

S,S'*-(But-2-yne-1,4-diyl)bis(L-cysteine) monohydrate*Yun-Mei Shi and Wen-Qin Zhang***

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Key indicators

Single-crystal X-ray study

 $T = 293\text{ K}$ Mean $\sigma(\text{C}-\text{C}) = 0.005\text{ \AA}$ R factor = 0.043 wR factor = 0.094

Data-to-parameter ratio = 6.4

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

In the title compound, $\text{C}_{10}\text{H}_{16}\text{N}_2\text{O}_4\text{S}_2\cdot\text{H}_2\text{O}$, both the (but-2-yne-1,4-diyl)bis(L-cysteine) moieties and the water molecule lie on crystallographic twofold axes. As a result of this symmetry, the two cysteine moieties (zwitterions), which are separated by the linear but-2-yne-1,4-diyl moiety, have exactly the same conformation. The conformation is characterized by the S atoms being *anti* to carboxyl groups and *gauche* to the protonated amino groups. There are hydrogen bonds which connect the structure in three dimensions.

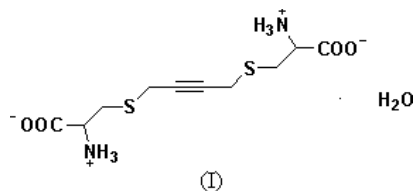
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Comment

It is widely known that L-cysteine and its derivatives exhibit remarkable bioactivities, which prompted us to synthesize new compounds containing two or more cysteine groups and investigate the relationships between structure and bioactivities. A few compounds containing two cysteine moieties bridged through their S atoms *via* different hydrocarbon diyls have been reported (Armstrong & Vigneaud, 1947; Struhar *et al.*, 1975; Hu *et al.*, 1999); however, the crystal structures of these derivatives are rarely studied (Bigoli *et al.*, 1982; Shi *et al.*, 2002). We report herein the crystal structure of a new compound *S,S'*-(but-2-yne-1,4-diyl)bis(L-cysteine) monohydrate, (I).



The trigonal unit cell contains three molecules of (I). The but-2-yne-1,4-diyl group is linear with a $\text{C4}-\text{C5}-\text{C5}^i$ angle of $178.8(4)^\circ$ [symmetry code: (i) $1 + x - y, 2 - y, \frac{1}{3} - z$]. The dihedral angle between the $\text{S1}/\text{C4}/\text{C5}$ and $\text{S1}^i/\text{C4}^i/\text{C5}^i$ planes is $30.2(4)^\circ$. The $\text{C5}\equiv\text{C5}^i$ triple-bond length is $1.191(7)\text{ \AA}$, which agrees with the value of $1.204(2)\text{ \AA}$ in ethyne (Weast, 1988–1989) and $1.200(4)\text{ \AA}$ in but-2-yne-1,4-diol (Steiner, 1996). There is little difference in the C–S bond lengths [$\text{C3}-\text{S1} = 1.799(3)\text{ \AA}$ and $\text{C4}-\text{S1} = 1.816(4)\text{ \AA}$] from that in *S,S'*-(but-2-ene-1,4-diyl)bis(L-cysteine) (BEDC; Shi *et al.*, 2002) and L-cysteine (Kerr & Ashmore, 1973). The $\text{C3}-\text{S1}-\text{C4}$ angle of $101.25(17)^\circ$ is slightly larger than that of 99.05° in dimethyl sulfide (Lide, 1992–1993), and lies between the values of $102.1(2)^\circ$ and $100.4(2)^\circ$ found in BEDC (Shi *et al.*, 2002).

The difference in the two C–O bond lengths [$\text{O1}-\text{C1} = 1.225(4)\text{ \AA}$ and $\text{O2}-\text{C1} = 1.239(4)^\circ$] is seemingly caused by the different hydrogen-bonding environments, in which atom O1 is involved in two hydrogen bonds, while O2 participates in

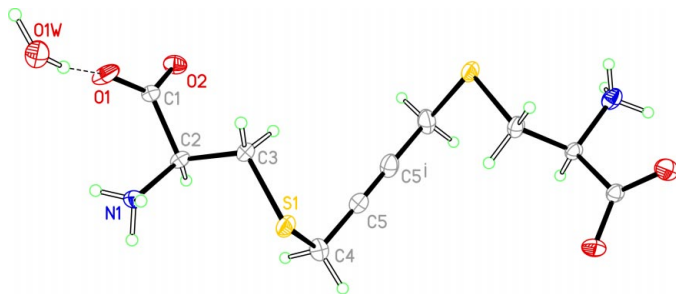


Figure 1
View of the molecular structure of (I), with 30% probability ellipsoids [symmetry code: (i) $1 + x - y, 2 - y, \frac{1}{3} - z$].

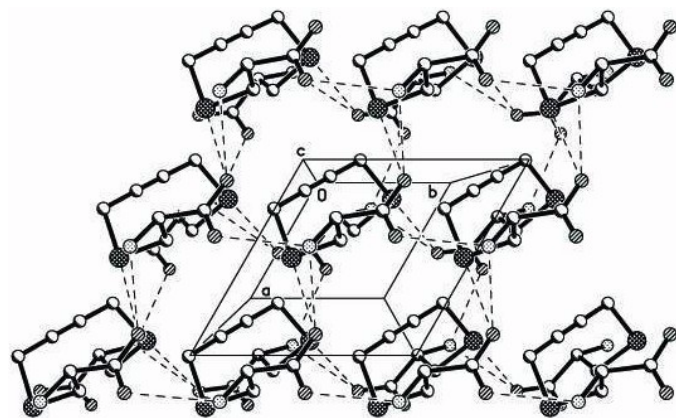


Figure 2
A section of the trigonal unit-cell contents of (I), viewed along the *c* axis.

just one (N1—H1B···O2) (see Table 2). The same situation is also found in BEDC (Shi *et al.*, 2002) and orthorhombic cysteine (Kerr & Ashmore, 1973).

The molecular conformation can be described by the position of the S atom, which is *gauche* to the protonated amino group [$S1-C3-C2-N1 = 52.1(3)^\circ$] and *anti* to the carboxyl group [$S1-C3-C2-C1 = 172.0(2)^\circ$], while in BEDC one S atom is *anti* to the carboxyl group and the other is *gauche* to it (Shi *et al.*, 2002). A Newman projection clearly shows the conformation of (I) (see Fig. 3).

The packing diagram (Fig. 4) shows the existence of some hydrogen bonds. Two distinct N—H···O hydrogen bonds are formed from two N—H bonds of the protonated amino group and two carboxyl O atoms from two different neighboring molecules, leading to the formation of an eight-membered ring with a water molecule situated inside. The water molecule also produces a hydrogen-bond interaction with the O atom from one of the four neighboring molecules of (I) (Table 2).

Experimental

The title compound was synthesized by a modified literature method (Kalopissis, 1975). Under the protection of nitrogen gas and cooled by an ice bath, a solution of 0.53 g (0.0025 mol) of 1,4-dibromo-2-butyne in 5 ml of ethanol was added dropwise to a mixture of 0.88 g (0.005 mol) of L-cysteine hydrochloride monohydrate, 0.001 mol (1 ml, 10 mol l⁻¹) of sodium hydroxide, 5 ml of water and 7.5 ml of ethanol. After that, the reaction mixture was stirred for another 24 h

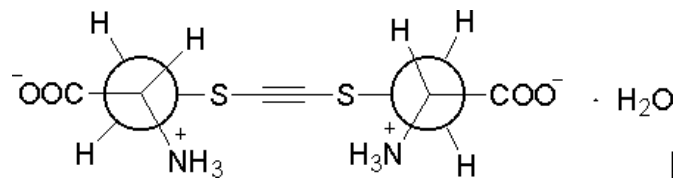


Figure 3
Newman projection of (I)

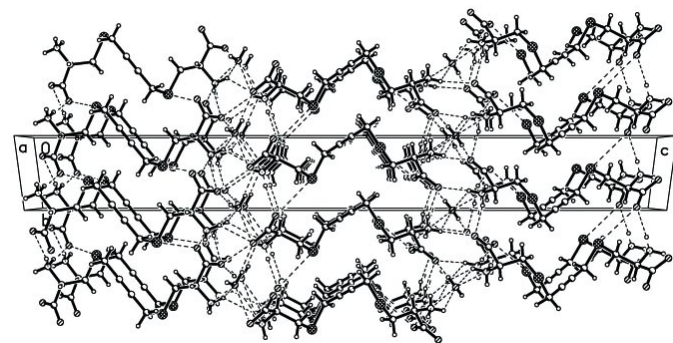


Figure 4
Packing diagram of (I), viewed along the *a* axis. Hydrogen bonds are shown dashed.

at room temperature. The precipitate was washed and recrystallized from water. Pale yellow flakes were obtained with a yield of 37%; m.p. 513–515 K (decomposition); IR (KBr) of (I): 3446 (*s*), 3226 (*b*), 2910 (*s*), 1599 (*vs*, *b*), 1501 (*s*), 1391 (*vs*), 1333 (*s*), 1300 (*w*), 1240 (*w*), 1169 (*w*), 1069 (*s*), 902 (*s*) cm⁻¹; ¹H NMR (D₂O): δ 3.43 (4H, *s*), 4.30 (2H, *q*), 3.20 (2H, *m*), 3.37 (2H, *dd*) p.p.m. 10 mg of (I) was dissolved in 15 ml of hot distilled water; after cooling and filtration, the solution was kept at room temperature for 60 d to yield single crystals of (I) suitable for X-ray analysis.

Crystal data

C₁₀H₁₆N₂O₄S₂·H₂O
M_r = 310.38
 Trigonal, *P*3₁21
a = 5.3906 (10) Å
c = 40.964 (15) Å
V = 1030.9 (5) Å³
Z = 3
D_x = 1.500 Mg m⁻³

Mo *K*α radiation
 Cell parameters from 691 reflections
 $\theta = 4.4\text{--}26.3^\circ$
 $\mu = 0.41\text{ mm}^{-1}$
T = 293 (2) K
 Prism, colorless
 0.30 × 0.25 × 0.20 mm

Data collection

Bruker SMART CCD area-detector diffractometer
 φ and ω scans
 Absorption correction: multi-scan (SADABS; Bruker, 1997)
T_{min} = 0.878, *T_{max}* = 1.000
 4241 measured reflections

1262 independent reflections
 1017 reflections with $I > 2\sigma(I)$
R_{int} = 0.048
 $\theta_{\text{max}} = 26.3^\circ$
h = -6 → 6
k = -6 → 6
l = -32 → 51

Refinement

Refinement on *F*²
R [*F*² > 2σ(*F*²)] = 0.043
wR (*F*²) = 0.094
S = 0.99
 1262 reflections
 197 parameters
 H atoms treated by a mixture of independent and constrained refinement

$w = 1/[\sigma^2(F_o^2) + (0.0519P)^2]$
 where $P = (F_o^2 + 2F_c^2)/3$
 $(\Delta/\sigma)_{\text{max}} < 0.001$
 $\Delta\rho_{\text{max}} = 0.89\text{ e \AA}^{-3}$
 $\Delta\rho_{\text{min}} = -0.21\text{ e \AA}^{-3}$
 Absolute structure: Flack (1983),
 341 Friedel pairs
 Flack parameter = 0.00 (16)

Table 1
Selected geometric parameters (Å, °).

S1—C3	1.799 (3)	C1—C2	1.545 (4)
S1—C4	1.816 (4)	C2—C3	1.524 (4)
N1—C2	1.488 (4)	C4—C5	1.459 (5)
O1—C1	1.225 (4)	C5—C5 ⁱ	1.191 (7)
O2—C1	1.239 (4)		
C3—S1—C4	101.25 (17)	N1—C2—C1	109.2 (2)
O1—C1—O2	126.6 (3)	C3—C2—C1	109.0 (2)
O1—C1—C2	117.4 (3)	C2—C3—S1	116.7 (2)
O2—C1—C2	115.9 (3)	C5—C4—S1	113.7 (3)
N1—C2—C3	110.3 (3)	C5 ⁱ —C5—C4	178.9 (4)
O1—C1—C2—N1	17.3 (4)	N1—C2—C3—S1	52.1 (3)
O2—C1—C2—N1	-164.3 (3)	C1—C2—C3—S1	172.0 (2)
O1—C1—C2—C3	-103.2 (3)	C4—S1—C3—C2	82.8 (3)
O2—C1—C2—C3	75.1 (3)	C3—S1—C4—C5	57.3 (3)

Symmetry code: (i) $1 + x - y, 2 - y, \frac{1}{3} - z$.**Table 2**
Hydrogen-bonding geometry (Å, °).

$D-H \cdots A$	$D-H$	$H \cdots A$	$D \cdots A$	$D-H \cdots A$
N1—H1B ⁱⁱ ···O2 ⁱⁱ	0.85 (11)	1.982 (12)	2.821 (4)	169 (6)
N1—H1C ⁱⁱⁱ ···O1 ⁱⁱⁱ	0.85 (11)	2.053 (13)	2.892 (4)	169 (6)
O1W—H1D ⁱⁱⁱ ···O1	0.90	1.94	2.820 (3)	166

Symmetry codes: (ii) $x - 1, y - 1, z$; (iii) $x, y - 1, z$.

The unique water H atom was located in a difference Fourier map and refined with riding-model constraints on its position. All other H atoms were positioned in difference Fourier maps. U_{iso} parameters were constrained for H atoms bonded to C, and refined freely for those attached to N and O.

Data collection: *SMART* (Bruker, 1997); cell refinement: *SMART*; data reduction: *SAINT* (Bruker, 1997) and *SHELXTL* (Bruker, 1997); program(s) used to solve structure: *SHELXS97* (Sheldrick, 1997); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *SHELXTL*; software used to prepare material for publication: *SHELXTL*.

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