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Three salts from the reactions of cysteamine and cystamine with L-(+)-tartaric acid

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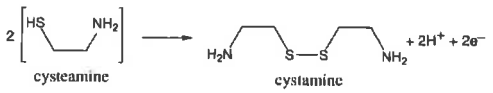
Reaction between cysteamine (systematic name: 2-aminoethanethiol, C_2H_7NS) and L-(+)-tartaric acid [systematic name: (2*R*,3*R*)-2,3-dihydroxybutanedioic acid, $C_4H_6O_6$] results in a mixture of cysteamine tartrate(1−) monohydrate, $C_2H_8NS^+\cdot C_4H_5O_6^-\cdot H_2O$, (I), and cystamine bis[tartrate(1−)] dihydrate, $C_4H_{14}N_2S_2^{2+}\cdot 2C_4H_5O_6^-\cdot 2H_2O$, (III). Cystamine [systematic name: 2,2′-dithiobis(ethylamine), $C_4H_{12}N_2S_2$], reacts with L-(+)-tartaric acid to produce a mixture of cystamine tartrate(2−), $C_4H_{14}N_2S_2^{2+}\cdot C_4H_4O_6^{2-}$, (II), and (III). In each crystal structure, the anions are linked by O—H···O hydrogen bonds that run parallel to the *a* axis. In addition, hydrogen bonding involving protonated amino groups in all three salts, and water molecules in (I) and (III), leads to extensive three-dimensional hydrogen-bonding networks. All three salts crystallize in the orthorhombic space group $P2_12_12_1$.

Comment

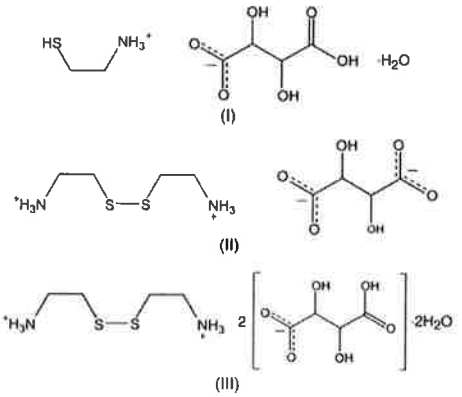
Nephropathic cystinosis is a rare autosomal recessive disease that is characterized by raised lysosomal levels of cystine in the cells of most organs. If untreated, the disease results in death from renal failure by the second decade of life. The condition is characterized by poor growth, renal Fanconi syndrome, renal glomerular failure, and impairment of other tissues and organs (*e.g.* thyroid, pancreas and central nervous system). If treatment is started just after birth this can attenuate the rate of renal failure, but glomerular damage present at the time of diagnosis (usually about 12 months of age) is irreversible and may result in the need for renal transplant (Gahl *et al.*, 2000, 2001, 2002; Cairns *et al.*, 2002). Although novel prodrug strategies are being researched (Kay *et al.*, 2007; McCaughan *et al.*, 2008), the main treatment for the disorder remains the administration of the aminothiol cysteamine as the tartrate(2−) salt, in the commercial preparation Cystagon® (Orphan Europe, Paris). Cysteamine lowers intracellular levels of cystine by forming a cysteamine–cysteine mixed disulfide that is spatially similar in structure to the amino acid lysine, and can egress the lysosome using the undamaged excretion pathway for lysine (Touchman *et al.*, 2000). The thiol cysteamine is known to auto-oxidize to form cystamine (Scheme 1).



Scheme 1

The known 2*R*,3*R* absolute configuration of L-(+)-tartaric acid can establish the absolute configuration of its chiral associations, where it can exist as a neutral molecule, a tartrate monoanion or a tartrate dianion. Its use in pharmaceutical salts also includes metoprolol tartrate, a β-adrenoceptor blocking agent used for migraines, and zolpidem tartrate, a hyponotic used for insomnia (Sweetman, 2011).

In this study, we have reacted cysteamine and cystamine with L-(+)-tartaric acid, and report on the formation and absolute molecular configuration of the three crystalline products, cysteamine tartrate(1−) monohydrate, (I), cystamine tartrate(2−), (II), and cystamine bis[tartrate(1−)] dihydrate, (III) (Scheme 2; Figs. 1–3).



Scheme 2

For (I), the cysteamine moiety remains unoxidized and salt formation results from the transfer of a proton from one of the two carboxylic acid groups in the tartaric acid molecule to the amino group of cysteamine. This results in a monohydrated tartrate monoanion (also known as a hydrogen tartrate anion or semi-tartrate anion) associated with a cysteaminium cation. In the carboxylic acid group, the single-bond character of C3—O1 [1.301 (2) Å] compares with the double-bond length of C3—O2 [1.224 (2) Å], whereas the lengths of the bonds in the carboxylate group [C6—O5 = 1.240 (2) Å and C6—O6 = 1.280 (2) Å] are closer to each other, but not equal, due to differences in hydrogen bonding. The conformation of the cation is described by a S1—C1—C2—N1 torsion angle of

  doi:10.1107/S0108270113012377

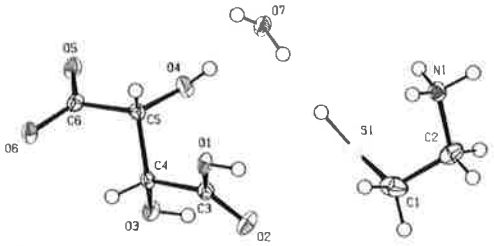


Figure 1
A view of hydrated salt (I), showing the atomic numbering scheme. Displacement ellipsoids are drawn at the 50% probability level.

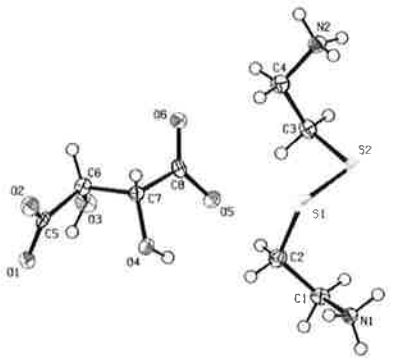


Figure 2
A view of salt (II), showing the atomic numbering scheme. Displacement ellipsoids are drawn at the 50% probability level.

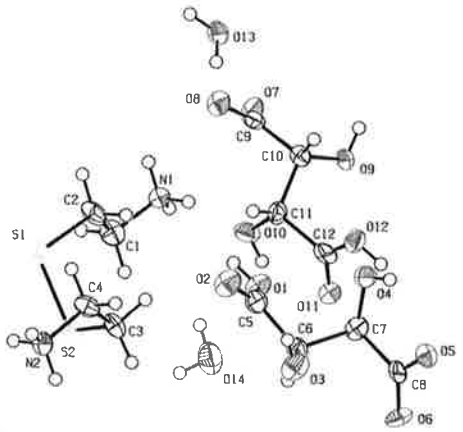


Figure 3
A view of hydrated salt (III), showing the atomic numbering scheme. Displacement ellipsoids are drawn at the 50% probability level.

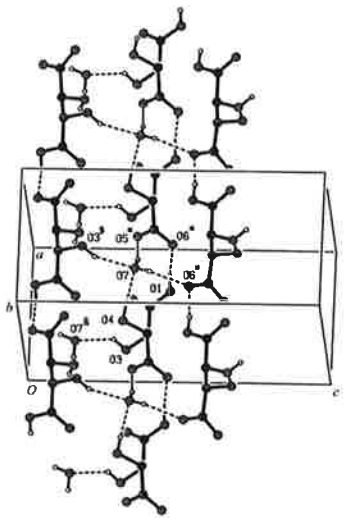


Figure 4
Part of the crystal structure of (I), showing the head-to-tail hydrogen-bonded chains of tartrate monoanions running parallel to [100] [O1···O6* = 2.4885 (18) Å] and crosslinked by water molecules, which act as double donors and double acceptors of hydrogen bonds. Atoms labelled with an asterisk (*), a hash symbol (#), a dollar sign ($) or an ampersand (&) are at the symmetry positions $(x+1, y, z)$, $(x+\frac{1}{2}, -y+\frac{1}{2}, -z+1)$, $(-x+1, y+\frac{1}{2}, -z+\frac{1}{2})$ or $(-x+1, y-\frac{1}{2}, -z+\frac{1}{2})$, respectively. Hydrogen bonds are shown as dashed lines and H atoms not involved in the interactions have been omitted.

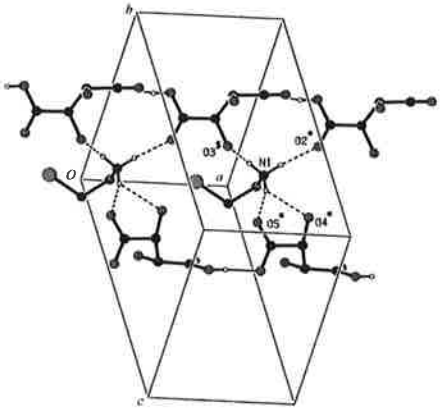


Figure 5
Part of the crystal structure of (I), showing the head-to-tail hydrogen-bonded chains of tartrate monoanions crosslinked by the protonated amino group of the cysteamine cation. One of the three hydrogen bonds is bifurcated. Atoms labelled with an asterisk (*), a hash symbol (#) or a dollar sign ($) are at the symmetry positions $(x+1, y, z)$, $(-x+2, y+\frac{1}{2}, -z+\frac{1}{2})$ or $(-x+1, y+\frac{1}{2}, -z+\frac{1}{2})$, respectively. Hydrogen bonds involving the amino groups are shown as dashed lines and H atoms not involved in the interactions have been omitted.

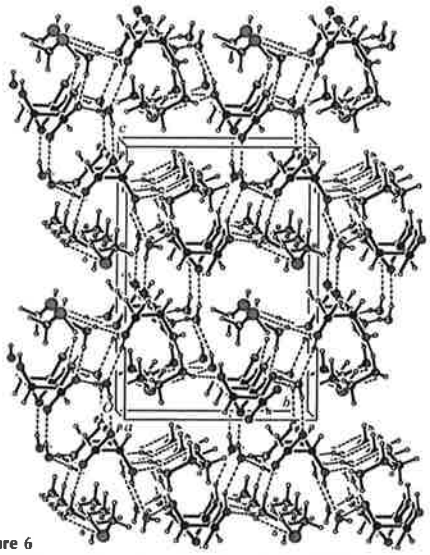


Figure 6
A view of the packing of the ions in the unit cell of (I). Hydrogen bonds are shown as dashed lines.

67.1 (2)° and differs from values of 61.7 (2), −60.3 (4) and 60.7 (4)° found in cysteamine hydrochloride (Ahmad *et al.*, 2010; Kim *et al.*, 2002), where chloride anions are engaged in hydrogen bonding. The S—H bond of 1.31 (3) Å compares with the value of 1.30 (5) Å in thiosalicylic acid (Steiner, 2000) and there are no short intermolecular contacts around the S atom. The tartrate monoanions are linked into chains running

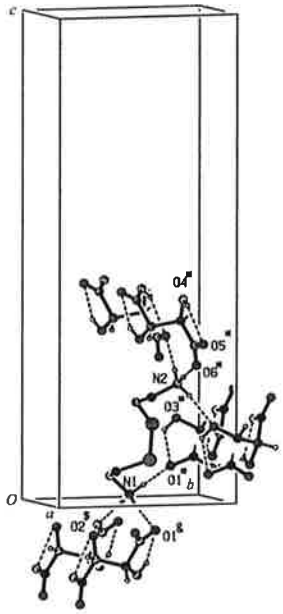


Figure 8
Part of the crystal structure of (II), showing the tartrate anions crosslinked by the protonated amino groups of the cystamine dication. Atoms labelled with an asterisk (*), a hash symbol (#), a dollar sign ($) or an ampersand (&) are at the symmetry positions $(-x+2, y+\frac{1}{2}, -z+\frac{1}{2})$, $(x-1, y, z)$, $(x-\frac{1}{2}, -y+\frac{1}{2}, -z)$ or $(x-\frac{1}{2}, -y+\frac{1}{2}, -z)$, respectively. Hydrogen bonds are shown as dashed lines and H atoms not involved in the interactions have been omitted.

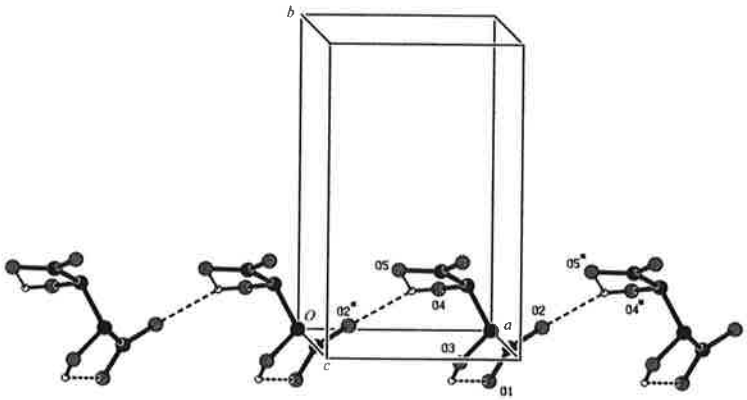


Figure 7
Part of the crystal structure of (II), showing intramolecular [O3···O1 = 2.588 (4) Å and O4···O5 = 2.613 (4) Å] and intermolecular [O4···O2$^{\#}$ = 2.889 (4) Å] hydrogen-bonded chains of tartrate dianions running parallel to [100]. Atoms labelled with an asterisk (*) or a hash symbol (#) are at the symmetry positions $(x+1, y, z)$ or $(x-1, y, z)$, respectively. Hydrogen bonds are shown as dashed lines and H atoms not involved in the interactions have been omitted.

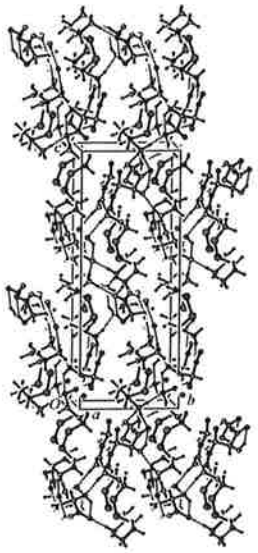


Figure 9
A view of the packing of the ions in the unit cell of (II). Hydrogen bonds are shown as dashed lines.

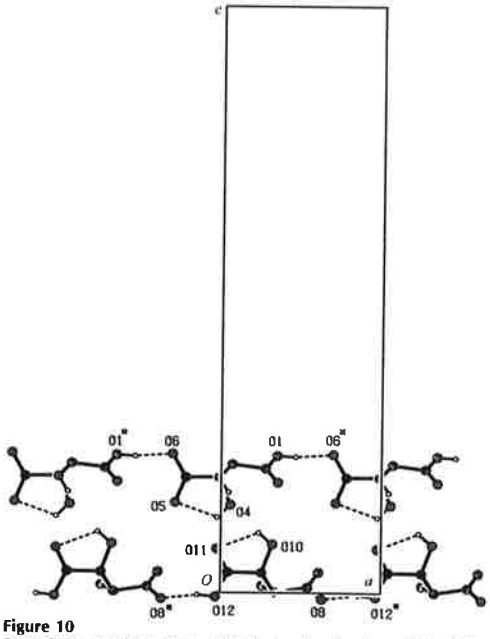


Figure 10
Part of the crystal structure of (III), showing the intra- [O4···O5 = 2.576 (7) Å and O10···O11 = 2.572 (7) Å] and intermolecular [O1···O6* = 2.554 (7) Å and O8···O12* = 2.476 (7) Å] hydrogen-bonded chains of the two independent tartrate monoanions, running parallel to [100]. Atoms labelled with an asterisk (*) or a hash symbol (#) are at the symmetry positions ($x + 1, y, z$) or ($x - 1, y, z$), respectively. Hydrogen bonds are shown as dashed lines and H atoms not involved in the interactions have been omitted.

parallel to (100) by a strong head-to-tail O1—H1···O6($x + 1$, y, z) hydrogen bond, with O1···O6($x + 1$, y, z) = 2.489 (2) Å. These chains are then interlinked by water molecules (Fig. 4) and cysteamine cations (*via* the three H atoms of the protonated amino group; Fig. 5). One of these three H atoms, H1*C*, is involved in bifurcated hydrogen bonding. The resulting honeycomb or columnar packing structure (Fig. 6) is similar to those found in quinolinium hydrogen (2*R*,3*R*)-tartrate monohydrate (Smith *et al.*, 2006) and pyridinium (2*R*,3*R*)-tartrate (Suresh *et al.*, 2006). Hydrogen bonds are given in Table 1.

Product (II) is an anhydrous salt formed by the transfer of both H atoms from the two carboxylic acid groups in L-(+)-tartaric acid to the two amino groups in cystamine. (When cysteamine is the starting material, cystamine is formed by auto-oxidation of cysteamine.) Similarities in bond character in the carboxylate groups are shown by C5—O1 = 1.257 (5) Å, C5—O2 = 1.244 (5) Å, C8—O5 = 1.258 (5) Å and C8—O6 = 1.251 (5) Å. The disulfide bond [S1—S2 = 2.0384 (16) Å] adopts a *gauche* orientation, with a C2—S1—S2—C3 torsion angle of 80.39 (19)°, and as the five torsion angles around this bond are all positive it may be designated +RHSpiral (Schmidt *et al.*, 2006). The tartrate dianions (Fig. 7) are linked into chains running parallel to (100) by a single O4—H4···O2($x - 1$, y, z) hydrogen bond (Table 2). In addition, each cystamine dication is hydrogen bonded to six tartrate anions *via* the two protonated amino groups (Fig. 8), resulting in the overall crystal packing shown in Fig. 9. Hydrogen bonds are listed in Table 2.

The quality of the data set related to the crystal for (III) was not as good as those obtained for (I) and (II), and discussion of the fine details of the product structure needs to be approached with caution. As in (II), both amino groups have acquired an additional H atom. Each of these two protons appears to have transferred from separate tartaric acid molecules, leaving a single charge on each of the two symmetry-independent tartrate monoanions. Evidence for this is based on bond lengths: for the carboxylic acid group, C5—O1 = 1.292 (9) Å and C5—O2 = 1.191 (8) Å, and, in the same anion, the carboxylate group has C8—O5 = 1.261 (8) Å and C8—O6 = 1.231 (8) Å. In the second tartrate monoanion, the bond character is less obvious but the carboxylic acid group has C12—O11 = 1.220 (9) Å and C12—O12 = 1.275 (9) Å, while in the carboxylate group these bonds are C9—O7 = 1.229 (8) Å and C9—O8 = 1.278 (8) Å. In this second anion, the intermolecular O8···O12 separation is very short at 2.476 (7) Å, and although a difference Fourier map indicated that atom H12 was closer to O12 than O8, a sharing of the donor–acceptor roles of these two O atoms could explain the similarities in C—O bond lengths. Refinements of other

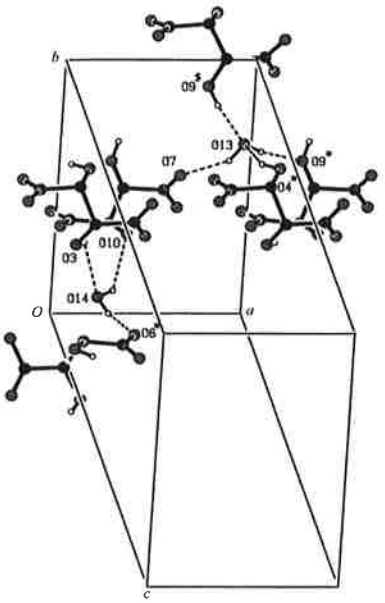


Figure 11
Part of the crystal structure of (III), showing the hydrogen-bonded tartrate monoanions crosslinked by water molecules, which act as donors and acceptors of hydrogen bonds. Atoms labelled with an asterisk (*), a hash symbol (#) or a dollar sign ($) are at the symmetry positions $(-x, y-\frac{1}{2}, -z+\frac{1}{2})$, $(x+1, y, z)$ or $(x+\frac{1}{2}, -y+\frac{3}{2}, -z)$, respectively. Hydrogen bonds are shown as dashed lines and H atoms not involved in the interactions have been omitted.

models involving H_3O^+ formation were unsatisfactory. The disulfide bond [S1—S2 = 2.038 (3) Å] adopts a *gauche* orientation, with a C2—S1—S2—C3 torsion angle of 75.3 (2)°, and may be designated ±RHSpiral (Schmidt *et al.*, 2006). Here, the N1—C1—C2—S1 torsion angle is −179.4 (5)° and this *trans*-planar arrangement is also present in cystamine hydrochloride (Vedavathi & Vijayan, 1979), whereas in (II) this arrangement is *gauche*. As in (I), each tartrate monoanion of (III) is linked into chains (Fig. 10) running parallel to (100) by a strong head-to-tail O1—H1···O6($x+1, y, z$) hydrogen bond, with O1···O6($x+1, y, z$) = 2.554 (7) Å. These chains are crosslinked by two independent water molecules (Fig. 11) acting as acceptors and donors of hydrogen bonds. Furthermore, each protonated amino group is linked to four tartrate monoanions (Fig. 12), with one of the three protons, H4, engaged in bifurcated hydrogen-bond formation. Numerous hydrogen bonds are present and some have short donor–acceptor separations (Table 3). The resulting crystal packing is shown in Fig. 13.

Experimental

For the preparation of cysteamine tartrate(1−) monohydrate (cysteamine hydrogen tartrate monohydrate), (I), millimolar amounts (1:1 ratio) of cysteamine and L-(+)-tartaric acid were weighed and transferred into a 50 ml conical flask. A small amount (5 ml) of hot ethanol was added to the mixture, and the flask and contents were placed in a water bath, with swirling, at 323 K. After 10 min both starting materials remained solid, and so to aid dissolution the flask was stirred and heated to 333 K on a hot plate. Further quantities of solvent were added dropwise to the mixture until a clear solution was obtained. The whole process lasted for about an hour and a total volume of 15 ml of ethanol was used. The solution was then filtered, covered with Parafilm and left in the fume cupboard for crystallization to take place by slow evaporation. After 5 d, clear rod-shaped crystals of (I) separated from the product mixture. The crystals were then collected by gravity filtration and allowed to dry on filter paper. Attempts to cut crystals of (I) to a smaller size without damaging the crystals were unsuccessful.

For the preparation of cystamine tartrate(2−), (II), and cystamine bis[tartrate(1−)] dihydrate (cystamine hydrogen tartrate dihydrate), (III), millimolar amounts (1:1 ratio) of cystamine and L-(+)-tartaric acid were weighed and transferred into a 50 ml conical flask. Hot ethanol (5 ml) was added, resulting in the formation of a white precipitate, and the flask placed in a water bath at 323 K with swirling. Ethanol was added dropwise until a clear solution was obtained. A total volume of 20 ml of solvent was used. The solution was filtered, covered with Parafilm and left in the fume cupboard for crystallization to take place by slow evaporation. After 24 h, crystals [blades of (II) and needles of (III)] formed, and these were collected by gravity filtration and allowed to dry on filter paper. Product (III) also formed as a noncrystalline mass in the preparation of (I). Attempts to obtain high-quality crystals of (III) were only partially successful.

Compound (I)

Crystal data

$C_2H_8NS^+·C_4H_5O_6^-·H_2O$
M_r = 245.25
Orthorhombic, $P2_12_12_1$
a = 7.0630 (2) Å
b = 10.3833 (5) Å
c = 14.8591 (7) Å
V = 1089.73 (8) Å^3
Z = 4
Mo $K\alpha$ radiation
μ = 0.32 mm^{-1}
T = 120 K
0.84 × 0.12 × 0.1 mm

Data collection

Bruker–Nonius KappaCCD area-detector diffractometer
Absorption correction: multi-scan (*SADABS*; Sheldrick, 2007)
T_{min} = 0.620, T_{max} = 0.746
9253 measured reflections
2485 independent reflections
2099 reflections with $I > 2\sigma(I)$
R_{int} = 0.051

Table 1
Hydrogen-bond geometry (Å, °) for (I).

D—H···A	D—H	H···A	D···A	D—H···A
O1—H1···O6^{i}	0.84	1.66	2.4885 (18)	169
O3—H3···O7^{ii}	0.84	2.13	2.819 (2)	139
O4—H4···O7	0.84	1.90	2.742 (2)	177
N1—H1*A*···O3^{iii}	0.91	2.00	2.813 (2)	148
N1—H1*B*···O2^{iv}	0.91	1.92	2.814 (2)	166
N1—H1*C*···O5^{i}	0.91	1.89	2.772 (2)	162
N1—H1*C*···O4^{i}	0.91	2.30	2.850 (2)	118
O7—H7*A*···O5^{v}	0.87	1.89	2.7455 (19)	168
O7—H7*B*···O6^{v}	0.77	2.14	2.8910 (19)	166

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

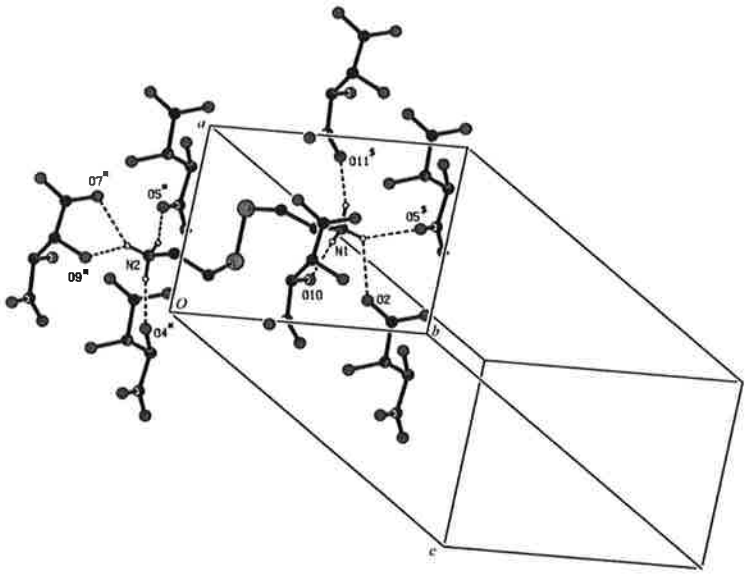


Figure 12
Part of the crystal structure of (III), showing the tartrate monoanions crosslinked by the protonated amino groups of the cystamine cation. Atoms labelled with an asterisk (*), a hash symbol (#) or a dollar sign ($) are at the symmetry positions $(x, y-1, z)$, $(x+1, y-1, z)$ or $(x+1, y, z)$. Hydrogen bonds are shown as dashed lines and H atoms not involved in the interactions have been omitted.

Refinement

$R[F^2 > 2\sigma(F^2)] = 0.039$
$wR(F^2) = 0.093$
$S = 1.06$
2485 reflections
143 parameters
H atoms treated by a mixture of independent and constrained refinement
$\Delta\rho_{max} = 0.27$ e Å^{-3}
$\Delta\rho_{min} = -0.25$ e Å^{-3}
Absolute structure: Flack (1983), 1027 Friedel pairs
Flack parameter: −0.04 (9)

Compound (II)

Crystal data

$C_4H_{14}N_2S_2^{2+}\cdot C_4H_4O_6^{2-}$
$M_r = 302.36$
Orthorhombic, $P2_12_12_1$
$a = 5.7281$ (3) Å
$b = 9.3699$ (5) Å
$c = 24.6770$ (14) Å
$V = 1324.46$ (12) Å^3
$Z = 4$
Mo $K\alpha$ radiation
$\mu = 0.42$ mm^{-1}
$T = 120$ K
0.36 × 0.14 × 0.03 mm

Data collection

Bruker–Nonius KappaCCD area-detector diffractometer
Absorption correction: multi-scan (*SADABS*; Sheldrick, 2007)
$T_{min} = 0.613$, $T_{max} = 0.746$
9158 measured reflections
3020 independent reflections
2273 reflections with $I > 2\sigma(I)$
$R_{int} = 0.083$

Refinement

$R[F^2 > 2\sigma(F^2)] = 0.060$
$wR(F^2) = 0.139$
$S = 1.05$
3020 reflections
165 parameters
H-atom parameters constrained
$\Delta\rho_{max} = 0.55$ e Å^{-3}
$\Delta\rho_{min} = -0.43$ e Å^{-3}
Absolute structure: Flack (1983), 1222 Friedel pairs
Flack parameter: 0.20 (13)

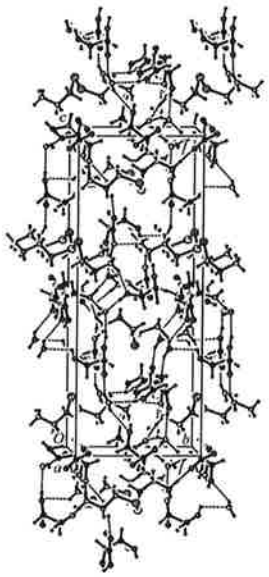


Figure 13
A view of the packing of the ions in the unit cell of (III). Hydrogen bonds are shown as dashed lines.

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

D—H···A	D—H	H···A	D···A	D—H···A
N1—H1A···O1^{i}	0.91	1.88	2.786 (4)	175
N1—H1B···O2^{ii}	0.91	1.82	2.705 (4)	162
N1—H1C···O1^{iii}	0.91	1.99	2.892 (4)	170
N2—H2A···O3^{iv}	0.91	1.99	2.871 (4)	161
N2—H2B···O6^{v}	0.91	1.77	2.684 (4)	177
N2—H2C···O5^{vi}	0.91	1.87	2.727 (4)	155
O3—H3···O1	0.84	2.09	2.588 (4)	117
O3—H3···S1^{vii}	0.84	2.92	3.703 (3)	156
O4—H4···O5	0.84	2.13	2.613 (4)	116
O4—H4···O2^{viii}	0.84	2.20	2.889 (4)	139

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

Table 3
Hydrogen-bond geometry (Å, °) for (III).

D—H···A	D—H	H···A	D···A	D—H···A
N1—H1A···O11^{i}	0.91	1.90	2.789 (8)	164
N1—H1B···O2	0.91	2.32	2.861 (8)	118
N1—H1B···O5^{i}	0.91	2.34	2.983 (8)	127
N1—H1C···O10	0.91	1.97	2.859 (7)	164
N2—H2A···O5^{ii}	0.91	1.87	2.741 (8)	160
N2—H2B···O7^{iii}	0.91	2.16	2.948 (8)	145
N2—H2B···O9^{iii}	0.91	2.27	2.987 (7)	136
N2—H2C···O4^{iii}	0.91	1.87	2.767 (7)	169
O1—H1···O6^{i}	0.84	1.73	2.554 (7)	167
O3—H3···O14	0.84	2.39	2.819 (8)	113
O4—H4···O5	0.84	2.07	2.576 (7)	118
O4—H4···O13^{iv}	0.84	2.23	2.941 (7)	143
O9—H9···O13^{v}	0.84	1.85	2.682 (7)	171
O10—H10···O11	0.84	2.05	2.572 (7)	119
O12—H12···O8^{iv}	0.84	1.66	2.476 (7)	165
O13—H13A···O7	0.85	1.99	2.743 (7)	148
O13—H13B···O9^{v}	0.85	1.99	2.833 (7)	170
O14—H14A···O10	0.86	2.51	3.170 (8)	135
O14—H14B···O6^{vi}	0.87	1.97	2.786 (8)	156

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

Compound (III)

Crystal data

$C_4H_{14}N_2S_2^{2+}·2C_4H_5O_6^-·2H_2O$
M_r = 488.48
Orthorhombic, $P2_12_12_1$
a = 7.3425 (5) Å
b = 10.5227 (8) Å
c = 26.983 (2) Å
V = 2084.8 (3) Å^3
Z = 4
Mo $K\alpha$ radiation
μ = 0.33 mm^{-1}
T = 120 K
0.22 × 0.02 × 0.02 mm

Data collection

Bruker–Nonius KappaCCD area-detector diffractometer
Absorption correction: multi-scan (*SADABS*; Sheldrick, 2007)
T_{min} = 0.363, T_{max} = 1.000
12189 measured reflections
3527 independent reflections
2471 reflections with $I > 2\sigma(I)$
R_{int} = 0.084

Refinement

$R[F^2 > 2\sigma(F^2)]$ = 0.078
$wR(F^2)$ = 0.152
S = 1.09
3527 reflections
271 parameters
H-atom parameters constrained
$\Delta\rho_{max}$ = 0.42 e Å^{-3}
$\Delta\rho_{min}$ = −0.39 e Å^{-3}
Absolute structure: Flack, (1983), 1396 Friedel pairs
Flack parameter: −0.1 (2)

Unless otherwise indicated below, H atoms were placed in geometrically idealized positions and constrained to ride on their parent atoms, with C—H = 1.00 (methine) or 0.99 Å (methylene), O—H = 0.84 Å and N—H = 0.91 Å, and with U_{iso}(H) = 1.2U_{eq}(carrier). For (I), the position of the S-bound H atom was refined freely, while those of the water H atoms were refined freely initially, but then constrained to ride on their parent O atom. The water and hydroxy H atoms were assigned U_{iso}(H) = 1.3U_{eq}(O). For (III), the water H-atom positions were refined initially, with distance restraints of O—H = 0.85 (2) Å and H···H = 1.34 (2) Å, but were then constrained to ride on their parent O atoms. The water and hydroxy H atoms were assigned U_{iso}(H) = 1.5U_{eq}(O).

For all compounds, data collection: *COLLECT* (Nonius, 1998); cell refinement: *DENZO* (Otwinowski & Minor, 1997) and *COLLECT*; data reduction: *DENZO* and *COLLECT*; 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*, *PLATON*, *publCIF* (Westrip, 2010) and *WinGX* (Farrugia, 2012).

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Supplementary data for this paper are available from the IUCr electronic archives (Reference: YP3029). Services for accessing these data are described at the back of the journal.

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