

C—C bonds and C—C—C angles within the ring (Fig. 2). Thus, the distortions arise mainly from the electronic structure and to a lesser degree from the molecular interaction as well as from the crystal packing forces. The S—O bonds of the SO₃[−] group are all intermediate in length between double S=O and single bonds (Allen *et al.*, 1987), indicating charge delocalization on to all O atoms of this group.

The C—S bond length in the crystal structure is shorter than that calculated for the gas-phase structure (1.841 Å), owing to the interactions of negatively charged SO₃[−] groups with the π -aromatic ring. In the crystal structure, this interaction decreases as a result of the hydrogen-bonding system, which reduces the charge on the SO₃[−] groups. The small differences between the experimental S—O bond lengths result from the strengths of the hydrogen bonds in which the O atoms are involved (Table 2).

The acidic H atom is dihydrated such that pairs of water molecules are joined together *via* a short O—H...O hydrogen bond to form a discrete H₅O₂⁺ ion. However, the acidic H atom is not located at the centre between the O atoms, but closer to one of the two water molecules (Table 2). This is in contrast to the results of molecular orbital (MO) calculations performed for an isolated H₅O₂⁺ cation, which is predicted to be symmetric (O...O = 2.42 Å, O—H = 1.21 Å and O—H—O = 177°), although in the crystal structure the cation is nonsymmetrical. *Ab initio* MO calculations indicate that substantial energy is involved in the hydration of the hydronium ion (*e.g.* H₃O⁺ + H₂O = H₅O₂⁺, 37 kcal mol^{−1}). The H₅O₂⁺ ion has a *gauche* conformation, with a dihedral angle of 99.5°, as defined by the dihedral angle between the O4/H41/H42 and O5/H51/H52 planes. Thus, the bonding arrangement together with the lone pair of electrons around each O atom in H₅O₂⁺ is tetrahedral. However, because of the hydrogen-bonding system and, especially, the lone pair of electrons on both O atoms, the tetrahedron is significantly distorted, since the lone pair of electrons affords a wider region than the bonding pair, as predicted by the valence-shell electron-pair repulsion model (Gillespie, 1963, 1992).

The molecular arrangement in the crystal structure of (I) is mainly determined by relatively strong and directional hydrogen bonds (Table 2), and to a lesser degree by a π – π interaction between the naphthalene ring systems, where the interplanar spacing is *ca* 3.53 Å (Fig. 3). This value is comparable to the sum of the C-atom van der Waals radii of

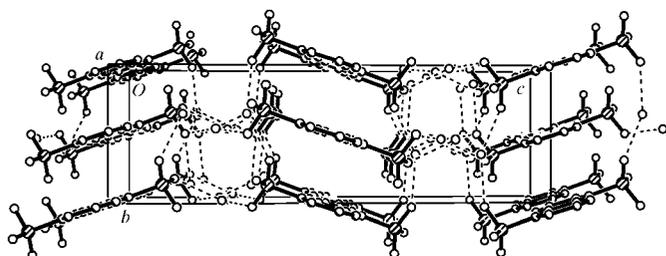


Figure 3

A view of the crystal packing in (I), showing the three-dimensional hydrogen-bonded network. H atoms have been omitted for clarity.

the π -ring system (Pauling, 1967). However, as a result of the mutual shift of the rings, the π – π interaction is not fully effective. The π – π overlapping between the rings takes place only *via* the outermost C—C bonds (C1—C5ⁱ and C5—C1ⁱ). The naphthalene-1,5-disulfonate anions are stacked in the crystal structure along the *b* axis at *z* = 0 and *z* = $\frac{1}{2}$, and they make an angle of 17.7° with the (010) plane, so forming sheets parallel to (001). The H₅O₂⁺ cations are located between these sheets and join together *via* O—H...O hydrogen bonds into a three-dimensional network. Each H₅O₂⁺ cation links four anions. Atom O1 of the SO₃[−] group is involved in two hydrogen bonds, while the other two O atoms of SO₃[−] are each involved in one hydrogen bond (Table 2).

Experimental

Suitable crystals of (I) were obtained by slow evaporation of an aqueous solution of naphthalene-1,5-disulfonic acid. MO calculations were performed using GAUSSIAN98 (Frisch *et al.*, 1998).

Crystal data

2H ₅ O ₂ ⁺ ·C ₁₀ H ₆ O ₆ S ₂ ^{2−}	<i>V</i> = 1481.3 (5) Å ³
<i>M_r</i> = 360.37	<i>Z</i> = 4
Monoclinic, <i>C2/c</i>	Mo <i>K</i> α radiation
<i>a</i> = 9.1183 (18) Å	μ = 0.41 mm ^{−1}
<i>b</i> = 7.1051 (14) Å	<i>T</i> = 295 (2) K
<i>c</i> = 22.954 (4) Å	0.32 × 0.28 × 0.11 mm
β = 95.08 (1)°	

Data collection

Kuma KM-4 diffractometer with CCD area detector	9288 measured reflections
Absorption correction: analytical, face-indexed (SHELXTL; Sheldrick, 1990b)	1835 independent reflections
<i>T_{min}</i> = 0.884, <i>T_{max}</i> = 0.961	1575 reflections with <i>I</i> > 2σ(<i>I</i>)
	<i>R_{int}</i> = 0.017

Refinement

<i>R</i> [<i>F</i> ² > 2σ(<i>F</i> ²)] = 0.030	H atoms treated by a mixture of independent and constrained refinement
<i>wR</i> (<i>F</i> ²) = 0.077	$\Delta\rho_{\max}$ = 0.28 e Å ^{−3}
<i>S</i> = 1.06	$\Delta\rho_{\min}$ = −0.28 e Å ^{−3}
1835 reflections	
116 parameters	

Table 1

Selected geometric parameters (Å, °).

S1—O3	1.4431 (12)	C1—C5 ⁱ	1.406 (2)
S1—O2	1.4475 (11)	C2—C3	1.4281 (18)
S1—O1	1.4683 (11)	C3—C4	1.411 (2)
S1—C2	1.7703 (13)	C3—C3 ⁱ	1.431 (2)
C1—C2	1.361 (2)	C4—C5	1.357 (2)
O3—S1—O2	113.54 (7)	O3—S1—C2	107.27 (7)
O3—S1—O1	111.35 (7)	O2—S1—C2	106.80 (7)
O2—S1—O1	111.02 (7)	O1—S1—C2	106.42 (6)

Symmetry code: (i) $-x + 1, -y, -z + 1$.

H atoms bonded to C atoms were treated as riding in geometrically idealized positions, with C—H distances of 0.93 Å and *U*_{iso}(H) values of 1.2*U*_{eq}(C). H atoms bonded to O atoms were located in difference maps and their coordinates were refined [with *U*_{iso}(H) = 1.5*U*_{eq}(O)], giving a range of O—H distances of 0.80 (4)–0.86 (4) Å for the terminal H atoms, and distances of 1.02 (4) and 1.42 (4) Å for the bridging H atom.

Table 2

Hydrogen-bond geometry (Å, °).

<i>D</i> —H... <i>A</i>	<i>D</i> —H	H... <i>A</i>	<i>D</i> ... <i>A</i>	<i>D</i> —H... <i>A</i>
O4—H2...O5	1.02 (4)	1.42 (4)	2.416 (2)	163 (3)
O4—H41...O1	0.86 (3)	1.76 (3)	2.6059 (19)	167 (2)
O4—H42...O2 ⁱⁱ	0.82 (3)	1.83 (3)	2.6294 (17)	164 (2)
O5—H51...O3 ⁱⁱⁱ	0.80 (4)	1.90 (4)	2.6562 (19)	156 (4)
O5—H52...O1 ^{iv}	0.86 (4)	1.83 (4)	2.6891 (19)	171 (4)

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

Data collection: *CrysAlis CCD* (Oxford Diffraction, 2005); cell refinement: *CrysAlis CCD*; data reduction: *CrysAlis RED* (Oxford Diffraction, 2005); program(s) used to solve structure: *SHELXS97* (Sheldrick, 1990a); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *SHELXTL* (Sheldrick, 1990b); software used to prepare material for publication: *SHELXL97*.

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Supplementary data for this paper are available from the IUCr electronic archives (Reference: GD3169). Services for accessing these data are described at the back of the journal.

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