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Graham Smith,^a* Urs D. Wermuth^a and Jonathan M. White^b

^aCentre for Instrumental and Developmental Chemistry, Queensland University of Technology, GPO Box 2434, Brisbane 4001, Australia, and ^bSchool of Chemistry, University of Melbourne, Parkville, Vic. 3052, Australia

Correspondence e-mail: g.smith@qut.edu.au

Key indicators

Single-crystal X-ray study T = 293 K Mean σ (C–C) = 0.002 Å R factor = 0.037 wR factor = 0.098 Data-to-parameter ratio = 12.2

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

The 1:1 proton-transfer compound of sulfanilamide with 3,5-dinitrosalicylic acid

The crystal structure of the proton-transfer compound from the reaction of 3,5-dinitrosalicylic acid (DNSA) with sulfanilamide (ABSA), *i.e.* 4-sulfonamidoanilinium 3,5-dinitrosalicylate, $C_6H_9N_2O_2S^+ \cdot C_7H_3N_2O_7^-$, shows an extensively hydrogenbonded polymeric structure in which the protonated amino group of sulfanilamide together with the amide group give a total of eight intermolecular interactions with most of the O atoms of the DNSA anions [N···O 2.822 (2)–3.172 (2) Å], together with both of the sulfonate O atoms of adjacent ABSA cations [N···O 2.867 (2) and 3.090 (2) Å].

Comment

3,5-Dinitrosalicylic acid (DNSA) provides one of the best chemical synthons for the construction of hydrogen-bonded structural motifs. The acid has provided examples of polymorphism in which associations with solvent molecules such as water (two examples), dioxane (four examples) and tert-butyl alcohol (one example) give a variety of hydrogen-bonded molecular assemblies (Smith et al., 1995; Kumar et al., 1999). The low pK_a of the acid (2.18) also means that with Lewis bases, protonation of the hetero-N atom usually occurs, giving further promotion of hydrogen bonding. We have synthesized and determined the structures of the proton-transfer compounds with the isomeric aminobenzoic acids (Smith et al., 1995), viz. 3-amino-1H-1,2,4-triazole (Smith et al., 1996), 8aminoquinoline (Smith, Wermuth, Bott et al., 2001), 8hydroxyquinoline (Smith, Wermuth & White, 2001), guanidine (Smith et al., 2001a) and 8-quinolylurea (Smith et al., 2001b). All of these are 1:1 except for the 1:2 adduct with 4-aminobenzoic acid.



In a continuation of the study of the nature of the interactions of DNSA with Lewis bases, reaction with sulfanilamide (4-aminobenzenesulfonamide, ABSA), gave large yellow crystals of the title compound [(ABSA)⁺(DNSA)⁻], (I). The structure determination has shown that the amine group of sulfanilamide is protonated (Fig. 1), subsequently giving an

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Figure 1

The molecular configuration and atom-numbering scheme for (I) with atoms shown as 30% probability ellipsoids.



Figure 2

Packing in the unit cell, showing hydrogen-bonding associations as broken lines.

extensively hydrogen-bonded network polymer in which all ABSA H atoms are involved in a total of eight associations [five to the protonated amine (two three-centred); three to the amide (one three-centred)], with DNSA oxygen acceptors or sulfonate O atoms of other ABSA molecules.

The sulfanilamide cations form centrosymmetric hydrogenbonded cyclic dimers through the sulfonamide groups $[N4-H4C \cdots O9\ 2.867\ (2)$ Å; symmetry code: -x, 2 - y, 2 - z] (Fig. 2). These dimers are linked by weak hydrogen bonds $[C10-H10 \cdots O8\ 3.171\ (2)$ Å; symmetry code: 1 - x, y, z] to form infinite chains extending along the *a* axis of the cell. Hydrogen bonds between the protonated amine groups and sulfanilamide O atoms $[N3-H3A\cdots O8\ 3.090\ (2)$ Å; symmetry code: 1 - x, 1 - y, 2 - z] form a two-dimensional network parallel to (001). The 3,5-dinitrosalicylate anions are stacked down the *a* cell direction and are linked peripherally to the ABSA framework sheets by $N-H\cdots O$ hydrogen bonds (Table 1). The usual intramolecular hydrogen bonding is found between the phenolic O atom and the *anti*-related H atom on the carboxyl group $[O2-H1\cdots O1 \ 2.462 \ (2) \ \text{Å}]$, comparing closely with the mean for the current series (2.461 Å). This arrangement with the H atom located on the carboxyl O atom rather than the phenolic O atom is found in 75% of the known proton-transfer compounds of DNSA with Lewis bases (Smith, Bott, Wermuth *et al.*, 2001).

Experimental

The synthesis of the title compound was carried out by heating, under reflux for 10 min, 1 mmol quantities of 3,5-dinitrosalicylic acid and sulfanilamide (4-aminobenzenesulfonamide) in 30 ml of 80% ethanol/water. Crystals were obtained after partial room-temperature evaporation of the solvent.

Z = 2

 $D_x = 1.702 \text{ Mg m}^{-3}$

Cell parameters from 25

Mo $K\alpha$ radiation

reflections

T = 293 (2) K

Prismatic, yellow

 $0.35 \times 0.25 \times 0.20$ mm

 $\begin{aligned} \theta &= 12\text{--}15^{\circ} \\ \mu &= 0.27 \text{ mm}^{-1} \end{aligned}$

Crystal data

 $\begin{array}{l} C_{7}H_{3}N_{2}O_{7}^{+}\cdot C_{6}H_{9}N_{2}O_{2}S^{-}\\ M_{r}=400.33\\ \text{Triclinic, }P\overline{1}\\ a=7.0167~(9)~\text{\AA}\\ b=9.137~(1)~\text{\AA}\\ c=12.430~(1)~\text{\AA}\\ \alpha=90.77~(1)^{\circ}\\ \beta=99.736~(9)^{\circ}\\ \gamma=95.70~(1)^{\circ}\\ V=781.17~(15)~\text{\AA}^{3} \end{array}$

Data collection

Nonius CAD-4 diffractometer $h = 0 \rightarrow 9$ $\omega - 2\theta$ scans $k = -11 \rightarrow 11$ 3867 measured reflections $l = -16 \rightarrow 15$ 3575 independent reflections3 standard reflections3080 reflections with $I > 2\sigma(I)$ frequency: 160 min $R_{int} = 0.010$ intensity decay: 5.0%

Refinement

Refinement on F^2 $R[F^2 > 2\sigma(F^2)] = 0.037$ $wR(F^2) = 0.098$ S = 1.053575 reflections 293 parameters All H-atom parameters refined $w = 1/[\sigma^{2}(F_{o}^{2}) + (0.0482P)^{2} + 0.3779P]$ where $P = (F_{o}^{2} + 2F_{c}^{2})/3$ $(\Delta/\sigma)_{max} = 0.006$ $\Delta\rho_{max} = 0.39 \text{ e}^{\Lambda^{-3}}$ $\Delta\rho_{min} = -0.35 \text{ e}^{\Lambda^{-3}}$ Extinction correction: *SHELXL97* (Sheldrick, 1997) Extinction coefficient: 0.008 (2)

Table 1Hydrogen-bonding geometry (Å, $^{\circ}$).

$D - H \cdot \cdot \cdot A$	D-H	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - \mathbf{H} \cdot \cdot \cdot A$
02-H1···O1	1.03 (4)	1.48 (4)	2.462 (2)	157 (3)
$N3-H3A\cdotsO6^{i}$	0.82 (3)	2.53 (2)	3.172 (2)	137 (2)
N3-H3A···O8 ⁱⁱ	0.82 (3)	2.46 (3)	3.090 (2)	135 (2)
N3−H3 <i>B</i> ···O3	0.84 (3)	2.10 (3)	2.934 (2)	170 (3)
$N4-H4A\cdots O1^{iii}$	0.91 (3)	1.93 (3)	2.822 (2)	166 (3)
$N4-H4A\cdots O7^{iii}$	0.91 (3)	2.41 (3)	2.870 (2)	111.2 (19)
$N4-H4B\cdots O2^{iv}$	0.93 (3)	2.01 (3)	2.926 (2)	172 (2)
$N4 - H4B \cdot \cdot \cdot O4^{v}$	0.93 (3)	2.51 (3)	2.880 (2)	104 (2)
$N4-H4C\cdots O9^{v}$	0.89(2)	1.97 (2)	2.867 (2)	176 (2)
$C4-H4\cdots O5$	0.88 (3)	2.42 (3)	2.711 (2)	100.0 (18)
C9−H9···O7 ^{vi}	0.94(2)	2.57 (2)	3.414 (2)	150.6 (16)
$C10-H10\cdots O8^{vii}$	0.96 (2)	2.43 (2)	3.171 (2)	133.5 (16)
C13-H13···O8	0.89 (2)	2.53 (2)	2.896 (2)	105.3 (15)

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

H atoms were located from a difference map and both positional and isotropic displacement parameters were refined. For H atoms: C-H range 0.88 (2)–0.96 (2) Å; N-H range 0.81 (3)–0.93 (3) Å, and the intramolecular O-H distance is 1.03 (4) Å.

Data collection: *CAD-4 Software* (Enraf–Nonius, 1989); cell refinement: *CAD-4 Software*; data reduction: *PROCESS DATA* (Gable *et al.*, 1994); program(s) used to solve structure: *SHELXS97* (Sheldrick, 1997); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *PLATON for Windows* (Spek, 1999).

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