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The Crystal Structure of L-Alanyl-L-alanine Hydrochloride

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The crystal structure of L-alanyl-L-alanine hydrochloride, $^+H_3NCH(CH_3)CONHCH(CH_3)COOH \cdot Cl^-$, has been determined. The crystal is orthorhombic with space group $P2_12_12$; the unit-cell dimensions are: $a=9.51$, $b=19.72$, $c=5.38$ Å. Final refinement was made by block-diagonal least-squares method to an R of 0.079 and this gave a standard deviation of about 0.012 Å in bond lengths among the non-hydrogen atoms. The bond lengths and angles agree with those found so far in amino acids and peptides. Both the carboxyl and the peptide group are planar within the limits of experimental error, and the dihedral angle between the planes is 27° . The internal rotation angles in the peptide backbone are similar to those in the antiparallel pleated sheet configuration of polypeptide.

Introduction

Accurate structure analyses by X-ray of various kinds of amino acids and peptides have been carried out at many places mainly with biochemical interest. Most of these peptides, however, contain at least one glycyl residue. The only example containing an alanyl residue is glycyl-L-alanine hydrochloride (Tranter, 1956), whereas alanine is one of the most frequently appearing components in proteins. The present work on L-alanyl-L-alanine hydrochloride has been undertaken in order to provide some fundamental knowledge on the conformations of the alanyl residues in proteins, in particular, this knowledge is of essential importance to the structure of tussah silk fibroin.

Experimental

L-Alanyl-L-alanine hydrochloride was obtained in the form of needle-like crystals elongated along the c axis by dissolving the peptide in a slight excess of 2*N* HCl and evaporating to dryness *in vacuo* at room temperature. Since the crystals are hygroscopic, the specimen was coated with a thin-film of collodion during the X-ray experiment.

Unit-cell dimensions were determined by the least-squares calculation, using 17 $0kl$ and 21 $hk0$ reflexions whose Bragg angles were measured on zero-layer Weissenberg photographs taken with Cu $K\alpha$ radiation and calibrated with aluminum powder lines. The density was measured by flotation in a benzene-carbon tetrachloride mixture.

Crystal data:

$$\begin{aligned} a &= 9.51 \pm 0.01 \text{ \AA} , & \rho_{\text{obs}} &= 1.29_0 \text{ g.cm.}^{-3} \\ b &= 19.72 \pm 0.01 \text{ \AA} , & \rho_{\text{cal}} &= 1.29_5 \text{ g.cm.}^{-3} \\ c &= 5.38 \pm 0.01 \text{ \AA} . & Z &= 4 . \end{aligned}$$

The systematic absence of the odd orders of $h00$ and $0k0$ reflexions were observed, hence the space group was found to be $P2_12_12$.

The three-dimensional intensity data for nickel-filtered Cu $K\alpha$ radiation were collected from multiple-film, equi-inclination Weissenberg photographs of the layer line 0-7 about the a axis and 0-4 about the c axis. The intensities were visually estimated by comparison with a standard scale. They were corrected for Lorentz and polarization factors; no absorption and extinction corrections were applied. Corrections for variation in spot-size on higher-layer photographs were made by the method presented by Phillips (1954). Since the intensity data from the c axis photographs seemed to be less reliable than those from the a axis, the former were used only for reflexions outside the region of the a axis photographs. Thus 1273 intensity data were obtained of which 183 were too weak to be observed.

Determination of the structure

The coordinates of the chloride ion were deduced from the Patterson function. The electron density distribution and the minimum function were synthesized on the basis of the coordinates of the chloride ion. All the non-hydrogen atoms were identified, though

some spurious peaks appeared. Successive Fourier syntheses did not show any spurious peak.

The positional and thermal parameters were refined by the block-diagonal least-squares method, minimizing $\sum w(|F_o| - |F_c|)^2$. The weighting scheme was; $w = \frac{1}{2}$ when $F_o = 0$ and $w = 1$ when $F_o \neq 0$. The scattering factors for H, C, N, O and Cl⁻ were taken from *International Tables for X-ray Crystallography* (1962). After three cycles with isotropic thermal parameters and two with anisotropic thermal parameters, the reliability index, R , was reduced to 0.114. At this stage, the seven non-methyl hydrogen atoms were assigned coordinates with reasonable bond distances and angles, and they

were confirmed in the difference-Fourier synthesis. The six hydrogen atoms of the methyl groups could also be located in this synthesis. After several cycles of the least-squares calculation including all 25 atoms, the maximum shift of the non-hydrogen atom coordinates became less than the estimated standard deviations; their mean value for C, N and O was 0.007 Å (0.005 – 0.011 Å). The R index was 0.079 ($R = 0.100$, for all 1273 reflexions).

The final atomic coordinates and thermal parameters for non-hydrogen atoms are given in Tables 1 and 2, and for the hydrogen atoms in Table 3. The absolute configuration of the molecule was not determined; the

Table 1. *The final atomic coordinates (fractional) and their standard deviations (Å)*

	x	$\sigma(x)$	y	$\sigma(y)$	z	$\sigma(z)$
C(1A)	-0.0080	0.007	0.3218	0.006	0.3941	0.008
C(1B)	-0.0640	0.008	0.3497	0.008	0.6407	0.010
C(1)	0.1402	0.007	0.3468	0.006	0.3389	0.007
C(2A)	0.2751	0.006	0.4398	0.007	0.1605	0.008
C(2)	0.2537	0.007	0.5168	0.007	0.1604	0.009
C(2B)	0.3224	0.009	0.4179	0.009	-0.1051	0.011
N(1)	-0.0030	0.006	0.2456	0.006	0.4126	0.007
N(2)	0.1434	0.006	0.4082	0.006	0.2298	0.007
O(1)	0.2442	0.005	0.3152	0.005	0.3969	0.006
O(2-1)	0.1417	0.006	0.5415	0.005	0.1508	0.009
O(2-2)	0.3680	0.006	0.5498	0.005	0.1662	0.009
Cl	0.1510	0.002	0.1999	0.002	0.9075	0.002

Table 2. *The thermal parameters and their standard deviations (multiplied by 10⁴)*

$$\text{Temperature factor} = \exp \{ -(\beta_{11}h^2 + \beta_{22}k^2 + \beta_{33}l^2 + \beta_{12}hk + \beta_{13}hl + \beta_{23}kl) \}.$$

	β_{11}	σ	β_{22}	σ	β_{33}	σ	β_{12}	σ	β_{13}	σ	β_{23}	σ
C(1A)	75	7	19	2	295	26	7	6	48	31	5	13
C(1B)	122	10	29	2	457	41	-1	8	222	39	-22	18
C(1)	64	7	21	2	307	27	-5	6	-33	28	-11	12
C(2A)	56	7	21	2	373	31	4	6	57	27	6	13
C(2)	58	7	25	2	451	36	-5	7	58	30	-1	15
C(2B)	129	11	38	3	461	40	-3	9	212	43	-61	21
N(1)	101	7	20	1	326	24	-17	6	-20	32	8	13
N(2)	60	6	23	2	373	26	1	6	-4	25	24	11
O(1)	77	5	26	1	394	22	6	5	-45	23	26	11
O(2-1)	101	7	23	1	1019	48	-2	6	155	39	4	16
O(2-2)	105	7	22	1	1098	52	-6	6	24	40	20	16
Cl	118	2	25	0	327	6	21	2	6	8	0	4

Table 3. *The hydrogen atom parameters*

	Bonded to	x	y	z	B
H(1) } H(2) } H(3) }	N(1)	0.055 0.051 -0.108	0.230 0.227 0.226	0.522 0.262 0.470	4.6 0.8 2.1
H(4) } H(5) }	C(1A)	-0.091 -0.166	0.332 0.328	0.261 0.677	1.6 4.1
H(6) } H(7) }	C(1B)	-0.086 0.038	0.395 0.350	0.630 0.788	1.0 1.1
H(8) } H(9) }	N(2)	0.048 0.365	0.423 0.435	0.145 0.277	3.1 0.9
H(10) } H(11) } H(12) }	C(2A)	0.346 0.417 0.241	0.370 0.437 0.426	-0.109 -0.161 -0.219	6.6 6.5 4.1
H(13)	O(2-2)	0.333	0.591	0.167	4.3

$\langle \sigma(x) \rangle = 0.080 \text{ \AA}$ $\langle \sigma(y) \rangle = 0.075 \text{ \AA}$ $\langle \sigma(z) \rangle = 0.088 \text{ \AA}$
 $\langle \sigma(B) \rangle = 2.1 \text{ \AA}^2$

All the numerical computations were done on the NEAC 2101 of this laboratory, the NEAC 2200 of the computation center of Osaka University and the HITAC 5020E of the computer center of the University of Tokyo.

Main programs used:

Unit cell dimension, written by A. Sugihara.
Lp and spot shape correction by N. Tanaka.
Patterson and minimum function by N. Yasuoka.
The least-squares calculation and Fourier synthesis by T. Ashida.
Bond lengths, angles and best planes by T. Ashida.

Discussion of the structure

Geometry of the molecule

The bond lengths and angles of the non-hydrogen atoms are shown in Fig. 3, while those involving the hydrogen atoms are shown in Table 5. The estimated standard deviations in the bond distances and angles among the non-hydrogen atoms are about 0.012 Å and 0.7°, respectively. In general, these structure data are

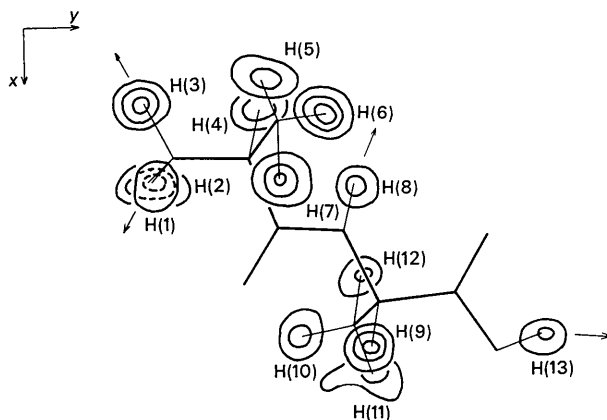


Fig. 2. A composite drawing of the final difference map, viewed along the c axis. The contributions of the hydrogen atoms were omitted from the amplitudes of F_c but were included in the phase angles. Contours are at intervals of $0.2 \text{ e.}\text{\AA}^{-3}$, beginning with the $0.2 \text{ e.}\text{\AA}^{-3}$ contour. The dotted contours are in the lower section.

in good agreement with those found so far in amino acids and peptides, and the peptide group in particular maintains good agreement with the standard conformation presented by Pauling & Corey (1953).

The two C–O bond lengths in the carboxyl group are 1.17 and 1.27 Å. The oxygen atom O(2–1) of the shorter C–O bond is an acceptor for an $\text{O}\cdots\text{H}-\text{N}$ hydrogen bond, while O(2–2) of the longer bond is the donor for the $\text{O}-\text{H}\cdots\text{Cl}$ hydrogen bond. In correlation with the bond lengths, the two O–C–C angles are different from each other, 113° and 122° .

The equations for the best planes of the carboxyl and the peptide group are given in Table 6, together with the deviations of the individual atoms from the planes. Each of the two groups is planar within the limits of error, and the dihedral angle between the planes is 27° .

Table 6. The equations of the least-squares planes through atoms

Peptide group		Carboxyl group	
$-0.0226X - 0.4528Y - 0.8913Z + 4.7634 = 0$		$0.0383X - 0.0017Y - 0.9993Z + 0.7801 = 0$	
Atom	Deviation	Atom	Deviation
C(1A)	0.002 Å	C(2A)	0.002 Å
O(1)	-0.007	C(2)	-0.007
C(1)	0.012	O(2-1)	0.003
N(2)	-0.014	O(2-2)	0.002
C(2A)	0.007	N(2)*	-0.417
N(1)*	0.593	C(2B)*	1.448
C(1B)*	-1.418	H(13)*	-0.017
C(2)*	-0.675		
C(2B)*	1.467		
H(8)*	0.282		

* These atoms were not included in the least-squares calculations.

The internal rotation angles in the peptide backbone (according to definitions proposed by Edsall, Flory, Kendrew, Liquori, Némelty & Ramachandran, 1966) are:

$$\begin{aligned} \psi_1[\text{C}(1\text{A})-\text{C}(1)] &= 334.2^\circ, & \omega[\text{C}(1)-\text{N}(2)] &= 0.8^\circ. \\ \phi[\text{N}(2)-\text{C}(2\text{A})] &= 26.5^\circ, & \psi_2[\text{C}(2\text{A})-\text{C}(2)] &= 341.3^\circ \\ & & & (\text{or } 161.3^\circ). \end{aligned}$$

Table 5. Bond distances and angles involving the hydrogen atoms

$d(\text{X}-\text{H})$		$\angle(\text{C}, \text{N}-\text{X}-\text{H})$	
C(1B)–H	0.91, 1.08, 1.25 Å	C, N–C(1A)–H(4)	105, 105, 119°
C(1A)–H(4)	1.09 Å	C, N–C(2A)–H(9)	101, 107, 120°
C(2A)–H(9)	1.06 Å	C(1A)–C(1B)–H	106, 109, 112°
C(2B)–H	0.97, 1.00, 1.02 Å	C(2A)–C(2B)–H	107, 111, 115°
N(1)–H	0.87, 1.03, 1.11 Å	C(1A)–N(1)–H	108, 110, 115°
N(2)–H(8)	1.05 Å	C(1)–N(2)–H(8)	115°
O(2-2)–H(13)	0.88 Å	C(2A)–N(2)–H(8)	121°
$\langle\sigma(d)\rangle = 0.09 \text{ \AA}$		C(2)–O(2-2)–H(13)	99°
		$\langle\sigma\rangle = 4.8^\circ$	
$\angle(\text{H}-\text{X}-\text{H})$			
H–C(1B)–H	101, 102, 126°		
H–C(2B)–H	98, 109, 116°		
H–N(1)–H	96, 105, 123°		
$\langle\sigma\rangle = 7.5^\circ$			

These are close to the expected values ($\varphi=38^\circ$, $\psi=325^\circ$, $\omega=0^\circ$; (Miyazawa, 1961) for an antiparallel pleated sheet configuration and also to those found in β -poly-L-alanine ($\varphi=41.4^\circ$, $\psi=314.7^\circ$, $\omega=1.5^\circ$; Arnott, Dover & Elliot, 1967).

The conformation about the two $C\alpha-C'$ bonds is similar to those of L-alanine (Simpson & Marsh, 1966) and DL-alanine (Donohue, 1950). The deviation of N(1) from the peptide plane is 0.59 Å, and that of N(2) from the carboxyl plane is 0.42 Å. Those in L- and DL-alanine are 0.44 Å and 0.38 Å, respectively.

Packing of the molecules

The drawings of the structure viewed along [001] and [100] are shown in Figs. 4 and 5, respectively. As clearly shown in Fig. 5, the molecules of L-alanyl-L-alanine make wave-like sheets parallel to the (001) joined with the hydrogen bonds, and these sheets are linked together along [001] by the chloride ions.

All five hydrogen atoms belonging to the nitrogen and the oxygen atoms take part in the hydrogen bonding. The hydrogen bond lengths and angles are given in Table 7. The terminal nitrogen atom, N(1), forms three hydrogen bonds – to two chloride ions and the oxygen atom, O(1), of the peptide group; the three acceptor atoms are approximately on the three vertices of a regular tetrahedron centered at N(1), with the carbon atom, C(1A), directed towards the fourth vertex. The peptide nitrogen atom, N(2), forms the

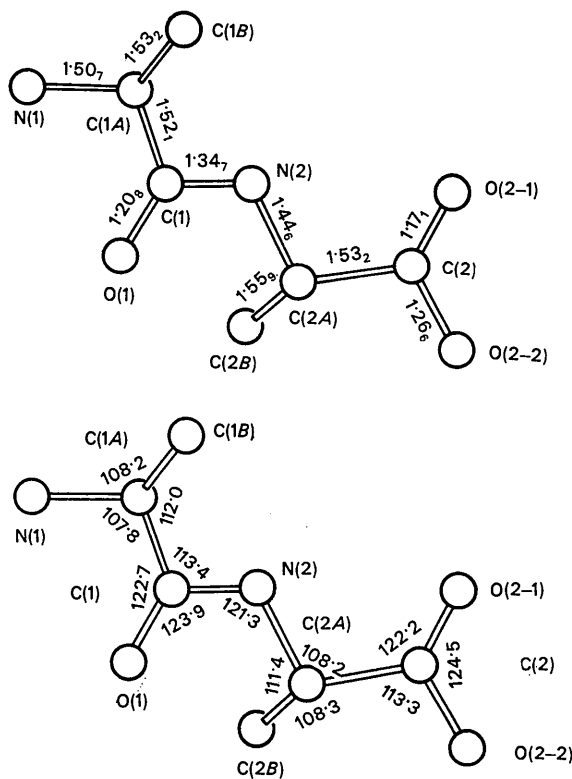


Fig. 3. Bond distances and angles.

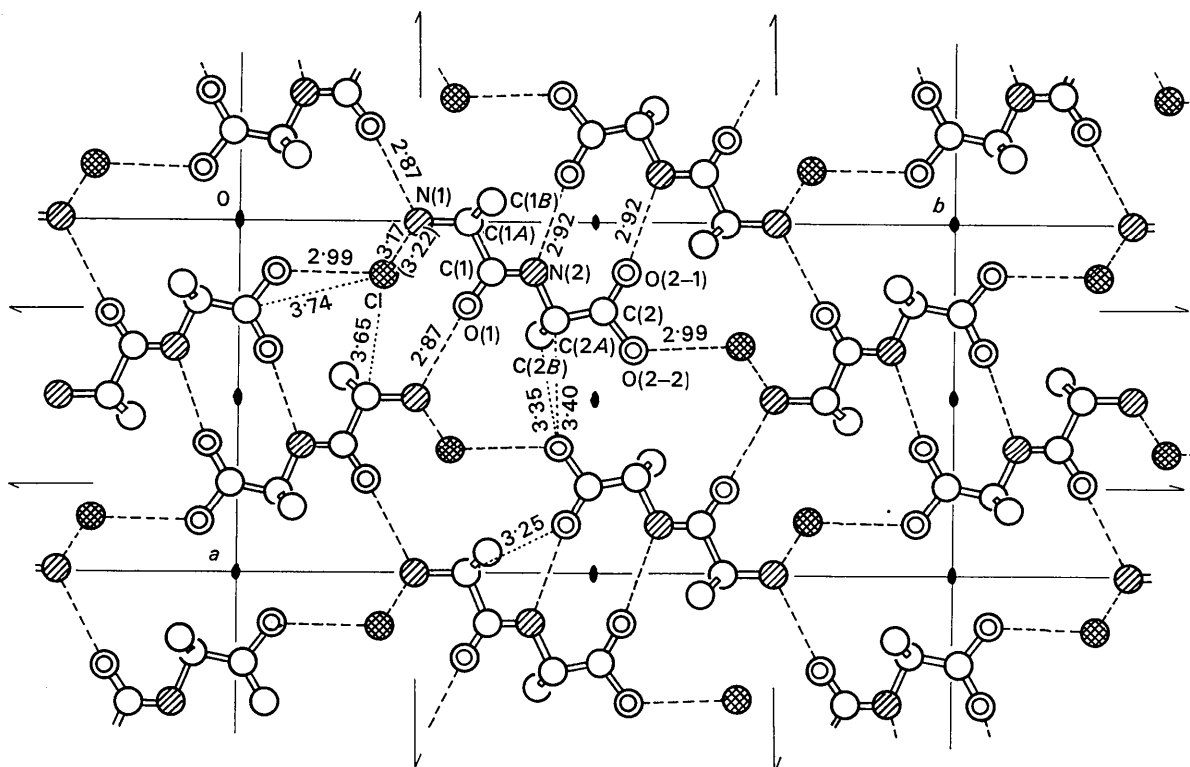


Fig. 4. A drawing of the structure viewed along [001]. Hydrogen bonds and van der Waals contacts are indicated by the broken and dotted lines, respectively.

Table 7. *Hydrogen bond lengths and angles*

Donor	H	Acceptor, at	$d(D \cdots A)$	$d(H \cdots A)$	$\angle(H-D \cdots A)$	$\angle(D-H \cdots A)$
N(1)	H(1)	Cl' (x, y, z)	3.17 Å	2.34 Å	14°	161°
N(1)	H(2)	Cl'' ($x, y, z-1$)	3.22	2.20	6	172
N(1)	H(3)	O(1) ($x-\frac{1}{2}, \bar{y}+\frac{1}{2}, \bar{z}+1$)	2.87	1.77	7	169
N(2)	H(8)	O(2-1) ($\bar{x}, \bar{y}+1, z$)	2.92	1.94	17	153
O(2-2)	H(13)	Cl''' ($\bar{x}+\frac{1}{2}, y+\frac{1}{2}, \bar{z}+1$)	2.99	2.19	20	152
$\angle(C-X \cdots A)$			$\angle(A \cdots N \cdots A)$			
C(1A)-N(1) \cdots Cl'	111°	Cl' \cdots N(1) \cdots Cl''	115°			
C(1A)-N(1) \cdots Cl''	104	Cl'' \cdots N(1) \cdots O(1)	124			
C(1A)-N(1) \cdots O(1)	114	O(1) \cdots N(1) \cdots Cl'	88			
C(2A)-N(2) \cdots O(2-1)	128					
C(1)-N(2) \cdots O(2-1)	110					
C(2)-O(2-2) \cdots Cl'''	117					

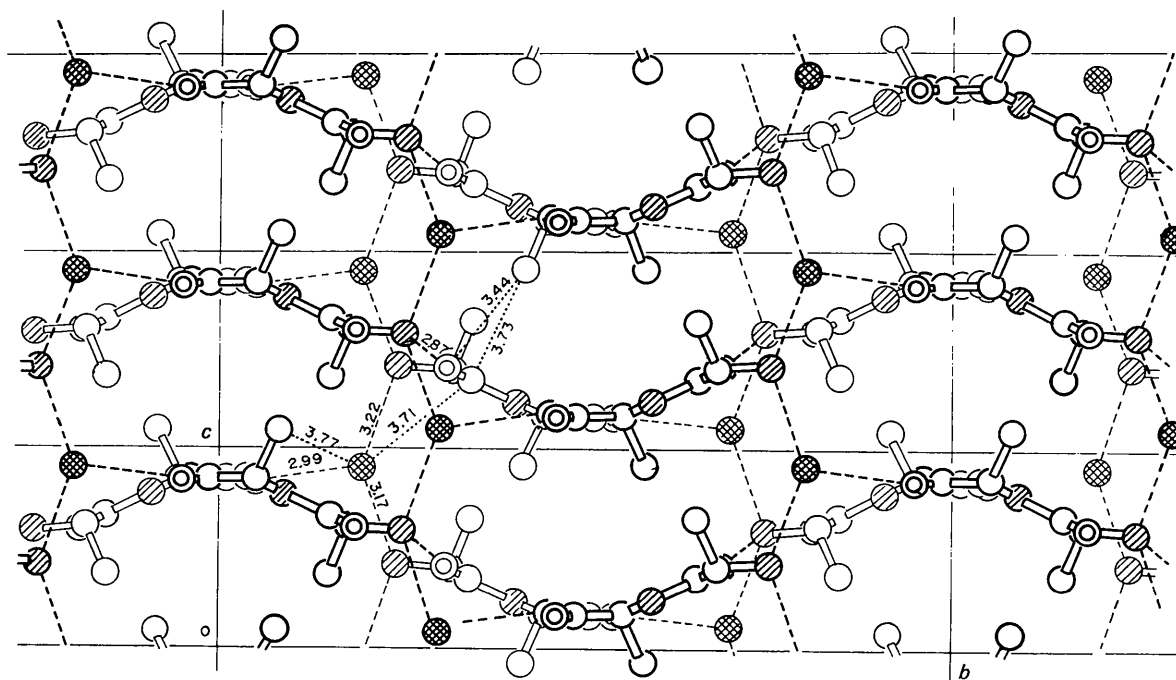


Fig.5. A drawing of the structure viewed along [100].

hydrogen bond to an oxygen atom, O(2-1), of the carboxyl group. This N(2)-H...O(2-1) hydrogen bond in the peptide group, 2.92 Å, is significantly longer (probably weaker) than the terminal N(1)-H...O(1) hydrogen bond of 2.87 Å. This is in agreement with a current survey of hydrogen bonding in peptides (Marsh & Donohue, 1967). The oxygen atom, O(2-2), of the carboxyl group forms the hydrogen bond with a chloride ion. The arrangement of these hydrogen bonds around the chloride ion is a trigonal pyramid with the chloride ion at the apex.

Some of the shorter intermolecular distances are indicated by the dotted lines in Figs.4 and 5. No unusually short contact is found in this crystal structure, and the shortest C...C, C...O and C...Cl distances are 3.73, 3.25 and 3.65 Å, respectively.

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