Structural Study on Solvates of Dopamine-Based Cyclic Imide Derivatives

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Received October 7, 2010; Revised Manuscript Received December 9, 2010



ABSTRACT: A structural study on two dopamine-based imide derivatives, namely, 2-(3,4-dihydroxyphenethyl)isoindole-1,3dione (1) and 2,6-bis-[2-(3,4-dihydroxyphenyl)ethyl]pyrrolo [3,4-f]isoindole-1,3,5,7-tetrone (2), and their solvates was carried out. The compound 1 (Z' = 2) was crystallized through a melt crystallization process, whereas its two solvates (Z' = 1 of each), containing one water molecule (1a) and the other containing two quinoline molecules (1b) in their crystal lattices, respectively, were obtained through solution crystallization. The reasons for Z' = 2 arising from symmetry nonequivalent molecules in the unit cell of 1 is attributed to the nonparallel arrangement of two layers of self-assembled molecules in crystal lattice, where one layer has $C-H\cdots\pi$ and another layer has $C=O\cdots\pi$ interactions. Four different solvates of compound 2 (Z' = 0.5 of each), containing two DMF molecules (2a), two DMSO molecules (2b), two pyridine molecules (2c), and six quinoline molecules (2d), were also obtained through solution crystallization of 2 in respective solvents. Solvate 2d has channels in its structure which are formed by interaction of 2 with quinoline molecules through $O-H\cdots N$ and $C-H\cdots\pi$ interactions. Additional quinoline molecules reside in these channels of approximately (11×12) Å dimension. Structural features of all the compounds and their solvates have been studied by single crystal X-ray structures, powder X-ray diffractions (PXRD), thermogravimetric analyses (TGA), and differential scanning calorimetric (DSC) measurements.

Introduction

Solvates are generally known as crystalline materials containing a host component and molecule/s of the solvent.^{1,2} The intermolecular interactions between organic host and solvent are responsible for the inclusion of solvent in crystal lattice.³ A promising method to obtain guest-free crystalline forms of host is melt crystallization.⁴ Among the solvates, hydrates are of special interest in the pharmaceutical industry due to their different physical properties from corresponding nonhydrates.⁵ Weak intermolecular interactions control the stability of the solvate and also affect their aggregation that may lead to crystal structure of particular conformation in the solid state.⁶ Moreover, the inclusion of solvent molecules tunes geometrical alignment of host molecules, which in turn affects the Z' value in crystals.⁷ Cyclic imide derivatives have versatility in the field of crystal engineering to control the molecular arrangements by various weak interactions.⁸ With an objective to understand the role of weak interactions in stabilizing various solvates of imide derivative tethered to catecholate unit, we describe here a structural study on two dopamine-based mono and diimide derivatives 2-(3.4-dihydroxyphenethyl)isoindole-1,3-dione (1) and 2,6-bis-[2-(3,4-dihydroxyphenyl)ethyl]pyrrolo[3,4-*f*]-isoindole-1,3,5,7-tetraone (2) (Chart 1) and their various solvates. Dopamine and its derivatives have biological applications as a neurotransmitter⁹ and as drugs for several diseases.¹⁰ They are of interest in theoretical chemistry as a computational study supported by experimental data has shown the existence of different conformers of dopamine derivatives due to C-C bond rotation.¹¹ The other purpose of this study is to understand the self-assembly of cyclic imide derivatives tethered to electronrich catechol unit/s.

Results and Discussion

The guest-free crystals of **1** were obtained by a melt crystallization process.⁴ The hydrated form of the crystals, **1a**, were obtained by crystallizing **1** from commercially available solvents such as ethanol, DMF, pyridine, etc., and the crystals of quinoline solvate **1b** were obtained from a quinoline solution of **1** (Scheme 1).

The compound 1 crystallized in monoclinic $P2_1/c$ space group. It possesses two symmetry independent molecules of 1 (X and Y) in its crystallographic asymmetric unit (Figure 1). Both the symmetry nonequivalent molecules exhibit O- $H \cdots O$ interactions. These molecules interact with each other via C-H···O (C20-H···O1 $d_{D...A}$ 3.28 Å, $\angle D$ -H···A 135.62°) interaction. Both the symmetry independent sets of molecules X and Y self-assemble themselves to form two independent one-dimensional (1D) layers in the lattice. One of the hydroxyl groups of molecule X involves discrete O-H···O (O4-H4A···O4 $d_{D...A}$ 2.98 Å, $\angle D$ -H···A 161.43°) interaction. The other hydroxyl group engages in a cyclic R_2^2 (7) hydrogen bond motif formed by the combination of O-H···O (O3-H3A···O2 $d_{\text{D...A}}$ 2.74 Å, $\angle D$ -H···A 166.05°) and C-H···O (C6-H···O3 d_D ...A 3.40 Å, $\angle D$ -H···A 146.94°) interactions, which further interacts by O-H··· π ($d_{O3...\pi}$ 3.55 Å) interaction in the lattice. Similar types of discrete O-H···O (O8-H8A···O8 $d_{D...A}$ 2.87 Å, $\angle D - H \cdots A$ 161.60°) interaction and cyclic R_2^2 (7) hydrogen bond motifs formed by the combination of O−H···O (O7−H7A···O6 $d_{D···A}$ 2.72 Å, ∠D−H···A 162.80°) and C-H···O (C22-H···O7 $d_{\text{D...A}}$ 3.31 Å, $\angle D$ -H···A 146.44°) interactions, along with O-H··· π $(d_{\rm O7}...\pi$ 3.50 Å) interaction, are observed among the Y molecules in the crystal lattice. Notably, both the hydroxyl groups of molecule Y involve bifurcated hydrogen bonding with the hydrogen atom of the phenyl ring of imide functionality

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Figure 1. Crystal packing of 1, showing the arrangement of symmetry independent molecules in crystal lattice (X and Y).





Scheme 1. Structures of Host 1 and Its Two Solvates



via C-H···O (C22-H···O7 and C22-H···O8 $d_{D...A}$ 3.34 Å, $\angle D$ -H···A 130.69°) interactions, which induces C-H··· π ($d_{C31...\pi}$ 3.70 Å) interactions among the Y molecules and aggregates them in a one-dimensional (1D) layer supported by strong $\pi \cdots \pi$ interactions. These types of bifurcated as well as C-H··· π interactions are absent in the assembly of X molecules. They assemble in a 1D layer structure by C=O··· π interactions present between the fivemember imide rings of X molecules. There is a clear distinction between the weak interactions in these two layers of X and Y molecules. Both the layers require an independent frame of coordinates to describe them. Thus, the subtle differences in weak interactions due to slight variations in orientations of molecules lead to symmetry nonequivalence in unit cell.¹²

The solvate **1a** crystallized in orthorhombic $Pna2_1$ space group. It has one molecule of **1** with a water molecule in asymmetric unit. In the crystal lattice, the O–H···O interactions between the host molecules are absent due to the presence of water molecules, which are engaged in O–H···O hydrogen bonds with host molecules and act as both donor and acceptor (Figure 2). One of the hydrogen atoms of water



Figure 2. (a) Weak interactions in 1a. (b) Edge to face $\pi \cdots \pi$ interactions between host molecules.

Table 1. Hydrogen Bond Parameters $(\text{\AA}, \circ)$ for 1a								
	d	d		d				
$D-H\cdots A$	(D-H)	$(H\!\cdot\!\cdot\!\cdot A)$	$\angle D - H \cdots A$	$(D \boldsymbol{\cdot} \boldsymbol{\cdot} \boldsymbol{\cdot} A)$				
O4−H4A…O5	0.82	2.15	159.00	2.93(3)				
[-x+2, -y+1, z-1/2]								
O4−H4A…O3	0.82	2.26	114.02	2.70(3)				
O3-H3AO5	0.82	1.90	163.56	2.69(3)				
O5-H5A···O4	0.78	2.25	166.32	3.02(3)				
[x, y, z+1]								
O5-H5B···O1	0.85	1.94	176.18	2.79(3)				
[-x+3/2, y-1/2, z+1/2]								
С16-Н16О2	0.93	2.56	159.25	3.44(4)				
[x, y, -1 + z]								



Figure 3. A part of crystal packing of 1b showing the weak interactions between the host and quinoline molecules.

molecule involves bifurcated donor hydrogen bonding with a host molecule through O5-H5A···O3 ($d_{D...A}$ 3.01 A, $\angle D - H \cdots A \ 108.96^{\circ}$) and O5 - H5A \cdots O4 ($d_{D} \cdots A \ 3.01 \ \text{\AA}$, $\angle D-H\cdots A$ 162.76°) interactions and the oxygen atom involves bifurcated acceptor hydrogen bonding through O3-H3A····O5 ($d_{D...A}$ 2.69 Å, $\angle D$ -H···A 164.88°) and O4-H4A···O5 ($d_{D...A}$ 2.92 Å, $\angle D$ -H···A 159.23°) interactions making a cyclic $R_3^{3}(6)$ hydrogen-bonded six-membered ring structure (Table 1). Another cyclic $R_2^2(7)$ hydrogen bond assembly is also formed in the lattice by the donor-acceptor O-H···O interactions between the host and water molecule involving O5-H5A····O3 and O4-H4A····O5 interactions. The other hydrogen atom of the water molecule forms a hydrogen bond with a carbonyl oxygen atom of the host molecule via O5–H5B····O1 ($d_{D...A}$, 2.79 Å, $\angle D$ –H···A 176.29°) interaction. This hydrogen atom further interacts to the host via O-H··· π ($d_{O5...\pi}$ 3.60 Å) interaction. Beside that, the host molecules also assemble in the lattice through



Figure 4. PXRD patterns of 1 and its two solvates.

C-H···O (C6-H···O1 $d_{D...A}$ 3.33 Å, $\angle D$ -H···A 129.58° and C16-H···O2 $d_{D...A}$ 3.44 Å, $\angle D$ -H···A 159.25° and C9-H9B···O2 $d_{D...A}$ 3.25 Å, $\angle D$ -H···A 123.88°) interactions and edge-to-face $\pi \cdot \cdot \pi$ interactions experienced between the five-member imide ring and phenyl ring bearing two hydroxyl groups.

The solvate **1b** crystallized in triclinic $P\overline{1}$ space group. The asymmetric unit of this has one molecule of 1 with two quinoline molecules (Figure 3). Because of the hierarchy of O-H···N interactions over O-H···O interactions, O-H...O interactions are not found between the host molecules in the crystal lattice. Two symmetry nonequivalent quinoline molecules interact with host molecules in different ways. One set of symmetry independent quinoline molecules interacts with host molecules via discrete O-H···N (O3-H3A···N3 $d_{\rm D...A}$ 2.93 Å, $\angle D-H\cdots A$ 146.30°) interaction and simultaneously involves bifurcated donor hydrogen bonding with the carbonyl oxygen of the imide ring of the host molecule through C-H···O (C32-H···O2 $d_{D...A}$ 3.33 Å, $\angle D$ -H···A 148.18° and C33-H···O2 $d_{D...A}$ 3.41 Å, $\angle D$ -H···A 136.48°) interactions and situated inside the alternate cavities formed between the host molecules via C-H···O (C6-H···O3 $d_{D...A}$ 3.31 Å, $\angle D$ -H···A 155.96°) hydrogen bonding interactions. Another set of quinoline molecules also interact by discrete O-H···N (O4-H4A····N2 $d_{D...A}$ 2.82 Å, $\angle D$ -H···A 176.91°) interactions with host molecules and involve bifurcated acceptor hydrogen bonding with the hydrogen atom of imide functionality through C-H··· π ($d_{C4...\pi}$ 3.69 Å and $d_{C4...\pi}$ 3.70 Å) interactions. The quinoline molecules further interact with each



Figure 5. (a) Weak interactions between the DMF and host molecules in **2a**. (b) 1D layer of host supported by $\pi \cdots \pi$ interactions (along the *a* axis). (c) Another 1D layer of host supported by C-H···O and C=O··· π interactions (along the *c* axis).

Scheme 2. Various Solvates of 2



other via C-H··· π ($d_{C21...\pi}$ 3.63 Å) interaction in the hydrogen-bonded assembly of **1b**.

Thermogravimetric analysis of **1a** reveals loss of 6% weight over the temperature range 65–115 °C, which corresponds to the loss of 1 equiv of water, whereas 45% weight loss corresponds to 2 equiv of quinoline molecules, occurs from **1b** in the temperature range between 75 and 170 °C. The endothermic peak at 121 °C and a broad endothermic peak at 152 °C in the DSC of **1a** and **1b**, respectively, confirm the loss of solvent molecules in this particular temperature range. Sharp endotherms appear in **1a** at 189 °C and in **1b** at 185 °C, are due to the melting of the solvates (Supporting Information).

Powder X-ray diffraction (PXRD) patterns obtained for 1 and its two solvates, 1a and 1b, show significant differences (Figure 4). The inclusion of different solvents in the crystal lattice of the host could easily be distinguished by dissimilar diffraction patterns obtained for different solvated forms

Table 2. Hydrogen Bond Parameters (Å, °) for Crystals 2a and 2d

compound	D-H···A	<i>d</i> (D–H)	$d(\mathbf{H}\cdots\mathbf{A})$	∠D−H···A	$d(\mathbf{D}\cdots\mathbf{A})$
2a	O4-H4A···O5 $[x + 1, y - 1, z]$	0.82	1.95	154.11	2.71(19)
	O4-H4AO3	0.82	2.30	113.10	2.73(19)
	$O3-H3A\cdots O1[x+1, y-1, z]$	0.82	1.93	169.70	2.74(2)
	$C7-H7A\cdots O2[x-1, y, z]$	0.97	2.55	152.95	3.44(2)
	C16-H16···O3 $[x - 1, y + 1, z]$	0.93	2.41	128.30	3.07(3)
2d	$O4-H4A\cdots N2[-x+2,-y+1,-z+1]$	0.82	1.94	176.31	2.76(3)
	$O3-H3A\cdots N3 [x + 1, y - 1, z]$	0.82	2.11	151.53	2.86(4)
	$O3-H3A\cdots O4$	0.82	2.33	111.36	2.74(3)
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Figure 6. (a) Weak interactions between the DMSO and host molecules in 2b. (b) 3D tetrameric assemblies of host molecules encapsulating the DMSO molecules (along the *c* axis). (c) Space filling model after removal of the DMSO molecules.

1a and **1b** which crystallize in different space groups. Comparison of PXRD patterns of all three different crystalline materials with simulated patterns from single crystal X-ray structures determined at 298 K shows good agreement (Supporting Information).

The crystal structures of four different solvates of **2** (Scheme 2) were also determined. Each of the solvates has half of the host molecule (Z' = 0.5) containing one DMF molecule (**2a**), one DMSO molecule (**2b**), one pyridine molecule (**2c**), and three quinoline molecules (**2d**) in the asymmetric unit of the crystal lattice.

The solvate **2a** crystallized in triclinic $P\overline{1}$ space group. It has half of the host molecule lying on the inversion center with one DMF molecule in the asymmetric unit (Figure 5). The DMF molecules interact with host molecules via both donor and acceptor types of interactions in the lattice. The carbonyl oxygen of DMF molecule acts as an acceptor and involves the $O-H\cdots O$ hydrogen bond (O4–H4A $\cdots O5 d_{D}\dots A 2.71$ Å, $\angle D-H\cdots A 154.07^{\circ}$) with one of the hydroxyl groups of the host molecule, whereas the hydrogen atom of DMF present on carbonyl carbon acts as a donor and involves $C-H\cdots O$ (C16– $H\cdots O3 d_{D}\dots A 3.07$ Å, $\angle D-H\cdots A 128.30^{\circ}$) interaction with the oxygen atom of another hydroxyl group of host molecule making a cyclic $R_2^2(8)$ type of hydrogen bond motif (Table 2). The methyl hydrogen of DMF also involves C-H···O interaction (C14-H14B···O4 d_{D} ···A 3.62 Å, $\angle D$ -H···A 168.52°) with the host molecule. The two carbonyl oxygen atoms of the host molecule involve two different types of bifurcated acceptor hydrogen bondings. One such hydrogen atom forms a bifurcated hydrogen bond via the combination of O-H···O (O3-H3A···O1 $d_{D...A}$ 2.74 Å, $\angle D$ -H···A 169.63°) and C-H···O (C9-H···O1 $d_{\rm D...A}$ 3.32 Å, $\angle D-H\cdots A$ 125.18°) interactions, whereas another via two C-H···O (C7-H7A···O2 $d_{D...A}$ 3.44 Å, $\angle D$ -H···A 152.94° and C13-H···O2 $d_{D...A}$ 3.47 Å, $\angle D-H\cdots A$ 141.80°) interactions. The later bifurcated hydrogen bonding results in the formation of C=O $\cdots \pi$ interactions between the host molecules making a 1D layered structure along the c axis. Moreover, the host molecules are also layered over each other in the lattice through strong $\pi \cdots \pi$ interactions constructing a 1D steplike structure along the c axis. These two different kinds of layers further grow along the b axis by interacting with DMF molecules, overall making a 3D hostguest arrangement in the crystal lattice of 2a.



Figure 7. (a) Weak interactions between the pyridine and host molecules in 2c. (b) $\pi \cdots \pi$ interactions between the two layers of host molecules (red) which holds the pyridine molecules (blue) via O-H···N and C-H···O interactions.

The solvate **2b** crystallized in triclinic $P\overline{1}$ space group. The asymmetric unit of 2b has half of the host molecule that lies on the inversion center with one DMSO molecule. In the structure of 2b (Figure 6), the oxygen atom of DMSO molecule is disordered over two positions having occupancies of 0.86 and 0.14, respectively. The hydroxyl groups of host molecules in the crystal structure of solvate **2b** form cyclic $R_2^{2}(10)$ hydrogen bond motifs interacting with each other via O-H···O $(O4-H4A\cdots O3 d_{D\cdots A} 2.78 \text{ Å}, \angle D-H\cdots A 146.54^{\circ})$ interactions, generating a 1D infinite zigzag chain and involve simultaneously $O \cdots \pi$ (O4-C4 = 3.17 Å) and $\pi \cdots \pi$ (C3-C11 = 3.37 Å) interactions, which overall construct a two-dimensional (2D) steplike structure of host molecules. The DMSO molecules form hydrogen bonds with host molecules via acceptor O-H···O (O3-H3A···O5 $d_{D...A}$ 2.58 Å, ∠D-H···A 175.25°) and donor C-H···O (C14-H14B-···O2 $d_{D...A}$ 3.36 Å, $\angle D-H\cdots A$ 162.34°) interactions and also interact with each other via C-H···O (C15-H15A- \cdots O5 $d_{D...A}$ 3.30 Å, \angle D-H \cdots A 152.75°) interaction in the crystal lattice. All these host-host, host-guest, and guestguest interactions result in the construction of repeated threedimensional (3D) tetrameric assemblies of host molecules allow the rectangular voids formation in the lattice filled by DMSO molecules when viewed along the c axis. The DMSO molecules generally coordinate to acidic OH groups through weak interactions,¹³ but in this case, the DMSO molecules are held in the interstitial positions.

The solvate 2c crystallized in monoclinic $P2_1/c$ space group. It includes half of the host molecule that lies on inversion center and one pyridine molecule in the asymmetric unit. The

crystal structure of 2c is devoid of cyclic hydrogen bond motifs and pyridine molecules are held with host molecules through discrete acceptor O-H···N (O4-H4A···N2 $d_{D...A}$ 2.74 Å, $\angle D-H\cdots A$ 163.01°) interaction with one of the hydroxyl groups of the host molecule as well as discrete donor C-H···O (C14-H···O1 $d_{D...A}$ 3.45 A, $\angle D$ -H···A 144.74°) interaction with one of the carbonyl oxygen atoms of the host molecule in the lattice (Figure 7). A cyclic $R_2^2(8)$ hydrogen bond motif forms between the host molecules when associated together via O-H···O (O3-H3A···O1 $d_{D...A}$ 2.80 Å, $\angle D$ -H···A 128.25°) and C-H···O (C7-H7B ···O3 $d_{D...A}$ 3.38 Å, $\angle D-H\cdots A$ 146.54°) interactions, generating a repeated tetrameric assembly of host molecules. These tetramers encapsulate pyridine molecules inside the assembly in the lattice. No weak interactions among the pyridine molecules are observed. The pyridine molecules generally form strong hydrogen bonds with acidic OH functional groups¹⁴ and also have tendency to remain in stacked assemblies in inclusion compounds.^{8j} The host molecules also assemble with each other via another type of C-H···O (C9–H···O2 $d_{D...A}$ 3.45 Å, ∠D–H···A 147.23°) C=O $\cdots \pi$ interaction. These multiple interactions found among the host molecules project them in two different directions, further making a three-dimensional layered arrangements supported by strong $\pi \cdots \pi$ interactions which exist between the five-member imide ring and phenyl ring bearing two hydroxyl groups. The pyridine molecules adopt a parallel position between the two sheets of host molecules interacting via discrete O-H···N and C-H···O interactions in the lattice of 2c.



Figure 8. (a) A part of the crystal structure of **2d** showing different types of weak interactions between the host and three symmetry independent quinoline molecules. (b) Channel formation in assembly of host and quinoline molecules (along the a axis). (c) Space filling model after removal of one set of quinoline molecules residing inside the channels.

The solvate **2d** crystallized in triclinic $P\overline{1}$ space group. The asymmetric unit of this structure has half of the host molecule lying on the inversion center with three symmetry nonequivalent quinoline molecules. Unlike the other solvates, the O-H···O and C-H···O interactions found between the host molecules are absent in the crystal structure of 2d (Figure 8). Apparently, the host molecules aggregate with each other via only weak C–H $\cdots \pi (d_{C7} \dots \pi 3.53 \text{ Å})$ hydrogen bonding interactions appearing between the methylene hydrogen of flexible arms and the five-member imide ring of host molecules. All the three symmetry independent quinoline molecules have different types of interactions with host molecules. The first set of quinoline molecules have three different types of interactions with host molecules in the lattice (i) discrete O-H···N (O3-H3A···N3 $d_{\text{D...A}}$ 2.86 Å, $\angle D-H\cdots A$ 151.48°) interaction with one of the hydroxy groups of the host; (ii) C-H···O (C30-H···O2 $d_{D...A}$ 3.36 Å, $\angle D$ -H···A 134.50°) interaction with one of the carbonyl oxygens, in the combination of acceptor C-H $\cdots \pi$ $(d_{C6...\pi} 3.76 \text{ Å})$ interaction with methylene hydrogen of host; (iii) bifurcated donor C-H··· π ($d_{C24...\pi}$ 3.68 Å and $d_{C24...\pi}$ 3.72 Å) interactions with the phenyl ring bearing two hydroxyl groups of the host molecules. Asecond set of quinoline molecules form a cyclic $R_2^{-1}(6)$ hydrogen bond motif by the combination of O-H···N (O4-H4A···N2 $d_{\rm D...A}$ 2.76 Å, $\angle D-H\cdots A 176.31^\circ$ and $C-H\cdots N (C12-H\cdots N2 d_{D\cdots A})$ 3.34 Å, $\angle D - H \cdots A$ 130.69°) interactions (Table 2). A third set of quinoline molecules do not facilitate by O-H···N interactions but form a cyclic $R_2^{2}(8)$ hydrogen bond motif by the combination of C-H···N (C3-H···N4 $d_{D...A}$ 3.51 Å, $\angle D$ -H···A 158.29°) and C-H···O (C32-H···O1 $d_{D...A}$ 3.53 Å, $\angle D - H \cdots A$ 150.96°) interactions in the lattice. The



Figure 9. PXRD patterns of 2 and its solvates.

quinoline molecules belong to the first and second set also interact with each other via $C-H\cdots\pi$ ($d_{C16}\ldots\pi$ 3.70 Å and $d_{C27...\pi}$ 3.52 Å) interaction. This creates tetrameric assemblies of quinoline molecules which adopts a chairlike geometry. Assemblies of pyridine derivatives held by $C-H\cdots\pi$ interactions are reported in the literature.¹⁴ The C-H \cdots π interactions present between the host molecules and quinoline molecules aggregate them in a 1D layer, which further results in the formation of a 3D channel-like structure by the interactions present between host and quinoline molecules. A third set of quinoline molecules do not participate in the channel formation. However, the channels created along the *a* axis accommodate these quinoline molecules (Figure 8). When the solvent molecules are omitted, these channels have (11×12) Å dimension (Figure 8c). It may be noted that the C-H bond next to the nitrogen atom of pyridine and quinoline participates in weak hydrogen bonding with carboxylic acid or related functional groups.^{8k,1} We have attempted to remove the quinoline molecules by pyridines but it was not possible. However, the reverse was possible; that is, the pyridine solvate (2c) led to quinoline solvate (2d) on crystallization from quinoline but not vice versa.

Thermogravimetric studies on these solvates show that solvate **2a** loses 2 equiv of DMF (21% weight loss) over the temperature range 60–102 °C, solvate **2b** loses 2 equiv of DMSO (17% weight loss) over the temperature range 95–138 °C, solvate **2c** loses 2 equiv of pyridine (23% weight loss) over the temperature range 65–118 °C, while solvate **2d** loses 6 equiv of quinoline molecules (56% weight loss) over the temperature range 75–150 °C. The results obtained from TGA are further confirmed by DSC analyses. The endothermic peaks at 100, 140, 120, and 130 °C appear due to the loss of solvent molecules in DSC profile of solvates **2a**, **2b**, **2c**, and **2d**, respectively (Supporting Information).

The PXRD patterns obtained for solvent-free host 2 and its different solvated forms 2a, 2b, 2c and 2d are shown in Figure 9. The differences in the position and intensity of diffraction peaks of the various solvates are due to the inclusion of different solvent molecules in the crystal lattice of host. The peaks obtained in the PXRD patterns of different

 Table 3. Crystallographic Parameters of 1, 1a, 1b, 2a, 2b, 2c, and 2d

compound no.	1	1 a	1b	2a	2b	2c	2d
formulas	C ₁₆ H ₁₃ NO ₄	C ₁₆ H ₁₅ NO ₅	C34H27N3 O4	C32H34N4 O10	C ₃₀ H ₃₂ N ₂ O ₁₀ S ₂	C36H30N4 O8	C80H62N8O8
formulawt	283.27	301.29	541.59	634.63	644.72	646.64	1263.38
crystal system	monoclinic	orthorhombic	triclinic	triclinic	triclinic	monoclinic	triclinic
space group	$P2_1/c$	$Pna2_1$	$P\overline{1}$	$P\overline{1}$	$P\overline{1}$	$P2_1/c$	$P\overline{1}$
a /Å	23.4842(15)	26.316(11)	8.6650(17)	6.3217(2)	9.4527(5)	14.9497(5)	8.790(3)
b /Å	5.0207(4)	7.329(4)	12.644(2)	8.5303(3)	9.4740(4)	8.8863(3)	12.746(4)
c /Å	25.7292(16)	7.737(3)	12.964(2)	15.5713(6)	9.7186(4)	12.1128(4)	15.130(5)
a/°	90.00	90.00	77.925(9)	80.929(2)	104.394(3)	90.00	101.030(13)
$\beta/^{\circ}$	115.859(4)	90.00	86.183(8)	89.670(2)	101.121(3)	98.096(2)	91.205(14)
$\gamma/^{\circ}$.	90.00	90.00	87.733(9)	69.818(2)	106.048(3)	90.00	99.449(12)
$V/\text{\AA}^3$	2729.9(3)	1492.2(12)	1385.4(5)	777.21(5)	777.52(6)	1593.12(9)	1638.7(10)
Z	8	4	2	1	1	2	1
density/Mg m ^{-3}	1.378	1.341	1.298	1.356	1.377	1.348	1.280
abs coeff $/\text{mm}^{-1}$	0.100	0.101	0.086	0.102	0.231	0.097	0.084
F(000)	1184	632	568	334	338	676	662
total no. of reflections	27295	9114	8789	7315	9245	17442	16165
reflections, $I > 2\sigma(I)$	2721	2273	3147	2190	1970	1989	2455
$\max 2\theta/^{\circ}$	50.00	50.00	50.00	50.00	50.00	50.00	50.00
ranges (h, k, l)	$-26 \le h \le 27$	$-31 \le h \le 31$	$-10 \le h \le 9$	$-7 \le h \le 7$	$-11 \le h \le 11$	$-17 \le h \le 17$	$-10 \le h \le 10$
	$-5 \le k \le 5$	$-8 \le k \le 8$	$-15 \le k \le 6$	$-10 \le k \le 9$	$-11 \le k \le 11$	$-10 \le k \le 10$	$-14 \le k \le 15$
	$-30 \le l \le 30$	$-8 \le l \le 9$	$-15 \le l \le 13$	$-18 \le l \le 18$	$-11 \le l \le 11$	$-14 \le l \le 13$	$-17 \le l \le 16$
complete to 2θ (%)	100.0	98.7	98.0	95.8	98.2	99.5	92.9
data/restraints/parameters	4781/0/379	2525/1/209	4778/0/372	2691/0/212	4212/0/264	2796/0/217	5355/0/435
$\operatorname{GOF}(F^2)$	0.925	1.073	1.050	1.068	1.025	0.997	1.016
R indices $[I > 2\sigma(I)]$	0.0452	0.0476	0.0673	0.0465	0.0809	0.0400	0.0585
R indices (all data)	0.0860	0.0529	0.0907	0.0532	0.1029	0.0603	0.1664

solvates correlate well with the simulated peaks of X-ray structures (Supporting Information).

Conclusions

The role of weak interactions of solvents with host molecules, namely, 2-(3,4-dihydroxyphenethyl) isoindole-1,3-dione (1) and 2,6-bis-[2-(3,4-dihydroxyphenyl)ethyl]pyrrolo [3,4flisoindole-1,3,5,7-tetraone (2), in changing their packing patterns are studied. The weak interactions play crucial roles in changing the packing patterns and a subtle difference in weak interactions such as $C-H\cdots\pi$ and $C=O\cdots\pi$ interactions distinguishes the symmetry nonequivalent molecules in the crystal lattice of 1. Hydrogen bonding interactions are responsible for forming a porous structure to accommodate DMSO molecules in the interstitial sites in the structure of **2b**. The quinoline molecules along with 2 act as a constituent for building a secondary host system to encapsulate additional molecules of quinoline. While forming such a structure, the quinoline molecules occupy positions in the crystal lattice which requires three independent sets of coordinates to describe their positions in the lattice.

Experimental Section

Structure Determination. The X-ray single crystal diffraction data were collected at 296 K with MoK α radiation ($\lambda = 0.71073$ Å) using a Bruker Nonius SMART CCD diffractometer equipped with a graphite monochromator. The SMART software was used for data collection and also for indexing the reflections and determining the unit cell parameters; the collected data were integrated using SAINT software. The structures were solved by direct methods and refined by full-matrix least-squares calculations using SHELXTL software. All the non-H atoms were refined in the anisotropic approximation against F^2 of all reflections. The H-atoms, except those attached to nitrogen and oxygen atoms, were placed at their calculated positions and refined in the isotropic approximation; those attached to nitrogen and oxygen were located in the difference Fourier maps, and refined with isotropic displacement coefficients. Crystallographic data collection was done at room temperature and the data are tabulated in Table 3. In structure 2b, the DMSO molecule is disordered and modeled by splitting occupancies of the oxygen atom.

Synthesis and Characterization of Compounds 1, 2, and Their Solvates. 2-(3,4-Dihydroxyphenethyl)isoindole-1,3-dione (1). A solution of phthalic anhydride (0.740 g, 5 mmol) and dopamine hydrochloride (0.945 g, 5 mmol) in acetic acid (20 mL) was refluxed for 3 h. The reaction mixture was cooled to room temperature, poured into ice cooled water (50 mL), and stirred for 15 min. A brown-colored crystalline material of the product was obtained. This was filtered and dried in open air. Yield: 85%; IR (KBr, cm⁻¹): 3373 (m), 3273 (m), 2929 (w), 1759 (m), 1693 (s), 1615 (m), 1531 (w), 1446 (s), 1435 (s), 1402 (s), 1357 (m), 1266 (m), 1242 (m), 1117 (w), 1090 (w), 1001 (w), 952 (w), 724 (m). ¹H NMR (400 MHz, DMSO-*d*₆): 8.79 (s, 1H), 8.68 (s, 1H), 7.82 (s, 4H), 6.56 (d, 2H, J = 7.6 Hz), 6.39 (d, 1H, J = 8.0 Hz), 3.70 (t, 2H, J = 7.2 Hz), 2.71 (t, 2H, J = 7.2 Hz). ¹³C NMR (DMSO-*d*₆): 167.8, 145.2, 143.8, 134.4, 131.6, 129.0, 132.1, 119.3, 116.0, 115.6, 33.2. ESI-MS: 284.115 $[M + H^+]$. The compound 1 was heated up to 200 °C in a test tube using oil bath and the resulting neat liquid phase was cooled rapidly, putting the test tube in ice cubes. Crystals of 1 were obtained immediately.

1a: The crystals of the solvate **1a** were obtained as colorless blocks from the corresponding solution of compound **1** in a variety of ordinary solvents such as ethanol, isopropanol, *t*-butanol, 1,4 dioxane, tetrahydrofurane, *N*,*N*-dimethylformamide, dimethylsulfoxide, and pyridine. The hydrated form **(1a)** was obtained from each solvent which was also confirmed by unit cell parameters. IR (KBr, cm⁻¹): 3340 (s), 3226 (s), 2948 (m), 1768 (m), 1692 (s), 1614 (m), 1529 (w), 1432 (s), 1403 (s), 1367 (s), 1263 (m), 1242 (m), 1199 (m), 1089 (w), 1002 (w), 952 (w), 861 (w), 720 (m). ¹H NMR (400 MHz, DMSO-*d*₆): 8.79 (s, 1H), 8.68 (s, 1H), 7.82 (s, 4H), 6.57 (d, 2H, *J* = 7.6 Hz), 6.39 (d, 1H, *J* = 8.0 Hz), 3.70 (t, 2H, *J* = 7.2 Hz), 3.55 (s, 2H), 2.71 (t, 2H, *J* = 7.2 Hz).

1b: The solvate **1b** was crystallized as brown-colored blocks from the quinoline solution of compound **1**. IR (KBr, cm⁻¹): 3477 (m), 3067 (m), 2944 (m), 1767 (w), 1707 (s), 1617 (m), 1503 (w), 1465 (w), 1434 (m), 1393 (s), 1353 (m), 1298 (w), 1186 (m), 1112 (w), 1087 (w), 955 (w), 944 (w), 805 (m), 787 (m), 721 (m). ¹H NMR (400 MHz, CDC1₃): 8.90 (m, 4H), 8.18 (d, 2H, J = 8.0 Hz), 8.11 (d, 2H, J = 8.4 Hz), 7.82 (d, 2H, J = 8.0 Hz), 7.77 (dd, 2H, J = 3.2 Hz), 7.72 (t, 2H, J = 7.2 Hz), 7.65 (dd, 2H, J = 3.2 Hz), 7.55 (t, 2H, J = 7.2 Hz), 7.42 (dd, 2H, J = 4.0 Hz), 6.79 (d, 2H, J = 8.0 Hz), 6.62 (d, 1H, J = 8.0 Hz), 3.83 (t, 2H, J = 7.6 Hz), 2.82 (t, 2H, J = 7.6 Hz).

2,6-Bis-[2-(3,4-dihydroxyphenyl)ethyl]pyrrolo[3,4-f]isoindole-1,3,-5,7-tetrone (2). A solution of pyromellitic dianhydride (1.09 g, 5 mmol) and dopamine hydrochloride (1.89 g, 10 mmol) in acetic acid (35 mL) was refluxed for 4 h. The reaction mixture was cooled to room temperature, poured into ice-cooled water (100 mL), and

stirred for 15 min. A yellow-colored precipitate of the product was filtered and air-dried. Yield: 90%. IR (KBr, cm⁻¹): 3461 (s), 3410 (s), 2949 (w), 1763 (m), 1702 (s), 1614 (m), 1518 (m), 1433 (m), 1396 (s), 1354 (s), 1302 (m), 1284 (w), 1234 (w), 1192 (m), 1179 (m), 1120 (w), 1096 (w), 1007 (w), 812 (w), 730 (w). ¹H NMR (400 MHz, DMSO- d_6): 8.77 (s, 2H), 8.67 (s, 2H), 8.15 (s, 2H), 6.57 (s, 4H), 6.40 (s, 2H), 3.75 (s, 4H), 2.74 (s, 4H). ¹³C NMR (DMSO- d_6): 166.1, 145.2, 143.8, 136.9, 128.8, 119.3, 117.3, 116.0, 115.6, 33.0. ESI-MS: 489.201 [M + H⁺].

2a: Solvate **2a** was crystallized from a solution of DMF as red block. IR (KBr, cm⁻¹): 3461 (s), 3408 (s), 2924 (w), 1763 (m), 1703 (s), 1661 (m), 1518 (w), 1434 (m), 1395 (s), 1354 (s), 1302 (w), 1283 (w), 1192 (w), 1152 (w), 1120 (m), 1095 (m), 1006 (w), 812 (w), 729 (w). ¹H NMR (400 MHz, DMSO- d_6): 8.80 (s, 2H), 8.70 (s, 2H), 8.16 (s, 2H), 7.94 (s, 2H), 6.57 (dd, 4H, J = 4.4 Hz), 6.40 (d, 2H, J = 8.0 Hz), 3.74 (t, 4H, J = 7.6 Hz), 2.88 (s, 12H), 2.73 (t, 4H, J = 7.6 Hz).

2b: The crystals of solvate **2b** were obtained as yellow blocks from a solution of compound **2** in DMSO. IR (KBr, cm⁻¹): 3461 (s), 3410 (s), 2935 (w), 1763 (m), 1702 (s), 1656 (w), 1620 (m), 1524 (m), 1435 (m), 1396 (s), 1354 (s), 1302 (m), 1284 (w), 1234 (w), 1192 (m), 1179 (m), 1120 (w), 1096 (w), 1075 (m), 1007 (w), 812 (w), 730 (w). ¹H NMR (400 MHz, DMSO- d_6): 8.81 (s, 2H), 8.72 (s, 2H), 8.20 (s, 2H), 6.61 (dd, 4H, J = 4.0 Hz), 6.47 (d, 2H, J = 8.0 Hz), 3.75 (t, 4H, J = 7.6 Hz).

2c: The solvate **2c** was obtained by crystallization of compound **2** from pyridine solution as yellow blocks. IR (KBr, cm⁻¹): 3460 (s), 3410 (s), 2945 (w), 1761 (m), 1707 (s), 1610 (m), 1517 (m), 1432 (m), 1395 (s), 1353 (m), 1297 (w), 1281 (w), 1178 (s), 1119 (s), 1094 (m), 1006 (m), 957 (w), 812 (w), 727 (w). ¹H NMR (400 MHz, DMSO*d*₆): 8.80 (s, 2H), 8.70 (s, 2H), 8.57 (d, 4H, J = 5.6 Hz), 8.16 (s, 2H), 7.84 (t, 4H, J = 7.6 Hz), 7.38 (t, 4H, J = 6.4 Hz), 6.57 (dd, 4H, J = 4.0 Hz), 6.41 (d, 2H, J = 8.0 Hz), 3.76 (t, 4H, J = 7.6 Hz), 2.76 (t, 4H, J = 7.6 Hz).

2d: A solution of compound **2** in pyridine and quinoline resulted in the formation of crystals of solvate **2d** as red blocks. IR (KBr, cm⁻¹): 3460 (s), 3412 (s), 2924 (w), 1763 (m), 1714 (s), 1597 (w), 1503 (w), 1434 (w), 1392 (s), 1353 (s), 1281 (w), 1194 (m), 1121 (m), 1094 (m),, 957 (w), 801 (w), 729 (w). ¹H NMR (400 MHz, DMSO-*d*₆): 8.89 (m, 4H), 8.77 (s, 6H), 8.36 (d, 6H, J = 8.0 Hz), 8.13 (s, 2H), 8.00 (dd, 12H, J = 8.0 Hz), 7.76 (t, 6H, J = 6.8 Hz), 7.61 (t, 6H, J = 6.8 Hz), 7.53 (dd, 6H, J = 4.4 Hz), 6.58 (dd, 4H, J = 4.0 Hz), 6.40 (d, 2H, J = 8.4 Hz), 3.74 (t,4H, J = 7.2 Hz), 2.74 (t, 4H, J =7.2 Hz).

Acknowledgment. The authors thank Department of Science and Technology, New Delhi (India), for financial support. D.S. is thankful to Council of Scientific and Industrial Research, New Delhi (India), for Senior Research Fellowship.

Supporting Information Available: The CIF of the structures are deposited to the Cambridge Crystallographic Database UK and has the CCDC nos. 793834–793840. The PXRD, TG, DSC of the compounds, and hydrogen bond table for 1 and 1b. This material is available free of charge via the Internet at http://pubs.acs.org.

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