

Salicylaldoximum 3,5-dinitrosalicylate dihydrate

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Key indicators

Single-crystal X-ray study

T = 295 K

Mean $\sigma(\text{C}-\text{C}) = 0.003 \text{ \AA}$

R factor = 0.048

wR factor = 0.110

Data-to-parameter ratio = 10.4

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

The crystal structure of the dihydrate of the 1:1 proton-transfer compound of 3,5-dinitrosalicylic acid with 2-hydroxybenzaldehyde oxime (salicylaldoxime), $\text{C}_7\text{H}_8\text{NO}_2^+ \cdot \text{C}_7\text{H}_3\text{N}_2\text{O}_7^- \cdot 2\text{H}_2\text{O}$, is a three-dimensional hydrogen-bonded polymer. In this, the oxime-N atom of salicylaldoxime is protonated and, together with the adjacent O—H group, gives primary cyclic asymmetric hydrogen-bonding associations with both carboxyl O atoms of the acid. These, together with hydrogen-bonding interactions among all species present, including the two water molecules, give an essentially planar ten-membered ring. Peripheral hydrogen bonding also links the water molecules to carboxyl and nitro-O atoms, giving rise to a three-dimensional polymer structure.

Comment

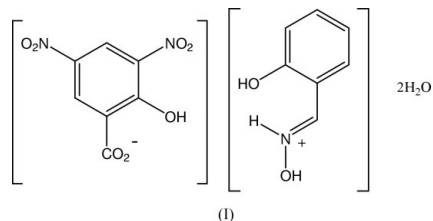
3,5-Dinitrosalicylic acid (DNSA) ($\text{pK}_a = 1.8$) is a sufficiently strong acid to protonate most amines with which it reacts (Issa *et al.*, 1980). Most compounds involving this molecule are, therefore, proton-transfer types, while others involving bases with particularly small pK_a values may form molecular complexes, which may or may not involve π - π stacking and electron transfer. The 1:1 adduct of the weak base phenazine ($\text{pK}_a = 1.2$) (Kumar *et al.*, 2002) is a rare example of a crystallographically characterized DNSA–Lewis base compound in which no proton transfer or electron transfer occurs. Other neutral DNSA complexes involving non-Lewis bases are more common, *e.g.* with urea (Smith *et al.*, 1997) and 1,1-diethylurea (Smith *et al.*, 2000) (both 1:1), and the pseudo-polymorphic solvate structures with water (two polymorphs: Smith *et al.*, 1995; Kumar *et al.*, 1999), 1,4-dioxane (four polymorphs: Kumar *et al.*, 1999) and *tert*-butyl alcohol (one polymorph: Kumar *et al.*, 1999). It was considered that, with a weak base such as an oxime, proton transfer may not occur with common carboxylic acids, *e.g.* the acetophenone oxime–benzoic acid compound (Maurin *et al.*, 1993) is non-transfer. Salicylaldoxime (SALOX) is a common analytical reagent used for the selective precipitation of copper(II) and palladium(II) (Vogel, 1964), achieved *via* formation of neutral square-planar bis-chelate complexes through both the phenolate-O ($\text{pK}_a = 9.1$) and the neutral oxime-N donor atoms. The structures of these complexes of SALOX with copper(II) (Jarski & Lingafelter, 1964) and palladium(II) (Pfluger *et al.*, 1970) are known, together with that of nickel(II), which is isomorphous with the Pd complex (Srivastava *et al.*, 1967). Examples of complexes involving these, as well as other metals and often with mixed ligands, *e.g.* platinum(II) (Kaplan *et al.*, 2001), nickel(II) (Lalia-Kantouri *et al.*, 1999) and tin(IV) (Willem *et al.*, 1996; Mercier *et al.*, 1998) are also known.

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With SALOX, the protonation of the oxime-N atom ($pK_a = 11.4$) might be considered feasible, particularly in the presence of carboxylic acids such as DNSA. This was found to be the case with the 1:1 compound reported here, obtained from the reaction of DNSA with SALOX, the dihydrate $\text{SALOX}^+\cdot\text{DNSA}^-\cdot 2\text{H}_2\text{O}$, (I).



In (I), the oxime-N atom of SALOX is protonated and is subsequently involved in a three-centred hydrogen-bonding interaction: an intramolecular hydrogen bond with the phenolic O atom of SALOX [N71—H71A···O21 2.645 (2) Å] and an intermolecular hydrogen bond to a carboxylate O atom [N71—H71A···O72 2.808 (2) Å] (Fig. 1). This intramolecular association in SALOX in (I) is similar to that found in the hydrogen-bonded cyclic dimeric structure of the parent oxime (Pfluger & Harlow, 1973). Completing an asymmetric cyclic $R_2^2(7)$ association in (I) is a strong O—H(oxime)···O(carboxyl) hydrogen bond [O81—H81···O71 2.556 (2) Å]. The two water molecules, together with the SALOX cation and the DNSA anion, complete a ten-membered and essentially planar hydrogen-bonded ring. This is extended peripherally in the b -axis direction, through the water molecules [O1W···O71ⁱ; symmetry code: (i) $x, 1 + y, z$] and *via* an n -glide operation [O2W···O32ⁱⁱ; symmetry code: (ii) $-x + \frac{1}{2}, y + \frac{1}{2}, -z + \frac{1}{2}$] (Fig. 2 and Table 1), to give a three-dimensional polymer structure.

The usual intramolecular hydrogen bond is found between the phenolic H atom and a carboxylate-O atom of DNSA [O2—H2···O72 2.431 (2) Å], making this one of the minority examples among proton-transfer compounds of DNSA, where the proton is located on the phenol group rather than the carboxyl group (Smith *et al.*, 2002, 2002a,b).

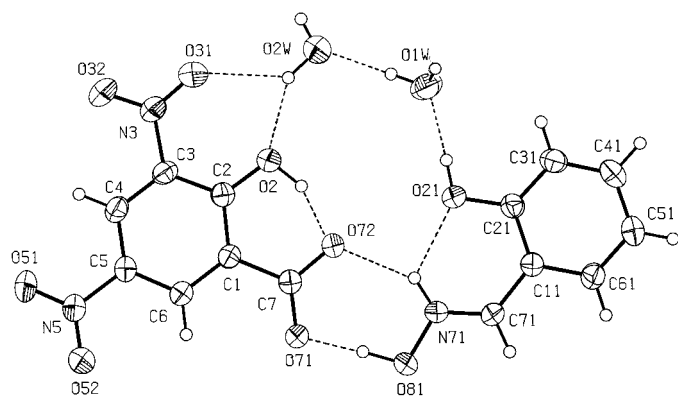


Figure 1
The molecular structure and atom-labelling scheme for the individual DNSA[−], SALOX⁺ and water molecules in (I). Non-H atoms are drawn as 40% probability ellipsoids

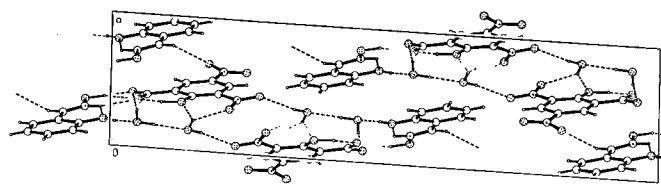


Figure 2
Perspective view of the packing in the unit cell, showing hydrogen-bonding associations as broken lines.

Experimental

The synthesis of the title compound, (I), was carried out by heating 1 mmol quantities of 3,5-dinitrosalicylic acid (DNSA) and 2-hydroxybenzaldehyde oxime (salicylaldehyde oxime = SALOX) in 50 ml of 80% ethanol/water for 10 min under reflux. After concentration to *ca* 30 ml, partial room-temperature evaporation of the hot-filtered solution gave yellow crystals (m.p. 375.5–379.0 K), suitable for X-ray analysis.

Crystal data

$\text{C}_7\text{H}_8\text{NO}_2^+\cdot\text{C}_7\text{H}_3\text{N}_2\text{O}_7^-\cdot 2\text{H}_2\text{O}$
 $M_r = 401.29$
 Monoclinic, $P2_1/n$
 $a = 7.0077$ (4) Å
 $b = 8.5126$ (5) Å
 $c = 28.5138$ (15) Å
 $\beta = 92.979$ (1) $^\circ$
 $V = 1698.66$ (17) Å³
 $Z = 4$

$D_x = 1.569$ Mg m^{−3}
 Mo $K\alpha$ radiation
 Cell parameters from 9872 reflections
 $\theta = 2.5$ – 25.0 $^\circ$
 $\mu = 0.14$ mm^{−1}
 $T = 295$ (2) K
 Block, yellow
 0.50 × 0.30 × 0.10 mm

Data collection

Bruker CCD area detector diffractometer
 φ and ω scans
 Absorption correction: none
 11631 measured reflections
 2985 independent reflections

2898 reflections with $I > 2\sigma(I)$
 $R_{\text{int}} = 0.019$
 $\theta_{\text{max}} = 25.0$ $^\circ$
 $h = -8 \rightarrow 8$
 $k = -10 \rightarrow 10$
 $l = -33 \rightarrow 33$

Refinement

Refinement on F^2
 $R[F^2 > 2\sigma(F^2)] = 0.048$
 $wR(F^2) = 0.110$
 $S = 1.21$
 2985 reflections
 286 parameters
 H atoms treated by a mixture of independent and constrained refinement

$w = 1/[\sigma^2(F_o^2) + (0.0322P)^2 + 0.9115P]$
 where $P = (F_o^2 + 2F_c^2)/3$
 $(\Delta/\sigma)_{\text{max}} = 0.003$
 $\Delta\rho_{\text{max}} = 0.28$ e Å^{−3}
 $\Delta\rho_{\text{min}} = -0.20$ e Å^{−3}
 Extinction correction: *SHELXTL*
 Extinction coefficient: 0.0094 (12)

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

D—H···A	D—H	H···A	D···A	D—H···A
O1W—H1A···O71 ⁱ	0.93 (4)	1.95 (4)	2.853 (2)	164 (3)
O1W—H1B···O2W	0.89 (3)	1.84 (3)	2.733 (3)	178 (3)
O2—H2···O72	1.07 (3)	1.40 (3)	2.431 (2)	161 (3)
O2W—H2A···O2	0.94 (4)	1.98 (4)	2.822 (3)	148 (3)
O2W—H2A···O31	0.94 (4)	2.17 (4)	2.911 (3)	134 (3)
O2W—H2B···O32 ⁱⁱ	0.80 (4)	2.15 (4)	2.947 (3)	173 (4)
O21—H21···O1W	0.91 (3)	1.68 (3)	2.590 (2)	176 (3)
N71—H71A···O21	0.92 (3)	2.05 (3)	2.645 (2)	121 (2)
N71—H71A···O72	0.92 (3)	2.00 (3)	2.808 (2)	145 (2)
O81—H81···O71	1.02 (3)	1.54 (3)	2.556 (2)	177 (2)
O81—H81···O72	1.02 (3)	2.50 (3)	3.162 (2)	121.9 (18)
C71—H71···O52 ⁱⁱⁱ	0.93	2.39	3.280 (3)	160

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

H atoms involved in hydrogen-bonding interactions (H2, H1A, H1B, H2A, H2B, H71A and H81) were located in difference maps and their positional and isotropic displacement parameters refined. Other H atoms were included in the refinement at calculated positions in the riding-model approximation. For refined H atoms, the oxime N–H distance is 0.92 (3) Å, the hydroxyl O–H range is 0.91 (3)–1.07 (3) Å and the water O–H range is 0.80 (4)–0.94 (4) Å.

Data collection: *SMART* (Bruker, 2000); cell refinement: *SMART*; data reduction: *SAINTE* (Bruker, 1999); program(s) used to solve structure: *SHELXTL* (Bruker, 1997); program(s) used to refine structure: *SHELXTL*; molecular graphics: *PLATON* for Windows (Spek, 1999); software used to prepare material for publication: *SHELXTL*.

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