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O-Phospho-L-tyrosine

TAMAMI SUGA, CHIKA INUBUSHI AND NOBUO OKABE

Faculty of Pharmaceutical Sciences, Kinki University, Kowakae 3-4-1, Higashiosaka, Osaka 577, Japan

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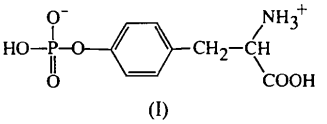
Abstract

Two conformers are present in the asymmetric unit cell of the title compound, $C_9H_{12}NO_6P$. Their conformations differ by rotation around the P—O—C ester bonds. In each conformer, the phosphate and the asymmetric C atom of the tyrosine moiety lie on opposite sides of the phenyl ring plane. Both the phosphate and the amino groups are charged. Molecules are held together by a hydrogen-bond network involving the phosphate, amino and carboxyl groups.

Comment

Phosphorylation or dephosphorylation of cellular proteins by protein kinases or phosphatases has an extremely important physiological role in cellular regulatory systems (Taborsky, 1974; Rubin & Rosen, 1975; Cohen, 1982; Martin, Mayes & Rodwell, 1983; Waksman, 1994; Mora, Lacombe & Pavia, 1995). The incorporation of the phosphate groups in the protein may change the conformation of the protein and its mode of interaction with ligands. It is known that phosphorylation of proteins occurs at seryl, threonyl and tyrosyl residues of the polypeptide chain. Therefore, it is important to obtain detailed structural information on the phosphorylated amino acids in order to understand their biological function in cell regulatory systems. The crystal structures of DL-serine phosphate (Putkey & Sundaralingam, 1970), L-serine phosphate (McCallum, Robertson & Sim, 1959) and DL-threonine phosphate (Maniukiewicz, Kwiatkowski & Blessing, 1996) have been reported previously. Recently, we determined the crystal structure of the chelate compound of L-serine phosphate and the calcium ion (Suga & Okabe, 1996). In this study, the crystal structure of *O*-phospho-L-tyrosine, (I), was determined.



(I)

O-Phospho-L-tyrosine appears as two conformers in the unit cell (forms *A* and *B*) (Fig. 1). The overall conformations of the two conformers resemble one another. Conformational difference is characterized by the torsion angles defining the phosphate group orientation with respect to the phenol ring, *i.e.* P(1*A*)—O(1*A*)—C(7*A*)—C(6*A*) of −117 (1)° and P(1*B*)—O(1*B*)—C(7*B*)—C(8*B*) of −82 (2)°. Both the amino and phosphate groups of the conformers are charged but the carboxyl groups are not. The molecular packing (Fig. 2) is stabilized by electrostatic interaction between the positively charged amino group

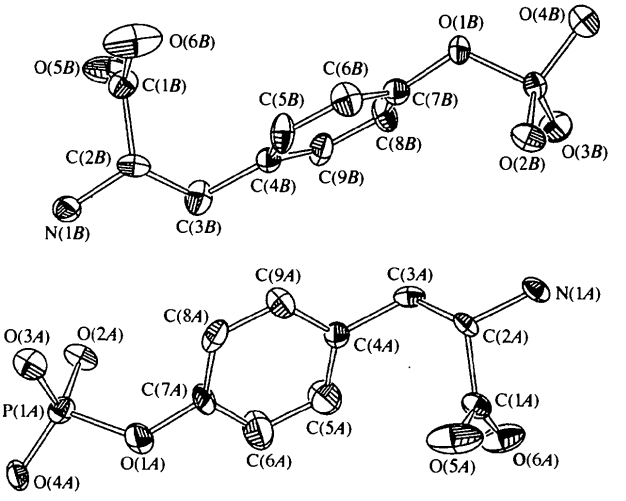


Fig. 1. *ORTEP*II (Johnson, 1976) drawing of the conformers (*A* and *B*) of the title compound with the atomic numbering scheme. Ellipsoids correspond to 50% probability and H atoms have been omitted for clarity.

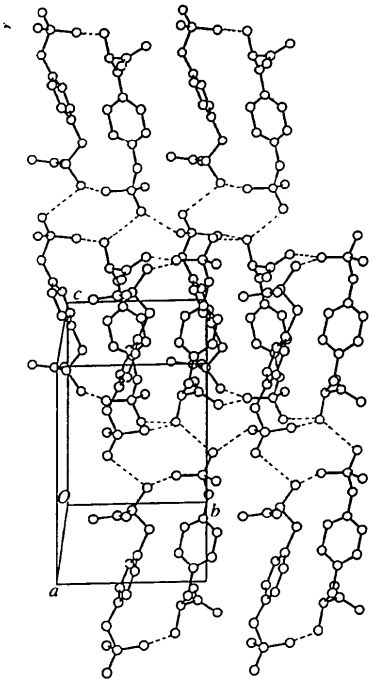


Fig. 2 Packing diagram of the title compound viewed down the *b* axis.

and the negatively charged phosphate group, and by a hydrogen-bond network involving the phosphate, amino and carboxyl groups.

Experimental

It is very difficult to obtain crystals of the title compound suitable for single-crystal X-ray diffraction. Crystals always appear as very thin needle crystals, like fibers, from various solvents. In this study, thin colorless plate crystals suitable for analysis were obtained by chance while trying to prepare the chelate compound of the title compound with silver sulfate by slow evaporation of an aqueous solution containing *O*-phospho-L-tyrosine and Ag_2SO_4 in a 1:2 molar ratio at room temperature.

Crystal data

$C_9H_{12}NO_6P$	Mo $K\alpha$ radiation
$M_r = 261.17$	$\lambda = 0.71069$ Å
Monoclinic	Cell parameters from 24 reflections
$P2_1$	$\theta = 4.3$–$7.4°$
$a = 11.480\,(5)$ Å	$\mu = 0.269$ mm^{-1}
$b = 8.114\,(3)$ Å	$T = 296$ K
$c = 11.882\,(4)$ Å	Plate
$\beta = 107.68\,(3)°$	0.30 × 0.20 × 0.10 mm
$V = 1054\,(1)$ Å^3	Colorless
$Z = 4$	
$D_x = 1.645$ Mg m^{-3}	
D_m not measured	

Data collection

Rigaku AFC-5*R* diffractometer	1998 reflections with $I > 0$
ω–2θ scans	$R_{int} = 0.060$
Absorption correction: ψ scans (North, Phillips & Mathews, 1968)	$\theta_{max} = 27.5°$
	$h = 0 \rightarrow 14$
	$k = -10 \rightarrow 0$
$T_{min} = 0.95$, $T_{max} = 1.00$	$l = -15 \rightarrow 13$
2719 measured reflections	3 standard reflections
2597 independent reflections	every 150 reflections
	intensity decay: 0.70%

Refinement

Refinement on F^2	$(\Delta/\sigma)_{max} = 0.018$
$R = 0.121$	$\Delta\rho_{max} = 0.98$ e Å^{-3}
$wR = 0.130$	$\Delta\rho_{min} = -1.35$ e Å^{-3}
$S = 1.23$	Extinction correction: none
1998 reflections	Scattering factors from *International Tables for X-ray Crystallography* (Vol. IV)
294 parameters	
H atoms not refined	
$w = 4F_o^2/\sigma^2(F_o^2)$	

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

P(1*A*)—O(1*A*)	1.637 (8)	C(1*B*)—C(2*B*)	1.54 (1)
P(1*A*)—O(2*A*)	1.498 (8)	C(2*A*)—C(3*A*)	1.53 (1)
P(1*A*)—O(3*A*)	1.568 (7)	C(2*B*)—C(3*B*)	1.53 (1)
P(1*A*)—O(4*A*)	1.472 (7)	C(3*A*)—C(4*A*)	1.53 (1)
P(1*B*)—O(1*B*)	1.581 (8)	C(3*B*)—C(4*B*)	1.52 (1)
P(1*B*)—O(2*B*)	1.517 (9)	C(4*A*)—C(5*A*)	1.35 (1)
P(1*B*)—O(3*B*)	1.562 (8)	C(4*A*)—C(9*A*)	1.41 (1)
P(1*B*)—O(4*B*)	1.502 (8)	C(4*B*)—C(5*B*)	1.41 (1)
O(1*A*)—C(7*A*)	1.40 (1)	C(4*B*)—C(9*B*)	1.37 (1)
O(1*B*)—C(7*B*)	1.42 (1)	C(5*A*)—C(6*A*)	1.39 (2)
O(5*A*)—C(1*A*)	1.28 (1)	C(5*B*)—C(6*B*)	1.39 (1)
O(5*B*)—C(1*B*)	1.31 (1)	C(6*A*)—C(7*A*)	1.37 (2)
O(6*A*)—C(1*A*)	1.20 (1)	C(6*B*)—C(7*B*)	1.35 (2)
O(6*B*)—C(1*B*)	1.18 (1)	C(7*A*)—C(8*A*)	1.36 (1)
N(1*A*)—C(2*A*)	1.50 (1)	C(7*B*)—C(8*B*)	1.37 (1)
N(1*B*)—C(2*B*)	1.52 (1)	C(8*A*)—C(9*A*)	1.37 (1)
C(1*A*)—C(2*A*)	1.50 (1)	C(8*B*)—C(9*B*)	1.37 (1)
O(1*A*)—P(1*A*)—O(2*A*)	104.5 (4)	N(1*B*)—C(2*B*)—C(3*B*)	108.6 (7)
O(1*A*)—P(1*A*)—O(3*A*)	103.2 (4)	C(1*B*)—C(2*B*)—C(3*B*)	113.0 (9)
O(1*A*)—P(1*A*)—O(4*A*)	106.9 (4)	C(2*A*)—C(3*A*)—C(4*A*)	115.1 (8)
O(2*A*)—P(1*A*)—O(3*A*)	106.5 (4)	C(2*B*)—C(3*B*)—C(4*B*)	112.8 (8)
O(2*A*)—P(1*A*)—O(4*A*)	121.5 (4)	C(3*A*)—C(4*A*)—C(5*A*)	120.8 (9)
O(3*A*)—P(1*A*)—O(4*A*)	112.5 (4)	C(3*A*)—C(4*A*)—C(9*A*)	119.6 (9)
O(1*B*)—P(1*B*)—O(2*B*)	108.3 (4)	C(5*A*)—C(4*A*)—C(9*A*)	120 (1)
O(1*B*)—P(1*B*)—O(3*B*)	106.8 (4)	C(3*B*)—C(4*B*)—C(5*B*)	122.4 (9)
O(1*B*)—P(1*B*)—O(4*B*)	103.7 (4)	C(3*B*)—C(4*B*)—C(9*B*)	121.5 (9)
O(2*B*)—P(1*B*)—O(3*B*)	111.0 (5)	C(5*B*)—C(4*B*)—C(9*B*)	116.1 (9)
O(2*B*)—P(1*B*)—O(4*B*)	115.0 (5)	C(4*A*)—C(5*A*)—C(6*A*)	121 (1)
O(3*B*)—P(1*B*)—O(4*B*)	111.4 (4)	C(4*B*)—C(5*B*)—C(6*B*)	121 (1)
P(1*A*)—O(1*A*)—C(7*A*)	125.5 (7)	C(5*A*)—C(6*A*)—C(7*A*)	119 (1)
P(1*B*)—O(1*B*)—C(7*B*)	122.8 (7)	C(5*B*)—C(6*B*)—C(7*B*)	119 (1)
O(5*A*)—C(1*A*)—O(6*A*)	122 (1)	O(1*A*)—C(7*A*)—C(6*A*)	116 (1)
O(5*A*)—C(1*A*)—C(2*A*)	114 (1)	O(1*A*)—C(7*A*)—C(8*A*)	123 (1)
O(6*A*)—C(1*A*)—C(2*A*)	124 (1)	C(6*A*)—C(7*A*)—C(8*A*)	121 (1)
O(5*B*)—C(1*B*)—O(6*B*)	126 (1)	O(1*B*)—C(7*B*)—C(6*B*)	118 (1)
O(5*B*)—C(1*B*)—C(2*B*)	113.5 (9)	O(1*B*)—C(7*B*)—C(8*B*)	119 (1)
O(6*B*)—C(1*B*)—C(2*B*)	121 (1)	C(6*B*)—C(7*B*)—C(8*B*)	122 (1)
N(1*A*)—C(2*A*)—C(1*A*)	107.6 (8)	C(7*A*)—C(8*A*)—C(9*A*)	120.4 (9)
N(1*A*)—C(2*A*)—C(3*A*)	107.5 (8)	C(7*B*)—C(8*B*)—C(9*B*)	117.7 (9)
C(1*A*)—C(2*A*)—C(3*A*)	114.9 (8)	C(4*A*)—C(9*A*)—C(8*A*)	119.2 (9)
N(1*B*)—C(2*B*)—C(1*B*)	111.0 (9)	C(4*B*)—C(9*B*)—C(8*B*)	124 (1)

All H atoms were located from difference Fourier maps, and included in the refinement calculations at fixed positions, but the H atom attached to O(5*B*) of the carboxyl group of conformer *B* could not be found in the final refinement. Both the C(4*A*) and C(4*B*) atoms were refined using isotropic displacement parameters, because anisotropic refinement of these atoms resulted in abnormal temperature factors.

Data collection: *MSC/AFC Diffractometer Control Software* (Molecular Structure Corporation, 1988). Cell refinement: *MSC/AFC Diffractometer Control Software*. Data reduction: *TEXSAN* (Molecular Structure Corporation, 1985). Program(s) used to solve structure: *SHELXS*86 (Sheldrick, 1985) and *DIRDIF* (Beurskens, 1984). Program(s) used to refine structure: *TEXSAN*. Molecular graphics: *ORTEP*II (Johnson, 1976).

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Supplementary data for this paper are available from the IUCr electronic archives (Reference: BS1022). Services for accessing these data are described at the back of the journal.

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Chiral Hydroxylamines. V.† (2*S*,3*S*)-*N*-Benzyl-*N*-[3-(*tert*-butoxycarbonylamino)-2-butyl]hydroxylamine‡

PEDRO MERINO, FRANCISCO L. MERCHAN, TOMAS TEJERO AND ANA LANASPA

Departamento de Química Orgánica, Instituto de Ciencia de Materiales de Aragon, Universidad de Zaragoza, E-50009 Zaragoza, Spain. E-mail: pmerino@posta.unizar.es

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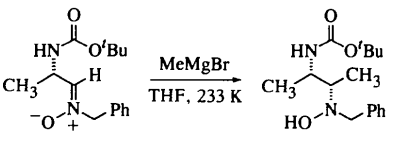
Abstract

The molecular structure of the title compound, $C_{16}H_{26}N_2O_3$, has been determined in order to establish the stereochemical effect of the addition of methyl magnesium bromide to the precursor nitrone. The molecular conformation is influenced by an intramolecular hydrogen-bonding interaction [O—H···O 2.714 (4) Å] and the packing in the crystal is mainly the result of van der Waals interactions.

Comment

In the course of our studies aimed at the synthesis of vicinal diamines, we have prepared the intermediate α-aminohydroxylamine (II) from the precursor nitrone (I), following our previously reported procedure (Merino



(I) (II)

et al., 1997*a*). The structure of (I) had been confirmed previously by X-ray crystallographic analysis (Merino *et al.*, 1996*a*). The hydroxylamine (II) was obtained in 66% diastereoselectivity with 83% chemical yield and was fully characterized by means of spectroscopic data (NMR, IR and MS). The *ORTEP*II (Johnson, 1976) diagram of (II) with the atom-numbering scheme is shown in Fig. 1.

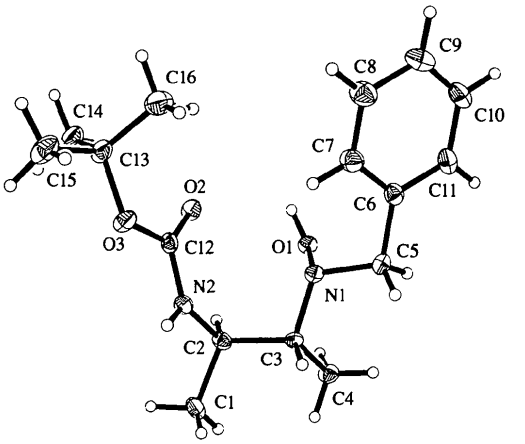


Fig. 1. The molecular structure of compound (II) showing the atom labelling. Displacement ellipsoids are shown at the 30% probability level.

We did not consider the absolute configuration of the title compound since the starting nitrone (I) was known to have an *S* configuration at the only chiral center [C2 in compound (II)]. The relative configuration at the second chiral atom, C3, is defined by the series of torsion angles given in Table 1.

As found in other α-(*tert*-butoxycarbonylamino)-hydroxylamines analyzed by X-ray crystallography (Merino *et al.*, 1996*b*, 1997*b*), an intramolecular hydrogen bond between the nitrone oxygen and the carbonyl group of the carbamate moiety is present, the distance between O1 and O2 being 2.714 (4) Å. The carbamate group is almost planar [N2—C12—O3—C13 −178.5 (4)°] as expected.

Experimental

The title compound was synthesized following our previously reported procedure for the addition of methylmagnesium bromide to α-amino nitrones (Merino *et al.*, 1997*a*). The hydroxylamine (II) was purified by column chromatography

† Part IV: Merino, Merchan, Tejero & Franco (1997).
‡ Alternative name: *tert*-butyl *N*-{(2*S*,3*S*)-3-[*N*-(hydroxy)benzylamino]-2-butyl}carbamate.