1474 measured reflections	3 standard reflections
1466 independent reflections	every 200 reflections
1168 reflections with	intensity decay: none
$I > 2\sigma(I)$	

. > 20(1

Refinement

Refinement on F^2	$(\Delta/\sigma)_{\rm max} < 1$
$R[F^2 > 2\sigma(F^2)] = 0.045$	$\Delta \rho_{\rm max} = 0.19$
$wR(F^2) = 0.125$	$\Delta \rho_{\min} = -0.$
S = 1.066	Extinction co
1466 reflections	SHELXL97
110 parameters	Extinction co
H atoms: see below	(14)
$w = 1/[\sigma^2(F_o^2) + (0.0610P)^2]$	Scattering fac
+ 0.0766 <i>P</i>]	Internation
where $P = (F_0^2 + 2F_c^2)/3$	Crystallogi

 $(\Delta/\sigma)_{max} < 0.001$ $\Delta\rho_{max} = 0.193 \text{ e } \text{\AA}^{-3}$ $\Delta\rho_{min} = -0.143 \text{ e } \text{\AA}^{-3}$ Extinction correction: *SHELXL97* Extinction coefficient: 0.066 (14) Scattering factors from *International Tables for Crystallography* (Vol. C)

 Table 4. Selected geometric parameters (Å, °) for (III)

 C1--C1¹
 1.480 (3)
 C2--C21
 1.5208 (19)

 Symmetry code: (i) 1 - x, 1 - y, 1 - z.

In all cases, rather large crystals were used because the specimens turned out to be very brittle and cracked into tiny pieces when we tried to cut them. All H atoms were located by difference syntheses and refined with fixed individual displacement parameters using a riding model [C—H(aromatic) = 0.93, C—H(secondary) = 0.97 and C—H(tertiary) = 0.98 Å], except for the hydroxyl H atoms in (I), whose coordinates were refined. As compound (II) contains only C, H and O atoms, and Mo $K\alpha$ radiation was used, its absolute structure could not be determined.

For all compounds, data collection: *DIF*4 (Stoe & Cie, 1984*a*); cell refinement: *DIF*4; data reduction: *REDU*4 (Stoe & Cie, 1984*b*); program(s) used to solve structures: *SHELXS97* (Sheldrick, 1997*a*); program(s) used to refine structures: *SHELXL97* (Sheldrick, 1997*b*); molecular graphics: *XP* in *SHELXTL-Plus* (Sheldrick, 1991); software used to prepare material for publication: *SHELXL97*.

We thank Professor Dr M. Lüttke (University of Göttingen) for providing us with the samples, Professor Dr E. Egert (University of Frankfurt) for helpful discussions and the Deutsche Forschungsgemeinschaft for financial support.

Supplementary data for this paper are available from the IUCr electronic archives (Reference: SK1161). Services for accessing these data are described at the back of the journal.

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6-Amino-9-(carboxymethyl)-2-methoxypurine Methyl Ester†

GEETA SOOD, CARL H. SCHWALBE AND WILLIAM FRASER

Pharmaceutical Sciences Institute, Aston University, Aston Triangle, Birmingham B4 7ET, England. E-mail: c.h.schwalbe@aston.ac.uk

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Abstract

The hydrogenolysis of 6-azido-9-(carboxymethyl)-2methoxypurine methyl ester, (3), formed in a single step from 2,6-dichloro-9-(carboxymethyl)purine ethyl ester, (2), gave the title compound, $C_9H_{11}N_5O_3$, (1). The side chain attached at N9 avoids steric hindrance with the heterocycle by emerging almost orthogonally [C8-N9-C10-C11 -104.5 (2)°] and the amino group at N6 donates intermolecular hydrogen bonds to the ring N1 and ester carbonyl O11 atoms.

Comment

2,6-Dichloro-9-(carboxymethyl)purine ethyl ester, (2) (Chan et al., 1995), with its displaceable Cl atoms, has provided a useful building block for the synthesis of base-modified intermediates (Sood et al., 1997a,b) for incorporation into peptidic nucleic acids (Hyrup & Nielsen, 1996). At elevated temperatures, prolonged treatment of (2) in the presence of excess sodium azide, acetone and methanol yields predominantly 2,6diazido-9-(carboxymethyl)purine ethyl ester through displacement of both chloro groups by azide. Two minor by-products arise from transesterification in situ, i.e. the methyl ester homologue (Sood et al., 1997a) and a second methyl ester bearing one azido group and one methoxyl group attached at the heterocyclic ring. Hydrogenolysis of the methoxyl-containing intermediate converted the azido group to an amino group giving compound (1). We undertook the crystal structure determination of (1) to unambiguously establish the substitution pattern at the heterocyclic ring. This revealed that the amino and methoxyl groups were attached at C6 and C2, respectively, in (1) and that the azido group was attached at C6 in the precursor (3).

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[†] Alternative name: methyl 6-amino-2-methoxypurine-9-acetate.



In the crystal structure, (1) exhibits none of the disorder apparent in the ethyl ester analogue where an amino group replaces the methoxyl group at C2 (Sood *et al.*, 1997*b*). Like other purine analogues containing methyl and ethyl acetate fragments attached at N9, the side chain in (1) avoids steric hindrance with the heterocycle by emerging almost orthogonally [C8—N9—C10—C11 -104.5 (2)°]. The atoms of the purine ring system are essentially coplanar within ± 0.011 (1) Å. The methyl group at O2 eclipses N3, with N3—C2—O2—C14 1.7 (2)°.

The amino group is involved in two weak hydrogen bonds, creating centrosymmetric dimers that are further linked along the screw axis (Table 2).



Fig. 1. ORTEPII view (Johnson, 1976) of the molecule of (1) with its numbering scheme. Displacement ellipsoids are shown at the 50% probability level.

Experimental

The title compound (1) was obtained on catalytic hydrogenolysis of (3) using a method analogous to that described previously (Sood *et al.*, 1997*b*). Recrystallization was from ethyl acetate-methanol solution.

Crystal data

$C_9H_{11}N_5O_3$	Cu $K\alpha$ radiation
$M_r = 237.23$	$\lambda = 1.54178 \text{ Å}$

Monoclinic $P2_1/n$ a = 11.085 (3) Å b = 7.7168 (6) Å c = 13.006 (2) Å $\beta = 99.97 (2)^{\circ}$ $V = 1095.8 (3) \text{ Å}^{3}$ Z = 4 $D_x = 1.438 \text{ Mg m}^{-3}$ $D_m \text{ not measured}$

Data collection

Enraf-Nonius CAD-4 diffractometer $\omega/2\theta$ scans Absorption correction: empirical via ψ scans (North et al., 1968) $T_{min} = 0.85, T_{max} = 0.94$ 2486 measured reflections 1946 independent reflections

Refinement

Refinement on F^2	$(\Delta/\sigma)_{\rm max} < 0.001$
$R[F^2 > 2\sigma(F^2)] = 0.038$	$\Delta \rho_{\rm max} = 0.175 \ {\rm e} \ {\rm \AA}^{-3}$
$vR(F^2) = 0.101$	$\Delta \rho_{\rm min}$ = -0.163 e Å ⁻³
S = 1.381	Extinction correction:
1946 reflections	SHELXL93
163 parameters	Extinction coefficient:
H atoms treated by a	0.0071 (6)
mixture of independent	Scattering factors from
and constrained refinement	International Tables for
$w = 1/[\sigma^2(F_o^2) + (0.0346P)^2]$	Crystallography (Vol. C)
+ 0.1761 <i>P</i>]	
where $P = (F_o^2 + 2F_c^2)/3$	

Cell parameters from 25

 $0.40 \times 0.40 \times 0.07 \text{ mm}$

1818 reflections with

 $I > 2\sigma(I)$

 $h = -2 \rightarrow 13$

 $l = -15 \rightarrow 15$

3 standard reflections

frequency: 120 min

intensity decay: 3%

 $k = 0 \rightarrow 9$

 $R_{\rm int} = 0.062$ $\theta_{\rm max} = 66.94^{\circ}$

reflections

 $\theta = 23.5 - 37.9^{\circ}$

T = 293 (2) K

Colourless

Plate

 $\mu = 0.947 \text{ mm}^{-1}$

	Table 1. Sel	lected g	geometric	parameters	(A,	°j)
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C202	1.346 (2)	C11011	1.200 (2)
C6N6	1.330 (2)		
N3-C2-N1	129.50 (13)	N1	117.79 (13)
N3-C2-O2-C14	1.7 (2)	N9-C10-C11-011	31.5 (2)
N1-C2-O2-C14	-179.48 (15)	011-C11-O12-C13	-0.8 (2)
C8-N9-C10-C11	-104.5 (2)		

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

D—H···A	D—H	H···A	$D \cdot \cdot \cdot A$	D — $H \cdot \cdot \cdot A$
N6H61····O11 ¹	0.89 (2)	2.26 (2)	3.111 (2)	160 (2)
N6H62· · · N1 ⁱⁱ	0.91 (2)	2.15 (2)	3.055 (2)	171 (2)
Symmetry codes: (i)	$\frac{1}{2} - x, \frac{1}{2} + y$	$\frac{1}{2} - z$; (ii)	1 - x, 1 - y	y, 1 - z.

H-atom treatment: N—H free, rigid methyl H atoms and others riding.

Data collection: CAD-4 Software (Enraf-Nonius, 1989). Cell refinement: CAD-4 Software. Data reduction: CADABS (Gould & Smith, 1986). Program(s) used to solve structure: MULTAN84 (Main et al., 1984). Program(s) used to refine structure: SHELXL93 (Sheldrick, 1993). Molecular graphics: ORTEPII (Johnson, 1976). Software used to prepare material for publication: SHELXL93.

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Supplementary data for this paper are available from the IUCr electronic archives (Reference: JZ1235). Services for accessing these data are described at the back of the journal.

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Knowledge of the solid-state structure of this ligand will enable further understanding of its chemical behaviour and coordination ability.



The molecule crystallizes in the space group $P2_1/c$, lying on a centre of symmetry, with the N atoms of the pyridyl rings *trans* to each other around the central bond. This conformation of the uncoordinated molecule contrasts with the *cisoid* arrangement necessary when it acts as a chelating ligand. The molecule is planar, with only the methyl H atoms deviating significantly from the plane. Bond lengths and angles are as expected for this type of system and compare favourably with those reported for other bipyridyl molecules (Nakatsu *et al.*, 1972; Troyanov *et al.*, 1989).



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6,6'-Dimethyl-2,2'-bipyridyl

ABDURRAHMAN SENGÜL, MICHAEL B. HURSTHOUSE, SIMON J. COLES* AND ROBERT D. GILLARD

Department of Chemistry, University of Wales, Cardiff, PO Box 912, Park Place, Cardiff CF1 3TB, Wales. E-mail: sacsjc@cardiff.ac.uk

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Abstract

In the solid state, the novel ligand 6,6'-dimethyl-2,2'bipyridyl (dmbp), $C_{12}H_{12}N_2$, is a planar centrosymmetric molecule in which the pyridyl N atoms have a *transoid* arrangement, by virtue of the symmetry.

Comment

Square-planar complexes of Pt^{II} containing the title dmbp ligand, *e.g.* [Pt(dmbp)Cl₂], have aroused much interest recently due to their unusual redox and physical properties (Zuleta *et al.*, 1990; Miskowski *et al.*, 1993).

Fig. 1. The molecular structure of dmbp shown with 50% probability ellipsoids.

Experimental

The title compound was prepared according to the method of Badger & Sasse (1956, 1963), with modifications (Case, 1966; Burstal, 1938; Parks et al., 1973; Newcome et al., 1981; Rodde & Breitmaier, 1987) in order to improve yield. 2-Picoline (Aldrich) was refluxed (96 h) over freshly degassed Raney-nickel catalyst (dried under vacuum for 3 h) using a Soxhlet apparatus. NaOH was added to the alloy at 353-363 K over a period of 15 min. After removal of unreacted 2-picoline by distillation, the crude product was dissolved in ethanol, heated to boiling point and filtered over decolourising charcoal. The resulting vellow solution was evaporated to dryness and sublimed at 373 K. Recrystallization from ethanol produced clear prismatic crystals, which were characterized by NMR using a Bruker AMX360 (DMSO- d_6); δ 2.52 (s, py-CH₃, 6H), 7.25 (d, 5,5'-py-H, J = 7.5 Hz, 2H), 7.76 (t, 4,4'-py-H, J = 7.7 Hz, 2H) and 8.14 (d, 3,3'-py-H, J = 7.8 Hz, 2H).