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#### Key indicators

Single-crystal X-ray study T = 293 K Mean  $\sigma$ (C–C) = 0.010 Å R factor = 0.070 wR factor = 0.218 Data-to-parameter ratio = 7.1

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

# L-Argininium dinitrate

In the title compound,  $C_6H_{16}N_4O_2^{2+}\cdot 2NO_3^{-}$ , the diprotonated argininium molecule is linked by a strong  $O-H\cdots O$  [2.653 (7) Å] hydrogen bond to the nitrate anion. The single-bonded O atom of the carboxyl group exhibits a very unusual *cis* conformation with respect to the  $\alpha$ -amino N atom. Chelated three-centered hydrogen bonds are observed in the case of the N<sup> $\alpha$ </sup> and N<sup> $\varepsilon$ </sup> atoms with the nitrate anions. The argininium molecules are connected by type *A*, *B* and *D* interactions through nitrate anions.

## Comment

L-Arginine is one of the essential amino acids widely distributed in biological substances. L-Arginine phosphate monohydrate is found to exhibit interesting non-linear optical properties (Jiang *et al.*, 1983). The strong basicity of the guanidyl group is responsible for the functions in living matter (Aoki *et al.*, 1971). The crystal structures of L-arginine dihydrate (Karle & Karle, 1964), L-arginine hydrochloride monohydrate (Dow *et al.*, 1970), L-arginine phosphate monohydrate (Aoki *et al.*, 1971). L-arginine perchlorate (Monaco *et al.*, 1987; Srinivasan & Rajaram, 1997) and L-arginine diarsenate (Zalkin *et al.*, 1989) have been reported. In the present study, the crystal structure of L-arginine dinitrate, (I), was undertaken to study conformational aspects.



The conformation of the arginine molecule may be characterized by three planar groups: (i) the carboxyl group, (ii) the side chain C atoms consisting of the  $\alpha$ -,  $\beta$ -,  $\gamma$ - and  $\delta$ -carbon (C12, C13, C14 and C15) and (iii) the guanidyl group including the  $\delta$ -C atom (C15, N4, C16, N5 and N6) (Aoki *et al.*, 1971). The conformation of the single-bonded carboxyl O atom is *cis* with respect to the amino N atom [-29.7 (10)°] for the diprotonated argininium molecule. In general, this conformation is found to be *trans*, whereas the present structure is different from earlier studies, *viz*. L-valine hydrochloride (Koetzle *et al.*, 1974), DL-valine hydrochloride (Di Blasio *et al.*, 1977), L-arginine diarsenate (Zalkin *et al.*, 1989), bis(DL-methioninium) sulfate (Srinivasan *et al.*, 2001), tri(L-isoleuci-

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### Figure 1

The molecular structure of the diprotonated argininium cation showing the atomic numbering scheme and 50% probability displacement ellipsoids (Johnson, 1976).

nium) sulfate bisulfate (Sridhar et al., 2001) and L-valine Lvalinium perchlorate monohydrate (Pandiarajan et al., 2001).

The side-chain conformation angle  $\chi^1$  has a *gauche* II form  $[-62.5 (8)^{\circ}]$ , while  $\chi^2$  and  $\chi^3$  are in the *trans* form [-168.6 (6)and 178.0  $(6)^{\circ}$ ] for the argininium molecule (Fig. 1). The other conformation angle, which has the guanidyl group at the end of the residue,  $\chi^4$  [-92.9 (10)°], is as expected and  $\chi^{51}$  and  $\chi^{52}$ are 6.6 (14) and -172.6 (8)°, respectively. These conformational angles are very similar to those on L-arginine diarsenate, except for  $\chi^4$  which is 148.8°. The argininium molecule, in the present study, is in a slightly folded conformation.

The guanidyl group is protonated and exists as a guanidinium ion. The three C-N bonds in this group are nearly equal in length with an average value of 1.313 (9) Å. The three N-C-N angles are very close to 120°, confirming the planarity of the guanidyl group. Like other arginine molecules, the C15 atom is only slightly displaced [0.15 (2) Å] from the plane of the guanidyl group. The two crystallographically independent nitrate anions have similar geometries.

The carboxyl O atom of the diprotonated argininium cation is linked through a strong  $O-H \cdots O$  hydrogen bond [2.653(7) Å] with the nitrate anion (Table 2), while the amino-N and the N atoms of the guanidyl group are linked through normal hydrogen bonds with the two nitrate anions.

Chelated three-centered hydrogen bonds are observed in the case of the N<sup> $\alpha$ </sup> and N<sup> $\varepsilon$ </sup> atoms (N3–H3C···O5<sup>ii</sup> and N3– H3C···O4<sup>ii</sup>, and N4-H4···O3<sup>iii</sup> and N4-H4···O2<sup>iii</sup>; Jeffrey & Saenger, 1991). The O atom (O2) of the nitrate anion links the carboxyl O atom (O1*B*),  $N^{\varepsilon}$  and  $N^{\eta 1}$  (N5) through a chain along the c axis. The O atoms of the second nitrate anion (O5 and O4) link the  $\alpha$ -amino N atom and N<sup> $\eta$ 2</sup> (N6) through a chain along the *a* axis. The intermolecular guanidyl-nitrate interactions are observed as (i) type D between N atoms  $\varepsilon$ ,  $\eta 1$ with O2; (ii) type A between N atoms  $\eta 1$ ,  $\eta 2$  with O3 and O1 and (iii) type B between N atoms  $\varepsilon$ ,  $\eta 1$  with O3 and O2 of the nitrate anions (Salunke & Vijayan, 1981). An intermolecular short contact of 2.903 (12) Å is observed between O4 and the carboxyl C11 $(1 - x, \frac{1}{2} + y, 1 - z)$  atom.

# **Experimental**

The title compound was crystallized in aqueous solution from a 1:2 stoichiometric ratio of L-arginine and nitric acid. Colorless needleshaped crystals were grown.

#### Crystal data

-	
$C_6H_{16}N_4O_2^{2+}\cdot 2NO_3^{-}$ $M_r = 300.25$	$D_m$ measured by flotation in a mixture of carbon tetrachloride
Monoclinic, P2 <sub>1</sub>	and xylene
a = 7.744(5) Å	Cu $K\alpha$ radiation
b = 7.284(5) Å	Cell parameters from 25
c = 11.653 (5)  Å	reflections
$\beta = 92.600 \ (5)^{\circ}$	$\theta = 14.9 - 26.9^{\circ}$
$V = 656.6 (7) \text{ Å}^3$	$\mu = 1.22 \text{ mm}^{-1}$
Z = 2	T = 293 (2)  K
$D_x = 1.519 \text{ Mg m}^{-3}$	Needle, colorless
$D_m = 1.519 \text{ Mg m}^{-3}$	$0.03 \times 0.02 \times 0.01 \text{ mm}$

1213 reflections with  $I > 2\sigma(I)$ 

 $\theta_{\rm max} = 68.0^{\circ}$  $h = -9 \rightarrow 9$ 

 $k = 0 \rightarrow 8$ 

 $l = 0 \rightarrow 14$ 

3 standard reflections

frequency: 60 min intensity decay: none

### Data collection

Enraf–Nonius sealed-tube				
diffractometer				
$\omega$ –2 $\theta$ scans				
Absorption correction: $\psi$ scan				
(North et al., 1968)				
$T_{\min} = 0.967, \ T_{\max} = 0.984$				
1284 measured reflections				
1284 independent reflections				

#### Refinement

Refinement on $F^2$	H-atom parameters constrained
$R[F^2 > 2\sigma(F^2)] = 0.070$	$w = 1/[\sigma^2 (F_o^2) + (0.2P)^2]$
$wR(F^2) = 0.218$	where $P = (F_o^2 + 2F_c^2)/3$
S = 1.08	$(\Delta/\sigma)_{\rm max} < 0.001$
1284 reflections	$\Delta \rho_{\rm max} = 0.35 \ {\rm e} \ {\rm \AA}^{-3}$
181 parameters	$\Delta \rho_{\rm min} = -0.44 \text{ e} \text{ Å}^{-3}$

## Table 1

Selected geometric parameters (Å, °).

1.201 (9)	C16-N6	1.308 (9)
1.320 (8)	C16-N5	1.336 (9)
1.296 (9)		
122.5 (6)	N6-C16-N5	118.0 (6)
119.4 (6)		
-29.7(10)	C14-C15-N4-C16	-92.9 (10)
-62.5 (8)	C15-N4-C16-N6	6.6 (14)
-168.6(6)	C15-N4-C16-N5	-172.6(8)
178.0 (6)		
	$\begin{array}{c} 1.201 \ (9) \\ 1.320 \ (8) \\ 1.296 \ (9) \\ 122.5 \ (6) \\ 119.4 \ (6) \\ -29.7 \ (10) \\ -62.5 \ (8) \\ -168.6 \ (6) \\ 178.0 \ (6) \end{array}$	

# Table 2

Hydrogen-bonding geometry (Å, °).

$D - H \cdot \cdot \cdot A$	D-H	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - H \cdot \cdot \cdot A$
$O1B - H1B \cdots O2^{i}$	0.82	1.85	2.653 (7)	166
$N3-H3A\cdots O1$	0.89	2.08	2.950 (8)	165
$N3-H3B\cdots O5$	0.89	1.94	2.823 (9)	170
$N3-H3C \cdot \cdot \cdot O5^{ii}$	0.89	2.00	2.855 (9)	161
N3-H3C···O4 <sup>ii</sup>	0.89	2.49	3.212 (9)	139
N4-H4···O3 <sup>iii</sup>	0.86	2.22	3.010 (8)	153
$N4-H4\cdots O2^{iii}$	0.86	2.36	3.138 (8)	151
N5-H5 $A$ ···O2 <sup>iii</sup>	0.86	2.34	3.086 (9)	146
$N5-H5B\cdotsO1^{iv}$	0.86	2.17	3.022 (8)	173
$N6-H6A\cdots O4^{v}$	0.86	2.18	2.998 (9)	158
N6-H6 $B$ ···O3 <sup>iv</sup>	0.86	2.10	2.957 (9)	177

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

Data collection: *CAD-4 Software* (Enraf–Nonius, 1989); cell refinement: *CAD-4 Software*; data reduction: *CAD-4 Software*; program(s) used to solve structure: *SHELXS*97 (Sheldrick, 1997); program(s) used to refine structure: *SHELXL*97 (Sheldrick, 1997); molecular graphics: *PLATON* (Spek, 1999); software used to prepare material for publication: *SHELXL*97.

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