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5-Chloro-1-phenyl-1H-pyrazol-4-amine

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5-Chloro-1-phenyl-1H-pyrazol-4-amine

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Key indicators: single-crystal X-ray study; T = 295 K; mean |C| - C) = 0.003 Å; R factor = 0.040; wR factor = 0.091; data-to-parameter ratio = 14.2.

In the crystal structure of the title compound, C9H8ClN3, amino–pyrazole N—H···N hydrogen bonds connect the molecules along the [010] direction; the chains interact with each other only by van der Waals-type interactions. The pyrazole and phenyl rings are inclined at a dihedral angle of 45.65 (6)°.

Related literature

For the synthesis, see: Tallec et al. (2000). For other 4-aminopyrazoles, see: Infantes et al. (1998, 1999); Schmidt et al. (2001). For a description of the Cambridge Structural Database, see: Allen (2002).

Experimental

Crystal data

\[
\begin{align*}
\text{C}_9\text{H}_8\text{ClN}_3 & \quad M_r = 193.63 \\
\text{Monoclinic, } P2_1/c & \\
a = 3.8926 (6) \text{ Å} & \\
b = 9.9679 (13) \text{ Å} & \\
c = 22.617 (2) \text{ Å} & \\
\beta = 92.795 (11)^\circ & \\
V = 876.52 (19) \text{ Å}^3 & \\
Z = 4 & \\
\mu = 0.39 \text{ mm}^{-1} & \\
T = 295 \text{ K} & \\
0.4 \times 0.07 \times 0.06 \text{ mm} & \\
\end{align*}
\]

Data collection

Agilent Xcalibur Sapphire2 diffractometer
Absorption correction: multi-scan (CrysAlis PRO; Agilent, 2010)
\[\text{R}(F^2) = 0.091\]
\[S = 1.02\]
1879 reflections
1340 reflections with \(I > 2\sigma(I)\)
\(R_{int} = 0.035\)

Refinement

\[R(F^2) = 0.040\]
\[wR(F^2) = 0.091\]
\[S = 1.02\]
1879 reflections
132 parameters

H atoms treated by a mixture of independent and constrained refinement
\[\Delta \rho_{min} = 0.17 \text{ e Å}^{-3}\]
\[\Delta \rho_{max} = -0.21 \text{ e Å}^{-3}\]

Table 1

Hydrogen-bond geometry (Å, °).

<table>
<thead>
<tr>
<th>D—H···A</th>
<th>D—H</th>
<th>H···A</th>
<th>D···A</th>
<th>D—H···A</th>
</tr>
</thead>
<tbody>
<tr>
<td>N4—H41···N2</td>
<td>0.85 (3)</td>
<td>2.31 (3)</td>
<td>3.144 (3)</td>
<td>169 (3)</td>
</tr>
</tbody>
</table>

Symmetry code: (i) \(-x, y - 1/2, -z + 1/2\).

Data collection: CrysAlis PRO (Agilent, 2010); cell refinement: CrysAlis PRO; data reduction: CrysAlis PRO; program(s) used to solve structure: SIR92 (Altomare et al., 1993); program(s) used to refine structure: SHELXL97 (Sheldrick, 2008); molecular graphics: SHELXTL (Sheldrick, 2008) and Mercury (Macrae et al., 2008); software used to prepare material for publication: SHELXL97.

References


Supplementary data and figures for this paper are available from the IUCr electronic archives (Reference: RK2288).
supplementary materials

5-Chloro-1-phenyl-1H-pyrazol-4-amine

A. Korzanski, P. Wagner and M. Kubicki

Comment

In the course of our studies on small heterocyclic ring derivatives we have determined the crystal structure of another member of 1-phenyl-4-amino-5-chloro-pyrazole, I, (Scheme 1). Some crystal structures of 4-aminopyrazoles were also reported, e.g. two polymorphic forms of 4-aminopyrazole (Infantes et al., 1998), 3,5-dimethyl-4-aminopyrazole (Infantes et al., 1999), and 4-amino-3,5-dinitropyrazole and its dimethylsulfoxide solvate (Schmidt et al., 2001).

The Fig. 1 shows the perspective view of I. Two planar fragments, pyrazole (maximum deviation 0.0025 (12)Å) and phenyl (0.0082 (13)Å) rings are inclined by 45.65 (6)°. This is quite a typical value, for 241 compounds with similar structural fragment (5-substituted pyrazole, non-o-substituted phenyl) found in the Cambridge Structural Database (Allen, 2002; ver. 5.32 of Nov. 2010, last update May 2011) mean value of the twist angle is around 43°, and such is also the median value. The NH₂-group is quite significantly twisted with respect to the pyrazole ring plane, the dihedral angle between two planes is 48 (2)°.

In the crystal structure the relatively weak N4—H41···N2_i hydrogen bonds join 21 screw-related molecules into the C(5) chains along y-direction. Symmetry code: (i) -x, y-1/2, -z+1/2. There are no other specific interactions, so apparently the chains are organized into three-dimensional structure by van der Waals forces.

Experimental

The compound was synthesized by electrochemical reduction of 4-nitro-1-phenylpyrazole in diluted hydrochloric acid to corresponding hydroxylamine and its in situ nucleophilic transformation into 5-chloro derivative. The compound was separated from post-reaction mixture with low yield. (Tallec et al., 2000).

Refinement

Hydrogen atoms from NH₂-group were found in the difference Fourier maps and freely refined with isotropic displacement parameters. All other hydrogen atoms were placed in idealized positions (C—H distance 0.93Å) and refined as a riding model with their U_iso = 1.2U_eq(C).

Figures

Fig. 1. The molecular structure of title compound with the atom numbering scheme. The displacement ellipsoids are drawn at 50% probability level. Hydrogen atoms are depicted as spheres of arbitrary radius.
supplementary materials

Fig. 2. The crystal packing as seen along [1 0 0] direction; hydrogen bonds are shown as dashed lines.

5-Chloro-1-phenyl-1H-pyrazol-4-amine

Crystal data

\[ C_9H_8ClN_3 \]

\[ M_r = 193.63 \]

Monoclinic, \( P2_1/c \)

Hall symbol: -P 2ybc

\[ a = 3.8926 (6) \ \text{Å} \]

\[ b = 9.9679 (13) \ \text{Å} \]

\[ c = 22.617 (2) \ \text{Å} \]

\[ \beta = 92.795 (11)^\circ \]

\[ V = 876.52 (19) \ \text{Å}^3 \]

\[ Z = 4 \]

\[ \text{Crystal data} \]

\[ F(000) = 400 \]

\[ D_x = 1.467 \ \text{Mg m}^{-3} \]

Mo K\( \alpha \) radiation, \( \lambda = 0.71073 \ \text{Å} \)

Cell parameters from 1285 reflections

\[ \theta = 2.0–27.8^\circ \]

\[ \mu = 0.39 \ \text{mm}^{-1} \]

Cell:

\[ T = 295 \ \text{K} \]

Needle, colourless

\[ V = 876.52 (19) \ \text{Å}^3 \]

\[ 0.4 \times 0.07 \times 0.06 \ \text{mm} \]

\[ 4 \times 4 \times 4 \]

\[ \text{Data collection} \]

Agilent Xcalibur Sapphire2 diffractometer

Radiation source: Enhance (Mo) X-ray Source graphite

Detector resolution: 8.1929 pixels mm\(^{-1}\)

\( \omega \) scans

Absorption correction: multi-scan

(CrysAlis PRO; Agilent, 2010)

\( T_{\text{min}} = 0.853, T_{\text{max}} = 1.000 \)

5036 measured reflections

1879 independent reflections

1340 reflections with \( I > 2\sigma(I) \)

\( \Delta\rho_{\text{max}} = 0.17 \ \text{e Å}^{-3} \)

Refinement

Refinement on \( F^2 \)

Least-squares matrix: full

\[ R[F^2 > 2\sigma(F^2)] = 0.040 \]

\[ wR(F^2) = 0.091 \]

\[ S = 1.02 \]

1879 reflections

132 parameters

Primary atom site location: structure-invariant direct methods

Secondary atom site location: difference Fourier map

Hydrogen site location: inferred from neighbouring sites

H atoms treated by a mixture of independent and constrained refinement

\[ w = 1/[\sigma^2(F_o^2) + (0.0382P)^2 + 0.093P] \]

where \( P = (F_o^2 + 2F_c^2)/3 \)

(H/\( \sigma \))\( _{\text{max}} < 0.001 \)

\[ \Delta\rho_{\text{max}} = 0.17 \ \text{e Å}^{-3} \]
0 restraints \[ \Delta \rho_{\text{min}} = -0.21 \text{ e Å}^{-3} \]

Special details

**Geometry.** All s.u.'s (except the s.u. in the dihedral angle between two l.s. planes) are estimated using the full covariance matrix. The cell s.u.'s are taken into account individually in the estimation of s.u.'s in distances, angles and torsion angles; correlations between s.u.'s in cell parameters are only used when they are defined by crystal symmetry. An approximate (isotropic) treatment of cell s.u.'s is used for estimating s.u.'s involving l.s. planes.

**Refinement.** Refinement of $F^2$ against ALL reflections. The weighted $R$–factor $wR$ and goodness of fit $S$ are based on $F^2$, conventional $R$–factors $R$ are based on $F$, with $F$ set to zero for negative $F^2$. The threshold expression of $F^2 > 2\sigma(F^2)$ is used only for calculating $R$–factors(gt) etc. and is not relevant to the choice of reflections for refinement. $R$–factors based on $F^2$ are statistically about twice as large as those based on $F$, and $R$–factors based on ALL data will be even larger.

**Fractional atomic coordinates and isotropic or equivalent isotropic displacement parameters (Å$^2$)**

<table>
<thead>
<tr>
<th>Atom</th>
<th>x</th>
<th>y</th>
<th>z</th>
<th>$U_{\text{iso}}$/$U_{\text{eq}}$</th>
</tr>
</thead>
<tbody>
<tr>
<td>N1</td>
<td>0.2024 (4)</td>
<td>1.056 (15)</td>
<td>0.1533 (6)</td>
<td>0.0333 (4)</td>
</tr>
<tr>
<td>C11</td>
<td>0.2744 (4)</td>
<td>1.179 (17)</td>
<td>0.125 (8)</td>
<td>0.0323 (4)</td>
</tr>
<tr>
<td>C12</td>
<td>0.1587 (5)</td>
<td>1.201 (2)</td>
<td>0.067 (8)</td>
<td>0.0398 (5)</td>
</tr>
<tr>
<td>H12</td>
<td>0.0415</td>
<td>1.135</td>
<td>0.0457</td>
<td>0.043 (6)*</td>
</tr>
<tr>
<td>C13</td>
<td>0.2187 (5)</td>
<td>1.323 (2)</td>
<td>0.04152 (9)</td>
<td>0.0476 (5)</td>
</tr>
<tr>
<td>H13</td>
<td>0.1442</td>
<td>1.3391</td>
<td>0.0024</td>
<td>0.070 (7)*</td>
</tr>
<tr>
<td>C14</td>
<td>0.3879 (5)</td>
<td>1.422 (2)</td>
<td>0.07319 (10)</td>
<td>0.0497 (6)</td>
</tr>
<tr>
<td>H14</td>
<td>0.4254</td>
<td>1.5056</td>
<td>0.0558</td>
<td>0.060 (7)*</td>
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<tr>
<td>C15</td>
<td>0.5023 (5)</td>
<td>1.3995 (2)</td>
<td>0.13093 (9)</td>
<td>0.0457 (5)</td>
</tr>
<tr>
<td>H15</td>
<td>0.6165</td>
<td>1.4670</td>
<td>0.1524</td>
<td>0.046 (6)*</td>
</tr>
<tr>
<td>C16</td>
<td>0.4486 (5)</td>
<td>1.277 (19)</td>
<td>0.15698 (8)</td>
<td>0.0377 (4)</td>
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<tr>
<td>H16</td>
<td>0.5292</td>
<td>1.2610</td>
<td>0.1957</td>
<td>0.039 (5)*</td>
</tr>
<tr>
<td>N2</td>
<td>0.0761 (4)</td>
<td>1.05812 (17)</td>
<td>0.2082 (6)</td>
<td>0.0400 (4)</td>
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<tr>
<td>C3</td>
<td>0.0204 (5)</td>
<td>0.9308 (2)</td>
<td>0.22098 (8)</td>
<td>0.0414 (5)</td>
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<tr>
<td>H3</td>
<td>-0.0687</td>
<td>0.9022</td>
<td>0.2563</td>
<td>0.057 (6)*</td>
</tr>
<tr>
<td>C4</td>
<td>0.1090 (5)</td>
<td>0.8444 (2)</td>
<td>0.17613 (8)</td>
<td>0.0400 (5)</td>
</tr>
<tr>
<td>N4</td>
<td>0.0706 (7)</td>
<td>0.7062 (2)</td>
<td>0.17291 (11)</td>
<td>0.0673 (7)</td>
</tr>
<tr>
<td>H42</td>
<td>0.231 (7)</td>
<td>0.668 (3)</td>
<td>0.1551 (14)</td>
<td>0.096 (12)*</td>
</tr>
<tr>
<td>H41</td>
<td>0.059 (7)</td>
<td>0.670 (3)</td>
<td>0.2067 (13)</td>
<td>0.090 (10)*</td>
</tr>
<tr>
<td>C5</td>
<td>0.2237 (5)</td>
<td>0.92795 (19)</td>
<td>0.13352 (7)</td>
<td>0.0343 (4)</td>
</tr>
<tr>
<td>C15</td>
<td>0.39097 (13)</td>
<td>0.88538 (6)</td>
<td>0.06812 (2)</td>
<td>0.04946 (19)</td>
</tr>
</tbody>
</table>

**Atomic displacement parameters (Å$^2$)**

<table>
<thead>
<tr>
<th></th>
<th>$U_{11}$</th>
<th>$U_{22}$</th>
<th>$U_{33}$</th>
<th>$U_{12}$</th>
<th>$U_{13}$</th>
<th>$U_{23}$</th>
</tr>
</thead>
<tbody>
<tr>
<td>N1</td>
<td>0.0408 (8)</td>
<td>0.0330 (9)</td>
<td>0.0265 (7)</td>
<td>0.0010 (7)</td>
<td>0.0052 (7)</td>
<td>−0.0009 (7)</td>
</tr>
<tr>
<td>C11</td>
<td>0.0326 (9)</td>
<td>0.0331 (10)</td>
<td>0.0316 (9)</td>
<td>0.0015 (8)</td>
<td>0.0051 (8)</td>
<td>0.0015 (8)</td>
</tr>
<tr>
<td>C12</td>
<td>0.0402 (10)</td>
<td>0.0455 (12)</td>
<td>0.0339 (10)</td>
<td>0.0005 (10)</td>
<td>0.0034 (8)</td>
<td>0.0001 (9)</td>
</tr>
<tr>
<td>C13</td>
<td>0.0519 (12)</td>
<td>0.0535 (14)</td>
<td>0.0378 (11)</td>
<td>0.0064 (11)</td>
<td>0.0082 (10)</td>
<td>0.0132 (10)</td>
</tr>
<tr>
<td>C14</td>
<td>0.0514 (12)</td>
<td>0.0404 (13)</td>
<td>0.0588 (14)</td>
<td>0.0034 (10)</td>
<td>0.0186 (11)</td>
<td>0.0133 (11)</td>
</tr>
<tr>
<td>C15</td>
<td>0.0459 (11)</td>
<td>0.0366 (12)</td>
<td>0.0552 (13)</td>
<td>−0.0017 (10)</td>
<td>0.0071 (10)</td>
<td>−0.0038 (10)</td>
</tr>
</tbody>
</table>
supplementary materials

\begin{tabular}{lllllll}
C16 & 0.0392 (10) & 0.0368 (11) & 0.0370 (10) & 0.0032 (9) & 0.0016 (8) & −0.0018 (9) \\
N2 & 0.0506 (9) & 0.0423 (10) & 0.0278 (8) & 0.0028 (8) & 0.0086 (7) & 0.0006 (7) \\
C3 & 0.0526 (12) & 0.0422 (12) & 0.0300 (9) & 0.0003 (10) & 0.0078 (9) & 0.0072 (9) \\
C4 & 0.0479 (11) & 0.0361 (11) & 0.0356 (10) & 0.0021 (9) & −0.0021 (9) & 0.0025 (9) \\
N4 & 0.113 (2) & 0.0338 (11) & 0.0560 (14) & −0.0017 (12) & 0.0120 (14) & 0.0028 (10) \\
C5 & 0.0367 (10) & 0.0377 (11) & 0.0283 (9) & 0.0018 (8) & 0.0007 (8) & −0.0021 (8) \\
Cl5 & 0.0591 (3) & 0.0560 (4) & 0.0338 (3) & 0.0070 (3) & 0.0076 (2) & −0.0094 (2) \\
\end{tabular}

\textit{Geometric parameters (Å, °)}

\begin{tabular}{lllll}
N1—N2 & 1.3566 (19) & C15—C16 & 1.375 (3) \\
N1—C5 & 1.358 (2) & C15—H15 & 0.9300 \\
N1—C11 & 1.417 (2) & C16—H16 & 0.9300 \\
C11—C16 & 1.373 (2) & N2—C3 & 1.322 (2) \\
C11—C12 & 1.386 (2) & C3—C4 & 1.387 (3) \\
C12—C13 & 1.369 (3) & C3—H3 & 0.9300 \\
C12—H12 & 0.9300 & C4—C5 & 1.365 (3) \\
C13—C14 & 1.371 (3) & C4—N4 & 1.387 (3) \\
C13—H13 & 0.9300 & N4—H42 & 0.85 (3) \\
C14—C15 & 1.379 (3) & N4—H41 & 0.85 (3) \\
C14—H14 & 0.9300 & C5—Cl5 & 1.6988 (18) \\
N2—N1—C5 & 110.30 (15) & C14—C15—H15 & 119.8 \\
N2—N1—C11 & 119.19 (15) & C15—C16—H15 & 120.4 \\
C5—N1—C11 & 130.45 (15) & C11—C16—H16 & 120.4 \\
C16—C11—C12 & 120.69 (17) & C15—C16—H16 & 120.4 \\
C16—C11—N1 & 118.89 (15) & C3—N2—N1 & 104.85 (15) \\
C12—C11—N1 & 120.37 (17) & N2—C3—C4 & 112.76 (17) \\
C13—C12—C11 & 119.35 (19) & N2—C3—H3 & 123.6 \\
C13—C12—H12 & 120.3 & C4—C3—H3 & 123.6 \\
C11—C12—H12 & 120.3 & C5—C4—C3 & 103.84 (18) \\
C12—C13—C14 & 120.42 (19) & C5—C4—N4 & 127.4 (2) \\
C12—C13—H13 & 119.8 & C3—C4—N4 & 128.7 (2) \\
C14—C13—H13 & 119.8 & C4—C3—N4 & 113 (2) \\
C13—C14—C15 & 119.9 (2) & C4—C3—H41 & 113 (2) \\
C13—C14—H14 & 120.0 & H42—N4—H41 & 108 (3) \\
C15—C14—H14 & 120.0 & N1—C5—C4 & 108.25 (16) \\
C16—C15—C14 & 120.4 (2) & N1—C5—C15 & 123.71 (14) \\
C16—C15—H15 & 119.8 & C4—C5—C15 & 127.94 (16) \\
N2—N1—C11—C16 & 45.7 (2) & C11—N1—N2—C3 & 176.97 (15) \\
C5—N1—C11—C16 & −137.71 (19) & N1—N2—C3—C4 & 0.4 (2) \\
N2—N1—C11—C12 & −131.79 (18) & N2—C3—C4—C5 & −0.4 (2) \\
C5—N1—C11—C12 & 44.8 (3) & N2—C3—C4—N4 & −176.6 (2) \\
C16—C11—C12—C13 & −0.2 (3) & N2—N1—C5—C4 & 0.1 (2) \\
N1—C11—C12—C13 & 177.24 (16) & C11—N1—C5—C4 & −176.81 (17) \\
C11—C12—C13—C14 & −0.8 (3) & N2—N1—C5—C15 & −176.49 (12) \\
C12—C13—C14—C15 & 0.8 (3) & C11—N1—C5—Cl5 & 6.7 (3) \\
C13—C14—C15—C16 & 0.2 (3) & C3—C4—C5—N1 & 0.2 (2) \\
C12—C11—C16—C15 & 1.1 (3) & N4—C4—C5—N1 & 176.4 (2) \\
N1—C11—C16—C15 & −176.34 (17) & C3—C4—C5—Cl5 & 176.55 (14) \\
\end{tabular}
### Hydrogen-bond geometry (Å, °)

<table>
<thead>
<tr>
<th></th>
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<th>H···A</th>
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<tr>
<td>N4—H41···N2&lt;sup&gt;i&lt;/sup&gt;</td>
<td>0.85 (3)</td>
<td>2.31 (3)</td>
<td>3.144 (3)</td>
<td>169 (3)</td>
</tr>
</tbody>
</table>

Symmetry codes: (i) −x, y+1/2, −z+1/2.
Fig. 2