Acta Crystallographica Section E Structure Reports Online

ISSN 1600-5368

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Key indicators

Single-crystal X-ray study T = 273 K Mean σ (C–C) = 0.002 Å R factor = 0.030 wR factor = 0.088 Data-to-parameter ratio = 31.2

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

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1-(4-Aminophenyl)-3-(3-bromophenyl)prop-2-en-1-one

The title molecule, $C_{15}H_{12}BrNO$, is approximately planar and the dihedral angle between the two aromatic rings is 9.6 (1)°. The crystal packing reveals that the molecules translated by one unit cell along the *a*-axis direction are linked into a chain by intermolecular N-H···O and C-H···O hydrogenbonding interactions. The screw-related molecules of adjacent chains are linked *via* N-H···N hydrogen bonds into a sheetlike structure parallel to the *ab* plane.

Comment

Chalcones (1,3-diarylpropen-1-ones) and their heterocyclic analogues possess a number of biological attributes and some of these have been reviewed. The antibacterial, fungistatic and fungicidal properties of these compounds have been reviewed by Opletalova (2000) and Opletalova & Sedivy (1999). The cytotoxic, anticancer, chemopreventative, mutagenic, antimicrobial, antiviral, antiprotozoal and insecticidal activities and enzyme-inhibitory properties of a variety of chalcones have also been reviewed (Dimmock et al., 1999). Photo-crosslinkable polymers containing the chalcone group act as negative photo-resist materials used in a wide variety of applications (Balaji et al., 2003). Chalcones are also used in designing effective second-order non-linear optical materials (Zhao et al., 2000). The structure determination of the title compound, (I), was undertaken as part of our study of chalcones.



Bond lengths and angles in (I) are comparable with those reported for related structures (Sathiya Moorthi, Chinnakali, Nanjundan, Radhika *et al.*, 2005; Sathiya Moorthi, Chinnakali, Nanjundan, Selvam *et al.*, 2005; Sathiya Moorthi, Chinnakali, Nanjundan, Unnithan *et al.*, 2005) The short H5···H8 (2.24 Å) contact causes the bond angles C5–C6–C7 [123.07 (14)°] and C6–C7–C8 [126.76 (14)°] to deviate significantly from 120°. Also, the short H8···H11 (2.08 Å) contact results in a slight widening of the C9–C10–C11 angle to 122.97 (15)°. The sum of the angles around atom N1 is 349.7° and the deviation of atom N1 from the C13/H1*A*/H1*B* plane is 0.19 (2) Å, indicating its pyramidal nature.

The molecule of (I) (Fig. 1) is approximately planar. The enone fragment of the molecule containing atoms C7, C8, C9

Received 23 September 2005 Accepted 26 September 2005 Online 30 September 2005

5338 independent reflections

 $R_{\rm int} = 0.023$ $\theta_{\rm max} = 38.2^{\circ}$

 $h = -13 \rightarrow 13$ $k = -7 \rightarrow 8$

 $l = -27 \rightarrow 27$

4831 reflections with $I > 2\sigma(I)$



Figure 1

The structure of (I), showing the atomic numbering scheme. Displacement ellipsoids are drawn at the 50% probability level. The dashed line indicates a hydrogen bond.



Figure 2 View of the hydrogen-bonded (dashed lines) sheets of (I).

and O1 is planar within ± 0.022 (2) Å. This plane makes dihedral angles of 3.1 (1) and 7.1 (1) $^{\circ}$, respectively, with the C1-C6 and C10-C15 benzene rings. The dihedral angle between the benzene rings is 9.6 $(1)^{\circ}$. The H atoms attached to C7 and C8 are trans to each other.

The weak intramolecular C7-H7···O1 interaction generates an S(5) ring motif. In the crystal structure, the molecules translated by one unit cell along the *a*-axis direction are linked by N1-H1A···O1¹ and C12-H12···O1¹ [symmetry code: (i) 1 + x, y, z hydrogen-bonding interactions to form a chain (Table 1). These interactions together constitute a pair of bifurcated acceptor bonds, generating an $R_2^1(6)$ motif (Bernstein et al., 1995). The screw-related molecules of adjacent chains are linked via N1-H1B···N1ⁱⁱ [symmetry code: (ii) 2 $x, \frac{1}{2} + y, -z$] hydrogen bonds into a sheet-like structure parallel to the ab plane (Fig. 2).

Experimental

Compound (I) was obtained by the Claisen-Schmidt condensation of 4-aminoacetophenone (5.4 g, 0.04 mol) and 3-bromobenzaldehyde (7.4 g, 0.04 mol) in a 20% solution of NaOH and ethanol at 273 K over a period of 24 h. The product was isolated by neutralizing the reaction mixture with dilute hydrochloric acid. The crude product was recrystallized from ethanol.

Crystal data

	D = 1.504 M = -3
$U_{15}H_{12}BrNO$	$D_x = 1.594 \text{ Mg m}^{-1}$
$M_r = 302.17$	Mo $K\alpha$ radiation
Monoclinic, P2 ₁	Cell parameters from 6184
a = 8.0012 (2) Å	reflections
b = 4.6257 (1) Å	$\theta = 2.6-37.8^{\circ}$
c = 17.1148 (5) Å	$\mu = 3.25 \text{ mm}^{-1}$
$\beta = 96.413 \ (1)^{\circ}$	T = 273 (2) K
$V = 629.47 (3) \text{ Å}^3$	Block, colourless
Z = 2	$0.45 \times 0.40 \times 0.15 \text{ mm}$

Data collection

Bruker SMART APEX2 CCD area-
detector diffractometer
ω scans
Absorption correction: multi-scan
(SADABS; Bruker, 2005)
$T_{\min} = 0.324, \ T_{\max} = 0.640$
9718 measured reflections

Refinement

Refinement on F^2	$w = 1/[\sigma^2(F_0^2) + (0.0546P)^2]$
$R[F^2 > 2\sigma(F^2)] = 0.030$	where $P = (F_0^2 + 2F_c^2)/3$
$wR(F^2) = 0.088$	$(\Delta/\sigma)_{\rm max} = 0.001$
S = 1.09	$\Delta \rho_{\rm max} = 1.36 \text{ e } \text{\AA}^{-3}$
5338 reflections	$\Delta \rho_{\rm min} = -0.50 \text{ e } \text{\AA}^{-3}$
171 parameters	Absolute structure: Flack (1983),
H atoms treated by a mixture of	1968 Friedel pairs
independent and constrained	Flack parameter: 0.008 (6)
refinement	

Table 1

Hydrogen-bond geometry (Å, °).

	ם ת	Ш 4		
$D - H \cdots A$	D-H	$H \cdots A$	$D \cdots A$	$D - H \cdots A$
$N1 - H1A \cdots O1^{i}$	0.89 (2)	2.11 (3)	2.943 (2)	155 (3)
$N1 - H1B \cdot \cdot \cdot N1^{ii}$	0.89 (2)	2.33 (2)	3.157 (2)	155 (2)
$C7 - H7 \cdots O1$	0.93	2.45	2.789 (2)	102
$C12 - H12 \cdots O1^{i}$	0.93	2.49	3.241 (2)	138

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

Amino H atoms were located in a difference Fourier map and both positional and isotropic displacement parameters were refined, with an N-H distance restraint of 0.90 (1) Å. The C-bound H atoms were placed in calculated positions and constrained to ride on their parent atoms, with C-H = 0.93 Å and $U_{iso}(H) = 1.2U_{eq}(C)$. The highest residual electron-density peak is located 0.76 Å from atom Br1.

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).

HKF thanks the Malaysian Government and Universiti Sains Malaysia for the Scientific Advancement Grant Allocation (SAGA) grant No. 304/PFIZIK/635003/A118.

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