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The 2:1 salt-type adduct formed between 6-amino-3-methyl-5-nitrosopyrimidine-2,4(1*H*,3*H*)-dione and piperidine: sheets containing 20 independent hydrogen bonds

Fabián Orozco,[a]‡ Braulio Insuasty,[a] Justo Cobo[b] and Christopher Glidewell[c]*

[a]Departamento de Química, Universidad de Valle, AA 25360 Cali, Colombia, [b]Departamento de Química Inorgánica y Orgánica, Universidad de Jaén, 23071 Jaén, Spain, and [c]School of Chemistry, University of St Andrews, Fife KY16 9ST, Scotland
Correspondence e-mail: cg@st-andrews.ac.uk

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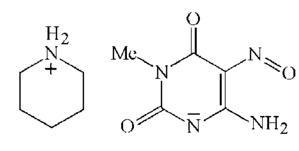
The title compound, piperidinium 6-amino-3-methyl-5-nitroso-2,4-dioxo-1,2,3,4-tetrahydropyrimidin-1-ide 6-amino-3-methyl-5-nitrosopyrimidine-2,4(1*H*,3*H*)-dione, $C_5H_{12}N^+\cdot C_5H_5N_4O_3^-\cdot C_5H_6N_4O_3$, (I), crystallizes with $Z' = 2$ in the space group $P\overline{1}$. There is an intramolecular N—H···O hydrogen bond in each pyrimidine unit and within the selected asymmetric unit the six independent components are linked by 11 hydrogen bonds, seven of the N—H···O type and four of the N—H···N type. These six-component aggregates are linked into sheets by five further hydrogen bonds, three of the N—H···O type and one each of the N—H···N and C—H···O types.

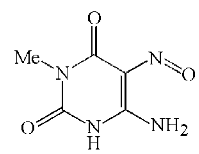
Comment

We report here the structure of the 2:1 adduct, (I), formed between 6-amino-3-methyl-5-nitrosopyrimidine-2,4(1*H*,3*H*)-dione and piperidine, and compare this structure with those of the parent pyrimidinedione, (II) (Godino Salido *et al.*, 2003), and the 1:1 salt, (III), formed with piperidine (Low *et al.*, 1999), and also with those of the hydrated complexes formed with a number of metals (Cuesta *et al.*, 2001; Low *et al.*, 2003; López Garzón *et al.*, 2003*a*,*b*).

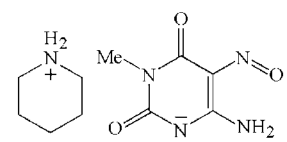
In the course of our development of synthetic routes to 2-substituted 6-amino-5-nitrosopyrimidines for use as intermediates in the synthesis of fused pyrimidine derivatives, we have recently reported examples of the substitution by a variety of amino groups of methoxy (Melguizo *et al.*, 2002) or methylsulfanyl (Orozco *et al.*, 2008) groups at the 2-position in the pyrimidine ring. Such nitrosopyrimidine derivatives often form intramolecular N—H···O hydrogen bonds and are thus interesting purine mimics (Low *et al.*, 2000). We have already introduced the morpholino group at C2 using the reactions of 6-amino-2-methylsulfanyl-5-nitrosopyrimidin-4(3*H*)-ones with morpholine (Orozco *et al.*, 2008), and accordingly we have employed similar reaction conditions with the aim of synthesizing an analogous 6-amino-2-piperidino-5-nitrosopyrimidin-4(3*H*)-one. However, instead of the expected substitution product, the hydrolysis product 6-amino-3-methyl-5-nitrosopyrimidine-2,4(1*H*,3*H*)-dione was formed which crystallized as the 2:1 salt, (I), with piperidine. By contrast, the corresponding reaction using 6-amino-2-methoxy-5-nitrosopyrimidin-4(3*H*)-one and the same molar ratio of piperidine to the pyrimidine gave instead the 1:1 salt, (III) (Low *et al.*, 1999).



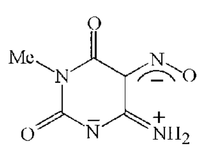
(I)



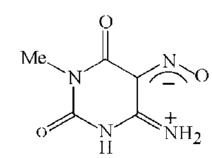
(II)



(III)



(I*a*)



(I*b*)

Compound (I) contains a 1:2 ratio of the piperidine and pyrimidine components and crystallizes with $Z' = 2$ in the space group $P\overline{1}$. Its constitution is that of a salt, in which a proton has been transferred to each of the piperidine units from two of the four pyrimidine units. With six independent molecular entities present in the structure, the selection of the asymmetric unit permits a considerable degree of choice. However, it is possible here to select a fairly compact asymmetric unit (Fig. 1) in which the six components are linked by 11 hydrogen bonds (Table 2), seven of the N—H···O type and four of the N—H···N type, where both piperidinium cations act as donors in three-centre N—H···(O,N) systems.

Within the selected asymmetric unit, there are two dioxopyrimidinide anions, with atom labels of the type N1*x*/C1*x* and N2*x*/C2*x*, and two formally neutral pyrimidinedione units, with atom labels of the type N3*x*/C3*x* and N4*x*/C4*x*. The anions of types 1 and 2 are linked to neutral molecules of types 4 and 3, respectively, *via* three hydrogen bonds. Within each such pair, two antiparallel N—H···O hydrogen bonds are flanked by a central N—H···N hydrogen bond, producing a linkage reminiscent of the three-point recognition between cytosine and

‡ Present address: Departamento de Química, Pontificia Universidad Javeriana, Kr 7 No. 43-82, Bogotá DC, Colombia.

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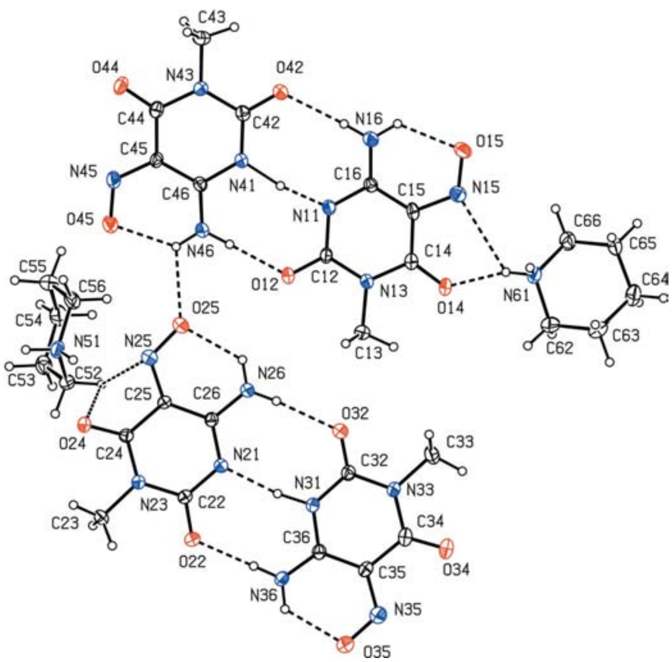

Figure 1
The independent components of compound (I), showing the atom-labelling scheme and the 15 hydrogen bonds (dashed lines) within the selected asymmetric unit. Displacement ellipsoids are drawn at the 30% probability level and H atoms are shown as small spheres of arbitrary radii.

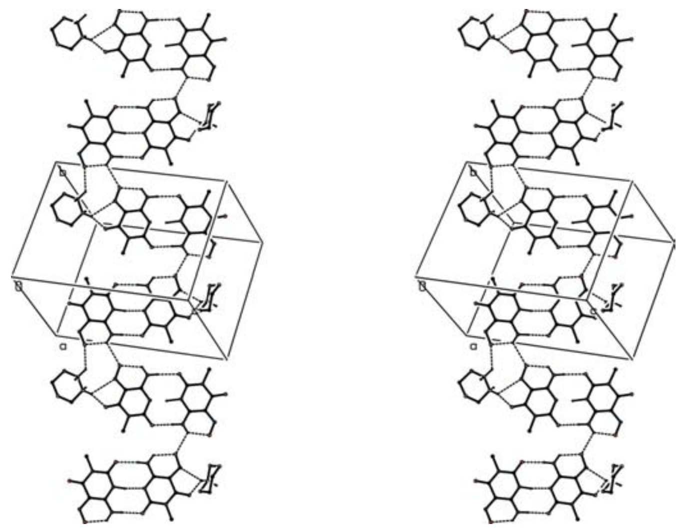

Figure 2
A stereoview of part of the crystal structure of compound (I), showing the formation of a hydrogen-bonded chain running parallel to the [1$\bar{1}$0] direction. For the sake of clarity, H atoms bonded to C atoms which are not involved in the motifs shown have been omitted.

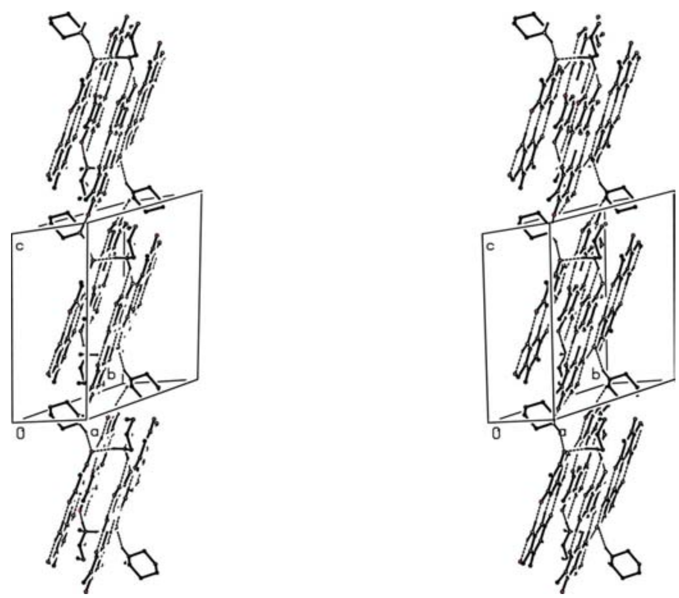

Figure 3
A stereoview of part of the crystal structure of compound (I), showing the formation of a hydrogen-bonded chain running parallel to the [001] direction. For the sake of clarity, H atoms bonded to C atoms have been omitted.

guanine in DNA. However, the N—H···N hydrogen bonds are somewhat unusual in that the bonded N—H distances are quite long, based upon the positions deduced from difference maps for atoms N31 and N41 (Table 2). The interatomic distances within the four pyrimidine units show no systematic differences between those units which are formally neutral and those which are formally anionic (Table 1). It is thus possible that the negative charges are dispersed very widely over the pyrimidine units. On the other hand, all of these components show the pattern of bond lengths typical of 6-amino-5-nitrosopyrimidines, namely having C*x*5—C*x*6 and C*x*6—N*x*6 bonds (where x = 1–4) which are, respectively, long and short for their formal types, and with a rather small difference in lengths between the C*x*5—N*x*5 and N*x*5—O*x*5 bonds, pointing to the importance of polarized forms such as (I*a*) and (I*b*) as contributors to the overall electronic structure.

The planarity of each individual pyrimidine unit may be controlled by the intramolecular N—H···O hydrogen bonds, which give each such unit an overall shape somewhat similar to that of a purine. Each hydrogen-bonded pair of neutral and anionic units is essentially planar, apart from the methyl H atoms, with approximate but noncrystallographic 2/*m* (C_{2h}) symmetry. However, this approximate 2/*m* symmetry is only local, as it is broken by the cations which are linked only to the anionic dioxopyrimidinide units, in each case *via* an asymmetric three-centre N—H···(O,N) hydrogen bond, Moreover, the possibility of any additional crystallographic symmetry is precluded, not only by the location of the cations but also by the different orientations of the two independent cations relative to the adjacent pyrimidine rings (Fig. 1). The dihedral angle between the mean plane of the piperidine ring based on atom N51 and the adjacent pyrimidine ring containing atom N21 is 83.5 (2)°, while the corresponding dihedral angle for the rings containing atoms N61 and N11 is only 19.4 (2)°.

The asymmetric unit (Fig. 1) thus contains four intramolecular hydrogen bonds and 11 intermolecular hydrogen bonds. Five further hydrogen bonds, three of the N—H···O type and one each of the N—H···N and C—H···O types, link the six-component aggregates into sheets, the formation of which is readily analysed in terms of two one-dimensional substructures. In the simpler of the two substructures, atoms

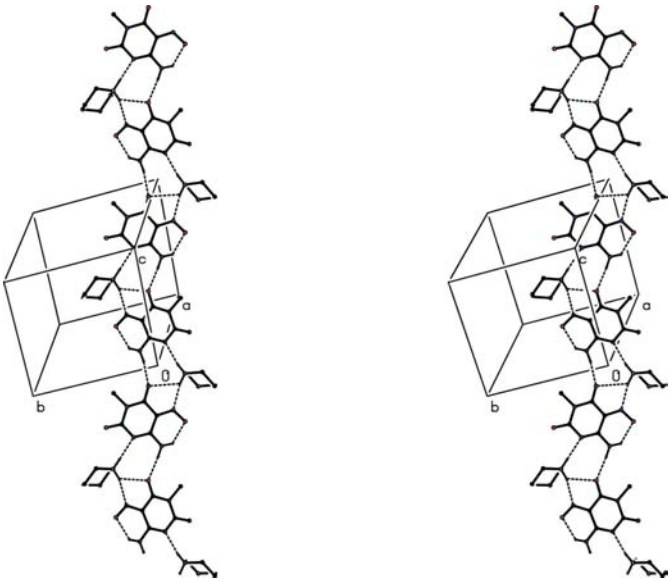

Figure 4
A stereoview of part of the crystal structure of compound (III) (Low *et al.*, 1999), showing the formation of a hydrogen-bonded chain running parallel to [101]. The original atomic coordinates have been employed and, for the sake of clarity, H atoms bonded to C atoms have been omitted.

N36 and C66 at (x, y, z) act as hydrogen-bond donors to, respectively, atom O15 at ($1+x$, $-1+y$, z) and O35 at ($-1+x$, $1+y$, z), so forming a complex chain running parallel to the [1$\overline{1}$0] direction (Fig. 2). Accordingly, atom N36 acts as donor in the three-centre N—H$\cdots$(O)$_2$ system, the longer component of which acts as the principal chain-forming interaction, just as atom N46 acts as donor in a similar three-centre interaction which links the two independent cation–anion–neutral aggregates within the asymmetric unit (Table 2 and Fig. 1). In the second substructure, atoms N51 and N61 at (x, y, z) act as hydrogen-bond donors to, respectively, atoms O44 and N45 at ($1-x$, $1-y$, $2-z$) and atom O24 at ($1-x$, $1-y$, $1-z$), so forming a complex chain of rings running parallel to the [001] direction (Fig. 3). The combination of chains along [001] and [1$\overline{1}$0] suffices to generate a sheet lying parallel to (110).

The two-dimensional hydrogen-bonded structure of salt (I) may be contrasted both with the three-dimensional hydrogen-bonded structure found in the neutral pyrimidinedione, (II), which is built from only three intermolecular hydrogen bonds (Godino Salido *et al.*, 2003), and with the one-dimensional aggregation in the 1:1 salt, (III) (Low *et al.*, 1999). Compound (III), like compound (I), crystallizes in the space group $P\overline{1}$, and a combination of four N—H$\cdots$O hydrogen bonds and four N—H$\cdots$N hydrogen bonds links the ionic components into a chain running parallel to the [101] direction (Fig. 4). Antiparallel pairs of such chains, related to one another by inversion, are linked by a single C—H$\cdots$O hydrogen bond to form a tube-like structure. Thus, the hydrogen-bonded structures of the closely related compounds (I)–(III) are, respectively, two-, three- and one-dimensional, with no straightforward correlation between the dimensionality of the overall structure and the number of hydrogen bonds formed per molecular entity.

Similar structural variation is also observed in the hydrated metal complexes derived from compound (II). The Zn derivative contains a monomeric complex (López Garzón *et al.*, 2003*b*), the Sr derivative contains a dimeric complex which is centrosymmtric (Low *et al.*, 2003), while the Na and Ba derivatives both contain one-dimensional coordination polymers, taking the form of a simple chain in the Ba compound (López Garzón *et al.*, 2003*a*) and a molecular ladder containing two types of rings between the uprights in the Na derivative (Cuesta *et al.*, 2001). However, a structural feature shared by all of these metal derivatives is the linking of the metal-containing units into three-dimensional frameworks by extensive series of hydrogen bonds.

Experimental

Piperidine (100 mmol) was added dropwise with stirring to a suspension of 6-amino-3-methyl-2-methylsulfanyl-5-nitrosopyrimidin-4(3*H*)-one (25 mmol) in methanol (80 ml). The reaction proceeded overnight with a change of colour from blue to violet and liberation of methanethiol. The resulting precipitate was collected by filtration and washed with cold methanol, yielding 3.51 g of a solid which was recrystallized from dimethylformamide–ethanol (10:1 *v*/*v*) to give red–violet crystals of (I) suitable for single-crystal X-ray diffraction.

Crystal data

$C_5H_{12}N^+\cdot C_5H_5N_4O_3^-\cdot C_5H_6N_4O_3$	$\gamma = 89.987\ (16)^\circ$
$M_r = 425.42$	$V = 1917.2\ (5)$ Å^3
Triclinic, $P\overline{1}$	$Z = 4$
$a = 9.3287\ (19)$ Å	Mo $K\alpha$ radiation
$b = 13.1352\ (10)$ Å	$\mu = 0.12$ mm^{-1}
$c = 16.2814\ (19)$ Å	$T = 120$ K
$\alpha = 87.815\ (10)^\circ$	$0.41 \times 0.25 \times 0.22$ mm
$\beta = 74.095\ (10)^\circ$	

Data collection

Bruker–Nonius KappaCCD area-detector diffractometer	44265 measured reflections
Absorption correction: multi-scan (*SADABS*; Sheldrick, 2003)	8768 independent reflections
$T_{min} = 0.922$, $T_{max} = 0.975$	3414 reflections with $I > 2\sigma(I)$
	$R_{int} = 0.107$

Refinement

$R[F^2 > 2\sigma(F^2)] = 0.069$	545 parameters
$wR(F^2) = 0.216$	H-atom parameters constrained
$S = 1.02$	$\Delta\rho_{max} = 0.54$ e Å^{-3}
8768 reflections	$\Delta\rho_{min} = -0.41$ e Å^{-3}

All H atoms were located in difference maps and then treated as riding. Apart from atom H31, lying between atoms N21 and N31, and atom H41, lying between atoms N11 and N41, the H atoms were allowed to ride in geometrically idealized positions, with C—H = 0.98 (CH_3) or 0.99 Å (CH_2) and N—H = 0.88 (planar N) or 0.92 Å (tetrahedral N), and with $U_{iso}(H) = kU_{eq}$(carrier), where $k = 1.5$ for the methyl groups, which were allowed to rotate but not to tilt, and 1.2 for the other H atoms. Atoms H31 and H41 were permitted to ride at the positions deduced from the difference maps, with $U_{iso}(H) = 1.2U_{eq}(N)$, giving the N—H distances listed in Table 2.

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*

Table 1
Selected bond lengths (Å).

N11—C12	1.376 (5)	N31—C32	1.373 (5)
C12—N13	1.372 (4)	C32—N33	1.371 (5)
N13—C14	1.390 (5)	N33—C34	1.404 (5)
C14—C15	1.439 (5)	C34—C35	1.454 (5)
C15—C16	1.427 (5)	C35—C36	1.417 (5)
C16—N11	1.352 (4)	C36—N31	1.358 (5)
C12—O12	1.229 (4)	C32—O32	1.221 (4)
C14—O14	1.226 (4)	C34—O34	1.214 (4)
C15—N15	1.368 (5)	C35—N35	1.361 (5)
N15—O15	1.267 (4)	N35—O35	1.261 (4)
C16—N16	1.311 (5)	C36—N36	1.311 (4)
N21—C22	1.356 (5)	N41—C42	1.360 (5)
C22—N23	1.397 (4)	C42—N43	1.396 (5)
N23—C24	1.376 (5)	N43—C44	1.399 (5)
C24—C25	1.444 (5)	C44—C45	1.450 (5)
C25—C26	1.428 (5)	C45—C46	1.419 (5)
C26—N21	1.348 (4)	C46—N41	1.356 (4)
C22—O22	1.245 (4)	C42—O42	1.233 (4)
C24—O24	1.242 (4)	C44—O44	1.222 (4)
C25—N25	1.347 (5)	C45—N45	1.349 (5)
N25—O25	1.277 (4)	N45—O45	1.275 (4)
C26—N26	1.322 (4)	C46—N46	1.318 (5)

(Sheldrick, 2008); molecular graphics: *PLATON* (Spek, 2009); software used to prepare material for publication: *SHELXL97* and *PLATON*.

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Supplementary data for this paper are available from the IUCr electronic archives (Reference: GG3200). Services for accessing these data are described at the back of the journal.

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

D—H$\cdots A$	D—H	H$\cdots A$	$D\cdots A$	D—H$\cdots A$
N31—H31···N21	1.05	1.80	2.842 (4)	172
N41—H41···N11	1.32	1.52	2.829 (4)	171
N16—H161···O42	0.88	2.02	2.899 (4)	176
N16—H162···O15	0.88	2.01	2.637 (4)	128
N26—H261···O32	0.88	2.02	2.893 (4)	175
N26—H262···O25	0.88	2.01	2.650 (4)	128
N36—H361···O22	0.88	1.90	2.786 (4)	178
N36—H362···O35	0.88	1.99	2.614 (4)	126
N36—H362···O15^{i}	0.88	2.42	2.940 (4)	118
N46—H461···O12	0.88	1.89	2.768 (4)	177
N46—H462···O45	0.88	1.98	2.620 (5)	128
N46—H462···O25	0.88	2.26	2.793 (4)	119
N51—H511···O24	0.92	2.12	2.872 (4)	138
N51—H511···N25	0.92	2.36	3.114 (4)	139
N51—H512···O44^{ii}	0.92	2.11	2.941 (5)	150
N51—H512···N45^{ii}	0.92	2.33	3.052 (5)	135
N61—H611···O14	0.92	1.83	2.706 (4)	159
N61—H611···N15	0.92	2.61	3.204 (5)	123
N61—H612···O24^{iii}	0.92	1.92	2.812 (4)	163
C66—H66*A*···O35^{iv}	0.99	2.29	3.033 (6)	131

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

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