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Hydrogen bonding in pyrimethamine hydrogen adipate

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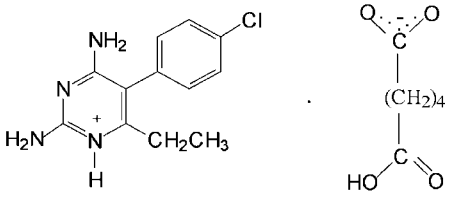
Key indicators: single-crystal X-ray study; T = 293 K; mean σ(C–C) = 0.004 Å; R factor = 0.054; wR factor = 0.155; data-to-parameter ratio = 16.1.

In 2,4-diamino-5-(*p*-chlorophenyl)-6-ethylpyrimidinium hydrogen adipate, $C_{12}H_{14}ClN_4^+\cdot C_6H_9O_4^-$, the protonated pyrimethamine cation interacts with the carboxylate group of the adipate ion through N—H···O hydrogen bonds, forming a cyclic hydrogen-bonded $R_2^2(8)$ motif. The carboxyl and carboxylate groups of the adipate ions are linked through O—H···O hydrogen bonds in a head-to-tail fashion, forming a chain. Anions and cations are further connected by an extensive network of N—H···O hydrogen bonds.

Related literature

For related literature, see: Allen (2002); Bakalbassis *et al.* (2001); Barker & Marsh (1964); Bernstein *et al.* (1995); Bucar *et al.* (2007); De *et al.* (1989); Devi *et al.* (2006); Etter (1990); Hemamalini *et al.* (2005); Kuyper (1990); Lynch & Jones (2004); Robert *et al.* (2001); Roy *et al.* (2005); Sansom *et al.* (1989); Sethuraman & Thomas Muthiah (2002); Sethuraman *et al.* (2003); Sharma *et al.* (2006); Stanley *et al.* (2002); Vallee & Auld (1993); Voet & Rich (1969, 1970); Zheng *et al.* (2000, 2001); Hitchings & Burchall (1965); Kraut & Matthews (1987); Muthiah *et al.* (2006); Vanier & Brisse (1983); Zuccotto *et al.* (1998).



Experimental

Crystal data

$C_{12}H_{14}ClN_4^+\cdot C_6H_9O_4^-$
M_r = 394.85
Triclinic, $P\overline{1}$
a = 8.154 (1) Å
b = 11.420 (2) Å
c = 12.238 (2) Å
α = 79.38 (2)°
β = 71.06 (2)°
γ = 71.20 (2)°
V = 1016 (3) Å^3
Z = 2
Mo $K\alpha$ radiation
μ = 0.22 mm^{-1}
T = 293 K
0.3 × 0.12 × 0.1 mm

Data collection

Bruker SMART CCD area-detector diffractometer
Absorption correction: none
9586 measured reflections
3988 independent reflections
3265 reflections with $I > 2\sigma(I)$
R_{int} = 0.017

Refinement

$R[F^2 > 2\sigma(F^2)]$ = 0.054
$wR(F^2)$ = 0.155
S = 1.03
3988 reflections
247 parameters
H-atom parameters constrained
$\Delta\rho_{max}$ = 0.75 e Å^{-3}
$\Delta\rho_{min}$ = −0.29 e Å^{-3}

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

D—H···A	D—H	H···A	D···A	D—H···A
N1—H1···O2	0.86	1.84	2.698 (5)	178
N2—H2A···O1^{i}	0.86	2.24	2.911 (5)	134
N2—H2B···O1	0.86	2.07	2.909 (5)	166
O4—H4···O2^{ii}	0.82	1.79	2.581 (5)	161
N4—H4A···O3^{i}	0.86	2.09	2.941 (5)	169
N4—H4B···O3^{iii}	0.86	2.30	2.986 (5)	136

Symmetry codes: (i) $-x+3, -y, -z+1$; (ii) $x+1, y, z$; (iii) $x-2, y+1, z$.

Data collection: *SMART* (Bruker, 1997); cell refinement: *SMART*; data reduction: *SAINT* (Bruker, 1997); program(s) used to solve structure: *SHELXS97* (Sheldrick, 1997); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *PLATON* (Spek, 2003) and *ORTEPII* (Johnson, 1976); software used to prepare material for publication: *PLATON*.

Supplementary data and figures for this paper are available from the IUCr electronic archives (Reference: BT2499).

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supplementary materials

Acta Cryst. (2007). E**63**, o4065-o4066 [**doi:10.1107/S1600536807044364**]

Hydrogen bonding in pyrimethamine hydrogen adipate

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Comment

Pyrimethamine [PMN] is an antimalarial drug widely employed in the chemotherapy of malaria. The drug selectively binds to the bacterial Dihydrofolate reductase enzyme (DHFR) with greater affinity than to the human enzyme inhibiting the synthesis of proteins and nucleic acids (Hitchings & Burchall, 1965). PMN [2,4-diamino-5- (*p*-chlorophenyl)-6-ethyl-pyrimidine] also used in combination with other drugs for treatment of protozoan disease like toxoplasmosis, bacterial infections and some types of cancer (Zuccotto *et al.*, 1998; Kraut & Matthews, 1987). Adipic acid is used as acidulant in baking powders, in beverages and as a gelatinizing agent. Supramolecular aggregates of adipic acid with amino acids like L– and DL-Lysine(Sharma *et al.*, 2006) and *L*-and DL-arginine (Roy *et al.*, 2005) have been reported in literature. Adipic acid also forms complexes with metals like Cu, Cd, Ni (Bakalbassis *et al.*, 2001) and co-crystal with caffeine (Bucar *et al.*, 2007). Pyrimidine and aminopyrimidines are biologically important compounds and occur in nature as components of nucleic acid. The diaminopyrimidines PMN and TMP (trimethoprim) are components of many drugs. The carboxyl group and carboxylate anion involve in hydrogen bonding interactions with aminopyrimidines (Vallee & Auld, 1993). These interactions play a vital role in protein-nucleic acid and drug-protein recognition processes (Kuyper, 1990). Crystal structures of pyrimethamine (Sethuraman & Thomas Muthiah, 2002), PMN salts (Sethuraman *et al.*, 2003), PMN hydrogen glutarate and PMN formate (Stanley *et al.*, 2002), PMN 3-chloro benzoate, PMN sulfosalicylate monohydrate (Hemamalini *et al.*, 2005) have been reported in our laboratory. The present study has been undertaken to study the hydrogen bonding patterns involving hydrogen adipate anion with the pyrimethamine cation. An *ORTEP* (II) view of the compound (I) is shown in Fig (1). The asymmetric unit contains one PMN cation and a hydrogen adipate anion. PMN is protonated at N1 as it is evident from the enhancement of internal angle at N1 from 116.3 (2)° in neutral PMN molecule A and 116.09 (18)° in molecule B (Sethuraman & Thomas Muthiah, 2002) to 121.32 (18)°. The conformation of PMN is described two angles namely dihedral and torsion angles. The dihedral angle between 2, 4 diamino pyrimidine and *p*-chlorophenyl rings is found to be 79.47 (10)°. The torsion angle C5—C6—C7—C8, which represents the deviation of the ethyl group from the pyrimidine ring is found to be 99.3 (3)°. The values are close to the modeling studies of DHFR-PMN complexes (Sansom *et al.*, 1989). The C5—C9 bond length connecting the pyrimidine and phenyl ring was found to be 1.504 (4) Å. This is in agreement with the reported value (De *et al.*, 1989). Adipic acid tends to deviate from the standard *trans* (Vanier & Brisse, 1983) conformation. This may be dueto increasing chain length of the lower aliphatic dicarboxylic acids and the flexibility of the bonds to adopt twisted conformations. The actual values of the torsion angles are −174.9 (2)°, −170.8 (2)° and −69.4 (3)° for C15—C16—C17—C18, C16—C17—C18—C19 and C17—C18—C19—C20 respectively. The angles indicate that the hydrogen adipate anion exhibits *trans-trans-gauche* conformation (Zheng *et al.*, 2000; Zheng *et al.*, 2001), which has been confirmed from CSD search of 46 adipic acid fragments (Allen & Kennard, 1993). The various hydrogen-bonding interactions are shown in Table 1. The protonated N1 cation interacts with the carboxyl ate group of the adipate ion *via* N—H···O hydrogen bonds forming cyclic hydrogen bonded ring motif represented by graph-set notation $R^2_2(8)$ (Etter, 1990; Bernstein *et al.*, 1995; Lynch & Jones, 2004). The ring motif further self assembles to form a complementary DDAA (D represents hydrogen bond donor and A represents hydrogen bond acceptor) array of quadruple hydrogen bonds. The graph set notation of three fused rings is designated as $R^2_2(8)$, $R^2_4(8)$, $R^2_2(8)$ shown in Fig(2). Similar type of interactions has also been observed

in crystal structures of TMP hydrogen adipate (Muthiah *et al.*, 2006), PMN *m*-chlorobenzoate (Devi *et al.*, 2006), TMP hydrogen glutarate (Robert *et al.*, 2001), and PMN hydrogen glutarate (Stanley *et al.*, 2002). The carboxyl and carboxylate ends of hydrogen adipate anion adopts a folded *syn* conformation so as to tie the 2-amino and 4-amino groups of the paired PMN cation on either sides to form a large 15 membered ring[$R^2_2(15)$]. Similar interactions are seen in crystal structure of TMP hydrogen adipate (Muthiah *et al.*, 2006). The hydrogen adipate ions are linked through O—H···O hydrogen bonds with the carboxylate group forming the head and carboxyl group forming the tail portions respectively. The infinite supramolecular chain [graph set: C(9)] is shown in Fig (3). This type of head to tail arrangement of hydrogen bonding has been observed in PMN hydrogen glutarate (Stanley *et al.*, 2002) and TMP hydrogen glutarate (Robert *et al.*, 2001). In adipate ions, the carbonyl O3 atoms of the free carboxyl group interacts with 4-amino groups of the pyrimethamine cations through N—H···O hydrogen bonds forming a quadrilateral ring $R^2_4(8)$, shown in Fig(2). This ring formation has also been observed in the crystal structures of cytosine (Barker & Marsh, 1964), 1-methyl cytosine and 5-fluoro-uracil complex (Voet & Rich, 1970) and cytosine and 5-fluoro-uracil complex (Voet & Rich, 1969).

Experimental

Pyrimethamine (62 mg, Shah Pharma Chem, India), adipic acid (36 mg, Merck) were mixed in 1:1 molar ratio in hot methanolic solution. The mixtures were allowed to cool at room temperature. Colourless needle shaped crystals were obtained after a few days.

Refinement

All the hydrogen atoms were fixed geometrically and were refined using a riding model with C—H = 0.93 Å-0.97 Å, N—H = 0.86Å and O—H 0.82Å and with U_{iso}(H)=1.2U_{eq}(parent atom).

Figures

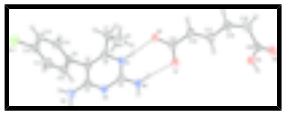

Fig. 1. An *ORTEPII* (Johnson, 1976) diagram of the asymmetric unit of (I), showing 50% probability displacement ellipsoids.

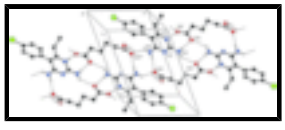

Fig. 2. Hydrogen bonding pattern of complementary DDAA array and quadrilateral ring. [Symmetry codes: (i) −*x* + 3, −*y*, −*z* + 1; (iii) *x* − 2, *y* + 1, *z*].

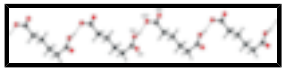

Fig. 3. Head-to-tail arrangement of supramolecular chain of adipate ions. [Symmetry code: (ii) *x* + 1, *y*, *z*].

2,4-diamino-5-(*p*-chlorophenyl)-6-ethylpyrimidinium hydrogen adipate

Crystal data

$C_{12}H_{14}ClN_4^+·C_6H_9O_4^-$	$Z = 2$
$M_r = 394.85$	$F_{000} = 416$
Triclinic, $P\bar{1}$	$D_x = 1.291$ Mg m^{-3}
Hall symbol: -P 1	Mo $K\alpha$ radiation

	λ = 0.71073 Å
a = 8.154 (1) Å	Cell parameters from 25 reflections
b = 11.420 (2) Å	θ = 1.8–27.1º
c = 12.238 (2) Å	μ = 0.22 mm^{-1}
α = 79.38 (2)º	T = 293 K
β = 71.06 (2)º	Needle, colourless
γ = 71.20 (2)º	0.3 × 0.12 × 0.1 mm
V = 1016 (3) Å^3	

Data collection

Bruker SMART CCD area-detector diffractometer	3265 reflections with $I > 2\sigma(I)$
Radiation source: fine-focus sealed tube	R_{int} = 0.017
Monochromator: graphite	θ_{max} = 27.1º
T = 293 K	θ_{min} = 1.8º
ω–scans	h = −10→10
Absorption correction: none	k = −14→14
9586 measured reflections	l = −14→15
3988 independent reflections	

Refinement

Refinement on F^2	Hydrogen site location: inferred from neighbouring sites
Least-squares matrix: full	H-atom parameters constrained
$R[F^2 > 2\sigma(F^2)]$ = 0.054	$w = 1/[\sigma^2(F_o^2) + (0.0761P)^2 + 0.4803P]$ where $P = (F_o^2 + 2F_c^2)/3$
$wR(F^2)$ = 0.155	$(\Delta/\sigma)_{max} < 0.001$
S = 1.03	$\Delta\rho_{max}$ = 0.75 e Å^{-3}
3988 reflections	$\Delta\rho_{min}$ = −0.29 e Å^{-3}
247 parameters	Extinction correction: shelxl97
Primary atom site location: structure-invariant direct methods	Extinction coefficient: 0.004 (2)
Secondary atom site location: difference Fourier map	

Special details

Geometry. Bond distances, angles *etc*. have been calculated using the rounded fractional coordinates. All e.s.d.'s are estimated from the variances of the (full) variance-covariance matrix. The cell e.s.d.'s are taken into account in the estimation of distances, angles and torsion angles

Refinement. Refinement on F^2 for ALL reflections except those flagged by the user for potential systematic errors. Weighted *R*-factors *wR* and all goodnesses of fit S are based on F^2, conventional *R*-factors *R* are based on F, with F set to zero for negative F^2. The observed criterion of $F^2 > 2\text{sigma}(F^2)$ is used only for calculating –*R*-factor-obs *etc*. and is not relevant to the choice of reflections for refinement. *R*-factors based on F^2 are statistically about twice as large as those based on F, and *R*-factors based on ALL data will be even larger.

Fractional atomic coordinates and isotropic or equivalent isotropic displacement parameters ($Å^2$)

	x	*y*	*z*	U_{iso}*/U_{eq}
Cl1	0.34022 (11)	0.32332 (8)	0.00817 (7)	0.0860 (3)
N1	1.1280 (2)	0.03254 (15)	0.34090 (15)	0.0420 (5)
N2	1.2397 (2)	0.07015 (18)	0.47705 (15)	0.0495 (6)
N3	0.9774 (2)	0.21031 (16)	0.44490 (14)	0.0436 (5)
N4	0.7145 (2)	0.34147 (17)	0.41299 (16)	0.0538 (6)
C2	1.1124 (3)	0.10668 (18)	0.42111 (16)	0.0391 (6)
C4	0.8543 (3)	0.24149 (18)	0.38477 (17)	0.0396 (6)
C5	0.8706 (3)	0.17170 (17)	0.29244 (17)	0.0389 (6)
C6	1.0088 (3)	0.06442 (18)	0.27514 (17)	0.0415 (6)
C7	1.0468 (3)	−0.0232 (2)	0.1858 (2)	0.0616 (9)
C8	1.1962 (5)	−0.0045 (4)	0.0776 (3)	0.1047 (16)
C9	0.7367 (3)	0.21222 (17)	0.22296 (17)	0.0396 (6)
C10	0.7511 (3)	0.3024 (2)	0.1302 (2)	0.0596 (8)
C11	0.6303 (4)	0.3365 (3)	0.0632 (2)	0.0671 (9)
C12	0.4946 (3)	0.2799 (2)	0.09055 (19)	0.0521 (7)
C13	0.4764 (3)	0.1909 (2)	0.1818 (2)	0.0597 (8)
C14	0.5978 (3)	0.1571 (2)	0.2481 (2)	0.0562 (8)
O1	1.5619 (2)	−0.13053 (15)	0.39195 (16)	0.0613 (6)
O2	1.3938 (2)	−0.18294 (14)	0.30789 (16)	0.0594 (6)
O3	2.3656 (3)	−0.48130 (16)	0.38775 (17)	0.0706 (7)
O4	2.2650 (2)	−0.33732 (15)	0.25569 (15)	0.0590 (6)
C15	1.5422 (3)	−0.1989 (2)	0.3318 (2)	0.0494 (7)
C16	1.7001 (3)	−0.3033 (3)	0.2752 (3)	0.0774 (10)
C17	1.8551 (3)	−0.3532 (2)	0.3244 (2)	0.0609 (8)
C18	2.0095 (3)	−0.4499 (2)	0.2505 (3)	0.0633 (9)
C19	2.1553 (4)	−0.5163 (2)	0.3095 (3)	0.0675 (9)
C20	2.2707 (3)	−0.4429 (2)	0.3223 (2)	0.0494 (7)
H1	1.21400	−0.03560	0.33110	0.0500*
H2A	1.23490	0.11370	0.52890	0.0590*
H2B	1.32630	0.00310	0.46110	0.0590*
H4A	0.70540	0.38320	0.46750	0.0650*
H4B	0.63330	0.36430	0.37670	0.0650*
H7A	0.93730	−0.01070	0.16440	0.0740*
H7B	1.08080	−0.10810	0.21960	0.0740*
H8A	1.16410	0.07980	0.04440	0.1570*
H8B	1.21240	−0.05990	0.02230	0.1570*
H8C	1.30670	−0.02140	0.09750	0.1570*
H10	0.84250	0.34080	0.11240	0.0710*
H11	0.64160	0.39670	0.00090	0.0810*
H13	0.38420	0.15340	0.19940	0.0720*
H14	0.58570	0.09670	0.31010	0.0670*
H4	2.32700	−0.30130	0.26990	0.0890*
H16A	1.65360	−0.37170	0.27590	0.0930*
H16B	1.74600	−0.27460	0.19450	0.0930*
H17A	1.81520	−0.39120	0.40240	0.0730*

H17B	1.89920	−0.28560	0.32940	0.0730*
H18A	1.96110	−0.51030	0.23500	0.0760*
H18B	2.06230	−0.40890	0.17670	0.0760*
H19A	2.09780	−0.54900	0.38640	0.0810*
H19B	2.23460	−0.58680	0.26670	0.0810*

Atomic displacement parameters (Å^2)

	U^{11}	U^{22}	U^{33}	U^{12}	U^{13}	U^{23}
Cl1	0.0792 (5)	0.1157 (7)	0.0790 (5)	−0.0179 (4)	−0.0553 (4)	−0.0043 (4)
N1	0.0379 (9)	0.0389 (9)	0.0504 (10)	−0.0029 (7)	−0.0203 (7)	−0.0073 (7)
N2	0.0413 (9)	0.0595 (11)	0.0510 (10)	−0.0062 (8)	−0.0222 (8)	−0.0108 (8)
N3	0.0399 (9)	0.0492 (10)	0.0424 (9)	−0.0077 (7)	−0.0156 (7)	−0.0077 (7)
N4	0.0514 (10)	0.0517 (10)	0.0576 (11)	0.0059 (8)	−0.0268 (9)	−0.0198 (8)
C2	0.0358 (10)	0.0458 (11)	0.0361 (10)	−0.0134 (8)	−0.0111 (8)	0.0001 (8)
C4	0.0389 (10)	0.0405 (10)	0.0390 (10)	−0.0095 (8)	−0.0134 (8)	−0.0013 (8)
C5	0.0391 (10)	0.0387 (10)	0.0404 (10)	−0.0094 (8)	−0.0156 (8)	−0.0025 (8)
C6	0.0421 (10)	0.0399 (10)	0.0457 (11)	−0.0094 (8)	−0.0186 (9)	−0.0041 (8)
C7	0.0614 (14)	0.0495 (13)	0.0829 (17)	0.0056 (10)	−0.0428 (13)	−0.0257 (12)
C8	0.109 (3)	0.123 (3)	0.078 (2)	−0.014 (2)	−0.013 (2)	−0.058 (2)
C9	0.0392 (10)	0.0390 (10)	0.0410 (10)	−0.0055 (8)	−0.0160 (8)	−0.0063 (8)
C10	0.0587 (14)	0.0644 (15)	0.0657 (15)	−0.0290 (12)	−0.0318 (12)	0.0168 (12)
C11	0.0696 (16)	0.0763 (17)	0.0595 (15)	−0.0255 (14)	−0.0343 (13)	0.0221 (13)
C12	0.0475 (12)	0.0641 (14)	0.0466 (12)	−0.0047 (10)	−0.0231 (10)	−0.0117 (10)
C13	0.0497 (13)	0.0736 (16)	0.0654 (15)	−0.0265 (12)	−0.0242 (11)	0.0012 (12)
C14	0.0548 (13)	0.0641 (14)	0.0545 (13)	−0.0247 (11)	−0.0239 (11)	0.0128 (11)
O1	0.0521 (9)	0.0558 (9)	0.0875 (12)	−0.0026 (7)	−0.0383 (9)	−0.0230 (9)
O2	0.0432 (8)	0.0513 (9)	0.0935 (12)	−0.0013 (7)	−0.0377 (8)	−0.0186 (8)
O3	0.0766 (12)	0.0603 (10)	0.0788 (12)	0.0042 (9)	−0.0453 (10)	−0.0157 (9)
O4	0.0568 (10)	0.0590 (10)	0.0756 (11)	−0.0168 (8)	−0.0378 (9)	−0.0049 (8)
C15	0.0419 (11)	0.0457 (11)	0.0665 (14)	−0.0071 (9)	−0.0270 (10)	−0.0076 (10)
C16	0.0483 (14)	0.0833 (19)	0.111 (2)	0.0037 (13)	−0.0370 (15)	−0.0481 (17)
C17	0.0466 (13)	0.0659 (15)	0.0725 (16)	−0.0073 (11)	−0.0219 (12)	−0.0183 (12)
C18	0.0436 (12)	0.0645 (15)	0.0900 (19)	−0.0100 (11)	−0.0199 (12)	−0.0345 (14)
C19	0.0623 (15)	0.0556 (14)	0.0877 (19)	−0.0121 (12)	−0.0227 (14)	−0.0198 (13)
C20	0.0428 (11)	0.0449 (11)	0.0579 (13)	0.0024 (9)	−0.0163 (10)	−0.0213 (10)

Geometric parameters (Å, °)

Cl1—C12	1.756 (4)	C11—C12	1.377 (5)
O1—C15	1.244 (3)	C12—C13	1.369 (4)
O2—C15	1.285 (4)	C13—C14	1.395 (4)
O3—C20	1.219 (4)	C7—H7A	0.9706
O4—C20	1.322 (3)	C7—H7B	0.9702
O4—H4	0.8201	C8—H8A	0.9606
N1—C6	1.377 (4)	C8—H8C	0.9599
N1—C2	1.361 (3)	C8—H8B	0.9600
N2—C2	1.341 (4)	C10—H10	0.9302
N3—C2	1.333 (3)	C11—H11	0.9298

N3—C4	1.352 (4)	C13—H13	0.9292
N4—C4	1.332 (3)	C14—H14	0.9293
N1—H1	0.8601	C15—C16	1.515 (5)
N2—H2A	0.8598	C16—C17	1.479 (5)
N2—H2B	0.8603	C17—C18	1.535 (4)
N4—H4A	0.8602	C18—C19	1.511 (5)
N4—H4B	0.8605	C19—C20	1.505 (5)
C4—C5	1.448 (4)	C16—H16A	0.9697
C5—C9	1.504 (4)	C16—H16B	0.9709
C5—C6	1.366 (4)	C17—H17A	0.9706
C6—C7	1.509 (4)	C17—H17B	0.9694
C7—C8	1.516 (5)	C18—H18A	0.9694
C9—C14	1.391 (4)	C18—H18B	0.9705
C9—C10	1.387 (4)	C19—H19A	0.9705
C10—C11	1.398 (5)	C19—H19B	0.9699
Cl1···C16^{i}	3.642 (6)	C16···H4^{iii}	3.0566
Cl1···H16B^{i}	2.9746	C20···H17B	2.9648
O1···N2	2.909 (5)	C20···H4A^{ii}	2.8597
O1···N2^{ii}	2.911 (5)	H1···O2	1.8377
O2···O4^{iii}	2.581 (5)	H1···H7B	2.3844
O2···C20^{iii}	3.386 (6)	H1···C15	2.7262
O2···N1	2.698 (5)	H1···H2B	2.2429
O3···N4^{ii}	2.941 (5)	H2A···H17B^{ii}	2.5878
O3···N4^{iv}	2.986 (5)	H2A···O1^{ii}	2.2442
O4···O2^{v}	2.581 (5)	H2B···O2	2.8943
O4···C17	3.228 (6)	H2B···O1	2.0656
O1···H2A^{ii}	2.2442	H2B···C15	2.8008
O1···H2B	2.0656	H2B···H1	2.2429
O1···H17B	2.6982	H4···H16A^{v}	2.5434
O1···H14^{v}	2.6486	H4···O2^{v}	1.7918
O2···H1	1.8377	H4···C15^{v}	2.7445
O2···H2B	2.8943	H4···C16^{v}	3.0566
O2···H7B	2.9078	H4···H7B^{v}	2.5930
O2···H4^{iii}	1.7918	H4A···O3^{ii}	2.0919
O3···H17A^{vi}	2.9045	H4A···C20^{ii}	2.8597
O3···H4B^{iv}	2.3038	H4B···C9	2.5491
O3···H16A^{v}	2.8515	H4B···O3^{viii}	2.3038
O3···H4A^{ii}	2.0919	H4B···C10	2.9983
O4···H7B^{v}	2.6026	H7A···C14	2.8015
O4···H17B	2.7154	H7A···C9	2.6263
O4···H18B	2.5561	H7B···O4^{iii}	2.6026
N1···O2	2.698 (5)	H7B···O2	2.9078
N1···C2^{vii}	3.384 (6)	H7B···H1	2.3844
N2···O1	2.909 (5)	H7B···H4^{iii}	2.5930

N2···O1^{ii}	2.911 (5)	H8B···C12^{i}	3.0324
N4···O3^{viii}	2.986 (5)	H8C···N1	2.9421
N4···O3^{ii}	2.941 (5)	H13···N1^{iii}	2.8102
N1···H8C	2.9421	H13···C2^{iii}	2.9805
N1···H13^{v}	2.8102	H14···O1^{iii}	2.6486
C2···C2^{vii}	3.446 (6)	H16A···O3^{iii}	2.8515
C2···N1^{vii}	3.384 (6)	H16A···H4^{iii}	2.5434
C7···C14	3.483 (6)	H16A···H18A	2.4417
C14···C7	3.483 (6)	H16B···H18B	2.5021
C16···Cl1^{i}	3.642 (6)	H16B···Cl1^{i}	2.9746
C17···O4	3.228 (6)	H17A···H19A	2.3993
C20···O2^{v}	3.386 (6)	H17A···O3^{vi}	2.9045
C2···H13^{v}	2.9805	H17B···O1	2.6982
C9···H7A	2.6263	H17B···O4	2.7154
C9···H4B	2.5491	H17B···C20	2.9648
C10···H4B	2.9983	H17B···H2A^{ii}	2.5878
C12···H8B^{i}	3.0324	H18A···H16A	2.4417
C12···H19B^{viii}	2.7608	H18B···O4	2.5561
C13···H19B^{viii}	2.7979	H18B···H16B	2.5021
C14···H7A	2.8015	H19A···H17A	2.3993
C15···H1	2.7262	H19B···C12^{iv}	2.7608
C15···H4^{iii}	2.7445	H19B···C13^{iv}	2.7979
C15···H2B	2.8008		
C20—O4—H4	109.48	H8A—C8—H8C	109.42
C2—N1—C6	121.32 (18)	H8B—C8—H8C	109.49
C2—N3—C4	117.41 (18)	C7—C8—H8C	109.50
C2—N1—H1	119.34	C11—C10—H10	119.54
C6—N1—H1	119.34	C9—C10—H10	119.45
C2—N2—H2A	120.04	C10—C11—H11	120.32
C2—N2—H2B	120.03	C12—C11—H11	120.46
H2A—N2—H2B	119.93	C14—C13—H13	120.36
C4—N4—H4A	119.98	C12—C13—H13	120.36
H4A—N4—H4B	120.03	C9—C14—H14	119.43
C4—N4—H4B	120.00	C13—C14—H14	119.43
N2—C2—N3	120.72 (19)	O1—C15—C16	120.7 (2)
N1—C2—N2	116.74 (19)	O2—C15—C16	115.6 (2)
N1—C2—N3	122.5 (2)	O1—C15—O2	123.6 (2)
N3—C4—C5	122.70 (19)	C15—C16—C17	118.7 (3)
N3—C4—N4	117.24 (18)	C16—C17—C18	111.8 (2)
N4—C4—C5	120.1 (2)	C17—C18—C19	112.2 (3)
C4—C5—C9	121.56 (18)	C18—C19—C20	117.7 (2)
C4—C5—C6	116.7 (2)	O3—C20—C19	121.4 (2)
C6—C5—C9	121.72 (19)	O4—C20—C19	115.3 (2)
N1—C6—C7	115.77 (19)	O3—C20—O4	123.2 (2)
C5—C6—C7	125.1 (2)	C15—C16—H16A	107.65

N1—C6—C5	119.10 (19)	C15—C16—H16B	107.64
C6—C7—C8	112.5 (2)	C17—C16—H16A	107.68
C5—C9—C10	121.2 (2)	C17—C16—H16B	107.65
C5—C9—C14	120.59 (18)	H16A—C16—H16B	107.01
C10—C9—C14	118.2 (2)	C16—C17—H17A	109.25
C9—C10—C11	121.0 (2)	C16—C17—H17B	109.32
C10—C11—C12	119.2 (2)	C18—C17—H17A	109.22
Cl1—C12—C13	119.2 (2)	C18—C17—H17B	109.29
Cl1—C12—C11	119.66 (19)	H17A—C17—H17B	107.89
C11—C12—C13	121.2 (2)	C17—C18—H18A	109.18
C12—C13—C14	119.3 (2)	C17—C18—H18B	109.16
C9—C14—C13	121.1 (2)	C19—C18—H18A	109.20
C6—C7—H7B	109.14	C19—C18—H18B	109.11
C8—C7—H7A	109.07	H18A—C18—H18B	107.90
C8—C7—H7B	109.10	C18—C19—H19A	107.82
H7A—C7—H7B	107.83	C18—C19—H19B	107.88
C6—C7—H7A	109.10	C20—C19—H19A	107.88
C7—C8—H8A	109.47	C20—C19—H19B	107.92
C7—C8—H8B	109.50	H19A—C19—H19B	107.18
H8A—C8—H8B	109.44		
C2—N1—C6—C5	−1.1 (3)	C5—C6—C7—C8	99.4 (3)
C2—N1—C6—C7	177.32 (19)	N1—C6—C7—C8	−78.9 (3)
C6—N1—C2—N2	−177.18 (19)	C5—C9—C10—C11	177.6 (2)
C6—N1—C2—N3	3.4 (3)	C5—C9—C14—C13	−177.8 (2)
C4—N3—C2—N1	−0.8 (3)	C14—C9—C10—C11	−0.4 (3)
C2—N3—C4—C5	−3.9 (3)	C10—C9—C14—C13	0.3 (3)
C4—N3—C2—N2	179.81 (19)	C9—C10—C11—C12	0.4 (4)
C2—N3—C4—N4	176.57 (19)	C10—C11—C12—C13	−0.1 (4)
N3—C4—C5—C6	6.0 (3)	C10—C11—C12—Cl1	179.2 (2)
N4—C4—C5—C9	2.6 (3)	C11—C12—C13—C14	0.0 (4)
N3—C4—C5—C9	−176.8 (2)	Cl1—C12—C13—C14	−179.37 (17)
N4—C4—C5—C6	−174.5 (2)	C12—C13—C14—C9	0.0 (3)
C9—C5—C6—N1	179.56 (19)	O2—C15—C16—C17	−161.3 (2)
C4—C5—C6—C7	178.5 (2)	O1—C15—C16—C17	22.4 (4)
C4—C5—C6—N1	−3.3 (3)	C15—C16—C17—C18	−174.9 (2)
C4—C5—C9—C14	−99.6 (2)	C16—C17—C18—C19	−170.8 (2)
C6—C5—C9—C10	−100.6 (3)	C17—C18—C19—C20	−69.4 (3)
C6—C5—C9—C14	77.5 (3)	C18—C19—C20—O4	−16.5 (4)
C4—C5—C9—C10	82.4 (3)	C18—C19—C20—O3	165.4 (3)
C9—C5—C6—C7	1.3 (3)		

Symmetry codes: (i) −*x*+2, −*y*, −*z*; (ii) −*x*+3, −*y*, −*z*+1; (iii) *x*−1, *y*, *z*; (iv) *x*+2, *y*−1, *z*; (v) *x*+1, *y*, *z*; (vi) −*x*+4, −*y*−1, −*z*+1; (vii) −*x*+2, −*y*, −*z*+1; (viii) *x*−2, *y*+1, *z*.

Hydrogen-bond geometry (Å, °)

D—H···*A*	*D*—H	H···*A*	*D*···*A*	*D*—H···*A*
N1—H1···O2	0.86	1.84	2.698 (5)	178
N2—H2A···O1^{ii}	0.86	2.24	2.911 (5)	134
N2—H2B···O1	0.86	2.07	2.909 (5)	166

O4—H4···O2^{v}	0.82	1.79	2.581 (5)	161
N4—H4A···O3^{ii}	0.86	2.09	2.941 (5)	169
N4—H4B···O3^{viii}	0.86	2.30	2.986 (5)	136

Symmetry codes: (ii) −*x*+3, −*y*, −*z*+1; (v) *x*+1, *y*, *z*; (viii) *x*−2, *y*+1, *z*.

Fig. 1

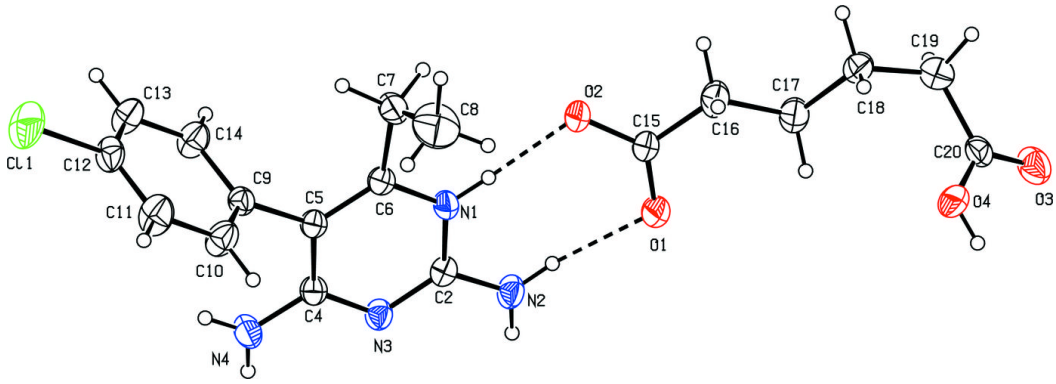
C13
C7
C8
O2
C19
C14
C15
C16
C17
C18
C20
Cl1
C12
C9
C5
C6
N1
O4
O3
C11
O1
C10
C2
N2
C4
N3
N4

Fig. 2

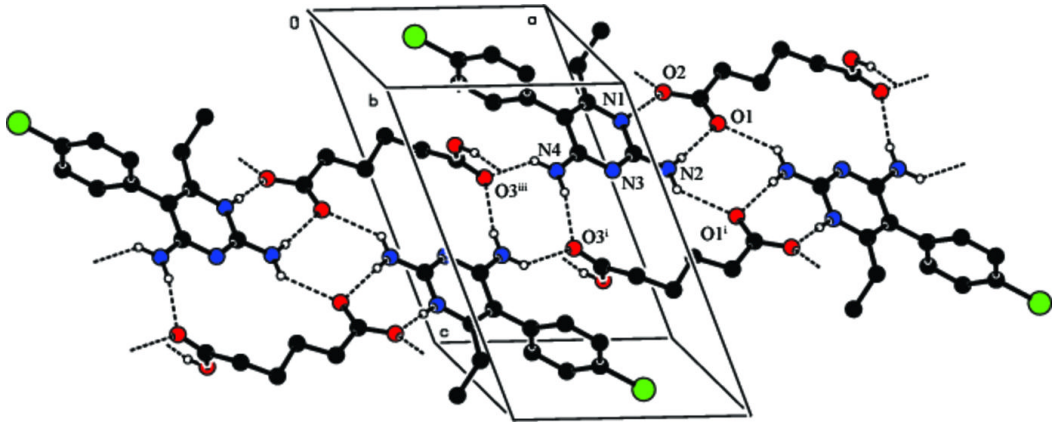

Fig. 3