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2,3,4-Tribromothiophene

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Key indicators: single-crystal X-ray study; T = 91 K; mean $\sigma(C-C) = 0.033 \text{ Å}$; R factor = 0.062; wR factor = 0.172; data-to-parameter ratio = 19.8.

In the title compound, C_4HBr_3S , there are two essentially planar molecules in the asymmetric unit. In the crystal structure, bifurcated $C-H\cdots Br$ hydrogen bonds link the molecules into chains. Weak $Br\cdots Br$ interactions $[Br\cdots Br=3.634\ (4)-3.691\ (4)\ Å]$ then lead to undulating sheets in the bc plane.

Related literature

For related polybromothiophene structures, see: Helmholdt *et al.* (2007); Murakami *et al.* (2002); Xie *et al.* (1997, 1998). For information on halogen···halogen contacts, see: Pedireddi *et al.* (1994). For details of the Cambridge Structural Database, see: Allen (2002).

Experimental

Crystal data

 C_4HBr_3S $M_r = 320.84$ Orthorhombic, $Pna2_1$ a = 12.4529 (11) Å b = 3.9724 (4) Å c = 28.846 (3) Å

Z = 8 Mo $K\alpha$ radiation $\mu = 17.14 \text{ mm}^{-1}$ T = 91 (2) K 0.17 × 0.06 × 0.02 mm

 $V = 1426.9 (2) \text{ Å}^3$

Data collection

Bruker APEXII CCD area-detector diffractometer Absorption correction: multi-scan (SADABS; Bruker, 2006) $T_{\min} = 0.434$, $T_{\max} = 0.710$

12082 measured reflections 2163 independent reflections 1852 reflections with $I > 2\sigma(I)$ $R_{\rm int} = 0.092$ $\theta_{\rm max} = 23.7^{\circ}$

Refinement

 $R[F^2 > 2\sigma(F^2)] = 0.061$ $wR(F^2) = 0.172$ S = 0.862163 reflections 109 parameters 1 restraint H-atom parameters constrained $\Delta \rho_{\rm max} = 3.39 \ {\rm e \ \mathring{A}^{-3}}$ $\Delta \rho_{\rm min} = -1.30 \ {\rm e \ \mathring{A}^{-3}}$ Absolute structure: Flack (1983), 1050 Friedel pairs Flack parameter: 0.11 (6)

Table 1Hydrogen-bond geometry (Å, °).

$\cdot A$

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

Data collection: *APEX2* (Bruker 2006); cell refinement: *APEX2* and *SAINT* (Bruker 2006); data reduction: *SAINT*; program(s) used to solve structure: *SHELXS97* (Sheldrick, 2008) and *TITAN* (Hunter & Simpson, 1999); program(s) used to refine structure: *SHELXL97* (Sheldrick, 2008) and *TITAN*; molecular graphics: *ORTEP-3* (Farrugia, 1997) and *Mercury* (Macrae *et al.*, 2006); software used to prepare material for publication: *SHELXL97*, *enCIFer* (Allen *et al.*, 2004) and *PLATON* (Spek, 2003).

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Supplementary data and figures for this paper are available from the IUCr electronic archives (Reference: HB2706).

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2,3,4-Tribromothiophene

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S1. Comment

Brominated thiophenes are very important intermediates in the construction of thiophene oligomers and polymers for use in optoelectronics. In some cases, it is important to have one or two α -positions free for further oxidative coupling. The 2,3,4-tribromo derivative is not easy to access, as the 2- and 5-positions are normally substituted first, and so it is normally synthesized *via* debromination from tetrabromothiophene (Xie *et al.*, 1998).

The asymmetric unit of the title compound, (I), $C_8H_2Br_6S_2$, consists of two discrete tribromothiophene molecules A & B (Fig. 1). Each molecule is essentially planar with r.m.s. deviations from the mean planes through all non-hydrogen atoms of 0.0194 and 0.0286 Å for A and B respectively. The dihedral angle between the A and B ring planes is 0.9 (4)° but they are well separated with a centroid to centroid distance of 6.3 Å.

In the crystal of (I) bifurcated C—H···Br hydrogen bonds (Table 1) form chains of like molecules that pack in an obverse fashion along a. The structure is further stabilized by an extensive network of weak Br···Br interactions with Br···Br distances in the range 3.634 (4)Å (Br3A···Br2Bⁱ, i = 1 - x, 1 - y, -1/2 + z; $\theta_1 = 156.7^{\circ}$ and $\theta_2 = 117.5^{\circ}$) (Pedireddi *et al.*, 1994) to 3.691 (4)Å (Br3A···Br2Aⁱⁱ ii = -1/2 + x, 1/2 - y, z; $\theta_1 = 161.8^{\circ}$ and $\theta_2 = 84.7^{\circ}$). These contacts link the chains of molecules into undulating sheets in the *bc* plane (Fig. 2).

S2. Experimental

2,3,4-Tribromothiophene, prepared by the method of Xie *et al.* (1998), was dissolved in methanol. Colourless plates of (I) were grown by slow diffusion of water into the solution.

S3. Refinement

The crystals were small and very weakly diffracting and little data were obtainable beyond $\theta = 23^{\circ}$. This clearly contributes to the relatively high R factor and poor precision of the data in this determination. The C-bound H atoms were placed geometrically (C—H = 0.95 Å) and refined as riding with $U_{\rm iso}(H) = 1.2 U_{\rm eq}(C)$. A number of high peaks were found in the final difference map in the vicinity of the Br atoms in both molecules. The deepest hole is 0.98Å from Br3B.

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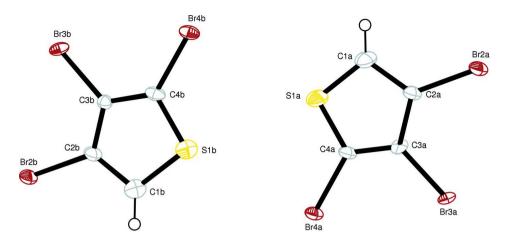


Figure 1The asymmetric unit of (I), with 50% displacement ellipsoids for the non-hydrogen atoms.

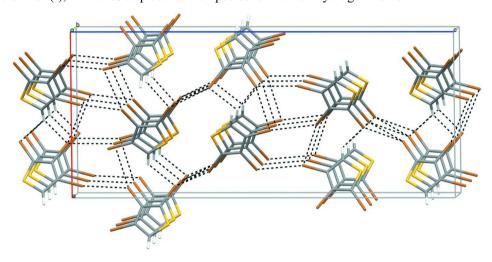


Figure 2Crystal packing of (I) with C—H···Br hydrogen bonds and Br···Br interactions drawn as dashed lines.

2,3,4-Tribromothiophene

Crystal data C₄HBr₃S

 $M_r = 320.84$ Orthorhombic, $Pna2_1$

Hall symbol: P 2c -2n

a = 12.4529 (11) Åb = 3.9724 (4) Å

c = 28.846 (3) Å

 $V = 1426.9 (2) \text{ Å}^3$

Z = 8

Data collection

Bruker APEXII CCD area-detector diffractometer

Radiation source: fine-focus sealed tube

F(000) = 1168

 $D_{\rm x} = 2.987 \; {\rm Mg \; m^{-3}}$

Mo $K\alpha$ radiation, $\lambda = 0.71073 \text{ Å}$

Cell parameters from 1448 reflections

 $\theta = 3.4-21.9^{\circ}$

 $\mu = 17.14 \text{ mm}^{-1}$

T = 91 K

Plate, colourless

 $0.17\times0.06\times0.02~mm$

Graphite monochromator

 ω scans

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Absorption correction: multi-scan	
(SADABS; Bruker, 2006)	
$T_{\min} = 0.434, T_{\max} = 0.710$	
12082 measured reflections	
2163 independent reflections	
1852 reflections with $I > 2\sigma(I)$	

$$R_{\text{int}} = 0.092$$

 $\theta_{\text{max}} = 23.7^{\circ}, \ \theta_{\text{min}} = 1.4^{\circ}$
 $h = -14 \rightarrow 14$
 $k = -4 \rightarrow 4$
 $l = -32 \rightarrow 32$

Refinement

Refinement on F^2 Least-squares matrix: full $R[F^2 > 2\sigma(F^2)] = 0.061$ $wR(F^2) = 0.172$ S = 0.862163 reflections 109 parameters 1 restraint Primary atom site location: structure-invariant direct methods Secondary atom site location: difference Fourier Hydrogen site location: inferred from neighbouring sites
H-atom parameters constrained $w = 1/[\sigma^2(F_o^2) + (0.1079P)^2 + 95.665P]$ where $P = (F_o^2 + 2F_c^2)/3$ $(\Delta/\sigma)_{max} = 0.001$ $\Delta\rho_{max} = 3.39 \text{ e Å}^{-3}$ $\Delta\rho_{min} = -1.30 \text{ e Å}^{-3}$ Absolute structure: Flack (1983), 1050 Friedel pairs
Absolute structure parameter: 0.11 (6)

Special details

map

Experimental. As the crystals were small and very weakly diffracting, data were collected using 55 sec exposures per frame.

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 F-factors based on ALL data will be even larger.

Fractional atomic coordinates and isotropic or equivalent isotropic displacement parameters (\mathring{A}^2)

	x	y	Z	$U_{ m iso}$ */ $U_{ m eq}$	
S1A	0.6553 (5)	0.6506 (19)	0.2528 (2)	0.0307 (15)	
C1A	0.723 (2)	0.726 (7)	0.2042 (10)	0.0307 (15)	
H1A	0.7916	0.8311	0.2015	0.037*	
C2A	0.6527 (19)	0.592 (6)	0.1649 (8)	0.0229 (6)	
Br2A	0.69172 (17)	0.6009 (6)	0.10260 (10)	0.0229 (6)	
C3A	0.5527 (17)	0.441 (7)	0.1819 (9)	0.021 (5)	
Br3A	0.44805 (17)	0.2573 (6)	0.14378 (10)	0.0183 (7)	
C4A	0.5485 (18)	0.455 (6)	0.2298 (8)	0.0197 (6)	
Br4A	0.43447 (16)	0.3131 (7)	0.26658 (9)	0.0197 (6)	
S1B	0.6092 (5)	0.3531 (17)	0.3764(2)	0.0268 (14)	
C1B	0.542(2)	0.270(6)	0.4273 (10)	0.0268 (14)	
H1B	0.4743	0.1617	0.4311	0.032*	
C2B	0.6136 (18)	0.407(7)	0.4637 (8)	0.0227 (6)	
Br2B	0.57498 (17)	0.4088 (6)	0.52692 (10)	0.0227 (6)	
C3B	0.7118 (17)	0.544 (6)	0.4479 (8)	0.016 (5)	
Br3B	0.82097 (17)	0.7329 (6)	0.48587 (10)	0.0193 (7)	

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C4B Br4B	0.7212 (1 0.83237 (· ·	23 (6) 820 (7)	0.4001 (8) 0.36312 (9)	0.0206 (6) 0.0206 (6)	
Atomic a	lisplacement para	meters (Ų)				
	U^{11}	U^{22}	U^{33}	U^{12}	U^{13}	U^{23}
S1A	0.017 (3)	0.039 (4)	0.037 (4)	0.000(3)	-0.004 (3)	0.002 (3)
C1A	0.017(3)	0.039(4)	0.037 (4)	0.000(3)	-0.004(3)	0.002(3)
C2A	0.0147 (12)	0.0294 (16)	0.0246 (13)	-0.0022(10)	0.0041 (10)	0.0019 (12)
Br2A	0.0147 (12)	0.0294 (16)	0.0246 (13)	-0.0022 (10)	0.0041 (10)	0.0019 (12)
C3A	0.005 (10)	0.035 (14)	0.024 (13)	0.008 (10)	-0.002(9)	-0.006(12)
Br3A	0.0104(11)	0.0209 (16)	0.0237 (16)	-0.0040(9)	-0.0040(10)	-0.0015(9)
C4A	0.0138 (12)	0.0212 (11)	0.0243 (14)	-0.0028(9)	0.0055 (9)	-0.0012(14)
Br4A	0.0138 (12)	0.0212 (11)	0.0243 (14)	-0.0028 (9)	0.0055 (9)	-0.0012 (14)
S1B	0.023 (3)	0.023 (3)	0.034 (4)	0.004(3)	0.001 (3)	-0.005(3)
C1B	0.023 (3)	0.023 (3)	0.034 (4)	0.004(3)	0.001 (3)	-0.005(3)
C2B	0.0142 (11)	0.0305 (15)	0.0235 (13)	-0.0007 (10)	0.0037 (10)	0.0040 (12)
Br2B	0.0142 (11)	0.0305 (15)	0.0235 (13)	-0.0007 (10)	0.0037 (10)	0.0040 (12)
СЗВ	0.016 (11)	0.015 (11)	0.017 (12)	0.000 (9)	0.000 (9)	0.002 (10)
Br3B	0.0090 (11)	0.0200 (16)	0.0290 (17)	0.0022 (10)	-0.0020 (10)	-0.0028 (10)
C4B	0.0125 (11)	0.0198 (10)	0.0295 (15)	0.0030 (10)	0.0056 (10)	0.0023 (14)
Br4B	0.0125 (11)	0.0198 (10)	0.0295 (15)	0.0030 (10)	0.0056 (10)	0.0023 (14)
Geometr	ic parameters (Å,	9				
S1A—C	44A	1.68 (2)		S1B—C4B		69 (2)
S1A—C	74A 71A	1.68 (2) 1.66 (3))	S1B—C1B	1.	72 (3)
S1A—C S1A—C C1A—C	4A 11A C2A	1.68 (2) 1.66 (3) 1.53 (4))	S1B—C1B C1B—C2B	1. ⁻ 1	72 (3) 48 (4)
S1A—C S1A—C C1A—C C1A—F	4A 11A 22A 111A	1.68 (2) 1.66 (3) 1.53 (4) 0.9500)	S1B—C1B C1B—C2B C1B—H1B	1. 1. 0.	72 (3) 48 (4) 9500
S1A—C S1A—C C1A—C C1A—H C2A—C	14A 11A 12A 11A 13A	1.68 (2) 1.66 (3) 1.53 (4) 0.9500 1.47 (3)))	S1B—C1B C1B—C2B C1B—H1B C2B—C3B	1. 1. 0. 1.	72 (3) 48 (4) 9500 41 (3)
S1A—C S1A—C C1A—C C1A—H C2A—C	44A 21A 22A 11A 23A 3r2A	1.68 (2) 1.66 (3) 1.53 (4) 0.9500 1.47 (3) 1.86 (2))))	S1B—C1B C1B—C2B C1B—H1B C2B—C3B C2B—Br2B	1. 1. 0. 1.	72 (3) 48 (4) 9500 41 (3) 89 (2)
S1A—C S1A—C C1A—C C1A—H C2A—C C2A—E C3A—C	44A C2A I1A C3A Br2A	1.68 (2) 1.66 (3) 1.53 (4) 0.9500 1.47 (3) 1.86 (2) 1.38 (3)))))	S1B—C1B C1B—C2B C1B—H1B C2B—C3B C2B—Br2B C3B—C4B	1. 1. 0. 1. 1.	72 (3) 48 (4) 9500 41 (3) 89 (2) 39 (3)
S1A—C S1A—C C1A—H C2A—C C2A—E C3A—C	44A 71A 72A 11A 73A 8r2A 74A 8r3A	1.68 (2) 1.66 (3) 1.53 (4) 0.9500 1.47 (3) 1.86 (2))))))	S1B—C1B C1B—C2B C1B—H1B C2B—C3B C2B—Br2B	1. 1. 0. 1. 1. 1.	72 (3) 48 (4) 9500 41 (3) 89 (2)
S1A—C S1A—C C1A—C C1A—H C2A—C C2A—E C3A—C C3A—E	44A 71A 72A 11A 73A 8r2A 74A 8r3A	1.68 (2) 1.66 (3) 1.53 (4) 0.9500 1.47 (3) 1.86 (2) 1.38 (3) 1.86 (2))))))	S1B—C1B C1B—C2B C1B—H1B C2B—C3B C2B—Br2B C3B—C4B C3B—Br3B	1. 1. 0. 1. 1. 1.	72 (3) 48 (4) 9500 41 (3) 89 (2) 39 (3) 90 (2)
S1A—C S1A—C C1A—C C1A—H C2A—C C2A—E C3A—C C3A—E C4A—E	44A 21A 22A 31A 33A 3r2A 3r3A 3r4A	1.68 (2) 1.66 (3) 1.53 (4) 0.9500 1.47 (3) 1.86 (2) 1.38 (3) 1.86 (2)))))))))))))))))))))))))))))))	S1B—C1B C1B—C2B C1B—H1B C2B—C3B C2B—Br2B C3B—C4B C3B—Br3B C4B—Br4B	1. 1. 0. 1. 1. 1. 97	72 (3) 48 (4) 9500 41 (3) 89 (2) 39 (3) 90 (2) 86 (2)
S1A—C S1A—C C1A—C C1A—F C2A—E C3A—C C3A—E C4A—E	44A C2A IIA C3A Br2A C4A Br3A Br4A	1.68 (2) 1.66 (3) 1.53 (4) 0.9500 1.47 (3) 1.86 (2) 1.38 (3) 1.86 (2) 98.9 (1)))))))))))))))))))))))))))))))	S1B—C1B C1B—C2B C1B—H1B C2B—C3B C2B—Br2B C3B—C4B C3B—Br3B C4B—Br4B	1. 1. 0. 1. 1. 1. 97	72 (3) 48 (4) 9500 41 (3) 89 (2) 39 (3) 90 (2) 86 (2)
S1A—C S1A—C C1A—C C1A—F C2A—C C2A—E C3A—E C4A—E C4A—S C2A—C	44A 71A 72A 811A 73A 812A 74A 813A 814A 814A—C1A	1.68 (2) 1.66 (3) 1.53 (4) 0.9500 1.47 (3) 1.86 (2) 1.86 (2) 1.86 (2) 98.9 (1) 105.5 ())))))))))))))))))))))))))))))	S1B—C1B C1B—C2B C1B—H1B C2B—C3B C2B—Br2B C3B—C4B C3B—Br3B C4B—Br4B C4B—S1B—C1B C2B—C1B—S1B	1. 1. 0. 1. 1. 1. 97 10	72 (3) 48 (4) 9500 41 (3) 89 (2) 39 (3) 90 (2) 86 (2) 7.7 (12) 93.8 (17)
S1A—C S1A—C C1A—C C1A—H C2A—C C2A—E C3A—E C4A—E C4A—S C2A—C S1A—C	24A 21A 22A 31A 23A 3r2A 24A 3r3A 3r4A 3r4A 3r4A 21A—C1A 21A—S1A	1.68 (2) 1.66 (3) 1.53 (4) 0.9500 1.47 (3) 1.86 (2) 1.38 (3) 1.86 (2) 1.86 (2) 98.9 (1) 105.5 (1)))))))) 3) 17)	\$1B—C1B C1B—C2B C1B—H1B C2B—C3B C2B—Br2B C3B—C4B C3B—Br3B C4B—Br4B C4B—S1B—C1B C2B—C1B—S1B C2B—C1B—H1B	1. 1. 0. 1. 1. 1. 97 10 12 12	72 (3) 48 (4) 9500 41 (3) 89 (2) 39 (3) 90 (2) 86 (2) 7.7 (12) 93.8 (17) 98.1
S1A—C S1A—C C1A—F C2A—C C2A—E C3A—C C3A—E C4A—S C2A—C C2A—C C2A—C	24A 21A 22A 31A 23A 3r2A 24A 3r3A 3r4A 3r4A 21A—C1A 21A—S1A 21A—H1A	1.68 (2) 1.66 (3) 1.53 (4) 0.9500 1.47 (3) 1.86 (2) 1.38 (3) 1.86 (2) 1.86 (2) 98.9 (1) 105.5 (1) 127.2 127.2)))))))))))))))))))))))))))))))))))	S1B—C1B C1B—C2B C1B—H1B C2B—C3B C2B—Br2B C3B—C4B C3B—Br3B C4B—Br4B C4B—S1B—C1B C2B—C1B—S1B C2B—C1B—H1B S1B—C1B—H1B	1. 0. 1. 1. 1. 1. 97 10 12 11	72 (3) 48 (4) 9500 41 (3) 89 (2) 39 (3) 90 (2) 86 (2) 7.7 (12) 93.8 (17) 98.1
S1A—C S1A—C C1A—F C2A—C C2A—E C3A—C C3A—E C4A—S C2A—C C2A—C C3A—C C3A—C	24A 21A 22A 31A 23A 3r2A 24A 3r3A 3r4A 3r4A 21A—C1A 21A—S1A 21A—H1A	1.68 (2) 1.66 (3) 1.53 (4) 0.9500 1.47 (3) 1.86 (2) 1.38 (3) 1.86 (2) 98.9 (1) 105.5 (127.2) 127.2 112 (2)))))))))))))))))))))))))))))))))))))))	S1B—C1B C1B—C2B C1B—H1B C2B—C3B C2B—Br2B C3B—C4B C3B—Br3B C4B—Br4B C4B—S1B—C1B C2B—C1B—S1B C2B—C1B—H1B S1B—C1B—H1B C3B—C2B—C1B	1. 0. 1. 1. 1. 1. 97 10 12 12 11	72 (3) 48 (4) 9500 41 (3) 89 (2) 39 (3) 90 (2) 86 (2) 7.7 (12) 93.8 (17) 98.1 98.1 99.1 9
S1A—C S1A—C C1A—C C1A—F C2A—E C3A—E C4A—E C4A—S C2A—C S1A—C C3A—C C3A—C	24A 21A 22A 31A 23A 3r2A 24A 3r3A 3r4A 3r4A 21A—C1A 21A—S1A 21A—H1A 21A—H1A 22A—C1A	1.68 (2) 1.66 (3) 1.53 (4) 0.9500 1.47 (3) 1.86 (2) 1.38 (3) 1.86 (2) 98.9 (1) 105.5 (127.2 127.2 112 (2) 123.5 ()))))))) () () () () () ()	S1B—C1B C1B—C2B C1B—H1B C2B—C3B C2B—Br2B C3B—C4B C3B—Br3B C4B—Br4B C4B—S1B—C1B C2B—C1B—S1B C2B—C1B—H1B S1B—C1B—H1B C3B—C2B—C1B C3B—C2B—C1B C3B—C2B—Br2B	1. 1. 0. 1. 1. 1. 97 10 12 11 12 12	72 (3) 48 (4) 9500 41 (3) 89 (2) 39 (3) 90 (2) 86 (2) 7.7 (12) 93.8 (17) 98.1 98.1 98.1 99.2 9
S1A—C S1A—C C1A—C C1A—H C2A—C C2A—E C3A—E C4A—E C4A—S C2A—C C3A—C C3A—C C3A—C C3A—C	24A 21A 22A 31A 23A 3r2A 24A 3r3A 3r4A 3r4A 3r4A 3r4A 3r4A 3r4A 3r	1.68 (2) 1.66 (3) 1.53 (4) 0.9500 1.47 (3) 1.86 (2) 1.38 (3) 1.86 (2) 1.86 (2) 1.98.9 (1) 105.5 (127.2 127.2 112 (2) 123.5 (123.9 ())))))))))))))))))))))))))))))))))))))	S1B—C1B C1B—C2B C1B—H1B C2B—C3B C2B—Br2B C3B—C4B C3B—Br3B C4B—Br4B C4B—S1B—C1B C2B—C1B—S1B C2B—C1B—H1B S1B—C1B—H1B C3B—C2B—C1B C3B—C2B—Br2B C1B—C2B—Br2B	1. 1. 0. 1. 1. 1. 1. 97 10 12 11 12 11	72 (3) 48 (4) 9500 41 (3) 89 (2) 39 (3) 90 (2) 86 (2) 7.7 (12) 93.8 (17) 98.1 98.1 98.1 99.2 9
S1A—C S1A—C C1A—F C2A—C C2A—E C3A—C C3A—E C4A—S C2A—C C2A—C C3A—C C3A—C C3A—C C3A—C C3A—C C3A—C	44A 61A 62A 61A 63A 63A 64A 63A 64A 63A 61A—C1A 61A—H1A 61A—H1A 62A—C1A 62A—C1A 62A—Br2A 63A—C2A	1.68 (2) 1.66 (3) 1.53 (4) 0.9500 1.47 (3) 1.86 (2) 1.38 (3) 1.86 (2) 1.86 (2) 1.85 (2) 1.27.2 127.2 127.2 112 (2) 123.5 (110 (2)	18) 18) 19)	S1B—C1B C1B—C2B C1B—H1B C2B—C3B C2B—Br2B C3B—C4B C3B—Br3B C4B—Br4B C4B—S1B—C1B C2B—C1B—H1B S1B—C1B—H1B C3B—C2B—C1B C3B—C2B—C1B C3B—C2B—Br2B C1B—C2B—Br2B C4B—C3B—C2B	1. 0. 1. 1. 1. 1. 97 10 12 11 12 11 12	72 (3) 48 (4) 9500 41 (3) 89 (2) 39 (3) 90 (2) 86 (2) 7.7 (12) 93.8 (17) 98.1 98.1 98.1 99.2 10.7 11.7 12.1 13.8 14.7 15.8 16.7 17.7 18.1 18.1 18.1 19.2 19.3 1
S1A—C S1A—C C1A—F C2A—C C2A—E C3A—C C3A—E C4A—S C4A—S C2A—C C3A—C C3A—C C3A—C C3A—C C3A—C C3A—C C4A—C	44A 61A 62A 61A 63A 672A 64A 673A 674A 61A—C1A 61A—S1A 61A—H1A 61A—H1A 62A—C1A 62A—C1A 62A—Br2A 62A—Br2A 63A—C2A 63A—C2A	1.68 (2) 1.66 (3) 1.53 (4) 0.9500 1.47 (3) 1.86 (2) 1.38 (3) 1.86 (2) 1.86 (2) 1.98.9 (1) 105.5 (127.2) 127.2 112 (2) 123.5 (123.9 (110 (2)) 125.6 (125.6 (125.6)	18) 18) 19)	S1B—C1B C1B—C2B C1B—H1B C2B—C3B C2B—Br2B C3B—C4B C3B—Br3B C4B—Br4B C4B—S1B—C1B C2B—C1B—S1B C2B—C1B—H1B S1B—C1B—H1B C3B—C2B—C1B C3B—C2B—Br2B C1B—C2B—Br2B C4B—C3B—C2B C4B—C3B—C2B	1. 1. 0. 1. 1. 1. 1. 97 10 12 11 12 12 11 12 12	72 (3) 48 (4) 9500 41 (3) 89 (2) 39 (3) 90 (2) 86 (2) 7.7 (12) 93.8 (17) 98.1 98.1 98.1 98.1 98.1 99.1 99.1 99.1
S1A—C S1A—C C1A—C C1A—E C2A—C C2A—E C3A—E C4A—E C4A—S C2A—C C3A—C C3A—C C1A—C C1A—C C4A—C C4A—C C4A—C	24A 21A 22A 211A 23A 24A 24A 27A 21A—C1A 21A—S1A 21A—H1A 21A—H1A 22A—C1A 22A—C1A 22A—Br2A 23A—Br2A 23A—Br3A 23A—Br3A	1.68 (2) 1.66 (3) 1.53 (4) 0.9500 1.47 (3) 1.86 (2) 1.38 (3) 1.86 (2) 1.86 (2) 1.98.9 (1) 105.5 (127.2 127.2 112 (2) 123.5 (123.9 (110 (2) 125.6 (124.0 (18) 18) 18) 19) 19) 18)	S1B—C1B C1B—C2B C1B—H1B C2B—C3B C2B—Br2B C3B—C4B C3B—Br3B C4B—Br4B C4B—S1B—C1B C2B—C1B—S1B C2B—C1B—H1B S1B—C1B—H1B C3B—C2B—C1B C3B—C2B—Br2B C1B—C2B—Br2B C4B—C3B—Br3B C4B—C3B—Br3B C2B—C3B—Br3B	1. 1. 0. 1. 1. 1. 1. 97 10 12 12 11 12 12 11 12 12	72 (3) 48 (4) 9500 41 (3) 89 (2) 39 (3) 90 (2) 86 (2) 7.7 (12) 93.8 (17) 98.1 98.1 98.1 99.2.1 (17) 99.2.1 (18) 99.2.1 (18) 99.2.1 (17) 99.2.1 (18) 99.2.1 (17) 99.2.1 (18) 99.2.1 (17) 99.2.1 (18) 99.2.1 (17) 99.2.1 (18) 99.2.1 (17) 99.2.1 (18) 99.2.1 (17)

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supporting information

Hydrogen-bond geometry (Å, °)

D—H···A	<i>D</i> —H	$H\cdots A$	D··· A	<i>D</i> —H··· <i>A</i>
$C1A$ — $H1A$ ···Br $3A^{i}$	0.95	3.04	3.89 (3)	149
C1A— $H1A$ ···Br $4A$ ⁱ	0.95	2.96	3.68 (3)	134
C1B— $H1B$ ···Br $3B$ ⁱⁱ	0.95	2.93	3.79 (3)	151
C1B— $H1B$ ···Br $4B$ ⁱⁱ	0.95	2.97	3.66 (2)	131

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

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