The Crystal Structure of Terephthalamide

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The crystal structure of terephthalamide, $C_6H_4(CONH_2)_2$, has been investigated using three-dimensional X-ray data collected by means of a three-circle diffractometer in conjunction with a proportional counter. The space group is PI and there is one molecule in the unit cell. A full-matrix least-squares refinement of the positional and anisotropic thermal vibration parameters gave a final R value of 0.088. The molecules are linked together in sheets by hydrogen bonds with the plane of the amide group making an angle of 23° with the plane of the benzene ring. The bond lengths have been corrected for librational motion, and are C-C (amido) = 1.491 ± 0.005, C-O = 1.247 ± 0.005, C-N = 1.305 ± 0.005, C-C = 1.409 ± 0.006, C-C = 1.382 ± 0.006 and C-C = 1.380 ± 0.008 Å.

Introduction

The crystal structure of terephthalamide has been investigated as part of a series of studies of amides and similar hydrogen bonded structures. Apart from the hydrogen bonding network and the geometry of the amide group, the degree of planarity of the molecule as a whole was of interest.

Crystal data

Terephthalamide is insoluble in most common organic solvents and virtually insoluble in water. Crystals were obtained by dissolving a commercial sample in aqueous formic acid and allowing the solvent to evaporate slowly at a temperature of 30 °C. The habit of the colourless crystals obtained suggested that terephthalamide is triclinic. Preliminary oscillation and Weissenberg photographs confirmed this.

Accurate cell dimensions were determined from θ measurements made on a three-circle diffractometer (Small & Travers, 1961) using an extrapolation method (Beagley & Small, 1964) to eliminate zero-crror settings of the circles. The corrected interplanar spacings calculated for a number of sets of planes were used to give a best least-squares fit for the cell parameters. The density was measured by the flotation method using a mixture of carbon tetrachloride and chlorobenzene. Crystal data are shown in Table 1.

Table 1. Crystal data

$a = 5.027 \pm 0.001$ Å	$V = 183.88 \text{ Å}^3$
$b = 5.355 \pm 0.001$	Z = 1
$c = 7.165 \pm 0.001$	$D_{\rm obs} = 1.47 {\rm g. cm^{-3}}$
$\alpha = 103.02 \pm 0.04^{\circ}$	$D_{calc} = 1.48 \text{ g.cm}^{-3}$
$\beta = 100.90 \pm 0.03$	
$\gamma = 92.17 \pm 0.02$	

The space group was taken to be $P\overline{1}$ on the evidence of a centric distribution of the three-dimensional data (Howells, Phillips & Rogers, 1950).

Determination of the structure

Three-dimensional data were collected using the threecircle diffractometer. At room temperature, 796 integrated intensities, for which $\theta < 82^{\circ}$, were measured using Cu K α radiation ($\lambda = 1.5418$ Å). The intensities were corrected for absorption on the Chilton ATLAS computer using the program *ABSCOR*.

The structure was solved by interpretation of twodimensional Patterson syntheses projected on (100) and (010). Refinement of the model obtained was carried out initially by two-dimensional least-squares calculations and subsequently by applying the fullmatrix least-squares program ORFLS (Busing, Martin & Levy, 1962) to the three-dimensional data. The atomic scattering factors used throughout were those listed in International Tables for X-ray Crystallography (1962). Initially all reflexions were weighted equally but in the later cycles a weighting scheme was applied with $\sqrt{w} = 0.43/(J)$ where (J) takes the maximum value of the three functions, $0.008|F_o| - 0.15$, σ or 0.43 for a particular reflexion, where σ is the standard deviation of the structure amplitude based on counting statistics. Refinement of the carbon, nitrogen and oxygen parameters continued until R reached 0.124, when a weighted $F_o - F_c$ Fourier synthesis was computed to give the positions of the four hydrogen atoms of the asymmetric unit. These hydrogen atoms were given anisotropic thermal parameters equal to those of the atoms to which they were bonded and included in the next two cycles of least-squares refinement when Rreached 0.099. The calculated structure amplitudes for the 011 and $1\overline{11}$ reflexions were considerably in excess of their observed magnitudes and, on the assumption that the difference was due to extinction, these reflexions were omitted from subsequent refinement cycles. In the last cycle the hydrogen atom positions were refined. The final R value was 0.088, the parameter shifts of the heavy atoms being less than one quarter of their estimated standard deviations.

An $F_o - F_c$ Fourier synthesis did not reveal any

further significant features. The final positional parameters are shown in Table 2 and the vibrational parameters of the heavier atoms in Table 3. Table 4 lists the final values of the observed and calculated structure amplitudes.

Table 2. Fractional atomic coordinates

The values of the fractional coordinates and the estimated standard deviations in parentheses are multiplied by 10⁴.

x	у	Z
57 (7)	7768 (6)	1999 (5)
-2181 (7)	4577 (7)	3432 (5)
2169 (7)	6722 (7)	5110 (5)
9 (6)	6326 (6)	3544 (4)
2269 (5)	8642 (6)	1769 (4)
-2247 (6)	8063 (6)	932 (4)
-2275 (81)	9106 (84)	-40 (65)
- 3931 (89)	7668 (83)	1344 (59)
3712 (79)	8194 (79)	5313 (58)
- 3965 (83)	4375 (81)	2181 (60)
	57 (7) -2181 (7) 2169 (7) 9 (6) 2269 (5) -2247 (6) -2275 (81) -3931 (89) $3712 (79)$	$\begin{array}{cccccccccccccccccccccccccccccccccccc$

Table 3. Thermal vibrational parameters

The values of the vibration parameters and the estimated standard deviations in parentheses are multiplied by 104. The temperature factor expression used is of the form

exp {	$(-(b_{11})h_{11})$	$k^{2} + b_{22}k^{2}$	$+b_{33}l^{2}+$	$-2b_{12}hk +$	2b13h	$l+2b_{23}k$	l)}.

	<i>b</i> 11	b22	b33	<i>b</i> ₁₂	<i>b</i> ₁₃	b ₂₃
C(1)	364 (14)	393 (15)	141 (7)	1 (11)	110 (8)	95 (8)
C(2)	381 (15)	470 (16)	138 (7)	-64(12)	60 (8)	106 (9)
C(3)	331 (14)	435 (16)	149 (7)	-45(12)	59 (8)	106 (9)
C(4)	319 (13)	368 (14)	133 (7)	-13(11)	87 (7)	78 (8)
0	359 (12)	702 (16)	244 (7)	- 36 (10)	130 (7)	239 (9)
N	366 (13)	506 (15)	183 (7)	-4(11)	86 (8)	169 (8)

Table 4. Observed and calculated structure amplitudes $\times 10^2$

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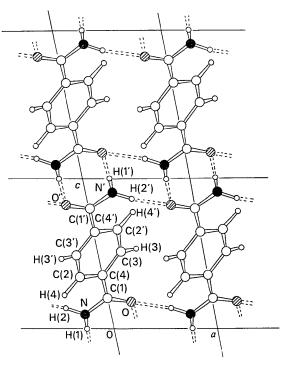


Fig. 1. The crystal structure projected on to (010).

Analysis of the anisotropic thermal motion

In order to correct bond lengths for librational motion the ellipsoids of vibration were analysed in terms of rotational oscillations of the molecule as a rigid body. Cruickshank (1956) has described a method in which rigid-body translational and rotational displacements are represented in terms of two symmetric tensors T and L. The method is only valid for libration about a centre of symmetry and, in other cases, correlation of the librational and translational motion can occur. Schomaker & Trueblood (1968) have considered this correlation by introducing a third tensor S. In the case of terephthalamide the centre of mass of the molecule is at a centre of symmetry and the thermal vibration can be interpreted in terms of the two tensors T and L. The thermal motion analysis program MGTLS of Gantzel & Trueblood was used to test the validity of rigid-body motion of the molecule. Table 5 gives the rigid-body parameters for the molecule. The U_{ii} values calculated from these parameters showed satisfactory agreement with the 'observed' U_{ij} values calculated from the b_{ij} values of the final least-squares refinement cycle (Table 6). The r.m.s. ΔU_{ij} , 0.0024 Å², derived for the rigid-body model, compared with the mean σU_{ij} value of 0.0014 Å² calculated from the estimated standard deviations of the b_{ij} values, provides evidence for the validity of the model. The bond lengths and angles were corrected for the thermal motion shown by the rigid-body analysis and the uncorrected and corrected values are given in Tables 7 and 8 respectively.

Table 5. Rigid-body thermal parameters referred to orthogonal axes a, b, c*

Estimated standard deviations of the elements of the T and L tensors are given in parentheses.

$$\mathbf{T} = \begin{pmatrix} 330 & (12) & -59 & (10) & 126 & (10) \\ & 458 & (11) & 27 & (10) \\ & 269 & (10) \end{pmatrix} \times 10^{-4} \text{ Å}^2$$
$$\mathbf{L} = \begin{pmatrix} 17 & (2) & 6 & (2) & 0 & (2) \\ & 101 & (7) & -97 & (7) \\ & & 109 & (8) \end{pmatrix} \times 10^{-4} \text{ rad}^2$$

Principal axes of T

R.m.s. amplitude (Å)	Direction	n cosines	(× 10 ³)
0.220	-465	870	- 163
0.203	- 629	-454	-631
0.126	- 623	- 191	758
Principal axes of L			
R.m.s. amplitude (rad)	Direction	1 cosines	(×103)
0.142	19	693	-720
0.043	930	252	267
0.025	364	- 676	- 641

Discussion of the crystal and molecular structure

The crystal structure of terephthalamide consists of molecules held together by hydrogen bonding in sheets. Chains of molecules are hydrogen-bonded end-to-end across centres of symmetry, and adjacent chains are linked by hydrogen bonds approximately parallel to the *a* axis. The hydrogen-bonded distances $(N \cdots O)$ are 2.90 and 2.94 Å respectively and the N-H \cdots O angles are 175.7 and 149.4°. There are no abnormal contact distances between atoms in adjacent sheets; the closest approach between heavy atoms is 3.43 Å for atoms C(2) and C(3). The crystal structure projected on to the (010) plane is illustrated in Fig. 1.

The bond lengths of the amide group and the benzene ring are comparable with those found in similar compounds. The carbon atoms of the benzene ring are coplanar within the limits of the experimental error, and the plane through the amide group makes an angle of 23° with this plane. The equations of these planes referred to the orthogonal axes a, b', c^* and the deviations of atoms from them are shown in Table 9. A similar twist, of magnitude 24.6° , has been found for benzamide (Blake & Small, 1972) in which the non-planarity is attributed to repulsion between an amide hydrogen atom and the *ortho* hydrogen atom rather than repulsion effects between adjacent hydrogen-bonded molecules. The same view is put forward for

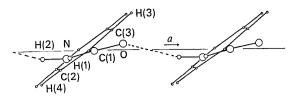


Fig. 2. Projection showing the side-to-side hydrogen bonding. For clarity only one of the amide groups is depicted.

the non-planarity of terephthalamide since the amide hydrogen atom, H(2), is involved in a close contact of 1.99 Å with the *ortho* hydrogen atom, H(4), whereas the closest approaches between adjacent molecules related by the **a** translation are 3.11 Å between atoms H(3) and H(4), 3.05 Å between atoms O and H(4) and 3.16 Å between atoms C(2) and H(3).

Table 7. Bond distances and their standard deviations

	Before libration correction	After libration correction
C(1)-C(4)	1·489 (5) Å	1·491 (5) Å
C(1)-O	1.244 (5)	1.247 (6)
$\hat{C}(1)-N$	1.298 (5)	1.305 (6)
C(2) - C(4)	1.397 (6)	1.409 (6)
C(3) - C(4)	1.377 (5)	1.382 (6)
C(3) - C(2')	1.379 (8)	1.380 (8)
N - H(1)	0.98 (5)	
NH(2)	0.98 (5)	
C(3) - H(3)	1.05 (4)	
C(2) - H(4)	1.12 (4)	

Tab	le ¦	8.	Bond	angle	es and	their	• stand	lard	deviations
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	Before libration	After libration
	correction	correction
C(4) - C(1) - O	119·7 (7)°	119·6 (7)°
C(4) - C(1) - N	118.0 (7)	117.7 (7)
$O_{}C(1)-N$	122.3 (9)	122.7 (9)
C(1) - C(4) - C(2)	121.2 (7)	121.1 (7)
C(1) - C(4) - C(3)	119.3 (7)	119-2 (7)
C(2) - C(4) - C(3)	119.5 (7)	119.8 (7)
C(3')-C(2)-C(4)	119.8 (9)	119.4 (9)
C(2') - C(3) - C(4)	120.7 (9)	120.6 (9)
C(1) - N - H(1)	119 (2)	
H(1) - N - H(2)	120 (4)	
C(1) - N - H(2)	119 (2)	
H(3)-C(3)-C(2')	118 (2)	
C(4) - C(3) - H(3)	121 (2)	
C(4) - C(2) - H(4)	118 (2)	
H(4)-C(2)-C(3')	122 (2)	

Table 6. Observed and calculated values of $(U_{ij} \times 10^4)$ in Å²

	U_{11}	U_{22}	U_{33}	U_{12}	U_{13}	U_{23}
	obs calc	obs calc	obs calc	obs calc	obs calc	obs calc
C(1)	406 392	503 547	334 343	-84 - 90	119 107	95 106
C(2)	469 439	604 560	326 346	-160 - 153	32 34	118 108
C(3)	405 432	557 576	353 382	-130 - 168	25 27	110 132
C(4)	365 345	482 479	314 285	-87 - 66	84 121	69 46
0	403 428	836 791	577 563	-199 - 173	96 65	303 324
N	432 444	607 635	434 419	-108 - 117	51 52	208 187

 Table 9. Deviations of atoms from least-squares planes

(a) Plane through the benzene-ring carbon atoms Equation of the plane, referred to orthogonal axes a, b', c^* is

C(2)	−0·001 Å	H(1)	0·516 Å
C(3)	-0.001	H(2)	0.939
C(4)	0.001	H(3)	0.124
C(1)	0.004	H(4)	0.058
0	-0.417		
N	0.420		

(b) Plane through atoms C(1), C(4), O and N

Equation of the plane, referred to orthogonal axes
$$a, b', c^*$$
 is

-0.2317x + 0.7189y + 0.6553z = 3.7368.			
C(1)	0.000 Å	N	0·000 Å
C(4)	0.000	H(1)	0.060
0	0.000	H(2)	0.190

Another feature of interest is the degree of planarity of the hydrogen-bonding system, which is very similar to that reported for benzamide. The planes of the amide groups involved in hydrogen bonding across the centre of symmetry have a separation of 0.31 Å (0.37 Å in benzamide) and for the amide groups hydrogen-bonded side-to-side the separation is 1.16 Å (1.15 Å in benzamide). Fig. 2 shows the side-to-side hydrogen-bonding network and illustrates the extent to which the 0.19 Å deviation of the amide hydrogen atom, H(2), from the amide plane places it further from the *ortho* hydrogen atom, H(4), and closer to a linear hydrogen-bonding direction.

The authors would like to thank Professor K. N. Trueblood for a listing of the rigid-body analysis program *MGTLS*.

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Kristall- und Molekülstruktur von 1-Hyoscyaminhydrobromid

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The crystal structure of 1-hyoscyamine hydrobromide ($C_{17}H_{24}O_3NBr$) has been investigated. The relationship between the molecular structure and the pharmacological mode of operation has been discussed with reference to the known properties of the acetylcholine receptor. Bonding to the receptor is achieved through the tertiary amino group with hydrogen bonds of 3.7 and 7.7 Å to the anionic site of the receptor.

Hyoscyamin ist ein Alkaloid der Atropingruppe, das sich in verschiedenen Pflanzen, z.B. Atropa belladonna (Tollkirsche) und Hyoscyamus niger (Bilsenkraut) findet. Es kommt in zwei optisch aktiven Formen vor. als (+)-Hyoscyamin und als (-)-Hyoscyamin. (-)-Hyoscyamin ist der Ester des Tropins und der (-)-Tropasäure. In der Natur findet man vorwiegend die linksdrehende Form. Seine pharmakologische Wirkung kommt dadurch zustande, dass Rezeptoren von Zellen, die auf Acetylcholin (ACh) ansprechen, für diese Transmittersubstanz unempfindlich gemacht werden. Die Wirkung von (-)-Hyoscyamin im peripheren Nervensystem ist allerdings beschränkt auf die glatte Muskulatur und die parasympatisch innervierten Drüsen. An der quergestreiften Muskulatur und an den Ganglien wirkt Hyoscyamin nicht als ACh-Antagonist. Die optischen Isomeren haben nicht dieselbe pharmakologische Wirksamkeit. (+)-Hyoscyamin beeinflusst das cholinerge periphere Nervensystem sehr viel weniger (Cushny, 1920), es kommt also bei der pharmakologischen Wirkung auf die räumliche Beziehung der Atomgruppen im Molekül an. Eine Aufklärung der Raumstruktur von Hyoscyamin und entsprechend wirkenden Verbindungen kann weitere Aufschlüsse über die Beziehungen zwischen chemischer Struktur und pharmakologischer Wirkung dieser Substanzen geben.

Material und Methode

Untersucht wurde das käufliche (-)-Hyoscyaminhydrobromid der Fa. Merck, Darmstadt.