& Rabinovich, 1978). These structures are symmetrically disposed about a crystallographic twofold axis, which is not the case for diphenic acid. The structure of biphenyl-2,2′-dicarbonyl dichloride (diphenic acid chloride) has both carbonyl O atoms directed toward the bond connecting the two rings (Leser & Rabinovich, 1978), whereas in diphenic acid only the O(3) carbonyl atom is located in this position. The differences in the structure of diphenic acid as compared to the other 2,2′-disubstituted biphenyls probably arise from intermolecular hydrogen bonding in the former.

The minimum-energy structure of diphenic acid calculated by extended Hückel theory methods as an isolated molecule (Botrel & Guerillot, 1974) has a dihedral angle of 85° with the acid groups *anti*, in agreement with the crystal structure. However, the calculated structure has the carboxyl groups orthogonal to the rings.

References

Bodewig, C. (1879). *Z. Kristallogr.* **3**, 413–415.

Botrel, A. & Guerillot, C.-R. (1974). *J. Chim. Phys. Phys. Chim. Biol.* **71**, 1240–1246.

Charton, M. (1971). *Prog. Phys. Org. Chem.* **8**, 235–317.

Chiari, G., Fronczek, F. R., Davis, S. T. & Gandour, R. D. (1981). *Acta Cryst.* B**37**, 1623–1625.

Clark, G. L. (1931). *J. Am. Chem. Soc.* **53**, 3826–3831.

Clark, G. L. & Pickett, L. W. (1931). *J. Am. Chem. Soc.* **53**, 167–177.

Cromer, D. T. (1974). *International Tables for X-ray Crystallography*, Vol. IV, Table 2.3.1. Birmingham: Kynoch Press. (Present distributor D. Reidel, Dordrecht, The Netherlands.)

Cromer, D. T. & Waber, J. T. (1974). *International Tables for X-ray Crystallography* Vol. IV, Table 2.2B. Birmingham: Kynoch Press. (Present distributor D. Reidel, Dordrecht, The Netherlands.)

Frenz, B. A. & Okaya, Y. (1980). *Enraf–Nonius Structure Determination Package*. Enraf–Nonius, Delft, The Netherlands.

Fronczek, F. R., Merrill, M. L. & Gandour, R. D. (1982). *Acta Cryst.* B**38**, 1340–1342.

Huggins, M. L. (1931). *J. Am. Chem. Soc.* **53**, 3823–3826.

Johnson, C. K. (1965). *ORTEP*. Report ORNL-3794. Oak Ridge National Laboratory, Tennessee, USA.

Leser, J. & Rabinovich, D. (1978). *Acta Cryst.* B**34**, 2260–2263.

Main, P., Hull, S. E., Lessinger, L., Germain, G., Declercq, J.-P. & Woolfson, M. M. (1978). *MULTAN78. A System of Computer Programs for the Automatic Solution of Crystal Structures from X-ray Diffraction Data*. Univs. of York, England, and Louvain, Belgium.

Ottersen, T. (1977). *Acta Chem. Scand. Ser. A*, **31**, 480–484.

Pauling, L. & Dickinson, R. G. (1931). *J. Am. Chem. Soc.* **53**, 3820–3823.

Pickett, L. W. (1936). *J. Am. Chem. Soc.* **58**, 2299–2303.

Rømming, C., Seip, H. M. & Øymo, I. A. (1974). *Acta Chem. Scand Ser. A*, **28**, 507–514.

Acta Cryst. (1987). C**43**, 1618–1621

Incipient Type II β-Turn, Internal Water Bridge and Head-to-Tail Sequence in the Structure of Tri-α-aminoisobutyric Acid Dihydrate

By A. N. Jayashree, C. G. Suresh and M. Vijayan

Molecular Biophysics Unit, Indian Institute of Science, Bangalore – 560 012, India

and C. Toniolo and G. M. Bonora

Biopolymer Research Centre, CNR, Department of Organic Chemistry, University of Padova, Padova 35131, *Italy*

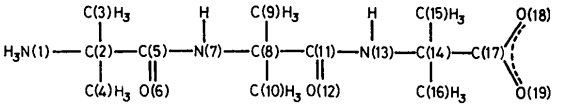
(*Received* 21 *January* 1987; *accepted* 13 *March* 1987)

Abstract. $C_{12}H_{23}N_3O_4.2H_2O$, $M_r = 309$, monoclinic, $P2_1$, $a = 8{\cdot}504\ (2)$, $b = 11{\cdot}287\ (2)$, $c = 8{\cdot}922\ (2)$ Å, $\beta = 108{\cdot}65\ (1)°$, $V = 811{\cdot}4\ (4)$ Å^3, $Z = 2$, $D_x = 1{\cdot}27\ (2)$, $D_m = 1{\cdot}26$ Mg m^{-3}, λ(Cu $K\alpha$) $= 1{\cdot}5418$ Å, $\mu = 8{\cdot}53$ cm^{-1}, $F(000) = 336$, $T = 293$ K, final $R = 0{\cdot}040$ for 1499 observed reflections. The bond angles in the central residue exhibit conformation-dependent asymmetry about C^α. The conformation of the molecule corresponds to an incipient type II′ (or type II) β-turn. The structure contains an internal water bridge, involving two water molecules, which connects the terminal amino group and the carbonyl group of the second residue. An interesting feature of the crystal is a zigzag head-to-tail sequence centred around a 2_1 screw axis.

Introduction. We have earlier shown that the most prominent feature of molecular aggregation in the crystals of unprotected peptides containing residues of common naturally occurring amino acids is the 'head-to-tail' sequence in which the terminal amino and carboxylate groups are brought into periodic proximity (Suresh & Vijayan, 1985*a*,*b*). Such sequences, which occur ubiquitously in amino acid crystal structures as

0108-2701/87/081618-04$01.50

well (Suresh & Vijayan, 1983*a*,*b*), have been suggested as of probable relevance to prebiotic polymerization (Vijayan, 1980). It is of interest to examine if such sequences occur in peptides containing α-aminoisobutyric acid (Aib), for two reasons. First, Aib is found in simulated experiments on prebiotic organic synthesis (Miller & Orgel, 1974, pp. 83–102) as well as in carbonaceous chondrites (Miller & Orgel, 1974, pp. 191–196). Secondly, Aib differs from most proteinous amino acids in that it is highly conformationally restricted and promotes folded structures (Toniolo, Bonora, Bavoso, Benedetti, Di Blasio, Pavone & Pedone, 1983; Prasad & Balaram, 1984). The crystal structures of several Aib-containing peptides have been published, but the terminal groups in almost all of them are blocked. As far as we are aware, the only crystal structure containing an unprotected Aib peptide is that of a tri-Aib copper complex (Diaddario, Robinson & Margerum, 1983). Metal complexation, however, often has an overriding influence in dictating crystal and molecular structure, and hence the structure of this complex does not provide useful information on the intrinsic structural propensities of Aib peptides. The crystal structure analysis of free, uncomplexed tri-Aib (I) was therefore undertaken.



(I)

Experimental. The synthesis of the free tripeptide (Kirksey, Neubecker & Margerum, 1979) was achieved by the catalytic dehydrogenation of benzyloxycarbonyl-tri-α-aminoisobutyrylbenzyl ester (Bonora, Mapelli, Toniolo, Wilkening & Stevens, 1984). The compound was crystallized by slow evaporation from slightly aqueous methanol. Space group ($0k0$, k odd systematically absent) and unit-cell dimensions determined from preliminary X-ray diffraction photographs. D_m measured by flotation in a mixture of benzene and carbon tetrachloride. Crystal of dimensions $0{\cdot}35 \times 0{\cdot}33 \times 0{\cdot}18$ mm. Computer-controlled CAD-4 diffractometer, ω–2θ scan to a maximum Bragg angle of 70°, graphite-monochromated Cu $K\alpha$ radiation. 25 reflections in the range $14 < \theta < 40°$ used for cell parameter refinement. Intensities not corrected for absorption. h 0 to 10, k 0 to 13, l −10 to 10. Maximum variation in intensity of standard reflections (303, 203, 311) 2%. 1732 reflections measured, 1628 unique, 1499 with $I > 2\sigma(I)$ used in refinement. $R_{int} = 0{\cdot}016$. The structure was solved using the direct-methods program *MULTAN*80 (Main, Fiske, Hull, Lessinger, Germain, Declercq & Woolfson, 1980). The non-H atoms were refined anisotropically and the H atoms, located from a difference Fourier map, isotropically on F using the block-diagonal least-squares method (9×9 and 4×4 matrices for non-H and H atoms respectively) employing a locally modified version of a program originally written by Dr R. Shiano. The y coordinate of N(1) was fixed to define the origin. Refinement converged at $R = 0{\cdot}040$, $wR = 0{\cdot}071$, $S = 0{\cdot}4306$ (max. $\Delta/\sigma = 0{\cdot}08$). The weighting scheme had the form $1/(a + bF_o + cF_o^2)$ with $a = 1{\cdot}1584$, $b = -0{\cdot}0589$ and $c = 0{\cdot}0291$. Maximum and minimum values in the final difference Fourier map were 0·016 and −0·20 e Å^{-3}, respectively. Form factors for non-H atoms taken from Cromer & Waber (1965) and those for H from Stewart, Davidson & Simpson (1965). Computations performed on a DEC-1090 system. The final positional parameters and equivalent isotropic thermal parameters (Hamilton, 1959) of the non-H atoms are given in Table 1.*

Table 1. *Positional parameters* ($\times 10^4$) *and equivalent isotropic temperature factors of non*-H *atoms* (Å^2) *with e.s.d.'s in parentheses*

$B_{eq} = \frac{4}{3}\sum_i\sum_j b_{ij}\mathbf{a}_i.\mathbf{a}_j$.

	x	y	z	B_{eq}
N1	5795 (3)	768	9722 (2)	3·71 (6)
C2	6701 (3)	1930 (3)	9976 (3)	3·42 (7)
C3	6148 (4)	2650 (3)	11161 (3)	5·14 (9)
C4	8564 (3)	1682 (3)	10595 (3)	3·92 (8)
C5	6156 (3)	2544 (3)	8334 (3)	3·62 (7)
O6	5143 (3)	2073 (2)	7210 (3)	4·36 (7)
N7	6813 (3)	3605 (3)	8269 (3)	3·96 (7)
C8	6251 (3)	4316 (3)	6810 (3)	4·54 (8)
C9	6939 (4)	5573 (4)	7196 (5)	5·74 (11)
C10	6882 (3)	3766 (4)	5534 (4)	6·72 (12)
C11	4338 (3)	4405 (3)	6335 (3)	4·01 (7)
O12	3670 (2)	4588 (2)	7361 (2)	4·90 (6)
N13	3512 (2)	4346 (2)	4806 (2)	3·99 (6)
C14	1719 (3)	4412 (3)	4048 (3)	3·72 (6)
C15	1034 (5)	5574 (4)	4434 (4)	5·45 (12)
C16	889 (4)	3313 (4)	4500 (3)	5·71 (9)
C17	1402 (3)	4333 (2)	2227 (3)	4·18 (7)
O18	2644 (3)	4156 (2)	1782 (2)	6·19 (7)
O19	−52 (3)	4437 (2)	1343 (2)	4·32 (6)
*W*1	2427 (3)	1064 (4)	8793 (5)	7·97 (12)
*W*2	1269 (4)	3357 (3)	8522 (3)	9·46 (11)

Discussion. The present structure provides an example of a peptide made up of optically inactive amino acid residues crystallizing in a chiral space group. Thus, the crystals contain only molecules of the same chirality. However, in as much as the absolute configuration has not been determined, it is not possible to say which of the two possible enantiomorphs is present in the crystal. The choice of the particular enantiomorph in the following discussion is purely arbitrary.

* Lists of structure factors, anisotropic thermal parameters and H-atom parameters have been deposited with the British Library Document Supply Centre as Supplementary Publication No. SUP 43881 (16 pp.). Copies may be obtained through The Executive Secretary, International Union of Crystallography, 5 Abbey Square, Chester CH1 2HU, England.

Table 2. *Bond lengths* (Å) *and angles* (°) *with e.s.d.'s in parentheses*

N1–C2	1·501 (3)	C8–C11	1·547 (4)
C2–C3	1·523 (4)	C11–O12	1·239 (4)
C2–C4	1·526 (4)	C11–N13	1·321 (3)
C2–C5	1·552 (4)	N13–C14	1·459 (3)
C5–O6	1·216 (3)	C14–C15	1·519 (5)
C5–N7	1·331 (4)	C14–C16	1·543 (5)
N7–C8	1·472 (4)	C14–C17	1·561 (3)
C8–C9	1·531 (5)	C17–O18	1·258 (4)
C8–C10	1·536 (5)	C17–O19	1·241 (3)
N1–C2–C3	108·2 (2)	C10–C8–C11	114·1 (3)
N1–C2–C4	108·6 (2)	C8–C11–O12	119·9 (2)
N1–C2–C5	105·3 (2)	C8–C11–N13	116·4 (2)
C3–C2–C4	111·2 (2)	O12–C11–N13	123·6 (3)
C3–C2–C5	110·6 (2)	C11–N13–C14	127·4 (2)
C4–C2–C5	112·7 (2)	N13–C14–C15	111·1 (2)
C2–C5–O6	120·2 (3)	N13–C14–C16	109·7 (2)
C2–C5–N7	116·1 (2)	N13–C14–C17	106·7 (2)
O6–C5–N7	123·6 (3)	C15–C14–C16	113·1 (3)
C5–N7–C8	120·5 (2)	C15–C14–C17	109·5 (3)
N7–C8–C9	108·3 (3)	C16–C14–C17	106·5 (2)
N7–C8–C10	110·1 (3)	C14–C17–O18	117·0 (2)
N7–C8–C11	107·1 (2)	C14–C17–O19	117·5 (2)
C9–C8–C10	110·0 (3)	O18–C17–O19	125·5 (3)

The bond lengths and valency angles in the structure, given in Table 2, are comparable to those observed in other Aib peptides (Benedetti, Bavoso, Di Blasio, Pavone, Pedone, Crisma, Bonora & Toniolo, 1982; Prasad & Balaram, 1984). It is, however, interesting to note the asymmetry of bond angles around the C^{α} of the central residue. Such asymmetry in helical Aib peptides has already been commented upon (Prasad & Balaram, 1984). In the present case, however. the residue falls in a non-helical region ($\varphi = 52{\cdot}9$ and $\psi = -141{\cdot}5°$) corresponding to a D residue in the Ramachandran map (Ramachandran & Sasisekharan, 1968). In this residue, the angles around C^{α} involving the C^{β} corresponding to the D configuration (C10) open up at the expense of the angles involving the C^{β} corresponding to the L configuration (C9). The reverse would hold in the enantiomorph in which the φ,ψ angles would correspond to an allowed region for an L residue in the Ramachandran map.

The torsion angles (°) that define the conformation (IUPAC–IUB Commission on Biochemical Nomenclature, 1970) of the molecule are:

N1–C2–C5–N7 (ψ_1)	180·0 (1)	C8–C11–N13–C14 (ω_2)	−179·7 (1)
C2–C5–N7–C8 (ω_1)	−173·8 (1)	C11–N13–C14–C17 (φ_3)	178·4 (1)
C5–N7–C8–C11 (φ_2)	52·9 (1)	N13–C14–C17–O18 (ψ_3')	4·6 (1)
N7–C8–C11–N13 (ψ_2)	−141·5 (1)	N13–C14–C17–O19 (ψ_3'')	176·2 (1).

A perspective view of the molecule is shown in Fig. 1. The conformation angles and the figure clearly show that the conformation of the molecule corresponds to an incipient type II′ (type II in the enantiomorph) β-turn (Venkatachalam, 1968). The second (central) residue in the peptide has conformational angles close to those of the residue in the first corner of such a turn. This seems to be the first instance where an Aib residue occupies such a position. Indeed, so far, no other non-terminal Aib residues with φ,ψ values close to 53, −142° have been observed. This unique conformation appears to have been made possible by the absence of terminal protecting groups. All the protected homotripeptides of Aib have a type III or III′ β-turn conformation (Benedetti, Bavoso, Di Blasio, Pavone, Pedone, Crisma, Bonora & Toniolo, 1982; Toniolo, Valle, Bonora, Crisma, Formaggio, Bavoso, Benedetti, Di Blasio, Pavone & Pedone, 1987).

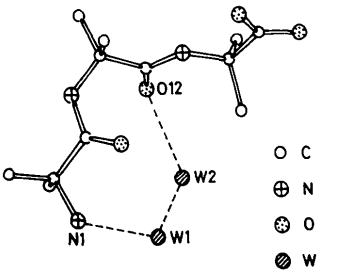


Fig. 1. A perspective view of the molecule. The water bridge is also indicated. Dotted lines represent hydrogen bonds.

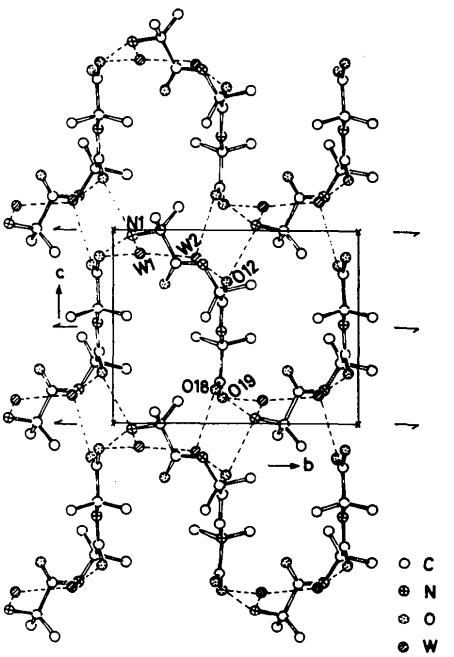


Fig. 2. The crystal structure projected onto the *bc* plane. Only atoms involved in hydrogen bonds are numbered. Dotted lines represent hydrogen bonds.

Table 3. *Hydrogen-bond parameters with e.s.d.'s in parentheses*

A–H···*B*	*A*···*B* (Å)	H–*A*···*B* (°)	Symmetry of atom *B*
N1–H3(N1)···*W*1	2·735 (3)	13 (4)	*x, y, z*
N1–H2(N1)···O12	2·828 (3)	5 (2)	$-x+1, \frac{1}{2}+y-1, -z+2$
N1–H1(N1)···O18	2·831 (3)	6 (3)	$-x+1, \frac{1}{2}+y-1, -z+1$
*W*1–H1(*W*1)···O19	2·703 (4)	4 (3)	$-x, \frac{1}{2}+y-1, -z+1$
*W*1–H2(*W*1)···*W*2	2·753 (6)	3 (3)	*x, y, z*
*W*2–H1(*W*2)···O18	2·910 (3)	15 (5)	*x, y, z*+1
*W*2–H2(*W*2)···O12	2·921 (4)	12 (5)	*x, y, z*

The packing diagram of the tripeptide is shown in Fig. 2. The parameters of the hydrogen bonds that stabilize the structure are given in Table 3. As expected, the terminal amino N atom is involved in three N—H···O hydrogen bonds as a donor. None of the peptide N atoms is involved in a hydrogen bond. One of the peptide carbonyl O atoms is not involved in any hydrogen bond whereas the other accepts two. One of the terminal carboxylate O atoms accepts two hydrogen bonds whereas the other accepts one. Both water molecules in the structure accept one proton and donate two.

An interesting feature of the structure is an internal water bridge which connects the terminal amino group and the carbonyl group of the second residue. Such internal bridges involving one water molecule have been observed before in short peptides (*e.g.* Nair, Nagaraj, Ramaprasad, Balaram & Vijayan, 1981; Aubry, Vitoux, Boussard & Marraud, 1981; Toniolo *et al.*, 1987) but two-membered water bridges connecting adjacent residues, like that in the present structure, are less usual.

The original objective of the present investigation was to see if stereochemically constrained folded peptides like those containing Aib residues form head-to-tail sequences. The tripeptide in the present crystal structure does so even in the presence of disturbing influences such as those of water molecules. The structure contains a zigzag head-to-tail sequence centred around a 2_1 screw axis. This sequence is stabilized by the N1—H···O19 hydrogen bond and its symmetry equivalents. The sequence, which runs parallel to the *b* axis, and its translational equivalents are stacked together along the *a* and the *c* axes to form the crystal.

Financial support from SERC, Department of Science and Technology, is acknowledged.

References

AUBRY, A., VITOUX, B., BOUSSARD, G. & MARRAUD, M. (1981). *Int. J. Pept. Protein Res.* **18**, 195–202.

BENEDETTI, E., BAVOSO, A., DI BLASIO, B., PAVONE, V., PEDONE, C., CRISMA, M., BONORA, G. M. & TONIOLO, C. (1982). *J. Am. Chem. Soc.* **104**, 2437–2444.

BONORA, G. M., MAPELLI, C., TONIOLO, C., WILKENING, R. R. & STEVENS, E. S. (1984). *Int. J. Biol. Macromol.* **6**, 179–188.

CROMER, D. T. & WABER, J. T. (1965). *Acta Cryst.* **18**, 104–109.

DIADDARIO, L. L., ROBINSON, W. R. & MARGERUM, D. W. (1983). *Inorg. Chem.* **22**, 1021–1025.

HAMILTON, W. C. (1959). *Acta Cryst.* **12**, 609–610.

IUPAC–IUB COMMISSION ON BIOCHEMICAL NOMENCLATURE (1970). *J. Mol. Biol.* **52**, 1–17.

KIRKSEY, S. T. JR, NEUBECKER, T. A. & MARGERUM, D. W. (1979). *J. Am. Chem. Soc.* **101**, 1631–1632.

MAIN, P., FISKE, S. J., HULL, S. E., LESSINGER, L., GERMAIN, G., DECLERCQ, J.-P. & WOOLFSON, M. M. (1980). *MULTAN80. A System of Computer Programs for the Automatic Solution of Crystal Structures from X-ray Diffraction Data.* Univs. of York, England, and Louvain, Belgium.

MILLER, S. L. & ORGEL, L. E. (1974). *The Origins of Life on Earth.* New Jersey: Prentice-Hall.

NAIR, C. M. K., NAGARAJ, R., RAMAPRASAD, S., BALARAM, P. & VIJAYAN, M. (1981). *Acta Cryst.* B**37**, 597–601.

PRASAD, B. V. V. & BALARAM, P. (1984). *CRC Crit. Rev. Biochem.* **16**, 307–348.

RAMACHANDRAN, G. N. & SASISEKHARAN, V. (1968). *Adv. Protein Chem.* **23**, 283–437.

STEWART, R. F., DAVIDSON, E. R. & SIMPSON, W. T. (1965). *J. Chem. Phys.* **42**, 3175–3187.

SURESH, C. G. & VIJAYAN, M. (1983*a*). *Int. J. Pept. Protein Res.* **22**, 129–143.

SURESH, C. G. & VIJAYAN, M. (1983*b*). *Int. J. Pept. Protein Res.* **22**, 617–621.

SURESH, C. G. & VIJAYAN, M. (1985*a*). *Int. J. Pept. Protein Res.* **26**, 311–328.

SURESH, C. G. & VIJAYAN, M. (1985*b*). *Int. J. Pept. Protein Res.* **26**, 329–336.

TONIOLO, C., BONORA, G. M., BAVOSO, A., BENEDETTI, E., DI BLASIO, B., PAVONE, V. & PEDONE, C. (1983). *Biopolymers*, **22**, 205–215.

TONIOLO, C., VALLE, G., BONORA, G. M., CRISMA, M., FORMAGGIO, F., BAVOSO, A., BENEDETTI, E., DI BLASIO, B., PAVONE, V. & PEDONE, C. (1987). *Biopolymers*. In the press.

VENKATACHALAM, C. M. (1968). *Biopolymers*, **6**, 1425–1436.

VIJAYAN, M. (1980). *FEBS Lett.* **112**, 135–137.

Acta Cryst. (1987). C**43**, 1621–1623

(1*R**,4*S**,10*S**)-2,2,10-Tribromo-1,2,3,4-tetrahydro-1,4-ethanonaphthalene

BY ÖMER ERGİN

Faculty of Necatibey Education, Department of Science, Uludağ University, Balıkesir, Turkey

AND MANSUR HARMANDAR AND METİN BALCI

Faculty of Science, Department of Chemistry, Atatürk University, Erzurum, Turkey

(*Received* 30 *September* 1985; *accepted* 1 *April* 1987)

Abstract. $C_{12}H_{11}Br_3$, $M_r = 394{\cdot}9$, monoclinic, $P2_1/c$, $a = 7{\cdot}334$ (6), $b = 15{\cdot}305$ (26), $c = 11{\cdot}612$ (16) Å, $\beta = 73{\cdot}58$ (6)°, $V = 1250{\cdot}25$ Å^3, $Z = 4$, $D_m = 2{\cdot}065$, $D_x = 2{\cdot}098$ Mg m^{-3}, λ(Mo $K\bar{\alpha}$) = 0·71069 Å, $\mu = 9{\cdot}45$ mm^{-1}, $F(000) = 752$, $T = 293$ K, $R = 0{\cdot}047$ for 816 unique reflections. The dibromocyclohexane frag-

0108-2701/87/081621-03$01.50