Queensland, Australia

## 4-amino-2-chloro-5-nitro-6-(propylamino)pyrimidine

## Author

McKeveney, D, Quinn, RJ, Janssen, CO, Healy, PC

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Declan McKeveney, ${ }^{\text {a }}$ Ronald J. Quinn, ${ }^{\text {a }}$ Christian O. Janssen ${ }^{\text {a }}$ and Peter C. Healy ${ }^{\text {b }}$ *<br>${ }^{\text {a }}$ Natural Product Discovery, Eskitis Institute, Griffith University, Nathan, Brisbane 4111, Australia, and ${ }^{\mathbf{b}}$ School of Science, Griffith<br>University, Nathan, Brisbane 4111, Australia

Correspondence e-mail: p.healy@griffith.edu.au

## Key indicators

Single-crystal X-ray study
$T=295 \mathrm{~K}$
Mean $\sigma(\mathrm{C}-\mathrm{C})=0.007 \AA$
$R$ factor $=0.050$
$w R$ factor $=0.158$
Data-to-parameter ratio $=13.1$

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

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# 4-Amino-2-chloro-5-nitro-6-(propylamino)pyrimidine 

The title compound, $\mathrm{C}_{7} \mathrm{H}_{10} \mathrm{ClN}_{5} \mathrm{O}_{2}$, was synthesized as part of a study to demonstrate the reactivity of 4-amino-2,6-dichloro-5-nitropyrimidine with respect to various amine substitutions. The structure determination allowed unambiguous assignment of the regioselectivity of the substitution of the propylamine group at the 6 -position. Intra- and intermolecular $\mathrm{N}-\mathrm{H} \cdots \mathrm{O}$ and $\mathrm{N}-\mathrm{H} \cdots \mathrm{N}$ hydrogen bonding yields polymeric chains of coplanar molecules. There are two independent molecules in the asymmetric unit.

## Comment

The title compound, (I), was synthesized by substitution of one chloro substituent of 4 -amino-2,6-dichloro-5-nitropyrimidine with propylamine. While it was clear from the spectroscopic data that monosubstitution had been achieved, the question remained as to whether the chloro group at the 2or 6-position had been substituted. NMR experiments could not answer this question satisfactorily and so crystals of (I) were grown. The determination of the crystal structure has allowed the assignment of the regioselectivity of the substitution at the 6-position.


The crystal structure of (I) contains two independent molecules in the asymmetric unit disposed across a pseudo-centre of symmetry (Fig. 1). Relevant bond lengths and angles are listed in Table 1. With the exception of the peripheral propylamine substituents, both molecules are essentially coplanar.

Each molecule exhibits two intramolecular $S(6)$ (Bernstein et al., 1995) $\mathrm{N}-\mathrm{H} \cdots \mathrm{O}$ hydrogen-bonding interactions. The first of these is between the ortho amine and the nitro groups on C4 and C5 (cf. McKeveney et al., 2004; Glidewell et al., 2003), and the second is between the ortho propylamine and the nitro groups on C6 and C5 (Table 2 and Fig. 2).

Two intermolecular hydrogen-bonding interactions are also observed between the two independent molecules. The first is an $R_{2}^{2}(8) \mathrm{N}-\mathrm{H} \cdots \mathrm{N}$ interaction between the ortho amino group and the ring N3 atom (cf. Glidewell et al., 2003; Lynch \& McClenaghan, 2004). The second is an $R_{2}^{2}(12) \mathrm{N}-\mathrm{H} \cdots \mathrm{O}$

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Figure 1
The two independent molecules of (I), showing the atomic numbering scheme. Displacement ellipsoids are drawn at the $30 \%$ probability level and H atoms are shown as small spheres of arbitrary radii.


Figure 2
The hydrogen-bonding interactions in (I), shown as dashed lines.
interaction between the ortho propylamine and the nitro groups (Table 2, Fig. 2). This complex hydrogen-bonding pattern results in the formation of polymeric chains of coplanar molecules, which lie approximately parallel to the $b c$ plane and along the direction of the crystallographic $c$ axis.

## Experimental

4-Amino-2,6-dichloro-5-nitropyrimidine ( $40 \mathrm{mg}, \quad 0.19 \mathrm{mmol}$ ) was taken up in $\mathrm{CHCl}_{3}(4 \mathrm{ml})$ at 273 K . Propylamine ( $32 \mu \mathrm{l}, 0.38 \mathrm{mmol}$ ), which had been distilled before use, was added and the reaction left to stir. After 4 h , thin-layer chromatography and gas chromato-graphy-mass spectroscopy analysis indicated the reaction was complete. Purification on a column (silica gel, $\mathrm{CHCl}_{3}$ ) followed by slow evaporation of the solvent gave a pale-yellow crystalline solid
suitable for X-ray diffraction studies ( $32 \mathrm{mg}, 72.7 \%$ yield; m.p. $463-$ 465 K ). Spectroscopic analysis: ${ }^{1} \mathrm{H}$ NMR ( $d_{6}$-DMSO, $\delta$, p.p.m.): 9.48 (brs, NH), 8.84 (brs, $\mathrm{NH}_{2}$ ), $3.43\left(\mathrm{CH}_{2}\right), 1.58\left(\mathrm{CH}_{2}\right), 0.89\left(t, \mathrm{CH}_{3}\right)$; ${ }^{13}$ C NMR ( $d_{6}$-DMSO, $\delta$, p.p.m.): $160.76,159.61,157.32,110.69,42.82$, 21.79, 11.11.

## Crystal data

$\mathrm{C}_{7} \mathrm{H}_{10} \mathrm{ClN}_{5} \mathrm{O}_{2}$

$$
Z=4
$$

$M_{r}=231.65$
$D_{x}=1.518 \mathrm{Mg} \mathrm{m}^{-3}$
Triclinic, $P \overline{1}$
$a=7.406$ (3) $\AA$
$b=11.074$ (3) $\AA$
Cell parameters from 25
$c=13.886$ (5) $\AA$
reflections
$\alpha=112.54$ (2) ${ }^{\circ}$
$\theta=12.7-17.4^{\circ}$
$\beta=94.82$ (3) ${ }^{\circ}$
$\mu=0.37 \mathrm{~mm}^{-1}$
$\gamma=101.69$ (3) ${ }^{\circ}$
$T=295 \mathrm{~K}$
Prism, pale yello
$0.30 \times 0.15 \times 0.10 \mathrm{~mm}$

## Data collection

Rigaku AFC-7R diffractometer $\omega / 2 \theta$ scans
Absorption correction: none 3994 measured reflections
3565 independent reflections 1948 reflections with $I>2 \sigma(I)$ $R_{\text {int }}=0.025$
$\theta_{\max }=25.0^{\circ}$
$h=-8 \rightarrow 8$
$k=-12 \rightarrow 13$
$l=-16 \rightarrow 7$
3 standard reflections every 150 reflections intensity decay: $2.9 \%$

## Refinement

Refinement on $F^{2}$
$R\left[F^{2}>2 \sigma\left(F^{2}\right)\right]=0.050$
$w R\left(F^{2}\right)=0.158$
$S=1.02$
3565 reflections
272 parameters
H -atom parameters constrained

$$
\begin{aligned}
& w=1 /\left[\sigma^{2}\left(F_{o}^{2}\right)+(0.0687 P)^{2}\right. \\
& +0.5417 P] \\
& \text { where } P=\left(F_{o}^{2}+2 F_{c}^{2}\right) / 3 \\
& (\Delta / \sigma)_{\max }<0.001 \\
& \Delta \rho_{\max }=0.41 \mathrm{e} \AA^{-3} \\
& \Delta \rho_{\min }=-0.32 \mathrm{e}^{-3}
\end{aligned}
$$

Table 1
Selected geometric parameters ( $\left({ }^{\circ},{ }^{\circ}\right)$.

| $\mathrm{C} 2 A-\mathrm{C} 2 A$ | 1.738 (4) | N6 $A-$ C7 $A$ | 1.453 (7) |
| :---: | :---: | :---: | :---: |
| $\mathrm{Cl} 2 B-\mathrm{C} 2 B$ | 1.732 (4) | $\mathrm{N} 1 B-\mathrm{C} 2 B$ | 1.316 (5) |
| $\mathrm{O} 51 A-\mathrm{N} 5 A$ | 1.228 (5) | N1 $B-\mathrm{C} 6 B$ | 1.355 (5) |
| O52A-N5 $A$ | 1.233 (4) | N3B-C2B | 1.316 (6) |
| $\mathrm{O} 51 B$ - $\mathrm{N} 5 B$ | 1.235 (5) | N3B-C4B | 1.356 (5) |
| $\mathrm{O} 52 B-\mathrm{N} 5 B$ | 1.239 (4) | $\mathrm{N} 4 B-\mathrm{C} 4 B$ | 1.324 (5) |
| $\mathrm{N} 1 A-\mathrm{C} 2 A$ | 1.306 (5) | N5B-C5B | 1.410 (5) |
| $\mathrm{N} 1 A-\mathrm{C} 6 A$ | 1.352 (5) | N6B-C6B | 1.323 (6) |
| N3A - C4A | 1.360 (5) | N6B-C7B | 1.469 (7) |
| $\mathrm{N} 3 A-\mathrm{C} 2 A$ | 1.314 (6) | $\mathrm{C} 4 A-\mathrm{C} 5 A$ | 1.430 (5) |
| $\mathrm{N} 4 A-\mathrm{C} 4 A$ | 1.319 (5) | C5A-C6A | 1.430 (6) |
| N5A - C5A | 1.406 (5) | C4B-C5B | 1.422 (5) |
| N6 $A$ - C6 $A$ | 1.327 (6) | C5B-C6B | 1.439 (6) |
| $\mathrm{C} 2 A-\mathrm{N} 1 A-\mathrm{C} 6 A$ | 115.7 (4) | $\mathrm{C} 4 A-\mathrm{C} 5 A-\mathrm{C} 6 A$ | 117.7 (3) |
| $\mathrm{C} 2 A-\mathrm{N} 3 A-\mathrm{C} 4 A$ | 115.6 (3) | N5A-C5A-C6A | 122.1 (3) |
| $\mathrm{O} 51 A-\mathrm{N} 5 A-\mathrm{O} 52 A$ | 120.0 (3) | N6 $A$ - C6 $A$ - C5 $A$ | 123.9 (4) |
| $\mathrm{O} 51 A-\mathrm{N} 5 A-\mathrm{C} 5 A$ | 121.1 (3) | $\mathrm{N} 1 A-\mathrm{C} 6 A-\mathrm{N} 6 A$ | 115.9 (4) |
| $\mathrm{O} 52 A-\mathrm{N} 5 A-\mathrm{C} 5 A$ | 118.9 (3) | $\mathrm{N} 1 A-\mathrm{C} 6 A-\mathrm{C} 5 A$ | 120.1 (4) |
| $\mathrm{C} 6 A-\mathrm{N} 6 A-\mathrm{C} 7 A$ | 124.9 (4) | $\mathrm{N} 6 A-\mathrm{C} 7 A-\mathrm{C} 8 A$ | 116.2 (5) |
| $\mathrm{C} 2 B-\mathrm{N} 1 B-\mathrm{C} 6 B$ | 115.9 (4) | $\mathrm{Cl} 2 B-\mathrm{C} 2 B-\mathrm{N} 1 B$ | 114.7 (3) |
| $\mathrm{C} 2 B-\mathrm{N} 3 B-\mathrm{C} 4 B$ | 115.7 (3) | $\mathrm{Cl} 2 B-\mathrm{C} 2 B-\mathrm{N} 3 B$ | 114.4 (3) |
| $\mathrm{O} 51 B-\mathrm{N} 5 B-\mathrm{O} 28$ | 119.8 (3) | $\mathrm{N} 1 B-\mathrm{C} 2 B-\mathrm{N} 3 B$ | 130.9 (4) |
| O52B-N5B-C5B | 119.6 (3) | $\mathrm{N} 4 B-\mathrm{C} 4 B-\mathrm{C} 5 B$ | 125.3 (3) |
| $\mathrm{O} 51 B-\mathrm{N} 5 B-\mathrm{C} 5 B$ | 120.6 (3) | N3B-C4B-C5B | 119.9 (3) |
| $\mathrm{C} 6 B-\mathrm{N} 6 B-\mathrm{C} 7 B$ | 124.5 (4) | $\mathrm{N} 3 B-\mathrm{C} 4 B-\mathrm{N} 4 B$ | 114.8 (3) |
| $\mathrm{Cl} 2 A-\mathrm{C} 2 A-\mathrm{N} 1 A$ | 114.5 (3) | N5B-C5B-C4B | 120.5 (3) |
| $\mathrm{C} 2 A-\mathrm{C} 2 A-\mathrm{N} 3 A$ | 114.2 (3) | $\mathrm{C} 4 B-\mathrm{C} 5 B-\mathrm{C} 6 B$ | 118.1 (3) |
| $\mathrm{N} 1 A-\mathrm{C} 2 A-\mathrm{N} 3 A$ | 131.2 (4) | N5B-C5B-C6B | 121.5 (3) |
| $\mathrm{N} 3 A-\mathrm{C} 4 A-\mathrm{C} 5 A$ | 119.7 (3) | $\mathrm{N} 1 B-\mathrm{C} 6 B-\mathrm{N} 6 B$ | 116.9 (4) |
| $\mathrm{N} 3 A-\mathrm{C} 4 A-\mathrm{N} 4 A$ | 115.1 (3) | N6B-C6B-C5B | 123.8 (4) |
| $\mathrm{N} 4 A-\mathrm{C} 4 A-\mathrm{C} 5 A$ | 125.2 (3) | $\mathrm{N} 1 B-\mathrm{C} 6 B-\mathrm{C} 5 B$ | 119.3 (4) |
| $\mathrm{N} 5 A-\mathrm{C} 5 A-\mathrm{C} 4 A$ | 120.2 (3) | N6B-C7B-C8B | 111.4 (5) |

Table 2
Hydrogen-bonding geometry $\left(\AA,{ }^{\circ}\right)$.

| $D-\mathrm{H} \cdots A$ | $D-\mathrm{H}$ | $\mathrm{H} \cdots A$ | $D \cdots A$ | $D-\mathrm{H} \cdots A$ |
| :--- | :--- | :--- | :--- | :--- |
| $\mathrm{~N} 6 A-\mathrm{H} 6 A \cdots \mathrm{O} 52 A$ | 0.95 | 1.91 | $2.601(5)$ | 128 |
| $\mathrm{~N} 6 A-\mathrm{H} 6 A \cdots \mathrm{O} 2 B$ | 0.95 | 2.24 | $3.076(5)$ | 147 |
| $\mathrm{~N} 6 B-\mathrm{H} 6 B \cdots \mathrm{O} 52 A$ | 0.95 | 2.22 | $3.052(5)$ | 146 |
| N6 $B-\mathrm{H} 6 B \cdots \mathrm{O} 52 B$ | 0.95 | 1.89 | $2.599(5)$ | 129 |
| N4 $A-\mathrm{H} 41 A \cdots \mathrm{O} 51 A$ | 0.95 | 1.94 | $2.607(4)$ | 125 |
| N4 $B-\mathrm{H} 41 B \cdots \mathrm{O} 51 B$ | 0.95 | 1.94 | $2.607(4)$ | 125 |
| N4 $A-\mathrm{H} 42 A \cdots \mathrm{~N} 3 B^{\mathrm{i}}$ | 0.95 | 2.07 | $3.024(4)$ | 177 |
| N4 $B-\mathrm{H} 42 B \cdots \mathrm{~N} 3 \mathrm{~A}^{\mathrm{ii}}$ | 0.95 | 2.06 | $3.003(4)$ | 176 |

Symmetry codes: (i) $x, y, z-1$; (ii) $x, y, 1+z$.
H atoms were constrained in the riding-model approximation, fixed to their parent C or N atoms, with $\mathrm{C}-\mathrm{H}$ and $\mathrm{N}-\mathrm{H}$ distances of $0.95 \AA$ and with $U_{\text {iso }}(\mathrm{H})=1.2 U_{\text {eq }}(\mathrm{C}, \mathrm{N})$.

Data collection: MSC/AFC-7 Diffractometer Control for Windows (Molecular Structure Corporation, 1999); cell refinement: MSC/AFC7 Diffractometer Control for Windows; data reduction: TEXSAN for Windows (Molecular Structure Corporation, 1997-2001); program(s) used to solve structure: TEXSAN for Windows; program(s) used to refine structure: TEXSAN for Windows and SHELXL97 (Sheldrick,
1997); molecular graphics: PLATON for Windows (Spek, 2001) and ORTEP-3 (Farrugia, 1997); software used to prepare material for publication: TEXSAN for Windows and PLATON for Windows.

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