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N-(5-Ethylsulfanyl-1,3,4-thiadiazol-2-yl)-2-(4,5,6,7-tetrahydrothieno[3,2-c]pyridin-5-yl)acetamide

Shuang Zhi,[a] Shuai Mu,[b] Ying Liu[c]* and Deng-Ke Liu[c]

[a]School of Environmental and Chemical Engineering, Tianjin Polytechnic University, Tianjin 300160, People's Republic of China, [b]School of Chemical Engineering and Technology, Tianjin University, Tianjin, 300072, People's Republic of China, and [c]Tianjin Institute of Pharmaceutical Research, Tianjin, 300193, People's Republic of China
Correspondence e-mail: liudk@tjipr.com

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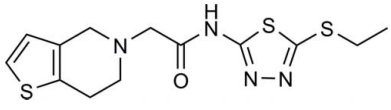
Key indicators: single-crystal X-ray study; T = 113 K; mean σ(C–C) = 0.002 Å; R factor = 0.030; wR factor = 0.079; data-to-parameter ratio = 18.2.

In the title compound, $C_{13}H_{16}N_4OS_3$, a thienopyridine-derivative, the tetrahydropyridine ring exhibits a half-chair conformation, and the folded conformation of the molecule is defined by the N—C—C—N torsion angle of −78.85 (16)°. The crystal packing features intermolecular C—H···N, N—H···N and C—H···O hydrogen bonds.

Related literature

The title compound is a potential antiplatelet agent. As irreversible P2Y12 antagonists, thienopyridines have proved the relevance of inhibiting signaling *via* the platelet-specific P2Y12 ADP receptor in the prevention of cardiovascular events, see: Iyengar (2009); Franchini & Mannucci, (2009); Van Giezen *et al.* (2009); Van Giezen & Humphries (2005). For a related structure, see: Chen *et al.* (2010). For the synthesis of the title compound, see: Liu *et al.* (2008).



Experimental

Crystal data

$C_{13}H_{16}N_4OS_3$
M_r = 340.48
Monoclinic, $P2_1/n$
a = 6.532 (4) Å
b = 9.788 (6) Å
c = 23.491 (15) Å
β = 95.524 (6)°
V = 1494.8 (16) Å^3
Z = 4
Mo $K\alpha$ radiation
μ = 0.50 mm^{-1}
T = 113 K
0.28 × 0.22 × 0.18 mm

Data collection

Rigaku Saturn CCD area-detector diffractometer
Absorption correction: multi-scan (*CrystalClear*; Rigaku/MSC, 2005)
T_{min} = 0.873, T_{max} = 0.916
12423 measured reflections
3545 independent reflections
2653 reflections with $I > 2\sigma(I)$
R_{int} = 0.036

Refinement

$R[F^2 > 2\sigma(F^2)]$ = 0.030
$wR(F^2)$ = 0.079
S = 1.03
3545 reflections
195 parameters
1 restraint
H atoms treated by a mixture of independent and constrained refinement
$\Delta\rho_{max}$ = 0.44 e Å^{-3}
$\Delta\rho_{min}$ = −0.23 e Å^{-3}

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

D—H···A	D—H	H···A	D···A	D—H···A
C12—H12B···N1^{i}	0.99	2.60	3.473 (3)	147
N2—H2···N3^{ii}	0.89 (1)	2.02 (1)	2.902 (2)	171 (2)
C5—H5···O1^{iii}	0.95	2.46	3.279 (2)	145

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

Data collection: *CrystalClear* (Rigaku/MSC, 2005); cell refinement: *CrystalClear*; data reduction: *CrystalClear*; program(s) used to solve structure: *SHELXS97* (Sheldrick, 2008); program(s) used to refine structure: *SHELXL97* (Sheldrick, 2008); molecular graphics: *SHELXTL* (Sheldrick, 2008); software used to prepare material for publication: *CrystalStructure* (Rigaku/MSC, 2005).

The authors thank Mr Hai-Bin Song of Nankai University for the X-ray crystallographic determination and for helpful suggestions.

Supplementary data and figures for this paper are available from the IUCr electronic archives (Reference: KP2327).

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supporting information

Acta Cryst. (2011). E**67**, o1490 [doi:10.1107/S1600536811017107]

N-(5-Ethylsulfanyl-1,3,4-thiadiazol-2-yl)-2-(4,5,6,7-tetrahydrothieno[3,2-*c*]pyridin-5-yl)acetamide

Shuang Zhi, Shuai Mu, Ying Liu and Deng-Ke Liu

S1. Comment

As irreversible P2Y12 antagonists, the thienopyridines (*e.g.*, clopidogrel and prasugrel) have been further proved the relevance of inhibiting signaling *via* the platelet-specific P2Y12 ADP receptor in the prevention of cardiovascular events (Iyengar, 2009; Van Giezen & Humphries, 2005; Franchini, *et al.*, 2009). The structure of the title compound (I), a new derivative of thienopyridine, is presented here.

The tetrahydropyridine ring is in a half-chair conformation (Fig. 1). The thiadiazole ring plane (r.m.s. deviation 0.0020Å) and the acidamide plane (r.m.s. deviation 0.0074 Å) are almost coplanar, with a dihedral angle of 3.24 (9)°. The dihedral angles formed between the thiadiazole ring plane and the thiophene ring plane, the acidamide plane and the thiophene ring plane are 76.19 (6)° and 78.47 (7)° , respectively. Crystal packing is via hydrogen bonds C—H···N, N—H···N and C—H···O (Table 1, Fig. 2).

S2. Experimental

Chloracetyl chloride was dropwised added into a mixture of 5-(ethylthio)-1,3,4-thiadiazol-2-amine, TEA and DMF at 268 K. After stirred for 3 h, the mixture was poured into cold water. 2-Chloro-*N*-(5-(ethylthio)-1,3,4-thiadiazol-2-yl)acetamide was precipitated as an intermediate. Then the intermediate, equimolar quantities thienopyridine salt and TEA were refluxed for 5 h in acetonitrile, and the product was obtained by silica gel column chromatography. Crystallisation of the obtained yellow solid from methanol afforded light-yellow crystals suitable for X-ray analysis.

S3. Refinement

The N–H bond was restrained to 0.90 Å, and other H atoms were positioned geometrioncally and refined using a riding model, with d(C—H)=0.95–0.99 Å, and U_{iso}(H)=1.2U_{eq}(C) of the parent atom.

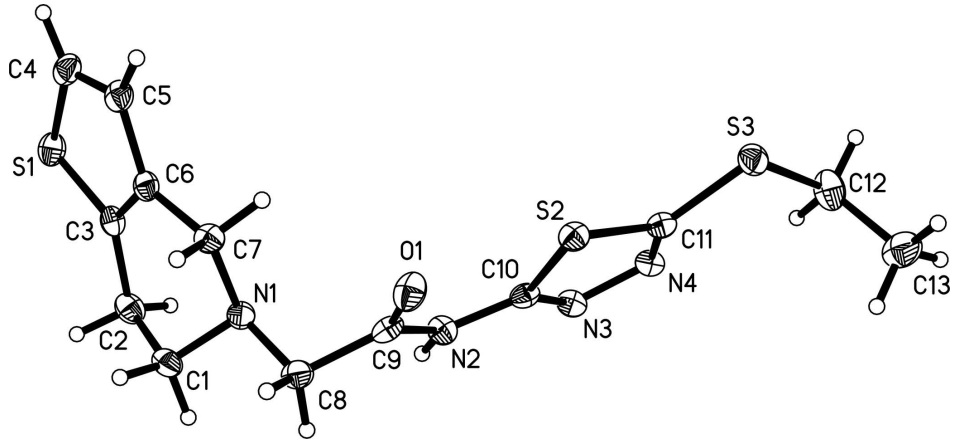

Figure 1

The molecular structure of (I), with the atom-numbering scheme and 50% probability displacement ellipsoids.

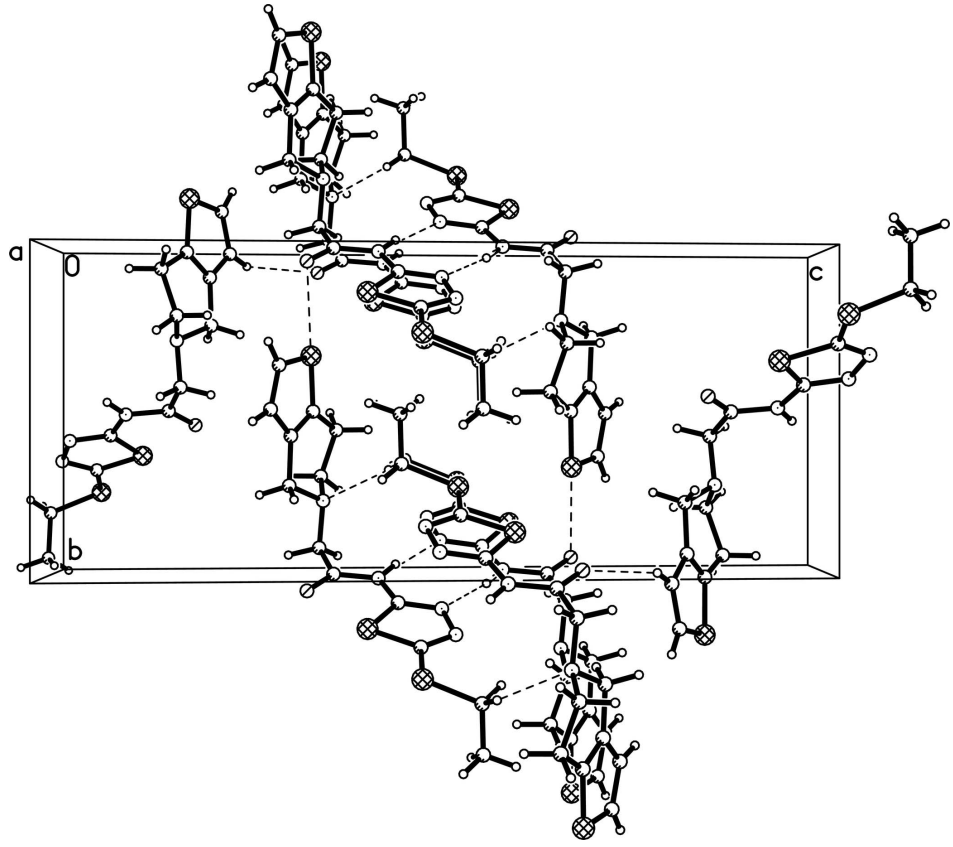

Figure 2

Packing diagram for (I) with hydrogen bonds drawn as dashed lines.

N-(5-Ethylsulfanyl-1,3,4-thiadiazol-2-yl)-2-(4,5,6,7- tetrahydrothieno[3,2-*c*]pyridin-5-yl)acetamide

Crystal data

$C_{13}H_{16}N_4OS_3$
M_r = 340.48
Monoclinic, $P2_1/n$
Hall symbol: -P 2yn
a = 6.532 (4) Å
b = 9.788 (6) Å

c = 23.491 (15) Å
β = 95.524 (6)°
V = 1494.8 (16) Å^3
Z = 4
F(000) = 712
D_x = 1.513 Mg m^{-3}
Mo $K\alpha$ radiation, λ = 0.71073 Å

Cell parameters from 4582 reflections
θ = 1.7–27.9°
μ = 0.50 mm^{-1}
T = 113 K
Prism, colourless
0.28 × 0.22 × 0.18 mm

Data collection

Rigaku Saturn CCD area-detector diffractometer
Radiation source: rotating anode
Multilayer monochromator
Detector resolution: 14.63 pixels mm^{-1}
ω and φ scans
Absorption correction: multi-scan (*CrystalClear*; Rigaku/MSC, 2005)
T_{min} = 0.873, T_{max} = 0.916

12423 measured reflections
3545 independent reflections
2653 reflections with $I > 2\sigma(I)$
R_{int} = 0.036
θ_{max} = 27.9°, θ_{min} = 1.7°
h = −8→8
k = −12→12
l = −28→30

Refinement

Refinement on F^2
Least-squares matrix: full
$R[F^2 > 2\sigma(F^2)]$ = 0.030
$wR(F^2)$ = 0.079
S = 1.03
3545 reflections
195 parameters
1 restraint
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
$w = 1/[\sigma^2(F_o^2) + (0.042P)^2]$ where $P = (F_o^2 + 2F_c^2)/3$
$(\Delta/\sigma)_{max}$ = 0.004
$\Delta\rho_{max}$ = 0.44 e Å^{-3}
$\Delta\rho_{min}$ = −0.23 e Å^{-3}

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 (Å^2)

	x	y	z	U_{iso}*/U_{eq}
S1	1.09432 (6)	−0.17109 (4)	0.167990 (17)	0.02366 (11)
S2	0.59937 (6)	0.64557 (4)	0.091056 (16)	0.01921 (10)
S3	0.24260 (6)	0.77190 (4)	0.021966 (17)	0.02324 (11)
O1	0.87853 (17)	0.54420 (11)	0.17006 (4)	0.0257 (3)
N1	1.16286 (18)	0.27779 (12)	0.15327 (5)	0.0188 (3)
N2	0.9587 (2)	0.51028 (13)	0.08012 (5)	0.0195 (3)
N3	0.76496 (19)	0.59529 (13)	−0.00107 (5)	0.0199 (3)
N4	0.58266 (19)	0.66332 (13)	−0.01858 (5)	0.0196 (3)

C1	1.3598 (2)	0.20466 (16)	0.15877 (7)	0.0220 (3)
H1A	1.4181	0.2046	0.1993	0.026*
H1B	1.4584	0.2513	0.1359	0.026*
C2	1.3270 (2)	0.05905 (16)	0.13799 (7)	0.0233 (3)
H2A	1.2955	0.0577	0.0959	0.028*
H2B	1.4531	0.0045	0.1479	0.028*
C3	1.1520 (2)	0.00006 (15)	0.16615 (6)	0.0194 (3)
C4	0.8868 (2)	−0.14081 (15)	0.20530 (7)	0.0234 (3)
H4	0.7989	−0.2103	0.2173	0.028*
C5	0.8627 (2)	−0.00627 (15)	0.21566 (6)	0.0214 (3)
H5	0.7562	0.0299	0.2360	0.026*
C6	1.0153 (2)	0.07498 (15)	0.19257 (6)	0.0184 (3)
C7	1.0281 (2)	0.22806 (15)	0.19494 (6)	0.0197 (3)
H7A	0.8889	0.2676	0.1865	0.024*
H7B	1.0824	0.2573	0.2338	0.024*
C8	1.1928 (2)	0.42478 (15)	0.15876 (7)	0.0220 (3)
H8A	1.3052	0.4538	0.1361	0.026*
H8B	1.2324	0.4484	0.1993	0.026*
C9	0.9969 (2)	0.49862 (14)	0.13783 (7)	0.0204 (3)
C10	0.7907 (2)	0.57771 (14)	0.05403 (6)	0.0181 (3)
C11	0.4826 (2)	0.69389 (15)	0.02453 (6)	0.0190 (3)
C12	0.2098 (3)	0.84165 (17)	−0.04979 (7)	0.0300 (4)
H12A	0.3070	0.7958	−0.0734	0.036*
H12B	0.0686	0.8216	−0.0669	0.036*
C13	0.2449 (3)	0.99201 (18)	−0.05141 (8)	0.0362 (4)
H13A	0.1524	1.0379	−0.0271	0.054*
H13B	0.2173	1.0249	−0.0908	0.054*
H13C	0.3879	1.0121	−0.0374	0.054*
H2	1.047 (2)	0.4714 (17)	0.0587 (7)	0.038 (5)*

Atomic displacement parameters (Å²)

	U^{11}	U^{22}	U^{33}	U^{12}	U^{13}	U^{23}
S1	0.0286 (2)	0.0204 (2)	0.0220 (2)	0.00424 (17)	0.00251 (17)	0.00018 (16)
S2	0.0206 (2)	0.02023 (18)	0.0177 (2)	0.00016 (15)	0.00653 (16)	−0.00083 (15)
S3	0.0217 (2)	0.0242 (2)	0.0244 (2)	0.00316 (16)	0.00550 (17)	0.00097 (16)
O1	0.0338 (7)	0.0255 (6)	0.0190 (6)	0.0047 (5)	0.0095 (5)	0.0034 (5)
N1	0.0177 (7)	0.0200 (6)	0.0189 (7)	0.0010 (5)	0.0038 (5)	0.0011 (5)
N2	0.0192 (7)	0.0222 (6)	0.0178 (7)	0.0017 (5)	0.0052 (5)	−0.0018 (5)
N3	0.0185 (7)	0.0228 (6)	0.0186 (7)	−0.0007 (5)	0.0030 (5)	−0.0029 (5)
N4	0.0179 (7)	0.0210 (6)	0.0200 (7)	−0.0015 (5)	0.0026 (5)	−0.0019 (5)
C1	0.0165 (8)	0.0283 (8)	0.0213 (8)	0.0002 (6)	0.0017 (6)	−0.0002 (6)
C2	0.0190 (8)	0.0286 (8)	0.0224 (8)	0.0039 (7)	0.0031 (7)	−0.0024 (7)
C3	0.0197 (8)	0.0213 (7)	0.0164 (8)	0.0025 (6)	−0.0016 (6)	0.0005 (6)
C4	0.0278 (9)	0.0243 (8)	0.0181 (8)	−0.0009 (7)	0.0020 (7)	0.0045 (6)
C5	0.0235 (8)	0.0252 (8)	0.0157 (8)	0.0019 (6)	0.0031 (6)	0.0020 (6)
C6	0.0198 (8)	0.0210 (7)	0.0141 (7)	0.0014 (6)	−0.0003 (6)	0.0012 (6)
C7	0.0198 (8)	0.0223 (7)	0.0174 (8)	0.0003 (6)	0.0042 (6)	−0.0009 (6)

C8	0.0216 (8)	0.0220 (8)	0.0223 (8)	−0.0037 (6)	0.0020 (7)	0.0002 (6)
C9	0.0248 (8)	0.0154 (7)	0.0216 (8)	−0.0056 (6)	0.0049 (7)	0.0010 (6)
C10	0.0191 (8)	0.0166 (7)	0.0195 (8)	−0.0025 (6)	0.0067 (6)	−0.0013 (6)
C11	0.0193 (8)	0.0176 (7)	0.0200 (8)	−0.0034 (6)	0.0024 (6)	−0.0011 (6)
C12	0.0335 (10)	0.0342 (9)	0.0216 (9)	0.0088 (8)	−0.0004 (7)	−0.0013 (7)
C13	0.0387 (11)	0.0375 (10)	0.0303 (10)	−0.0098 (8)	−0.0067 (8)	0.0095 (8)

Geometric parameters (Å, º)

S1—C4	1.7096 (18)	C2—H2A	0.9900
S1—C3	1.7186 (18)	C2—H2B	0.9900
S2—C10	1.7232 (16)	C3—C6	1.352 (2)
S2—C11	1.7372 (18)	C4—C5	1.351 (2)
S3—C11	1.7396 (18)	C4—H4	0.9500
S3—C12	1.812 (2)	C5—C6	1.423 (2)
O1—C9	1.2179 (18)	C5—H5	0.9500
N1—C8	1.456 (2)	C6—C7	1.501 (2)
N1—C7	1.4614 (18)	C7—H7A	0.9900
N1—C1	1.467 (2)	C7—H7B	0.9900
N2—C9	1.359 (2)	C8—C9	1.510 (2)
N2—C10	1.373 (2)	C8—H8A	0.9900
N2—H2	0.885 (9)	C8—H8B	0.9900
N3—C10	1.300 (2)	C12—C13	1.490 (3)
N3—N4	1.3914 (18)	C12—H12A	0.9900
N4—C11	1.2921 (19)	C12—H12B	0.9900
C1—C2	1.515 (2)	C13—H13A	0.9800
C1—H1A	0.9900	C13—H13B	0.9800
C1—H1B	0.9900	C13—H13C	0.9800
C2—C3	1.491 (2)		
C4—S1—C3	91.75 (7)	C5—C6—C7	125.60 (13)
C10—S2—C11	85.86 (8)	N1—C7—C6	110.02 (11)
C11—S3—C12	102.89 (8)	N1—C7—H7A	109.7
C8—N1—C7	110.75 (11)	C6—C7—H7A	109.7
C8—N1—C1	111.43 (12)	N1—C7—H7B	109.7
C7—N1—C1	110.99 (12)	C6—C7—H7B	109.7
C9—N2—C10	123.21 (13)	H7A—C7—H7B	108.2
C9—N2—H2	117.7 (13)	N1—C8—C9	110.00 (13)
C10—N2—H2	119.1 (13)	N1—C8—H8A	109.7
C10—N3—N4	112.50 (12)	C9—C8—H8A	109.7
C11—N4—N3	111.23 (13)	N1—C8—H8B	109.7
N1—C1—C2	109.60 (13)	C9—C8—H8B	109.7
N1—C1—H1A	109.8	H8A—C8—H8B	108.2
C2—C1—H1A	109.8	O1—C9—N2	121.50 (15)
N1—C1—H1B	109.8	O1—C9—C8	122.81 (15)
C2—C1—H1B	109.8	N2—C9—C8	115.69 (13)
H1A—C1—H1B	108.2	N3—C10—N2	121.95 (13)
C3—C2—C1	108.17 (12)	N3—C10—S2	114.88 (12)

C3—C2—H2A	110.1	N2—C10—S2	123.17 (12)
C1—C2—H2A	110.1	N4—C11—S2	115.51 (12)
C3—C2—H2B	110.1	N4—C11—S3	126.62 (13)
C1—C2—H2B	110.1	S2—C11—S3	117.83 (9)
H2A—C2—H2B	108.4	C13—C12—S3	113.02 (12)
C6—C3—C2	124.21 (14)	C13—C12—H12A	109.0
C6—C3—S1	111.17 (12)	S3—C12—H12A	109.0
C2—C3—S1	124.61 (11)	C13—C12—H12B	109.0
C5—C4—S1	111.89 (12)	S3—C12—H12B	109.0
C5—C4—H4	124.1	H12A—C12—H12B	107.8
S1—C4—H4	124.1	C12—C13—H13A	109.5
C4—C5—C6	112.24 (14)	C12—C13—H13B	109.5
C4—C5—H5	123.9	H13A—C13—H13B	109.5
C6—C5—H5	123.9	C12—C13—H13C	109.5
C3—C6—C5	112.94 (14)	H13A—C13—H13C	109.5
C3—C6—C7	121.45 (13)	H13B—C13—H13C	109.5

C10—N3—N4—C11	0.50 (17)	C7—N1—C8—C9	−70.74 (16)
C8—N1—C1—C2	−165.54 (12)	C1—N1—C8—C9	165.18 (12)
C7—N1—C1—C2	70.53 (16)	C10—N2—C9—O1	2.6 (2)
N1—C1—C2—C3	−49.63 (17)	C10—N2—C9—C8	−178.09 (13)
C1—C2—C3—C6	16.2 (2)	N1—C8—C9—O1	100.49 (17)
C1—C2—C3—S1	−165.28 (12)	N1—C8—C9—N2	−78.85 (16)
C4—S1—C3—C6	−0.65 (13)	N4—N3—C10—N2	178.63 (12)
C4—S1—C3—C2	−179.37 (14)	N4—N3—C10—S2	−1.53 (16)
C3—S1—C4—C5	0.16 (13)	C9—N2—C10—N3	175.29 (14)
S1—C4—C5—C6	0.36 (18)	C9—N2—C10—S2	−4.5 (2)
C2—C3—C6—C5	179.69 (14)	C11—S2—C10—N3	1.57 (12)
S1—C3—C6—C5	0.97 (17)	C11—S2—C10—N2	−178.59 (13)
C2—C3—C6—C7	0.9 (2)	N3—N4—C11—S2	0.73 (16)
S1—C3—C6—C7	−177.84 (12)	N3—N4—C11—S3	−176.86 (10)
C4—C5—C6—C3	−0.9 (2)	C10—S2—C11—N4	−1.29 (12)
C4—C5—C6—C7	177.88 (15)	C10—S2—C11—S3	176.53 (10)
C8—N1—C7—C6	−174.53 (12)	C12—S3—C11—N4	−16.16 (16)
C1—N1—C7—C6	−50.20 (16)	C12—S3—C11—S2	166.30 (9)
C3—C6—C7—N1	15.4 (2)	C11—S3—C12—C13	−103.33 (14)
C5—C6—C7—N1	−163.23 (14)		

Hydrogen-bond geometry (Å, º)

D—H···*A*	*D*—H	H···*A*	*D*···*A*	*D*—H···*A*
C12—H12*B*···N1^{i}	0.99	2.60	3.473 (3)	147
N2—H2···N3^{ii}	0.89 (1)	2.02 (1)	2.902 (2)	171 (2)
C5—H5···O1^{iii}	0.95	2.46	3.279 (2)	145

Symmetry codes: (i) −*x*+1, −*y*+1, −*z*; (ii) −*x*+2, −*y*+1, −*z*; (iii) −*x*+3/2, *y*−1/2, −*z*+1/2.