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2-Cyano-*N*-(4,6-dimethoxypyrimidin-2-yl)acetamide: complex sheets built from N—H···O and C—H···O hydrogen bonds

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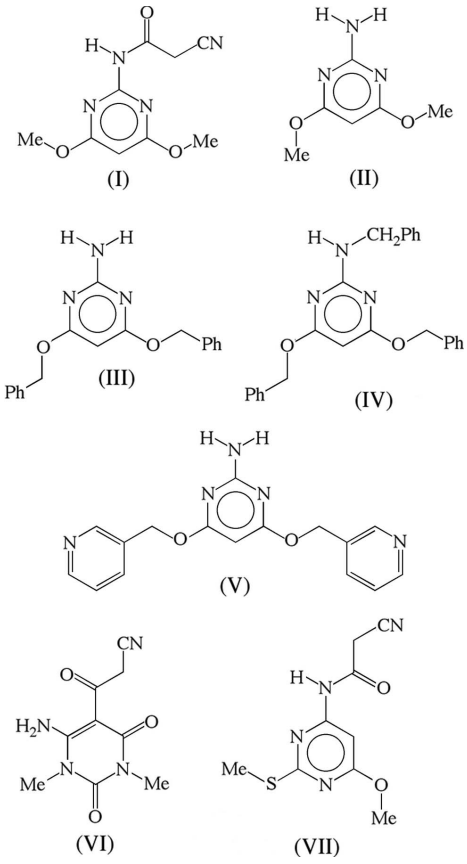
Molecules of the title compound, $C_9H_{10}N_4O_3$, (I), are linked into complex sheets by a combination of one N—H···O hydrogen bond and two C—H···O hydrogen bonds. Comparisons are drawn between (I) and some related compounds in respect of both their molecular conformations and their hydrogen-bonding arrangements.

Comment

Pyrido[2,3-*d*]pyrimidines are attractive fused heterocyclic compounds from the biological and medical point of view. In an attempt to prepare novel intermediates for the synthesis of 7-aryl-6-cyanopyrido[2,3-*d*]pyrimidin-5-ones, we isolated 2-cyano-*N*-(4,6-dimethoxypyrimidin-2-yl)acetamide, (I), instead of the expected 5-cyanoacetylpyrimidine in a cyanoacetylation reaction from 2-amino-4,6-dimethoxypyrimidine (Quiroga *et al.*, 2009). We report here the molecular and supramolecular structure of (I) (Fig. 1) which we compare with those of the related compounds (II)–(V) (Low *et al.*, 2002; Quesada *et al.*, 2002, 2004), the isomeric compound (VI) and the monosulfur analogue (VII) (Trilleras *et al.*, 2008).

The molecule of (I) is very nearly planar, as indicated by the key torsion angles (Table 1). The molecule could, in principle, exhibit exact mirror symmetry, with all of the non-H atoms lying on a crystallographic mirror plane. In fact, while the pyrimidine ring is planar within experimental uncertainty, with maximum deviations from the mean plane through the ring atoms of only 0.004 (2) Å for atoms N3 and C4, most of the exocyclic atoms are slightly displaced from this plane. The maximum displacements are those for atoms O22 [0.234 (2) Å] and C23 [0.269 (2) Å], displaced on opposite sides of the pyrimidine ring plane. These displacements are sufficient to preclude any possibility of imposed mirror symmetry. The bond distances and interbond angles present no unexpected values.



The molecular conformation, in which both of the methoxy C atoms are directed away from the ring C—H bond (Fig. 1), is in sharp contrast to that found in related compounds (II) (Low *et al.*, 2002), (III) (Quesada *et al.*, 2002) and (IV) (Low *et al.*, 2002), where only one of the alkoxy groups is directed away from the pyrimidine ring C—H bond, although in (V) (Quesada *et al.*, 2004) the alkoxy groups adopt a conformation

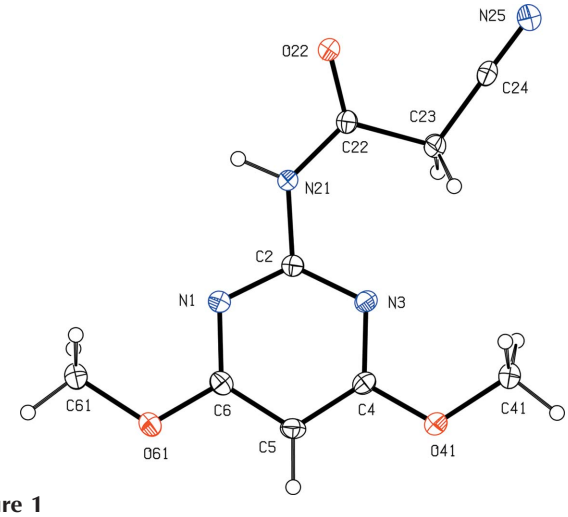


Figure 1
The molecular structure of (I), showing the atom-labelling scheme. Displacement ellipsoids are drawn at the 30% probability level.

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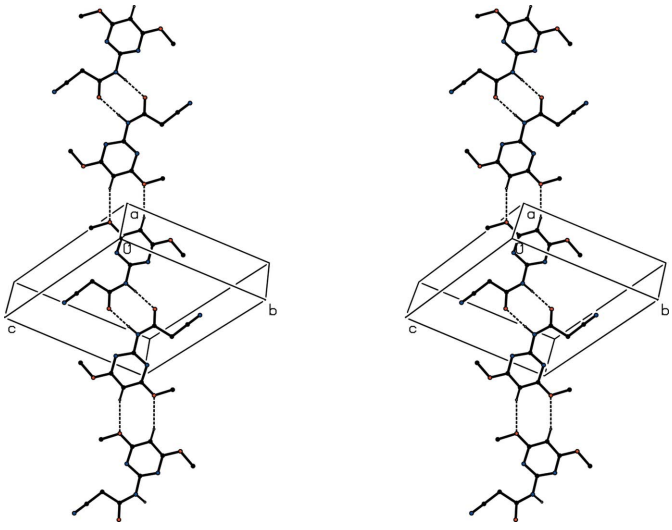

Figure 2
A stereoview of part of the crystal structure of (I), showing the formation of a hydrogen-bonded chain parallel to [$2\bar{1}\bar{1}$] and containing two different types of centrosymmetric $R_2^2(8)$ ring. For the sake of clarity, H atoms not involved in the motifs shown have been omitted.

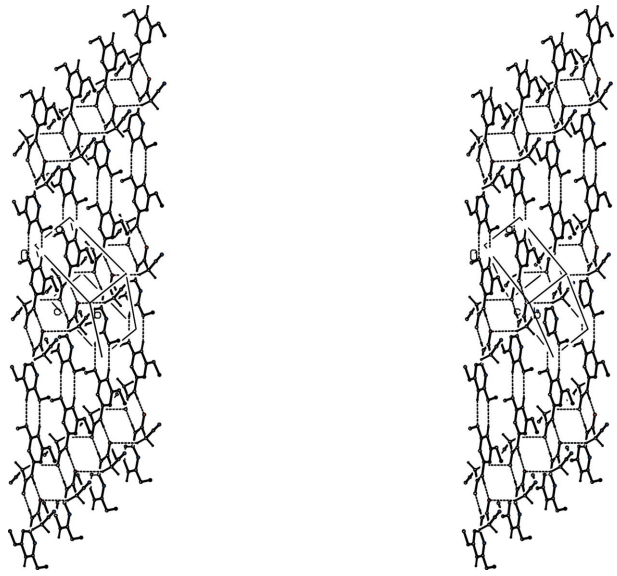

Figure 3
A stereoview of part of the crystal structure of (I), showing the formation of a hydrogen-bonded sheet parallel to (01$\bar{1}$). Methyl H atoms have been omitted for the sake of clarity.

similar to that in (I). One plausible interpretation of these differences might be in terms of the direction-specific intermolecular interactions, specifically the intermolecular hydrogen bonds. However, there appears to be no obvious pattern connecting the hydrogen-bonding arrangements in these compounds with the molecular conformations. Thus, only one of the alkoxy O atoms is utilized as a hydrogen-bond acceptor in (I) (see below). In (II), neither of the O atoms is used but both ring N atoms act as hydrogen-bond acceptors. Compound (III) uses one O atom and the less hindered of the ring N atoms as acceptors. Compound (IV) uses neither of the O atoms, just the less hindered ring N atom. In (V), which crystallizes with $Z' = 3$, all six of the pyridine N atoms act as hydrogen-bond acceptors but the O atoms and the ring N atoms play no part in the hydrogen bonding.

The molecules of (I) are linked into sheets by a combination of one N—H···O and two C—H···O hydrogen bonds (Table 2). Although there are three O atoms in the molecule of (I) potentially available as hydrogen-bond acceptors, methoxy atom O61 in fact plays no part in the hydrogen bonding; instead, amidic atom O22 acts as a double acceptor of hydrogen bonds. Neither of the ring N atoms acts as a hydrogen-bond acceptor, as access to these sites is effectively prevented by the adjacent methyl groups, along with the H atoms on atom C23 in the case of access to ring atom N3 (Fig. 1).

Two nearly linear hydrogen bonds, with atoms N21 and C5 as the donor atoms, link the molecules of (I) into a chain running parallel to the [$2\bar{1}\bar{1}$] direction and containing two independent types of centrosymmetric $R_2^2(8)$ ring (Bernstein *et al.*, 1995). The rings containing inversion-related pairs of N—H···O hydrogen bonds are centred at $(2n, \frac{1}{2} - n, \frac{1}{2} - n)$, where n represents an integer, and these alternate with the rings containing inversion-related pairs of C—H···O hydrogen bonds which are centred at $(1 + 2n, -n, -n)$, where n again represents an integer (Fig. 2). A second, weaker, C—H···O hydrogen bond, utilizing methylene atom C23 as donor, links chains related by translation along [100] into a complex sheet lying parallel to (01$\bar{1}$) (Fig. 3).

It is of interest briefly to compare the hydrogen-bonding arrangements in (II)–(V) with that found here for (I). Of (II)–(V), (IV) (Low *et al.*, 2002) is closest to (I) in overall constitution, but the molecules of (IV) are simply linked into centrosymmetric $R_2^2(8)$ rings by pairs of inversion-related N—H···N hydrogen bonds; N—H···O and C—H···O interactions are absent from the structure of (IV). The only hydrogen bonds present in the structures of compounds (II) (Low *et al.*, 2002) and (V) (Quesada *et al.*, 2004) are again of N—H···N type, giving a chain containing two types of $R_2^2(8)$ ring in (II) and two distinct types of chain containing only $R_2^2(20)$ rings in (V), where $Z' = 3$. One type of chain, which contains only one type of molecule, is formed by inversion, while the other, containing two types of molecule, is generated by translation. The aggregation in (III) (Quesada *et al.*, 2002) takes the form of a molecular ladder, where pairs of antiparallel $C(6)$ chains built from N—H···O hydrogen bonds provide the uprights and $R_2^2(8)$ rings formed by pairs of N—H···N hydrogen bonds provide the rungs of the ladder.

Compound (VI) (Trilleras *et al.*, 2008) is isomeric with (I), although of somewhat different chemical constitution. The molecules of (VI) are linked into centrosymmetric dimers by pairs of both N—H···N and N—H···O hydrogen bonds. More similar to (I) in overall constitution is compound (VII) (Trilleras *et al.*, 2008), where the molecules are linked into simple $C(6)$ chains by an N—H···N hydrogen bond, rather than by an N—H···O hydrogen bond as might perhaps have been expected.

Experimental

2-Amino-4,6-dimethoxypyrimidine (1.9 mmol) was added to a solution of cyanoacetic acid (1.9 mmol) in acetic anhydride (2.5 ml) at 340 K, and the mixture was then heated at 360 K for 5 min. During this period, 2-cyano-*N*-(4,6-dimethoxypyrimidin-2-yl)acetamide started to crystallize. After heating for 5 min, the reaction mixture was allowed to cool to ambient temperature, and the solid product was collected by filtration, washed with ethanol and recrystallized from dimethylformamide–ethanol (1:1 *v*/*v*). Colourless crystals of (I) suitable for single-crystal X-ray diffraction were obtained by slow evaporation, at ambient temperature and in air, of a solution in dimethyl sulfoxide (yield 74%, m.p. 573–575 K). MS (EI, 70 eV), *m*/*z* (relative abundance, %): 222 (57, M^+), 221 (42), 154 (100), 155 (30), 83 (43), 69 (74), 68 (71).

Crystal data

$C_9H_{10}N_4O_3$
M_r = 222.21
Triclinic, $P\overline{1}$
a = 4.1760 (6) Å
b = 11.296 (2) Å
c = 12.070 (3) Å
α = 116.929 (15)°
β = 90.478 (13)°
γ = 95.767 (15)°
V = 504.13 (18) Å^3
Z = 2
Mo $K\alpha$ radiation
μ = 0.11 mm^{-1}
T = 120 K
0.40 × 0.32 × 0.19 mm

Data collection

Bruker–Nonius KappaCCD area-detector diffractometer
Absorption correction: multi-scan (*SADABS*; Sheldrick, 2003)
T_{min} = 0.961, T_{max} = 0.979
12440 measured reflections
2325 independent reflections
1564 reflections with $I > 2\sigma(I)$
R_{int} = 0.050

Refinement

$R[F^2 > 2\sigma(F^2)]$ = 0.058
$wR(F^2)$ = 0.163
S = 1.10
2325 reflections
147 parameters
H-atom parameters constrained
$\Delta\rho_{max}$ = 0.34 e Å^{-3}
$\Delta\rho_{min}$ = −0.31 e Å^{-3}

Table 1
Selected torsion angles (°).

N1—C2—N21—C22	−178.0 (2)	N21—C22—C23—C24	−179.0 (2)
C2—N21—C22—O22	−172.6 (2)	N3—C4—O41—C41	7.5 (3)
C2—N21—C22—C23	9.4 (4)	N1—C6—O61—C61	4.0 (3)

All H atoms were located in difference maps. They were then treated as riding in geometrically idealized positions, with C—H = 0.95 (pyrimidine), 0.98 (CH_3) or 0.99 Å (CH_2) and N—H = 0.88 Å, and with U_{iso}(H) = kU_{eq}(C,N), where k = 1.5 for the methyl groups, which were permitted to rotate but not to tilt, and 1.2 for all other H atoms.

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* and *PLATON*.

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

D—H···*A*	*D*—H	H···*A*	*D*···*A*	*D*—H···*A*
N21—H21···O22^{i}	0.88	1.97	2.845 (3)	174
C5—H5···O41^{ii}	0.95	2.48	3.401 (3)	164
C23—H23*B*···O22^{iii}	0.99	2.58	3.372 (3)	137

Symmetry codes: (i) $-x, -y+1, -z+1$; (ii) $-x+2, -y, -z$; (iii) $x+1, y, z$.

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Supplementary data for this paper are available from the IUCr electronic archives (Reference: SK3387). Services for accessing these data are described at the back of the journal.

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