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Key indicators

Single-crystal X-ray study
 $T = 294$ K
Mean $\sigma(\text{C}-\text{C}) = 0.003$ Å
 R factor = 0.041
 wR factor = 0.116
Data-to-parameter ratio = 14.7For details of how these key indicators were
automatically derived from the article, see
<http://journals.iucr.org/e>.

4-(Cyclohexyliminomethyl)phenol

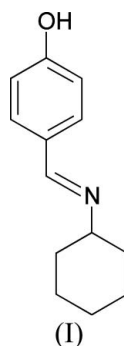
The title compound, $\text{C}_{13}\text{H}_{17}\text{NO}$, was prepared by reductive amination from 4-hydroxybenzaldehyde and cyclohexanamine. The crystal packing is stabilized by $\text{O}-\text{H}\cdots\text{N}$ hydrogen bonds.

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Comment

Schiff base derivatives are widely synthesized *via* reductive amination reactions. Recently we have reported the synthesis and crystal structure of a new Schiff base compound with a hindered phenol group (Yan *et al.*, 2006). As part of our ongoing research in this field, the title compound, (I), has been prepared by reductive amination from 4-hydroxybenzaldehyde and cyclohexanamine, and its crystal structure is reported here.



In (I), bond lengths and angles are as expected for a molecule of this kind (Allen *et al.*, 1987). The cyclohexyl ring adopts a chair conformation with puckering parameters $Q = 0.554$ (2) Å, $\varphi_2 = -85.4$ (8)° and $\theta_2 = 178.6$ (2)° (Cremer & Pople, 1975).

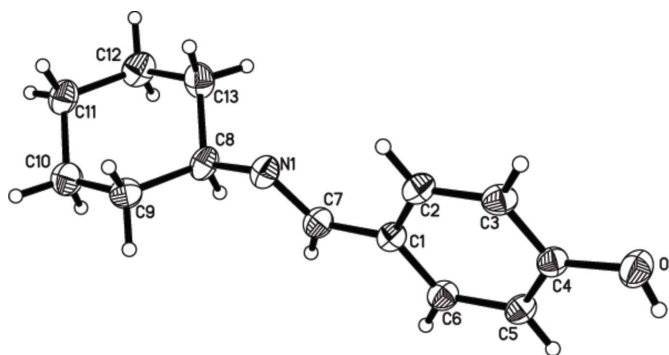


Figure 1

A view of the molecular structure of (I). Displacement ellipsoids are drawn at the 30% probability level and H atoms are shown as small spheres of arbitrary radii.

The crystal structure is stabilized by intermolecular O—H...N hydrogen bonds (Table 1).

Experimental

A mixture of 4-hydroxybenzaldehyde (6.1 g, 0.05 mol) and cyclohexanamine (4.95 g, 0.05 mol) in toluene (100 ml) was heated at 383 K and refluxed for 4 h. The solvent was then evaporated under reduced pressure to afford the title compound in 98% yield (9.96 g). Single crystals suitable for X-ray analysis were obtained by slow evaporation of a dichloromethane/ethanol solution (6:1 v/v; m.p. 446–448 K).

Crystal data

| | |
|--------------------------------|---|
| $C_{13}H_{17}NO$ | $Z = 4$ |
| $M_r = 203.28$ | $D_x = 1.164 \text{ Mg m}^{-3}$ |
| Monoclinic, $P2_1/n$ | Mo $K\alpha$ radiation |
| $a = 5.6582 (16) \text{ \AA}$ | $\mu = 0.07 \text{ mm}^{-1}$ |
| $b = 17.453 (5) \text{ \AA}$ | $T = 294 (2) \text{ K}$ |
| $c = 11.833 (3) \text{ \AA}$ | Block, colourless |
| $\beta = 97.102 (5)^\circ$ | $0.26 \times 0.24 \times 0.22 \text{ mm}$ |
| $V = 1159.5 (6) \text{ \AA}^3$ | |

Data collection

| | |
|---|--|
| Bruker SMART CCD area-detector diffractometer | 5807 measured reflections |
| φ and ω scans | 2043 independent reflections |
| Absorption correction: multi-scan (SADABS; Sheldrick, 1996) | 1346 reflections with $I > 2\sigma(I)$ |
| $T_{\min} = 0.981$, $T_{\max} = 0.984$ | $R_{\text{int}} = 0.034$ |
| | $\theta_{\text{max}} = 25.0^\circ$ |

Refinement

| | |
|--|--|
| Refinement on F^2 | $w = 1/[\sigma^2(F_o^2) + (0.0543P)^2 + 0.1411P]$ |
| $R[F^2 > 2\sigma(F^2)] = 0.041$ | where $P = (F_o^2 + 2F_c^2)/3$ |
| $wR(F^2) = 0.116$ | $(\Delta/\sigma)_{\text{max}} < 0.001$ |
| $S = 1.04$ | $\Delta\rho_{\text{max}} = 0.13 \text{ e \AA}^{-3}$ |
| 2043 reflections | $\Delta\rho_{\text{min}} = -0.19 \text{ e \AA}^{-3}$ |
| 139 parameters | |
| H atoms treated by a mixture of independent and constrained refinement | |

Table 1

Hydrogen-bond geometry (\AA , $^\circ$).

| $D-H\cdots A$ | $D-H$ | $H\cdots A$ | $D\cdots A$ | $D-H\cdots A$ |
|--------------------|----------|-------------|-------------|---------------|
| $O1-H1\cdots N1^i$ | 0.94 (2) | 1.83 (2) | 2.755 (2) | 168 (2) |

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

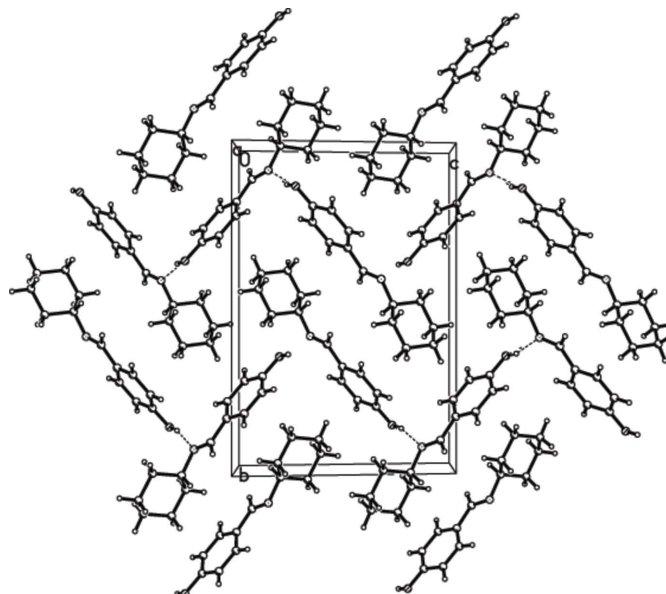


Figure 2

Packing diagram of (I) viewed along the a axis, showing the intermolecular O—H...N hydrogen interactions (dashed lines).

The H atom of the hydroxy group was located in a difference Fourier map and refined with the O—H distance restrained to 0.82 \AA . All other H atoms were positioned geometrically and refined using a riding model, with $C-H = 0.93-0.98 \text{ \AA}$ and with $U_{\text{iso}}(\text{H}) = 1.2U_{\text{eq}}(\text{C})$.

Data collection: SMART (Bruker, 1997); cell refinement: SAINT (Bruker, 1997); data reduction: SAINT; program(s) used to solve structure: SHELXS97 (Sheldrick, 1997); program(s) used to refine structure: SHELXL97 (Sheldrick, 1997); molecular graphics: SHELXTL (Bruker, 1997); software used to prepare material for publication: SHELXTL.

References

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