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Key indicators

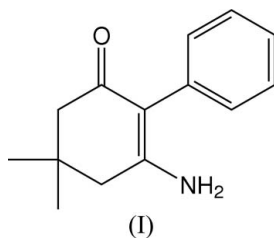
Single-crystal X-ray study
 $T = 100$ K
Mean $\sigma(\text{C}-\text{C}) = 0.005$ Å
 R factor = 0.052
 wR factor = 0.147
Data-to-parameter ratio = 11.1For details of how these key indicators were
automatically derived from the article, see
<http://journals.iucr.org/e>.

3-Amino-5,5-dimethyl-2-phenylcyclohex-2-en-1-one

In the title compound, $\text{C}_{14}\text{H}_{17}\text{NO}$, there are two crystallographically independent molecules in the asymmetric unit. The cyclohexene rings adopt an envelope conformation. Adjacent molecules are linked *via* $\text{N}-\text{H}\cdots\text{O}$ hydrogen bonds to form dimers and these form one-dimensional chains along the $[20\bar{1}]$ direction. These chains are interconnected by weak intermolecular $\text{C}-\text{H}\cdots\text{O}$ interactions. $\text{N}-\text{H}\cdots\pi$ interactions are also observed in the crystal structure.

Comment

Arynes used as reagents in synthetic organic chemistry have received much attention. There has recently been a renewed interest in exploring new benzyne reactions after Kobayashi described a mild method for the *in situ* preparation of benzyne at moderate temperatures that exploits the fluoride-induced elimination of *ortho*-silyl aryl triflates (Himeshima *et al.*, 1983). Here we report the crystal structure of the title compound, (I), which was obtained by the reaction of benzyne with the cyclic enamionone 3-amino-5,5-dimethylcyclohex-2-enone.



The asymmetric unit of (I) contains two molecules, *A* and *B*, in which the orientation of the benzene ring with respect to the cyclohexene ring is different (Fig. 1). The corresponding bond lengths and angles of these two molecules agree with each other and show normal values (Allen *et al.*, 1987). In both molecules *A* and *B*, the cyclohexene rings adopt an envelope conformation, with puckering parameters (Cremer & Pople 1975) $Q = 0.450$ (4) Å, $\theta = 52.3$ (4)° and $\varphi = 117.9$ (6)° in molecule *A* [$Q = 0.452$ (4) Å, $\theta = 129.1$ (5)° and $\varphi = 297.1$ (6)° in molecule *B*] and atom C3 having the maximum deviation of 0.318 (4) Å in molecule *A* [0.319 (4) Å in molecule *B*] from the mean plane of C1/C2/C4–C6. The C7–C12 benzene rings are oriented at angles of 73.63 (14)° in molecule *A* [79.56 (12)° in molecule *B*] with respect to the cyclohexene ring. The dihedral angle between the C7–C12 benzene ring and the mean plane of C1/C2/C4–C7/N1/O1 is 73.63 (14)° in molecule *A* [79.56 (12)° in molecule *B*]. The dihedral angle between the two benzene rings of molecules *A* and *B* is 39.86 (15)°.

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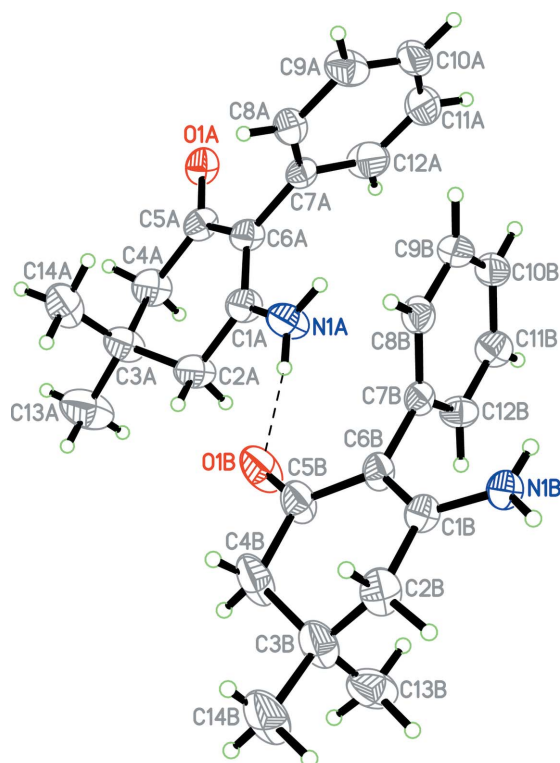


Figure 1

The asymmetric unit of (I), showing 60% probability displacement ellipsoids and the atomic numbering. The dashed line indicates a hydrogen bond.

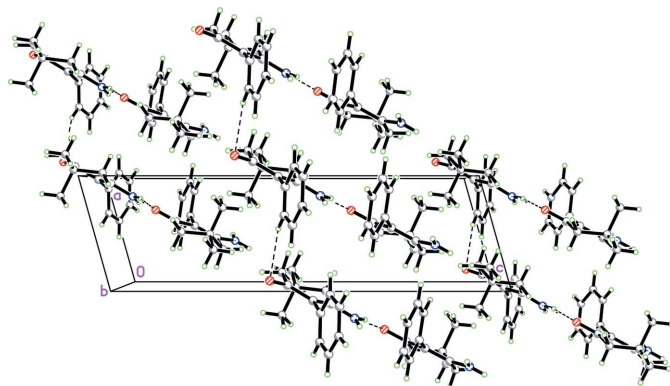


Figure 2

The crystal packing of (I), viewed down the *b* axis. Hydrogen bonds are shown as dashed lines.

In the crystal the two unique molecules in the asymmetric unit are linked into dimers by N—H···O hydrogen bonds (Table 1) and these dimers are arranged into one-dimensional chains along the $[20\bar{1}]$ direction. The chains are interconnected by weak C—H···O interactions (Fig. 2). N—H··· π interactions were also observed (Table 2); Cg1 is the centroid of the C7B–C12B benzene ring.

Experimental

Compound (I) was prepared by the reaction of 3-amino-5,5-dimethylcyclohex-2-enone (43.2 μ l, 0.4 mmol, 1.0 equiv.) with 2-

(trimethylsilyl)phenyl trifluoromethanesulfonate (121.4 μ l, 0.5 mmol, 1.25 equiv.) in the presence of caesium fluoride (152 mg, 1.0 mmol, 2.5 equiv.). The title compound was isolated using silica gel column chromatography using petroleum ether (b.p. 333–363 K) and ethyl acetate as eluents. Pale-yellow single crystals suitable for X-ray diffraction analysis were obtained by slow evaporation of the solvent from a petroleum ether/ethyl acetate solution (3:1 *v/v*), m.p. 443–444 K.

Crystal data

$C_{14}H_{17}NO$	$Z = 4$
$M_r = 215.29$	$D_x = 1.174 \text{ Mg m}^{-3}$
Monoclinic, <i>Pc</i>	Mo $K\alpha$ radiation
$a = 6.1044 (1) \text{ \AA}$	$\mu = 0.07 \text{ mm}^{-1}$
$b = 10.1495 (2) \text{ \AA}$	$T = 100.0 (1) \text{ K}$
$c = 20.4177 (4) \text{ \AA}$	Block, pale yellow
$\beta = 105.691 (1)^\circ$	$0.60 \times 0.20 \times 0.12 \text{ mm}$
$V = 1217.87 (4) \text{ \AA}^3$	

Data collection

Bruker SMART APEX2 CCD area-detector diffractometer	20888 measured reflections
ω scans	3248 independent reflections
Absorption correction: multi-scan (SADABS; Bruker, 2005)	2641 reflections with $I > 2\sigma(I)$
$T_{\min} = 0.957$, $T_{\max} = 0.991$	$R_{\text{int}} = 0.042$
	$\theta_{\text{max}} = 29.0^\circ$

Refinement

Refinement on F^2	$w = 1/[\sigma^2(F_o^2) + (0.0821P)^2 + 0.1433P]$
$R[F^2 > 2\sigma(F^2)] = 0.052$	where $P = (F_o^2 + 2F_c^2)/3$
$wR(F^2) = 0.147$	$(\Delta/\sigma)_{\text{max}} < 0.001$
$S = 1.06$	$\Delta\rho_{\text{max}} = 0.33 \text{ e \AA}^{-3}$
3248 reflections	$\Delta\rho_{\text{min}} = -0.22 \text{ e \AA}^{-3}$
293 parameters	
H-atom parameters constrained	

Table 1

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

<i>D</i> —H··· <i>A</i>	<i>D</i> —H	H··· <i>A</i>	<i>D</i> ··· <i>A</i>	<i>D</i> —H··· <i>A</i>
N1A—H2NA···O1B	0.86	1.99	2.839 (4)	169
N1B—H2NB···O1A ⁱ	0.86	2.03	2.877 (3)	171
C8A—H8AA···O1A ⁱⁱ	0.93	2.51	3.296 (4)	143
N1A—H1NA···Cg1	0.86	2.61	3.111 (3)	118

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

All H atoms were positioned geometrically and refined using a riding model with C—H = 0.93 \AA , $U_{\text{iso}}(\text{H}) = 1.2U_{\text{eq}}(\text{C})$ for aromatic, C—H = 0.97 \AA , $U_{\text{iso}}(\text{H}) = 1.2U_{\text{eq}}(\text{C})$ for CH_2 , C—H = 0.96 \AA , $U_{\text{iso}}(\text{H}) = 1.5U_{\text{eq}}(\text{C})$ for CH_3 and N—H = 0.86 \AA , $U_{\text{iso}}(\text{H}) = 1.2U_{\text{eq}}(\text{N})$ for NH atoms. A rotating group model was used for the methyl groups. A total of 2769 Friedel pairs were merged before final refinement as there is no significant anomalous dispersion for the determination of the absolute structure.

Data collection: APEX2 (Bruker, 2005); cell refinement: APEX2; data reduction: SAINT (Bruker, 2005); program(s) used to solve structure: SHELXTL (Sheldrick, 1998); program(s) used to refine structure: SHELXTL; molecular graphics: SHELXTL; software used to prepare material for publication: SHELXTL and PLATON (Spek, 2003).

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