

An orthorhombic modification of 4,4'-diaminobenzophenone

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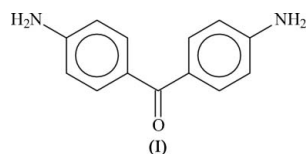
Key indicators

Single-crystal X-ray study
T = 291 K
Mean $\sigma(\text{C}-\text{C}) = 0.002 \text{ \AA}$
R factor = 0.032
wR factor = 0.088
Data-to-parameter ratio = 7.6For details of how these key indicators were automatically derived from the article, see <http://journals.iucr.org/e>.The molecule of the title compound, $\text{C}_{13}\text{H}_{12}\text{N}_2\text{O}$, uses one of its amine groups to hydrogen bond to two other molecules, affording a layer motif in the crystal structure.

Received 4 April 2006

Accepted 4 April 2006

Comment

The crystal structure of 4,4'-diaminobenzophenone, (I), was reported in the trigonal space group $P3_1$ (Velden & Noordik, 1980); the compound adopts a linear hydrogen-bonded chain structure. The orthorhombic modification also has the atoms of the molecule lying in general positions, but the less densely packed structure features hydrogen bonds that give rise to a hydrogen-bonded layer motif (Fig. 1). Only one amine group is involved in the interactions.

Experimental

A mixture of cadmium acetate dihydrate (0.133 g, 0.5 mmol) and 4,4'-diaminobenzophenone-3,3'-dicarboxylic acid (0.075 g, 0.25 mmol) in water (16 ml) was placed in a 25 ml Teflon-lined stainless steel Parr bomb. The bomb was heated to 433 K for 72 h. It was cooled to room temperature over 3 d to furnish orange prismatic crystals.

Crystal data

$\text{C}_{13}\text{H}_{12}\text{N}_2\text{O}$	<i>Z</i> = 4
<i>M_r</i> = 212.25	<i>D_x</i> = 1.301 Mg m ⁻³
Orthorhombic, $P2_12_12_1$	Mo <i>K</i> α radiation
<i>a</i> = 5.4982 (5) Å	μ = 0.08 mm ⁻¹
<i>b</i> = 8.1110 (7) Å	<i>T</i> = 291 (2) K
<i>c</i> = 24.306 (2) Å	Prism, orange
<i>V</i> = 1084.0 (2) Å ³	0.40 × 0.30 × 0.08 mm

Data collection

Rigaku Mercury CCD area-detector diffractometer	8288 measured reflections
ω scans	1470 independent reflections
Absorption correction: multi-scan (<i>CrystalClear</i> ; Rigaku/MS, 2000)	1416 reflections with $I > 2\sigma(I)$
<i>T</i> _{min} = 0.702, <i>T</i> _{max} = 1.000	<i>R</i> _{int} = 0.023
	θ_{max} = 27.5°

Refinement

Refinement on F^2	$w = 1/[\sigma^2(F_o^2) + (0.0594P)^2 + 0.165P]$
$R[F^2 > 2\sigma(F^2)] = 0.032$	where $P = (F_o^2 + 2F_c^2)/3$
$wR(F^2) = 0.088$	$(\Delta/\sigma)_{\text{max}} = 0.001$
<i>S</i> = 1.02	$\Delta\rho_{\text{max}} = 0.20 \text{ e \AA}^{-3}$
1470 reflections	$\Delta\rho_{\text{min}} = -0.13 \text{ e \AA}^{-3}$
193 parameters	
All H-atom parameters refined	

Table 1

Hydrogen-bond geometry (Å, °).

$D-H\cdots A$	$D-H$	$H\cdots A$	$D\cdots A$	$D-H\cdots A$
$N1-H1n1\cdots O1^i$	0.86 (1)	2.08 (1)	2.917 (2)	165 (2)
$N1-H1n2\cdots O1^{ii}$	0.86 (1)	2.27 (1)	3.047 (2)	152 (2)

Symmetry codes: (i) $x, y + 1, z$; (ii) $x + \frac{1}{2}, -y + \frac{3}{2}, -z$.

In the absence of significant anomalous scattering effects, Friedel pairs were merged. H atoms were located in difference Fourier maps and refined with distance restraints of $N-H = 0.85$ (1) Å and $C-H = 0.95$ (1) Å; their displacement parameters were freely refined.

Data collection: *CrystalClear* (Rigaku/MS, 2000); cell refinement: *CrystalClear*; data reduction: *CrystalClear*; program(s) used to solve structure: *SHELXS97* (Sheldrick, 1997); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *SHELXTL* (Bruker, 1998); software used to prepare material for publication: *SHELXL97*.

The authors thank the Foundation of the Zhejiang Key Laboratory for Reactive Chemistry on Solid Surfaces (No. 0506) and the University of Malaya (No. F0712/2005c) for supporting this study.

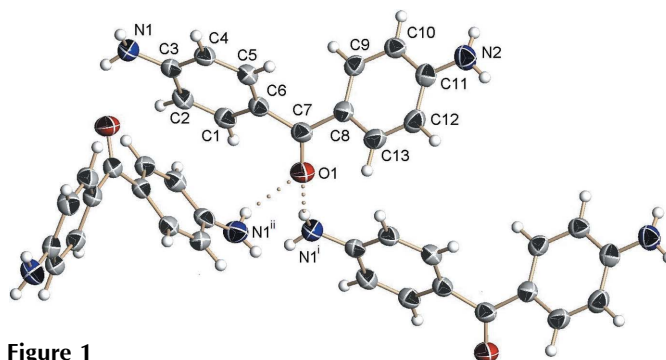


Figure 1

Three molecules of (I), with displacement ellipsoids drawn at the 50% probability level and H atoms shown as spheres of arbitrary radii. [Symmetry codes: (i) $x, 1 + y, z$; (ii) $\frac{1}{2} + x, \frac{1}{2} - y, -z$.] Dotted lines indicate hydrogen bonds.

References

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