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Key indicators

Single-crystal X-ray study T = 150 KMean $\sigma(C-C) = 0.003 \text{ Å}$ R factor = 0.039 wR factor = 0.105 Data-to-parameter ratio = 11.3

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

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2-Amino-6-nitrobenzo-1,3-thiazole hydrate

The structure of the title compound, $C_7H_5N_3O_2S \cdot H_2O$, comprises molecules of the thiazole in an extensive hydrogen-bonding network with lattice water molecules. The essentially planar thiazole forms centrosymmetric, hydrogenbonded dimers *via* a pair of $N-H \cdot \cdot \cdot N$ ($H \cdot \cdot \cdot N$ 2.11 Å) associations. The second amino H atom hydrogen bonds to the water O atom, while the water associates to one nitro O atom and two other water molecules. Complexity in the hydrogenbonding network arises because the water molecule is close to an inversion centre, thus producing an $Ow \cdot \cdot Ow$ interaction.

Comment

A multitude of crystal structures of 2-aminobenzo-1,3-thiazole and its derivatives have been determined and provide an interesting subset of compounds in the 2-amino-1,3-thiazole range. Of the structures reported, most are pure organics that have fragments attached to the amino N atom. The structure of 2-aminobenzo-1,3-thiazole itself is unknown, but of the ring-substituted compounds, the structures of the 6-fluoro (Jainhuknan et al., 1997), and both 4-nitro (Lokaj et al., 1996) and 6-nitro (Glidewell et al., 2001) analogues have been determined. In these three cases, the recorded hydrogen-bonding patterns are noteworthy, as well as the bond distances in the two nitro derivatives. In 2-amino-4-nitrobenzo-1,3-thiazole, the C–NH₂ and ring C–N distances are equal to within 2σ [1.315 (2) and 1.312 (2) Å, respectively], a feature indicating complete π -electron delocalization. The corresponding bond distances in 2-amino-6-nitrobenzo-1,3-thiazole are 1.331 (3) and 1.321 (3) Å, and in 2-amino-6-fluorobenzo-1,3-thiazole are 1.358 (2) and 1.295 (2) Å, respectively [average values: 1.336 (17) and 1.313 (11) Å; Allen et al., 1987]. The hydrogenbonding patterns in all three structures include a dimer formation about the N21-H···N3 association and, for both nitro analogues, at least one nitro O atom is also involved in the hydrogen-bonding array.



In this paper, the single-crystal structure of 2-amino-6nitrobenzo-1,3-thiazole hydrate, (I), is reported as an addition to the non-hydrate structure. The hydrate structure was obtained from attempts to produce adducts of 2-amino-6nitrobenzo-1,3-thiazole with aromatic carboxylic acids, as performed for 2-aminobenzo-1,3-thiazole (Lynch *et al.*, 1998, 1999). Received 12 September 2002 Accepted 18 September 2002 Online 27 September 2002

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The molecular configuration and atom-numbering scheme for the title compound, showing 50% probability ellipsoids.

The structure of (I) (Fig. 1) comprises the thiazole molecule associated in an extensive hydrogen-bonded network with the water molecule. Hydrogen-bonding parameters are listed in Table 2. The bond lengths across the N21–C2–N3 site show a similar pattern to the 4-nitro analogue, with both bond lengths being equal [1.320 (3) Å]. The formation of dimers *via* the N21–H···N3 association is expected for this type of compound, but the location of the water molecule so near to a symmetry element provides an interesting hydrogen-bonding network (Fig. 2). The water network extends parallel to the *a* axis, while the thiazole molecules are inclined to the (100) plane. The water O atom is bound by the second amino H atom, while H1W associates to a nitro O atom. The suggested position of H2W allows for a three-centre association, linking two symmetry-generated water molecules.

Experimental

Crystals of the title compound were separated from a partially evaporated ethanol solution containing an equimolar amount of 3-aminobenzoic acid.

Crystal data

$C_7H_5N_3O_2S \cdot H_2O$	
$M_r = 213.22$	
Monoclinic, $P2_1/c$	
a = 3.8930(2) Å	
b = 10.8743 (5) Å	
c = 20.6378 (8) Å	
$\beta = 91.335 \ (4)^{\circ}$	
$V = 873.44 (7) \text{ Å}^3$	
Z = 4	

Data collection

Bruker–Nonius KappaCCD area-
detector diffractometer
φ and ω scans
Absorption correction: multi-scan
(SORTAV; Blessing, 1995)
$T_{\min} = 0.933, T_{\max} = 0.970$
5105 measured reflections

Refinement

Refinement on F^2 $R[F^2 > 2\sigma(F^2)] = 0.039$ $wR(F^2) = 0.105$ S = 1.141504 reflections 133 parameters H-atom parameters constrained

D = 1 (21) M = -3						
$D_x = 1.621 \text{ Mg m}^{-3}$						
Mo $K\alpha$ radiation						
Cell parameters from 5386						
reflections						
$\theta = 2.9 - 32.0^{\circ}$						
$\mu = 0.35 \text{ mm}^{-1}$						
T = 150 (2) K						
Block, yellow						
$0.20 \times 0.15 \times 0.10 \text{ mm}$						

1504 independent reflections 1247 reflections with $I > 2\sigma(I)$ $R_{int} = 0.037$ $\theta_{max} = 25.0^{\circ}$ $h = -4 \rightarrow 4$ $k = -12 \rightarrow 12$ $l = -20 \rightarrow 24$

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w = 1/[\sigma^{2}(F_{o}^{2}) + (0.0469P)^{2} + 0.3321P]
where P = (F_{o}^{2} + 2F_{c}^{2})/3
(\Delta/\sigma)_{max} < 0.001
\Delta\rho_{max} = 0.32 \text{ e} \text{ Å}^{-3}
\Delta\rho_{min} = -0.25 \text{ e} \text{ Å}^{-3}
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Figure 2

Packing diagram for the title compound. Hydrogen-bonding associations are shown as dotted lines.

Table 1

Selected interatomic distances (Å).

S1-C8	1.740 (2)	C2-N3	1.320 (3)
S1-C2	1.766 (2)	C2-N21	1.320 (3)

Table 2

Hydrogen-bonding geometry (Å, °).

$D - H \cdots A$	D-H	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - \mathbf{H} \cdot \cdot \cdot A$
$N21 - H21 \cdots N3^{i}$	0.88	2.11	2.970 (3)	165
$N21 - H22 \cdot \cdot \cdot O1W^{ii}$	0.88	2.11	2.946 (3)	159
$O1W - H1W \cdot \cdot \cdot O61^{iii}$	0.84	2.06	2.894 (3)	175
$O1W - H2W \cdot \cdot \cdot O1W^{iv}$	0.81	2.17	2.772 (6)	132
$O1W - H2W \cdots O1W^{v}$	0.81	2.30	2.651 (8)	107

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

All thiazole H atoms were included in the refinement, at calculated positions, as riding models, with C-H set to 0.95 Å and N-H set to 0.88 Å. H1W was initially located in a difference synthesis, while H2W was generated at the most probable position based on the position of H1W and the positions of adjacent symmetry-generated water molecules. Both H1W and H2W were restrained to an O-H distance of 0.83 Å and an H···H distance of 1.35 Å, while displacement parameters were refined as riding models.

Data collection: *DENZO* (Otwinowski & Minor, 1997) and *COLLECT* (Hooft, 1998); cell refinement: *DENZO* and *COLLECT*; data reduction: *DENZO* and *COLLECT*; program(s) used to solve structure: *SHELXS*97 (Sheldrick, 1997); program(s) used to refine

structure: *SHELXL*97 (Sheldrick, 1997); molecular graphics: *PLATON*97 (Spek, 1997); software used to prepare material for publication: *SHELXL*97.

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