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Karimah Kassim,^a Hadariah Bahrom^a and Bohari M. Yamin^b*

^aDepartment of Chemistry, Universiti Teknologi MARA, Shah Alam, Selangor, Malaysia, and ^bSchool of Chemical Sciences and Food Technology, Universiti Kebangsaan Malaysia, 43600 Bangi, Selangor, Malaysia

Correspondence e-mail: bohari@pkrisc.cc.ukm.my

Key indicators

Single-crystal X-ray study T = 298 KMean σ (C–C) = 0.003 Å R factor = 0.056 wR factor = 0.165 Data-to-parameter ratio = 16.1

For details of how these key indicators were automatically derived from the article, see http://journals.iucr.org/e. The non-planar molecule of the title compound, $C_{18}H_{20}N_2$, is centrosymmetric about the central point of the ethylene bond and posses *E* configuration across each azomethine C=N bond.

(*E*,*E*)-*N*,*N*'-Bis(4-tolylmethylidene)ethylenediamine

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Comment

The continuing interest in the Schiff bases of ethylenediamine derivatives is driven by the development of supramolecular assemblies (Thalladi *et al.*, 1995), complexations with metals, and their biological activities (Patel *et al.*, 2005). The title compound, (I), is similar to (E,E)-N,N'-bis(1-phenylethyl-idene)ethylenediamine, (II) (Benson *et al.*, 2006), except that the methyl group is attached at the 4-position of the benzene ring instead of the azomethine group.



In the molecule of the title compound, (I) (Fig. 1), the bond lengths and angles are within normal ranges (Allen *et al.*, 1987). Like in (II), the molecule maintains its centrosymmetry about the ethylene bridge and the *E* configuration about the azomethine C=N bonds. It also adopts a staggered conformation about the C9–C9ⁱ bond, required by the centrosymmetry. The C1–C8 tolylmethyledine fragment is nearly planar, having a total puckering amplitude, $Q_{\rm T}$, of 0.074 (3) Å (Cremer & Pople, 1975). In contrast to compound (II), the



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Figure 1 The molecular structure with the atom-numbering scheme. Displacement ellipsoids are drawn at the 50% probability level.

entire molecule is not planar because the dihedral angle between the planar bridging $N1/C9/C9^i/N1^i$ and C1–C8 tolyl-methyledine fragments is 61.65 (17)°.

In the crystal structure, although there are no significant π - π interactions, there are C-H··· π interactions, the closest H···centroid distance being 2.80 Å, occurring between C2/H2 and the ring centroid of (C1-C6)ⁱⁱ with an angle at H of 138° [symmetry code: (ii) $-\frac{1}{2} - x$, $-\frac{1}{2} + y$, $\frac{3}{2} - z$]. These interactions lead to the formation of columns along the *a* axis.

Experimental

A mixture of ethylenediammine (0.45 g, 0.015 mol) and 4-methylbenzaldehyde (4.0 g, 0.030 mol) in absolute ethanol (100 ml) was heated in a water bath at 323 K for 3 h. The mixture was then cooled to 273 K in an ice bath. The resulting white precipitate was filtered off, washed with cold ethanol and then dried under vacuum. Crystals suitable for X-ray investigation were obtained by recrystallization from a mixture of chloroform and ethanol (1:1) (yield 3.23 g, 81.5%; m.p. 415.2–416.5 K).

Crystal data

 $\begin{array}{l} C_{18}H_{20}N_2\\ M_r = 264.36\\ Monoclinic, P2_1/n\\ a = 6.842 \ (2) \ \AA\\ b = 7.531 \ (2) \ \AA\\ c = 14.933 \ (5) \ \AA\\ \beta = 100.801 \ (7)^\circ\\ V = 755.8 \ (4) \ \AA^3 \end{array}$

Data collection

Bruker SMART APEX CCD areadetector diffractometer ω scans Absorption correction: multi-scan (*SADABS*; Bruker, 2000) $T_{\min} = 0.971, T_{\max} = 0.989$ Z = 2 $D_x = 1.162 \text{ Mg m}^{-3}$ Mo K α radiation $\mu = 0.07 \text{ mm}^{-1}$ T = 298 (2) K Block, colorless $0.42 \times 0.28 \times 0.16 \text{ mm}$

4098 measured reflections 1484 independent reflections 935 reflections with $I > 2\sigma(I)$ $R_{\text{int}} = 0.025$ $\theta_{\text{max}} = 26.0^{\circ}$

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Refinement on F^2	$w = 1/[\sigma^2(F_0^2) + (0.0854P)^2]$
$R[F^2 > 2\sigma(F^2)] = 0.056$	+ 0.0506P]
$wR(F^2) = 0.165$	where $P = (F_0^2 + 2F_c^2)/3$
S = 1.05	$(\Delta/\sigma)_{\rm max} < 0.001$
1484 reflections	$\Delta \rho_{\rm max} = 0.18 \ {\rm e} \ {\rm \AA}^{-3}$
92 parameters	$\Delta \rho_{\rm min} = -0.12 \ {\rm e} \ {\rm \AA}^{-3}$
H-atom parameters constrained	

H atoms were positioned geometrically with C–H = 0.93, 0.96 and 0.97 Å for aromatic, methyl and methylene H atoms, respectively, and constrained to ride on their parent atoms, with $U_{iso}(H) = xU_{eq}(C,N)$ where x = 1.5 for methyl H and x = 1.2 for all other H atoms.

Data collection: *SMART* (Bruker, 2000); cell refinement: *SAINT*; data reduction: *SAINT*; program(s) used to solve structure: *SHELXS97* (Sheldrick, 1997*a*); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997*a*); molecular graphics: *SHELXTL* (Sheldrick, 1997*b*); software used to prepare material for publication: *SHELXTL*, *PARST* (Nardelli, 1995) and *PLATON* (Spek, 2003).

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