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## The Crystal and Molecular Structure of 2,7-Dichlorodibenzo-*p*-dioxin

BY F. P. BOER AND P. P. NORTH

*Analytical Laboratory, The Dow Chemical Company, Midland, Michigan 48640, U.S.A.*

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The crystal and molecular structure of 2,7-dichlorodibenzo-*p*-dioxin has been determined from three-dimensional single-crystal X-ray diffraction data. This compound crystallizes in the triclinic space group  $P\bar{1}$  with lattice parameters  $a = 3.878 \pm 0.003$ ,  $b = 6.755 \pm 0.009$ ,  $c = 10.265 \pm 0.015$  Å,  $\alpha = 99.46 \pm 0.01$ ,  $\beta = 100.63 \pm 0.03$ , and  $\gamma = 99.73 \pm 0.03^\circ$ , giving a calculated density  $\rho = 1.647$  g.cm<sup>-3</sup> for C<sub>12</sub>H<sub>6</sub>O<sub>2</sub>Cl<sub>2</sub> and  $Z = 1$ . The intensities of 1152 unique reflections were measured, using the  $\theta$ - $2\theta$  scan mode of a Picker automatic diffractometer (Mo  $K\alpha$  radiation). The structure was solved from the Patterson function and was refined by full-matrix least-squares analysis to a final  $R$  value of 5.7% for the 1030 reflections above background. In the final model, Cl, O, and C atoms were assigned anisotropic thermal parameters, while the hydrogen atoms were restricted to isotropic thermal parameters. The molecules are situated on crystallographic inversion centers; because they are planar, the approximate molecular symmetry is  $C_{2h}$ . The C-Cl bond distance is  $1.742 \pm 0.004$  Å, the C-O distances are 1.380 and 1.382 Å ( $\pm 0.004$ ), and the six C-C distances vary between 1.370 and 1.397 Å ( $\pm 0.005$ ). The C-O-C angle in the heterocyclic ring is  $116.3 \pm 0.2^\circ$ .

### Introduction

As part of an effort to establish the chemical and biological properties of the chlorinated derivatives of dibenzo-*p*-dioxin, we are undertaking the structure determinations of key compounds in this series by X-ray diffraction. This paper describes the crystal and molecular structure of 2,7-dichlorodibenzo-*p*-dioxin. The preparation, isolation, and X-ray powder diffraction pattern of this compound are being communicated separately (Boer, van Remoortere & Muelder, 1972).

Although the primary purpose of this work is to assist researchers in making a rapid and positive identification of these materials, the molecular conformations are of some interest, since in principle the molecules are capable of folding along their transverse bisectors. Indeed, severe folding is encountered in

heterocyclic analogs containing sulfur, such as thianthrenes (Lynton & Cox, 1956; Rowe & Post, 1958) and thioxanthenes (Ternay, Chasar & Sax, 1967), and some slight folding is reported for 1,2,3,7,8,9-hexachlorodibenzo-*p*-dioxin (Cantrell, Webb & Mabis, 1969). On the other hand, 2,3,7,8-tetrachlorodibenzo-*p*-dioxin (TCBD) is planar (Boer, van Remoortere, North & Neuman, 1972).

### Experimental

A sample of dichlorodibenzo-*p*-dioxin was received from W. W. Muelder. This material was isolated from sodium 2,4-dichlorophenolate that had been heated to 180°C for 16 hours. The dichlorodibenzo-*p*-dioxin forms colorless crystals of a lath-like habit, which tend to be very thin between the {010} faces and are

elongated along the *a* axis, corresponding to the shortest dimension of the unit cell. A crystal suitable for X-ray analysis was selected, sealed within a thin-walled Lindemann glass capillary, and aligned on its *a* axis on a Weissenberg goniometer. A preliminary survey of the reciprocal lattice, as recorded on the oscillation and *0kl* and *1kl* Weissenberg levels, indicated that the crystal system was triclinic. The crystal was then carefully centered on a Picker automatic four-circle diffractometer, and lattice constants were determined by least-squares refinement of the setting angles of 24 reflections (Mo *K* $\alpha$  radiation,  $\lambda$  0.71069 Å).

### Crystal data

Molecular formula	$C_{12}H_6O_2Cl_2$
Molecular weight	253.086
Crystal habit	Lath
Crystal size	$1.50 \times 0.022 \times 0.096$ mm ( <i>a</i> , <i>b</i> , and <i>c</i> directions)
Space group	$P\bar{1}$ (No. 2- <i>C</i> <sub>1</sub> )
Cell constants (reduced cell), 25°C	
<i>a</i>	$3.878 \pm 0.003$ Å
<i>b</i>	$6.755 \pm 0.009$
<i>c</i>	$10.265 \pm 0.015$
$\alpha$	$99.46 \pm 0.01^\circ$
$\beta$	$100.63 \pm 0.03$
$\gamma$	$99.73 \pm 0.03$
Volume <i>V</i>	$255.2 \pm 0.1$ Å <sup>3</sup>
Density $\rho_{\text{calc}}$	$1.647$ g.cm <sup>-3</sup> ( <i>Z</i> = 1)
Absorption coefficient $\mu$ (Mo <i>K</i> $\alpha$ )	$5.26$ cm <sup>-1</sup>
Number of independent reflections	
observed	1152

The errors given for the cell constants are those determined by the precision of least-squares fit, multiplied by a factor of 10. This factor, chosen arbitrarily, allows for some systematic errors in measurement at a level consistent with our ability to reproduce results with different crystals and/or orientations. The requirement of one formula unit per unit cell can be accommodated by either a molecule situated on an inversion center in space group  $P\bar{1}$ , or by a molecule in general space in  $P1$ .

Intensity data were gathered, using the  $\theta$ - $2\theta$  scan mode of the diffractometer and Mo *K* $\alpha$  radiation selected by the 002 reflection of a highly oriented graphite crystal monochromator. The take-off angle of the X-ray tube was 3°, and a counter aperture  $6.0 \times 6.0$  mm was placed 30 cm from the crystal; 1.5 mm diameter incident- and exit-beam collimators restricted stray radiation. The scan speed was  $2^\circ \text{ min}^{-1}$  over  $2\theta$  angles of  $2^\circ + \Delta$ , where  $\Delta$  is the separation of the *K* $\alpha$  doublet; this range was sufficient to allow for the observed mosaic spread of the crystal. Two stationary-crystal stationary-counter background counts of 10 sec were taken at each end of the scan. The reciprocal lattice was recorded out to  $\sin \theta = 0.461$ , equivalent to the Cu *K* $\alpha$  sphere. Attenuators

were used to prevent counting rates in excess of 12,000 per sec. The test reflection  $1\bar{1}\bar{1}$ , monitored after every 50 measurements, showed a root-mean-square deviation of intensity of 1%, and a maximum deviation of 3% from the mean. An error  $\sigma(I) = [(0.02I)_0 + N_0 + k^2N_b]^{1/2}$  was assigned to the net intensity  $I = N_0 - kN_b$  of each reflection, in order to establish the weights  $w(F) = 4F^2/\sigma^2(F^2)$  for subsequent least-squares refinement, where the quantity  $\sum w(|F_o| - |F_c|)^2$  was minimized. Here,  $N_0$  is the gross count,  $N_b$  is the background count,  $k$  is the ratio of scan time to background time, and the  $F^2$  are the intensities corrected for Lorentz and polarization effects by the expression  $(Lp)^{-1} = \sin 2\theta(1 + \cos^2 2\theta_m)/(1 + \cos^2 2\theta \cos^2 2\theta_m)$ , where  $2\theta_m$  is the monochromator setting angle. The 122 reflections for which  $I < 0$  or  $I/\sigma(I) < 2.0$  were denoted absent and omitted from the refinement. An absorption correction was applied to the data. Transmission factors ranged from 0.942 to 0.986. No correction for secondary extinction appeared necessary, and none was applied. An overall scale factor and temperature factor were computed by Wilson's (1942) method. The intensity statistics matched an ideal centric distribution much more closely than an acentric distribution.

Quantity	Found	Theoretical (centric)	Theoretical (acentric)
$\langle  E  \rangle$	0.828	0.798	0.886
$\langle E^2 \rangle$	1.000	1.000	1.000
$\langle  E^2 - 1  \rangle$	0.911	0.968	0.736
% > 1	29.69	32.00	37.00
% > 2	4.95	5.00	1.80
% > 3	0.09	0.30	0.01

Stringent precautions are recommended to avoid exposure of laboratory personnel to chlorinated dioxins. The procedures followed during this experiment were identical to those described for the X-ray diffraction study of 2,3,7,8-tetrachlorodibenzo-*p*-dioxin (Boer *et al.*, 1972).

### Solution and refinement of the structure

The C, O, and Cl atoms were located from their vector interactions with Cl in a three-dimensional normal-sharpened Patterson function. A trial structure was generated by using these vectors to position an idealized model of the molecule (with normal bond distances and angles, and including hydrogen atoms). Because the Patterson synthesis was consistent with the presence of an inversion center, refinement was begun assuming space group  $P\bar{1}$ . The initial values of *R* for this model were  $R_1 = \sum ||F_o| - |F_c|| / \sum |F_o| = 0.239$  and  $R_2 = \{ \sum w[F_o - F_c]^2 / \sum wF_o^2 \}^{1/2} = 0.259$ . In successive cycles of full-matrix least-squares refinement, we introduced the heavy-atom positions, the heavy-atom isotropic temperature factors, the hydrogen positions, and finally the hydrogen isotropic temperature factors as variables. Four additional cycles of isotropic refine-

ment with these 45 variables converged at R1=0.1284 and R2=0.1309, and gave reasonable numbers (see below) for interatomic distances and angles and for the thermal parameters.

At this time we undertook further tests to determine whether the true space group might be P1. Refinement of the 86 variables in the acentric model converged to R1=0.1153 for the 1030 reflections above background. The ratio R=R1(centric)/R2(acentric)=1.1136 is well in excess of R41,944,0.01=1.0336 extrapolated from Hamilton's (1965) tables (41 is the dimension of the hypothesis and 944 is the number of degrees of freedom), and it implies that we can reject the hypothesis that the space group is centric with less than a 1% probability of error. Nevertheless, inspection of the results after refinement in P1 showed clearly that the acentric model was inappropriate for determining meaningful metric or thermal parameters for dichloro-dibenzo-p-dioxin. This point is brought out in Table 1, where high and low values of selected parameters from the P1 and P1 refinements are summarized, and where certain numbers from the acentric refinement, which ought to be equivalent or nearly so, can be seen to exhibit an unreasonably large range of values. The

explanation for this scatter is believed to be the high correlations that occur between atomic parameters related by the molecular center. In addition, the system may be attempting to compensate for anisotropic thermal motion. In view of these results, we decided to continue refinement in space group P1. Because reasonable values were obtained for the final atomic parameters and R values, we are confident that P1 is a satisfactory model for refining this structure. In this context, it is worth noting that very similar problems were encountered in the study of 2,3,7,8-tetrachloro-dibenzo-p-dioxin, and that its structure could be refined

Table 1. High and low values of selected parameters from the P1 and P1 refinements

Table with columns: Parameter, Distances, P1 Low, P1 High, P1 Low, P1 High. Rows include C-Cl, C-O, C-C, C-H, B, Cl, O, C, H.

Table 2. Observed and calculated structure factors in e and scaled by a factor of 48.12

Large table containing observed and calculated structure factors for various h, k, l reflections. Columns are labeled with h, k, l and corresponding observed (O) and calculated (C) values.

to a very respectable  $R_1$  of 3.6% in the centric space group. The results of the above calculations suggest that judgement should be exercised in accepting the results of  $R$  value ratio tests when the matrix equations are not well-behaved, as, for example, in the vicinity of symmetry elements not explicitly incorporated in the normal equations, and that intensity statistics may often be the preferred method for distinguishing between two space groups.

Full-matrix least-squares refinement was then continued, assuming anisotropic thermal parameters for the Cl, O, and C atoms, and introducing a dispersion correction for Cl. The final  $R$  values were  $R_1=0.057$  and  $R_2=0.062$ . That reasonable convergence was attained is indicated by the values  $(\Delta/\sigma)_{\max}=0.05$  for nonhydrogen atoms and 0.33 for hydrogen atoms. A final difference Fourier showed no positive peaks greater than  $0.34 \text{ e.}\text{\AA}^{-3}$  and no negative regions below  $-0.41 \text{ e.}\text{\AA}^{-3}$ . The largest negative peak occurred at the origin.

Observed and calculated structure factors are given in Table 2, and the final atomic parameters and their standard deviations, as calculated in the last least-squares cycle, are listed in Table 3. Intramolecular distances and angles are summarized in Table 4, and the amplitudes and directions of anisotropic thermal motion are listed in Table 5 and displayed in Fig. 1. The standard deviations in Tables 4 and 5 were computed from the variance-covariance matrix obtained in the last least-squares cycle.

Table 4. Bond distances and angles in 2,7-dichlorodibenzo-*p*-dioxin

Distances (Å)			
Cl—C(6)	1.742 (4)	C(3)—C(5)	1.378 (5)
O—C(1)	1.382 (4)	C(4)—C(6)	1.386 (5)
O'—C(2)	1.380 (4)	C(5)—C(6)	1.378 (5)
C(1)—C(2)	1.397 (5)	C(3)—H(3)	0.96 (3)
C(1)—C(3)	1.373 (5)	C(4)—H(4)	0.93 (4)
C(2)—C(4)	1.370 (5)	C(5)—H(5)	0.88 (3)

Table 3. Atomic parameters for 2,7-dichlorodibenzo-*p*-dioxin

	$x$	$y$	$z$	$10^4\beta_{11}$	$10^4\beta_{22}$	$10^4\beta_{33}$	$10^4\beta_{12}$	$10^4\beta_{13}$	$10^4\beta_{23}$
Cl	-0.4292 (3)	-0.3654 (1)	0.3777 (1)	945 (9)	240 (2)	106 (1)	85 (3)	142 (2)	63 (1)
O	0.0466 (7)	0.2155 (3)	0.0479 (2)	1110 (25)	134 (5)	72 (2)	82 (8)	114 (6)	15 (3)
C(1)	-0.0668 (8)	0.0749 (5)	0.1228 (3)	587 (26)	159 (7)	66 (3)	74 (11)	36 (7)	30 (4)
C(2)	-0.1125 (8)	-0.1359 (5)	0.0757 (3)	569 (26)	165 (2)	66 (3)	77 (11)	35 (7)	21 (4)
C(3)	-0.1340 (9)	0.1467 (5)	0.2468 (3)	694 (29)	166 (8)	78 (4)	74 (12)	64 (8)	3 (4)
C(4)	-0.2219 (9)	-0.2706 (5)	0.1534 (3)	599 (28)	160 (9)	84 (4)	63 (11)	41 (8)	32 (4)
C(5)	-0.2452 (9)	0.0123 (5)	0.3255 (3)	640 (29)	213 (9)	77 (4)	110 (12)	84 (8)	25 (5)
C(6)	-0.2894 (8)	-0.1955 (5)	0.2782 (3)	453 (24)	208 (8)	89 (4)	89 (11)	55 (7)	58 (4)
<i>B</i>									
H(3)	-0.094 (4)	0.293 (5)	0.278 (3)	3.5 (8)					
H(4)	-0.240 (9)	-0.411 (6)	0.124 (4)	4.4 (9)					
H(5)	-0.283 (9)	0.058 (5)	0.406 (4)	4.0 (9)					

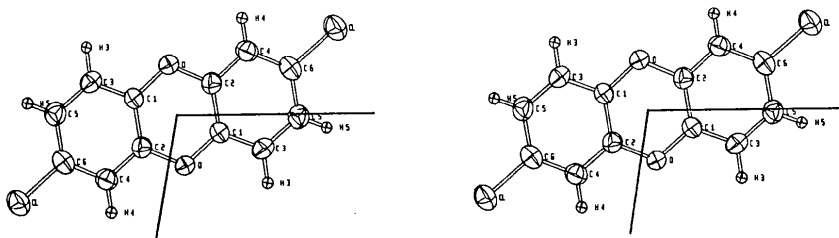


Fig. 1. Stereoscopic view of a molecule of 2,7-dichlorodibenzo-*p*-dioxin showing the ellipsoids of thermal motion and indicating the numbering system.

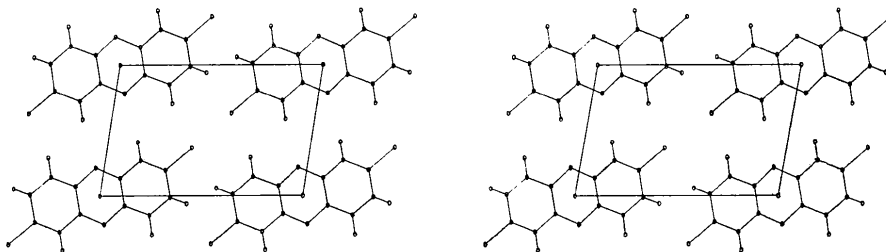


Fig. 2. Stereoscopic view of molecular packing in the  $yz$  plane of 2,7-dichlorodibenzo-*p*-dioxin. The unit cell outline in this plane is drawn.

Table 4 (cont.)

Angles (°)							
Vertex	Atom 1	Atom 2		Vertex	Atom 1	Atom 2	
O	C(1)	C(2')	116.3 (2)				
C(1)	O	C(2)	121.7 (3)	C(2)	O'	C(1)	122.0 (3)
	O	C(3)	118.5 (3)		O'	C(4)	118.0 (3)
	C(2)	C(3)	119.8 (3)		C(1)	C(4)	120.1 (3)
C(3)	C(1)	C(5)	120.6 (3)	C(4)	C(2)	C(6)	119.4 (3)
	C(1)	H(3)	118 (2)		C(2)	H(4)	120 (2)
	C(5)	H(3)	121 (2)		C(6)	H(4)	121 (2)
C(5)	C(3)	C(6)	119.2 (3)	C(6)	C(4)	C(5)	121.0 (3)
	C(3)	H(5)	121 (2)		C(4)	Cl	119.7 (3)
	C(6)	H(5)	120 (2)		C(5)	Cl	119.3 (3)

\* Primed atoms are related by the center at (0,0,0). Errors in parentheses are referred to the last significant digit cited.

Table 5. *R.m.s. amplitudes of thermal motion along the principal axes\**

	Axis 1	Axis 2	Axis 3
Cl	0.1831 (12)	0.2375 (12)	0.2691 (13)
O	0.166 (3)	0.181 (3)	0.282 (3)
C(1)	0.171 (4)	0.190 (4)	0.205 (4)
C(2)	0.181 (4)	0.186 (4)	0.203 (4)
C(3)	0.173 (5)	0.212 (4)	0.223 (5)
C(4)	0.181 (4)	0.202 (5)	0.210 (5)
C(5)	0.179 (5)	0.210 (4)	0.222 (5)
C(6)	0.174 (5)	0.180 (4)	0.229 (4)

\* Ordered on increasing magnitude.

The atomic scattering factors for Cl, C, and O were taken from the *International Tables for X-ray Crystallography* (1962). The scattering factor for hydrogen is that calculated by Stewart, Davidson & Simpson (1965). Fourier summations, least-squares refinements, and error analysis were based on adaptations of standard programs by Gvildys (1964, 1965a, b, 1967), and illustrations were prepared using a local version of the thermal ellipsoid plot program of Johnson (1965).

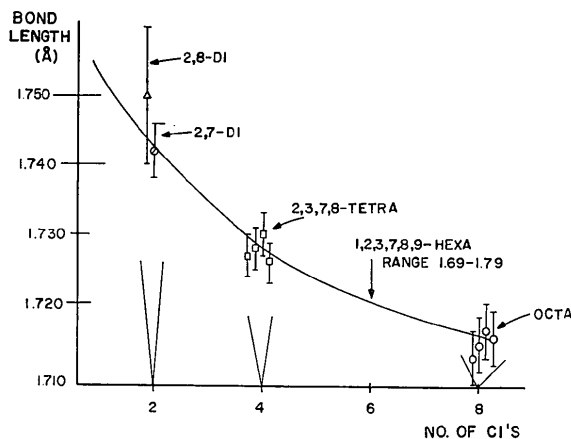


Fig. 3. Carbon-chlorine bond lengths (Å) in chlorinated dibenzo-*p*-dioxins as a function of the degree of chlorine substitution.

## Discussion

2,7-Dichlorodibenzo-*p*-dioxin is found to be planar within experimental error; because it is situated on a crystallographic inversion center, the approximate molecular symmetry in the crystal is  $C_{2h}$ . For the unique atoms, the calculated (Gvildys, 1965b) deviations from the least-squares plane, based on the nonhydrogen atoms, are Cl, 0.005; O, 0.003; C(1), -0.004; C(2), -0.008; C(3), -0.002; C(4), -0.001; C(5), 0.001; C(6), -0.002; H(3), 0.024; H(4), 0.042; and H(5), 0.025 (Å). Deviations for the 11 atoms related by the center are, of course, equal but opposite in sign. The equation of the plane is  $3.489x - 1.338y + 2.682z = 0$ .

The crystal contains only one unusually short intermolecular interaction: the Cl...Cl contact of 3.402 Å across the inversion center at  $(\frac{1}{2}, \frac{1}{2}, \frac{1}{2})$ . This distance is approximately 0.2 Å less than the sum of two chlorine van der Waals radii (3.6 Å), and, interestingly, is comparable to several short Cl...Cl intermolecular distances (3.44, 3.46, 3.47 Å) occurring in 1,2,3,7,8,9-hexachlorodibenzo-*p*-dioxin (Cantrell, *et al.*, 1969). The only other nonhydrogen contacts below 3.6 Å in the crystal occur between molecules stacked in the short (3.878 Å) cell translation along *x*. Distances between atoms related directly by this translation are C(4)...C(6), 3.526; C(1)...C(3), 3.528; O...C(3), 3.591; C(2)...C(6), 3.596; and C(1)...C(5), 3.600 (Å); whereas those based on the inversion center at  $(\frac{1}{2}, 0, 0)$  are O...C(2), 3.527; C(1)...C(2), 3.575; and O...C(4), 3.585 (Å). The perpendicular distance between planes related by the lattice period along *x* is 3.489 Å; the normal to the molecular plane forms an angle of 25.9° with the *x* axis. A view of the molecular packing in the *yz* planes is given in Fig. 2.

The C-Cl bond,  $1.742 \pm 0.004$  Å, is within experimental error of the value (Fig. 3) determined for 2,8-dichlorodibenzo-*p*-dioxin (Boer, Neuman & Aniline, 1972). It is 3-4 standard deviations longer than the C-Cl bond lengths determined for 2,3,7,8-tetrachlorodibenzo-*p*-dioxin and 6-7 standard deviations longer than C-Cl bonds in octachlorodibenzo-*p*-dioxin (Neuman, North & Boer, 1972). These results reveal an

interesting trend toward bond shortening with increasing chlorine substitution on the rings. The accuracy and internal agreement of the data are such as to suggest that these differences are real; they also persist when the bond distances are corrected assuming rigid-body thermal motion (Schomaker & Trueblood 1968). We attribute this effect to a reduction in the effective electronegativity difference between C and Cl atoms as more electron density is withdrawn from the aromatic ring upon increased substitution; as a result, the C-Cl bonds have increased covalent character and exhibit shorter distances.

Other bond distances and angles are quite regular. The C-O distances of 1.380 and 1.382 ( $\pm 0.004$ ) Å are very close to the average value of 1.378 Å in TCBD. Similarly, the C-C distances, which range between 1.370 and 1.397 ( $\pm 0.005$ ) Å, vary by no more than 0.01 Å from values for the corresponding ring positions in TCBD. The C-H distances of 0.88, 0.93, and 0.96 Å are subject both to larger random errors and to systematic shortening from the true internuclear separation, due to the attraction of electron density from the hydrogen nucleus toward the bonding region (Stewart *et al.*, 1965). The C-O-C angle in the central ring is  $116.3 \pm 0.2^\circ$  (compare  $115.6^\circ$  and  $115.8^\circ$  in TCBD), while the corresponding C-C-O angles in the heterocycle are  $121.7$  and  $122.0^\circ$ . The angle of  $121.0 \pm 0.3^\circ$  at C(6) might be significantly different ( $3\sigma$ ) from  $120^\circ$ ; if so, the increased angle could also be accounted for by rehybridization resulting from withdrawal of *p*-character from carbon by the more electronegative chlorine atom (Bent, 1961). Bond angles at the remaining carbon atoms are indistinguishable from the trigonal angle within the accuracy of this experiment.

That the chlorine and oxygen atoms display the most thermal anisotropy can be seen from Table 5. For the chlorine, the largest thermal amplitude is in the molecular plane in a direction perpendicular to the C-Cl bond (Fig. 1), whereas for the oxygen the largest vibrational component forms an angle of  $18.0 \pm 1.3^\circ$

with the *x* axis and is thus roughly orthogonal to the plane of the molecule.

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