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4-(4-Methylphenylsulfonyl)piperazin-1-ium trifluoroacetate

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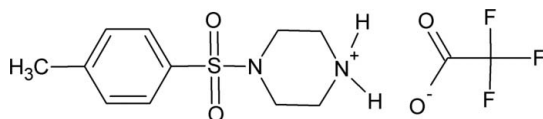
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Key indicators: single-crystal X-ray study; $T = 100$ K; mean $\sigma(\text{C}-\text{C}) = 0.003$ Å; R factor = 0.037; wR factor = 0.094; data-to-parameter ratio = 12.8.

In the title salt, $\text{C}_{11}\text{H}_{17}\text{N}_2\text{O}_2\text{S}^+\cdot\text{CF}_3\text{COO}^-$, the cation is protonated at the secondary piperazine N atom. The dihedral angle between the benzene ring and the piperazine mean plane is $85.54(10)^\circ$. In the crystal, cations and anions are connected by two types of strong $\text{N}-\text{H}\cdots\text{O}$ hydrogen bonds into chains extending along $[101]$. The chains are further assembled into $(10\bar{1})$ layers *via* stacking interactions between benzene rings of the cations [centroid-centroid distance = $3.7319(13)$ Å] and a $\text{C}-\text{H}\cdots\text{O}$ interaction involving a piperazine C-H group and a sulfonyl O atom. Another $\text{C}-\text{H}\cdots\text{O}$ interaction between the piperazine ring and the sulfonyl group connects the ions into a three-dimensional network.

Related literature

For the synthesis, characterization and biological activity of piperazine derivatives, see: Gan *et al.* (2009*a,b*). For hydrogen-bond motifs, see: Bernstein *et al.* (1995).



Experimental

Crystal data

$\text{C}_{11}\text{H}_{17}\text{N}_2\text{O}_2\text{S}^+\cdot\text{C}_2\text{F}_3\text{O}_2^-$
 $M_r = 354.35$
 Monoclinic, $P2_1/n$
 $a = 7.8796(6)$ Å
 $b = 22.5891(15)$ Å
 $c = 9.4626(7)$ Å

$\beta = 110.446(3)^\circ$
 $V = 1578.2(2)$ Å³
 $Z = 4$
 Mo $K\alpha$ radiation

$\mu = 0.26$ mm⁻¹
 $T = 100$ K
 $0.24 \times 0.22 \times 0.20$ mm

Data collection

Bruker APEXII diffractometer
 Absorption correction: multi-scan
 (SADABS; Bruker, 2009)
 $T_{\min} = 0.941$, $T_{\max} = 0.950$

11562 measured reflections
 2781 independent reflections
 2417 reflections with $I > 2\sigma(I)$
 $R_{\text{int}} = 0.030$

Refinement

$R[F^2 > 2\sigma(F^2)] = 0.037$
 $wR(F^2) = 0.094$
 $S = 1.04$
 2781 reflections
 217 parameters
 1 restraint

H atoms treated by a mixture of independent and constrained refinement
 $\Delta\rho_{\max} = 0.86$ e Å⁻³
 $\Delta\rho_{\min} = -0.55$ e Å⁻³

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

$D-\text{H}\cdots A$	$D-\text{H}$	$\text{H}\cdots A$	$D\cdots A$	$D-\text{H}\cdots A$
$\text{N}2-\text{H}1\text{N}2\cdots\text{O}4^{\text{i}}$	0.87 (3)	1.91 (3)	2.782 (2)	174 (2)
$\text{C}8-\text{H}8\text{B}\cdots\text{O}1^{\text{ii}}$	0.97	2.45	3.328 (2)	150
$\text{C}9-\text{H}9\text{B}\cdots\text{O}2^{\text{iii}}$	0.97	2.43	3.146 (2)	130
$\text{N}2-\text{H}2\text{N}2\cdots\text{O}3$	0.86 (2)	1.86 (2)	2.690 (2)	163 (2)

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

Data collection: APEX2 (Bruker, 2009); cell refinement: APEX2 and SAINT-Plus (Bruker, 2009); data reduction: SAINT-Plus and XPREP (Bruker, 2009); program(s) used to solve structure: SHELXS97 (Sheldrick, 2008); program(s) used to refine structure: SHELXL97 (Sheldrick, 2008); molecular graphics: Mercury (Macrae *et al.*, 2008); software used to prepare material for publication: SHELXL97.

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Supplementary data and figures for this paper are available from the IUCr electronic archives (Reference: GK2578).

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supporting information

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4-(4-Methylphenylsulfonyl)piperazin-1-ium trifluoroacetate

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S1. Comment

Numerous piperazine derivatives like aryl amide, sulfonamides, Mannich bases, Schiff bases, thiazolidinones, azetidinones, imidazolinones have shown a wide spectrum of biological activities *viz.* anti-inflammatory, antibacterial, antimalarial, anticonvulsant, antipyretic, antitumor, anthelmintics, analgesic, antidepressant, antifungal, antitubercular, anticancer, antidiabetic (Gan *et al.*, 2009*a,b*). Keeping this in mind, we synthesized the title compound and here we report its crystal structure.

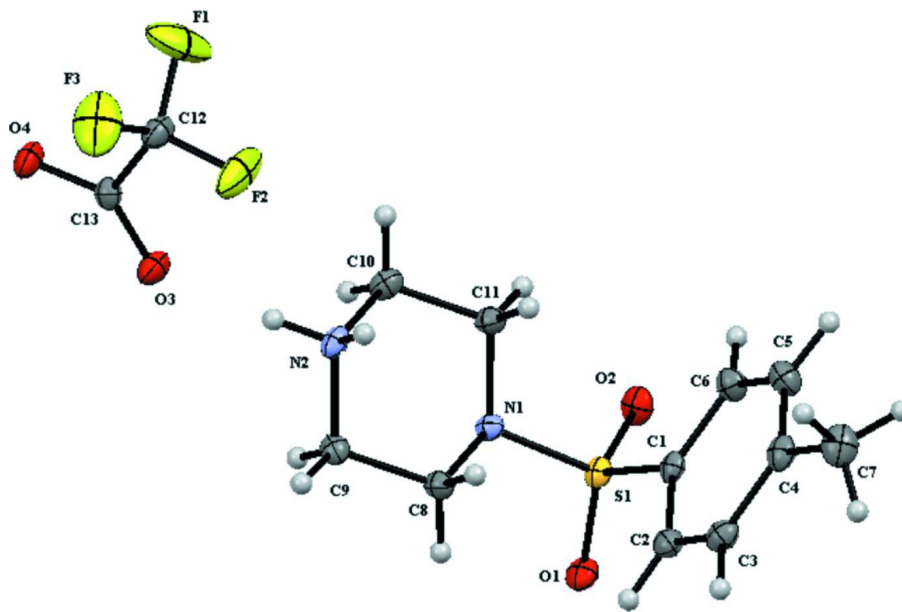
The title molecular salt, $C_{11}H_{17}SO_2N_2^+.CF_3COO^-$, crystallizes in monoclinic crystal system and $P2_1/n$ space group. The cation is protonated at the secondary N atom of the piperazine ring (Fig. 1). The piperazine ring adopts a chair conformation and the dihedral angle between the benzene ring and the piperazine ring (considering the mean plane formed by all the non-hydrogen atoms) in the cation is $85.54 (10)^\circ$. In the crystal, the ions are connected by strong $N2-H1(N2)\cdots O4$ and $N2-H2(N2)\cdots O3$ hydrogen bonds (Fig. 2, Table 1). The cations are further connected through weak $C8-H8B\cdots O1$ and $C9-H9B\cdots O2$ interactions forming chain $C(6)$ and ring $R_2^2(8)$ motifs (Bernstein *et al.* 1995) (Fig. 3, Table 1). The crystal structure is further stabilized by aromatic $\pi-\pi$ stacking interactions.

S2. Experimental

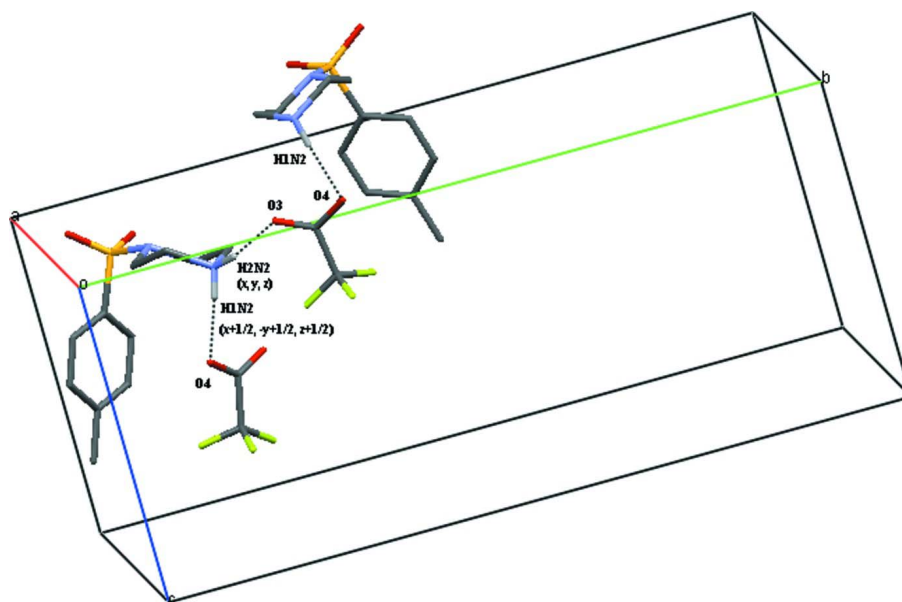
A mixture of *tert*-butyl 4-[(4-methylphenyl)sulfonyl]piperazine-1-carboxylate (0.002 moles, 1 gram) (1), trifluoroacetic acid (TFA) (0.013 moles, 1 ml) in 1,2-dichloroethane (10 ml) was refluxed for 2 h. Reaction mixture was then cooled to room temperature and concentrated to get crude pale yellow colored solid 1-[(4-methylphenyl)sulfonyl]piperazine (2). The crude compound (2) was purified by column chromatography using petroleum ether:ethyl acetate (7:3) as eluent to get white coloured solid (melting point = 518 K), which was further recrystallized from petroleum ether/ dichloromethane (1:1) to obtain colorless crystals suitable for diffraction studies.

S3. Refinement

The hydrogen atoms attached to N were located in difference maps. The distance $H1N2-N2$ was restrained to $0.86 (2) \text{ \AA}$ whereas $H2N2$ was freely refined. The remaining H atoms were positioned with idealized geometry using a riding model with $C-H = 0.93 - 0.97 \text{ \AA}$. The isotropic displacement parameters for all H atoms were set to 1.2 times U_{eq} of the parent atom or 1.5 times that of the parent atom for CH_3 group.

**Figure 1**

Molecular structure of the title compound, showing the atom-labeling scheme. Displacement ellipsoids are drawn at the 50% probability level.

**Figure 2**

Chain of anions and cations connected *via* N—H...O hydrogen bonds. The hydrogen bonds are shown as dashed lines and the hydrogen atoms not involved in hydrogen bonds are omitted.

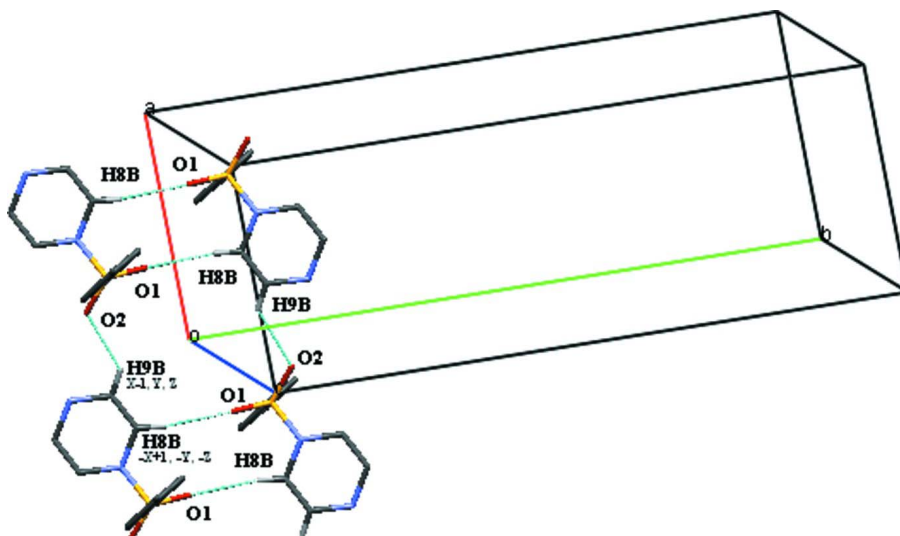


Figure 3

Molecular packing in the title compound displaying $R_2^2(10)$ rings and C(6) chains. Trifluoroacetate ion is omitted for clarity.

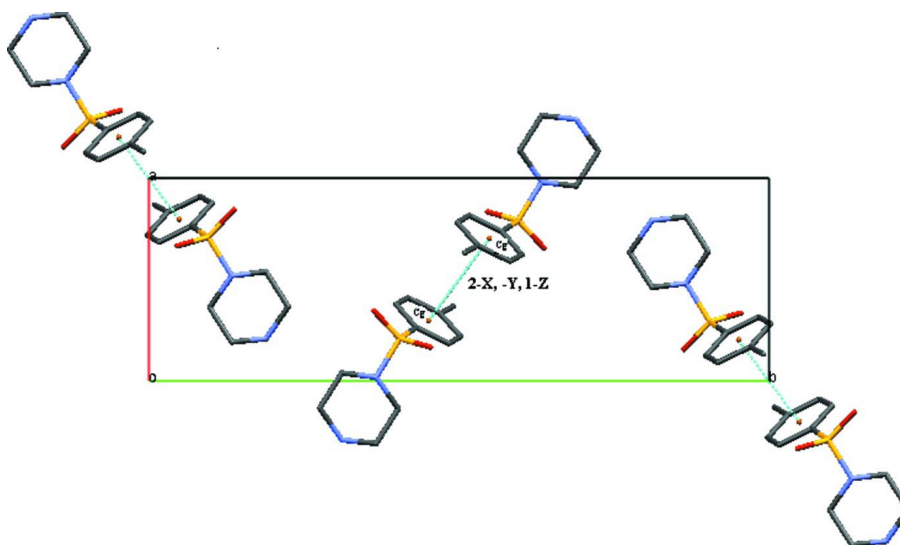


Figure 4

Aromatic π - π stacking interactions observed in the crystal structure.

4-(4-Methylphenylsulfonyl)piperazin-1-ium trifluoroacetate

Crystal data

$C_{11}H_{17}N_2O_2S^+ \cdot C_2F_3O_2^-$

$M_r = 354.35$

Monoclinic, $P2_1/n$

Hall symbol: -P 2yn

$a = 7.8796$ (6) Å

$b = 22.5891$ (15) Å

$c = 9.4626$ (7) Å

$\beta = 110.446$ (3)°

$V = 1578.2$ (2) Å³

$Z = 4$

$F(000) = 736$

prism

$D_x = 1.491$ Mg m⁻³

Melting point: 518 K

Mo $K\alpha$ radiation, $\lambda = 0.71073$ Å

Cell parameters from 2417 reflections

$\theta = 1.8$ – 25.0 °

$\mu = 0.26$ mm⁻¹

$T = 100$ K $0.24 \times 0.22 \times 0.20$ mm
 Prism, colourless

Data collection

Bruker APEXII diffractometer Radiation source: fine-focus sealed tube Graphite monochromator Detector resolution: 1.03 pixels mm ⁻¹ phi and ω scans Absorption correction: multi-scan (SADABS; Bruker, 2009) $T_{\min} = 0.941$, $T_{\max} = 0.950$	11562 measured reflections 2781 independent reflections 2417 reflections with $I > 2\sigma(I)$ $R_{\text{int}} = 0.030$ $\theta_{\text{max}} = 25.0^\circ$, $\theta_{\text{min}} = 1.8^\circ$ $h = -9 \rightarrow 9$ $k = -26 \rightarrow 24$ $l = -11 \rightarrow 10$
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Refinement

Refinement on F^2 Least-squares matrix: full $R[F^2 > 2\sigma(F^2)] = 0.037$ $wR(F^2) = 0.094$ $S = 1.04$ 2781 reflections 217 parameters 1 restraint 0 constraints Primary atom site location: structure-invariant direct methods	Secondary atom site location: difference Fourier map Hydrogen site location: inferred from neighbouring sites H atoms treated by a mixture of independent and constrained refinement $w = 1/[\sigma^2(F_o^2) + (0.042P)^2 + 1.4486P]$ where $P = (F_o^2 + 2F_c^2)/3$ $(\Delta/\sigma)_{\text{max}} = 0.001$ $\Delta\rho_{\text{max}} = 0.86 \text{ e } \text{\AA}^{-3}$ $\Delta\rho_{\text{min}} = -0.55 \text{ e } \text{\AA}^{-3}$
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Special details

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

Refinement. Refinement of F^2 against ALL reflections. The weighted R -factor wR and goodness of fit S are based on F^2 , conventional R -factors R are based on F , with F set to zero for negative F^2 . The threshold expression of $F^2 > \sigma(F^2)$ is used only for calculating R -factors(gt) etc. and is not relevant to the choice of reflections for refinement. R -factors based on F^2 are statistically about twice as large as those based on F , and R -factors based on ALL data will be even larger.

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

	x	y	z	$U_{\text{iso}}^*/U_{\text{eq}}$
C1	0.7630 (2)	0.06870 (8)	0.2940 (2)	0.0153 (4)
C2	0.6839 (3)	0.01633 (9)	0.3194 (2)	0.0183 (4)
H2	0.6086	-0.0057	0.2388	0.022*
C3	0.7192 (3)	-0.00242 (9)	0.4665 (2)	0.0196 (4)
H3	0.6670	-0.0373	0.4841	0.023*
C4	0.8315 (3)	0.03019 (9)	0.5883 (2)	0.0192 (4)
C5	0.9097 (3)	0.08191 (9)	0.5598 (2)	0.0214 (4)
H5	0.9856	0.1038	0.6404	0.026*
C6	0.8771 (3)	0.10158 (9)	0.4140 (2)	0.0198 (4)
H6	0.9307	0.1362	0.3967	0.024*
C7	0.8684 (3)	0.00917 (10)	0.7478 (2)	0.0259 (5)
H7A	0.9878	0.0212	0.8105	0.039*
H7B	0.8600	-0.0332	0.7488	0.039*

H7C	0.7809	0.0261	0.7855	0.039*
C8	0.3628 (2)	0.09780 (8)	0.0749 (2)	0.0167 (4)
H8A	0.3811	0.0860	0.1777	0.020*
H8B	0.3528	0.0623	0.0149	0.020*
C9	0.1909 (3)	0.13368 (9)	0.0128 (2)	0.0171 (4)
H9A	0.1691	0.1438	-0.0917	0.020*
H9B	0.0889	0.1106	0.0168	0.020*
C10	0.3658 (3)	0.22462 (9)	0.1004 (2)	0.0193 (4)
H10A	0.3766	0.2598	0.1617	0.023*
H10B	0.3462	0.2371	-0.0022	0.023*
C11	0.5387 (3)	0.18885 (8)	0.1599 (2)	0.0175 (4)
H11A	0.6391	0.2118	0.1521	0.021*
H11B	0.5646	0.1794	0.2654	0.021*
C12	-0.0777 (3)	0.32181 (9)	0.1546 (2)	0.0218 (5)
C13	-0.1238 (2)	0.30961 (9)	-0.0157 (2)	0.0167 (4)
F1	0.0057 (3)	0.37256 (7)	0.19613 (16)	0.0589 (5)
F2	0.0210 (2)	0.27979 (6)	0.24299 (14)	0.0485 (4)
F3	-0.2294 (2)	0.32421 (8)	0.18855 (15)	0.0523 (4)
N1	0.5186 (2)	0.13357 (7)	0.07164 (17)	0.0146 (3)
N2	0.2087 (2)	0.18872 (7)	0.10346 (19)	0.0162 (4)
O1	0.66600 (18)	0.04597 (6)	0.00690 (15)	0.0202 (3)
O2	0.84473 (18)	0.13710 (6)	0.10568 (15)	0.0213 (3)
O3	-0.05244 (19)	0.26533 (6)	-0.04921 (15)	0.0215 (3)
O4	-0.22722 (19)	0.34645 (6)	-0.10056 (15)	0.0231 (3)
S1	0.70876 (6)	0.09536 (2)	0.10835 (5)	0.01538 (15)
H1N2	0.222 (3)	0.1792 (10)	0.196 (3)	0.029 (6)*
H2N2	0.114 (2)	0.2104 (9)	0.066 (2)	0.021 (6)*

Atomic displacement parameters (Å²)

	U^{11}	U^{22}	U^{33}	U^{12}	U^{13}	U^{23}
C1	0.0127 (9)	0.0189 (10)	0.0163 (10)	0.0046 (8)	0.0074 (8)	0.0021 (8)
C2	0.0177 (10)	0.0179 (10)	0.0197 (10)	0.0016 (8)	0.0071 (8)	-0.0026 (8)
C3	0.0210 (10)	0.0178 (10)	0.0232 (11)	0.0021 (8)	0.0120 (9)	0.0019 (8)
C4	0.0158 (10)	0.0249 (11)	0.0191 (10)	0.0050 (8)	0.0091 (8)	0.0016 (8)
C5	0.0190 (10)	0.0263 (11)	0.0181 (10)	-0.0031 (8)	0.0053 (8)	-0.0028 (8)
C6	0.0162 (10)	0.0218 (11)	0.0222 (11)	-0.0026 (8)	0.0078 (8)	0.0001 (8)
C7	0.0269 (12)	0.0338 (12)	0.0201 (11)	0.0035 (9)	0.0120 (9)	0.0036 (9)
C8	0.0149 (10)	0.0162 (10)	0.0207 (10)	-0.0021 (8)	0.0084 (8)	-0.0026 (8)
C9	0.0158 (10)	0.0212 (10)	0.0152 (10)	0.0002 (8)	0.0066 (8)	-0.0025 (8)
C10	0.0229 (10)	0.0162 (10)	0.0213 (10)	0.0017 (8)	0.0108 (8)	0.0016 (8)
C11	0.0182 (10)	0.0150 (10)	0.0210 (10)	-0.0004 (8)	0.0089 (8)	-0.0023 (8)
C12	0.0272 (11)	0.0196 (11)	0.0181 (10)	0.0076 (9)	0.0071 (9)	0.0025 (8)
C13	0.0141 (9)	0.0194 (10)	0.0169 (10)	0.0003 (8)	0.0058 (8)	0.0015 (8)
F1	0.0970 (14)	0.0423 (9)	0.0240 (8)	-0.0291 (9)	0.0041 (8)	-0.0078 (6)
F2	0.0775 (11)	0.0456 (9)	0.0158 (7)	0.0377 (8)	0.0080 (7)	0.0068 (6)
F3	0.0497 (9)	0.0871 (12)	0.0294 (8)	0.0198 (9)	0.0253 (7)	0.0013 (8)
N1	0.0143 (8)	0.0145 (8)	0.0172 (8)	0.0000 (6)	0.0080 (7)	-0.0012 (6)

N2	0.0178 (9)	0.0181 (9)	0.0142 (9)	0.0062 (7)	0.0075 (7)	0.0028 (7)
O1	0.0220 (7)	0.0234 (8)	0.0177 (7)	0.0056 (6)	0.0099 (6)	-0.0016 (6)
O2	0.0165 (7)	0.0269 (8)	0.0244 (8)	0.0003 (6)	0.0119 (6)	0.0045 (6)
O3	0.0274 (8)	0.0201 (8)	0.0177 (7)	0.0089 (6)	0.0087 (6)	0.0027 (6)
O4	0.0254 (8)	0.0254 (8)	0.0168 (7)	0.0122 (6)	0.0054 (6)	0.0030 (6)
S1	0.0137 (3)	0.0193 (3)	0.0159 (3)	0.00225 (18)	0.00858 (19)	0.00105 (18)

Geometric parameters (Å, °)

C1—C6	1.392 (3)	C9—H9B	0.9700
C1—C2	1.397 (3)	C10—N2	1.488 (3)
C1—S1	1.7623 (19)	C10—C11	1.514 (3)
C2—C3	1.387 (3)	C10—H10A	0.9700
C2—H2	0.9300	C10—H10B	0.9700
C3—C4	1.394 (3)	C11—N1	1.480 (2)
C3—H3	0.9300	C11—H11A	0.9700
C4—C5	1.391 (3)	C11—H11B	0.9700
C4—C7	1.510 (3)	C12—F1	1.312 (3)
C5—C6	1.385 (3)	C12—F2	1.323 (2)
C5—H5	0.9300	C12—F3	1.343 (3)
C6—H6	0.9300	C12—C13	1.548 (3)
C7—H7A	0.9600	C13—O3	1.242 (2)
C7—H7B	0.9600	C13—O3	1.242 (2)
C7—H7C	0.9600	C13—O4	1.243 (2)
C8—N1	1.479 (2)	N1—S1	1.6576 (16)
C8—C9	1.510 (3)	N2—H1N2	0.87 (3)
C8—H8A	0.9700	N2—H2N2	0.860 (16)
C8—H8B	0.9700	O1—S1	1.4332 (14)
C9—N2	1.489 (2)	O2—S1	1.4340 (14)
C9—H9A	0.9700		
C6—C1—C2	120.75 (18)	N2—C10—H10A	109.6
C6—C1—S1	119.58 (15)	C11—C10—H10A	109.6
C2—C1—S1	119.60 (15)	N2—C10—H10B	109.6
C3—C2—C1	119.12 (18)	C11—C10—H10B	109.6
C3—C2—H2	120.4	H10A—C10—H10B	108.1
C1—C2—H2	120.4	N1—C11—C10	109.58 (15)
C2—C3—C4	121.03 (19)	N1—C11—H11A	109.8
C2—C3—H3	119.5	C10—C11—H11A	109.8
C4—C3—H3	119.5	N1—C11—H11B	109.8
C5—C4—C3	118.68 (18)	C10—C11—H11B	109.8
C5—C4—C7	120.96 (18)	H11A—C11—H11B	108.2
C3—C4—C7	120.36 (19)	F1—C12—F2	108.37 (18)
C6—C5—C4	121.48 (19)	F1—C12—F3	106.73 (18)
C6—C5—H5	119.3	F2—C12—F3	104.68 (17)
C4—C5—H5	119.3	F1—C12—C13	112.23 (17)
C5—C6—C1	118.94 (18)	F2—C12—C13	113.76 (16)
C5—C6—H6	120.5	F3—C12—C13	110.57 (16)

C1—C6—H6	120.5	O3—C13—O4	128.86 (18)
C4—C7—H7A	109.5	O3—C13—O4	128.86 (18)
C4—C7—H7B	109.5	O3—C13—C12	116.54 (16)
H7A—C7—H7B	109.5	O3—C13—C12	116.54 (16)
C4—C7—H7C	109.5	O4—C13—C12	114.60 (17)
H7A—C7—H7C	109.5	C8—N1—C11	112.06 (14)
H7B—C7—H7C	109.5	C8—N1—S1	114.04 (12)
N1—C8—C9	109.67 (15)	C11—N1—S1	114.21 (12)
N1—C8—H8A	109.7	C10—N2—C9	110.79 (15)
C9—C8—H8A	109.7	C10—N2—H1N2	110.0 (15)
N1—C8—H8B	109.7	C9—N2—H1N2	109.2 (16)
C9—C8—H8B	109.7	C10—N2—H2N2	106.9 (15)
H8A—C8—H8B	108.2	C9—N2—H2N2	110.2 (15)
N2—C9—C8	109.43 (15)	H1N2—N2—H2N2	110 (2)
N2—C9—H9A	109.8	O1—S1—O2	120.15 (8)
C8—C9—H9A	109.8	O1—S1—N1	106.33 (8)
N2—C9—H9B	109.8	O2—S1—N1	106.28 (8)
C8—C9—H9B	109.8	O1—S1—C1	108.66 (9)
H9A—C9—H9B	108.2	O2—S1—C1	108.65 (9)
N2—C10—C11	110.41 (16)	N1—S1—C1	105.87 (8)
C6—C1—C2—C3	0.6 (3)	C9—C8—N1—C11	58.60 (19)
S1—C1—C2—C3	-176.24 (14)	C9—C8—N1—S1	-169.70 (12)
C1—C2—C3—C4	0.1 (3)	C10—C11—N1—C8	-57.2 (2)
C2—C3—C4—C5	-0.6 (3)	C10—C11—N1—S1	171.14 (12)
C2—C3—C4—C7	179.94 (18)	C11—C10—N2—C9	-58.0 (2)
C3—C4—C5—C6	0.5 (3)	C8—C9—N2—C10	58.8 (2)
C7—C4—C5—C6	179.90 (18)	O4—C13—O3—O3	0.00 (8)
C4—C5—C6—C1	0.2 (3)	C12—C13—O3—O3	0.00 (7)
C2—C1—C6—C5	-0.7 (3)	C8—N1—S1—O1	52.91 (14)
S1—C1—C6—C5	176.09 (15)	C11—N1—S1—O1	-176.43 (13)
N1—C8—C9—N2	-58.22 (19)	C8—N1—S1—O2	-177.97 (13)
N2—C10—C11—N1	56.2 (2)	C11—N1—S1—O2	-47.32 (14)
F1—C12—C13—O3	117.9 (2)	C8—N1—S1—C1	-62.54 (14)
F2—C12—C13—O3	-5.6 (3)	C11—N1—S1—C1	68.11 (14)
F3—C12—C13—O3	-123.07 (19)	C6—C1—S1—O1	153.58 (15)
F1—C12—C13—O3	117.9 (2)	C2—C1—S1—O1	-29.56 (17)
F2—C12—C13—O3	-5.6 (3)	C6—C1—S1—O2	21.24 (18)
F3—C12—C13—O3	-123.07 (19)	C2—C1—S1—O2	-161.90 (14)
F1—C12—C13—O4	-61.4 (2)	C6—C1—S1—N1	-92.56 (16)
F2—C12—C13—O4	175.05 (18)	C2—C1—S1—N1	84.30 (16)
F3—C12—C13—O4	57.6 (2)		

Hydrogen-bond geometry (\AA , $^\circ$)

$D-H\cdots A$	$D-H$	$H\cdots A$	$D\cdots A$	$D-H\cdots A$
N2—H1N2 \cdots O4 ⁱ	0.87 (3)	1.91 (3)	2.782 (2)	174 (2)
C8—H8B \cdots O1 ⁱⁱ	0.97	2.45	3.328 (2)	150

C9—H9B···O2 ⁱⁱⁱ	0.97	2.43	3.146 (2)	130
N2—H2N2···O3	0.86 (2)	1.86 (2)	2.690 (2)	163 (2)

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