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## Key indicators

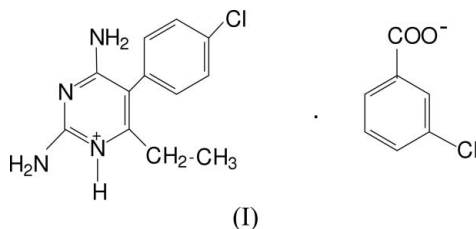
Single-crystal X-ray study  
 $T = 170$  K  
Mean  $\sigma(\text{C}-\text{C}) = 0.004$  Å  
 $R$  factor = 0.044  
 $wR$  factor = 0.122  
Data-to-parameter ratio = 14.8For details of how these key indicators were  
automatically derived from the article, see  
<http://journals.iucr.org/e>.Hydrogen-bonding patterns in pyrimethaminium  
3-chlorobenzoate

In the crystal structure of the title compound, 2,4-diamino-5-(4-chlorophenyl)-6-ethylpyrimidin-1-ium 3-chlorobenzoate,  $\text{C}_{12}\text{H}_{14}\text{ClN}_4^+ \cdot \text{C}_7\text{H}_4\text{ClO}_2^-$ , the cation interacts with the carboxylate group of the anion through a pair of  $\text{N}-\text{H} \cdots \text{O}$  hydrogen bonds, forming a cyclic hydrogen-bonded motif [graph-set notation  $R_2^2(8)$ ]. This motif self-assembles through a complementary  $DDAA$  array of quadruple hydrogen bonds. The pyrimethamine cations are paired about inversion centers through  $\text{N}-\text{H} \cdots \text{N}$  hydrogen bonds involving a pyrimidine N atom and the 4-amino group of the pyrimethamine cations. Concurrent with hydrogen bonding are  $\text{Cl} \cdots \text{Cl}$  and sandwich stacking interactions.

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## Comment

Pyrimethamine (PMN, 2,4-diamino-5-(4-chlorophenyl)-6-ethylpyrimidine) is an antimalarial drug (Tarnchompoo *et al.*, 2002). It selectively binds with DHFR enzyme through several hydrogen bonds (Hitchings & Burchall, 1965). The crystal structures of PMN (Sethuraman & Muthiah, 2002), PMN sulfosalicylate monohydrate (Hemamalini *et al.*, 2005) and PMN benzoate complexes (Stanley *et al.*, 2005) have been reported from our laboratory. The present study has been undertaken to study the hydrogen-bonding patterns in pyrimethaminium 3-chlorobenzoate (PMMB), (I).



PMN is protonated at N1 (Fig. 1), as is evident from the enhancement of the internal angle at N1 from  $116.25$  ( $18$ )° in neutral PMN molecule *A* and  $116.09$  ( $18$ )° in molecule *B* (Sethuraman & Muthiah, 2002) to  $121.4$  ( $2$ )°. In PMMB, the dihedral angle between the pyrimidine and 4-chlorophenyl rings was found to be  $87.65$  ( $12$ )° and the torsion angle  $\text{C}5-\text{C}6-\text{C}7-\text{C}8$  is  $-83.2$  ( $4$ )°. These values are close to those from modeling studies on dihydrofolate reductase-pyrimethamine complexes (Sansom *et al.*, 1989). The bond connecting the pyrimidine ring and the  $\text{C}5-\text{C}9$  benzene ring is  $1.495$  ( $3$ ) Å in length (De *et al.*, 1989). The PMN cation interacts with atoms O1 and O2 of the carboxylate group, forming a cyclic hydrogen-bonded  $R_2^2(8)$  dimer (Lynch & Jones, 2004). Two such motifs, related by inversion, are hydrogen-bonded to give a complementary  $DDAA$  ( $D$  = hydrogen-bond donor,  $A$  = hydrogen-bond acceptor) array of

quadruple hydrogen-bonding patterns, comprising fused  $R_2^2(8)$ ,  $R_4^2(8)$  and  $R_2^2(8)$  motifs (Fig. 2 and Table 1). The same pattern has been observed previously in PMN nitrobenzoate salts (Stanley *et al.*, 2005) and in some TMP (trimethoprim) salts with oxy acids (Giuseppetti *et al.*, 1984; Cody, 1984; Umadevi *et al.*, 2002; Baskar Raj *et al.*, 2002). The quadruple *DDAA* arrays are further extended into ladders by pairs of N—H...N hydrogen bonds involving atom N3 and the N4 amino group from two inversion-related pyrimidine rings. While this type of hydrogen bonding is present in many diaminopyrimidine salts (37 hits in the November 2005 release of the Cambridge Structural Database; Allen, 2002), the combination of both motifs in one crystal structure is far less common and has been observed only in *m*- and *p*-nitrobenzoate salts of PMN (Stanley *et al.*, 2005), and in the ethanesulfonate salts of both 2,4-diamino-5-(4-isopropenyl-3,5-dimethoxybenzyl)pyrimidine (Cody, 1984) and 2,4-diamino-5-(4,5-dichlorobenzyl)pyrimidine (Cody, 1983). At the edges of the ladder, we observe type II (Desiraju & Parthasarathy, 1989) Cl...Cl interactions that involve Cl atoms from both cation and anion [Cl...Cl = 3.297 (13) Å;  $\theta$  angles are 155.4 (1) and 162.7 (1)°]. Inversion-related (symmetry code:  $-x, 1 - y, -z$ ) 3-chlorobenzoate anions are involved in sandwich stacking interactions with a perpendicular separation of 3.367 Å, a slip angle of 28.9°, and a centroid-to-centroid distance of 3.845 (2) Å (Hunter, 1994).

## Experimental

PMMB was prepared by mixing hot methanol solutions (20 ml each) of pyrimethamine (62 mg, Shah Pharma Chem, India) and 3-chlorobenzoic acid (39 mg, s.d. Fine Chem, India) in a 1:1 molar ratio. Colorless prismatic crystals were obtained after a few days on slow cooling at room temperature.

### Crystal data

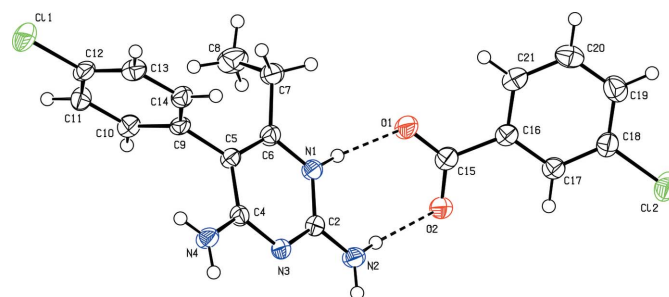
$C_{12}H_{14}ClN_4^+ \cdot C_7H_4ClO_2^-$	$V = 931.8 (4) \text{ \AA}^3$
$M_r = 405.27$	$Z = 2$
Triclinic, $P\bar{1}$	$D_x = 1.444 \text{ Mg m}^{-3}$
$a = 9.139 (2) \text{ \AA}$	Mo $K\alpha$ radiation
$b = 10.337 (2) \text{ \AA}$	$\mu = 0.37 \text{ mm}^{-1}$
$c = 11.121 (2) \text{ \AA}$	$T = 170 (2) \text{ K}$
$\alpha = 65.90 (3)^\circ$	Prism, colorless
$\beta = 82.80 (3)^\circ$	$0.4 \times 0.3 \times 0.1 \text{ mm}$
$\gamma = 76.45 (3)^\circ$	

### Data collection

Kuma KM-4-CCD $\kappa$ -geometry diffractometer	7913 measured reflections
$\omega$ scans	3616 independent reflections
Absorption correction: numerical ( <i>CrysAlis RED</i> ; Clark & Reid, 1995; Oxford Diffraction, 2004)	2359 reflections with $I > 2\sigma(I)$
$T_{\min} = 0.770$ , $T_{\max} = 0.924$	$R_{\text{int}} = 0.055$
	$\theta_{\text{max}} = 26.1^\circ$

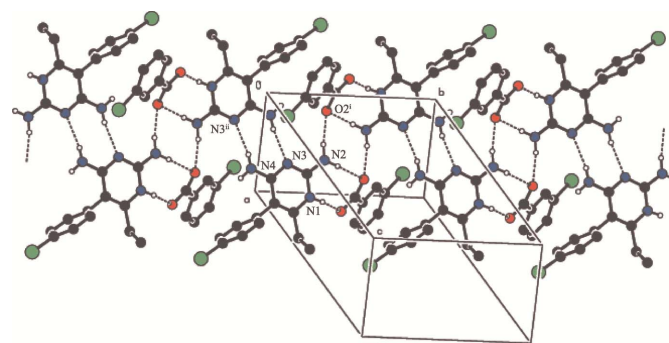
### Refinement

Refinement on $F^2$	H-atom parameters constrained
$R[F^2 > 2\sigma(F^2)] = 0.044$	$w = 1/[\sigma^2(F_o^2) + (0.0619P)^2]$
$wR(F^2) = 0.122$	where $P = (F_o^2 + 2F_c^2)/3$
$S = 0.97$	$(\Delta/\sigma)_{\text{max}} < 0.001$
3616 reflections	$\Delta\rho_{\text{max}} = 0.24 \text{ e \AA}^{-3}$
245 parameters	$\Delta\rho_{\text{min}} = -0.26 \text{ e \AA}^{-3}$



**Figure 1**

The asymmetric unit of (I) with 50% probability displacement ellipsoids (arbitrary spheres for H atoms). Dashed lines indicate hydrogen bonds.



**Figure 2**

Hydrogen-bonding patterns (dashed lines) in compound (I) [symmetry codes: (i)  $1 - x, 1 - y, -z$ ; (ii)  $1 - x, -y, -z$ ]. H atoms not involved in hydrogen bonding have been omitted.

**Table 1**

Hydrogen-bond geometry (Å, °).

$D-H \cdots A$	$D-H$	$H \cdots A$	$D \cdots A$	$D-H \cdots A$
N1—H1...O1	0.86	1.83	2.643 (3)	158
N2—H2A...O2 <sup>i</sup>	0.86	2.03	2.856 (3)	161
N2—H2B...O2	0.86	2.03	2.877 (3)	167
N4—H4A...N3 <sup>ii</sup>	0.86	2.28	3.091 (3)	157
C11—H11...O2 <sup>iii</sup>	0.93	2.59	3.477 (4)	160

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

Methyl H atoms were placed in idealized positions, with C—H = 0.96 Å and  $U_{\text{iso}}(\text{H}) = 1.5U_{\text{eq}}(\text{C})$ . Other H atoms were placed in idealized positions, with C—H = 0.97 (methylene) and 0.93 Å (aromatic), and N—H = 0.86 Å, and refined as riding on their carrier atoms, with  $U_{\text{iso}}(\text{H}) = 1.2U_{\text{eq}}(\text{C}, \text{N})$ .

Data collection: *CrysAlis CCD* (Oxford Diffraction, 2004); cell refinement: *CrysAlis RED* (Oxford Diffraction, 2004); data reduction: *CrysAlis RED*; program(s) used to solve structure: *SHELXS97* (Sheldrick, 1997); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *ORTEPII* (Johnson, 1976); software used to prepare material for publication: *PLATON* (Spek, 2003).

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