X-ray Crystal and Molecular Structure and Absolute Configuration of (Dihydrogen tripolyphosphato)tetraamminecobalt(III) Monohydrate, $Co(NH_3)_4H_2P_3O_{10}\cdot H_2O$. A Model for a Metal–Nucleoside Polyphosphate Complex†

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ABSTRACT: Single crystal X-ray diffraction analysis of the title compound has established its absolute configuration and molecular geometry. This has allowed identification for the first time of the handedness of the MgATP substrate for PRPP synthetase and its optical antipode which is a substrate for yeast hexokinase. The NMR and CD spectra of this and related metal–nucleotide complexes can now be interpreted in terms of their absolute configuration. The title compound is a degradation product of $Co(NH_3)_4$-ATP, and consists of a distorted octahedral complex of Co(III) with four ammonias and the β- and γ-phosphates of the tripolyphosphate chain. The phosphate chain is found to be in an extended conformation, with torsion angles of 80° and 115° about the central phosphodiester P–O bonds. The bond angles are 127° and 128° at the bridging oxygen atoms. The six-atom chelate ring is in a flattened twist-boat conformation, stabilized by two intramolecular interligand hydrogen bonds N(1)–O(8) and N(4)–O(4) involving the ammonia and a γ-phosphate hydroxyl on one side of the ring and the ammonia and the bridge oxygen on the opposite side. These hydrogen bonds can be switched to N(1)– O(6) and N(4)–O(9) by pseudorotation of the chelate ring. The two conformational states for the chelate ring might be intimately related to the mode of recognition and action of the enzymes. Of the network of intermolecular hydrogen bonds, the two donated by phosphate hydroxyls are short at 2.56 and 2.50 Å.

The nucleotides are frequent participants in biological reactions. Enzymes which utilize one of the nucleotides as a cofactor or substrate will typically require a specific complex of the nucleotide with a metal ion for activity. One or more of the phosphate groups from the nucleotide may be liganded to the metal ion; each phosphate may potentially be liganded through one or two oxygens. This flexibility leads to the possibility of a number of mono-, bi-, and tridentate coordination geometries about the metal ion, and one may reasonably expect that specific enzymes will prefer some of these forms over the others as substrates. A determination of which configurations are actually found in solution and which are selected by enzyme specificity will shed light on the modes of enzyme–nucleotide recognition and interaction.

Although in vivo the complexed metal ion is most commonly Mg^{2+}, enzyme function can be studied using nucleotide complexes with other metals as well. Whereas diastereomers of the Mg–nucleotide complexes may interconvert with a half-life on the order of 10^{-5} s, equivalent complexes containing Cr(III) or Co(III) are stable enough to allow separation and characterization. Cleland and co-workers have prepared substitution-inert complexes of Co(III) and Cr(III) with ADP and ATP (DePamphilis and Cleland, 1973; Cornelius et al., 1977) and these have been used to elucidate the kinetic mechanism of a number of enzymes (Schimerlik and Cleland, 1973; Janson and Cleland, 1974; Bar-Tana and Cleland, 1974; Brummond and Cleland, 1974; Danenberg and Cleland, 1975; Armbruster and Rudolph, 1976; Raushel and Cleland, 1977; Cornelius and Cleland, 1978). The cobalt complexes have proved particularly useful in that the coordination state of the nucleotide may be followed using ^1H and ^{31}P NMR.[1] There are seven coordination diastereomers of CoATP complexes observed in solution: four stereomerically distinct tridentate forms in which the α-, β-, and γ-phosphates of ATP are each liganded to the metal through a single oxygen; two stereomerically distinct bidentate forms in which the β- and γ-phosphates are liganded; and a single monodentate form in which the γ-phosphate alone is liganded to the metal (Cornelius et al., 1977). Similarly, there are three coordination geometries of CoADP observed: two bidentate and one monodentate. The stereoisomerism arises due to the asymmetry of the nucleotide itself and the chirality of the chelate ring formed by the phosphate chain and the metal ion. Figure 1 shows a schematic representation of the observed bidentate and tridentate forms. The various coordination isomers, including the diastereomers, are distinguishable through their NMR and CD spectra. However, until now the assignment of absolute configuration to distinct spectra had not been made. This assignment has now been made by X-ray crystallography.

We have undertaken to determine the three-dimensional structures and configurations of the several observed metal–nucleotide coordination isomers. We report here the structure and chirality of (dihydrogen tripolyphosphato)tetraamminecobalt(III), $Co(NH_3)_4H_2P_3O_{10}$, a degradation product of one of the known biologically active stereomers: β,γ-bidentate (ATP)tetraamminecobalt. The importance of the determination lies in the fact that enzymes requiring the metal–nucleotide complex can distinguish among the several isomers of the complex which may be present. When the configuration is fairly stable, as it is for the cobalt complexes, only those

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[1] Abbreviations used: PRPP, 5-phosphoribosyl α-1-pyrophosphate; NMR, nuclear magnetic resonance; CD, circular dichroism.

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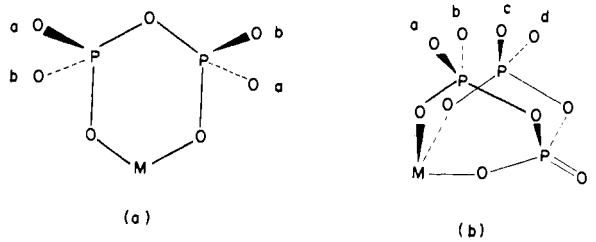

FIGURE 1: The observed bidentate and tridentate coordination geometries of a polyphosphate chelated to a metal ion. (a) The four sites in the bidentate geometry at which the remainder of the ligand (e.g., AMP) may be attached to the chelate ring are labeled a and b. The two a sites are stereochemically equivalent, as are the two b sites. The phosphates illustrated may be the β- and γ-phosphates of ATP or the α- and β-phosphates of ADP. (b) All four labeled sites in the tridentate geometry are stereochemically distinct. The tridentate geometry shown here is a facial arrangement. Meridional tridentate coordination complexes in which all three phosphates are in a plane are probably sterically impossible.

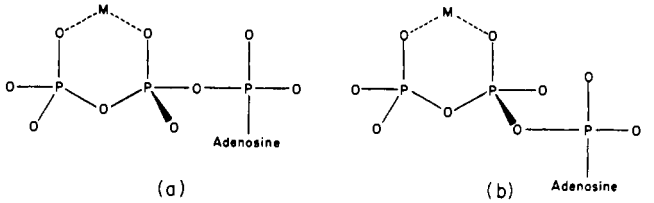

FIGURE 2: The two β,γ-bidentate diastereomers of ATP complexed with a metal ion. Figures 2a and 2b correspond to the b and a sites labeled in Figure 1a. (a) The left-handed diastereomer: $(\Lambda)\beta,\gamma$-bidentate metal-ATP, the substrate for yeast hexokinase. (b) The right-handed diastereomer: $(\Delta)\beta,\gamma$-bidentate metal-ATP, the substrate for PRPP synthetase. Cleavage between the adenosine and the α-phosphate yields the (Δ)-metal-tripolyphosphate structure described in the text.

complexes with the proper configuration are utilized as substrate. Other configurations may bind but not react, or react extremely slowly. This yields information about the active-site conformation of the enzyme and potentially about the reaction mechanism. of the two possible diastereomers of β,γ-bidentate (ATP)tetraamminecobalt, one is selectively recognized as a substrate by yeast hexokinase (Cornelius and Cleland, 1978, following paper in this issue), while the other is selectively recognized as substrate by PRPP synthetase (Li et al., 1978). The X-ray structure determination reported here has established the chirality of the latter as the Δ diastereomer (by the convention described below) and the former as the Λ diastereomer. The two diastereomers are shown in Figure 2. Creatine kinase, on the other hand, is thought to utilize one or more of the tridentate isomers in preference to either of the bidentate forms (Schimerlik and Cleland, 1973). Henceforth, the specificity of any given enzyme may be easily determined provided only that it will accept the equivalent cobaltammine substitution complex in lieu of its natural metal-nucleotide substrate. Characterization of the cobaltammine nucleotides is done by cation-exchange chromatography followed by CD and NMR spectrophotometry (Cornelius et al., 1977).

Experimental Section

(Dihydrogen tripolyphosphato)tetraamminecobalt(III), $Co(NH_3)_4H_2P_3O_{10}$, was prepared from bidentate ATP-$Co(NH_3)_4$ by a degradation scheme involving cleavage with periodate and treatment with aniline at pH 5 (Cornelius et al., 1977). Each of the two diastereomers of the parent ATP complex was used as starting material. The $Co(NH_3)_4H_2P_3O_{10}$ produced from the diastereomer found to be inactive with respect to yeast hexokinase formed red-purple crystals suitable for diffraction work after being stored in an ethanol/water mixture for several weeks at −20 °C. The crystals were extremely thin plates elongated along the unique axis. A crystal measuring about 0.30 × 0.75 × 0.03 mm was used in the X-ray work. The unit-cell constants were measured on an Enraf-Nonius CAD4 Kappa-geometry automated diffractometer. Table I summarizes the pertinent crystal data. Intensity data were collected using Ni-filtered Cu Kα radiation (λ 1.5418 Å). There were 1494 unique reflections measured, of which 1487 were judged observed [$F_o > 3\sigma(F_o)$]. Each reflection was collected using a $\theta - 2\theta$ scan at a minimum absorption position if possible (CAD4 "flat" mode); the 755 reflections for which the minimum absorption position was unattainable due to the diffractometer geometry were later scaled in shells of 20° on Ψ about the minimum absorption position.

TABLE I: Crystal Data for (Dihydrogen tripolyphosphato)tetraamminecobalt(III) Monohydrate.

compound:	$Co(NH_3)_4H_2P_3O_{10}\cdot H_2O$
unit-cell dimensions:	a = 8.162 Å (0.002)
	b = 10.229 Å (0.002)
	c = 7.585 Å (0.001)
	β = 99.44° (0.01)
	V = 624.71 Å^3
space group:	$P2_1$
	ρ_{calcd} = 2.123 g cm^{-3}
	Z = 2

Crystal decay was monitored using four standard reflections measured after every 90 min of exposure time. Lorentz polarization and decay corrections were applied during data reduction. A set of data consisting of 223 Bijvoet pairs of reflections for $\theta < 30°$ was collected in bisecting geometry and reduced similarly.

Determination of Structure and Absolute Configuration

Normalized structure factors were calculated based on an empirical analysis of the data. An origin-removed Patterson map using the normalized structure factors showed the Harker vectors ($2x$, $\frac{1}{2}$, $2z$) due to the cobalt atom and the three phosphorus atoms, as well as the cobalt-phosphorus cross vectors. These four atoms were refined using the Wilson isotropic temperature factor by the method of full-matrix least squares. A difference Fourier map calculated phased on the refined positions revealed all but two of the expected nonhydrogen atoms. After three further rounds of refinement, a second difference Fourier map revealed these two atoms as well as a water of crystallization. At this point the agreement index R ($= \Sigma||F_o| - |F_c||/\Sigma|F_o|$) was 0.135.

It was possible to determine the absolute configuration of this structure using Bijvoet's method (Bijvoet et al., 1951) in a straightforward fashion, because of the appreciable anomalous scattering of Cu Kα radiation by the Co atom. Bijvoet first demonstrated that in an acentric crystal the anomalous scattering atoms cause the intensities of inverse reflections to be unequal $F(hkl) \neq F(\bar{h}\bar{k}\bar{l})$, and the diffraction symmetry is the true point group symmetry rather than the Laue symmetry. By comparing the observed and calculated Bijvoet differences, $F(hkl) - F(\bar{h}\bar{k}\bar{l})$, the chirality of the structure can be established. The set of Bijvoet pairs measured was used to calculate a Bijvoet difference Fourier map (Kraut, 1968) using phases generated from the atomic coordinates without including the anomalous ($\Delta f''$) term. This map showed a large positive peak, twice as high as the next largest peak, at the site of the Co atom. The negative peaks were at noise level. This

TABLE II: Fractional Coordinates of the Atoms in (Dihydrogen tripolyphosphato)tetraamminecobalt(III) Monohydrate.

	atom	x	y	z
1	Co	−0.2233 (1)	0.5000 (0)	0.3570 (1)
2	F(1)	0.3580 (2)	0.4867 (2)	0.7821 (2)
3	P(2)	0.1582 (2)	0.5494 (2)	0.4450 (2)
4	P(3)	0.0452 (2)	0.3286 (2)	0.2166 (2)
5	O(4)	0.1841 (6)	0.5092 (8)	0.6504 (8)
6	O(5)	−0.0166 (6)	0.5966 (7)	0.3939 (8)
7	O(10)	−0.1180 (7)	0.3425 (6)	0.2826 (8)
8	O(7)	0.1814 (8)	0.4132 (8)	0.3518 (11)
9	O(6)	0.2930 (7)	0.6401 (8)	0.4127 (9)
10	O(3)	0.4774 (7)	0.4222 (7)	0.6811 (9)
11	O(8)	0.0337 (8)	0.4039 (9)	0.0381 (9)
12	O(9)	0.1138 (8)	0.1967 (7)	0.2120 (10)
13	O(2)	0.4230 (8)	0.6273 (7)	0.8323 (10)
14	O(1)	0.3184 (8)	0.4143 (9)	0.9384 (9)
15	N(1)	−0.2600 (10)	0.5650 (13)	0.1113 (11)
16	N(2)	−0.4270 (8)	0.3998 (8)	0.3143 (11)
17	N(3)	−0.3329 (8)	0.6446 (8)	0.4427 (13)
18	N(4)	−0.1781 (8)	0.4340 (8)	0.6035 (10)
19	O(W1)	−0.3411 (19)	0.2388 (12)	0.9014 (14)
20	H(11)	−0.191	0.534	0.053
21	H(12)	−0.252	0.646	0.108
22	H(13)	−0.354	0.545	0.058
23	H(21)	−0.411	0.325	0.278
24	H(22)	−0.469	0.392	0.407
25	H(23)	−0.498	0.435	0.237
26	H(31)	−0.333	0.709	0.376
27	H(32)	−0.432	0.627	0.449
28	H(33)	−0.287	0.667	0.545
29	H(41)	−0.262	0.438	0.652
30	H(42)	−0.148	0.356	0.607
31	H(43)	−0.103	0.477	0.666
32	H(81)	0.159	0.405	0.000
33	H(2W)	0.340	0.656	0.870

TABLE III: Bond Angles Not Given in Figure 4, with Standard Deviations in the Last Significant Digit in Parentheses.

N(1)-Co-N(2)	91.6 (4)°	N(4)-Co-O(5)	90.8 (3)°
N(1)-Co-N(3)	93.1 (4)°	N(4)-Co-O(10)	178.0 (3)°
N(1)-Co-N(4)	178.0 (3)°	O(5)-Co-O(10)	92.8 (3)°
N(1)-Co-O(5)	87.6 (3)°		
N(1)-Co-O(10)	90.6 (4)°	O(1)-P(1)-O(3)	116.0 (4)°
N(2)-Co-N(3)	91.7 (3)°	O(2)-P(1)-O(4)	104.4 (4)°
N(2)-Co-N(4)	90.0 (3)°		
N(2)-Co-O(5)	178.0 (3)°	O(4)-P(2)-O(5)	107.8 (3)°
N(2)-Co-O(10)	85.5 (3)°	O(6)-P(2)-O(7)	109.1 (4)°
N(3)-Co-N(4)	88.1 (4)°		
N(3)-Co-O(5)	90.1 (3)°	O(7)-P(3)-O(9)	102.9 (4)°
N(3)-Co-O(10)	175.4 (3)°	O(9)-P(3)-O(10)	117.3 (4)°

showed that the original coordinate set had the correct chirality.

We also generated a set of coordinates for the opposite chirality by negating the y coordinates of each atom. Both the original and the inverted set of coordinates, representing the two possible enantiomers, were refined with isotropic temperature factors and including anomalous dispersion terms in the structure factor calculations. The R value for the inverted set of coordinates converged to only 0.15 compared to that for the uninverted set which converged to 0.12.

We also checked several other crystals obtained in different crystallization experiments by collecting 120 Bijvoet pairs with the largest expected Bijvoet differences. In every case, we found the chirality to be the same.

These studies establish our crystalline material as the Δ enantiomer and thus the parent $Co(NH_3)_4ATP$ as (Δ) β,γ-bidentate (ATP)tetraamminecobalt(III). This is the configuration of the MgATP substrate of PRPP synthetase (Li et al., 1978). The opposite chirality (Λ) corresponds to the substrate of yeast hexokinase (Cornelius and Cleland, 1978).

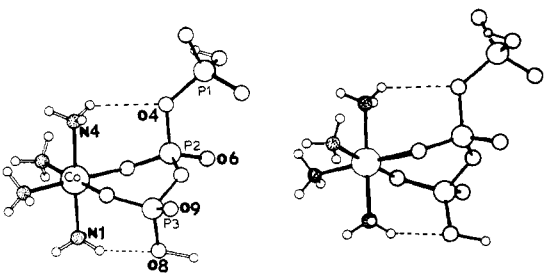

FIGURE 3: $Co(NH_3)_4H_2P_3O_{10}$ (Δ enantiomer left and Λ enantiomer right. Notice the extended conformation of the phosphate chain.)

Further refinement using anisotropic temperature factors for the atoms dropped the R value to 0.087. The largest parameter shift was 0.35σ and the average was 0.11σ during the final cycle of refinement, where σ is the esd in the associated parameter. A difference Fourier map calculated using the 878 reflections for which $\sin\theta/\lambda < 0.465$ revealed the positions of the phosphate hydroxyl hydrogens and few of the ammine hydrogens. Thus, many of the amine and the water hydrogen atoms could not be located unambiguously. The remaining ammine hydrogen atoms were fixed in tetrahedral geometry about the nitrogen with an N-H bond distance of 0.83 Å and a Co-N-H bond angle of 112° and were so oriented to give reasonable hydrogen-bonding geometry. Inclusion of these 14 hydrogen atoms in the structure factor calculations reduced the R value only slightly to 0.085. We attribute the relatively high final R value to the large absorption of the bladelike crystal. All least-squares refinements reported in this paper were done using full-matrix least squares. Reflections were weighted based on counting statistics by the formula $w = [\sigma^2_{F_o} + (pF_o)^2]^{-1}$, where the constant p was chosen as 0.05. Atomic scattering factors were taken from Cromer and Waber (1965). Final atomic coordinates are given in Table II.

Description of the Structure

An ORTEP plot (Johnson, 1965) of the molecule is shown in Figure 3. The structure is comprised of an octahedral Co(III) ion liganded to four ammine nitrogen atoms and one oxygen atom each from the β- and γ-phosphates of a tripolyphosphate chain. In this crystal form a single molecule of water is present for each molecule of the cobalt complex. Figure 4 and Table III give the bond angles and the bond distances.

Nomenclature and Chirality of Metal–Nucleoside Polyphosphates. The separation and identification of diastereomers of nucleotide complexes have created a need for a nomenclature which readily identifies the handedness of the coordination without reference to the identity of individual atoms. Only with such a nomenclature can the names of related complexes directly reflect the similarities and differences in the stereochemistry of the complexes.[2]

[2] The difficulty with the *R,S* system for naming these complexes is illustrated by the (Λ) bidentate isomers of $Co(NH_3)_4ATP$, $Co(NH_3)_4ADP$, MgATP, and MgADP. The first three are *R* and the fourth is *S*, despite their similar stereochemistry. This situation results from the fact that magnesium is heavier than carbon but lighter than phosphorus, while cobalt is heavier than all the others. Note that when the asymmetric center in the chelate ring (the β phosphorus in the complexes discussed here) has a chiral group such as adenosine or AMP attached to it the isomers will be diastereomers. In the tripolyphosphate complexes, where none of the groups attached to the central phosphorus are chiral, the isomers are enantiomers.

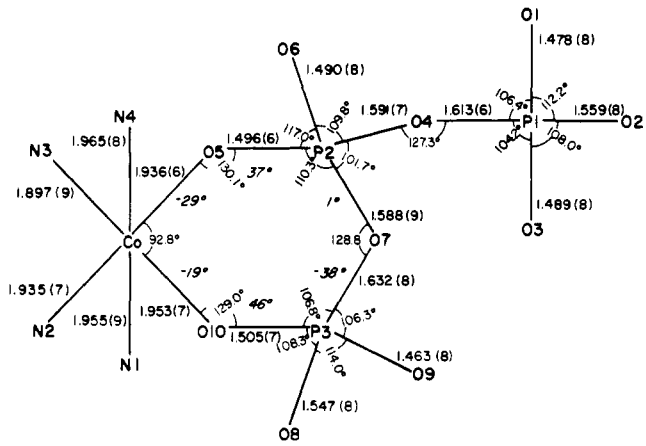

FIGURE 4: Bond distances and bond angles (see also Table III). Estimated standard deviations in the bond lengths are given in parentheses. Estimated standard deviations in the bond angles average 0.4°. Torsion angles around the chelate ring are shown in italics.

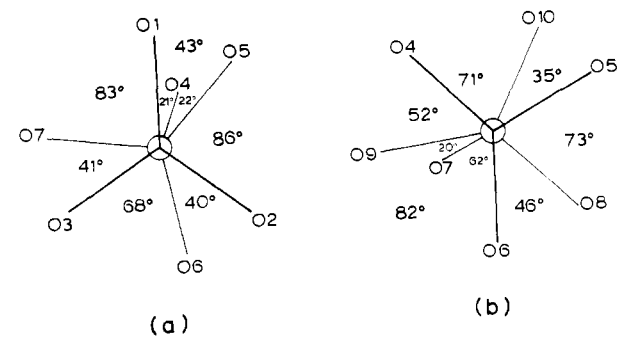

FIGURE 5: Phosphate stagger along the P(1)-P(2) virtual bond (a) and the P(2)-P(3) virtual bond (b).

Our nomenclature adopts the symbols Δ and Λ to indicate right or left handedness of the isomers. The handedness is defined according to the following rule: Place the chelate ring so that bond connecting it to the rest of the ligand points *toward* the viewer. If the shortest path around the ring from the metal to this bond is clockwise, then the isomer is right handed (Δ). If the shortest path around the ring from metal to the attaching bond is counter-clockwise, then the isomer is left handed (Λ). For ADP complexes, attachment of adenosine at either of the positions marked a in Figure 1a gives the Δ isomer; that is, viewed from the adenosine side of the chelate ring the shortest path from the metal to the α-phosphorus is counter-clockwise. Attachment of adenosine at either of the b positions gives the Λ isomer. Similarly, for ATP complexes, attachment of AMP at a or b gives the Δ or Λ isomers, respectively.

The present structure is the Δ enantiomer of $Co(NH_3)_4H_2P_3O_{10}$. This can be seen by noting that the chelate ring is formed by the β- and γ-phosphates of the tripolyphosphate ligand. The remaining portion of the ligand, the α-phosphate, is attached to the chelate ring at P(2). Viewed from the P(2)-O(4) bond side of the chelate ring, the shortest path from Co to P(2) is clockwise. This convention for determining the enantiomer can be followed visually using Figure 3.

Tridentate-ATP complexes are considered to be generated from the corresponding bidentate isomer. When the α-phosphate enters the coordination sphere, its coordination position is determined by the handedness of the bidentate complex. Thus, the Λ-bidentate-ATP complex gives rise to two Λ tridentate isomers, with adenosine attached at either position a or b in Figure 1b. The Δ-bidentate isomer gives rise to two Δ-tridentate isomers, with adenosine attached at either c or d. The tridentate isomers are further designated endo or exo depending on the configuration about the new chelate ring formed when the α-phosphate becomes coordinated. The designation is endo if the γ-phosphate and the rest of the molecule are on the same side of this ring and exo if they are on opposite sides of the ring. In Figure 1b, attachment of adenosine at a or d puts adenosine and the γ-phosphate on opposite sides of the ring and gives exo isomers. Attachment at b or c puts the groups on the same side of the ring and gives endo isomers. Thus, attachment at a, b, c, or d gives the Λ-exo, Λ-endo, Δ-endo, and Δ-exo isomers.

While this nomenclature is applied here to six-membered chelate rings formed by phosphates, it is also applicable to other five- and six-membered rings in metal chelates.

Conformation and Coordination Geometry. The conformation of the polyphosphate chain may be described using torsion angles about the virtual P-P bonds. The geometry above these virtual bonds is shown in Figure 5. The phosphate groups are seen to be staggered, although not ideally so (average torsion angle about the virtual bond: 43°). The bond angles of 127° and 129° at the two bridging oxygens are at the lower end of the range of angles reported for tripolyphosphate (Averbuch-Pouchot and Guitel, 1976; Averbuch-Pouchot et al., 1976). The chain torsion angles about the P-O bonds of the central phosphate are 80° and 115°, an extended conformation corresponding to a P-P-P virtual bond angle of 116°.

An important feature of the structure is the coordination geometry. As a bidentate coordination complex it differs significantly from the previously reported structures of RbADP (Viswamitra et al., 1976a,b) and Na_2ATP (Kennard et al., 1972). In the RbADP structure two oxygen atoms from each of the two phosphates are liganded to a single metal ion. This results in an irregular coordination geometry and does not correspond to any of the coordination states which we find in solution via NMR for the transition metal complexes. The Na_2ATP structure was determined from a crystal form with two independent molecules of ATP. In both molecules the triphosphate chain forms a tridentate coordination complex about a Na^+ ion, with one oxygen atom from each phosphate liganded to the metal. This corresponds to the tridentate $Co(NH_3)_3H_2P_3O_{10}$ structure we reported earlier rather than to the present structure (Merritt and Sundaralingam, 1977). The sodium tridentate coordination complex exhibits a "folded" conformation of the triphosphate chain (virtual P-P-P angles of 91° and 100° in the two molecules) as opposed to the present extended conformation.

Chelate Ring Pucker. The pucker of the chelate ring is a flattened twist-boat. The four ring atoms O(5), P(2), O(7), P(3) are essentially coplanar. The remaining ring atoms, Co and O(10), are both on the same side of this plane, deviating from the plane by 0.907 and 0.873 Å, respectively. The conformation of the chelate ring is stabilized by two intramolecular interligand hydrogen bonds, one between N(1) and O(8) on one side of the ring and the other a possibly weaker hydrogen bond between N(4) and the ester oxygen O(4) on the opposite side. We have previously observed similar intramolecular interligand hydrogen bonds in the crystal of the corresponding pyrophosphate structure, $Co(NH_3)_4HP_2O_7$ (Merritt and Sundaralingam, 1977). We notice that an alternate chelate ring conformation can be assumed by the present compound, in which the ring assumes the opposite conformation with inverted signs for the chelate ring torsion angles. Interconversion between these two conformers results from pseudorotation of

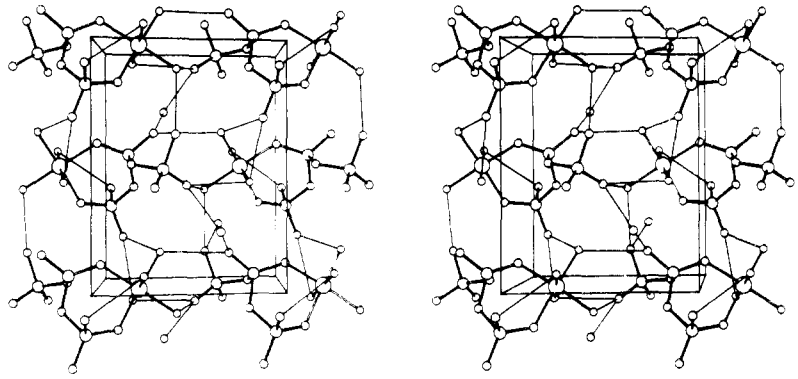

FIGURE 6: Stereo pair of the unit-cell contents of $Co(NH_3)_4H_2P_3O_{10}\cdot H_2O$ viewed approximately along the z axis. Fine lines are hydrogen bonds, except that those between the pairs of atoms N(1)-O(2), N(1)-O(9), N(3)-O(3), and N(4)-O(4) are not shown.

TABLE IV: Hydrogen-Bonding Distances.

donor atom	acceptor atom	D-A dist (Å)	symmetry code of acceptor[a]
O(8)	O(1)	2.561	(1; 0 0 −1)
O(2)	O(W1)	2.504	(2; 0 0 2)
O(W1)	O(3)	2.774	(1; −1 0 0
O(W1)	O(6)	2.675	(2; 0 −1 1)
N(1)	O(8)	3.035	(1; 0 0 0)
N(1)	O(2)	3.127	(1; −1 0 −1)
N(1)	O(9)	3.196	(2; 0 0 0)
N(2)	O(2)	3.003	(2; 0 −1 1)
N(2)	O(3)	3.019	(1; −1 0 0)
N(3)	O(6)	3.025	(1; −1 0 0)
N(3)	O(9)	2.968	(2; 0 0 1)
N(3)	O(3)	3.158	(2; 0 0 1)
N(4)	O(3)	2.968	(1; −1 0 0)
N(4)	O(9)	3.036	(2; 0 0 1)
N(4)	O(4)	3.019	(1; 0 0 0)

[a] The symmetry-related molecule containing the acceptor atom is given by the equivalent positions (1) x, y, z, and (2) $\bar{x}, {}^1/_2 + y, \bar{z}$. After application of the symmetry, the translations along a, b, c are made as indicated by the last three integers.

the chelate ring. The inversion of the ring pucker will rupture the existing hydrogen bonds and form two analogous intramolecular hydrogen bonds N(4)-O(9) and N(1)-O(6). These hydrogen bonds to the anionic phosphate oxygens are equivalent to the pyrophosphate structure (Merritt and Sundaralingam, 1977). In both ring conformers the hydrogen bonds involve the axial phosphate oxygens. We notice that such "complementary states" of the metal-phosphate chelate ring are seen in Na_2ATP, where the chelate rings in the two crystallographically independent molecules are close to being inversions of each other. We visualize that such interligand hydrogen bonds are possible in metal-nucleotide complexes where water or other ligands, rather than ammonia, completes the metal coordination sphere. The two chelate ring conformations may be a general feature of bidentate isomers of metal-nucleotide complexes. This would explain the two, separable, chromatographic bands observed for Cr(III)-ATP-bidentate complexes (Dunaway-Mariano, 1978). Further, the interconversion of ring puckers may have an important role in enzyme recognition and reaction mechanisms involving metal-nucleotide complexes.

Crystal Packing. A packing diagram showing the hydrogen-bonding scheme is given in Figure 6. There are two particularly short hydrogen bonds, both donated by a phosphate hydroxyl. The distance from phosphate oxygen O(8) to phosphate oxygen O(1) of the molecule related by translation along c is 2.561 Å. The water oxygen is involved in three hydrogen bonds, each to a different symmetry-related molecule. Of these, the distance from donor O(2) to acceptor O(W1) is short at 2.504 Å. A list of probable hydrogen bonds is given in Table IV.

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