (V) and (VI) are one-dimensional. The sharp contrast between this behaviour and that of (I) can be traced directly to the space group for (I), *viz.* $Pna2_1$, where the combination of two hydrogen bonds connecting molecules related by a glide plane and a screw axis, respectively, generates a three-dimensional array. But this simply raises the question of why (I) crystallizes in the relatively uncommon space group $Pna2_1$, representing only *ca* 1.4% of the entries in the Cambridge Strcutural Database (release 5.31, November 2009; Allen, 2002), rather than $P\overline{1}$ (23.0% of entries) or $C2/c$ (8.0% of entries).

Experimental

Glacial acetic acid (3 drops) was added to a solution of 6-chloro-4-(4-chlorophenyl)-3-methyl-1-phenyl-1*H*-pyrazolo[3,4-*b*]pyridine-5-carbaldehyde (0.64 mmol) and benzene-1,2-diamine (0.64 mmol) in ethanol (5 ml) and the mixture was heated under reflux for 1 h. The mixture was then cooled to ambient temperature and the resulting precipitate was collected by filtration, washed with cold ethanol and recrystallized from ethanol to afford yellow crystals of (I) suitable for single-crystal X-ray diffraction (yield 80%, m.p. 474–476 K). MS (EI, 70 eV) *m*/*z* (%): 475/473/471 (M^+, 2/5/10), 359 (5), 119 (100), 77 (11). Analysis found: C 66.3, H 4.0, N 14.6%; $C_{26}H_{19}Cl_2N_5$ requires: C 66.1, H 4.1, N 14.8%.

Crystal data

$C_{26}H_{19}Cl_2N_5$
M_r = 472.36
Orthorhombic, $Pna2_1$
a = 10.013 (2) Å
b = 12.3487 (12) Å
c = 17.666 (4) Å
V = 2184.4 (7) Å^3
Z = 4
Mo $K\alpha$ radiation
μ = 0.32 mm^{-1}
T = 120 K
0.37 × 0.06 × 0.04 mm

Data collection

Bruker–Nonius KappaCCD area-detector diffractometer
Absorption correction: multi-scan (*SADABS*; Sheldrick, 2003)
T_{min} = 0.899, T_{max} = 0.987
15595 measured reflections
3777 independent reflections
2630 reflections with $I > 2\sigma(I)$
R_{int} = 0.104

Refinement

$R[F^2 > 2\sigma(F^2)]$ = 0.057
$wR(F^2)$ = 0.127
S = 1.10
3777 reflections
306 parameters
1 restraint
H atoms treated by a mixture of independent and constrained refinement
$\Delta\rho_{max}$ = 0.39 e Å^{-3}
$\Delta\rho_{min}$ = −0.34 e Å^{-3}
Absolute structure: Flack (1983), with 1792 pairs
Flack parameter: 0.12 (10)

All H atoms were located in difference maps. H atoms bonded to C atoms were 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_{iso}(H) = kU_{eq}(C), where k = 1.5 for the methyl group, which was permitted to rotate but not to tilt, and 1.2 for all other H atoms bonded to C atoms. The coordinates of the H atoms bonded to N52 were refined with U_{iso}(H) = 1.2U_{eq}(N), giving N—H distances of 1.00 (6) and 1.02 (6) Å. The correct orientation of the structure with respect to the polar-axis direction was established by

Table 1
Selected geometric parameters (Å, °).

N1—N2	1.397 (6)	C5—C6	1.414 (7)
N2—C3	1.304 (7)	C6—N7	1.308 (7)
C3—C3*A*	1.424 (7)	N7—C7*A*	1.336 (6)
C3*A*—C4	1.373 (7)	C7*A*—N1	1.341 (6)
C4—C5	1.402 (7)	C3*A*—C7*A*	1.397 (7)
N2—N1—C11—C12	158.1 (5)	C5—C57—N57—C51	−176.5 (5)
C3*A*—C4—C41—C42	71.8 (7)	C57—N57—C51—C52	143.2 (5)
C4—C5—C57—N57	−175.1 (5)		

Table 2
Hydrogen-bond geometry (Å, °).

D—H···*A*	*D*—H	H···*A*	*D*···*A*	*D*—H···*A*
N52—H52*A*···N2^{i}	1.02 (6)	2.07 (6)	3.082 (7)	170 (5)
C46—H46···N7^{ii}	0.95	2.46	3.367 (7)	160

Symmetry codes: (i) $-x+\frac{1}{2}, y+\frac{1}{2}, z-\frac{1}{2}$; (ii) $x+\frac{1}{2}, -y+\frac{3}{2}, z$.

means of the Flack *x* parameter (Flack, 1983), *x* = 0.12 (10), and the Hooft *y* parameter (Hooft *et al.*, 2008), *y* = 0.15 (8), both calculated with 1792 Bijvoet pairs (96.4% 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* (Sheldrick, 2008) and *PLATON* (Spek, 2009).

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Supplementary data for this paper are available from the IUCr electronic archives (Reference: SK3364). Services for accessing these data are described at the back of the journal.

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