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Key indicators

Single-crystal X-ray study
 $T = 293\text{ K}$
Mean $\sigma(\text{C}-\text{C}) = 0.004\text{ \AA}$
 R factor = 0.057
 wR factor = 0.160
Data-to-parameter ratio = 17.1

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

Hydrogen-bonding patterns in bis(trimethoprim) dipicolinate pentahydrate

In the title compound, $2\text{C}_{14}\text{H}_{19}\text{N}_4\text{O}_3^+ \cdot \text{C}_7\text{H}_3\text{NO}_4^{2-} \cdot 5\text{H}_2\text{O}$, the asymmetric unit contains two trimethoprim cations (*A* and *B*), a dipicolinate anion and five water molecules. One of the picolinate carboxylate groups interacts with cation *A* via a pair of $\text{N}-\text{H} \cdots \text{O}$ hydrogen bonds, forming a ring motif $R_2^2(8)$. A loop of $\text{O}-\text{H} \cdots \text{O}$ hydrogen bonds is formed between four water molecules and the two carboxylate groups to form a supramolecular chain along the *a* axis. Molecules *A* and *B* constitute a base pair via $\text{N}-\text{H} \cdots \text{N}$ hydrogen bonds, and these base pairs are cross-linked by $\text{N}-\text{H} \cdots \text{O}$ and $\text{C}-\text{H} \cdots \text{O}$ hydrogen bonds.

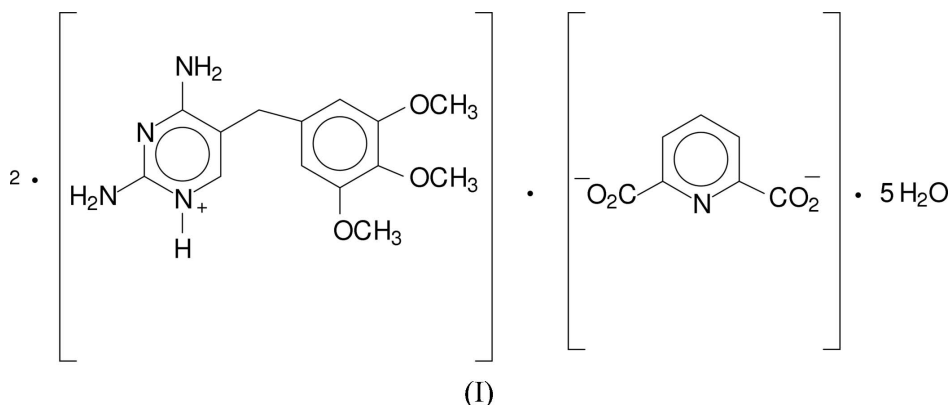
Received 21 April 2005

Accepted 27 June 2005

Online 6 July 2005

Comment

Trimethoprim [2,4-diamino-5-(3',4',5'-trimethoxybenzyl)-pyrimidine, TMP] is a well known antifolate drug. It selectively inhibits the bacterial dihydrofolate reductase (DHFR) enzyme. The present study was undertaken to explore the hydrogen-bonding patterns involving aminopyrimidine-carboxylate interactions. The crystal structure of dipicolinic acid (pyridine-2,6-dicarboxylic acid) has already been reported (Carranza Téllez *et al.*, 2002). Dipicolinic acid is a multi-chelating ligand capable of forming monomeric or polymeric complexes (Guerrero *et al.*, 1987; Kjell *et al.*, 1993; Abboud *et al.*, 1998).



In the crystal structure of trimethoprim dipicolinate pentahydrate (TMPDIP), (I), the asymmetric unit contains two trimethoprim cations (*A* and *B*), a dipicolinate anion and five water molecules. A diagram of the asymmetric unit with the atom-labelling scheme is shown in Fig. 1.

Both trimethoprim molecules are protonated at N1, as evident from the increase of the internal angle at N1 from $115.5(5)^\circ$ in neutral TMP (Koetzle & Williams, 1976) to $119.8(2)^\circ$ (cation *A*) and $120.0(2)^\circ$ (cation *B*) (Table 1) in (I).

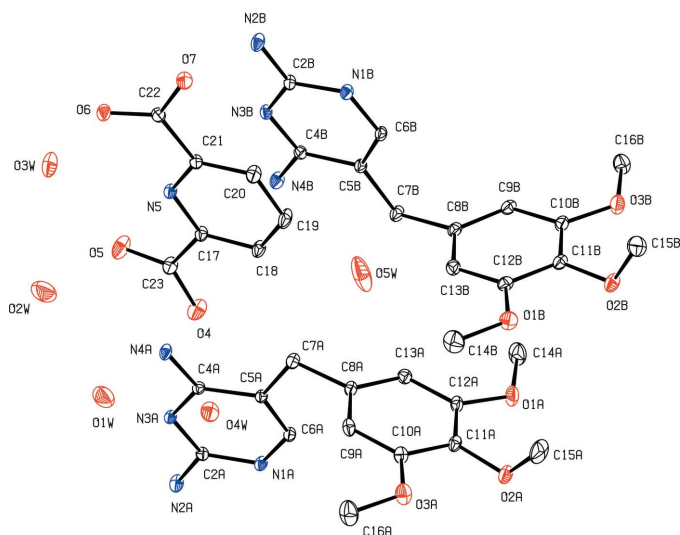


Figure 1

A view of (I), with the atom-labelling scheme and 50% probability displacement ellipsoids. H atoms have been omitted for clarity.

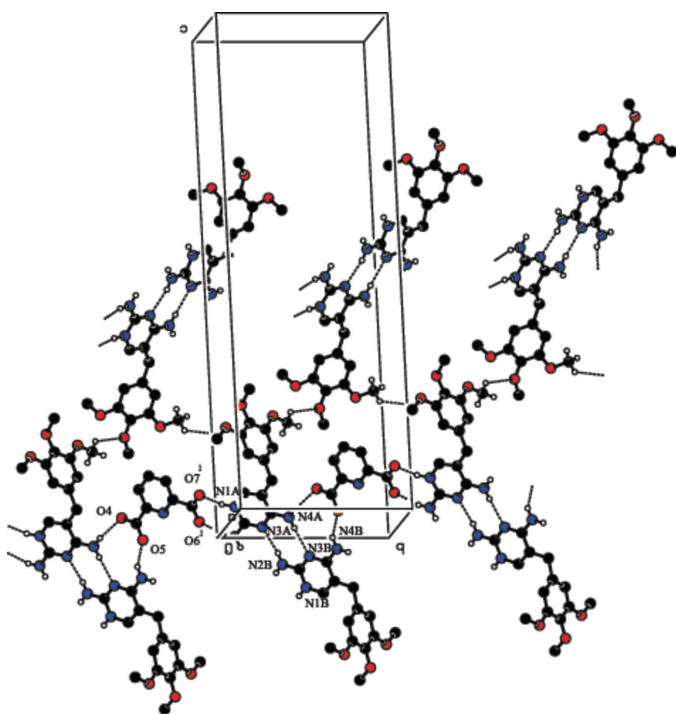


Figure 2

The hydrogen-bonding patterns (dashed lines) of (I). [Symmetry code: (i) $x - 1, y - 1, z$.]

The conformation of the trimethoprim cation is described by the two torsion angles, $C4A-C5A-C7A-C8A$ and $C5A-C7A-C8A-C9A$ [$159.9(2)$ and $-90.8(3)^\circ$] and $C4B-C5B-C7B-C8B$ and $C5B-C7B-C8B-C9B$ [$-169.7(2)$ and $-100.7(3)^\circ$] for cations *A* and *B*, respectively. The benzene ring makes dihedral angles of $77.55(12)$ (cation *A*) and $82.28(12)^\circ$ (cation *B*) with the corresponding pyrimidine plane. These values agree closely with the range of values observed in previously reported compounds (Giuseppetti *et al.*, 1984).

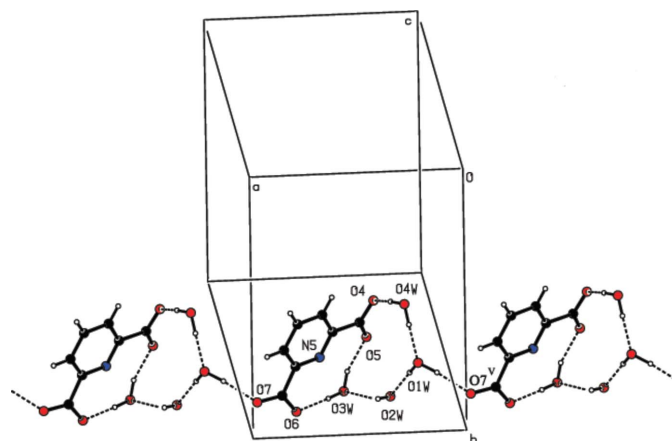


Figure 3

A view of the $O-H \cdots O$ hydrogen bonds (dashed lines) in (I). [Symmetry code: (v) $x - 1, y, z$.]

The $C-O-C$ (aromatic) angles at the methoxy groups differ significantly. This difference is also observed in the crystal structure of neutral trimethoprim and can be attributed to the close approaches involving the atoms of the three methoxy groups (Koetzle & Williams, 1976).

The geometries of the hydrogen-bonding interactions in (I) are given in Table 2. One of the carboxylate groups ($C22/O6/O7$) interacts with cation *A* via a pair of $N-H \cdots O$ hydrogen bonds, forming an $R_2^2(8)$ ring motif (Etter, 1990; Bernstein *et al.*, 1995). This motif is present in the DHFR-trimethoprim complex (Kuyper, 1989).

Cations *A* and *B* constitute a base pair via $N4A-H \cdots N3B$ and $N2B-H \cdots N3A$ hydrogen bonds. The two 4-amino groups of cations *A* and *B* are further bridged by the carboxylate group via an $N-H \cdots O$ hydrogen bond, forming an $R_3^3(10)$ ring, as shown in Fig. 2. A loop of $O-H \cdots O$ hydrogen bonds is formed between four water molecules and the carboxylate groups, to form a supramolecular chain along the *a* axis (Fig. 3). There are also $C-H \cdots O$ hydrogen bonds involving the methoxy groups, but these are not discussed in detail here.

Experimental

Trimethoprim (145 mg; obtained as a gift sample from Shilpa Antibiotics Ltd) and dipicolinic acid (41 mg; Merck) were mixed in a 2:1 molar ratio in hot ethanol (50 ml) and warmed for 30 min over a water bath. On slow evaporation, blocks of crystals of (I) were obtained.

Crystal data

$2C_{14}H_{19}N_4O_3^+ \cdot C_7H_3NO_4^{2-} \cdot 5H_2O$
 $M_r = 837.85$
 Monoclinic, $P2_1/n$
 $a = 9.713(2) \text{ \AA}$
 $b = 12.025(3) \text{ \AA}$
 $c = 35.703(3) \text{ \AA}$
 $\beta = 94.23(3)^\circ$
 $V = 4158.7(14) \text{ \AA}^3$
 $Z = 4$

$D_x = 1.338 \text{ Mg m}^{-3}$
 Mo $K\alpha$ radiation
 Cell parameters from 25 reflections
 $\theta = 3.1-27.0^\circ$
 $\mu = 0.11 \text{ mm}^{-1}$
 $T = 293 \text{ K}$
 Block, colourless
 $0.38 \times 0.26 \times 0.19 \text{ mm}$

Data collection

Philips PW1100 diffractometer
 ω scans
 Absorption correction: refined from ΔF (SHELXA; Sheldrick, 1997)
 $T_{\min} = 0.961$, $T_{\max} = 0.980$
 9210 measured reflections
 9074 independent reflections
 4170 reflections with $I > 2\sigma(I)$

$R_{\text{int}} = 0.023$
 $\theta_{\text{max}} = 27.0^\circ$
 $h = -12 \rightarrow 12$
 $k = 0 \rightarrow 15$
 $l = 0 \rightarrow 45$
 1 standard reflection every 100 reflections
 intensity decay: none

Refinement

Refinement on F^2
 $R[F^2 > 2\sigma(F^2)] = 0.057$
 $wR(F^2) = 0.160$
 $S = 0.96$
 9074 reflections
 532 parameters
 H-atom parameters constrained

$w = 1/[\sigma^2(F_o^2) + (0.0728P)^2]$
 where $P = (F_o^2 + 2F_c^2)/3$
 $(\Delta/\sigma)_{\text{max}} < 0.001$
 $\Delta\rho_{\text{max}} = 0.33 \text{ e } \text{Å}^{-3}$
 $\Delta\rho_{\text{min}} = -0.35 \text{ e } \text{Å}^{-3}$
 Extinction correction: SHELXL97 (Sheldrick, 1997)
 Extinction coefficient: 0.0032 (5)

Table 1

Selected geometric parameters (Å , $^\circ$).

O1A—C12A	1.370 (3)	O2B—C11B	1.375 (3)
O1A—C14A	1.411 (4)	O3B—C10B	1.365 (3)
O2A—C11A	1.378 (3)	O3B—C16B	1.414 (4)
O2A—C15A	1.390 (4)	N1B—C2B	1.357 (3)
O3A—C10A	1.358 (3)	N1B—C6B	1.356 (3)
O3A—C16A	1.416 (5)	N2B—C2B	1.320 (3)
N1A—C2A	1.346 (3)	N3B—C2B	1.329 (3)
N1A—C6A	1.367 (3)	N3B—C4B	1.346 (3)
N2A—C2A	1.336 (3)	N4B—C4B	1.328 (3)
N3A—C4A	1.350 (3)	O4—C23	1.248 (3)
N3A—C2A	1.330 (3)	O5—C23	1.231 (4)
N4A—C4A	1.320 (3)	O6—C22	1.251 (3)
O1B—C12B	1.362 (3)	O7—C22	1.257 (3)
O1B—C14B	1.421 (4)	N5—C21	1.338 (3)
O2B—C15B	1.422 (4)	N5—C17	1.336 (3)
C12A—O1A—C14A	118.2 (2)	N2B—C2B—N3B	120.3 (2)
C11A—O2A—C15A	117.0 (2)	N1B—C2B—N2B	117.7 (2)
C10A—O3A—C16A	117.9 (2)	N4B—C4B—C5B	119.8 (2)
C2A—N1A—C6A	119.8 (2)	N3B—C4B—C5B	122.4 (2)
C2A—N3A—C4A	118.3 (2)	N3B—C4B—N4B	117.8 (2)
N1A—C2A—N3A	122.2 (2)	N1B—C6B—C5B	122.1 (2)
N2A—C2A—N3A	120.6 (2)	O3B—C10B—C9B	124.4 (2)
N1A—C2A—N2A	117.2 (2)	O3B—C10B—C11B	115.6 (2)
N3A—C4A—C5A	122.2 (2)	O2B—C11B—C12B	119.6 (2)
N4A—C4A—C5A	121.0 (2)	O2B—C11B—C10B	120.5 (2)
N3A—C4A—N4A	116.8 (2)	O1B—C12B—C13B	125.3 (2)
N1A—C6A—C5A	122.1 (2)	O1B—C12B—C11B	115.1 (2)
O3A—C10A—C9A	124.6 (2)	C17—N5—C21	118.9 (2)
O3A—C10A—C11A	115.7 (2)	N5—C17—C18	121.9 (2)
O2A—C11A—C10A	120.0 (2)	N5—C17—C23	116.9 (2)
O2A—C11A—C12A	120.1 (2)	N5—C21—C20	121.9 (2)
O1A—C12A—C13A	124.1 (2)	N5—C21—C22	116.3 (2)
O1A—C12A—C11A	115.3 (2)	O7—C22—C21	117.1 (2)
C12B—O1B—C14B	117.8 (2)	O6—C22—C21	118.9 (2)
C11B—O2B—C15B	115.6 (2)	O6—C22—O7	123.9 (2)
C10B—O3B—C16B	118.2 (2)	O4—C23—C17	116.1 (2)
C2B—N1B—C6B	120.0 (2)	O4—C23—O5	125.2 (3)
C2B—N3B—C4B	118.1 (2)	O5—C23—C17	118.7 (3)
N1B—C2B—N3B	122.0 (2)		

Table 2

Hydrogen-bond geometry (Å , $^\circ$).

$D-H \cdots A$	$D-H$	$H \cdots A$	$D \cdots A$	$D-H \cdots A$
N1A—H1A \cdots O7 ⁱ	0.99	1.75	2.730 (3)	168
N1B—H1B \cdots O4W ⁱⁱ	0.92	1.81	2.728 (3)	176
N2A—H2A \cdots O2W ⁱⁱⁱ	0.86	2.52	3.138 (4)	129
N2A—H2B \cdots O6 ⁱ	0.86	2.05	2.892 (3)	165
N4A—H4A \cdots N3B ^{iv}	0.86	2.26	3.113 (3)	174
N4A—H4B \cdots O4	0.86	2.09	2.900 (3)	156
O1W—H11 \cdots O7 ^v	0.97	1.82	2.754 (4)	160
O1W—H12 \cdots O2W	0.98	1.76	2.712 (5)	165
O2W—H21 \cdots O3W	0.98	2.20	3.139 (4)	160
N2B—H21A \cdots N3A ^{iv}	0.86	2.16	3.009 (3)	170
O2W—H22 \cdots O5W ^{vi}	0.86	2.51	2.976 (5)	114
N2B—H22B \cdots O1W ⁱⁱ	0.86	2.50	3.265 (4)	149
O3W—H31 \cdots O6	0.95	1.90	2.854 (3)	178
O3W—H31 \cdots N5	0.95	2.52	2.898 (3)	104
O3W—H32 \cdots O5	0.94	1.85	2.759 (4)	162
O3W—H32 \cdots N5	0.94	2.40	2.898 (3)	113
O4W—H41 \cdots O1W	0.95	1.81	2.738 (3)	165
N4B—H41A \cdots O5 ^{iv}	0.86	2.05	2.798 (3)	145
O4W—H42 \cdots O4	0.97	1.79	2.733 (3)	164
O5W—H51 \cdots O6 ^{vii}	0.93	2.00	2.821 (4)	146
O5W—H52 \cdots O3W ^{iv}	0.96	1.69	2.594 (4)	155
C7A—H7B \cdots O4	0.97	2.27	3.176 (3)	155
C13A—H13A \cdots O5W	0.93	2.52	3.384 (4)	154
C16A—H16A \cdots O2A ^{viii}	0.96	2.38	3.061 (4)	128

Symmetry codes: (i) $x - 1, y - 1, z$; (ii) $x + 1, y, z$; (iii) $-x, -y + 1, -z$; (iv) $-x + 1, -y + 1, -z$; (v) $x - 1, y, z$; (vi) $x, y + 1, z$; (vii) $x, y - 1, z$; (viii) $-x + \frac{1}{2}, +y + \frac{1}{2}, -z + \frac{1}{2}$.

The H atoms of the aromatic groups were positioned geometrically and those of the water molecule were located in difference Fourier maps. All H atoms were treated as riding, with C—H, O—H and N—H bond lengths of 0.93–0.97 Å, 0.86–0.97 Å and 0.86–0.99 Å, respectively, and with $U_{\text{iso}}(\text{H}) = 1.2U_{\text{eq}}(\text{parent})$.

Data collection: FEBO (Belletti, 1996); cell refinement: MolEN (Fair, 1990); data reduction: MolEN; program(s) used to solve structure: SHELXS97 (Sheldrick, 1997); program(s) used to refine structure: SHELXL97 (Sheldrick, 1997); molecular graphics: ORTEPII (Johnson, 1976) and PLATON (Spek, 2003); software used to prepare material for publication: PLATON.

MH thanks the Council of Scientific and Industrial Research (CSIR), India, for the award of a Senior Research Fellowship (SRF) [reference No. 9/475(123)/2004-EMR-I].

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