Acta Crystallographica Section C
Crystal Structure Communications
ISSN 0108-2701

N-(6-Amino-3,4-dihydro-3-methyl-5-nitroso-4-oxopyrimidin-2-yl)-(*S*)-glutamic acid: a three-dimensional framework structure built from O—H···O, N—H···O and O—H···N hydrogen bonds

Paloma Arranz Mascarós,[a] M. Dolores Gutiérrez Valero,[a] John N. Low[b]† and Christopher Glidewell[c]*

[a]Departamento de Química Inorgánica y Orgánica, Universidad de Jaén, 23071 Jaén, Spain, [b]Department of Chemistry, University of Aberdeen, Meston Walk, Old Aberdeen AB24 3UE, Scotland, and [c]School of Chemistry, University of St Andrews, St Andrews, Fife KY16 9ST, Scotland
Correspondence e-mail: cg@st-andrews.ac.uk

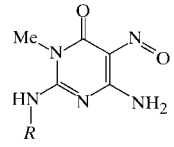
Received 10 March 2003
Accepted 12 March 2003
Online 31 March 2003

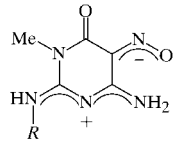
The title compound, $C_{10}H_{13}N_5O_6$, exhibits a highly polarized molecular–electronic structure and the conformation is influenced by two intramolecular N—H···O hydrogen bonds. The molecules are linked into a single framework by hydrogen bonds of types O—H···O [O—H = 1.22, H···O = 1.38, O···O = 2.558 (6) Å and O—H···O = 160°], N—H···O [H···O = 2.26, N···O = 2.866 (6) Å and N—H···O = 126°] and O—H···N [O—H = 1.26, H···N = 1.56, O···N = 2.811 (6) Å and O—H···N = 170°]. The substructure generated by the O—H···O and N—H···O hydrogen bonds takes the form of a double helix.

Comment

The neutral *N*-(6-amino-3,4-dihydro-3-methyl-5-nitroso-4-oxopyrimidin-2-yl) derivatives of the amino acids glycine, valine, serine, threonine and methionine, (I)–(V), all exhibit highly polarized molecular–electronic structures and supramolecular structures that are characterized by the formation of extremely short O—H···O hydrogen bonds (Low *et al.*, 2000). In each compound, the carboxyl group provides the donor and the O atom of the nitroso group provides the acceptor in the short hydrogen bond, where the O···O distance is generally less than 2.50 Å. By contrast, in the analogue (VI), derived from glycylglycine (Low *et al.*, 2002), there are no O—H···O hydrogen bonds at all, but instead the nitroso group acts as an acceptor of both N—H···O and O—H···N intermolecular hydrogen bonds, in which the donors are the peptide N—H and carboxyl groups, respectively.

Continuing our structural investigation of compounds of this type, we have now extended this study to encompass a derivative, (VII) (Fig. 1), of the dicarboxylic amino acid (*S*)-glutamic acid [(*S*)-(+)-2-aminopentane-1,5-dioic acid, $C_5H_9NO_4$]. We report here on the polarized molecular–electronic structure and the three-dimensional supramolecular structure of (VII).





(VII*a*)

(I) *R* = $CH_2COOH_2{\cdot}H_2O$
(II) *R* = $CH(COOH)CH_2CH_2SMe$
(III) *R* = $CH(COOH)CHMe_2$
(IV) *R* = $CH(COOH)CH_2OH{\cdot}H_2O$
(V) *R* = $CH(COOH)CH(OH)Me$
(VI) *R* = $CH_2CONHCH_2COOH$
(VII) *R* = $CH(COOH)CH_2CH_2COOH$

The intramolecular distances associated with the heterocyclic ring and its immediate substituents (Table 1) show the general pattern of behaviour now expected for aminonitrosopyrimidines of this type, but the polarization appears from the individual bond distances to be less extreme than that observed in the derivatives of the monocarboxylic amino acids (I)–(V). The distances in (VII) are, however, very similar to those in the glycylglycine derivative, (VI). Overall the intramolecular distances indicate that the polarized form, (VII*a*), is an important contributor to the molecular–electronic structure.

Within the molecule of (VII) there are two intramolecular N—H···O hydrogen bonds (Table 2). In addition to the usual intramolecular hydrogen bond, which has the nitroso O atom as acceptor, there is a second such bond between atoms N2 and O23, which probably influences the overall molecular conformation. In the absence of this hydrogen bond, a chain-extended conformation might have been expected for the glutamic fragment.

The formation of the three-dimensional supramolecular structure depends on just three intermolecular hydrogen bonds, one each of types O—H···O, N—H···O and O—H···N (Table 2), and the supramolecular structure is most readily analysed by considering the effect of each of these hydrogen bonds in turn. Note the absence from (VII) of both of the hydrogen-bond motifs that are so characteristic of simple carboxylic acids, *viz*. $R_2^2(8)$ dimer-forming rings and $C(4)$ chains.

Carboxyl atom O24 in the molecule at (x, y, z) acts as hydrogen-bond donor to nitrosyl atom O5 in the molecule at ($1-x$, $1-y$, $-1+z$), while O24 at ($1-x$, $1-y$, $-1+z$) in turn acts as donor to O5 at (x, y, $-2+z$), so producing a helical $C(13)$ chain running parallel to the [001] direction (Fig. 2). The repeat period of this helix means that there are in fact two such chains, which form a double helix and which are

† Postal address: Department of Electrical Engineering and Physics, University of Dundee, Dundee DD1 4HN, Scotland.

  DOI: 10.1107/S0108270103005754

related to one another by the twofold rotation axis along $(\frac{1}{2}, \frac{1}{2}, z)$ (Fig. 3). The paired helices are linked by intermolecular N—H···O hydrogen bonds. Amino atom N4 in the molecule at (x, y, z) acts as hydrogen-bond donor, *via* H4*A*, to carboxyl atom O23 in the molecule at $(x, y, 1 + z)$. Since the molecules at (x, y, z) and $(x, y, 1 + z)$ lie in different $C(13)$ helices, this interaction serves to link together the two chains of the double helix. Two double helices of this type run through each unit cell, along the axes at $(0, 0, z)$ and $(\frac{1}{2}, \frac{1}{2}, z)$, and the helices are all linked into a single continuum by the action of the O—H···N hydrogen bond.

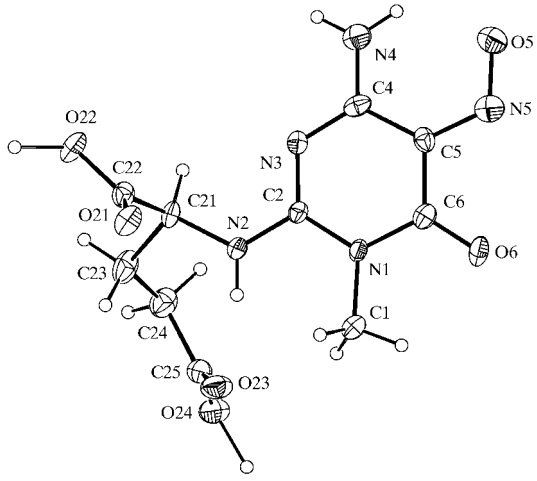


Figure 1
The molecular structure of (VII), showing the atom-labelling scheme. Displacement ellipsoids are drawn at the 30% probability level.

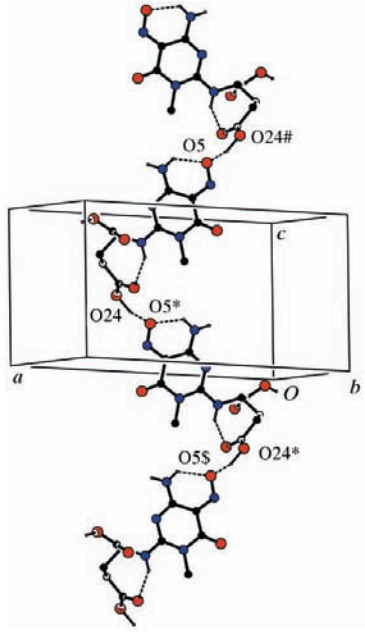


Figure 2
Part of the crystal structure of (VII), showing the formation of a $C(13)$ chain along [001]. For the sake of clarity, H atoms bonded to C atoms have been omitted. Atoms marked with an asterisk (*), hash (#) or dollar sign ($) are at the symmetry positions $(1 - x, 1 - y, 1 + z)$, $(1 - x, 1 - y, 1 + z)$ and $(x, y, 2 + z)$, respectively.

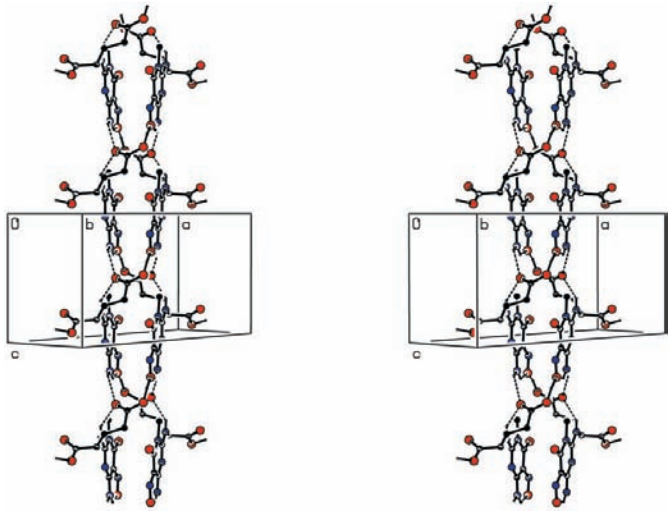


Figure 3
A stereoview of part of the crystal structure of (VII), showing the formation of a double helix around the $(\frac{1}{2}, \frac{1}{2}, z)$ axis. For the sake of clarity, H atoms bonded to C atoms have been omitted.

Carboxyl atom O22 in the molecule at (x, y, z) lies in the double helix along $(\frac{1}{2}, \frac{1}{2}, z)$ and acts as hydrogen-bond donor to nitroso atom N5, which is in the molecule at $(\frac{1}{2} + x, \frac{3}{2} - y, 2 - z)$ and lies in the double helix along $(1, 1, z)$. Nitroso atom N5 at (x, y, z) similarly accepts a hydrogen bond from O22, which is in the molecule at $(-\frac{1}{2} + x, \frac{3}{2} - y, 2 - z)$ and lies in the double helix along $(0, 1, z)$. Propagation of this hydrogen bond by the twofold axis links the $(\frac{1}{2}, \frac{1}{2}, z)$ helix to those along $(0, 0, z)$ and $(1, 0, z)$; hence each double helix is linked to the four adjacent helices (Fig. 4), so generating a single three-dimensional framework.

In the O—H···O hydrogen bond in (VII), the O···O distance is greater than those in (I)–(V), and this fact may be readily associated with the lesser polarization of the molecular–electronic structure in (VII). On the other hand, (VII)

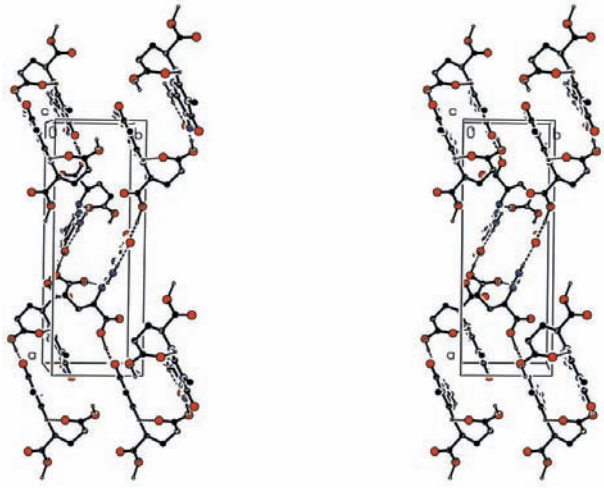


Figure 4
A stereoview of part of the crystal structure of (VII), showing the linking of the double helix into a three-dimensional framework. For the sake of clarity, H atoms bonded to C atoms have been omitted.

exhibits an O—H···N(nitroso) hydrogen bond, which has previously been observed in this series only in (VI). The presence of additional hydrogen-bonding functionality in the side chain *R* of compounds of this type may yet provide further unexpected patterns in the supramolecular aggregation.

Experimental

The title compound was prepared by adding 6-amino-3,4-dihydro-3-methyl-2-methoxy-5-nitroso-4-oxopyrimidine (2.66 mmol) to a solution of the potassium salt of (*S*)-glutamic acid (2.66 mmol) in methanol (40 ml). The mixture was stirred at 293 K for 2 d. After removal of the solvent, the residue was dissolved in distilled water and the pH was adjusted to 2.15 by dropwise addition of hydrochloric acid. Slow evaporation of this solution provided crystals suitable for single-crystal X-ray diffraction. Analysis found: C 40.6, H 5.1, N 24.1%; $C_{10}H_{13}N_5O_6$ requires: C 40.1, H 4.4, N 23.4%.

Crystal data

$C_{10}H_{13}N_5O_6$
M_r = 299.25
Orthorhombic, $P2_12_12$
a = 19.4182 (10) Å
b = 6.9420 (10) Å
c = 9.0534 (10) Å
V = 1220.4 (2) Å^3
Z = 4
D_x = 1.629 Mg m^{-3}
Mo $K\alpha$ radiation
Cell parameters from 1614 reflections
θ = 3.1–27.4°
μ = 0.14 mm^{-1}
T = 120 (2) K
Plate, orange
0.56 × 0.32 × 0.03 mm

Data collection

Nonius KappaCCD diffractometer
φ scans, and ω scans with κ offsets
Absorption correction: multi-scan (*DENZO–SMN*; Otwinowski & Minor, 1997)
T_{min} = 0.925, T_{max} = 0.996
13 181 measured reflections
1614 independent reflections
881 reflections with $I > 2\sigma(I)$
R_{int} = 0.140
θ_{max} = 27.4°
$h = -24 \rightarrow 25$
$k = -8 \rightarrow 8$
$l = -11 \rightarrow 11$

Refinement

Refinement on F^2
$R[F^2 > 2\sigma(F^2)]$ = 0.057
$wR(F^2)$ = 0.153
S = 0.99
1614 reflections
191 parameters
H-atom parameters constrained
$w = 1/[\sigma^2(F_o^2) + (0.0816P)^2]$ where $P = (F_o^2 + 2F_c^2)/3$
$(\Delta/\sigma)_{max}$ = 0.002
$\Delta\rho_{max}$ = 0.37 e Å^{-3}
$\Delta\rho_{min}$ = −0.30 e Å^{-3}

Table 1
Selected geometric parameters (Å, °).

N1—C2	1.370 (6)	N1—C1	1.461 (7)
C2—N3	1.318 (6)	C2—N2	1.320 (6)
N3—C4	1.317 (7)	C4—N4	1.315 (7)
C4—C5	1.450 (7)	C5—N5	1.345 (7)
C5—C6	1.442 (7)	N5—O5	1.279 (6)
C6—N1	1.391 (7)	C6—O6	1.230 (6)
N1—C2—N2—C21	−177.3 (4)	C2—N2—C21—C22	−96.6 (5)
C2—N2—C21—C23	145.0 (5)	N2—C21—C22—O21	−19.9 (7)
N2—C21—C23—C24	−50.4 (7)	C23—C24—C25—O23	−21.4 (8)
C21—C23—C24—C25	87.6 (7)	C4—C5—N5—O5	4.8 (8)

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

D—H···A	D—H	H···A	D···A	D—H···A
N2—H2···O23	0.88	2.09	2.779 (6)	134
N4—H4B···O5	0.88	1.97	2.617 (6)	129
O24—H24···O5^{i}	1.22	1.38	2.558 (6)	160
N4—H4A···O23^{ii}	0.88	2.26	2.866 (6)	126
O22—H22···N5^{iii}	1.26	1.56	2.811 (6)	170

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

Crystals of (VII) are orthorhombic and the space group $P2_12_12$ was uniquely assigned from the systematic absences. H atoms bonded to C and N atoms were treated as riding, with C—H distances of 0.98 (CH_3), 0.99 (CH_2) or 1.00 Å (CH) and N—H distances of 0.88 Å. H atoms bonded to O atoms were located from difference maps and allowed to ride at the distances deduced from the maps. In the absence of any significant anomalous scattering, the Flack (1983) parameter was indeterminate (Flack & Bernardinelli, 2000). Hence the Friedel equivalents were merged and the absolute structure was set by reference to the known configuration of the (*S*)-glutamic acid employed in the synthesis.

Data collection: *KappaCCD Server Software* (Nonius, 1997); cell refinement: *DENZO–SMN* (Otwinowski & Minor, 1997); data reduction: *DENZO–SMN*; program(s) used to solve structure: *SHELXS*97 (Sheldrick, 1997); program(s) used to refine structure: *SHELXL*97 (Sheldrick, 1997); molecular graphics: *PLATON* (Spek, 2003); software used to prepare material for publication: *SHELXL*97 and *PRPKAPPA* (Ferguson, 1999).

X-ray data were collected at the EPSRC X-ray Crystallographic Service, University of Southampton, England; the authors thank the staff for all their help and advice. JNL thanks NCR Self-Service, Dundee, for grants that have provided computing facilities for this work.

Supplementary data for this paper are available from the IUCr electronic archives (Reference: SK1626). Services for accessing these data are described at the back of the journal.

References

Ferguson, G. (1999). *PRPKAPPA*. University of Guelph, Canada.
Flack, H. D. (1983). *Acta Cryst.* A**39**, 876–881.
Flack, H. D. & Bernardinelli, G. (2000). *J. Appl. Cryst.* **33**, 1143–1148.
Low, J. N., López, M. D., Arranz Mascarós, P., Cobo Domingo, J., Godino, M. L., López Garzon, R., Gutiérrez, M. D., Melguizo, M., Ferguson, G. & Glidewell, C. (2000). *Acta Cryst.* B**56**, 882–892.
Low, J. N., Quesada, A., Glidewell, C., Fontecha, M. A., Arranz, P., Godino, M. L. & López, R. (2002). *Acta Cryst.* E**58**, o942–o945.
Nonius (1997). *KappaCCD Server Software*. Windows 3.11 Version. Nonius BV, Delft, The Netherlands.
Otwinowski, Z. & Minor, W. (1997). *Methods in Enzymology*, Vol. 276, *Macromolecular Crystallography*, Part A, edited by C. W. Carter Jr & R. M. Sweet, pp. 307–326. New York: Academic Press.
Sheldrick, G. M. (1997). *SHELXS*97 and *SHELXL*97. University of Göttingen, Germany.
Spek, A. L. (2003). *J. Appl. Cryst.* **36**, 7–13.