

C(20)	0.1834 (9)	-0.1214 (8)	0.5586 (4)	0.047 (3)
C(21)	0.2628 (9)	0.0491 (8)	0.5576 (4)	0.056 (3)
C(22)	0.2962 (9)	0.0986 (7)	0.4787 (4)	0.051 (3)
N(23)	0.1450 (9)	-0.1723 (9)	0.6429 (4)	0.068 (3)
O(24)	0.0574 (10)	-0.3218 (8)	0.6410 (3)	0.112 (3)
O(25)	0.2031 (9)	-0.0636 (7)	0.7094 (3)	0.097 (3)

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## Orthorhombic Form of Thiopurinol: 1,5-Dihydro-4*H*-pyrazolo[3,4-*d*]pyrimidine- 4-thione

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### Abstract

Thiopurinol crystallizes in two forms. The crystal structure of the monoclinic form has been reported [Gadret, Goursole & Leger (1974). *Acta Cryst.* **B30**, 1598–1602]. The orthorhombic form reported here has a hydrogen-bonded layered structure similar to the monoclinic form but differs from it in the stacking pattern of the purine bases. The interlayer separation (3.292 Å) is slightly smaller than that in the monoclinic form (3.426 Å). The H atom on the diazole ring is bonded to N(9). The relative magnitudes of the two exocyclic bond angles at N(9) subtended by H(9) are similar to those in the monoclinic form and in allopurinol, but differ from those in hypoxanthine, the related normal nucleobase. This trend for N(8)-purines is corroborated by *ab initio* molecular-orbital calculations and a literature search for related structures *via* the Cambridge Structural Database [Allen, Kennard & Taylor (1983). *Acc. Chem. Res.* **16**, 146–153].

### Comment

The title compound (*Ia*) is the thio analog of allopurinol (*Ib*) and possesses very similar biochemical and pharmacological properties. Thus, both allopurinol and thiopurinol riboside monophosphates inhibit guanosine monophosphate reductase and, therefore, affect the synthesis of adenosine triphosphate from guanine (Looker, Marr & Berens, 1986). Both inhibit ribonucleic acid biosynthesis thus affecting protein synthesis (Looker *et al.*, 1986). Both are potent

Table 2. Geometric parameters (Å, °)

C(1)—O(2)	1.425 (7)	C(1)—C(7)	1.500 (9)
O(2)—N(3)	1.397 (6)	N(3)—C(4)	1.252 (9)
C(4)—O(5)	1.340 (8)	C(4)—C(16)	1.518 (9)
O(5)—C(6)	1.447 (6)	C(6)—C(17)	1.518 (9)
C(7)—C(8)	1.390 (8)	C(7)—C(12)	1.388 (10)
C(8)—C(9)	1.380 (9)	C(9)—C(10)	1.382 (10)
C(10)—C(11)	1.383 (8)	C(10)—N(13)	1.474 (8)
C(11)—C(12)	1.383 (9)	N(13)—O(14)	1.201 (8)
N(13)—O(15)	1.200 (9)	C(16)—F(1)	1.266 (14)
C(16)—F(2)	1.290 (10)	C(16)—F(3)	1.251 (10)
C(17)—C(18)	1.389 (8)	C(17)—C(22)	1.374 (8)
C(18)—C(19)	1.361 (9)	C(19)—C(20)	1.365 (8)
C(20)—C(21)	1.367 (9)	C(20)—N(23)	1.484 (9)
C(21)—C(22)	1.388 (9)	N(23)—O(24)	1.211 (9)
N(23)—O(25)	1.208 (8)		
O(2)—C(1)—C(7)	109.8 (5)	C(1)—O(2)—N(3)	105.9 (4)
O(2)—N(3)—C(4)	112.8 (5)	N(3)—C(4)—O(5)	134.1 (5)
N(3)—C(4)—C(16)	116.0 (6)	O(5)—C(4)—C(16)	109.7 (6)
C(4)—O(5)—C(6)	119.7 (4)	O(5)—C(6)—C(17)	107.1 (4)
C(1)—C(7)—C(8)	117.4 (6)	C(1)—C(7)—C(12)	123.8 (5)
C(8)—C(7)—C(12)	118.7 (6)	C(7)—C(8)—C(9)	121.5 (6)
C(8)—C(9)—C(10)	117.8 (5)	C(9)—C(10)—C(11)	122.6 (6)
C(9)—C(10)—N(13)	118.1 (5)	C(11)—C(10)—N(13)	119.3 (6)
C(10)—C(11)—C(12)	118.1 (6)	C(7)—C(12)—C(11)	121.2 (5)
C(10)—N(13)—O(14)	118.1 (6)	C(10)—N(13)—O(15)	118.1 (5)
O(14)—N(13)—O(15)	123.7 (6)	C(4)—C(16)—F(1)	112.8 (7)
C(4)—C(16)—F(2)	111.3 (7)	F(1)—C(16)—F(2)	102.7 (7)
C(4)—C(16)—F(3)	114.4 (7)	F(1)—C(16)—F(3)	108.8 (9)
F(2)—C(16)—F(3)	106.1 (7)	C(6)—C(17)—C(18)	117.7 (5)
C(6)—C(17)—C(22)	122.5 (5)	C(18)—C(17)—C(22)	119.8 (6)
C(17)—C(18)—C(19)	120.2 (5)	C(18)—C(19)—C(20)	119.4 (6)
C(19)—C(20)—C(21)	122.1 (6)	C(19)—C(20)—N(23)	119.8 (6)
C(21)—C(20)—N(23)	118.1 (5)	C(20)—C(21)—C(22)	118.6 (5)
C(17)—C(22)—C(21)	119.9 (5)	C(20)—N(23)—O(24)	117.6 (6)
C(20)—N(23)—O(25)	118.6 (6)	O(24)—N(23)—O(25)	123.7 (7)

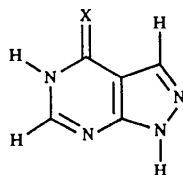
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Lists of structure factors, anisotropic displacement coefficients, H-atom coordinates and least-squares-planes data have been deposited with the British Library Document Supply Centre as Supplementary Publication No. SUP 55937 (12 pp.). Copies may be obtained through The Technical Editor, International Union of Crystallography, 5 Abbey Square, Chester CH1 2HU, England. [CIF reference: LI1038]

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inhibitors of xanthine oxidase (Robins *et al.*, 1985) and are effective antigout (Feigelson, Davidson & Robins, 1957), antiparasitic (Nelson, Bugge, Elion, Berens & Marr, 1979) and antithrombotic (Dikshit, Srivastava, Kar & Srimal, 1987; Srivastava, Mishra, Pratap, Bhakuni & Srimal, 1989) agents. The structure and intermolecular interactions of these compounds are, therefore, important in considering their interactions with biological macromolecules.



(Ia) X = S

(Ib) X = O

Crystal structures of allopurinol (Prusiner & Sundaralingam, 1972) and thiopurinol in the monoclinic form (Gadret, Goursole & Leger, 1974) have been reported previously. We have been able to crystallize thiopurinol in an orthorhombic form (see *Experimental*) for which we report the structure here and compare it to that of the monoclinic form. In addition, we point out some interesting features of the structure of N(8)-purines obtained from the Cambridge Structural Database (CSD; Allen, Kennard & Taylor, 1983) and *ab initio* molecular-orbital calculations.

An *ORTEP* (Johnson, 1965) view of thiopurinol with the atomic numbering scheme is shown in Fig. 1. The bond lengths and bond angles of thiopurinol in the two crystal structures are within  $3\sigma$  of each other. The crystal packing in the two structures, however, is different, as expected (Figs. 2 and 3). The planar purine molecules in the orthorhombic form (Fig. 2) are hydrogen bonded in layers and pack in crystallographic mirror planes perpendicular to the *c* axis at  $z = 0$  and  $\frac{1}{2}$ . The interplanar separation is 3.292 Å ( $\frac{1}{2}z$ ). The molecules in the monoclinic form (Gadret *et al.*, 1974) are hydrogen bonded in exactly the same way with an interlayer separation of 3.426 Å, but the base stacking pattern between adjacent layers is quite different (Fig. 3). The two crystal forms, therefore, result from two different stacking patterns of identically hydrogen-bonded thiopurinol molecular layers. In the orthorhombic form the stacked bases, Fig. 2, are related to each other by the *c*-glide plane which is perpendicular to the *a* axis and to the base planes, and which passes approximately through the midpoints of C(4)—N(9) and C(5)—C(7) bonds. The four atoms comprising these bonds, therefore, have more interactions with each other

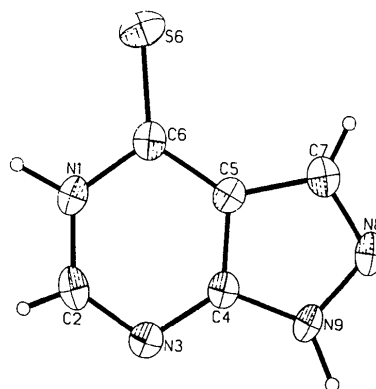


Fig. 1. *ORTEP* (Johnson, 1965) drawing of the thiopurinol molecule showing the labeling of the non-H atoms. Thermal ellipsoids are shown at the 50% probability level. Small circles represent H atoms.

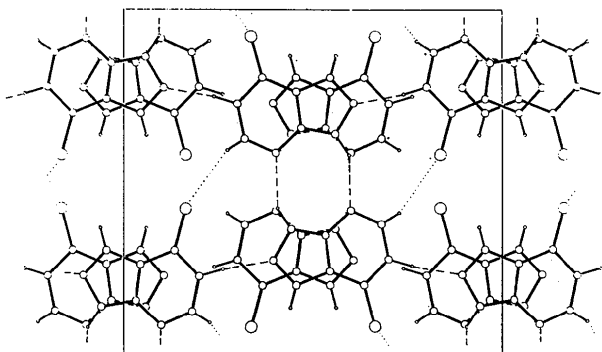


Fig. 2. A view of two adjacent molecular layers lying in crystallographic mirror planes perpendicular to the *c* axis at  $z = 0$  and  $\frac{1}{2}$  showing hydrogen bonding (in the top layer only) and base stacking. Hydrogen bonds are shown as dashed lines and C—H...S interactions as dotted lines. The larger circles represent S atoms and the smaller ones H atoms. The origin is in the lower left-hand corner with the *a* axis horizontal and the *b* axis vertical.

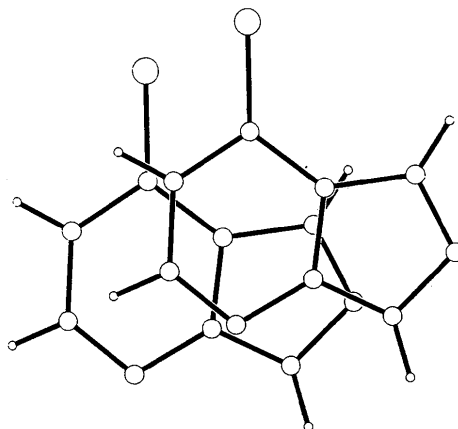


Fig. 3. Base stacking in the monoclinic form of thiopurinol (Gadret *et al.*, 1974) shown for comparison with that in the orthorhombic form presented in Fig. 2.

than other atoms.† All of them, except those involving symmetry-related atoms (*e.g.* C4...C4 *etc.*), occur twice (Fig. 2), since overlapped atoms are present in pairs. Only one of these interactions [C(5)...C(7) at 3.335 Å] is, however, less than the sum of the respective van der Waals radii (Bondi, 1964; Pauling, 1960).

The hydrogen-bonding arrangement in orthorhombic thiopurinol is identical to that in monoclinic thiopurinol (Gadret *et al.*, 1974) and in allopurinol (Prusiner & Sundaralingam, 1972). The hydrogen-bond distances and angles in the orthorhombic form are given in Table 3. All available hydrogen-bond donors and acceptors participate in hydrogen bonding in both crystal forms of thiopurinol and in allopurinol. In addition, there is a C(2)—H...S(6) interaction in thiopurinol similar to the C(2)—H...O(6) hydrogen bond proposed in allopurinol (Prusiner & Sundaralingam, 1972). It has been observed previously (Singh & Hodgson, 1977) that the hydrogen-bond acceptor strength of atom N(8) in 8-azapurines and of atom N(6) in 6-azapyrimidines is related to their Mulliken charges. The charge at N(8) in thiopurinol is  $-0.28 e$  (at the 6-31G\*\* level of approximation) which is large enough (Singh & Hodgson, 1977) for it to participate in hydrogen bonding, as observed in both crystal forms of thiopurinol.

Nucleosides whose base component is an 8-azapurine, *e.g.*, thio- or allopurinol, or a 6-azapyrimidine, have a curious structural feature in that, with few exceptions, the glycosyl torsion angle,  $\chi$ , lies either in the so-called 'high-*anti*' or *syn* region (Prusiner, Brennan & Sundaralingam, 1973; Singh & Hodgson, 1977; Saenger, 1983). These conformations for  $\chi$  would be facilitated in 8-azapurine nucleosides if the exocyclic bond angle C(4)—N(9)—H(9) ( $A_1$  in Table 4) in the corresponding purine were larger than the angle N(8)—N(9)—H(9) ( $A_2$  in Table 4) since this would relieve steric crowding between the sugar and the bulk of the base atoms. The relative magnitudes of these angles in 8-azapurines and their metal complexes† taken from the 1991 version of the CSD show  $A_1$  to be larger than  $A_2$  in every case with the mean difference ( $A_1 - A_2$ ) being  $10^\circ$ ; minimum and maximum differences are 1 and  $22^\circ$ . For thiopurinol the difference  $A_1 - A_2$  is  $13^\circ$  in the monoclinic form (Gadret *et al.*, 1974) and  $16(3)^\circ$  in the orthorhombic form (present work). A similar search for normal C(8)—H purines (including their metal complexes) in the CSD showed 36 entries with wide variations in the values of  $A_1$  and  $A_2$ , the mean difference  $A_1 - A_2$  being  $-1^\circ$  and the minimum and maximum being  $-26$  and  $15^\circ$ , respectively (a search excluding metal complexes, and no exocyclic bond to

N(7), yielded basically the same result). Molecular-orbital calculations using GAUSSIAN90 (Frisch *et al.*, 1990) at the STO 3-21G\* basis set level of approximation on two N(8)-purines and two normal purines, show the same trend in the relative magnitudes of the exocyclic bond angle,  $A_1$  and  $A_2$ , as that observed in the crystal (Table 4). It seems, therefore, that in general the exocyclic bond angle  $A_1$  is larger than  $A_2$  in 8-azapurines but could be either larger or smaller in other purines, which would explain partially the preponderance of high-*anti* or *syn* conformation around the glycosyl bond in 8-azapurine nucleosides.

## Experimental

### Crystal data

C <sub>5</sub> H <sub>4</sub> N <sub>4</sub> S	Mo K $\alpha$ radiation
$M_r = 152.19$	$\lambda = 0.71073 \text{ \AA}$
Orthorhombic	Cell parameters from 25 reflections
<i>I</i> bam	$\theta = 7.5\text{--}12.5^\circ$
$a = 14.597(5) \text{ \AA}$	$\mu = 0.42 \text{ mm}^{-1}$
$b = 13.153(5) \text{ \AA}$	$T = 298 \text{ K}$
$c = 6.584(3) \text{ \AA}$	Thin needle
$V = 1264(1) \text{ \AA}^3$	$0.20 \times 0.07 \times 0.04 \text{ mm}$
$Z = 8$	Pale yellow
$D_x = 1.60 \text{ Mg m}^{-3}$	

### Data collection

Siemens R3m/ $\mu$ diffractometer	$\theta_{\max} = 25^\circ$
$\theta/2\theta$ scans	$h = 0 \rightarrow 17$
Absorption correction: none	$k = 0 \rightarrow 15$
616 measured reflections	$l = 0 \rightarrow 7$
616 independent reflections	2 standard reflections monitored every 48 reflections
492 observed reflections [ $I \geq 2\sigma(I)$ ]	intensity variation: 1.5%

### Refinement

Refinement on $F$	$\Delta\rho_{\max} = 0.27 e \text{ \AA}^{-3}$
Final $R = 0.043$	$\Delta\rho_{\min} = -0.28 e \text{ \AA}^{-3}$
$wR = 0.060$	Extinction correction: Zachariasen
$S = 1.40$	Extinction coefficient: $4(3) \times 10^{-7}$
492 reflections	Atomic scattering factors from <i>International Tables for X-ray Crystallography</i> (1974, Vol. IV, Table 2.2B)
74 parameters	
All H-atom parameters refined	
$w = 1/[\sigma^2(F_o) + 0.001F_o^2]$	
$(\Delta/\sigma)_{\max} = 0.04$	

Table 1. Atomic coordinates and isotropic or equivalent isotropic thermal parameters ( $\text{\AA}^2$ )

H atoms were refined isotropically. For non-H atoms equivalent isotropic  $U$  is defined as one third of the trace of the orthogonalized  $U_{ij}$  tensor.

	$x$	$y$	$z$	$U_{\text{iso}}/U_{\text{eq}}$
N(1)	$-0.1997(2)$	$0.7742(2)$	$0.0$	$0.038(1)$
C(2)	$-0.1807(3)$	$0.8745(3)$	$0.0$	$0.043(1)$
N(3)	$-0.0993(2)$	$0.9157(2)$	$0.0$	$0.038(1)$

† See deposition footnote.

C(4)	-0.0321 (2)	<b>0.8438 (3)</b>	<b>0.0</b>	0.028 (1)
C(5)	-0.0448 (2)	<b>0.7394 (3)</b>	<b>0.0</b>	0.029 (1)
C(6)	-0.1343 (2)	<b>0.6984 (3)</b>	<b>0.0</b>	0.034 (1)
S(6)	-0.1638 (1)	<b>0.5781 (1)</b>	<b>0.0</b>	0.072 (1)
C(7)	0.0451 (3)	<b>0.6987 (3)</b>	<b>0.0</b>	0.036 (1)
N(8)	0.1061 (2)	<b>0.7722 (2)</b>	<b>0.0</b>	0.036 (1)
N(9)	0.0583 (2)	<b>0.8615 (3)</b>	<b>0.0</b>	0.033 (1)
H(1)	-0.2612 (42)	<b>0.7533 (37)</b>	<b>0.0</b>	0.060 (13)
H(2)	-0.2268 (35)	<b>0.9082 (32)</b>	<b>0.0</b>	0.048 (13)
H(7)	0.0605 (26)	<b>0.6352 (35)</b>	<b>0.0</b>	0.039 (12)
H(9)	0.0945 (36)	<b>0.9233 (32)</b>	<b>0.0</b>	0.049 (13)

Table 2. Geometric parameters (Å, °)

N(1)—C(2)	1.349 (5)	N(1)—C(6)	1.379 (5)
N(1)—H(1)	0.939 (61)	C(2)—N(3)	1.306 (5)
C(2)—H(2)	0.806 (49)	N(3)—C(4)	1.362 (5)
C(4)—C(5)	1.386 (5)	C(4)—N(9)	1.340 (4)
C(5)—C(6)	1.414 (5)	C(5)—C(7)	1.418 (5)
C(6)—S(6)	1.640 (4)	C(7)—N(8)	1.314 (5)
C(7)—H(7)	0.865 (46)	N(8)—N(9)	1.366 (5)
N(9)—H(9)	0.970 (45)		
C(2)—N(1)—C(6)	124.4 (3)	C(2)—N(1)—H(1)	118.8 (30)
C(6)—N(1)—H(1)	116.8 (30)	N(1)—C(2)—N(3)	126.3 (4)
N(1)—C(2)—H(2)	111.5 (32)	N(3)—C(2)—H(2)	122.2 (32)
C(2)—N(3)—C(4)	111.6 (3)	N(3)—C(4)—C(5)	126.3 (3)
N(3)—C(4)—N(9)	126.1 (3)	C(5)—C(4)—N(9)	107.6 (3)
C(4)—C(5)—C(6)	120.1 (3)	C(4)—C(5)—C(7)	104.5 (3)
C(6)—C(5)—C(7)	135.4 (4)	N(1)—C(6)—C(5)	111.4 (3)
N(1)—C(6)—S(6)	121.0 (3)	C(5)—C(6)—S(6)	127.6 (3)
C(5)—C(7)—N(8)	110.5 (4)	C(5)—C(7)—H(7)	127.1 (26)
N(8)—C(7)—H(7)	122.4 (26)	C(7)—N(8)—N(9)	106.7 (3)
C(4)—N(9)—N(8)	110.7 (3)	C(4)—N(9)—H(9)	133.0 (31)
N(8)—N(9)—H(9)	116.2 (31)		

Table 3. Possible hydrogen-bond distances (Å) and angles (°)

A—H...B	A—H	H...B	A...B	A—H...B
N(1)—H...N(8)	0.94	1.97	2.900	173
N(9)—H...N(3 <sup>a</sup> )	0.97	2.12	2.991	149
C(2)—H...S(6 <sup>b</sup> )	0.81	2.75	3.510	159

Symmetry code: (i)  $-0.5 + x, 1.5 - y, -z$ ; (ii)  $-x, 2 - y, -z$ ; (iii)  $-0.5 - x, 0.5 + y, z$ .

Table 4. Comparison of the exocyclic bond angles 4—9—H(9) (A1) and 8—9—H(9) (A2) (°) of relevant purines or nucleosides, the latter having a C atom in place of H(9), as determined crystallographically and by molecular-orbital calculations (Gaussian STO 3-21G\*)

	Crystal		3-21G*	
	A1	A2	A1	A2
Thiopurinol	133°, 131 <sup>b</sup>	116°, 117 <sup>a</sup>	128.7	120.3
8-Azaadenine	128.4 <sup>c</sup>	121.8 <sup>c</sup>	130.0	120.5
Hypoxanthine	117, 123 <sup>d</sup>	136, 130	125.5	128.3
Adenine	124.3 <sup>e</sup> , 130 <sup>f</sup>	130 <sup>e</sup> , 123 <sup>f</sup>	125.5	127.7

Notes: (a) present study; (b) Gadret *et al.* (1974); (c) from the corresponding nucleoside, 8-azadenosine (Singh & Hodgson, 1974); (d) two independent molecules (Schmalle, Hänggi & Dubler, 1988); (e) from the corresponding nucleoside, adenosine (Lai & Marsh, 1972); (f) Tret'yak, Mitkevich & Sukhodub (1987).

Thiopurinol was purchased from Aldrich Chemical Company (Milwaukee, WI, USA) and was used without further purification. The compound was dissolved at 323 K in an 80/20 dimethylformamide/2-propanol mixture and the solution left to evaporate at room temperature for 10–12 weeks. Small single crystals grew as needles emanating from clumps of the powdered material. These crystals possessed orthorhombic symmetry. Crystals of the same compound grown by Gadret *et al.*

(1974) from dimethylformamide alone had monoclinic symmetry. The orthorhombic unit cell was chosen by Sparks' cell-reduction routine which is part of the diffractometer software package. The monoclinic cell reported by Gadret *et al.* (1974) was subjected to cell reduction by the NRC program *CREDOC* (Le Page, 1982) which showed it to be the properly reduced cell of highest symmetry. Our crystals are, therefore, different from those of Gadret *et al.* (1974). (To check the crystalline homogeneity of the sample, the remainder of the recrystallized sample was crushed and a powder pattern was taken on a diffractometer; this showed the sample to contain crystals of the orthorhombic form only.) The structure was solved by direct methods and difference Fourier techniques and was refined by blocked-cascade least-squares technique (Sparks, 1961). Crystallographic calculations were performed on a Data General desktop Microclipse computer using *SHELXTL* (Sheldrick, 1985) and *ORTEP* (Johnson, 1965). Molecular-orbital calculations were performed with *GAUSSIAN90* (Frisch *et al.*, 1990) using STO 3-21G\* basis set. Initial dimensions for each purine molecule were taken from its crystal structure except those involving H atoms. The latter were placed in standard positions. All bond distances and angles in the purine ring, which was assumed to be planar, were optimized. The initial value for the C(4)—N(9)—H(9) angle for each molecule was taken to be 125°. The final optimized values for this angle are compared with the crystallographic values in Table 4. The geometry optimization was performed on a Multi-flow Trace 14/300 workstation.

We are grateful to Professor S. B. Weed of the Department of Soil Science, NCSU, for the X-ray powder pattern, Dr Peter White of UNC-Chapel Hill for supplying us with a copy of the personal-computer version of the cell-reduction program *CREDOC*, Dr David Hoel for support and encouragement, and the National Science Foundation for financial support (grant No. CHE 8307022) towards upgrading the X-ray diffractometer at North Carolina State University.

Lists of structure factors, anisotropic thermal parameters, intermolecular distances up to 3.81 Å between overlapped molecules, including distances between atoms of the diazole moiety, and a CSD survey of exocyclic bond angles at N(9) have been deposited with the British Library Document Supply Centre as Supplementary Publication No. SUP 55941 (10 pp.). Copies may be obtained through The Technical Editor, International Union of Crystallography, 5 Abbey Square, Chester CH1 2HU, England. [CIF reference: CR1037]

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## Structure of 1,3,5-Trichloro-2,4,6-trinitrobenzene

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### Abstract

The three formula units in the asymmetric unit are stacked in almost planar layers. The average inter-layer distance is 4.062 (6) Å, much greater than the

normal spacing observed between benzene rings as a result of the large rotation of the nitro groups out of the ring planes by 72.3–88.2°. N and Cl atoms are within the benzene average planes [deviations 0.066 (4) and 0.064 (1) Å, respectively]. The three molecules are virtually connected by a pseudo-threefold axis, leading to a hexagonal habit and a strong twinning of the crystals.

### Comment

In an effort to correlate the sensitivity of explosives with their structure, the Société Nationale des Poudres et Explosifs (SNPE, France) has undertaken a screening of trinitroaromatic compounds. The one at issue was synthesized, purified and named PICL3 by the SNPE. In nitroaromatic compounds, it is well known that a Cl atom induces strong twist angles of nitro groups in  $\alpha$  positions (Table 3). In less-symmetrical compounds than PICL3, a deviation of Cl towards the less-rotated nitro group has been observed: in picryl chloride by Willis, Stewart, Ammon, Preston, Gluyas & Harris (1971); in 1,3-dichloro-2,4,6-trinitrobenzene by Holden & Dickinson (1967); and in 1-chloro-2,4-dinitrobenzene by Wilkins, Small & Gleghorn (1990). This feature is not observed in more symmetrical molecules such as 1,2,4,5-tetrachloro-3,6-dinitrobenzene, in which C–N torsion reaches 90°, or in 1,3,5-trichloro-2,4-dinitrobenzene (Wigand, Walz, Weiden & Weiss, 1987), or here in PICL3.

In all these compounds it is observed that the greater the twist at the C–N bond, the greater its length. In PICL3, where such twist angles (listed in Table 3) are very strong, these bonds are in the range 1.484–1.498 Å, among the highest observed in polynitroaromatics. The most common explanation is that strong torsion makes the resonance of NO<sub>2</sub> with the ring unlikely (*e.g.* Bhattacharjee & Ammon, 1981), although such resonance, even in a planar unit, has been recently challenged by Politzer, Lane, Jayasuriya & Domelsmith (1987), and such correlation challenged by Holden & Dickinson (1977). The three molecules of PICL3 show enlarged endocyclic angles (Table 2) at the C-bearing nitro groups, a feature explained by their strong withdrawing effect (Domenicano, Vaciego & Coulson, 1975).

Molecules are stacked in nearly planar sheets, almost parallel to (11 $\bar{1}$ ) (Table 3). Average spacing between sheets is constant within experimental precision [4.062 (6) Å], but much greater than the normal spacing [3.4 Å] of benzene rings. There is no contact within a layer except O15...Cl35 [3.219 (3) Å]. No short O...O contact from layer to layer exists, but some C...O contacts are observed, the shortest (Table 3) involving C-bearing Cl atoms of the molecule 3, and O atoms of the two others,