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2-Amino-4-(4-chlorophenylthio)-5-phenyl-6-(1-piperidyl)pyrimidine

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Key indicators

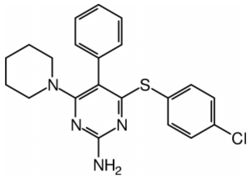
Single-crystal X-ray study
T = 120 K
Mean σ(C–C) = 0.004 Å
R factor = 0.047
wR factor = 0.124
Data-to-parameter ratio = 13.6

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

The structure of the title compound, $C_{21}H_{21}ClN_4S$, comprises a fully substituted pyrimidine ring that packs in a 2-aminopyrimidine-type hydrogen-bonded polymer chain. However, hindrance from the chlorophenylthio group, in turn altered by the presence of the phenyl ring, creates a convoluted hydrogen-bonded chain. The dihedral angle between the thiophenyl and pyrimidine rings is 70.10 (7)°, while the dihedral angle between the phenyl and pyrimidine rings is 56.14 (8)°. Neither the S nor the Cl atoms is involved in the hydrogen-bonding network.

Comment

We recently discussed the occurrence of N—H···S hydrogen-bonding associations in a series of nine 2-amino-4-sulfur-substituted pyrimidines (Lynch *et al.*, 2002). In the packing motifs of the ten structures studied (one compound had two polymorphs), all displayed $R_2^2(8)$ hydrogen-bonded 2-aminopyrimidine dimers, to varying degrees of polymerization, whereas six packing modes additionally included N—H···S interactions, the majority being three-centre with an N—H···N interaction. The title compound, (I), prepared by the sequential addition of piperidine and 4-chlorothiophenol to 2-amino-5-phenylpyrimidine, has the appropriate S-substituent to be compared with these previously studied pyrimidine structures.


(I)

In (I), the presence of the 5-phenyl ring prevents the thiophenyl group from taking on a similar conformation to that in 2-amino-4-(4-chlorophenylthio)-6-morpholinopyrimidine, in which the direction of the thiophenyl group opposes that of the pyrimidine N atoms. Instead, the thiophenyl group adopts a conformation that turns it towards the heterocyclic N atoms (Fig. 1). The dihedral angle between the 5-phenyl and pyrimidine rings is 56.14 (8)°, while the dihedral angle between the thiophenyl and pyrimidine rings is 70.10 (7)°. Previously reported 2-amino-5-phenylpyrimidine-type structures, and the dihedral angles between their 5-phenyl and pyrimidine rings, are 2,4-diamino-5-(3′,4′-dichlorophenyl)-6-methylpyrimidinium ethanesulfonate [71.7 (1)°; Cody, 1983], 2,4-diamino-5-(3′,4′-dichlorophenyl)-6-methylpyrimidine [78.2 (5) and 88.4 (5)°; De *et al.*, 1989] and methyl-

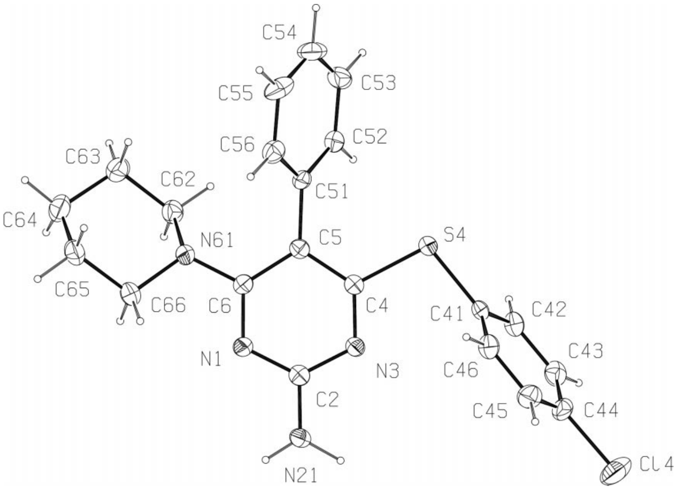


Figure 1
The molecular configuration and atom-numbering scheme for the title compound, showing ellipsoids at the 50% probability level.

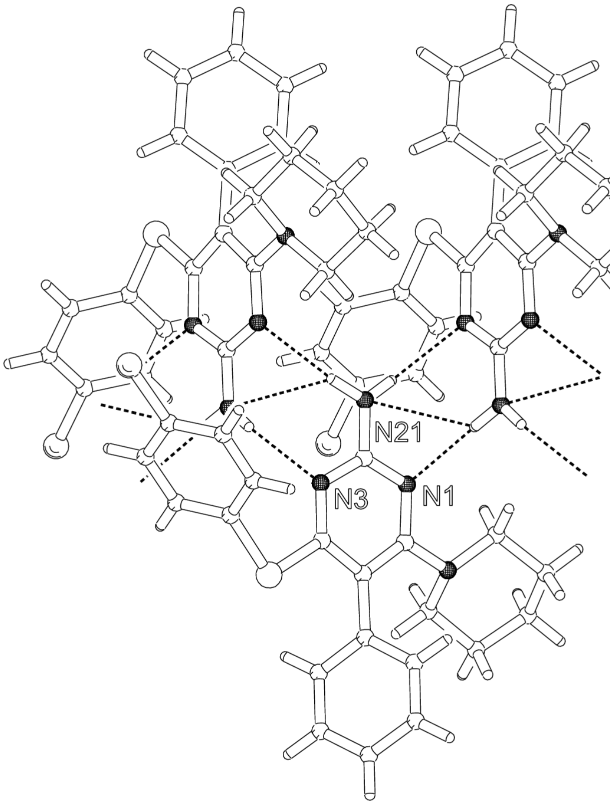


Figure 2
Partial packing diagram for the title compound, showing the convoluted 2-aminopyrimidine hydrogen-bonded chain.

benzoprim [75.4 (2) and 73.5 (2)°; Denny *et al.*, 1992]. The latter two compounds have two independent molecules in the asymmetric unit.

Hindrance from the 5-phenyl ring to neighbouring molecules and the conformation of the thiophenyl ring not only prevent any hydrogen-bonding associations to the S atom, but the latter also causes the resultant 2-aminopyrimidine hydrogen-bonded polymer chain to be convoluted (Fig. 2), similar to the packing of both 2-amino-4-chloro-6-(4-fluorophenylthio)pyrimidine and 2-amino-4-[4-(2,3-dimethylphenyl)piperazino]-6-phenylthiopyrimidine (Lynch *et al.*, 2002). However, the hydrogen-bonding pattern for (I) (Table 1) does differ from these two aforementioned structures in that there is a three-centre association from one 2-amino H atom to both the adjacent pyrimidine N atom and the adjacent 2-amino N atom. This is due to the high angle (*ca* 90°) in which the 2-aminopyrimidines approach each other to form the hydrogen-bonded chain, thus allowing one 2-amino H atom closer to both N atoms and not just the pyrimidine N. Such a high angle of incidence is due to hindrance from both the thiophenyl and piperidyl substituents, because in lesser-substituted 2-aminopyrimidines any resultant hydrogen-bonded chains have a high likelihood of being essentially planar. In this respect, it is surprising that the packing network of (I) displays any $R_2^2(8)$ dimers, let alone a full chain, especially when the Cl atom is available for hydrogen-bonding associations in an unhindered position [compare this with the structure of 2-amino-4-(4-(2-ethoxyphenyl)piperazino)-6-(4-chlorophenylthio)pyrimidine in Lynch *et al.* (2002)].

Experimental

The title compound was obtained from Key Organics Ltd and crystals were grown from an ethanol solution.

Crystal data

$C_{21}H_{21}ClN_4S$
$M_r = 396.93$
Monoclinic, $P2_1/c$
$a = 14.645$ (3) Å
$b = 6.4302$ (13) Å
$c = 20.954$ (4) Å
$\beta = 98.67$ (3)°
$V = 1950.8$ (7) Å^3
$Z = 4$
$D_x = 1.351$ Mg m^{-3}
Mo $K\alpha$ radiation
Cell parameters from 9868 reflections
$\theta = 2.9$–27.5°
$\mu = 0.32$ mm^{-1}
$T = 120$ (2) K
Plate, colourless
0.40 × 0.12 × 0.02 mm

Data collection

Bruker Nonius KappaCCD area-detector diffractometer
φ and ω scans
Absorption correction: multi-scan (*SORTAV*; Blessing, 1995)
$T_{\min} = 0.884$, $T_{\max} = 0.994$
14972 measured reflections
3422 independent reflections
2637 reflections with $I > 2\sigma(I)$
$R_{\rm int} = 0.105$
$\theta_{\max} = 25.0°$
$h = -17 \rightarrow 16$
$k = -7 \rightarrow 7$
$l = -24 \rightarrow 24$

Refinement

Refinement on F^2
$R[F^2 > 2\sigma(F^2)] = 0.047$
$wR(F^2) = 0.124$
$S = 1.09$
3422 reflections
252 parameters
H atoms treated by a mixture of independent and constrained refinement
$w = 1/[\sigma^2(F_o^2) + (0.0616P)^2 + 0.0316P]$ where $P = (F_o^2 + 2F_c^2)/3$
$(\Delta/\sigma)_{\max} < 0.001$
$\Delta\rho_{\max} = 0.49$ e Å^{-3}
$\Delta\rho_{\min} = -0.48$ e Å^{-3}

Table 1
Hydrogen-bonding geometry (Å, °).

D—H···A	D—H	H···A	D···A	D—H···A
N21—H21···N1$^{\rm i}$	1.00 (3)	2.17 (3)	3.130 (3)	160 (2)
N21—H21···N21$^{\rm i}$	1.00 (3)	2.63 (3)	3.219 (3)	118 (2)
N21—H22···N3$^{\rm ii}$	0.88 (3)	2.19 (3)	2.978 (3)	150 (2)

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

All H atoms were included in the refinement, at calculated positions, in the riding model approximation, with C—H set at 0.95 (Ar—H) and 0.99 Å (CH_2), while the isotropic displacement parameters were set equal to $1.25U_{eq}(C)$, except for the 2-amino H atoms, which were located in a difference synthesis and for which both positional and displacement parameters were refined. The high R_{int} value of 0.105 is the result of weak high-angle data.

Data collection: *DENZO* (Otwinowski & Minor, 1997) and *COLLECT* (Hooft, 1998); cell refinement: *DENZO* and *COLLECT*; data reduction: *DENZO* and *COLLECT*; program(s) used to solve structure: *SHELXS*97 (Sheldrick, 1997); program(s) used to refine structure: *SHELXL*97 (Sheldrick, 1997); molecular graphics: *PLUTON*94 (Spek, 1994) and *PLATON*97 (Spek, 1997); software used to prepare material for publication: *SHELXL*97.

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