

## An independent refinement of H-atom coordinates from laboratory X-ray powder data in tetraformaltrisazine

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## Key indicators

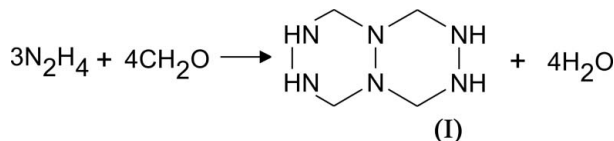
Powder X-ray study  
 $T = 298$  K  
Mean  $\sigma(\text{N-N}) = 0.009$  Å  
 $R$  factor = 0.025  
 $wR$  factor = 0.008For details of how these key indicators were automatically derived from the article, see <http://journals.iucr.org/e>.

The structure of centrosymmetric tetraformaltrisazine (systematic name: 1,2,3,4,5,6,7,8-octahydro-1,2,4,5-tetrazino-[1,2-*a*][1,2,4,5]tetrazine),  $\text{C}_4\text{H}_{12}\text{N}_6$ , has been solved by simulated annealing from X-ray laboratory powder data and refined by Rietveld refinement without any restraints for non-H atoms. The coordinates of H atoms forming hydrogen bonds were refined independently. Tetraformaltrisazine can be used as a biologically active compound.

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## Comment

The condensation of formaldehyde with hydrazine may lead to different products. One of the most easily obtainable is tetraformaltrisazine, (I) (Neureiter, 1959). For further study of this compound, the structure of the molecule needs to be known. Since we failed to obtain a single crystal of (I), the structure was determined using X-ray powder techniques.



It is evident (Fig. 1) that tetraformaltrisazine is a hexaaza-derivative of decalin, in which all four H atoms attached to N atoms are in axial positions, forming eight hydrogen bonds around one molecule (Fig. 2 and Table 2). The molecule has a centre of symmetry.

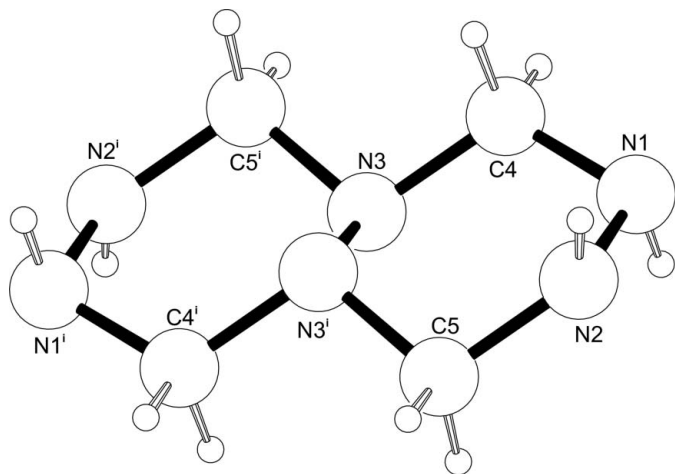
## Experimental

Paraformaldehyde (12 g, 0.4 mol) was added slowly to hydrazine hydrate (15 g, 0.3 mol) with cooling and stirring. Stirring was continued for 20 min at room temperature, and then the reaction mixture was left to stand at room temperature for 2 d. The mixture was filtered and the precipitate was washed with hot propan-2-ol (yield 8 g, 56%; m.p. 488–490 K). Analysis found: C 32.80, H 8.27, N 57.28%;  $\text{C}_4\text{H}_{12}\text{N}_6$  requires: C 33.31, H 8.40, N 58.28%. <sup>1</sup>H NMR ( $\text{D}_2\text{O}$ , 250 MHz,  $\delta$ , p.p.m.): 3.6 (s), 3.9 (s) (4H, NH); 4.1 (s), 4.9 (s) (8H,  $\text{CH}_2$ ).

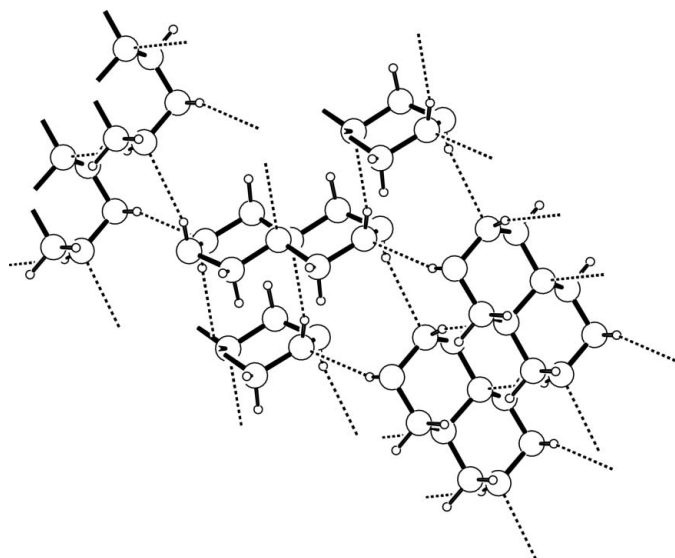
## Crystal data

$\text{C}_4\text{H}_{12}\text{N}_6$   
 $M_r = 144.20$   
Monoclinic,  $P2_1/n$   
 $a = 6.3243$  (4) Å  
 $b = 4.8633$  (3) Å  
 $c = 11.3322$  (9) Å  
 $\beta = 92.042$  (14)°  
 $V = 348.32$  (4) Å<sup>3</sup>  
 $Z = 2$

$D_x = 1.375$  Mg m<sup>-3</sup>  
Cu  $K\alpha_1$  radiation  
 $\mu = 0.81$  mm<sup>-1</sup>  
Specimen shape: flat sheet  
15 × 15 × 0.5 mm  
Specimen prepared at 298 K  
Particle morphology: lump-like,  
colourless



**Figure 1**  
 PLATON (Spek, 2003) view of the title compound, with the atom-numbering scheme. Symmetry code as in Table 1.



**Figure 2**  
 Hydrogen bonds (dashed lines) in the packing of the title compound.

#### Data collection

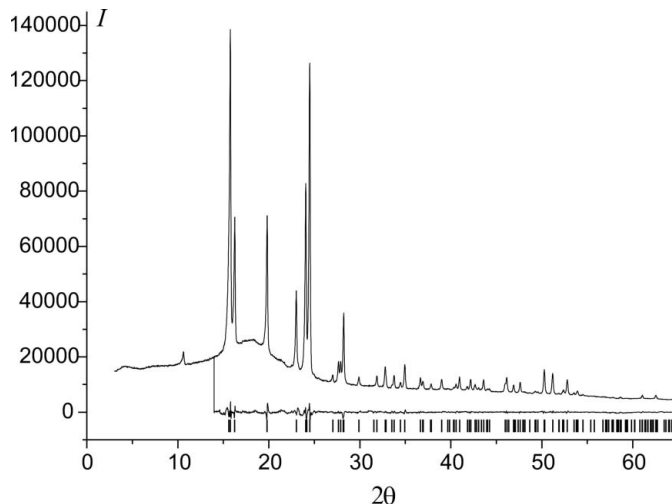
Huber Guinier G670 diffractometer  
 Specimen mounting: pressed as a thin layer in the specimen holder  
 Specimen mounted in transmission mode

Scan method: step  
 Absorption correction: none  
 $2\theta_{\min} = 3.0$ ,  $2\theta_{\max} = 65.0^\circ$   
 Increment in  $2\theta = 0.01^\circ$

#### Refinement

Refinement on  $I_{\text{net}}$   
 $R_{\text{wp}} = 0.025$   
 $R_{\text{exp}} = 0.008$   
 $R_B = 0.019$   
 $S = 2.87$   
 Wavelength of incident radiation:  
 1.54059 Å  
 Excluded region(s): 3.00–13.99  
 Profile function: split-type pseudo-Voigt

68 parameters  
 H atoms treated by a mixture of independent and constrained refinement  
 Weighting scheme based on measured s.u.'s;  $w = 1/I_{\text{obs}}$   
 $(\Delta/\sigma)_{\text{max}} = 0.01$   
 Preferred orientation correction: none



**Figure 3**  
 Rietveld plot for the title compound. The upper trace is the observed profile and the lower trace is the difference between observed and calculated; indexed lines are shown with dashes.

**Table 1**

Selected geometric parameters (Å, °).

N1–N2	1.440 (15)	N3–C4	1.489 (9)
N1–C4	1.432 (9)	N3–N3 <sup>i</sup>	1.484 (9)
N2–C5	1.474 (9)	C5–N3 <sup>i</sup>	1.480 (9)
N2–N1–C4	106.5 (5)	C5–N2–H2	116 (2)
N2–N1–H1	104 (2)	N1–C4–N3	117.1 (3)
C4–N1–H1	106 (2)	C4–N3–N3 <sup>i</sup>	103.7 (5)
N1–N2–C5	119.6 (4)	C4–N3–C5 <sup>i</sup>	107.7 (5)
N1–N2–H2	108 (3)	C5 <sup>i</sup> –N3–N3 <sup>i</sup>	109.8 (6)

Symmetry code: (i)  $-x, -y, -z$ .

**Table 2**

Hydrogen-bond geometry (Å, °).

$D-H\cdots A$	$D-H$	$H\cdots A$	$D\cdots A$	$D-H\cdots A$
N1–H1 $\cdots$ N2 <sup>ii</sup>	0.85 (4)	2.40 (4)	3.209 (9)	159 (3)
N2–H2 $\cdots$ N3 <sup>iii</sup>	0.85 (2)	2.44 (3)	3.271 (8)	165 (3)

Symmetry codes: (ii)  $-x + \frac{1}{2}, y + \frac{1}{2}, -z + \frac{1}{2}$ ; (iii)  $x, y - 1, z$ .

Monoclinic cell dimensions were determined with *TREOR90* (Werner *et al.*, 1985) using the first 53 peak positions. The structure was solved by the simulated annealing method and refined by Rietveld refinement using *MRIA* (Zlokazov & Chernyshev, 1992). The diffraction profile and the difference between the measured and calculated profiles after the final Rietveld refinement are shown in Fig. 3. This centrosymmetric small molecule has only five non-H atoms per asymmetric unit; this, as well as good diffraction data, allowed us to refine all non-H atoms isotropically without any bond length or  $U_{\text{iso}}$  restraints. H atoms bonded to N atoms were found in difference maps and their coordinates were refined independently, with  $U_{\text{iso}}(\text{H}) = 0.05 \text{ \AA}^2$ . H atoms bonded to C atoms were placed in geometrically calculated positions with  $U_{\text{iso}}(\text{H}) = 1.2U_{\text{iso}}(\text{C})$ . The specimen turned out to be texture-free.

Data collection: *HUBER G670* (HUBER Diffraktionstechnik GmbH, version 4.3); cell refinement: *MRIA* (Zlokazov & Chernyshev, 1992); data reduction: *HUBER G670*; program(s) used to solve

structure: *MRIA*; program(s) used to refine structure: *MRIA*; molecular graphics: *PLATON* (Spek, 2003); software used to prepare material for publication: *MRIA*.

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## References

- Neureiter, N. P. (1959). *J. Am. Chem. Soc.* **81**, 2910.  
Spek, A. L. (2003). *J. Appl. Cryst.* **36**, 7–13.  
Werner, P.-E., Eriksson, L. & Westdahl, M. (1985). *J. Appl. Cryst.* **18**, 367–370.  
Zlokazov, V. B. & Chernyshev, V. V. (1992). *J. Appl. Cryst.* **25**, 447–451.