L-Methionyl-L-tyrosine monohydrate

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The study of the oxidation of various proteins necessitates scrutiny of the amino acid sequence. Since methionine (Met) and tyrosine (Tyr) are easily oxidized, peptides that contain these amino acids are frequently studied using a variety of oxidation methods, including, but not limited to, pulse radiolysis, electro-chemical oxidation, and laser flash photolysis. To date, the oxidation of the Met–Tyr dipeptide is not fully understood. Several investigators have proposed a mechanism of intramolecular electron transfer between the sulfide radical of Met and the Tyr residue. Our elucidation of the structure and absolute configuration of L-Met–L-Tyr monohydrate, $C_{14}H_{20}N_2O_4S\cdot H_2O$ (systematic name: (2S)-2-{[(2S)-2-amino-4-methylsulfanylbutanoyl]amino}-3-(4-hydroxy-phenyl)propanoic acid monohydrate) is presented herein and provides information about the zwitterionic nature of the dipeptide. We suspect that the zwitterionic state of the dipeptide and its interaction within the solvent medium may play a major role in the oxidation of the dipeptide. In the crystal, all the potential donor atoms interact via strong N—H···O, C—H···O, O—H···S, and O—H···O hydrogen bonds.

3D view
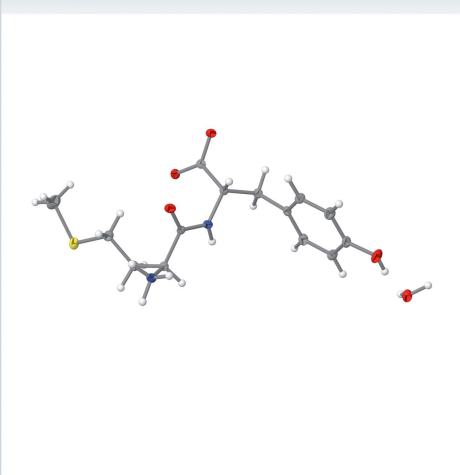
Chemical scheme
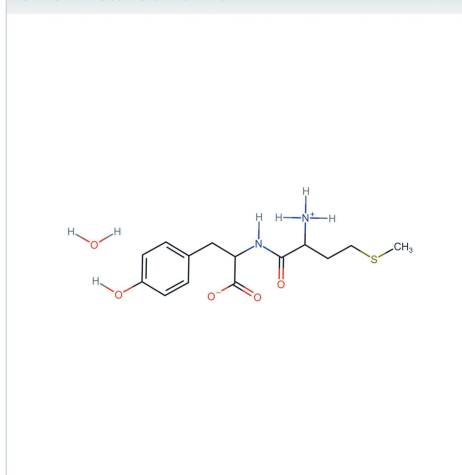
Structure description

Protein oxidation is an important physiological and pathological mechanism (Berlett & Stadtman, 1997; Wojcik et al., 2008). Oxidation of tyrosine (Tyr) and methionine (Met) residues play a role in the etiology of inflammatory diseases (Gu et al., 2015; Meredith et al., 2014). Studies have shown that the Met–Tyr dipeptide has a significant antioxidant activity against the radical cation of 2,2′-azinobis(3-ethylbenzothiazoline-6-sulfonic acid) (ABTS$^{+\cdot}$) and peroxyl radicals, while the Tyr–Met dipeptide does not have any reaction with those radicals (Torkova et al., 2015). The presence of a C-terminal Met group to Tyr had somewhat conflicting results with many oxidation systems (Zhang et al., 2009; Wojcik

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

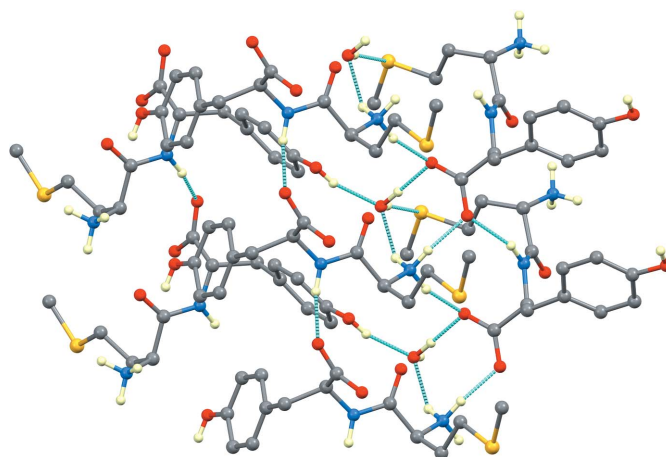| $D—H\cdots A$	$D—H$	$H\cdots A$	$D\cdots A$	$D—H\cdots A$
N1—H1$N\cdots$O2^{i}	0.97 (3)	1.95 (3)	2.863 (2)	156 (2)
N2—H21$N\cdots$O1W^{ii}	0.91 (3)	2.01 (3)	2.805 (2)	145 (2)
N2—H22$N\cdots$O3^{iii}	0.95 (3)	1.91 (3)	2.827 (2)	162 (2)
N2—H23$N\cdots$O2^{iv}	0.95 (3)	1.80 (3)	2.743 (2)	171 (2)
C6—H6$\cdots$O1W	0.95	2.61	3.290 (3)	129
C11—H11$\cdots$O1^{v}	1.00	2.66	3.359 (2)	127
C11—H11$\cdots$O4^{i}	1.00	2.49	3.108 (2)	119
C12—H12$A\cdots$O2^{i}	0.99	2.65	3.440 (2)	137
C13—H13$B\cdots$O2^{iv}	0.99	2.53	3.472 (2)	159
O1W—H1$W\cdots$S1^{vi}	0.85 (3)	2.54 (3)	3.3674 (16)	165 (3)
O1W—H2$W\cdots$O3^{vii}	0.90 (3)	1.82 (3)	2.716 (2)	179 (3)

Symmetry codes: (i) $x-1, y, z$; (ii) $x+\frac{1}{2}, -y+\frac{3}{2}, -z+1$; (iii) $-x+1, y+\frac{1}{2}, -z+\frac{1}{2}$; (iv) $-x+2, y+\frac{1}{2}, -z+\frac{1}{2}$; (v) $x-\frac{1}{2}, -y+\frac{3}{2}, -z+1$; (vi) $-x+\frac{1}{2}, -y+1, z+\frac{1}{2}$; (vii) $-x+\frac{3}{2}, -y+1, z+\frac{1}{2}$.

et al., 2008; Nagy *et al.*, 2009). Several studies have suggested that the mechanism of oxidation is through intramolecular electron transfer from Met to Tyr phenoxy radicals (Bergès *et al.*, 2011; Houée-Lévin *et al.*, 2015; Kciuk *et al.*, 2005; Zhang *et al.*, 2009). The diverse oxidation ability of the dipeptides could be attributed to the structural differences, particularly the configuration of the zwitterion and their interaction with solvent molecules. With this in mind, we have elucidated the structure of L-Met–L-Tyr to better understand its role in the oxidation and nitration process.

The title compound, L-Met–L-Tyr monohydrate, $C_{14}H_{20}N_2O_4S\cdot H_2O$ (Fig. 1), has been analyzed as part of broader studies on the redox properties of Met-containing dipeptides.
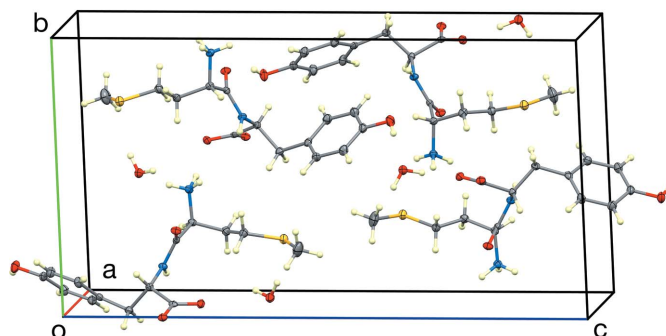

Figure 2
The hydrogen-bonding network, showing only the H atoms involved in hydrogen bonds.

Within the dipeptide, the amine group of Met is protonated and the carboxyl group of tyrosine is deprotonated, thereby generating a zwitterionic configuration. The conformation of the dipeptide molecule can be quantified by four torsion angles. Besides the expected essentially planar peptide linkage, the tyrosine portion has C10—N1—C8—C7 = 165.36 (17)° and N1—C8—C7—C4 = −71.1 (2)°. The methionine portion has C10—C11—C12—C13 = −45.6 (2)° and the sulfur-containing substituent shows an extended conformation with C11—C12—C13—S1 = −173.31 (13)°.

This structure has been reported recently (Babu *et al.*, 2023). The title compound (Fig. 1), derived from two amino acids, L-Met and L-Tyr, crystallized as a monohydrate and was structurally analyzed as a part of broader studies on the redox properties of Met dipeptides. The absolute configuration determined from the X-ray data agrees with that of the starting materials.

In the crystal, the molecules interact with each other *via* strong intermolecular N—H$\cdots$O, C—H$\cdots$O, O—H$\cdots$S, and O—H$\cdots$O hydrogen bonds, forming a three-dimensional network (Table 1 and Fig. 2). All the hydrogen-bond donors in the hydroxy, amidine, and carboxylate groups, as well as the solvent water molecule, are involved. It is interesting to note

Figure 1
The asymmetric unit of the title compound, shown with 50% probability displacement ellipsoids.

Figure 3
The unit cell, viewed approximately down [100].

Table 2
Experimental details.

Crystal data	
Chemical formula	$C_{14}H_{20}N_2O_4S \cdot H_2O$
M_r	330.39
Crystal system, space group	Orthorhombic, $P2_12_12_1$
Temperature (K)	100
a, b, c (Å)	5.4826 (3), 12.4971 (7), 23.5451 (13)
V (Å^3)	1613.23 (15)
Z	4
Radiation type	Cu $K\alpha$
μ (mm^{-1})	2.01
Crystal size (mm)	$0.29 \times 0.08 \times 0.02$
Data collection	
Diffractometer	Bruker Kappa APEXII DUO CCD
Absorption correction	Multi-scan (*SADABS*; Krause *et al.*, 2015)
T_{min}, T_{max}	0.777, 0.961
No. of measured, independent and observed [$I > 2\sigma(I)$] reflections	14990, 3002, 2854
R_{int}	0.040
$(\sin\theta/\lambda)_{max}$ (Å^{-1})	0.607
Refinement	
$R[F^2 > 2\sigma(F^2)]$, $wR(F^2)$, S	0.025, 0.064, 1.06
No. of reflections	3002
No. of parameters	221
H-atom treatment	H atoms treated by a mixture of independent and constrained refinement
$\Delta\rho_{max}, \Delta\rho_{min}$ (e Å^{-3})	0.22, −0.18
Absolute structure	Flack x determined using 1154 quotients [$(I^+) - (I^-)$]/[$(I^+) + (I^-)$] (Parsons *et al.*, 2013)
Absolute structure parameter	0.031 (7)

Computer programs: *APEX2* and *SAINT* (Bruker, 2016), *SHELXS97* (Sheldrick, 2008), *SHELXL2014* (Sheldrick, 2015), *Mercury* (Macrae *et al.*, 2020), *ORTEP-3 for Windows* (Farrugia, 2012), and *publCIF* (Westrip, 2010).

that the dipeptide crystallized as a monohydrate. The water molecule is approximately tetrahedrally surrounded by four hydrogen bonds. In particular, a hydrogen bond exists between atom O1*W* of the water molecule and atom O3 of the Tyr carboxylate group and atom S1 of Met. The amine N1 group of Met forms hydrogen bonds with atoms O2 and O3 of the Tyr carboxylate group, while the protonated amine N2 group of Met hydrogen bonds not only with atoms O2 and O3 of the Tyr carboxylate group, but also with atom O1*W* of the water molecule. Several weak C—H···O hydrogen bonds also occur (Table 1). The unit cell is shown in Fig. 3.

Synthesis and crystallization

The dipeptide L-Met–L-Tyr was obtained commercially (Chemimpex International, Inc., Wood Dale, IL, USA). To about 100 mg of the dipeptide in a small tube, 2 ml of ethanol was added and mixed throughly on a vortex mixer. Additional solvent was added as required in small increments, while mixing on a vortex mixer and keeping the contents at 60 °C in a water bath. A small amount of water was added at the end to dissolve the peptide completely. The solution was left undisturbed at room temperature for slow evaporation and crystallization.

Refinement

Crystal data, data collection and structure refinement details are summarized in Table 2.

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full crystallographic data

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Crystal data

$C_{14}H_{20}N_2O_4S \cdot H_2O$	$D_x = 1.360$ Mg m^{-3}
$M_r = 330.39$	Cu $K\alpha$ radiation, $\lambda = 1.54184$ Å
Orthorhombic, $P2_12_12_1$	Cell parameters from 7969 reflections
$a = 5.4826$ (3) Å	$\theta = 3.8$–69.4°
$b = 12.4971$ (7) Å	$\mu = 2.01$ mm^{-1}
$c = 23.5451$ (13) Å	$T = 100$ K
$V = 1613.23$ (15) Å^3	Lath, colourless
$Z = 4$	$0.29 \times 0.08 \times 0.02$ mm
$F(000) = 704$	

Data collection

Bruker Kappa APEXII DUO CCD diffractometer	14990 measured reflections
Radiation source: IμS microfocus	3002 independent reflections
QUAZAR multilayer optics monochromator	2854 reflections with $I > 2\sigma(I)$
φ and ω scans	$R_{int} = 0.040$
Absorption correction: multi-scan (SADABS; Krause *et al.*, 2015)	$\theta_{max} = 69.4°$, $\theta_{min} = 4.0°$
	$h = -4 \rightarrow 6$
	$k = -14 \rightarrow 15$
$T_{min} = 0.777$, $T_{max} = 0.961$	$l = -28 \rightarrow 28$

Refinement

Refinement on F^2	H atoms treated by a mixture of independent and constrained refinement
Least-squares matrix: full	
$R[F^2 > 2\sigma(F^2)] = 0.025$	$w = 1/[\sigma^2(F_o^2) + (0.033P)^2 + 0.2455P]$ where $P = (F_o^2 + 2F_c^2)/3$
$wR(F^2) = 0.064$	
$S = 1.06$	$(\Delta/\sigma)_{max} = 0.001$
3002 reflections	$\Delta\rho_{max} = 0.22$ e Å^{-3}
221 parameters	$\Delta\rho_{min} = -0.18$ e Å^{-3}
0 restraints	Absolute structure: Flack x determined using 1154 quotients [(I+)-(I-)]/[(I+)+(I-)] (Parsons *et al.*, 2013)
Primary atom site location: structure-invariant direct methods	
Hydrogen site location: mixed	Absolute structure parameter: 0.031 (7)

Special details

Geometry. All esds (except the esd in the dihedral angle between two l.s. planes) are estimated using the full covariance matrix. The cell esds are taken into account individually in the estimation of esds in distances, angles and torsion angles; correlations between esds in cell parameters are only used when they are defined by crystal symmetry. An approximate (isotropic) treatment of cell esds is used for estimating esds involving l.s. planes.

Refinement. All H atoms were located in difference maps and those on C atoms were treated thereafter as riding in geometrically idealized positions, with C—H = 0.95 Å for phenyl, 0.99 Å for CH_2 and 0.98 Å for methyl H atoms. The coordinates of the N—H and O—H H atoms were refined. The U_{iso}(H) values were assigned as $1.5U_{eq}$ of the attached atom methyl, OH, and ammonium H atoms, and as $1.2U_{eq}$ otherwise.

Fractional atomic coordinates and isotropic or equivalent isotropic displacement parameters (Å^2)

	x	y	z	U_{iso}*/U_{eq}
S1	0.45672 (10)	0.72942 (4)	0.10139 (2)	0.01932 (13)
O1	0.6522 (3)	0.64462 (13)	0.60560 (7)	0.0234 (3)
H1OH	0.526 (6)	0.613 (2)	0.6171 (13)	0.035*
O2	1.2758 (2)	0.52566 (10)	0.29568 (6)	0.0150 (3)
O3	0.9501 (3)	0.54361 (10)	0.23911 (6)	0.0152 (3)
O4	0.8826 (2)	0.79919 (11)	0.28382 (6)	0.0159 (3)
N1	0.6958 (3)	0.65289 (13)	0.32141 (7)	0.0131 (3)
H1N	0.543 (5)	0.6144 (19)	0.3235 (10)	0.016*
N2	0.4517 (3)	0.90575 (13)	0.27842 (7)	0.0143 (3)
H21N	0.507 (5)	0.927 (2)	0.3129 (12)	0.022*
H22N	0.298 (5)	0.938 (2)	0.2718 (11)	0.022*
H23N	0.557 (5)	0.941 (2)	0.2526 (11)	0.022*
C1	0.6961 (4)	0.61434 (16)	0.55052 (9)	0.0177 (4)
C2	0.9078 (4)	0.65037 (18)	0.52474 (9)	0.0206 (4)
H2	1.0162	0.6960	0.5448	0.025*
C3	0.9612 (4)	0.61967 (16)	0.46948 (9)	0.0188 (4)
H3	1.1061	0.6452	0.4520	0.023*
C4	0.8066 (4)	0.55226 (16)	0.43912 (8)	0.0151 (4)
C5	0.5910 (4)	0.52002 (16)	0.46491 (9)	0.0183 (4)
H5	0.4796	0.4765	0.4444	0.022*
C6	0.5353 (4)	0.55030 (17)	0.52031 (9)	0.0193 (4)
H6	0.3874	0.5272	0.5374	0.023*
C7	0.8751 (4)	0.51252 (15)	0.38059 (9)	0.0153 (4)
H7A	0.7422	0.4661	0.3663	0.018*
H7B	1.0237	0.4679	0.3838	0.018*
C8	0.9225 (4)	0.60106 (15)	0.33686 (8)	0.0127 (4)
H8	1.0308	0.6558	0.3549	0.015*
C9	1.0589 (4)	0.55304 (14)	0.28579 (8)	0.0127 (4)
C10	0.6979 (3)	0.74683 (14)	0.29371 (8)	0.0117 (4)
C11	0.4474 (4)	0.78691 (14)	0.27481 (8)	0.0136 (4)
H11	0.3216	0.7592	0.3018	0.016*
C12	0.3816 (3)	0.75003 (16)	0.21469 (8)	0.0156 (4)
H12A	0.3336	0.6737	0.2163	0.019*
H12B	0.2376	0.7912	0.2017	0.019*
C13	0.5835 (4)	0.76236 (17)	0.17061 (8)	0.0171 (4)
H13A	0.7207	0.7137	0.1796	0.020*
H13B	0.6454	0.8368	0.1706	0.020*
C14	0.7332 (5)	0.7195 (2)	0.06034 (11)	0.0367 (6)
H14A	0.8149	0.7893	0.0596	0.055*
H14B	0.6935	0.6976	0.0215	0.055*

H14C	0.8415	0.6664	0.0776	0.055*
O1W	0.2853 (3)	0.50422 (12)	0.64496 (7)	0.0195 (3)
H1W	0.240 (5)	0.447 (2)	0.6281 (13)	0.029*
H2W	0.372 (6)	0.487 (2)	0.6762 (14)	0.029*

Atomic displacement parameters (Å²)

	U^{11}	U^{22}	U^{33}	U^{12}	U^{13}	U^{23}
S1	0.0240 (2)	0.0196 (2)	0.0143 (2)	−0.0005 (2)	−0.0008 (2)	−0.00063 (19)
O1	0.0273 (8)	0.0285 (8)	0.0144 (7)	−0.0058 (7)	0.0056 (7)	−0.0028 (6)
O2	0.0133 (7)	0.0133 (6)	0.0185 (7)	0.0011 (5)	0.0002 (6)	−0.0008 (6)
O3	0.0163 (7)	0.0156 (6)	0.0136 (6)	−0.0017 (6)	−0.0017 (6)	−0.0014 (5)
O4	0.0127 (7)	0.0136 (7)	0.0214 (7)	−0.0007 (5)	0.0007 (5)	0.0018 (5)
N1	0.0116 (8)	0.0115 (7)	0.0161 (8)	−0.0002 (7)	0.0001 (6)	0.0010 (6)
N2	0.0142 (8)	0.0134 (8)	0.0154 (8)	0.0014 (7)	0.0003 (7)	0.0010 (7)
C1	0.0229 (11)	0.0181 (10)	0.0123 (10)	0.0032 (8)	0.0012 (8)	0.0002 (8)
C2	0.0220 (11)	0.0228 (10)	0.0171 (10)	−0.0029 (9)	−0.0004 (9)	−0.0016 (8)
C3	0.0165 (9)	0.0229 (10)	0.0169 (10)	−0.0017 (9)	0.0018 (9)	0.0018 (8)
C4	0.0181 (10)	0.0133 (9)	0.0139 (10)	0.0042 (8)	0.0005 (8)	0.0038 (8)
C5	0.0210 (11)	0.0179 (9)	0.0160 (10)	−0.0031 (8)	−0.0017 (8)	0.0009 (8)
C6	0.0180 (10)	0.0226 (10)	0.0175 (10)	−0.0008 (9)	0.0023 (9)	0.0021 (8)
C7	0.0181 (10)	0.0120 (9)	0.0158 (10)	0.0015 (8)	0.0012 (8)	0.0017 (7)
C8	0.0141 (10)	0.0117 (8)	0.0124 (9)	0.0009 (8)	−0.0007 (8)	−0.0006 (7)
C9	0.0135 (9)	0.0076 (8)	0.0169 (10)	−0.0029 (8)	0.0000 (8)	0.0010 (7)
C10	0.0136 (9)	0.0109 (9)	0.0105 (9)	0.0012 (7)	0.0015 (7)	−0.0018 (7)
C11	0.0141 (9)	0.0122 (9)	0.0145 (9)	0.0001 (8)	0.0010 (8)	0.0019 (7)
C12	0.0149 (9)	0.0162 (9)	0.0158 (10)	−0.0023 (7)	−0.0025 (7)	0.0014 (8)
C13	0.0186 (10)	0.0177 (9)	0.0149 (10)	−0.0014 (8)	0.0012 (8)	−0.0016 (7)
C14	0.0377 (14)	0.0502 (16)	0.0222 (13)	0.0036 (13)	0.0064 (10)	−0.0097 (12)
O1W	0.0249 (8)	0.0188 (7)	0.0147 (7)	−0.0028 (6)	−0.0006 (6)	−0.0001 (6)

Geometric parameters (Å, º)

S1—C14	1.802 (3)	C5—C6	1.392 (3)
S1—C13	1.819 (2)	C5—H5	0.9500
O1—C1	1.372 (3)	C6—H6	0.9500
O1—H1OH	0.84 (3)	C7—C8	1.534 (3)
O2—C9	1.259 (3)	C7—H7A	0.9900
O3—C9	1.256 (2)	C7—H7B	0.9900
O4—C10	1.228 (2)	C8—C9	1.538 (3)
N1—C10	1.343 (2)	C8—H8	1.0000
N1—C8	1.448 (3)	C10—C11	1.528 (3)
N1—H1N	0.97 (3)	C11—C12	1.532 (3)
N2—C11	1.488 (2)	C11—H11	1.0000
N2—H21N	0.91 (3)	C12—C13	1.525 (3)
N2—H22N	0.95 (3)	C12—H12A	0.9900
N2—H23N	0.95 (3)	C12—H12B	0.9900
C1—C2	1.385 (3)	C13—H13A	0.9900

C1—C6	1.387 (3)	C13—H13B	0.9900
C2—C3	1.388 (3)	C14—H14A	0.9800
C2—H2	0.9500	C14—H14B	0.9800
C3—C4	1.392 (3)	C14—H14C	0.9800
C3—H3	0.9500	O1W—H1W	0.85 (3)
C4—C5	1.388 (3)	O1W—H2W	0.90 (3)
C4—C7	1.512 (3)		
C14—S1—C13	100.05 (11)	N1—C8—C9	113.30 (16)
C1—O1—H1OH	109 (2)	C7—C8—C9	109.01 (15)
C10—N1—C8	120.38 (16)	N1—C8—H8	108.0
C10—N1—H1N	117.9 (14)	C7—C8—H8	108.0
C8—N1—H1N	120.5 (14)	C9—C8—H8	108.0
C11—N2—H21N	110.3 (16)	O3—C9—O2	125.79 (19)
C11—N2—H22N	113.9 (16)	O3—C9—C8	119.33 (17)
H21N—N2—H22N	109 (2)	O2—C9—C8	114.87 (17)
C11—N2—H23N	116.0 (16)	O4—C10—N1	124.39 (18)
H21N—N2—H23N	104 (2)	O4—C10—C11	120.75 (16)
H22N—N2—H23N	104 (2)	N1—C10—C11	114.86 (16)
O1—C1—C2	118.13 (19)	N2—C11—C10	107.23 (16)
O1—C1—C6	122.15 (19)	N2—C11—C12	110.91 (15)
C2—C1—C6	119.7 (2)	C10—C11—C12	112.47 (16)
C1—C2—C3	119.8 (2)	N2—C11—H11	108.7
C1—C2—H2	120.1	C10—C11—H11	108.7
C3—C2—H2	120.1	C12—C11—H11	108.7
C2—C3—C4	121.3 (2)	C13—C12—C11	115.31 (16)
C2—C3—H3	119.3	C13—C12—H12A	108.4
C4—C3—H3	119.3	C11—C12—H12A	108.4
C5—C4—C3	117.98 (19)	C13—C12—H12B	108.4
C5—C4—C7	120.98 (19)	C11—C12—H12B	108.4
C3—C4—C7	121.01 (19)	H12A—C12—H12B	107.5
C4—C5—C6	121.2 (2)	C12—C13—S1	108.02 (14)
C4—C5—H5	119.4	C12—C13—H13A	110.1
C6—C5—H5	119.4	S1—C13—H13A	110.1
C1—C6—C5	119.9 (2)	C12—C13—H13B	110.1
C1—C6—H6	120.1	S1—C13—H13B	110.1
C5—C6—H6	120.1	H13A—C13—H13B	108.4
C4—C7—C8	114.64 (16)	S1—C14—H14A	109.5
C4—C7—H7A	108.6	S1—C14—H14B	109.5
C8—C7—H7A	108.6	H14A—C14—H14B	109.5
C4—C7—H7B	108.6	S1—C14—H14C	109.5
C8—C7—H7B	108.6	H14A—C14—H14C	109.5
H7A—C7—H7B	107.6	H14B—C14—H14C	109.5
N1—C8—C7	110.24 (16)	H1W—O1W—H2W	110 (3)
O1—C1—C2—C3	178.66 (19)	C4—C7—C8—C9	163.90 (16)
C6—C1—C2—C3	−1.9 (3)	N1—C8—C9—O3	−13.3 (2)
C1—C2—C3—C4	−0.5 (3)	C7—C8—C9—O3	109.8 (2)

C2—C3—C4—C5	2.7 (3)	N1—C8—C9—O2	167.13 (16)
C2—C3—C4—C7	−175.37 (19)	C7—C8—C9—O2	−69.7 (2)
C3—C4—C5—C6	−2.7 (3)	C8—N1—C10—O4	−6.3 (3)
C7—C4—C5—C6	175.42 (19)	C8—N1—C10—C11	174.12 (16)
O1—C1—C6—C5	−178.65 (19)	O4—C10—C11—N2	−33.4 (2)
C2—C1—C6—C5	1.9 (3)	N1—C10—C11—N2	146.24 (16)
C4—C5—C6—C1	0.4 (3)	O4—C10—C11—C12	88.8 (2)
C5—C4—C7—C8	123.7 (2)	N1—C10—C11—C12	−91.57 (19)
C3—C4—C7—C8	−58.3 (3)	N2—C11—C12—C13	74.5 (2)
C10—N1—C8—C7	165.36 (17)	C10—C11—C12—C13	−45.6 (2)
C10—N1—C8—C9	−72.2 (2)	C11—C12—C13—S1	−173.31 (13)
C4—C7—C8—N1	−71.1 (2)	C14—S1—C13—C12	−167.63 (16)

Hydrogen-bond geometry (Å, °)

D—H⋯A	D—H	H⋯A	D⋯A	D—H⋯A
N1—H1*N*⋯O2^i	0.97 (3)	1.95 (3)	2.863 (2)	156 (2)
N2—H21*N*⋯O1*W*^{ii}	0.91 (3)	2.01 (3)	2.805 (2)	145 (2)
N2—H22*N*⋯O3^{iii}	0.95 (3)	1.91 (3)	2.827 (2)	162 (2)
N2—H23*N*⋯O2^{iv}	0.95 (3)	1.80 (3)	2.743 (2)	171 (2)
C6—H6⋯O1*W*	0.95	2.61	3.290 (3)	129
C11—H11⋯O1^v	1.00	2.66	3.359 (2)	127
C11—H11⋯O4^i	1.00	2.49	3.108 (2)	119
C12—H12*A*⋯O2^i	0.99	2.65	3.440 (2)	137
C13—H13*B*⋯O2^{iv}	0.99	2.53	3.472 (2)	159
O1*W*—H1*W*⋯S1^{vi}	0.85 (3)	2.54 (3)	3.3674 (16)	165 (3)
O1*W*—H2*W*⋯O3^{vii}	0.90 (3)	1.82 (3)	2.716 (2)	179 (3)

Symmetry codes: (i) $x-1, y, z$; (ii) $x+1/2, -y+3/2, -z+1$; (iii) $-x+1, y+1/2, -z+1/2$; (iv) $-x+2, y+1/2, -z+1/2$; (v) $x-1/2, -y+3/2, -z+1$; (vi) $-x+1/2, -y+1, z+1/2$; (vii) $-x+3/2, -y+1, z+1/2$.