tive temperature factor' represents not only true thermal vibration but also some spread in position of the atom due to spatial disorder.

Table 3 lists isotropic *B* values determined in the course of the refinement procedure for the measurements on Schmirntal albite at 20, 300 and 600°C, and on Ramona albite at -180° C (Williams, 1961). When plotted against absolute temperature (Fig. 2) it is seen that for each kind of atom the *B*-*T* variation is very closely linear in the range -180 to 300°C, so that extrapolation to T=0 is justified. For sodium, aluminium and silicon atoms the extrapolation gives values of *B* very close to 0, whereas for oxygen atoms (at T=0) B>0.

Table 3. Low albite. Isotropic temperature factors $B(Å^2)$

	(WM, 1964) - 180°C	(S ₂) 20°C	(S ₂) 300°C	(S ₂) 600°C
Na	1.0 (3)	3.2 (1)	5.6 (1)	6.7 (2)
Al	0.15 (6)	0.72(6)	1.04 (9)	1.1 (1)
Si (average)	0.18 (6)	0.63 (4)	0.94 (6)	1.20 (8)
O (average)	0.38 (6)	1.01 (6)	1.65 (7)	2.0 (1)

Notes. Standard deviations are in brackets and refer to the last figure given.

Measurements on Schmirntal second fragment (S_2) and from Williams & Megaw (1964).

The difference between Na, Al and Si on the one hand, and O on the other, may be taken as evidence in support of a model in which the *position* of the Na atom is as clearly defined as are the positions of Al and Si atoms at the centres of their tetrahedral groups. Its large anisotropy is then due to anisotropic thermal vibration, not to positional disorder. By contrast, the O atoms show some positional disorder arising from the differences in Si–O and Al–O bond lengths and incomplete Al,Si order.

6. Conclusion

Measurements of diffraction intensities from low albite at 300 and 600°C have been used to study the anisotropy of the sodium atom as seen in [100] projection. Comparison with previous studies at room temperature and at -180° C provides strong support for the view that the observed anisotropy represents a true anisotropic thermal vibration of the sodium atom.

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The Molecular and Crystal Structure of Hippuric Acid

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Hippuric acid, C_6H_5 .CO.NH.CH₂.COOH, crystallizes with four molecules in an orthorhombic unit cell with a=8.874, b=10.577, c=9.117 Å, space group $P2_12_12_1$. The structure has been determined by direct methods and refined by full-matrix least-squares computations. The final *R* value is 5.8%. The benzene ring, the peptide part and the carboxylic group are planar and twisted with respect to each other. The molecules are held together in three dimensions by one O-H...O and one N-H...O hydrogen bond to the peptide oxygen atom.

Introduction

Hippuric acid



is formed in mammals when benzoic acid is detoxicated by conjugation with glycine. It is excreted in urine and constitutes about a half per cent of the nitrogen excretion in man. The crystallographic and optical data of hippuric acid have been given by Ringertz (1969).

Experimental

Commercially available hippuric acid was recrystallized in water. The cell axes a and b were determined from photographic measurements of high-angle reflexions with Cu $K\alpha$ radiation ($\lambda_{k\alpha 1} = 1.54051$ Å). The *c* axis was determined with a Philips automatic singlecrystal diffractometer PAILRED using Mo $K\alpha$ radia-

Table 1. Final observed and calculated structure factors

The sign * represents a 'less than' reflexion. The columns are l, $10F_o$, $10F_c$, 10A and 10B.

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Fig. 1. Diagrams showing bond lengths and angles in the hippuric acid molecule.

tion. The following dimensions of the orthorhombic unit-cell were observed. The refractive indices refer to the crystallographic axes.

$a = 8.874 \pm 2$ Å	$\beta = 1.592^{\circ}$
$b = 10.577 \pm 3$	$\gamma = 1.760$
c = 9.117 + 3	$\alpha = 1.535$

Systematic absences were h00, 0k0 and 00l with h, kand l respectively equal to 2n+1, space group $P2_12_12_1$. $D_{obs} = 1.385$ g.cm⁻³ and $D_{calc} = 1.390$ g.cm⁻³, assuming Z = 4. Two sets of reflexion data were recorded using two small crystals measuring approximately $0.15 \times 0.15 \times 0.15$ mm. The first data set was collected using Ni-filtered Cu $K\alpha$ radiation and a General Electric single-crystal orienter which was operated manually. The second set of data was collected with a Philips automatic single-crystal diffractometer, PAIL- RED, using monochromatized Mo $K\alpha$ radiation. In the first case 1098 structure amplitudes were obtained of which the 112 weakest were regarded as not observable. The two sets of data were corrected for Lorentz and polarization factors and put on an absolute scale. It was found that there was strong extinction of the most intense reflexions in the first data set and accordingly the 25 highest structure amplitudes were taken from the second data set. The *E* values were then calculated, giving the following statistical averages

	$\{ E \}$	$\{ E \}$	$\{ E^2-1 \}$
Observed	0.840	1.000	0.797
Theoretical for acentric	0.886	1.000	0.736
Theoretical for centric	0.798	1.000	0.968

Structure determination

The determination of the structure took four years and most crystallographic methods have been applied. However the optical indicatrix and the strength of the 102 and 202 reflexions indicated planar molecules with all parts parallel to the *b* axis and with the molecules inclined about 70° to each other. Spherical Patterson sections at 1.4 and 2.4 could be explained in detail by an essentially planar molecular model. In retrospect all assumptions were found to have been correct except that the carboxyl group was inclined at 85° with respect to the rest of the molecule and not coplanar with it.

The structure was finally solved using direct methods in a computer program series, GAASA 1-7 (Lindgren, Lindqvist & Nyborg, 1970). 273 reflexions with $E \ge 1.2$ were used in a symbolic addition procedure having a basic set of 10 symbols which were given to the strongest normalized structure factors taking part in the largest number of Sayre triplets. The number of symbols was then reduced on a statistical basis until 4 were left after 7 cycles:



Fig. 2. Thermal ellipsoid representation of a hippuric acid molecule showing the labelling of the atoms. The ellipsoids enclose 50% probability. The hydrogen atoms are indicated by small spheres.

h	k	l	E	Phase
5	0	6	3.1	0
8	7	0	2.9	0
0	7	5	2.7	π
1	12	5	2.6	π

These symbols were then given the above tabulated phase values to fix the origin and the enantiomorph. From the given values 152 preliminary phases were calculated and an iterative use of the tangent formula (Karle & Hauptman, 1956) was started. At the end of these calculations an E value map was calculated from all 273 phases and then automatically scanned for peaks. From the 22 highest peaks two geometrically perfect molecular arrangements could be found. These two models were perfectly alike and related to each other by a 1.4 Å translation along the b axis. None of the two molecular positions converged, however, when refined by least-squares methods. When hydrogen bonding possibilities were taken into consideration the position exactly between the two was refined to R=14% after 3 cycles.

Refinement of the structure

Introduction of anisotropic temperature factors reduced the R value to 9.8%. At this stage a difference synthesis was performed revealing all nine hydrogen atom positions. The hydrogen positional parameters were refined but the hydrogen atoms were given the same anisotropic temperature factors as that of the covalently bonded 'heavy' atom. A weighting scheme of the form $w=1/(3+F_o+F_o^2/55)$ (Cruickshank, 1965, p. 114) was used. The final R value obtained after two



Fig. 3. Drawing of the crystal structure projected along the *a* axis showing the hydrogen bonding system.

additional cycles was 5.8 %. The average and maximum positional shifts of the non-hydrogen atoms in the final cycle were 23 and 72 % respectively of the estimated standard deviations. Observed and calculated structure factors are listed in Table 1.

Results and discussion

Molecular arrangement

The hippuric acid molecule is not extended to its maximum length. The carboxyl group has been rotated around the N-C(8) bond forming an approximate right angle with the rest of the molecule. This brings one of the carboxyl oxygen atoms into a hydrogen bonding position with respect to the peptide oxygen atom in the molecule related to the original by the

 Table 2. Final fractional atomic positional parameters and anisotropic temperature factor parameters, all with estimated standard errors

The thermal parameters are in the form: exp $(-\beta_{11}h^2 - \beta_{22}k^2 - \beta_{33}l^2 - 2\beta_{12}hk - 2\beta_{23}kl - 2\beta_{13}hl)$.

All values are $\times 10^4$

										•								
	x/a	σ	y/b	σ	z/c	σ	β_{11}	σ	β_{22}	σ	β_{33}	σ	β_{12}	σ	β_{13}	σ	β_{23}	σ
O(1)	1164	4	5256	3	10275	3	123	5	59	3	78	4	12	3	14	4	-10	3
O(2)	4628	4	6634	3	9341	5	119	5	67	3	172	6	10	4	- 53	5	1	4
O(3)	3726	4	8527	3	8717	4	111	5	49	3	150	5	-5	3	- 33	5	1	3
N	2131	5	5433	3	8009	4	100	5	49	3	74	4	-9	3	2	5	-3	3
C(1)	1460	5	3364	4	8897	5	71	5	48	3	77	5	1	4	-9	5	-1	3
C(2)	2200	6	2711	4	7761	5	106	6	54	4	99	6	- 3	4	14	6	-4	4
C(3)	2070	6	1409	4	7674	6	122	7	53	4	128	7	6	5	11	7	-9	5
C(4)	1221	6	739	4	8709	6	102	6	54	4	146	8	-2	5	-13	7	4	5
C(5)	479	6	1382	4	9826	6	105	7	65	4	127	7	- 8	5	6	6	22	5
C(6)	587	5	2697	4	9924	6	98	6	61	4	95	6	-9	4	6	5	3	4
C(7)	1575	4	4763	4	9111	5	67	5	51	3	78	5	1	4	-10	4	-2	4
C(8)	2215	6	6823	4	8105	6	90	6	46	4	110	6	1	4	-5	6	4	4
C(9)	3668	5	7274	4	8798	5	97	6	53	4	87	5	0	4	2	6	-4	4
H(l)	2939	71	3224	55	7044	64												
H(2)	2561	68	945	54	6702	75												
H(3)	1075	68	-192	54	8559	72												
H(4)	-177	69	1072	53	10691	72												
H(5)	-238	68	3157	51	10643	66												
H(6)	2124	70	5308	54	7045	70												
H(7)	1880	70	7214	55	7035	69												
H(8)	1306	70	7155	53	8660	68												
H(0)	4388	74	8794	56	9107	78												

Non-hydr	ogen						
intramolecular distances							
C(1)-C(2)	1·407 (7) Å						
C(1) - C(6)	1.405 (6)						
C(1) - C(7)	1.496 (6)						
C(2) - C(3)	1.384 (6)						
C(3) - C(4)	1.400 (8)						
C(4) - C(5)	1.391 (8)						
C(5) - C(6)	1.396 (7)						
C(8) - C(9)	1.513 (7)						
C(7)-N	1.336 (6)						
C(8)-N	1.454 (6)						
C(7)-O(1)	1.238 (5)						
C(9)-O(2)	1.196 (6)						
C(9)–O(3)	1.328 (5)						
Angles involving not	n-hydrogen atoms						
C(2)-C(1)-C(6)	120·1 (4)°						
C(2) - C(1) - C(7)	123.3 (4)						
C(6) - C(1) - C(7)	116.6 (4)						
C(1) - C(2) - C(3)	119.5 (5)						
C(2)-C(3)-C(4)	120.6 (5)						
C(3)-C(4)-C(5)	120.1 (4)						
C(4) - C(5) - C(6)	120.1 (5)						
C(5)-C(6)-C(1)	119.7 (4)						
C(1)-C(7)-N	117.9 (4)						
C(1)-C(7)-O(1)	120.6 (4)						
N - C(7) - O(1)	121.5 (4)						
C(7) - N - C(8)	121.2 (4)						
N - C(8) - C(9)	112.5 (4)						
C(8)-C(9)-O(2)	127.0 (4)						
C(8) - C(9) - O(3)	108.9 (4)						
O(2)-C(9)-O(3)	124.1 (4)						

Table 3. Distances and angles of the hippuric acid molecule, with estimated standard deviations

twofold screw axis parallel to the *a* axis. The molecules are further held together by a N-H···O hydrogen bond to the peptide oxygen atom in the *c* axis screwrelated molecule. The molecules are oriented with their long dimension essentially parallel to the *b* axis with the non-carboxyl parts of the molecule tilted about 35° with respect to the (100) plane. The molecular arrangement can be seen in Fig. 1.

Molecular structure

The labelling and the thermal displacement ellipsoids of the atoms can be seen in Fig. 2 and the final positional and vibrational parameters in Table 2. From these values the interatomic distances and angles have been calculated and they are shown in Fig. 3, and are shown together with their estimated standard deviations in Table 3. The root-mean-square components of thermal displacement along the three principal axes are tabulated in Table 4 together with the angles between these principal axes and the unit-cell axes.

The configuration of the molecule is in agreement with earlier structure determinations on similar structures. Compared with the structure of *N*-acetylglycine, CH₃.CO.NH.CH₂.COOH (Carpenter & Donohue, 1950) the average deviations for comparable nonhydrogen bond lengths and angles are 0.008 Å and 1.3° respectively and no single deviation is significant. The dimensions of the peptide part of the molecule are in relatively good agreement with the averaged values given by Marsh & Donohue (1967). In this case the

Distances to	hydrogen atoms
C(2) - H(1)	1·07 (6) Å
C(3) - H(2)	1.10 (7)
C(4) - H(3)	1.00 (6)
C(5) - H(4)	1.03 (6)
C(6) - H(5)	1.10 (6)
N-H(6)	0.89 (6)
C(8) - H(7)	1.10 (6)
C(8) - H(8)	1.02 (6)
O(3) - H(9)	0.74 (7)
. , ,	

Angles	
involving hydroger	n atoms
C(1) - C(2) - H(1)	119 (3)°
C(3) - C(2) - H(1)	121 (3)
C(2) - C(3) - H(2)	117 (3)
C(4) - C(3) - H(2)	122 (3)
C(3) - C(4) - H(3)	118 (4)
C(5) - C(4) - H(3)	121 (4)
C(4) - C(5) - H(4)	132 (3)
C(6) - C(5) - H(4)	108 (3)
C(5) - C(6) - H(5)	116 (3)
C(1) - C(6) - H(5)	123 (3)
C(7) - N - H(6)	130 (4)
C(8) - N - H(6)	103 (4)
NC(8)-H(7)	108 (3)
C(9)-C(8)-H(7)	119 (3)
NC(8)H(8)	109 (3)
C(9) - C(8) - H(8)	111 (3)
H(7)-C(8)-H(8)	96 (5)
C(9)-O(3)-H(9)	113 (5)

mean deviations for bonds and angles are 0.006 Å and 1.3° respectively. The benzene ring has a normal configuration with an average aromatic C-C bond length of 1.397 Å.

The least-squares planes of the structure

Table 5 shows some least-squares planes calculated through the molecule including only non-hydrogen atoms given equal weight. In the benzene ring (plane I) none of the atoms deviates more than 0.005 Å and that part is accordingly perfectly planar within the experimental error. The significant deviations of the atoms from planarity in the peptide (plane II) and carboxyl (plane III) planes depends essentially on the N-C(8) bond which deviates from both of these planes.

The twist of the molecule can be described in terms of two rotations in the same direction. The peptide plane (plane II) is rotated 14° with respect to the benzene ring (plane I) and the carboxyl group (plane III) 83° with respect to the peptide group. The rotations are around the C(1)-C(7) and N-C(8) bonds respectively.

Hydrogen bonding

Both available non-carbon-bonded hydrogen atoms are involved in hydrogen bonds to the peptide oxygen atom. This is demonstrated in Fig. 1 and the distances and angles involved are tabulated in Table 6. The N-H···O bond (3.01 Å) thus connects the molecules forming infinite rows along the *c* axis and the O-H···O

Table 4. Principal axes (i) of anisotropic temperature factors, referred to the crystallographic axes ABC

The r.m.s. displacements $\bar{\mu}_i$ are in Å and the direction angles, V, are in degrees.

O(1)	<i>i</i> 1 2 3	$\begin{array}{ccc} \bar{\mu}_i & \sigma \\ 0.160 & 5 \\ 0.195 & 5 \\ 0.228 & 4 \end{array}$	Va 71 91 161	σ 3 6 3	$ \begin{array}{ccc} V_b & \sigma \\ 131 & 5 \\ 45 & 6 \\ 104 & 5 \end{array} $	V _c σ 48 5 45 6 77 5
O(2)	1 2 3	0·179 6 0·202 5 0·292 5	135 61 60	6 8 2	54 9 36 9 87 2	$ \begin{array}{rrrrrrrrrrrrrrrrrrrrrrrrrrrrrrrrrrrr$
O(3)	1	0·164 5	100	8	169 8	87 4
	2	0·193 5	30	4	100 8	117 3
	3	0·265 5	62	3	92 2	28 3
N	1	0·162 6	106	7	158 10	76 16
	2	0·177 6	101	11	102 16	164 15
	3	0·203 5	160	7	72 6	83 11
C(1)	1	0·162 7	61	11	86 13	29 11
	2	0·165 6	148	33	75 86	63 22
	3	0·186 6	78	75	16 83	101 41
C(2)	1 2 3	0·173 6 0·190 7 0·219 7	92 135 135	14 9 9	$\begin{array}{rrrr} 171 & 11 \\ 95 & 18 \\ 82 & 6 \end{array}$	81 14 135 10 46 9
C(3)	1	0·169 7	79	6	165 7	79 5
	2	0·218 7	30	15	75 7	64 15
	3	0·238 7	118	15	85 6	29 14
C(4)	1	0·174 6	93	14	176 8	93 5
	2	0·199 6	14	7	92 14	104 6
	3	0·250 7	76	6	93 4	14 6
C(5)	1	0·173 7	110	9	147 6	115 5
	2	0·209 7	20	9	109 9	98 9
	3	0·243 7	91	9	116 5	26 5
C(6)	1	0·177 7	122	11	143 13	107 13
	2	0·199 7	111	33	59 20	141 36
	3	0·206 7	140	23	72 23	56 37
C(7)	1	0·158 6	154	9	86 24	64 10
	2	0·170 5	90	23	10 19	100 19
	3	0·187 6	64	9	81 17	27 10
C(8)	1	0·162 7	87	11	174 8	95 6
	2	0·189 6	11	12	86 11	101 12
	3	0·217 6	79	12	95 6	12 11
C(9)	1	0·172 6	89	13	165 14	75 14
	2	0·192 6	110	54	104 15	155 44
	3	0·198 6	160	53	87 18	71 52

Table 5. Equations of some least-squares planes in the hippuric acid molecule and the distances of the atoms from these planes

Equations are expressed in the form lA+mB+nC=D where A, B, C and D are in Å and A, B and C are along the crystallographic axes respectively.

Plane	Atoms in plan	e	1	m		n	D
Ι	C(1), C(2), C(3), C(4),	C(5), C(6)	0.8070	-0.0975		0.5824	5.4172
II	C(1), C(7), C(8), N, O	(1)	0.9257	-0.0988		0.3651	3.8232
III	C(8), C(9), N, O(2), O	(3)	-0.4774	0.0360		0.8779	5.7560
	Plane I		Plane II			Plane II	I
	C(1) - 0.005	C(1)	0.014		C(8)	-0.052	
	C(2) 0.000	C(7)	-0.005		Č(9)	-0.009	
	$C(3) \qquad 0.005$	C(8)	0.019		N	0.041	
	C(4) = -0.005	N	-0.023		O(2)	-0.013	
	C(5) = 0.000	Q(1)	-0.004		O(3)	0.033	
	$ $						

Table 6. Some distances and angles involved in the hydrogen bonds

Donor	Acceptor	Hydrogen	$X - H \cdots O$	σ	$H \cdots O$	σ	Х-Н-О	σ
Ν	$O(1)(\frac{1}{2}-x; 1-y; z-\frac{1}{2})$	H(6)	3·011	6	2∙30 Å	6	137°	5
O(3)	$O(1)(\frac{1}{2}+x;1\frac{1}{2}-y;2-z)$	H(9)	2.680	6	1.95	6	166	6

bonds (2.68 Å) connect the molecules in infinite rows along the a axis. Together these two hydrogen bonds form a stabilized three-dimensional intermolecular network.

The proposed intramolecular hydrogen bond for hippuric acid in solution (Schätzle & Rottenberg, 1963) between the unprotonized carboxyl oxygen atom and the nitrogen atom is found to be sterically impossible in the solid state.

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The Crystal Structure of Disodium Dihydrogen Hypophosphate Hexahydrate (Na₂H₂P₂O₆.6H₂O) and

Disodium Dihydrogen Pyrophosphate Hexahydrate (Na₂H₂P₂O₇.6H₂O)

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The crystal structures of the isomorphous disodium hypophosphate hexahydrate (Na₂H₂P₂O₆.6H₂O) and disodium dihydrogen pyrophosphate hexahydrate (Na₂H₂P₂O₇.6H₂O) have been determined with diffractometer data. The space group is C2/c and a unit cell contains four formula units. The unit-cell dimensions of Na₂H₂P₂O₆.6H₂O are a=14.090 (3), b=6.998 (1), c=12.700 (6) Å, $\beta=115.94$ (2)° and those of Na₂H₂P₂O₇.6H₂O are a=14.099 (6), b=6.959 (4), c=13.455 (8) Å, $\beta=117.69$ (4)°. The hypophosphate ion has C_2 symmetry with a P-P distance of 2.190 (1) Å. The mean terminal P-O distance is 1.506 (2) Å while the terminal P-O(H) distance is 1.588 (2) Å. The pyrophosphate ion also has C_2 symmetry. The bridge P-O-P bonds make an angle of 136.1 (1)° and the P-O (bridge) distance is 1.598 (1) Å. The mean value of the terminal P-O distance is 1.494 (2) Å while the terminal P-O(H) distance is 1.569 (2) Å. The bridge oxygen atom of the pyrophosphate is not involved in any appreciable intermolecular bonding and the packing of the ions is similar in both structures.

Introduction

The unit-cell dimensions and space groups for a number of hydrated sodium hypophosphate and pyrophosphate salts have been reported by Corbridge (1957). In both the tetrasodium decahydrate and disodium dihydrogen hexahydrate series the hypophosphate salt (containing a phosphorus-phosphorus bond) and the pyrophosphate salt (containing a phosphorus-oxygen-phosphorus bridge) have the same space group and similar unit-cell dimensions. Corbridge suggested that these two hypophosphate-pyrophosphate salt pairs were isomorphous and interpreted his preliminary b axis projections in the disodium dihydrogen series to indicate that the P-O-P bond in the pyrophosphate was linear with the oxygen atom either on a twofold axis or at a center of symmetry. He found the P-P bond in the hypophosphate to be in a similar orientation.

We have determined the crystal structures with diffractometer data of both the disodium dihydrogen hypophosphate hexahydrate ($Na_2H_2P_2O_6.6H_2O$) and