**Discussion.** The atomic coordinates are listed in Table 1, and bond distances and angles are given in Table 2.\* A view of the molecule and the numbering scheme are shown in Fig. 1. The packing scheme is presented in Fig. 2.

Bond distances and angles are normal. Refinement of H atoms with isotropic thermal parameters and free coordinates was not successful. The H atoms had to be used as riding atoms with the C-H distance fixed until acceptable results were obtained. Earlier structural studies of chlorinated dibenzo-p-dioxins, viz. 2.3.7.8tetrachloro- (TCDD) (Boer, van Remoortere, North & Neuman, 1972), 2,7-dichloro- (Boer & North, 1972), octachloro- (Neuman, North & Boer, 1972) and 2.8-dichlorodibenzo-p-dioxin (Boer, Neuman & Aniline, 1972), confirmed the assumed planarity of these molecules. The compound under study is less planar than the chlorinated dibenzo-p-dioxins just mentioned, but the deviations are so small that the molecule can be regarded as planar {largest deviation 0.081 (4) Å [Cl(2)] from least-squares plane}.

On the basis of the molecular dimensions of TCDD, Poland (Poland & Knutson, 1982) proposed that the TCDD molecule fits exactly into a particular receptor, disturbing its normal functioning and causing the toxic effects observed. The dimensions of this rectangular receptor would be  $10 \times 3$  Å. Recently Gillner *et al.* (1985) improved Poland's theory by using instead molecular dimensions and van der Waals radii to evaluate the size of the dioxin receptor; namely, the receptor size proposed by Poland cannot explain the similar toxic effects observed for polycyclic aromatic hydrocarbons (PAH). The receptor size as expanded by the van der Waals radii is  $13 \cdot 7 \times 6 \cdot 8$  Å. The van der Waals expanded dimensions of the title compound are length 10.905 Å and height 7.928 Å. The height of 1,2,3,4-tetrachlorodibenzo-*p*-dioxin is thus too great for the molecule to fit exactly into the dioxin receptor. The compound does not, therefore, have similar toxic effects to TCDD and other molecules that fit into the dioxin receptor.

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# Structure of (3R,6S)-3-Neopentyl-1,4-diazabicyclo[4.3.0]nonane-2,5-dione

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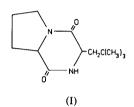
(Received 7 April 1986; accepted 23 September 1986)

Abstract.  $C_{12}H_{20}N_2O_2$ ,  $M_r = 224.30$ , orthorhombic,  $1.19(1) \text{ g cm}^{-3}$ ,  $\lambda(\text{Cu } K\alpha) = 1.5418 \text{ Å}$ ,  $\mu = 6.19 \text{ cm}^{-1}$ ,  $P_{2_12_12_1}$ , a = 10.006(2), b = 19.696(6), c = F(000) = 488, T = 295 K, final R = 0.067 for 1178 6.365(1) Å,  $V = 1254.4(5) \text{ Å}^3$ , Z = 4,  $D_x = unique observed reflections. The 2,5-piperazinedione <math>0108-2701/87/030490-04\$01.50$  © 1987 International Union of Crystallography

<sup>\*</sup> Lists of structure factors, anisotropic thermal parameters, least-squares planes and H-atom parameters have been deposited with the British Library Document Supply Centre as Supplementary Publication No. SUP 43434 (11 pp.). Copies may be obtained through The Executive Secretary, International Union of Crystallography, 5 Abbey Square, Chester CH1 2HU, England.

ring is in a twist-boat conformation containing slightly non-planar amide groups related by  $C_2$  symmetry. The *tert*-butyl group is oriented out of the ring plane. The 3R,6S diastereoisomer was confirmed. The molecules are connected by N-H···O hydrogen bonds into antiparallel helices along the c axis.

Introduction. The estimation of the geometry of the 2,5-piperazinedione ring is part of the amide-group investigation project (Ealick & van der Helm, 1977; Bláha *et al.*, 1978; Bláha & Maloň, 1980; Kálal, Bláha & Langer, 1984; Symerský, Kálal, Bláha & Langer, 1986; Tichý, Farag, Maloň & Bláha, 1984; Bláha *et al.*, 1984). The cyclodipeptide under study contains a non-coded amino acid neopentylglycine.



Experimental. Colorless long prismatic crystals grown by slow evaporation from ethanol solution kindly prepared by Dr J. Pospišek, Institute of Organic Chemistry and Biochemistry, Praha. Density measurement was not performed because there was insufficient material. Preliminary cell dimensions and space group determined from oscillation and Weissenberg photographs recorded with  $Cu K\alpha$  radiation. Syntex  $P2_1$  automated diffractometer with graphite monochromator, Cu Kα radiation,  $[(\sin\theta)/\lambda]_{max} =$  $0.6095 \text{ Å}^{-1}$ , crystal  $0.20 \times 0.40 \times 0.15 \text{ mm}$ , final cell dimensions refined on 25 diffractometer reflections with  $8.9 < 2\theta < 26.5^{\circ}$ .  $\theta - 2\theta$  scan technique, no background measurement, intensities and their respective e.s.d.'s were calculated using combined methods of profile analysis (Lehmann & Larsen, 1974) and mask procedure (Sjölin & Wlodawer, 1981).  $0 \le h \le 12, 0 \le k \le 23$ ,  $0 \le l \le 7$ ; in range up to  $2\theta = 140^{\circ}$ ; 1385 unique reflections measured, 1178 observed with  $I > 1.96\sigma_I$ . Check reflections 400, 0,12,0 and 002 monitored after every 47 reflections showed decreasing intensity throughout data collection (to 63, 66, 67%, respectively, of initial intensity). The measurements were reduced to the same scale with INTER (Langer, 1973). Corrections made for Lorentz and polarization factors, not for absorption. The phase problem was solved using direct methods (MULTAN80; Main, Fiske, Hull, Lessinger, Germain, Declercq & Woolfson, 1980). The enantiomorph assigned by the program agreed with the declared (S)-proline chirality known from chemical synthesis. Refinement on |F| by full-matrix LS method with SHELX76 (Sheldrick, 1976). Some H atoms were located on the  $\Delta \rho$  map, others were calculated in

theoretical positions. Most of the H atoms were unstable during refinement, therefore they were put in theoretical positions and refined using a riding model with fixed  $U_{iso} = 0.1 \text{ Å}^2$  for methyl H atoms and  $U_{iso}$  $= 0.08 \text{ Å}^2$  for other H atoms not found on the  $\Delta \rho$  map. Empirical correction for secondary extinction as  $F_c^{\rm corr}$  $=F_{c}(1-gF_{c}^{2}/\sin\theta)$ , where g=1.2 (3) × 10<sup>-6</sup>. Number of parameters refined 184, refinement stopped when  $(\Delta/\sigma)_{max} = 0.07$ . Final R = 0.0667, wR = 0.0814 for observed reflections, 0.0795 and 0.0882 respectively for all reflections, with  $w = 1.080/[\sigma_F^2 + (0.03F)^2]$ , where  $\sigma_{\rm F}$  is taken from counting statistics. The max. in final  $\Delta \rho$  map on all reflections was 0.22 and min.  $-0.30 \text{ e} \text{ Å}^{-3}$ . Atomic scattering factors from International Tables for X-ray Crystallography (1974). Final geometrical features of the molecule calculated with PARST83 (Nardelli, 1983).

**Discussion.** The compound investigated is a model for cyclodipeptides (diketopiperazines). A view of the molecule with the numbering scheme is shown in Fig. 1. The fractional atomic coordinates and  $B_{eq}$  values are given in Table 1, selected bond lengths and angles in Table 2.\* The crystal packing and hydrogen bonds are shown in Fig. 2. The hydrogen-bond parameters are:  $N(16)-H(161) = 0.87(6), H(161)\cdots O(8) = 2.09(6),$  $N(16)\cdots O(8) = 2.930(6) \text{ Å}$  and  $N(16)-H(161)\cdots$  $O(8) = 163 (5)^{\circ}$ . The molecules are connected by these hydrogen bonds into antiparallel helices along the caxis. The six-membered 2,5-piperazinedione ring has a twist-boat conformation, the  $\chi^2$  value for its weighted mean plane is 6360; the C(12) atom of the proline ring is an equatorial substituent and C(5) of the neopentyl is an axial one. From the (S)-proline chirality, known from the chemical synthesis, the 3R, 6S configuration was found. The bulky tert-butyl group is oriented out of the plane of the ring, with torsional angle [N(16)-

<sup>\*</sup> Lists of structure factors, anisotropic thermal parameters, H-atom coordinates and thermal parameters along with weak hydrogen contacts have been deposited with the British Library Document Supply Centre as Supplementary Publication No. SUP 43429 (12 pp.). Copies may be obtained through The Executive Secretary, International Union of Crystallography, 5 Abbey Square, Chester CH1 2HU, England.

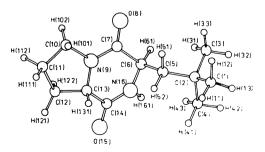


Fig. 1. Projection of the structure with numbering scheme.

C(6)-C(5)-C(2)] 80 (1)°. Comparison with the structure of cyclo(-L-Pro-D-tert-Leu-) (Sklenář & Ječný, 1979) (*tert*-Leu = 2-amino-3.3-dimethylbutyryl) shows no strong influence by the same bulky aliphatic substituent on the geometry of the 2,5-piperazinedione ring with respect to the distance from the ring. Deviations of the two amide groups from planarity are described by the torsion parameter  $\tau'$ , following Winkler & Dunitz (1971) and by the pyramidal parameters  $\chi_{\rm C}$ and  $\chi_N$  following Warshel, Levitt & Lifson (1970) and these are listed in Table 3.

The slightly non-planar arrangement of the amide groups is due to a torsion around the C-N amide bond  $(\tau)$ . Comparison of the corresponding atomic coordinates for the amide groups did not show significant differences in any projection. The two amide groups are approximately related by  $C_2$  symmetry. The proline ring has approximate  $C_2$  symmetry, with the  $\hat{C}_2$  axis

Table 1. Fractional atomic coordinates  $(\times 10^4)$  and  $B_{eq}$  (Å<sup>2</sup>) values with e.s.d.'s in parentheses

	x	У	z	$B_{eq}^*$
C(13)	2430 (5)	3131 (2)	9633 (8)	4.0(1)
C(3)	2909 (8)	1261 (3)	2465 (10)	6.5 (2)
O(8)	3973 (4)	3279 (2)	4531 (6)	5.1 (1)
N(16)	1385 (4)	2347 (2)	7217 (7)	4.2 (1)
C(14)	1320 (4)	2644 (2)	9098 (8)	4.0 (1)
N(9)	3117 (4)	3391 (2)	7801 (6)	3.8(1)
C(7)	3265 (5)	3063 (2)	6005 (8)	3.9 (1)
C(6)	2503 (4)	2395 (2)	5761 (8)	3.8 (1)
O(15)	417 (4)	2538 (2)	10360 (7)	5.9(1)
C(5)	3515 (5)	1809 (2)	5892 (9)	4.3 (1)
C(2)	3154 (5)	1135 (2)	4785 (9)	4.4 (1)
C(12)	1969 (5)	3785 (3)	10722 (10)	5-1 (1)
C(11)	3136 (7)	4271 (3)	10276 (12)	6.4 (2)
C(10)	3733 (6)	4049 (3)	8235 (10)	5.1(1)
C(4)	1936 (7)	801 (3)	5772 (13)	6.3 (2)
C(1)	4365 (7)	664 (3)	5060 (13)	6.9 (2)
	* ~			

\* 
$$B_{\rm eq} = \frac{8}{3}\pi^2 \sum_i \sum_j U_{ij} a_i^* a_j^* \mathbf{a}_i \cdot \mathbf{a}_j$$

### Table 2. Bond lengths (Å) and angles (°) for the molecule

C(13)-N(9) 1.4 C(13)-C(12) 1.5 C(3)-C(2) 1.5 O(8)-C(7) 1.2 N(16)-C(14) 1.3	506 (6) 447 (6) 534 (7) 517 (9) 250 (6) 134 (7) 156 (6)	$\begin{array}{l} N(9)-C(10) \\ C(7)-C(6) \\ C(6)-C(5) \\ C(5)-C(2) \\ C(2)-C(1) \\ C(2)-C(4) \\ C(12)-C(11) \end{array}$	1.461 (7) 1.529 (6) 1.538 (6) 1.546 (6) 1.536 (8) 1.521 (9) 1.536 (9)
C(14)-O(15) 1.2	227 (6) 321 (6)	C(11)-C(10)	1.495 (10)
$\begin{array}{l} N(9)-C(13)-C(12)\\ C(14)-C(13)-C(12)\\ C(14)-C(13)-N(9)\\ C(14)-N(16)-C(6)\\ C(13)-C(14)-N(16)\\ N(16)-C(14)-O(15)\\ C(13)-C(14)-O(15)\\ C(13)-N(9)-C(10)\\ C(13)-N(9)-C(10)\\ C(13)-N(9)-C(10)\\ C(7)-N(9)\\ N(9)-C(7)-C(6)\\ O(8)-C(7)-C(6)\\ O(8)-C(7)-C(6)\\ \end{array}$	102-1 (4) 114-5 (4) 113-2 (4) 125-5 (4) 123-3 (4) 120-2 (4) 111-2 (4) 125-3 (4) 123-4 (4) 123-4 (4) 123-1 (4) 116-9 (4) 120-0 (4)	$\begin{array}{l} N(16)-C(6)-C(7)\\ C(7)-C(6)-C(5)\\ N(16)-C(6)-C(5)\\ C(6)-C(5)-C(2)\\ C(3)-C(2)-C(4)\\ C(5)-C(2)-C(4)\\ C(3)-C(2)-C(1)\\ C(3)-C(2)-C(1)\\ C(1)-C(2)-C(1)\\ C(1)-C(2)-C(1)\\ C(12)-C(11)-C(1)\\ N(9)-C(10)-C(1)\\ N(1)-C(10)-C(1)\\ N(1)-C(10)-C(1)\\ N(1)-C(10)-C(1)\\ N(1)-C(10)-C(1)\\ N(1)-C(1)-C(1)\\ N(1)-C(1$	0) 106-4 (5)

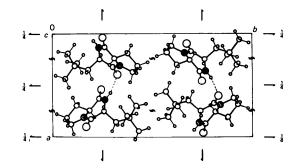


Fig. 2. Crystal packing in the projection along the c axis. N atoms are shaded. The hydrogen bonds are shown.

### Table 3. Parameters and angles (°) describing the geometry of the amide group

(1) Amide group at N(16)						
ω,		$\omega$ [C(13)–C(14)–N(16)–C(6)]	7.4 (7)			
ω,		$\omega$ [O(15)–C(14)–N(16)–H(161)]	5 (4)			
ω,		$\omega$ [O(15)-C(14)-N(16)-C(6)]	-172.7 (4)			
ώ		$\omega$ [C(13)–C(14)–N(16)–H(161)]	-175 (4)			
τ'	=	$\omega_1 + \omega_2$	12 (4)			
χc	=	$\omega_1 - \omega_3 + 180$ mod 360°	0.1 (7)			
χn	=	$\omega_2 - \omega_3 + 180$	-2 (4)			
(2) Amide group at N(9)						
$\omega_1$		$\omega$ [C(6)–C(7)–N(9)–C(13)]	8.0 (7)			
ω,		$\omega$ [O(8)–C(7)–N(9)–C(10)]	1.8 (8)			
ω,		$\omega[O(8)-C(7)-N(9)-C(13)]$	-173-0 (4)			
$\omega_{4}$		$\omega$ [C(6)–C(7)–N(9)–C(10)]	<i>−</i> 177·3 (4)			
τ'	=	$\omega_1 + \omega_2$ )	9-8 (8)			
χ <sub>c</sub>	=	$\omega_1 - \omega_3 + 180 \rangle \mod 360^\circ$	1.0 (7)			
χ'n	=	$\omega_2 - \omega_3 + 180$	-5.2 (8)			

running through C(10) and the centre of the C(13)-C(12) bond. Note that the H(161) atom of the amide group was found on the  $\Delta \rho$  map after five cycles of isotropic refinement of the non-H atoms and was successfully refined without constraints.

The authors thank Drs V. Petříček and J. Fábry for preliminary measurements on a Hilger & Watts diffractometer with Mo  $K\alpha$  radiation at the Institute of Physics, Czechoslovak Academy of Sciences, Praha.

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## N-(4-Acetylphenyl)acetohydroxamic Acid

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Abstract.  $C_{10}H_{11}NO_3$ ,  $M_r = 193.20$ , monoclinic,  $P2_1/n$ , a=23.539(5), b=8.473(2), c=9.540Å,  $\beta = 99.44(2)^\circ$ , V = 1876.9(7)Å<sup>3</sup>, Z = 8,  $D_x = 1.367$  g cm<sup>-3</sup>, Ni-filtered Cu K $\alpha$ ,  $\lambda = 1.5418$ Å,  $\mu = 7.55$  cm<sup>-1</sup>, F(000) = 816, T = 138(2) K, R = 0.057for 3018 data. The hydroxamate groups of the two crystallographically unique molecules have a *trans* conformation. Both molecules are roughly planar and have similar molecular conformations and identical dimensions, which are compared with those of other *N*-substituted acetohydroxamic acids. The molecules are linked by two intermolecular hydrogen bonds with lengths 2.631(2) and 2.636(2) Å.

Introduction. Under iron-limiting conditions, microorganisms produce a variety of small chelating agents which solubilize ferric iron in the environment and transport the iron to the cell. Many of these metabolites chelate the iron through hydroxamic acid groups. Both naturally occurring and synthetic hydroxamic acids have been used as therapeutic agents for treatment of iron overload (Anderson & Hiller, 1977). Crystal structures of synthetic hydroxamic acids with a trans N,N'-dihydroxy-N,N'-diisoconformation include propylhexanediamide (hipa) (Smith & Raymond, 1980), N-(4-cyanophenyl)acetohydroxamic acid (pcnpa) (Mocherla, Powell, Barnes & van der Helm, 1983) and N-(3-cyanophenyl)acetohydroxamic acid (m-cnpa) (Mocharla, Powell & van der Helm, 1984). This article describes the crystal and molecular structure of N-(4-acetylphenyl)acetohydroxamic acid (apa).

Experimental. A sample of the title compound was kindly supplied by Dr A. L. Crumbliss, P. M. Gross Chemical Laboratory, Department of Chemistry, Duke University, Durham, North Carolina. Colorless plateshaped crystals were grown by diffusing benzene into a solution of the compound in ethyl acetate. Crystal:  $0.08 \times 0.25 \times 0.50$  mm, Enraf-Nonius CAD-4, 48 reflections used for lattice constants, systematic absences: h0l, h + l = 2n + 1, 0k0, k = 2n + 1, no absorption correction applied, all data  $2\theta < 150^{\circ}$  in  $-29 \le h \le 29$ ,  $0 \le k \le 10$ ,  $0 \le l \le 11$  collected, three intensity monitors had a maximum difference of 0.074 and an e.s.d. of 0.019, 3826 unique data measured, 808 unobserved data  $[F < 3 \cdot 8\sigma(F)]$ , solved by MULTAN (Main, Fiske, Hull, Lessinger, Germain, Declercq & Woolfson, 1980), refined by block full-matrix least squares minimizing  $\sum w(|F_{o}| - |F_{c}|)^{2}$ , hydrogens located on a difference electron density map, all heavy atoms refined anisotropically, hydrogens refined isotropically, R = 0.057, wR = 0.078, S = 2.79, w = $1/\sigma^2(F)$ , maximum and average shift-to-e.s.d. ratios = 0.48, 0.10, maximum and minimum on final difference map = 0.35 and  $0.34 \text{ e} \text{ Å}^{-3}$ , C, N and O scattering factors from Cromer & Mann (1968), H scattering factors from Stewart, Davidson & Simpson (1965), programs used include SHELX (Sheldrick, 1976) and ORTEP (Johnson, 1965).

**Discussion.** The final coordinates of the nonhydrogen atoms are given in Table 1. The atom-numbering scheme is shown in Fig. 1 (Johnson, 1965). Bond

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