

Acta Crystallographica Section E

Structure Reports

Online

ISSN 1600-5368

5-Chloropyrimidin-2-amine

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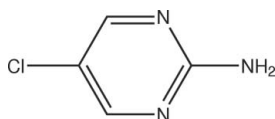
Received 19 October 2009; accepted 22 October 2009

Key indicators: single-crystal X-ray study; $T = 293$ K; mean $\sigma(\text{C}-\text{C}) = 0.002$ Å; R factor = 0.033; wR factor = 0.116; data-to-parameter ratio = 12.1.

The complete molecule of the title compound, $\text{C}_4\text{H}_3\text{ClN}_3$, is generated by crystallographic mirror symmetry, with the Cl atom, one N atom and two C atoms lying on the reflecting plane. In the crystal structure, intermolecular $\text{N}-\text{H}\cdots\text{N}$ hydrogen bonds link the molecules into chains propagating in [100].

Related literature

For general background, see: Hannouta & Johnson (1982). For bond-length data, see: Allen *et al.* (1987).



Experimental

Crystal data

$\text{C}_4\text{H}_3\text{ClN}_3$
 $M_r = 129.55$
 Orthorhombic, $Cmca$

$a = 7.6380$ (15) Å
 $b = 8.2240$ (16) Å
 $c = 17.100$ (3) Å

$V = 1074.1$ (4) Å³
 $Z = 8$
 Mo $K\alpha$ radiation

$\mu = 0.59$ mm⁻¹
 $T = 293$ K
 $0.30 \times 0.20 \times 0.10$ mm

Data collection

Enraf–Nonius CAD-4 diffractometer
 Absorption correction: ψ scan (North *et al.*, 1968)
 $T_{\min} = 0.844$, $T_{\max} = 0.944$
 1047 measured reflections

534 independent reflections
 462 reflections with $I > 2I$
 $R_{\text{int}} = 0.020$
 3 standard reflections every 200 reflections
 intensity decay: 1%

Refinement

$R[F^2 > 2\sigma(F^2)] = 0.033$
 $wR(F^2) = 0.116$
 $S = 0.92$
 534 reflections

44 parameters
 H-atom parameters constrained
 $\Delta\rho_{\max} = 0.20$ e Å⁻³
 $\Delta\rho_{\min} = -0.22$ e Å⁻³

Table 1

Hydrogen-bond geometry (Å, °).

$D-H\cdots A$	$D-H$	$H\cdots A$	$D\cdots A$	$D-H\cdots A$
$\text{N2}-\text{H2A}\cdots\text{N1}^i$	0.90	2.22	3.087 (2)	161

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

Data collection: *CAD-4 EXPRESS* (Enraf–Nonius, 1994); cell refinement: *CAD-4 EXPRESS*; data reduction: *XCAD4* (Harms & Wocadlo, 1995); program(s) used to solve structure: *SHELXS97* (Sheldrick, 2008); program(s) used to refine structure: *SHELXL97* (Sheldrick, 2008); molecular graphics: *SHELXTL* (Sheldrick, 2008); software used to prepare material for publication: *PLATON* (Spek, 2009).

Supplementary data and figures for this paper are available from the IUCr electronic archives (Reference: HB5158).

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supplementary materials

Acta Cryst. (2009). E65, o2863 [doi:10.1107/S1600536809043645]

5-Chloropyrimidin-2-amine

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Experimental

Guanidine (20 g) and 2-chloromalonaldehyde (16 g) were added to concentrated H₂SO₄ (50g) with cooling; the mixture was allowed to stand for two hours at room temperature, the product poured into ice water, neutralized with NH₄OH, the precipitated filtered, made strongly alkaline with NH₄OH, and the precipitate was recrystallized from alcohol or sublimed to give the title compound. Colourless blocks of (I) were obtained by slow evaporation of an methanol solution.

Refinement

H atoms were positioned geometrically (N—H = 0.86 Å, C—H = 0.93–0.98Å) and refined as riding with U_{iso}(H) = 1.2U_{eq}(C,N) or 1.5U_{eq}(methyl C).

Figures

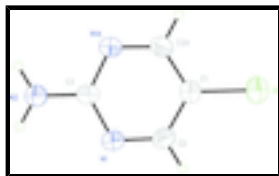


Fig. 1. The molecular structure of (I) showing 50% displacement ellipsoids.

5-Chloropyrimidin-2-amine

Crystal data

C₄H₄ClN₃

M_r = 129.55

Orthorhombic, *Cmca*

Hall symbol: -C 2bc 2

a = 7.6380 (15) Å

b = 8.2240 (16) Å

c = 17.100 (3) Å

V = 1074.1 (4) Å³

Z = 8

F(000) = 528

D_x = 1.602 Mg m⁻³

Melting point: 506 K

Mo *K*α radiation, λ = 0.71073 Å

Cell parameters from 25 reflections

θ = 10–13°

μ = 0.59 mm⁻¹

T = 293 K

Block, colourless

0.30 × 0.20 × 0.10 mm

Data collection

Enraf-Nonius CAD-4
diffractometer

462 reflections with *I* > 2σ(*I*)

supplementary materials

Radiation source: fine-focus sealed tube	$R_{\text{int}} = 0.020$
graphite	$\theta_{\text{max}} = 25.3^\circ$, $\theta_{\text{min}} = 2.4^\circ$
$\omega/2\theta$ scans	$h = 0 \rightarrow 9$
Absorption correction: ψ scan (North <i>et al.</i> , 1968)	$k = 0 \rightarrow 9$
$T_{\text{min}} = 0.844$, $T_{\text{max}} = 0.944$	$l = -20 \rightarrow 20$
1047 measured reflections	3 standard reflections every 200 reflections
534 independent reflections	intensity decay: 1%

Refinement

Refinement on F^2	Secondary atom site location: difference Fourier map
Least-squares matrix: full	Hydrogen site location: inferred from neighbouring sites
$R[F^2 > 2\sigma(F^2)] = 0.033$	H-atom parameters constrained
$wR(F^2) = 0.116$	$w = 1/[\sigma^2(F_o^2) + (0.1P)^2 + 0.2P]$
$S = 0.92$	where $P = (F_o^2 + 2F_c^2)/3$
534 reflections	$(\Delta/\sigma)_{\text{max}} < 0.001$
44 parameters	$\Delta\rho_{\text{max}} = 0.20 \text{ e } \text{\AA}^{-3}$
0 restraints	$\Delta\rho_{\text{min}} = -0.22 \text{ e } \text{\AA}^{-3}$
Primary atom site location: structure-invariant direct methods	Extinction correction: <i>SHELXL97</i> (Sheldrick, 2008), $F_c^* = kFc[1 + 0.001 \times Fc^2 \lambda^3 / \sin(2\theta)]^{-1/4}$
	Extinction coefficient: 0.025 (4)

Special details

Geometry. All esds (except the esd in the dihedral angle between two l.s. planes) are estimated using the full covariance matrix. The cell esds are taken into account individually in the estimation of esds in distances, angles and torsion angles; correlations between esds in cell parameters are only used when they are defined by crystal symmetry. An approximate (isotropic) treatment of cell esds is used for estimating esds 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 (\AA^2)

	<i>x</i>	<i>y</i>	<i>z</i>	$U_{\text{iso}}^*/U_{\text{eq}}$
Cl	0.5000	0.22728 (9)	0.27440 (4)	0.0527 (4)
N1	0.65713 (16)	-0.11849 (18)	0.41923 (8)	0.0360 (5)
C3	0.5000	-0.1761 (3)	0.44284 (14)	0.0319 (6)
N2	0.5000	-0.3014 (3)	0.49308 (15)	0.0432 (7)
H2A	0.6021	-0.3434	0.5099	0.052*
C2	0.6542 (2)	0.0027 (2)	0.36821 (10)	0.0364 (5)
H2C	0.7598	0.0457	0.3507	0.044*
C1	0.5000	0.0674 (3)	0.34019 (13)	0.0347 (6)

Atomic displacement parameters (\AA^2)

	U^{11}	U^{22}	U^{33}	U^{12}	U^{13}	U^{23}
C1	0.0488 (6)	0.0514 (6)	0.0580 (6)	0.000	0.000	0.0225 (3)
N1	0.0258 (9)	0.0398 (9)	0.0424 (9)	-0.0007 (6)	0.0004 (5)	0.0045 (6)
C3	0.0278 (12)	0.0325 (13)	0.0354 (12)	0.000	0.000	-0.0039 (11)
N2	0.0288 (11)	0.0450 (13)	0.0559 (14)	0.000	0.000	0.0179 (11)
C2	0.0296 (10)	0.0379 (10)	0.0418 (9)	-0.0033 (7)	0.0032 (7)	0.0013 (7)
C1	0.0353 (13)	0.0328 (13)	0.0359 (13)	0.000	0.000	0.0026 (10)

Geometric parameters (\AA , $^\circ$)

C1—C1	1.730 (2)	N2—H2A	0.9000
N1—C2	1.325 (2)	C2—C1	1.378 (2)
N1—C3	1.3519 (18)	C2—H2C	0.9300
C3—N2	1.341 (4)	C1—C2 ⁱ	1.378 (2)
C3—N1 ⁱ	1.3519 (18)		
C2—N1—C3	116.44 (14)	N1—C2—H2C	118.9
N2—C3—N1 ⁱ	117.41 (11)	C1—C2—H2C	118.9
N2—C3—N1	117.41 (11)	C2—C1—C2 ⁱ	117.4 (2)
N1 ⁱ —C3—N1	125.2 (2)	C2—C1—C1	121.28 (11)
C3—N2—H2A	120.0	C2 ⁱ —C1—C1	121.28 (11)
N1—C2—C1	122.25 (15)		
C2—N1—C3—N2	178.5 (2)	N1—C2—C1—C2 ⁱ	1.0 (4)
C2—N1—C3—N1 ⁱ	-0.8 (4)	N1—C2—C1—C1	179.28 (14)
C3—N1—C2—C1	-0.1 (3)		

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

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

$D-H\cdots A$	$D-H$	$H\cdots A$	$D\cdots A$	$D-H\cdots A$
N2—H2A \cdots N1 ⁱⁱ	0.90	2.22	3.087 (2)	161

Symmetry codes: (ii) $-x+3/2, -y-1/2, -z+1$.

Fig. 1

