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Key indicators

Single-crystal X-ray study T = 296 KMean σ (C–C) = 0.006 Å R factor = 0.072 wR factor = 0.203 Data-to-parameter ratio = 13.5

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

3-{4-[4-(3-Oxo-1,3-dihydroisobenzofuran-1-ylamino)benzyl]phenylamino}isobenzofuran-1(3*H*)-one dimethylformamide solvate

The crystal structure of the title compound, $C_{29}H_{22}N_2O_4$. C_3H_7NO , is stabilized by two N-H···O and six C-H···O intermolecular hydrogen bonds and C-H··· π and π - π interactions. The intermolecular hydrogen bonds generate $R_1^2(6)$ and $R_2^2(32)$ ring motifs.

Comment

Benzolactones are found in plants and they show several pharmacological effects, such as fungicidal, bactericidal, herbicidal and analgesic activities (Aoki *et al.*, 1973; Lacova, 1973). The present work is a part of our systematic research on the crystal structure analysis of 3-substituted phthalides (3-substituted benzolactones) synthesized from reactions of aromatic amines and phthalaldehydic acid.



In (I), the molecules have a planar configuration at the N atoms. The molecular conformation (Fig. 1) and relative orientation of the solvent molecule are defined by ten dihedral angles $[A/B = 58.35 (15)^{\circ}, A/C = 45.04 (15)^{\circ}, A/D = 71.49 (11)^{\circ}, A/E = 36.9 (4)^{\circ}, B/C = 78.50 (18)^{\circ}, B/D = 62.89 (15)^{\circ}, B/E = 37.3 (4)^{\circ}, C/D = 54.82 (15)^{\circ}, C/E = 73.6 (4)^{\circ}$ and $D/E = 72.2 (4)^{\circ}$], and these angles show that the molecules do not exhibit even approximate rotational symmetry but the orientations of A-B and C-D rings are similar for the two independent phenylphthalide units within the molecule.

The asymmetric unit (Fig. 1) contains one 3-{4-[4-(3-oxo-1,3-dihydroisobenzofuran-1-ylamino)benzyl]phenylamino}isobenzofuran-1(3H)-one molecule and one dimethylformamide (DMF) molecule, which are linked by N2– H2…O5 and C34–H34…O5 hydrogen bonds (Table 2), forming a six-membered ring with graph-set notation $R_2^1(6)$ (Etter, 1990; Bernstein *et al.*, 1995). This motif further selforganizes through N–H…O hydrogen bonds (Fig. 2), generating an array of two hydrogen bonds, the ring having graph-set notation $R_2^2(32)$. These hydrogen-bonded rings are linked into a complex three-dimensional framework by a combination of C–H…O hydrogen bonds (Table 2 and Fig. 3). There are also C–H… π (Table 2) and π – π interactions. The π – π interaction occurs between the O2/C1/C2/

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3-Substituted phthalides, Part XVI



Figure 1

A view of (I), showing the atomic numbering scheme, with displacement ellipsoids drawn at the 30% probability level. The labels A, B, C and D denote the ring planes and E the DMF molecular plane excluding the H atom.



Figure 2

Part of the crystal structure of (I), showing the formation of two hydrogen-bonded ring motifs. For the sake of clarity, H atoms not involved in the motifs shown have been omitted. Atoms marked with an (i) are at the symmetry position $(x - 1, y + \frac{1}{2}, z + \frac{1}{2})$.



The packing of (I). H atoms have been omitted. The dashed lines indicate the intramolecular hydrogen bonds.

C7/C8 rings of the phthalide units at (x, y, z) and (2 - x, -y, -z), with a centroid-to-centroid distance of 3.506 (2) Å and a plane-to-plane separation of 3.411 Å.

Experimental

The title compound, (I), was prepared as described by Odabaşoğlu & Büyükgüngör (2006), using phthalaldehydic acid and 4-(4-aminobenzyl)benzenamine as starting materials (yield 88%; m.p. 512–513 K). Crystals of (I) suitable for X-ray analysis were obtained by slow evaporation of a DMF solution at room temperature.

V = 1382.5 (2) Å³

 $D_x = 1.287 \text{ Mg m}^{-3}$ Mo *K* α radiation

 $0.71 \times 0.34 \times 0.11 \text{ mm}$

16524 measured reflections

5014 independent reflections

2712 reflections with $I > 2\sigma(I)$

Long prismatic stick, light brown

 $\mu = 0.09 \text{ mm}^{-1}$

T = 296 K

 $R_{\rm int} = 0.101$

 $\theta_{\rm max} = 25.3^\circ$

 $\Delta \rho_{\rm min} = -0.34 \text{ e} \text{ Å}^{-3}$

Z = 2

Crystal data

 $C_{29}H_{22}N_2O_4 \cdot C_3H_7NO$ $M_r = 535.58$ Triclinic, *P*1 a = 8.0267 (7) Å b = 12.6709 (11) Å c = 14.6529 (13) Å $\alpha = 98.911$ (7)° $\beta = 100.893$ (7)° $\gamma = 104.746$ (6)°

Data collection

Stoe IPDS-2 diffractometer ω scans Absorption correction: integration (*X-RED32*; Stoe & Cie, 2002) $T_{\min} = 0.951, T_{\max} = 0.988$

Refinement

Refinement on F^2	H atoms treated by a mixture of
$R[F^2 > 2\sigma(F^2)] = 0.072$	independent and constrained
$wR(F^2) = 0.203$	refinement
S = 0.96	$w = 1/[\sigma^2(F_o^2) + (0.1127P)^2]$
5014 reflections	where $P = (F_0^2 + 2F_c^2)/3$
371 parameters	$(\Delta/\sigma)_{\rm max} < 0.001$
	$\Delta \alpha = 0.41 \text{ e} $

Table 1 Selected geometric parameters (Å, °).

C1-O1	1.204 (5)	C21-O4	1.338 (5)
C1-O2	1.357 (5)	C22-C27	1.376 (5)
C2-C7	1.375 (5)	C28-N2	1.394 (4)
C8-N1	1.383 (5)	C35-O5	1.207 (7)
C21-O3	1.204 (4)		
O1-C1-O2	121.6 (4)	O3-C21-O4	121.5 (3)
O1-C1-C2	129.3 (4)	O3-C21-C22	129.3 (4)
N1-C8-O2	113.6 (3)	N2-C28-O4	111.0 (3)

Table 2

Hydrogen-bond geometry (Å, °).

Cg1 is the centroid of the C29-C34 ring.

$D - H \cdots A$	D-H	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - \mathbf{H} \cdots A$
N2-H2···O5	0.845 (18)	2.06 (2)	2.886 (5)	165 (4)
C34—H34…O5	0.93	2.81	3.505 (6)	133
N1-H1···O3 ⁱ	0.871 (19)	2.10(2)	2.956 (4)	168 (4)
C5−H5···O2 ⁱⁱ	0.93	2.53	3.413 (6)	160
C8−H8···O1 ⁱⁱⁱ	0.98	2.88	3.573 (5)	129
$C25-H25\cdots O4^{iv}$	0.93	2.54	3.408 (4)	155
C36−H36b···O3 ^v	0.96	2.85	3.669 (13)	143
C37−H37c···O1 ^{vi}	0.96	2.60	3.208 (10)	121
$C14-H14\cdots Cg1^{iv}$	0.93	3.00	3.735 (4)	137

Symmetry codes: (i) -x, -y + 1, -z + 1; (ii) x - 1, y, z; (iii) -x, -y + 2, -z + 2; (iv) x + 1, y, z; (v) -x + 1, -y, -z + 1; (vi) x + 1, y - 1, z.

All C-bound H atoms were refined using the riding-model approximation, with C-H = 0.93 Å for aromatic, 0.97 Å for methylene and 0.98 Å for methine H atoms $[U_{iso}(H) = 1.2U_{eq}(C)]$ and C-H = 0.96 Å for methyl H atoms $[U_{iso}(H) = 1.5U_{eq}(C)]$. The amino atoms H1 and H2 were located in a Fourier difference map and refined with a distance restraint of 0.87 (2) Å.

Data collection: X-AREA (Stoe & Cie, 2002); cell refinement: X-AREA; data reduction: X-RED32 (Stoe & Cie, 2002); program(s) used to solve structure: SHELXS97 (Sheldrick, 1990); program(s) used to refine structure: SHELXL97 (Sheldrick, 1997); molecular graphics: ORTEP-3 for Windows (Farrugia, 1997); software used to prepare material for publication: WinGX (Farrugia, 1999).

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