

hydrogen bonding interaction. Table 5 shows that the phenylalanyl ring has large thermal parameters while the tyrosine ring does not. The tyrosine is not fixed by hydrogen bonding, so the reason for the difference must be the packing of the groups around the rings. The motion of the phenylalanine ring is relatively unrestricted in the direction of the thermal ellipsoids. On the other hand, the tyrosine ring is held in place by its own symmetry-related partner, the phenylalanine ring and the carboxyl group.

In most of the molecules containing peptide-type linkages that have been studied in the solid state by X-ray crystallography, the atoms surrounding the peptide bonds have been found to be coplanar. The non-planar peptides which have been found to this date have been in small cyclic compounds or in peptides containing proline (Winkler & Dunitz, 1971; Ramachandran, 1968). Although the peptide group in this molecule is in a *trans* configuration, the dihedral angle about the peptide bond is 17·7° [$\omega = 162\cdot3(4)$ °]. Table 7 shows the results of fitting a least-squares plane to the atoms comprising the peptide group. In this molecule, the twist in the peptide plane must be caused by the crystal-packing forces. The molecule is not forced into its configuration by internal bonding as in cyclic compounds. It seems likely that if such forces can produce a nonplanar peptide in a small polypeptide, the various interactions in a protein structure could also produce nonplanar peptides.

Table 7. Deviations from the least-squares plane through C(3), C(4), O(2), N(2), C(5)

C(3)	0·090 Å
C(4)	-0·062
O(2)	-0·007
N(2)	-0·129
C(5)	0·108

Acta Cryst. (1973). **B29**, 2878

The Crystal and Molecular Structure of *cis*-1,3-Diethyl-2,4-diphenyl-2,4-dithiocyclodiphosphazane

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(Received 29 June 1973; accepted 30 June 1973)

Crystals of the title compound, $[NEtP(S)Ph]_2$, are monoclinic, $a = 7\cdot17$, $b = 16\cdot27$, $c = 16\cdot59$ Å, $\beta = 96\cdot0^\circ$, space group $C2/c$, $Z = 4$. The atomic positions have been determined by least-squares refinement from X-ray diffractometer intensities, the final R being 0·075 for 1574 reflexions. The molecules possess exact symmetry C_2 . The phosphazane ring is non-planar with the bond angles N-P-N 84·5° and P-N-P 95·0°, the departure from planarity being attributed to steric overcrowding in the molecule. The bond lengths: P-N 1·695, P-S 1·922, P-C 1·797, and N-C 1·46 Å, are not significantly different from the corresponding lengths in the *trans* isomer.

Introduction

The possibility of *cis-trans* isomerism in the cyclodiphosphazanes (**I**) was first suggested by Trippett

As in all crystallographic studies that are undertaken to study the chemistry of the molecules, questions must be raised concerning the structures of the molecules when not in the crystal. Because of the crystal-packing forces, it is possible that the structure of the molecule in the crystal is not the same as that in biological systems or in solution. This could obviate any chances of explaining the kinetics of the pepsin catalyzed hydrolysis on the basis of the solid-state results. Nevertheless, the structure found is useful for comparative purposes and as a point of departure for other methods. Other techniques such as n.m.r. spectroscopy or energy minimization programs would be useful in determining the structure of the molecule in solution.

We wish to thank the members of the local X-ray crystallographic community for many helpful discussions.

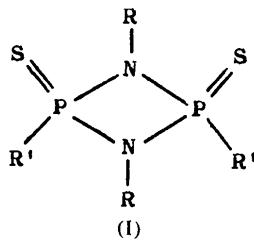
This work was supported by USPHS Grant GM-10828 from the National Institutes of Health.

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(1962) but until recently pairs of isomers had not been separated. Flint, Ibrahim, Shaw, Smith & Thakur (1971) were able to isolate two isomers of 1,3-diethyl-2,4-dithiocyclodiphosphazane (**I**: R = Et,

$R' = \text{Ph}$) and to assign *cis* and *trans* configurations to them on the basis of spectral data. We have studied the crystal structures of both these isomers. The structure of the *trans* isomer (melting point 144°C) was described in an earlier paper (Bullen, Rutherford & Tucker, 1973) and we now present the results on the *cis* isomer (m.p. 137°C) for comparison. A crystallographic analysis of 1,3-dimethyl-2,4-dichloro-2,4-dithiocyclo-diphosphazane (I : $R = \text{Me}$, $R' = \text{Cl}$) failed to establish whether its configuration was *cis* or *trans*, because the chlorine and sulphur atoms could not be distinguished (Weiss & Hartmann, 1966). With this possible exception, no information has been available on the detailed molecular geometry of *cis*-cyclodiphosphazanes.



Experimental

Crystals of *cis*-[NEtP(S)Ph]₂ are monoclinic six-sided plates on {001} bounded by the forms {110} and {010}. Their unit-cell dimensions were measured from precession photographs and are given in Table 1 with other data.

Table 1. *Crystal data*

<i>cis</i> -[NEtP(S)Ph] ₂ , m.p. 137°C*	$V = 1925 \text{ \AA}^3$
Monoclinic	$Z = 4$
$a = 7.17 (\pm 0.02) \text{ \AA}$	$D_m = 1.26 \text{ g cm}^{-3}$
$b = 16.27 (\pm 0.03)$	(by flotation)
$c = 16.59 (\pm 0.03)$	$D_c = 1.26 \text{ g cm}^{-3}$
$\beta = 96.0 (\pm 0.02)^\circ$	$F(000) = 768$
Space group $C2/c$ (No. 15)	$\lambda(\text{Mo } K\alpha) = 0.7107 \text{ \AA}$ $\mu(\text{Mo } K\alpha) = 4.1 \text{ cm}^{-1}$

Systematic absences: hkl when $h+k$ is odd, and $h0l$ when l is odd.

* Our measurement. Flint *et al.* (1971) report 134°C.

X-ray intensities comprising the 11 layers of reflexions 0–10, k , l were measured at 22–25°C on a Philips PAILRED diffractometer with monochromated Mo $K\alpha$ radiation. 1589 reflexions with $I > 2\sigma(I)$ were obtained by measuring all reflexions with $\sin \theta/\lambda$ less than 0.7 \AA^{-1} and some in the range 0.7 – 0.8 \AA^{-1} . The crystal used was approximately $0.4 \times 0.3 \times 0.1 \text{ mm}$ in size. The intensities were corrected for Lorentz and polarization effects but not for absorption.

The least-squares refinement was carried out initially at the Atlas Computer Laboratory, Chilton, with the X-RAY 63 program package, and in the final stages on the University of Essex PDP-10 computer with a program written by G. M. Sheldrick. The atomic

scattering factors were calculated by the analytic function $f = C + \sum_{i=1}^4 A_i \exp(-B_i \sin^2 \theta/\lambda^2)$, the parameters A , B , and C being taken from Cromer & Waber (1965) for sulphur, phosphorus, nitrogen, and carbon, and from Forsyth & Wells (1959) for hydrogen.

Structure determination

The systematic absences indicate space group Cc or $C2/c$. The positions of the phosphorus and sulphur atoms were deduced from the Patterson function, in which the distribution of peaks corresponded to the centrosymmetric space group $C2/c$. This choice of space group was confirmed by the subsequent analysis and refinement.

The carbon and nitrogen atoms were located from Fourier syntheses phased on the heavier atoms. Five cycles of full-matrix least-squares refinement with isotropic temperature factors reduced R to 0.16. Hydrogen atoms were then inserted, the positions of those in the phenyl and methylene groups being calculated from the molecular geometry with a C–H bond length of 1.05 Å. Those in the methyl group were located from a difference synthesis and their positions adjusted to make the C–H distances equal to 1.05 Å.

Least-squares refinement was continued with anisotropic temperature factors for all atoms except hydrogen. In the later cycles the weighting scheme $w = (9.5 - 0.4|F_o| + 0.0065|F_o|^2)^{-1}$ was used to make the average $w\Delta^2$ (where $\Delta = |F_o| - |F_c|$) similar in size over

Table 2. *Fractional atomic coordinates with estimated standard deviations*

	x/a	y/b	z/c
S	0.17825 (23)	0.31134 (9)	0.13677 (9)
P	0.09576 (17)	0.21641 (8)	0.19159 (7)
N	0.1333 (5)	0.2094 (3)	0.2935 (2)
C(1)	0.1704 (7)	0.1215 (3)	0.1508 (3)
C(2)	0.1854 (8)	0.1148 (3)	0.0674 (3)
C(3)	0.2411 (10)	0.0415 (4)	0.0360 (4)
C(4)	0.2915 (11)	-0.0242 (4)	0.0855 (4)
C(5)	0.2768 (13)	-0.0181 (4)	0.1677 (4)
C(6)	0.2163 (11)	0.0546 (4)	0.1995 (3)
C(7)	0.2980 (9)	0.2334 (5)	0.3470 (3)
C(8)	0.3381 (11)	0.1790 (6)	0.4158 (5)

Table 3. *Components of thermal vibration tensors ($\text{\AA}^2 \times 10^3$) and their estimated standard deviations*

	U_{11}	U_{22}	U_{33}	U_{23}	U_{13}	U_{12}
S	68.5 (10)	49.2 (8)	47.8 (8)	13.3 (6)	23.1 (7)	3.2 (7)
P	41.3 (6)	41.3 (7)	26.1 (5)	3.2 (5)	9.2 (4)	5.4 (6)
N	40 (2)	57 (3)	29 (2)	4 (2)	5 (1)	-1 (2)
C(1)	51 (3)	45 (3)	34 (2)	3 (2)	13 (2)	8 (2)
C(2)	67 (4)	56 (3)	37 (3)	2 (2)	21 (2)	9 (3)
C(3)	91 (5)	68 (4)	51 (3)	-10 (3)	22 (3)	6 (4)
C(4)	103 (6)	61 (4)	67 (4)	-12 (3)	20 (4)	21 (4)
C(5)	128 (7)	62 (4)	57 (4)	6 (3)	6 (4)	30 (4)
C(6)	111 (6)	55 (4)	43 (3)	2 (3)	15 (3)	18 (4)
C(7)	54 (3)	99 (5)	41 (3)	6 (3)	-6 (2)	-14 (3)
C(8)	73 (5)	149 (8)	69 (5)	30 (5)	-25 (4)	-4 (5)

Table 4. Fractional coordinates and mean-square amplitudes of thermal vibration assigned to hydrogen atoms (numbered according to the carbon atom to which they are attached)

	<i>x/a</i>	<i>y/b</i>	<i>z/c</i>	$\overline{u^2}$ (\AA^2)
H(2)	0.154	0.165	0.029	0.08
H(3)	0.246	0.036	-0.027	0.08
H(4)	0.340	-0.079	0.061	0.08
H(5)	0.312	-0.068	0.206	0.08
H(6)	0.206	0.059	0.262	0.08
H(7a)	0.414	0.237	0.314	0.08
H(7b)	0.279	0.294	0.368	0.08
H(8a)	0.448	0.196	0.457	0.10
H(8b)	0.359	0.120	0.395	0.10
H(8c)	0.217	0.172	0.446	0.10

the whole range of $|F_o|$ and $\sin \theta/\lambda$. 15 weak reflexions for which $4|F_c| < |F_o|$ were excluded from the refine-

ment. Neither the positions nor the temperature factors of hydrogen atoms were refined. The final R is 0.075 for 1574 reflexions and R' [$=(\sum w\Delta^2/\sum w|F_o|^2)^{1/2}$] is 0.085. For the total set of 1589 reflexions $R=0.078$. In the last cycle all parameter changes were less than 0.12σ . An attempt to refine the structure in the space group *Cc* gave no improvement.

The final atomic coordinates and thermal parameters with estimated standard deviations are listed in Tables 2-4. The molecular shape and the numbering of the atoms are shown in Fig. 1. Observed and calculated structure factors are given in Table 5. Bond lengths and bond angles are listed in Table 6. The orientation and magnitudes of the principal axes of the vibration ellipsoids are given in Table 7. The anisotropic thermal parameters were analysed in terms of a rigid-body motion for the central part of the mol-

Table 5. Observed and calculated structure factors ($\times 10$)

L	$ F_o $	F_c	L	$ F_o $	F_c	L	$ F_o $	F_c	L	$ F_o $	F_c	L	$ F_o $	F_c	L	$ F_o $	F_c	L	$ F_o $	F_c	L	$ F_o $	F_c			
o, 22, L	9.624	-0.21	9.624	-0.21	9.624	-0.21	15.188	-0.65	17.188	-0.65	5.295	2.64	2.128	1.23	1.188	0.56	2.128	1.23	2.128	-0.66	3.128	-0.56	1.128	-0.26	1.128	-0.26
6, 243, L	8.243	-2.52	-1.1, 21, L	14.168	-1.74	18.138	-1.29	4.288	2.88	2.128	1.23	1.188	0.56	2.128	1.23	1.188	-0.56	3.128	-0.56	1.128	-0.26	1.128	-0.26			
7, 483, 501	7.483	501	13.189	1.11	21.135	1.33	3.191	1.005	2.1388	-1.212	5.365	3.89	21.117	-1.04	1.456	0.73	9.89	0.78	11.291	0.68	10.685	0.676	10.685	0.676		
1, 123, 41	6.123	41	2.135	-0.83	9.227	0.24	1.1, 5, L	5.230	0.24	1.1, 5, L	4.191	-2.17	19.166	1.23	2.125	-1.74	7.128	-0.66	6.179	-0.175	7.128	-0.66	12.265	-0.264		
1, 143, 153	6.143	153	2.135	-0.27	4.130	0.93	5.230	0.24	1.1, 5, L	4.191	-2.17	19.166	1.23	1.188	-0.56	6.162	0.516	6.192	0.263	4.130	0.79	10.149	-0.133			
o, 26, L	3.297	-2.93	1, 10, L	6.193	-2.11	2.138	1.35	-1, 1, L	5.197	-2.25	19.113	1.32	2.029	0.756	1.106	-1.82	11.154	1.32	6.292	0.263	-3.13, L	2.196	2.196	2.196		
12, 118, -86	1.923	953	9.160	1.67	4.179	0.73	3.162	1.65	3.357	0.95	6.336	2.75	-2.12, L	1.165	-1.62	7.322	-0.83	2.12, L	1.165	-1.62	7.322	-0.83	21.156	-0.137		
2, 105, 119	6.688	-653	2.167	-1.26	3.162	1.62	3.162	1.62	3.162	1.62	6.627	0.95	2.12, L	1.165	-1.62	7.322	-0.83	2.12, L	1.165	-1.62	7.322	-0.83	21.156	-0.137		
2, 215, -238	1.215	-238	2.167	-0.51	7.161	0.51	6.688	-0.68	2.163	1.54	11.133	1.28	6.323	-0.350	2.164	0.641	1.317	-0.161	2.164	0.641	17.112	-0.53				
o, 165, -83	6.165	-83	9.167	1.65	1.682	-0.59	1.682	-0.59	1.682	-0.59	1.392	-0.63	1.681	-0.59	1.392	-0.63	3.254	0.264	1.623	-0.193	3.254	0.264	3.254	0.264		
o, 18, L	2.103	-1.77	-1, 10, L	1.141	-0.44	9.261	2.94	6.263	2.04	3.292	0.52	1.132	-0.56	1.132	-0.56	3.291	-0.262	3.291	-0.262	3.291	-0.262	3.291	-0.262			
15, 188, -29	1.127	-1.11	4.138	1.24	1.127	-0.51	1.127	-0.51	1.127	-0.51	1.127	-0.51	4.214	1.98	5.85	-0.86	12.185	-1.87	6.139	1.18	10.183	-0.124				
11, 123, 76	7.123	76	1.127	1.82	2.159	-2.27	8.376	0.52	12.159	1.36	5.97	0.79	1.127	-0.51	14.345	-1.32	6.139	-0.139	15.119	-0.139	15.119	-0.139				
10, 135, 143	1.286	143	7.183	-1.63	2.268	-2.95	7.532	0.344	12.159	1.36	5.97	0.79	1.127	-0.51	20.242	-0.261	11.296	-0.258	10.227	-0.255	10.227	-0.255				
8, 240, -245	14.106	-245	1.127	1.11	3.113	-1.11	6.502	-0.312	12.158	1.35	9.233	-0.226	2.127	1.23	12.255	1.241	9.245	-0.254	12.255	1.241	9.245	-0.254				
4, 142, 153	1.142	153	6.164	-0.77	1.127	1.11	5.464	-0.688	21.163	1.54	11.133	1.28	6.323	-0.350	23.164	0.641	13.162	0.181	8.261	0.255	8.261	0.255				
2, 143, -121	1.143	-121	1.294	-0.266	15.167	-0.98	1.164	-0.78	6.673	-0.68	1.127	-0.51	1.127	-0.51	1.127	-0.51	1.127	-0.51	1.127	-0.51	1.127	-0.51				
1, 228, 266	9.393	987	11.232	2.44	19.270	-2.40	2.155	1.58	1.127	-0.51	1.127	-0.51	1.127	-0.51	1.127	-0.51	1.127	-0.51	1.127	-0.51	1.127	-0.51				
8, 481, 387	8.481	387	10.111	-0.25	11.257	-0.24	1.127	-0.51	1.127	-0.51	1.127	-0.51	1.127	-0.51	1.127	-0.51	1.127	-0.51	1.127	-0.51	1.127	-0.51				
0, 16, L	8.161	-1.26	8.226	-1.24	1.127	-0.51	1.127	-0.51	1.127	-0.51	1.127	-0.51	1.127	-0.51	1.127	-0.51	1.127	-0.51	1.127	-0.51	1.127	-0.51				
14, 202, 104	5.699	-566	6.131	-116	15.183	2.00	1.127	-0.51	1.127	-0.51	1.127	-0.51	1.127	-0.51	1.127	-0.51	1.127	-0.51	1.127	-0.51	1.127	-0.51				
10, 313, -303	4.661	-386	5.219	218	16.322	-319	2.1421	-1.533	4.127	-1.07	1.127	-0.51	1.127	-0.51	1.127	-0.51	1.127	-0.51	1.127	-0.51	1.127	-0.51				
8, 339, 336	3.129	1235	2.146	-125	17.157	-0.96	3.832	0.84	18.128	-1.32	3.286	1.94	1.127	-0.51	1.127	-0.51	1.127	-0.51	1.127	-0.51	1.127	-0.51				
4, 246, -256	1.246	-256	9.96	-0.94	19.173	1.67	4.699	0.543	1.127	-0.51	1.127	-0.51	1.127	-0.51	1.127	-0.51	1.127	-0.51	1.127	-0.51	1.127	-0.51				
3, 156, 163	1.367	-156	1.127	-0.51	20.141	0.91	8.632	0.785	2.127	2.29	8.279	-0.297	1.127	-0.51	1.127	-0.51	1.127	-0.51	1.127	-0.51	1.127	-0.51				
2, 112, 116	0.373	379	-1, 17, L	7.714	-0.62	1.119	0.23	8.886	-0.613	1.127	-0.51	1.127	-0.51	1.127	-0.51	1.127	-0.51	1.127	-0.51	1.127	-0.51					
0, 14, L	8.14	4, L	3.186	-1.79	1.127	-0.51	8.886	-0.613	1.127	-0.51	1.127	-0.51	1.127	-0.51	1.127	-0.51	1.127	-0.51	1.127	-0.51	1.127	-0.51				
17, 188, -87	21.141	188	7.360	-366	8.284	-2.63	14.193	-0.88	2.128	1.23	1.127	-0.51	1.127	-0.51	1.127	-0.51	1.127	-0.51	1.127	-0.51	1.127	-0.51				
16, 119, 158	16.166	-174	9.146	-142	17.154	1.66	12.477	-0.67	4.391	0.293	1.127	-0.51	1.127	-0.51	1.127	-0.51	1.127	-0.51	1.127	-0.51	1.127	-0.51				
15, 186, 166	16.186	124	11.136	-0.89	14.198	0.56	13.543	-0.334	3.669	0.721	2.128	1.23	1.127	-0.51	1.127	-0.51	1.127	-0.51	1.127	-0.51	1.127	-0.51				
14, 160, -109	14.160	-109	13.135	-120	18.141	0.41	14.211	-0.197	1.127	-0.51	1.127	-0.51	1.127	-0.51	1.127	-0.51	1.127	-0.51	1.127	-0.51	1.127	-0.51				
12, 109, -98	12.109	-98	12.146	-121	18.141	0.41	14.211	-0.197	1.127	-0.51	1.127	-0.51	1.127	-0.51	1.127	-0.51	1.127	-0.51	1.127	-0.51	1.127	-0.51				
19, 412, 484	13.378	-386	1.127	-0.51	6.191	-0.68	7.419	-0.56	1.127	-0.51	1.127	-0.51	1.127	-0.51	1.127	-0.51	1.127	-0.51	1.127	-0.51	1.127	-0.51				
9, 194, -185	12.163	-173	1.127	-0.51	6.166	-0.66	7.419	-0.56	1.127	-0.51	1.127	-0.51	1.127	-0.51	1.127	-0.51	1.127	-0.51	1.127	-0.51	1.127	-0.51				
5, 334, -344	11.133	-127	5.484	-0.415	1.127	-0.51	1.127	-0.51	1.127	-0.51	1.127	-0.51	1.127	-0.51	1.127	-0.51	1.127	-0.51	1.127	-0.51	1.127	-0.51				
7, 299, -86	2.299	-86	3.538	-516	3.538	-516	1.127	-0.51	1.127	-0.51	1.127	-0.51	1.127	-0.51	1.127	-0.51	1.127	-0.51	1.127	-0.51	1.127	-0.51				
13, 339, 335	21.166	-335	4.129	-111	5.369	-565	10.166	1.00	10.166	1.00	1.127	-0.51	1.127	-0.51	1.127	-0.51	1.127	-0.51	1.127	-0.51	1.127	-0.51				
17, 157, 177	2.157	-177	8.287	-395	8.287	-395	3.128	-0.57	1.127	-0.51	1.127	-0.51	1.127	-0.51	1.127	-0.51	1.127	-0.51	1.127	-0.51	1.127	-0.51				
16, 153, -152	2.153	-152	2.142	-148	11.244	2.22	7.488	0.381	0.242	-0.217	1.127	-0.51	1.127	-0.51	1.127	-0.51	1.127	-0.51	1.127	-0.51	1.127	-0.51				
12, 242, 292	23.197	-43	3.282	-359	3.282	-359	12.288	-1.95	5.405	-0.378	-2.12, L	1.127	-0.51	1.127	-0.51	1.127	-0.51	1.127	-0.51	1.127	-0.51	1.127	-0.51			
13, 199, 231	21.199	-136	3.282	-359	3.282	-359	12.288	-1.95	5.																	

Table 5 (cont.)

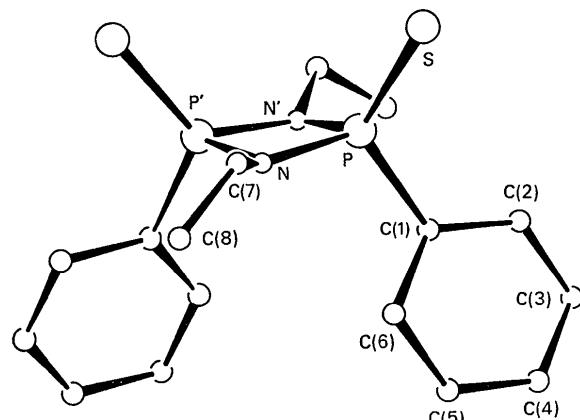


Fig. 1. Molecular shape and numbering of the atoms. A primed atom is related to the corresponding unprimed atom by rotation about the diad axis of the molecule.

ecule comprising the phosphazane ring, sulphur atoms, and carbon atoms C(1), C(1'), C(7), and C(7'). The remaining carbon atoms were not included because it was thought unlikely that the whole molecule behaves as a rigid body. The translational and librational tensors (Table 8) are referred to axes parallel to the inertial axes of this group of 10 atoms but the position of the origin of the librational axes was varied to give the best fit of observed and calculated U_{ij} values (Pawley, 1963). Because of the molecular symmetry, one of the axes of T and ω (chosen as axis 3) must coincide with the crystallographic diad axis so that $T_{13} = T_{23} = 0$ and $\omega_{13} = \omega_{23} = 0$. Axis 1 is very nearly parallel to the P...P' line and axis 2 to the N'...N line. The position obtained for the origin (0, 0.196, 0.250) is displaced from the phosphazane ring by 0.3 Å towards the side occupied by the phenyl groups, *i.e.* towards the centre of gravity of the whole molecule. Since ω_{12} is also zero

(Table 8) the principal axes of ω are parallel to the inertial axes of the group of 10 atoms. This is not the case for the translational tensor. Bond lengths corrected for the effect of the molecular oscillations

(Cruickshank, 1956, 1961) are given in Table 6(b). The correction is particularly important for the P-S bond but comparable to the standard deviation for the P-N and P-C bonds. For the bond angles the correction is negligible.

Table 6. Bond lengths (\AA) and bond angles ($^\circ$) with estimated standard deviations

(a) Bond lengths from the least-squares refinement

P-N	1.688 (4)	P-C(1)	1.791 (5)
P-N'	1.690 (4)	C(1)-C(2)	1.403 (6)
P-S	1.917 (2)	C(2)-C(3)	1.378 (8)
		C(3)-C(4)	1.373 (9)
N-C(7)	1.454 (7)	C(4)-C(5)	1.382 (9)
		C(5)-C(6)	1.383 (8)
C(7)-C(8)	1.450 (10)	C(6)-C(1)	1.375 (8)
		Mean	1.382 (11)

(b) Corrected for molecular oscillations

P-N	1.693 (4)	P-C(1)	1.797 (5)
P-N'	1.696 (4)		
Mean	1.695 (5)*	N-C(7)	1.457 (7)

(c) Bond angles

N-P-N'	84.5 (3)	P-N-C(7)	128.8 (3)
P-N-P'	95.0 (3)	P'-N-C(7)	129.2 (3)
S-P-C(1)	113.4 (2)	P-C(1)-C(2)	119.7 (4)
		P-C(1)-C(6)	121.6 (4)
N-P-S	120.3 (2)	C(1)-C(2)-C(3)	119.7 (5)
N'-P-S	118.5 (2)	C(2)-C(3)-C(4)	121.1 (5)
N-P-C(1)	107.3 (2)	C(3)-C(4)-C(5)	119.4 (6)
N'-P-C(1)	109.3 (2)	C(4)-C(5)-C(6)	119.9 (6)
N-C(7)-C(8)	113.4 (6)	C(5)-C(6)-C(1)	121.1 (5)
		C(6)-C(1)-C(2)	118.7 (5)

* These standard deviations have been enlarged to allow for possible error in the unit-cell parameters.

Table 7. Root-mean-square amplitudes of thermal vibration (\AA) along the principal axes of the vibration ellipsoids

The direction of each principal axis is specified by the angles it makes with the orthogonal axes a' , b , and c .

	a'	b	c		a'	b	c		
S	0.281	35°	73°	61°	C(4)	0.334	22	69	85
	0.229	119	36	71		0.275	82	124	36
	0.174	107	120	36		0.203	110	42	55
P	0.219	45	48	77	C(5)	0.374	21	69	94
	0.190	49	138	83		0.247	96	62	28
	0.153	104	94	15		0.217	110	36	118
N	0.239	92	8	82	C(6)	0.341	17	73	87
	0.201	4	88	87		0.223	106	17	96
	0.169	93	98	9		0.203	95	85	7
C(1)	0.242	36	58	75	C(7)	0.324	108	21	80
	0.199	118	32	105		0.236	40	69	122
	0.173	111	85	21		0.190	56	89	34
C(2)	0.277	30	66	72	C(8)	0.403	100	25	68
	0.229	111	24	101		0.311	137	112	55
	0.167	111	86	21		0.196	48	100	43
C(3)	0.307	16	83	76					
	0.270	91	24	114					
	0.199	106	67	28					

Discussion

Molecular geometry

The isomer of 1,3-diethyl-2,4-diphenyl-2,4-dithiocyclodiphosphazane with melting point 137°C has the *cis* configuration as proposed by Flint *et al.* (1971). The molecules possess exact C_2 symmetry but the phosphazane ring is significantly non-planar [see Table 9, plane (i)]. There is a dihedral angle of 11.5° between the two halves of the ring which meet in the P...P line and of 10.5° between the halves which meet in the N...N line (the difference arises from the inequality of the bond angles at the phosphorus and nitrogen atoms). The torsion angles of the ring bonds are all 7.8°, the symmetry of the ring being $C_{2v}(mm2)$. In contrast the phosphazane ring in the *trans* isomer is planar (Bullen, Rutherford & Tucker, 1973), as are the rings in *trans*-[NMeP(S)Ph]₂ (Ibrahim *et al.*, 1971) and *trans*-[NPhP(S)Ph]₂ (Peterson & Wagner, 1973). The (B-N)₂ ring in [Cl₂BNMe₂]₂ is also planar (Hess, 1963) but non-planar four-membered rings are known for (C-C)₂ in cyclobutane (Dunitz & Schomaker, 1952) and its derivatives (Owen & Hoard, 1951; Le-

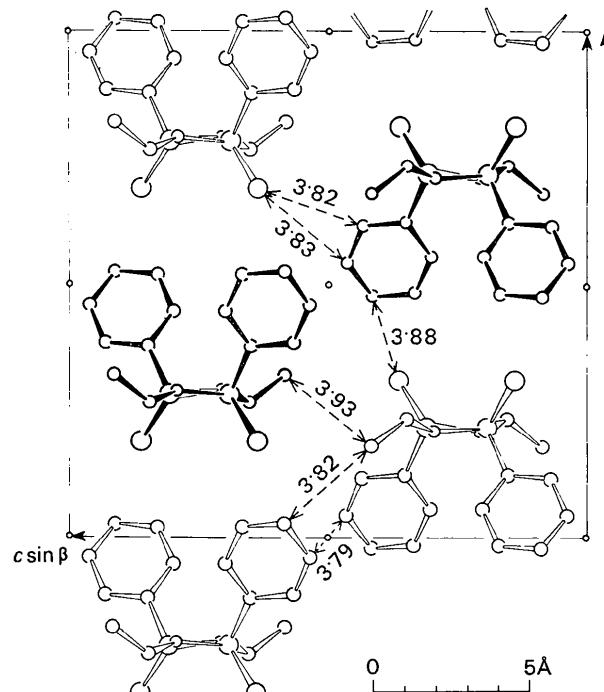


Fig. 2. Projection of the structure down a showing intermolecular S...C and C...C distances (\AA). The lightly shaded molecules are at a height $x=0$ and the heavily shaded molecules at $x=\frac{1}{2}$.

Table 8. *Translational* (T , Å²) and *librational* (ω , deg²) tensors for the central part of the molecule

See text for definition of the axial system; the origin of ω is at (0, 0.196, 0.250).

$$T = \begin{pmatrix} 0.031(3) & -0.006(3) & 0 \\ 0.033(3) & 0 & 0 \\ 0 & 0.043(4) & \end{pmatrix} \quad \omega = \begin{pmatrix} 27(3) & 0(3) & 0 \\ 4(3) & 0 & 0 \\ 10(3) & 0 & \end{pmatrix}$$

Table 9. Equations of mean planes through sets of atoms and distances (Å) of atoms from the plane (in square brackets)

Coordinates in Å are referred to orthogonal axes a' , b , and c .

Plane (i): P, N, P', N' $Y=3.464$
 [P, P' 0.057; N, N' -0.057]

Plane (ii): P, N, P', C(7) $-0.082X + 0.995Y - 0.053Z = 3.234$
 [P, P' 0.049; N -0.175, C(7) 0.077]

Plane (iii): C(1)-C(6) $0.947X + 0.320Y + 0.040Z = 1.878$
 [C(1) 0.001, C(2) 0.011, C(3) -0.018, C(4) 0.012, C(5) 0.000, C(6) -0.006, P 0.020]

maire & Livingston, 1952) and for (P-B)₂ in [(Ph₂P)BI₂]₂ (Bullen & Mallinson, 1972). It is presumed that these rings are bent in order to allow greater clearance between the exocyclic atoms or groups, and this is probably also the reason for the bending in *cis*-[NEtP(S)Ph]₂, since with a planar ring the two phenyl rings would come closer together. (Close contact between the phenyl rings is also relieved by a twist about the P-C bond, see below.) In the *trans*-cyclo-diphosphazanes the phenyl groups lie on opposite sides of the ring, so allowing it to be planar.

The molecular dimensions of *cis*- and *trans*-[NEtP(S)Ph]₂, compared in Table 10, are for the most part very similar. The comments on the P-N, P-S, and P-C bond lengths and on the coordination of the nitrogen and phosphorus atoms made in discussion of *trans*-[NEtP(S)Ph]₂ (Bullen, Rutherford & Tucker, 1973) apply also to the *cis* isomer. The C-C bond in the ethyl group of the *cis* isomer is surprisingly short and we have no explanation for this. The S-P-C-C torsion angle is not the same for the *cis* and *trans* isomers. The small angle in the *trans* isomer signifies that the phenyl group is almost eclipsed with the P=S bond, a conformation which produces a close intra-

molecular non-bonded S···C contact. As the eclipsed conformation occurs also in *trans*-[NMeP(S)Ph]₂ and *trans*-[NPhP(S)Ph]₂ it seems unlikely to have been caused by intermolecular forces (Bullen, Rutherford & Tucker, 1973). The larger twist of the phenyl group in the *cis* isomer is almost certainly caused by repulsion between the two phenyl groups within the molecule: C(6) and C(6') are only 3.68 Å apart. The conformation of the ethyl group (P-N-C-C torsion angle 144°) is remarkably similar to the conformation in one of the molecules in the *trans* isomer structure.

Intermolecular distances

The arrangement of the molecules in the unit cell is shown in Fig. 2. The molecular packing is controlled mainly by close S···C and C···C contacts. In addition to those marked in Fig. 2, there are close contacts between molecules separated by the a translation: S···C(7') (1+x, y , z) 3.95, C(8)···C(2') (1+x, y , z) 3.56, and C(8)···C(3') (1+x, y , z) 3.77 Å. Four of the five C···C contacts quoted involve the methyl carbon atom C(8). The shortest S···C contact is the same length (3.82 Å) in the *cis* and *trans* isomers and the distances between ethyl groups are also very similar in the two structures. There is a short S···S distance in *trans*-[NEtP(S)Ph]₂ but this type of contact does not occur in the *cis* isomer.

Table 10. Molecular dimensions in the two isomers of [NEtP(S)Ph]₂

Bond lengths	<i>cis</i>	<i>trans</i>
P-N	1.695 (5) Å	1.688 (5) Å
P-S	1.922 (4)	1.928 (4)
P-C	1.797 (5)	1.807 (5)
N-C	1.457 (7)	1.468 (6)
C-C	1.450 (10)	1.503 (9)
Bond angles		
N-P-N'	84.5 (3)°	83.3 (2)°
P-N-P'	95.0 (3)	96.8 (2)
P-N-C	129.0 (2)	129.0 (3)
S-P-C	113.4 (2)	113.5 (2)
Torsion angles		
S-P-C-C	35°	12°
P-N-C-C	144	80, 145

We are indebted to Professor R. A. Shaw (Birkbeck College, London) for supplying a sample of the diphosphazane, the University of Essex Computing Centre and the Atlas Computer Laboratory, Chilton for the use of their facilities, Dr G. M. Sheldrick for making his computer program available, Mr N. Lewis for the preparation of diagrams, and the Science Research Council for the award of a research studentship (to P.A.T.).

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The Crystal Structure of Histamine Sulphate Monohydrate

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(Received 17 February 1973; accepted 13 June 1973)

Histamine sulphate crystallizes in the space group $P2_1$ with four formula units, $(C_5H_{11}N_3^{2+} \cdot SO_4^{2-} \cdot H_2O)$, in the unit cell of dimensions $a=13.124$, $b=7.037$, $c=10.983$ Å and $\beta=104.16^\circ$. The structure was determined by the heavy-atom method and refined by least-squares calculations to $R=0.089$. The imidazole ring is protonated and the bond angle $C^{\prime\prime}-N^{\delta}-C^{\epsilon}$ in the protonated ring is larger than that for an unprotonated one. The skeleton of the histamine molecule is roughly planar, although in histamine phosphate the imidazole ring and the aliphatic chain are nearly perpendicular to each other. There is a partial disorder associated with one of the water molecules. The hydrogen-bond scheme is complicated, there being three bifurcated hydrogen bonds and two $C-H \cdots O$ hydrogen bonds.

Introduction

The tertiary structures of many enzymes have been determined by X-ray diffraction, and it has become clear that histidine often plays a key role in the catalytic activity of enzymes. In particular, the imidazole group, the functional side chain of histidine, participates in the activity of many enzymes.

Accurate structure determinations of histidine have been done by Donohue & Caron (1964), Bennett, Davidson, Harding & Morelle (1970) and Madden, McGandy & Seeman (1972). On the other hand, only a few analyses have been reported for the structure of histamine which is obtained from histidine by decarboxylation. The substance has also an important physiological activity. The structure analyses of its phosphate and sulphate were therefore both performed in our laboratory. In this paper only the structure of histamine sulphate will be described, because the structure of the phosphate has already been reported by Veidis, Palenik, Schaffrin & Trotter (1969).

Experimental

The colourless and transparent crystals elongated along the monoclinic b axis were obtained by dissolving commercial histamine in 2*N* sulphuric acid. They are hygroscopic and deteriorate quickly on exposure to air: hence all the X-ray data were taken with the crystal coated in a collodion film.

The crystal data are summarized in Table 1. The systematic absence of $0k0$ reflexions with k odd shows that the space group is either $P2_1$ or $P2_1/m$. The $N(z)$ test suggested the space group to be $P2_1$. The $h0l$ reflexions are weak when $h+l$ is odd, so there exists a pseudo-*n*-glide symmetry.

Table 1. *Crystal data*

$C_5H_{11}N_3^{2+} \cdot SO_4^{2-} \cdot H_2O$
$a=13.124$, $b=7.037$, $c=10.983$ Å, $\beta=104.16^\circ$
$V=983.5$ Å ³ , F.W. 227.24
$D_x=1.535$ g cm ⁻³ for $Z=4$
D_m (flotation)=1.52 g cm ⁻³
$\mu=3.31$ cm ⁻¹ (Mo $K\alpha$)
Systematic absence: $0k0$, $k=2n+1$
Space group: $P2_1$

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