Acta Crystallographica Section C Crystal Structure Communications ISSN 0108-2701

3-{[4-Amino-6-methoxy-2-(methylsulfanyl)pyrimidin-5-yl]amino}-1,2'biindenylidene-1',3'-dione dimethyl sulfoxide solvate: π -stacked sheets of hydrogen-bonded chains of edge-fused rings

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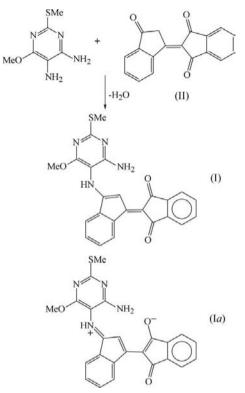
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Received 18 March 2009 Accepted 26 March 2009 Online 18 April 2009

In the title compound, $C_{24}H_{18}N_4O_3S \cdot C_2H_6OS$, the biindenylidene component shows evidence of polarization of the electronic structure. The dimethyl sulfoxide solvent molecules are disordered over two sites, and they are linked to the biindenylidenedione components *via* N-H···O and C-H···O hydrogen bonds. A combination of N-H···N and N-H···O hydrogen bonds links the nonsolvent components into a chain of edge-fused centrosymmetric $R_2^2(8)$ and $R_2^2(22)$ rings, and these chains are linked into sheets by a single aromatic π - π stacking interaction.

Comment

In order to explore synthetic routes to new pyrimido[4,5-*b*]-[1,4]diazepine derivatives incorporating fused and/or spirane residues at the diazepine moiety (of interest in view of their potential biological activity), we have utilized 1,2'-biindenylidene-1',3,3'(2*H*)-trione, (II), prepared by autocondensation of indan-1,3-dione, as a novel chalcone reagent in reactions with 4,5-diaminopyrimidines (Orozco *et al.*, 2008). However, in the reaction with one such 4,5-diaminopyrimidine, *viz.* 4,5diamino-6-methoxy-2-(methylsulfanyl)pyrimidine, rather than the expected 7'*H*-spiro[indene-1,6'-indeno[1,2-*e*]pyrimido-[4,5-*b*][1,4]diazepine]-3,5'-diol, we have obtained instead the title compound, (I), the product of simple condensation at the 5-amino group. A similar condensation was found to occur between the same chalcone reagent and 2,5,6-triaminopyrimidin-4(3*H*)-one, where the condensation product was accompanied by a modest yield of the biindenetrione oxidation product dispiro[indene-2,5'-indeno[2,1-*a*]fluorene-6',2''indene]-1,1'',3,3'',11',12'-hexaone (Orozco *et al.*, 2008). As a continuation of this study, we report here the structure and supramolecular aggregation of the title compound, (I).



The title compound is a stoichiometric monosolvate with dimethyl sulfoxide. The solvent molecules are disordered over two orientations, with refined site occupancies of 0.5505(15) and 0.4495(15) (Fig. 1). For each orientation of the solvent

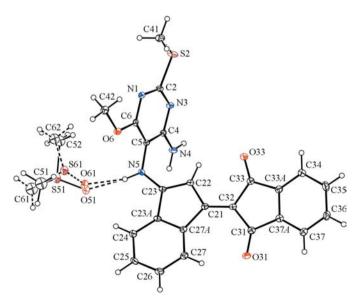


Figure 1

The molecular components of compound (I), showing the atom-labelling scheme. Displacement ellipsoids are drawn at the 30% probability level.

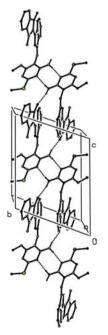
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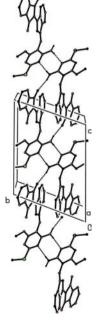
component, the dimethyl sulfoxide molecule is linked to the biindenylidene component by an almost linear $N-H\cdots O$ hydrogen bond (Table 2); there is also a fairly long, but nearly linear, $C-H\cdots O$ hydrogen bond for each orientation of the solvent and these may augment the linkage between the biindenylidene and solvent components. However, the solvent molecules play no other role in the supramolecular aggregation and it is possible that they are present primarily to fill what would otherwise be void space, centred near $(0, 0, \frac{1}{2})$ and amounting to some 23.6% of the total unit-cell volume.

The pyrimidine ring is nearly planar but it shows a slight distortion towards a very shallow boat conformation, with atoms C2 and C5 displaced by 0.036 (3) and 0.039 (3) Å, respectively, to one side of the mean plane, and all the remaining ring atoms displaced to the other side of this plane by distances ranging from 0.011 (3) Å for N3 to 0.026 (3) Å for C4. The rest of the molecular conformation in the nonsolvent molecule can be described in terms of five torsion angles (Table 1). The methyl atoms in the methoxy and methylsulfanyl substituents lie fairly close to the mean plane of the pyrimidine ring, with displacements from the mean plane of this ring of 0.220 (2) and 0.521 (4) Å for atoms S2 and C41, respectively, on one side of the mean plane, and 0.76 (2) and 0.211 (4) Å for atoms O6 and C42, respectively, on the other side. The two five-membered rings of the biindenylidene fragment are not coplanar, and there is a dihedral angle between them of $11.4 (2)^{\circ}$; this may be compared with the corresponding dihedral angle of 6.0° in biindene itself [CSD (Allen, 2002) refcode BIINDO (Bravic et al., 1976); unfortunately, there are no s.u. values associated with the deposited coordinates retrieved from the CSD]. The pyrimidine ring is twisted out of the plane of the adjacent five-membered ring by almost 70° (Table 1). Accordingly, the molecules have no internal symmetry so that they are conformationally chiral, but the centrosymmetric space group accommodates equal numbers of the two enantiomers.

While the bond distances within the pyrimidine unit in (I) show no unusual features, there are some interesting patterns amongst the bond distances in the aminobiindenvlidenedione unit (Table 1). Within the C33A/C34-C37/C37A ring, the range of C–C distances is only 0.013 (5) Å, consistent with normal aromatic delocalization; by contrast, in the C23A/C24-C27/C27A ring, the bond distances show regular alternation, with the C23A-C24, C25-C26 and C27-C27A distances significantly shorter than those for the intermediate bonds, indicative of some bond fixation in this ring (see scheme). In addition, the C23-N5, C21-C22 and C32-C33 bonds are all short for their types (Allen et al., 1987), while the C22-C23 and C21-C32 bonds are long for their types, suggesting some contribution from the polarized form 1-{[4-amino-6-methoxy-2-(methylsulfanyl)pyrimidin-5-yl]iminio}-1'-oxo-3H,1'H-1,2'biinden-3'-olate [see (Ia) in scheme].

In addition to the hydrogen bonds within the selected asymmetric unit (Table 2), two further hydrogen bonds, one each of the $N-H\cdots N$ and $N-H\cdots O$ types, link the nonsolvent molecules into a chain of edge-fused rings from which the solvent molecules are pendent, playing no further role in the hydrogen bonding. Pairs of molecules related by inversion are linked by paired $N-H\cdots N$ hydrogen bonds to form $R_2^2(8)$ (Bernstein *et al.*, 1995) rings, while paired $N-H\cdots O$ hydrogen





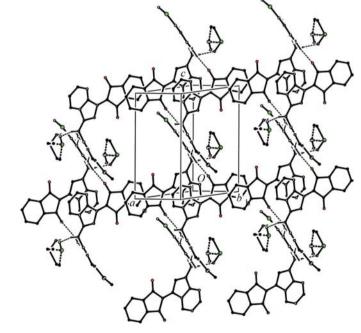


Figure 2

A stereoview of part of the crystal structure of (I), showing the formation of a hydrogen-bonded chain of edge-fused rings along [001]. For clarity, the disordered solvent molecules have been omitted and only the H atoms involved in the motif are included.

Figure 3

A view of part of the crystal structure of (I), showing the formation of a sheet of π -stacked hydrogen-bonded chains. For clarity, H atoms bonded to C atoms have all been omitted.

bonds link pairs of molecules forming a centrosymmetric $R_2^2(22)$ motif. Propagation by inversion of these two hydrogen bonds then generates a chain of edge-fused rings running parallel to the [001] direction in which $R_2^2(8)$ rings centred at $(\frac{1}{2}, \frac{1}{2}, \frac{1}{2} + n)$, where *n* represents an integer, alternate with centrosymmetric $R_2^2(22)$ rings centred at $(\frac{1}{2}, \frac{1}{2}, n)$, where *n* represents an integer (Fig. 2).

Chains of this type are linked into sheets by a single aromatic π - π stacking interaction. The fully aromatic C33*A*/C34-C37/C37*A* rings at (x, y, z) and (2 - x, -y, -z) are strictly parallel with an interplanar spacing of 3.543 (2) Å; the ring-centroid separation is 3.839 (2) Å, corresponding to an almost ideal ring-centroid offset of 1.477 (2) Å. The two molecules involved form parts, respectively, of the hydrogenbonded chains along $(\frac{1}{2}, \frac{1}{2}, z)$ and $(\frac{3}{2}, -\frac{1}{2}, z)$, so that propagation by inversion of this interaction links the chains into a sheet parallel to (110) (Fig. 3).

The supramolecular aggregation of compound (I) may be compared with that in its precursor trione, (II), where a single $C-H\cdots O$ hydrogen bond links the molecules into simple C(4) chains (Bravic *et al.*, 1976; Orozco *et al.*, 2008).

Experimental

A solution of 4,5-diamino-6-methoxy-2-(methylsulfanyl)pyrimidine (1.1 mmol) and 1,2'-biindene-1',3,3'(2H)-trione (1.1 mmol) in a mixture of absolute ethanol (10 ml) and glacial acetic acid (1 ml) was heated under reflux for 6 h, while the progress of the reaction was monitored using thin-layer chromatography. The resulting precipitate was collected by filtration, washed with ethanol, dried and recrystallized from ethanol (yield 57%, m.p. 605 K). Purple crystals of the monosolvate (I) suitable for single-crystal X-ray diffraction were grown from a solution in dimethyl sulfoxide (DMSO).

Crystal data

$C_{24}H_{18}N_4O_3S \cdot C_2H_6OS$	$\gamma = 64.484 \ (7)^{\circ}$
$M_r = 520.71$	V = 1245.6 (2) Å ³
Triclinic, $P\overline{1}$	Z = 2
a = 10.6056 (5) Å	Mo $K\alpha$ radiation
b = 10.9946 (11) Å	$\mu = 0.26 \text{ mm}^{-1}$
c = 12.6770 (11) Å	T = 120 K
$\alpha = 69.780 \ (13)^{\circ}$	$0.21 \times 0.15 \times 0.10 \text{ mm}$
$\beta = 76.523 \ (5)^{\circ}$	

Data collection

Bruker–Nonius KappaCCD
diffractometer
Absorption correction: multi-scan
(SADABS; Sheldrick, 2003)
$T_{\rm min} = 0.922, \ T_{\rm max} = 0.975$

Refinement

 $R[F^2 > 2\sigma(F^2)] = 0.068$ $wR(F^2) = 0.132$ S = 1.045681 reflections 334 parameters H-atom parameters constrained $\Delta \rho_{max} = 0.56 \text{ e} \text{ Å}^{-3}$ $\Delta \rho_{min} = -0.51 \text{ e} \text{ Å}^{-3}$

21189 measured reflections

 $R_{\rm int} = 0.071$

5681 independent reflections

3324 reflections with $I > 2\sigma(I)$

It was apparent from an early stage in the refinement process that the structure contained disordered DMSO molecules, and these were modelled using two orientations to give site occupancies with values

Table 1

Selected geometric parameters (Å, °).

C21-C22	1.423 (4)	C31-C32	1.484 (4)
C22-C23	1.372 (4)	C32-C33	1.485 (4)
C23-C23A	1.479 (4)	C33–C33A	1.490 (4)
C23A-C24	1.372 (4)	C33A-C34	1.382 (4)
C24-C25	1.407 (4)	C34-C35	1.382 (5)
C25-C26	1.379 (5)	C35-C36	1.395 (5)
C26-C27	1.403 (4)	C36-C37	1.382 (5)
C27-C27A	1.375 (4)	C37-C37A	1.386 (4)
C27A-C21	1.501 (4)	C37A-C31	1.493 (4)
C23A-C27A	1.409 (4)	C33A-C37A	1.392 (4)
C21-C32	1.377 (4)	C31-O31	1.227 (3)
C23-N5	1.349 (4)	C33-O33	1.228 (3)
N1-C2-S2-C41	7.9 (3)	C5-N5-C23-C22	-4.9 (4)
N1 - C2 - 32 - C41 N1 - C6 - O6 - C42	3.4 (4)	$C_{22} - C_{21} - C_{32} - C_{31}$	-171.9(3)
C4-C5-N5-C23	69.8 (4)	022-021-032-051	171.9 (3)

Table 2	
Hydrogen-bond geometry (Å, °).	

$D - H \cdots A$	$D-{\rm H}$	$H \cdots A$	$D \cdots A$	$D - \mathbf{H} \cdots A$
N5-H5···O51	0.88	1.97	2.840 (11)	172
N5−H5···O61	0.88	1.93	2.777 (15)	160
$N4-H41\cdots N3^{i}$	0.88	2.17	3.026 (5)	165
N4-H42···O31 ⁱⁱ	0.88	2.13	3.002 (3)	169
C24-H24···O51	0.95	2.51	3.394 (10)	154
C24-H24···O61	0.95	2.56	3.419 (14)	151

Symmetry codes: (i) -x + 1, -y + 1, -z + 1; (ii) -x + 1, -y + 1, -z.

summing to unity within experimental uncertainty and giving final values of 0.5505 (15) (major orientation, S51) and 0.4495 (15) (minor orientation, S61) (Fig. 1). For both orientations of the solvent molecule, the C atoms were refined isotropically; attempts to refine these atom sites anisotropically led to unsatisfactory outcomes. All H atoms were located in difference maps and then treated as riding atoms in geometrically idealized positions, such that the methyl groups were permitted to rotate about the adjacent C-X bonds (X = O or S) but not to tilt, with distances C-H = 0.95 (aromatic) or 0.98 Å (CH₃) and N-H = 0.88 Å, and with $U_{iso}(H) = kU_{iso}(carrier)$, where k = 1.5 for the methyl groups and 1.2 for all other H atoms.

Data collection: *COLLECT* (Hooft, 1999); cell refinement: *DIRAX/LSQ* (Duisenberg *et al.*, 2000); data reduction: *EVALCCD* (Duisenberg *et al.*, 2003); program(s) used to solve structure: *SHELXS97* (Sheldrick, 2008); program(s) used to refine structure: *SHELXL97* (Sheldrick, 2008); molecular graphics: *PLATON* (Spek, 2009); software used to prepare material for publication: *SHELXL97* and *PLATON*.

The authors thank Servicios Técnicos de Investigación of Universidad de Jaén and the staff for data collection. JC thanks the Consejería de Innovación, Ciencia y Empresa (Junta de Andalucía, Spain), the Universidad de Jaén (project reference No. UJA_07_16_33), and Ministerio de Ciencia e Innovación (project reference No. SAF2008-04685-C02-02) for financial support. BI and FO thank COLCIENCIAS and UNIVALLE (Universidad del Valle, Colombia) for financial support. Supplementary data for this paper are available from the IUCr electronic archives (Reference: GG3196). Services for accessing these data are described at the back of the journal.

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