*Refinement*

Refinement on $F^2$
$R[F^2 > 2\sigma(F^2)] = 0.056$
$wR(F^2) = 0.162$
$S = 1.068$
2117 reflections
80 parameters
H atoms: see below
$w = 1/[\sigma^2(F_o^2) + (0.0955P)^2 + 0.346P]$ where $P = (F_o^2 + 2F_c^2)/3$
$(\Delta/\sigma)_{max} = 0.001$
$\Delta\rho_{max} = 0.355$ e Å$^{-3}$
$\Delta\rho_{min} = -0.201$ e Å$^{-3}$
Extinction correction: *SHELXL*96
Extinction coefficient: 0.014 (4)
Scattering factors from *International Tables for Crystallography* (Vol. C)

Table 1. *Fractional atomic coordinates and equivalent isotropic displacement parameters* (Å$^2$)

$U_{eq} = (1/3)\Sigma_i\Sigma_j U^{ij} a_i^* a_j^* \mathbf{a}_i.\mathbf{a}_j$.

| | $x$ | $y$ | $z$ | $U_{eq}$ |
|---|---|---|---|---|
| B1 | 0.12738 (10) | 0.39998 (8) | 0.27444 (10) | 0.0310 (2) |
| N1 | 0.23964 (8) | 0.44035 (7) | 0.36486 (9) | 0.0399 (3) |
| C11 | 0.23101 (13) | 0.49365 (10) | 0.48373 (12) | 0.0500 (3) |
| C12 | 0.37380 (11) | 0.43480 (11) | 0.34414 (14) | 0.0545 (4) |
| N2 | 0.14302 (9) | 0.31287 (6) | 0.20691 (9) | 0.0398 (3) |
| C21 | 0.05408 (14) | 0.28068 (9) | 0.08588 (12) | 0.0496 (3) |
| C22 | 0.24049 (15) | 0.24075 (10) | 0.26201 (16) | 0.0601 (4) |
| N3† | 0 | 0.44841 (8) | 1/4 | 0.0300 (3) |
| C31† | 0 | 0.55328 (10) | 1/4 | 0.0386 (3) |

† Site occupancy = 0.5.

Table 2. *Selected geometric parameters* (Å, °)

| | | | |
|---|---|---|---|
| B1—N2 | 1.4271 (14) | B1—N3 | 1.4548 (12) |
| B1—N1 | 1.4361 (15) | | |
| N2—B1—N1 | 119.18 (9) | N1—B1—N3 | 120.34 (9) |
| N2—B1—N3 | 120.47 (9) | B1—N3—B1$^i$ | 124.53 (11) |

Symmetry code: (i) $-x, y, \frac{1}{2} - z$.

H atoms were included in calculated positions using a riding model. The torsion angle of the methyl groups was determined by a circular difference Fourier synthesis. The isotropic displacement parameter was set to $1.5U_{iso}$ of the parent atom. The H atoms of the methyl group, C31, are disordered about the twofold axis.

Data collection: *DIF*4 (Stoe & Cie, 1991*a*). Cell refinement: *DIF*4. Data reduction: *REDU*4 (Stoe & Cie, 1991*b*). Program(s) used to solve structure: *SHELXS*86 (Sheldrick, 1990). Program(s) used to refine structure: *SHELXL*96 (Sheldrick, 1996). Molecular graphics: *ZORTEP* (Zsolnai, Pritzkow & Huttner, 1996). Software used to prepare material for publication: *SHELXL*96.

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Supplementary data for this paper are available from the IUCr electronic archives (Reference: LN1012). Services for accessing these data are described at the back of the journal.

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# Diphenyl (−)-(*R*)-1-[(*S*)-Isoleucyl]pyrrolidine-2-phosphonate Hydrochloride

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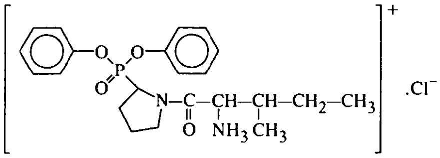
## Abstract

The crystal structure of the title compound, $C_{22}H_{30}N_2O_4P^+.Cl^-$, was determined in order to ascertain its absolute configuration. The pyrrolidine ring is markedly flattened and adopts a conformation intermediate between an envelope and a half-chair.

## Comment

The title compound, (I), belongs to a series of *L-AA*–Pro$^P$ dipeptides (*L-AA* is an amino acid residue and Pro$^P$ is proline diphenyl phosphonate). These compounds were synthesized as potential inhibitors of proline-specific serine proteases. Only the (−) diastereomers acted as inhibitors (Belyaev *et al.*, 1995). To obtain the absolute configuration of (I), its crystal structure has been determined from single-crystal diffraction data.



(I)

The bond lengths and angles display no unusual features. Puckering parameters [$q_2$ = 0.249 (3) Å and $\varphi_2$ = 7.0 (8)°] and asymmetry parameters [$\Delta C_s$(N7) = 0.023 (2)] indicate that the conformation of the pyrrolidine ring is intermediate between an envelope and a half-chair with a pseudo-mirror plane through the N atom. As a result of the $sp^2$ hybridization of the N atom, the ring is markedly flattened. The packing of the molecules in the unit cell is essentially achieved through hydrogen bonds between the H atoms of the protonated terminal amino group and the $Cl^-$ anion.

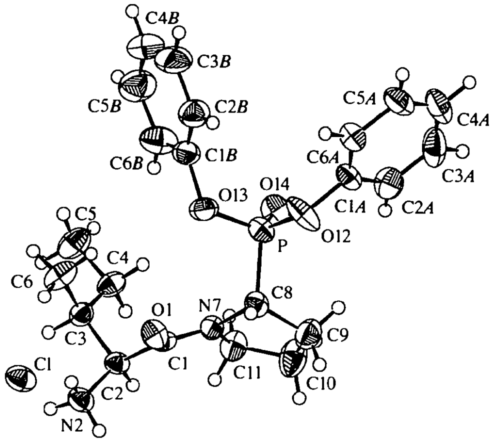


Fig. 1. Perspective view of the title compound with the atomic numbering scheme. Displacement ellipsoids are drawn at the 40% probability level.

## Experimental

The synthesis of (I) is described by Belyaev *et al.* (1995). Suitable crystals were obtained by slow evaporation from an ethyl acetate–methanol (10:1) solution.

### *Crystal data*

$C_{22}H_{30}N_2O_4P^+.Cl^-$
$M_r$ = 452.90
Orthorhombic
$P2_12_12_1$
$a$ = 6.0144 (6) Å
$b$ = 13.8744 (8) Å
$c$ = 27.517 (2) Å
$V$ = 2296.2 (3) Å$^3$
$Z$ = 4
$D_x$ = 1.310 Mg m$^{-3}$
$D_m$ not measured

Cu $K\alpha$ radiation
$\lambda$ = 1.54184 Å
Cell parameters from 32 reflections
$\theta$ = 13–28°
$\mu$ = 2.380 mm$^{-1}$
$T$ = 293 K
Needle
0.80 × 0.05 × 0.03 mm
Colourless

### *Data collection*

Siemens $P4$ four-circle diffractometer
$\omega/2\theta$ scans
Absorption correction: $\psi$ scan (*XEMP*; Siemens, 1989)
$T_{\min}$ = 0.639, $T_{\max}$ = 0.931

1732 reflections with $F^2 > 2\sigma(F^2)$
$R_{\text{int}}$ = 0.022
$\theta_{\max}$ = 57.19°
$h = -6 \rightarrow 6$
$k = -15 \rightarrow 15$
$l = -30 \rightarrow 30$

3735 measured reflections
1841 independent reflections

3 standard reflections every 100 reflections intensity decay: 2.0%

### *Refinement*

Refinement on $F^2$
$R[F^2 > 2\sigma(F^2)]$ = 0.033
$wR(F^2)$ = 0.084
$S$ = 1.069
3119 reflections
275 parameters
H-atom parameters constrained
$w = 1/[\sigma^2(F_o^2) + (0.0442P)^2 + 0.4975P]$ where $P = (F_o^2 + 2F_c^2)/3$
$(\Delta/\sigma)_{\max}$ = 0.001

$\Delta\rho_{\max}$ = 0.17 e Å$^{-3}$
$\Delta\rho_{\min}$ = −0.17 e Å$^{-3}$
Extinction correction: *SHELXL93* (Sheldrick, 1993)
Extinction coefficient: 0.0058 (3)
Scattering factors from *International Tables for X-ray Crystallography* (Vol. IV)
Flack parameter for absolute configuration determination = 0.00 (2)

Table 1. *Selected geometric parameters (Å, °)*

| | | | |
|---|---|---|---|
| P—C8 | 1.811 (3) | C3—C6 | 1.525 (4) |
| P—O12 | 1.575 (2) | C4—C5 | 1.524 (4) |
| P—O13 | 1.582 (2) | N7—C8 | 1.468 (3) |
| P—O14 | 1.452 (2) | N7—C11 | 1.470 (3) |
| C1—O1 | 1.230 (3) | C8—C9 | 1.538 (4) |
| C1—C2 | 1.533 (3) | C9—C10 | 1.491 (5) |
| C1—N7 | 1.345 (3) | C10—C11 | 1.492 (4) |
| C2—N2 | 1.488 (3) | O12—C1*A* | 1.410 (3) |
| C2—C3 | 1.542 (3) | O13—C1*B* | 1.411 (3) |
| C3—C4 | 1.525 (4) | | |
| O13—P—O14 | 114.6 (1) | C1—N7—C11 | 128.8 (2) |
| O12—P—O14 | 116.0 (1) | C1—N7—C8 | 119.8 (2) |
| O12—P—O13 | 104.2 (1) | C8—N7—C11 | 109.4 (2) |
| C8—P—O14 | 117.0 (1) | P—O12—C1*A* | 128.1 (2) |
| C8—P—O13 | 102.5 (1) | P—O13—C1*B* | 121.2 (2) |
| C8—P—O12 | 100.6 (1) | | |
| O14—P—C8—N7 | −63.8 (2) | C1—C2—C3—C4 | 75.9 (3) |
| O13—P—C8—N7 | 62.4 (2) | C1—C2—C3—C6 | −51.8 (3) |
| O12—P—C8—N7 | 169.7 (2) | C2—C3—C4—C5 | 170.7 (2) |
| N7—C1—C2—C3 | −88.2 (3) | C1—N7—C8—P | −102.1 (2) |
| N7—C1—C2—N2 | 152.6 (2) | | |

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

| *D*—H···*A* | *D*—H | H···*A* | *D*···*A* | *D*—H···*A* |
|---|---|---|---|---|
| N2—H2*B*···Cl | 0.890 | 2.51 | 3.311 (2) | 151 |
| N2—H2*A*···Cl$^{i}$ | 0.890 | 2.56 | 3.217 (2) | 131 |
| N2—H2*C*···Cl$^{ii}$ | 0.890 | 2.24 | 3.078 (2) | 157 |

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

The structure was solved by direct methods and refined by full-matrix least squares on $F^2$ for all reflections. H atoms were calculated at geometrical positions and allowed to ride on their parent atom.

Data collection: *XSCANS* (Siemens, 1994). Cell refinement: *XSCANS*. Data reduction: *XSCANS*. Program(s) used to solve structure: *SIR92* (Altomare *et al.*, 1994). Program(s) used to refine structure: *SHELXL93* (Sheldrick, 1993). Molecular graphics: *DIAMOND* (Bergerhoff, 1996). Software used to prepare material for publication: *PARST* (Nardelli, 1983).

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Supplementary data for this paper are available from the IUCr electronic archives (Reference: NA1308). Services for accessing these data are described at the back of the journal.

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# L-Proline Monohydrate at 100 K

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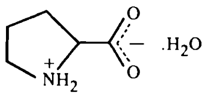
## Abstract

A new crystalline modification of proline was identified by the present X-ray analysis as a monoclinic L-proline monohydrate, $C_5H_9NO_2.H_2O$. The pyrrolidine rings are in a $C_2$–$C^{\gamma}$-*exo*–$C^{\delta}$-*endo* conformation. The C4 atom ($C^{\gamma}$) is in a *trans* position with respect to the carboxyl group. In the crystal lattice, columns of L-proline molecules are stabilized by intermolecular hydrogen bonds. These columns are interconnected by water molecules. The water molecules in the structure form non-linear hydrogen-bonded chains parallel to the *c* axis. One H atom of the water molecule chain is disordered.

## Comment

L-Proline is a cyclic amino acid. It contains a pyrrolidine ring whose presence in a protein chain can disrupt the $\alpha$-helix and can also give rise to the specific collagen spiral (Rich & Crick, 1961; Nagai & Noda, 1957; Miller & Wray, 1971; Stacey *et al.*, 1988; Kadler *et al.*, 1991; Horovitz, Matthews & Fersht, 1992; Bella *et al.*, 1994; Schulman & Kim, 1996; Fields & Prockop, 1996).

The crystal structure of L-proline monohydrate, (I), has not been determined previously, only the space group and unit-cell dimensions have been mentioned by Sasisekharan (1959). During attempts to recrystallize L-proline itself to obtain suitable crystals for a charge density determination, we obtained a monoclinic modification which previously has been mentioned by Sasisekharan (1959). Therefore, we determined the crystal structure and present here the full structural details of this modification.



(I)

At room temperature [$a$ = 20.553 (5), $b$ = 6.304 (2), $c$ = 5.164 (2) Å and $\beta$ = 93.61 (3)], the C4 atom (see Fig. 1) has unusually large vibrational amplitudes in the direction perpendicular to the pyrrolidine ring plane; therefore, this crystal was measured again at a lower temperature of 100 (2) K. A similar behaviour for the $C^{\gamma}$ atom can be found in DL-proline hydrochloride (Mitsui, Tsuboi & Iitaka, 1969) and in some oligopeptides containing L-proline (Leung & Marsh, 1958; Ukei *et al.*, 1969). At low temperature, the anisotropic displacement parameters for the C4 atom are comparable with those of the other atoms. Geometric details of the room and low temperature analyses do not differ significantly so the following discussion of results can be based on the low-temperature data only.

The conformation of the pyrrolidine ring in the L-proline molecule (Fig. 1) may be described, in a similar manner to the ring in the crystal structure of DL-proline monohydrate (Padmanabhan, Suresh & Vijayan, 1995), as $C_2$–$C^{\gamma}$-*exo*–$C^{\delta}$-*endo* or $C_s$–$C^{\gamma}$-*exo* or $C_s$–$C^{\delta}$-*endo* (IUPAC–IUB Commission on Biochemical Nomenclature, 1970; Balasubramanian *et al.*, 1971;

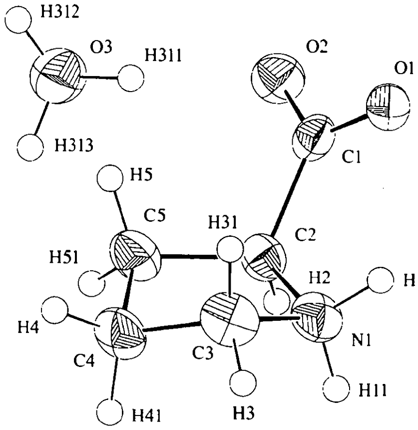


Fig. 1. *ORTEP*II (Johnson, 1971) drawing showing the molecular structure of the title compound and the crystallographic numbering scheme (50% probability displacement ellipsoids). The H312 and H313 atoms have an occupation factor of 0.5.

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