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Key indicators

Single-crystal X-ray study T = 100 KMean $\sigma(C-C) = 0.002 \text{ Å}$ Disorder in main residue R factor = 0.046 wR factor = 0.131 Data-to-parameter ratio = 18.2

For details of how these key indicators were automatically derived from the article, see http://journals.iucr.org/e.

p-Diisocyanotetramethylbenzene, p-C₆(CH₃)₄(NC)₂, crystallizes in the monoclinic space group C2/c. One-half of the molecule is crystallographically independent, with the other half being generated by an inversion centre located at the centre of the molecule.

p-Diisocyanotetramethylbenzene

Comment

In the course of our work on isonitrile-bridged and capped molybdenum complexes, we isolated and structurally characterized *p*-diisocyanotetramethylbenzene, (I). The bisisocyanide is located on an crystallographic inversion centre, with only one-half of the molecule crystallographically independent. Both crystallographically independent methyl groups show disorder of the H atoms; these have been refined as idealized disordered methyl groups with the two positions rotated from each other by 60° and the site distributions have been refined to be approximately 0.90:0.10 (2) and 0.72:0.28 (2). Bond lengths and angles are in the expected ranges for aromatic isonitriles.



The compound was found to be isostructural with its cyanoisomer, dicyanodurene, $p-C_6(CH_3)_4(NC)_2$ (Britton & Van Rij, 1991). Cell parameters and the orientation of the molecules are essentially identical.

Experimental

1,4-Diisocyano-2,3,5,6-tetramethylbenzene was synthesized from the corresponding formamide by reacting tetramethyl-*p*-phenylenediamine with 75% formic acid under reflux for two hours. Addition of water precipitated the formamide, which was washed with water until neutral and dried *in vacuo*. The isocyanide was synthesized as described by Efraty *et al.* (1980) for 1,4-diisocyanobenzene. The isocyanide was purified by sublimation *in vacuo*. Single crystals were grown by sublimation *in vacuo*.

Crystal data	
$C_{12}H_{12}N_2$	$D_x = 1.221 \text{ Mg m}^{-3}$
$M_r = 184.24$	Mo K α radiation
Monoclinic, $C2/c_{\perp}$	Cell parameters from 4202
a = 17.1518 (17) Å	reflections
b = 5.1324 (5) Å	$\theta = 2.6 - 28.3^{\circ}$
c = 12.3670 (12) Å	$\mu = 0.07 \text{ mm}^{-1}$
$\beta = 112.010 \ (2)^{\circ}$	T = 100 (2) K
$V = 1009.32 (17) \text{ Å}^3$	Block, colourless
Z = 4	$0.50 \times 0.35 \times 0.35$ mm

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Data collection

Bruker AXS SMART APEX CCD diffractometer
ω scans
Absorption correction: none
4935 measured reflections
1257 independent reflections

Refinement

Refinement on F^2 $R[F^2 > 2\sigma(F^2)] = 0.046$ $wR(F^2) = 0.131$ S = 1.051257 reflections 69 parameters H-atom parameters constrained

Table 1

Selected geometric parameters (Å, °).

N1-C1	1.1628 (14)	C3-C5	1.5106 (13)
N1-C2	1.4045 (12)	C4-C6	1.5105 (13)
C3-C4	1.4008 (13)	$C2-C4^{i}$	1.4065 (13)
C3-C2	1.4070 (13)		
C1-N1-C2	178.30 (10)	C3-C4-C6	121.39 (8)
C4-C3-C2	117.65 (9)	$C2^{i} - C4 - C6$	120.69 (9)
C4-C3-C5	121.14 (8)	$N1-C2-C4^{i}$	117.59 (8)
C2-C3-C5	121.20 (9)	N1-C2-C3	117.99 (8)
$C3 - C4 - C2^{i}$	117.92 (9)	$C4^{i} - C2 - C3$	124.42 (9)

1181 reflections with $I > 2\sigma(I)$

 $w = 1/[\sigma^2(F_o^2) + (0.0698P)^2]$

Extinction correction: SHELXL

Extinction coefficient: 0.011 (4)

+ 0.6662P] where $P = (F_o^2 + 2F_c^2)/3$

 $(\Delta/\sigma)_{\rm max} = 0.016$

 $\Delta \rho_{\rm max} = 0.32 \ {\rm e} \ {\rm \AA}^{-3}$

 $\Delta \rho_{\rm min} = -0.27 \text{ e } \text{\AA}^{-3}$

 $\begin{aligned} R_{\rm int} &= 0.080\\ \theta_{\rm max} &= 28.3^\circ \end{aligned}$

 $h = -22 \rightarrow 21$

 $\begin{array}{l} k=-6\rightarrow 6\\ l=-16\rightarrow 16 \end{array}$

Symmetry code: (i) $\frac{1}{2} - x, \frac{3}{2} - y, 1 - z$.

Both crystallographically independent methyl groups show rotational disorder. The H atoms were refined as idealized disordered methyl groups, with the two positions rotated from each other by 60°. They were geometrically positioned with a fixed C—H distance of 0.98 Å. Isotropic displacement parameters are 1.5 times $U_{\rm eq}$ of the parent atom. The major site occupancies were refined to be approximately 0.90 (2) and 0.72 (2).

The s.u. values of the cell parameters are derived from the software, and are unreasonably small (Herbstein, 2000).

Data collection: *SMART* (Bruker 1997–2000); cell refinement: *SAINT-Plus* (Bruker 1997–1999); data reduction: *SAINT-Plus*;



Figure 1

Molecular structure of (I), showing 30% probability displacement ellipsoids.

program(s) used to solve structure: *SHELXS*97 (Sheldrick, 1997); program(s) used to refine structure: *SHELXL*97 (Sheldrick, 1997); molecular graphics: *SHELXL*97; software used to prepare material for publication: *SHELXL*97.

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