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Hydrogen-bonded structures and interaction energies in two forms of the SGLT-2 inhibitor sotagliflozin

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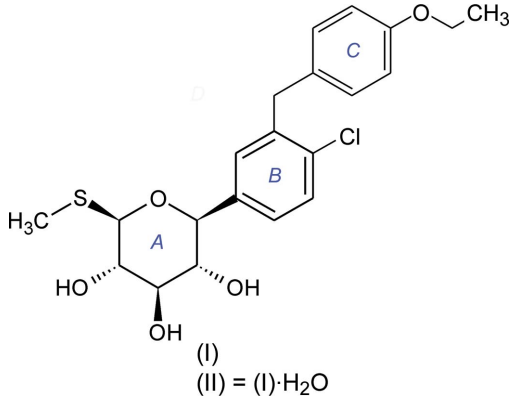
CCDC references: 1567263; 1567262

Supporting information: this article has supporting information at journals.iucr.org/c

The sotagliflozin molecule exhibits two fundamentally different molecular conformations in form 1 {systematic name: (2*S*,3*R*,4*R*,5*S*,6*R*)-2-[4-chloro-3-(4-ethoxybenzyl)phenyl]-6-(methylsulfanyl)tetrahydro-2*H*-pyran-3,4,5-triol, $C_{21}H_{25}ClO_5S$, (I)} and the monohydrate [$C_{21}H_{25}ClO_5S{\cdot}H_2O$, (II)]. Both crystals display hydrogen-bonded layers formed by intermolecular interactions which involve the three –OH groups of the xyloside fragment of the molecule. The layer architectures of (I) and (II) contain a non-hydrogen-bonded molecule–molecule interaction along the short crystallographic axis (*a* axis) whose total *PIXEL* energy exceeds that of each hydrogen-bonded molecule–molecule pair. The hydrogen-bonded layer of (I) has the topology of the 4-connected **sql** net and that formed by the water and sotagliflozin molecules of (II) has the topology of a 3,7-connected net.

1. Introduction

Sotagliflozin [systematic name: (2*S*,3*R*,4*R*,5*S*,6*R*)-2-[4-chloro-3-(4-ethoxybenzyl)phenyl]-6-(methylsulfanyl)tetrahydro-2*H*-pyran-3,4,5-triol; see Scheme], is an experimental drug aimed at controlling blood glucose concentrations in patients with type 2 diabetes. It is an orally available L-xyloside-based compound that inhibits gastrointestinal absorption and renal reabsorption of glucose through the sodium–glucose cotransporter (SGLT) (Lapuerta *et al.*, 2015). The existence of two anhydrous crystalline forms of sotagliflozin, labelled form 1



(I)
(II) = (I)·H_2O

(m.p. 396 K) and form 2 (m.p. 407 K), was reported by De Paul *et al.* (2010). We report herein the crystal structures of form 1, denoted (I), and a monohydrate, denoted (II), of sotagliflozin and discuss the molecular conformations, hydrogen-bonded structures and intermolecular interaction energies.

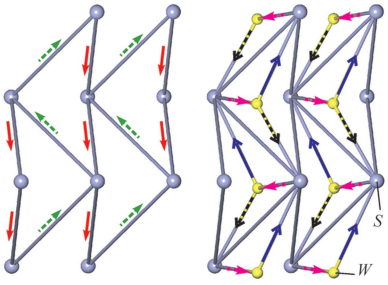


Table 1
Experimental details.

	(I)	(II)
Crystal data		
Chemical formula	$C_{21}H_{25}ClO_5S$	$C_{21}H_{25}ClO_5S\cdot H_2O$
M_r	424.92	442.93
Crystal system, space group	Orthorhombic, $P2_12_12_1$	Orthorhombic, $P2_12_12_1$
Temperature (K)	253	173
a, b, c (Å)	5.3945 (4), 9.1577 (5), 43.475 (4)	4.4659 (3), 9.8994 (8), 48.073 (5)
V (Å^3)	2147.7 (3)	2125.3 (3)
Z	4	4
Radiation type	Cu $K\alpha$	Cu $K\alpha$
μ (mm^{-1})	2.73	2.81
Crystal size (mm)	0.15 × 0.08 × 0.04	0.08 × 0.08 × 0.05
Data collection		
Diffractometer	Rigaku Xcalibur Ruby (Gemini ultra)	Rigaku Xcalibur Ruby (Gemini ultra)
Absorption correction	Multi-scan (*CrysAlis PRO*; Rigaku Oxford Diffraction, 2015)	Multi-scan (*CrysAlis PRO*; Rigaku Oxford Diffraction, 2015)
T_{min}, T_{max}	0.678, 1.000	0.560, 1.000
No. of measured, independent and observed [$I > 2\sigma(I)$] reflections	12259, 3849, 3081	11848, 3737, 3253
R_{int}	0.065	0.083
(sin $\theta/\lambda)_{max}$ (Å^{-1})	0.602	0.600
Refinement		
$R[F^2 > 2\sigma(F^2)]$, $wR(F^2)$, S	0.044, 0.108, 1.07	0.073, 0.149, 1.35
No. of reflections	3849	3737
No. of parameters	269	279
No. of restraints	3	8
H-atom treatment	H atoms treated by a mixture of independent and constrained refinement	H atoms treated by a mixture of independent and constrained refinement
$\Delta\rho_{max}$, $\Delta\rho_{min}$ (e Å^{-3})	0.17, −0.20	0.68, −0.39
Absolute structure	Flack x determined using 1021 quotients $[(I^+) - (I^-)]/[(I^+) + (I^-)]$ (Parsons *et al.*, 2013).	Flack *x* determined using 1098 quotients $[(I^+) - (I^-)]/[(I^+) + (I^-)]$ (Parsons *et al.*, 2013)
Absolute structure parameter	0.031 (18)	0.02 (3)

Computer programs: *CrysAlis PRO* (Rigaku Oxford Diffraction, 2015), *SHELXT* (Sheldrick, 2015*a*), *SHELXL2014* (Sheldrick, 2015*b*), *XP* (Bruker, 1998), *Mercury* (Macrae *et al.*, 2006), *TOPOS* (Blatov, 2006), *PLATON* (Spek, 2009) and *publCIF* (Westrip, 2010).

2. Experimental

2.1. Synthesis and crystallization

The title compound was synthesized in eight synthetic steps according to the procedure described by Goodwin *et al.* (2009), starting from commercially available (3a*S*,5*S*,6*R*,6a*S*)-5-hydroxymethyl-2,2-dimethyltetrahydrofuro[2,3-*d*]-1,3-dioxol-6-ol. Dissolving sotagliflozin in propan-2-ol at reflux temperature (80 mg ml^{-1}) and slow cooling of the solution yielded single crystals of (I). Single crystals of (II) were extracted from a mixture of (I) and (II) obtained after the slow addition of water to a methanol solution of sotagliflozin (80 mg ml^{-1}) at room temperature. The powder X-ray diffractogram (see Fig. S1 of the supporting information), as well as the melting point of (I) (396 K), correspond with the data of form 1 disclosed by De Paul *et al.* (2010). The existence of the monohydrate (II) has not been reported previously. This phase has a melting point of 344 K and the experimental powder pattern is shown in Fig. S2 of the supporting information.

2.2. Refinement

Crystal data, data collection and structure refinement details are summarized in Table 1. All H atoms were identified in difference maps. Methyl H atoms were idealized and included as rigid groups allowed to rotate but not tip and refined with $U_{iso}(H) = 1.5U_{eq}(C)$. All other H atoms bonded to C atoms were positioned geometrically and refined with $U_{iso}(H) = 1.2U_{eq}(C)$. Hydroxy H atoms were refined with restrained distances [O—H = 0.84 (1) Å; in (II), additionally, C4···H10 = 1.84 (1) Å and C5···H11 = 1.85 (1) Å] and their $U_{iso}(H)$ parameters were refined freely in the case of (I) and set at $1.2U_{eq}(O)$ in the case of (II). The water molecule of (II) was refined with restrained 1,1- and 1,2-distances [O—H = 0.82 (1) Å and H···H = 1.34 (1) Å], and the $U_{iso}(H)$ value was set at $1.5U_{eq}(O)$. The absolute structures of (I) and (II) were established by anomalous-dispersion effects and are consistent with the synthetic procedure. Two outlier reflections were omitted from the refinement of (I) and one outlier reflection was omitted from the refinement of (II).

2.3. Analysis of crystal structure data

The topologies of the hydrogen-bonded structures were determined and classified with the programs *ADS* and *IsoTest* of the *TOPOS* package (Blatov, 2006), in the manner described by Baburin & Blatov (2007).

Intermolecular interaction energies were calculated using the *PIXEL-CLP* package (Gavezzotti, 2002, 2003, 2011). C—H and O—H distances were recalculated to standard lengths by the *CLP* program. No optimization of molecular

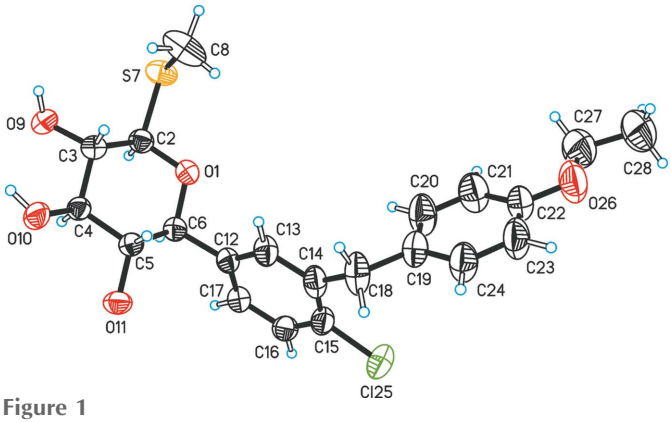


Figure 1
The asymmetric unit of (I), with displacement ellipsoids drawn at the 50% probability level and H atoms drawn as spheres of arbitrary size.

geometries was performed. An electron-density map was calculated on a three-dimensional grid, with a step size of 0.08 Å at the MP2/6-31G(d,p) level using *GAUSSIAN03* (Frisch *et al.*, 2004). A *PIXEL* condensation factor of 4 was applied, giving superpixels with a dimension of 0.32 × 0.32 × 0.32 Å. Details of the *PIXEL* results for (I) and (II) are contained in the supporting information.

3. Results and discussion

In the molecular structure of (I) (Fig. 1), six-membered ring *A* (atoms O1/C2–C6) of the L-xyloside fragment adopts a chair conformation. The orientation of the methanethiol substituent is such that an O1—C2—S7—C8 torsion angle of −63.5 (4)° is formed. The mean plane of ring *B* (atoms C12–C17) forms angles of 82.0 (1) and 85.5 (1)°, respectively, with the mean planes of rings *A* and *C* (atoms C19–C24). The ethoxy group is nearly coplanar with the benzyl ring.

Each of the three –OH groups of the xyloside unit donates one hydrogen bond and also accepts one such bond, resulting in the three intermolecular interactions O9—H9···O10^{i}, O10—H10···O11^{i} and O11—H11···O9^{ii} (Fig. 2*a*, and the

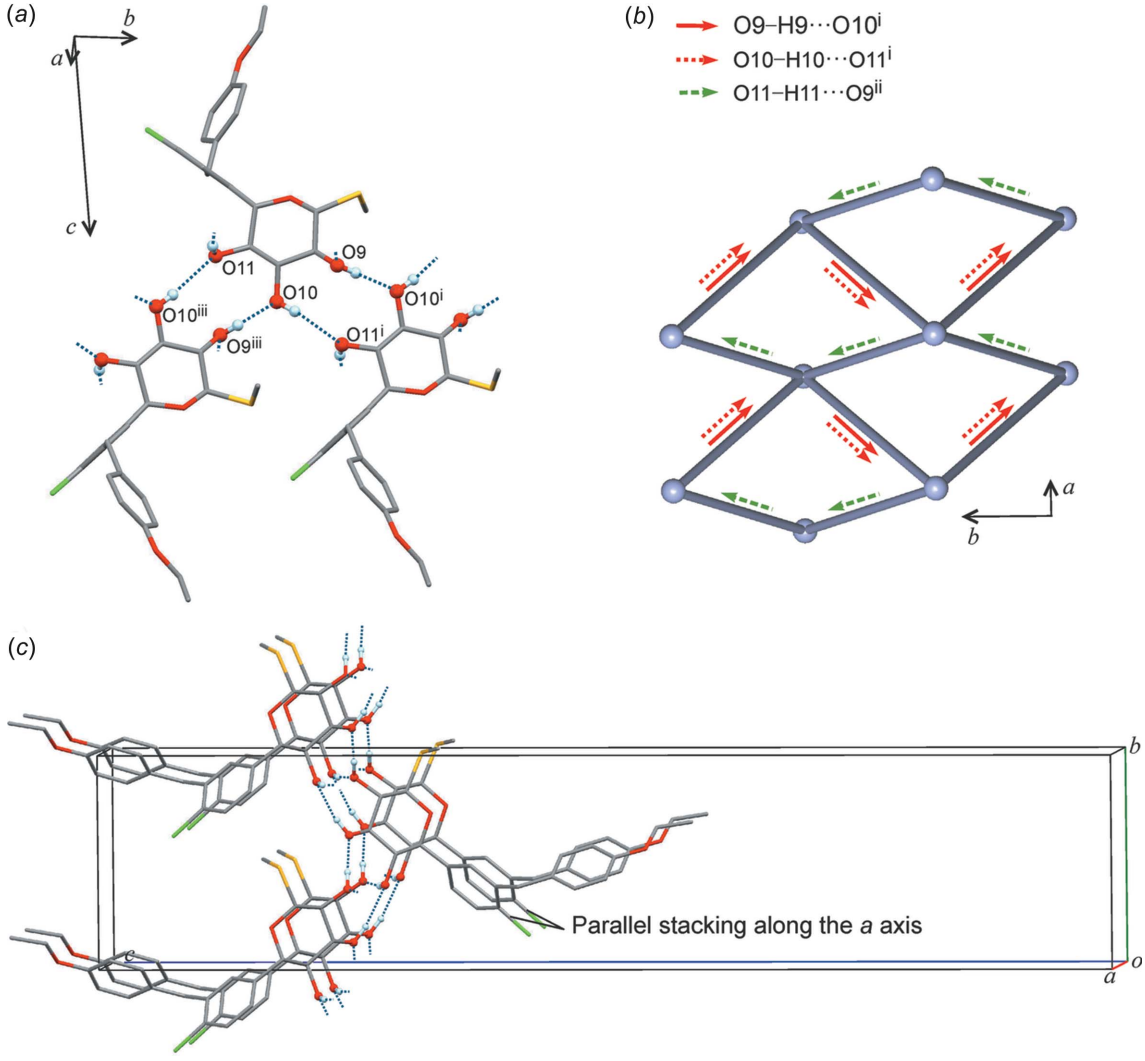


Figure 2
The hydrogen-bonded structure of (I). (*a*) A fragment of the hydrogen-bonded layer structure, showing two $R_2^2(10)$ rings. The symmetry codes are as defined in Table 2, and additionally (iii) $-x+2, y+\frac{1}{2}, -z+\frac{3}{2}$. (*b*) A representation of the L6$_4$[4^{4}6^2-**sql**] structure (viewed along the *c* axis) generated by depicting molecules as nodes and intermolecular hydrogen bonds as the links between nodes, with arrows indicating the type and direction of the hydrogen-bond interactions. (*c*) View of a hydrogen-bonded layer structure, highlighting the internal stacking of the non-hydrogen-bonded molecules.

Table 2
Hydrogen-bond geometry (Å, °) for (I).

D—H···A	D—H	H···A	D···A	D—H···A
O9—H9···O10^{i}	0.84 (1)	1.85 (2)	2.686 (4)	175 (5)
O10—H10···O11^{i}	0.84 (1)	2.23 (3)	2.970 (4)	147 (5)
O11—H11···O9^{ii}	0.84 (1)	2.01 (2)	2.837 (5)	170 (6)

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

Table 3
Hydrogen-bond geometry (Å, °) for (II).

D—H···A	D—H	H···A	D···A	D—H···A
O9—H9···O10^{i}	0.84 (1)	1.99 (2)	2.807 (7)	166 (7)
O10—H10···O1W	0.84 (1)	1.79 (2)	2.621 (7)	177 (3)
O11—H11···O9^{ii}	0.84 (1)	2.14 (4)	2.825 (7)	138 (5)
O1W—H1W···S7^{ii}	0.82 (1)	2.47 (2)	3.282 (5)	170 (8)
O1W—H2W···O11^{iii}	0.82 (1)	1.90 (3)	2.694 (6)	162 (7)

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

symmetry codes are as defined in Table 2). Therefore, six hydrogen bonds link each molecule to four neighbouring molecules *via* two one-point connections and *via* two two-point connections. The latter connections result in a chain consisting of fused $R_2^2(10)$ rings (Etter *et al.*, 1990; Bernstein *et al.*, 1995) which contains a twofold screw axis and propagates parallel to [010]. Altogether, O—H···O interactions connect molecules into a layer structure which lies parallel to the *ab* plane and has the topology of a square lattice ($4^4.6^2$-**sql**; Figs. 2*b* and 2*c*). The short descriptor of the hydrogen-bonded structure of (I) according to Hursthouse *et al.* (2015) is therefore L6_4[$4^4.6^2$-**sql**].

The asymmetric unit of (II) contains one formula unit (Fig. 3). The overlay in Fig. 4 illustrates that the conformation of the sotagliflozin molecule in (II) differs considerably from the geometry found in (I). Specifically, the O1—C2—S7—C8 torsion angle involving the methanethiol group at xyloside ring *A* is 66.4 (5)° and differs by approximately 130° from the corresponding parameter in (I). The angles between the mean plane of ring *B* on the one hand and those of planes *A* and *C* on the other are 42.7 (2) and 72.5 (2)°, respectively (differences of 40 and 13° in comparison to form 1). As observed in (I), the ethoxy substituent of the benzyl ring lies approximately in the plane of the ring.

Each sotagliflozin molecule of (II) is hydrogen bonded by a single O9—H9···O10^{i} or O11—H11···O9^{ii} interaction to each of four other sotagliflozin molecules (the symmetry codes are as defined in Table 3). The resulting hydrogen-bonded layer structure lies in the *ab* plane and exhibits the **sql** topology (Fig. 5*b*, left). The water molecule donates hydrogen bonds to a hydroxy group (O1W—H2W···O11^{iii}) and an S atom (O1W—H1W···S7^{ii}) of two different sotagliflozin molecules. Additionally, it also accepts a hydrogen bond from a third sotagliflozin molecule (O10—H10···O1W). The hydrogen-bonded layer structure contains chains of fused $R_3^3(9)$ and $R_3^3(12)$ rings (Fig. 5*a*), possesses twofold screw symmetry and lies parallel to the *b* axis. All together, each sotagliflozin molecule is hydrogen bonded to seven other (four sotagliflozin and three water) molecules. In the resulting binodal 3,7-connected net (Fig. 5*b*, right), each water molecule serves as an additional bridge for each of two pairs of hydrogen-bonded sotagliflozin molecules and also serves as a bridge between two sotagliflozin molecules that are indirectly linked to one another *via* a third such molecule. The topology of the 3,7-connected net can be described as $(3^2.4)(3^4.4^8.5^4.6^5)$. The descriptor for the overall hydrogen-bonded structure of (II) according to Hursthouse *et al.* (2015) is therefore L$3_3.7_7$[$(3^2.4)(3^4.4^8.5^4.6^5)$].

The *PIXEL-CLP* software was used to assess the relative importance of individual intermolecular interactions in (I) and (II) (Gavezzotti, 2002, 2003, 2011). A total *PIXEL* energy

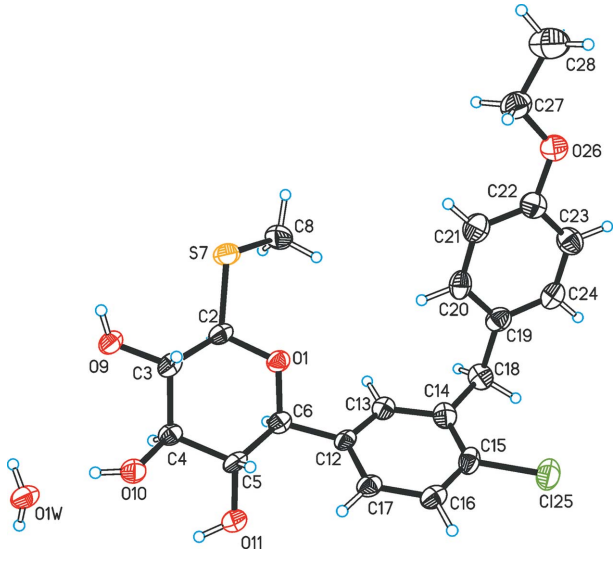


Figure 3
The asymmetric unit of (II), with displacement ellipsoids drawn at the 50% probability level and H atoms drawn as spheres of arbitrary size.

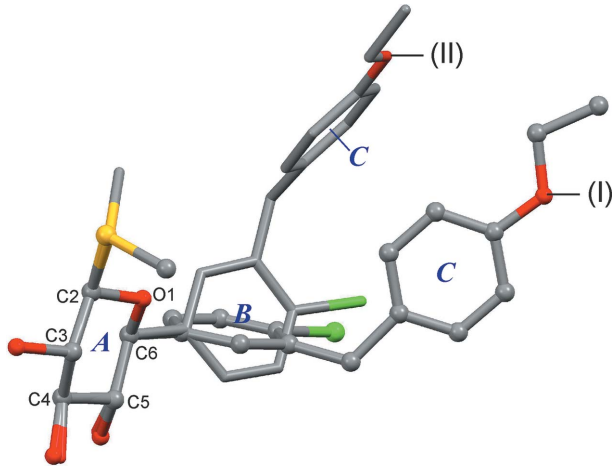


Figure 4
An overlay of the sotagliflozin molecules of (I) (atoms drawn as spheres) and (II), obtained by a least-squares fitting of the six-membered rings of their L-xyloside fragments (atoms O1/C2–C6).

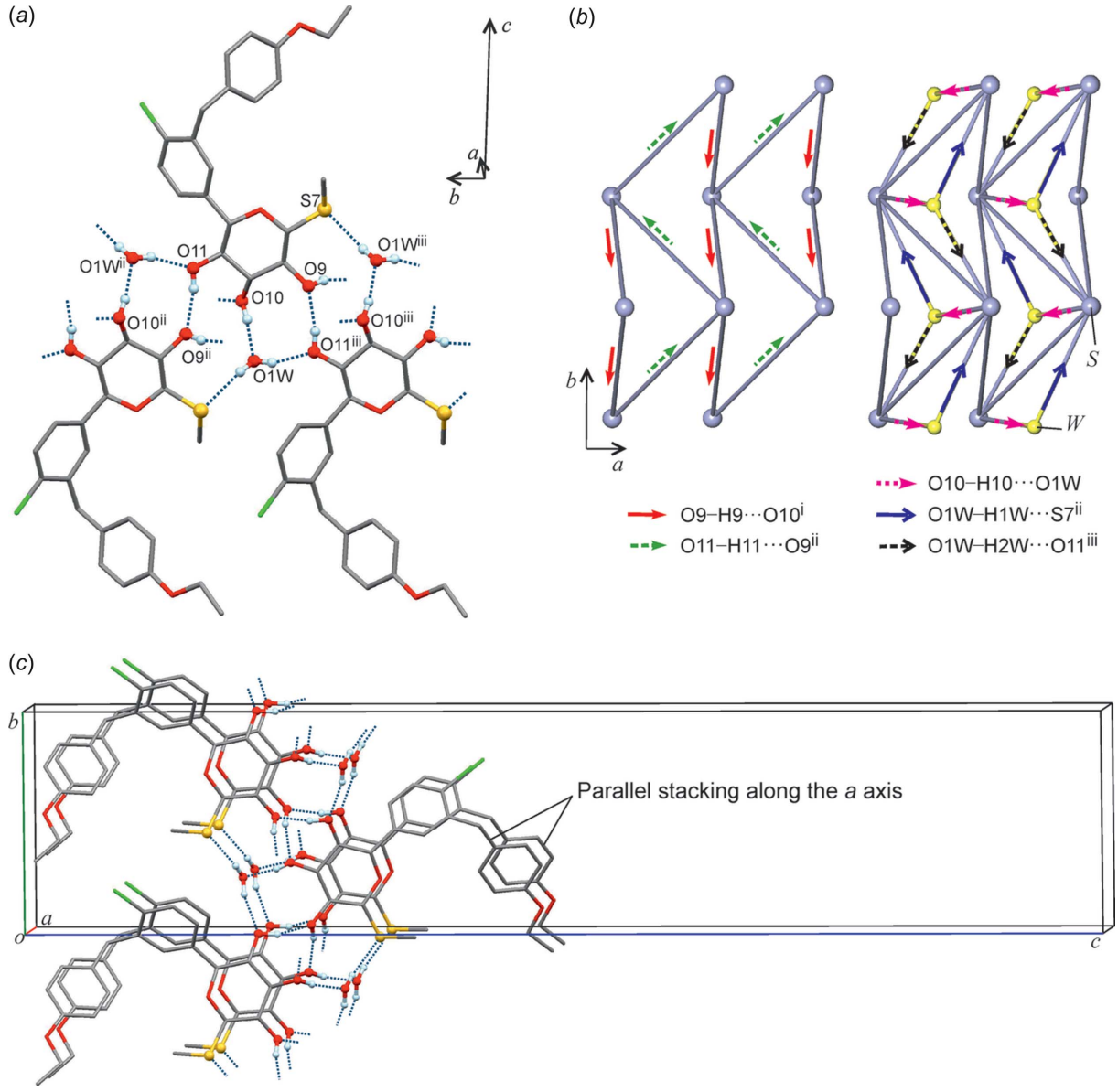


Figure 5
The hydrogen-bonded structure of (II). (*a*) A fragment of the layer structure, showing a sequence of fused $R_3^3(9)$ and $R_3^3(12)$ rings. The symmetry codes are as defined in Table 3. (*b*) Representations of (left) the $L4_4[4^46^2$-**sql**] substructure of hydrogen-bonded sotagliflozin molecules and (right) the complete $L3_3.7_7[(3^2.4)(3^4.4^8.5^4.6^5)]$ structure of hydrogen-bonded sotagliflozin (*S*) and water (*W*) molecules (certain details of the sotagliflozin–sotagliflozin interactions have been omitted for clarity). (*c*) The hydrogen-bonded layer structure, highlighting the internal stacking of non-hydrogen-bonded molecules.

(E_T) is calculated for each molecule–molecule interaction and separated into contributions from Coulombic, polarization, dispersion and repulsion terms.

In (I), the two-point O—H···O hydrogen-bond connection between two molecules (E_T = −53 kJ mol^{-1}) is significantly more attractive than the corresponding one-point connection (E_T = −35 kJ mol^{-1}). However, the largest contribution to the lattice energy results from the parallel stacking of molecules *via* a translation along *a* (E_T = −64 kJ mol^{-1}). The parallel stacking of the two molecules results in a large contact area of their van der Waals surfaces and E_T is dominated by the dispersion term, whilst significant directed intermolecular interactions are absent. However, these two molecules belong to the same hydrogen-bonded layer structure even though they are not connected directly to one another by hydrogen bonding (Fig. 2*c*).

In hydrate structure (II), two sotagliflozin–sotagliflozin interactions involving the O9—H9···O10^{i} and O11—H11···O9^{ii} hydrogen bonds (Table 3) have E_T values of −27 and −26 kJ mol^{-1}. The *PIXEL* energies for the three sotagliflozin–water interaction pairs in which the O10—H10···O1*W*, O1*W*—H1*W*···S7^{ii} and O1*W*—H2*W*···O11^{iii} hydrogen bonds are involved contribute −30, −21 and −21 kJ mol^{-1}, respectively, to the lattice energy. By far the highest contribution of E_T = −82 kJ mol^{-1} originates from the interaction between two sotagliflozin molecules related by a

translation along the *a* axis and is not associated with hydrogen bonding. This feature matches the situation found in (I) in that the hydrogen-bonded layer structure contains stacks of parallel aligned non-hydrogen-bonded sotagliflozin molecules with extensive van der Waals contacts whose interaction energy is dominated by the dispersion term (Fig. 5*c*).

The two sotagliflozin forms investigated in this study show fundamentally different molecular geometries, but both contain hydrogen-bonded layers formed by interactions of the three –OH groups of the xyloside fragment. Remarkably, the layer architectures of (I) and (II) both exhibit a non-hydrogen-bonded molecule–molecule interaction along the short crystallographic axis whose total *PIXEL* energy exceeds that of each hydrogen-bonded molecule–molecule pair.

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supporting information

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Computing details

For both structures, data collection: *CrysAlis PRO* (Rigaku Oxford Diffraction, 2015); cell refinement: *CrysAlis PRO* (Rigaku Oxford Diffraction, 2015); data reduction: *CrysAlis PRO* (Rigaku Oxford Diffraction, 2015); program(s) used to solve structure: SHELXT (Sheldrick, 2015a); program(s) used to refine structure: *SHELXL2014* (Sheldrick, 2015b); molecular graphics: *XP* (Bruker, 1998), *Mercury* (Macrae *et al.*, 2006) and TOPOS (Blatov, 2006); software used to prepare material for publication: *PLATON* (Spek, 2009) and *publCIF* (Westrip, 2010).

(2*S*,3*R*,4*R*,5*S*,6*R*)-2-[4-Chloro-3-(4-ethoxybenzyl)phenyl]-6-(methylsulfanyl)tetrahydro-2*H*-pyran-3,4,5-triol (I)

Crystal data

$C_{21}H_{25}ClO_5S$
M_r = 424.92
Orthorhombic, $P2_12_12_1$
a = 5.3945 (4) Å
b = 9.1577 (5) Å
c = 43.475 (4) Å
V = 2147.7 (3) Å^3
Z = 4
$F(000)$ = 896
D_x = 1.314 Mg m^{-3}
Cu $K\alpha$ radiation, λ = 1.54184 Å
Cell parameters from 2082 reflections
θ = 4.0–67.4°
μ = 2.73 mm^{-1}
T = 253 K
Prism, colourless
0.15 × 0.08 × 0.04 mm

Data collection

Rigaku Xcalibur Ruby (Gemini ultra) diffractometer
Radiation source: fine-focus sealed X-ray tube, Enhance Ultra (Cu) X-ray Source
Mirror monochromator
Detector resolution: 10.3575 pixels mm^{-1}
ω scans
Absorption correction: multi-scan (CrysAlis PRO, Rigaku Oxford Diffraction, 2015)
T_{min} = 0.678, T_{max} = 1.000
12259 measured reflections
3849 independent reflections
3081 reflections with $I > 2\sigma(I)$
R_{int} = 0.065
θ_{max} = 68.1°, θ_{min} = 4.1°
h = −6→6
k = −10→10
l = −49→51

Refinement

Refinement on F^2
Least-squares matrix: full
$R[F^2 > 2\sigma(F^2)]$ = 0.044
$wR(F^2)$ = 0.108
S = 1.07
3849 reflections
269 parameters
3 restraints
Primary atom site location: structure-invariant direct methods
Secondary atom site location: difference Fourier map
Hydrogen site location: mixed

H atoms treated by a mixture of independent and constrained refinement
$w = 1/[\sigma^2(F_o^2) + (0.0315P)^2 + 0.2004P]$ where $P = (F_o^2 + 2F_c^2)/3$
$(\Delta/\sigma)_{max} = 0.001$
$\Delta\rho_{max} = 0.17$ e Å^{-3}
$\Delta\rho_{min} = -0.21$ e Å^{-3}
Absolute structure: Flack x determined using 1021 quotients [(I+)-(I-)]/[(I+)+(I-)] (Parsons, Flack and Wagner, Acta Cryst. B69 (2013) 249-259).
Absolute structure parameter: 0.031 (18)

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.

Fractional atomic coordinates and isotropic or equivalent isotropic displacement parameters (Å²)

	x	*y*	*z*	U_{iso}*/U_{eq}
O1	0.5532 (6)	0.7137 (3)	0.67757 (6)	0.0416 (7)
C2	0.5324 (8)	0.8155 (4)	0.70215 (9)	0.0388 (9)
H2	0.3816	0.7912	0.7136	0.047*
C3	0.7474 (8)	0.7994 (4)	0.72382 (9)	0.0353 (8)
H3	0.9001	0.8289	0.7133	0.042*
C4	0.7747 (8)	0.6434 (4)	0.73522 (8)	0.0338 (8)
H4	0.6379	0.6224	0.7494	0.041*
C5	0.7656 (8)	0.5334 (4)	0.70900 (8)	0.0346 (8)
H5	0.9159	0.5446	0.6966	0.041*
C6	0.5402 (8)	0.5661 (4)	0.68863 (8)	0.0369 (8)
H6	0.3901	0.5559	0.7011	0.044*
S7	0.4926 (2)	0.99677 (11)	0.68675 (3)	0.0521 (3)
C8	0.7782 (13)	1.0243 (7)	0.66669 (16)	0.0871 (19)
H8A	0.9136	1.0195	0.6810	0.131*
H8B	0.7765	1.1185	0.6570	0.131*
H8C	0.7978	0.9498	0.6513	0.131*
O9	0.7144 (5)	0.8871 (3)	0.75063 (6)	0.0411 (6)
H9	0.807 (8)	0.960 (4)	0.7491 (12)	0.058 (15)*
O10	1.0025 (7)	0.6281 (3)	0.75158 (6)	0.0462 (6)
H10	1.015 (11)	0.699 (3)	0.7635 (9)	0.056 (13)*
O11	0.7565 (6)	0.3873 (3)	0.72033 (7)	0.0431 (7)
H11	0.618 (5)	0.376 (6)	0.7287 (12)	0.064 (17)*
C12	0.5191 (8)	0.4648 (4)	0.66126 (8)	0.0391 (9)
C13	0.6882 (9)	0.4738 (5)	0.63690 (9)	0.0468 (10)
H13	0.8096	0.5459	0.6373	0.056*
C14	0.6789 (9)	0.3773 (5)	0.61211 (9)	0.0493 (11)
C15	0.4919 (10)	0.2720 (4)	0.61243 (9)	0.0491 (10)
C16	0.3231 (10)	0.2630 (5)	0.63612 (10)	0.0491 (11)
H16	0.1994	0.1923	0.6356	0.059*
C17	0.3373 (9)	0.3583 (5)	0.66051 (9)	0.0434 (10)
H17	0.2241	0.3512	0.6766	0.052*
C18	0.8757 (10)	0.3829 (7)	0.58731 (10)	0.0629 (14)
H18A	0.9515	0.2870	0.5860	0.075*

H18B	1.0034	0.4504	0.5940	0.075*
C19	0.7951 (10)	0.4271 (6)	0.55509 (10)	0.0566 (12)
C20	0.5988 (11)	0.5178 (8)	0.54861 (11)	0.0737 (16)
H20	0.5002	0.5516	0.5646	0.088*
C21	0.5444 (12)	0.5601 (7)	0.51875 (12)	0.0758 (16)
H21	0.4097	0.6207	0.5149	0.091*
C22	0.6903 (12)	0.5121 (6)	0.49492 (11)	0.0654 (14)
C23	0.8842 (12)	0.4198 (7)	0.50102 (12)	0.0754 (17)
H23	0.9831	0.3861	0.4850	0.090*
C24	0.9329 (11)	0.3770 (7)	0.53060 (11)	0.0668 (14)
H24	1.0625	0.3124	0.5342	0.069 (17)*
Cl25	0.4717 (4)	0.14452 (15)	0.58310 (3)	0.0790 (5)
O26	0.6608 (10)	0.5511 (5)	0.46459 (8)	0.0909 (14)
C27	0.4644 (17)	0.6439 (8)	0.45612 (14)	0.094 (2)
H27A	0.4767	0.7358	0.4671	0.113*
H27B	0.3069	0.5989	0.4612	0.113*
C28	0.481 (2)	0.6698 (9)	0.42195 (14)	0.115 (3)
H28A	0.3348	0.7201	0.4151	0.173*
H28B	0.4938	0.5779	0.4115	0.173*
H28C	0.6244	0.7281	0.4175	0.173*

Atomic displacement parameters (Å²)

	U^{11}	U^{22}	U^{33}	U^{12}	U^{13}	U^{23}
O1	0.0534 (19)	0.0379 (13)	0.0336 (13)	0.0018 (13)	−0.0008 (13)	0.0029 (11)
C2	0.042 (2)	0.0351 (18)	0.0397 (19)	0.0028 (18)	−0.0013 (19)	0.0017 (15)
C3	0.035 (2)	0.0323 (18)	0.038 (2)	0.0004 (17)	0.0036 (17)	0.0003 (15)
C4	0.035 (2)	0.0309 (18)	0.0355 (19)	0.0024 (16)	−0.0036 (17)	−0.0010 (15)
C5	0.036 (2)	0.0311 (19)	0.0366 (19)	−0.0005 (16)	0.0008 (16)	−0.0009 (15)
C6	0.040 (2)	0.0355 (17)	0.0348 (18)	0.0016 (17)	0.0005 (18)	−0.0003 (15)
S7	0.0537 (6)	0.0399 (5)	0.0626 (6)	0.0086 (5)	−0.0028 (6)	0.0117 (5)
C8	0.077 (4)	0.089 (4)	0.096 (4)	0.008 (3)	0.011 (4)	0.048 (4)
O9	0.0440 (16)	0.0346 (14)	0.0446 (15)	−0.0014 (13)	−0.0011 (13)	−0.0072 (12)
O10	0.0509 (16)	0.0379 (13)	0.0497 (14)	0.0080 (15)	−0.0195 (15)	−0.0073 (12)
O11	0.048 (2)	0.0300 (13)	0.0515 (17)	0.0027 (14)	−0.0070 (15)	0.0022 (12)
C12	0.044 (2)	0.0401 (19)	0.0336 (18)	0.002 (2)	−0.0064 (19)	0.0009 (14)
C13	0.048 (2)	0.057 (3)	0.036 (2)	−0.005 (2)	−0.0033 (19)	−0.0002 (19)
C14	0.051 (3)	0.065 (3)	0.032 (2)	0.011 (2)	−0.0040 (19)	−0.001 (2)
C15	0.062 (3)	0.049 (2)	0.036 (2)	0.010 (2)	−0.010 (2)	−0.0060 (17)
C16	0.061 (3)	0.040 (2)	0.046 (2)	−0.005 (2)	−0.017 (2)	0.0011 (19)
C17	0.051 (3)	0.044 (2)	0.035 (2)	0.001 (2)	−0.0025 (18)	0.0004 (17)
C18	0.051 (3)	0.102 (4)	0.036 (2)	0.014 (3)	0.000 (2)	−0.007 (3)
C19	0.058 (3)	0.073 (3)	0.039 (2)	0.002 (3)	0.004 (2)	−0.008 (2)
C20	0.070 (4)	0.106 (4)	0.045 (3)	0.026 (3)	0.007 (2)	−0.004 (3)
C21	0.075 (4)	0.096 (4)	0.056 (3)	0.023 (3)	0.002 (3)	0.003 (3)
C22	0.085 (4)	0.073 (3)	0.039 (2)	−0.003 (3)	0.001 (2)	0.000 (2)
C23	0.091 (4)	0.095 (4)	0.039 (2)	0.021 (3)	0.012 (3)	−0.005 (3)
C24	0.069 (4)	0.087 (4)	0.045 (2)	0.016 (3)	0.002 (2)	−0.006 (3)

Cl25	0.1166 (13)	0.0693 (7)	0.0513 (6)	0.0050 (9)	−0.0106 (8)	−0.0229 (5)
O26	0.122 (4)	0.107 (3)	0.0438 (19)	0.027 (3)	−0.002 (2)	0.006 (2)
C27	0.118 (6)	0.096 (4)	0.068 (3)	0.016 (5)	−0.017 (4)	0.008 (3)
C28	0.170 (8)	0.110 (5)	0.064 (3)	0.019 (6)	−0.020 (5)	0.021 (3)

Geometric parameters (Å, º)

O1—C2	1.423 (5)	C14—C18	1.514 (7)
O1—C6	1.436 (5)	C15—C16	1.377 (7)
C2—C3	1.501 (6)	C15—Cl25	1.732 (4)
C2—S7	1.803 (4)	C16—C17	1.376 (6)
C2—H2	0.9800	C16—H16	0.9300
C3—O9	1.427 (5)	C17—H17	0.9300
C3—C4	1.519 (5)	C18—C19	1.522 (7)
C3—H3	0.9800	C18—H18A	0.9700
C4—O10	1.427 (5)	C18—H18B	0.9700
C4—C5	1.522 (5)	C19—C20	1.375 (8)
C4—H4	0.9800	C19—C24	1.377 (7)
C5—O11	1.426 (5)	C20—C21	1.386 (8)
C5—C6	1.534 (6)	C20—H20	0.9300
C5—H5	0.9800	C21—C22	1.373 (8)
C6—C12	1.513 (5)	C21—H21	0.9300
C6—H6	0.9800	C22—C23	1.371 (9)
S7—C8	1.788 (7)	C22—O26	1.375 (6)
C8—H8A	0.9600	C23—C24	1.370 (8)
C8—H8B	0.9600	C23—H23	0.9300
C8—H8C	0.9600	C24—H24	0.9300
O9—H9	0.836 (14)	O26—C27	1.407 (9)
O10—H10	0.838 (14)	C27—C28	1.507 (9)
O11—H11	0.839 (14)	C27—H27A	0.9700
C12—C17	1.383 (6)	C27—H27B	0.9700
C12—C13	1.400 (6)	C28—H28A	0.9600
C13—C14	1.395 (6)	C28—H28B	0.9600
C13—H13	0.9300	C28—H28C	0.9600
C14—C15	1.396 (7)		

C2—O1—C6	111.2 (3)	C13—C14—C18	120.2 (5)
O1—C2—C3	110.3 (3)	C15—C14—C18	122.5 (4)
O1—C2—S7	109.5 (2)	C16—C15—C14	121.8 (4)
C3—C2—S7	114.5 (3)	C16—C15—Cl25	117.9 (4)
O1—C2—H2	107.4	C14—C15—Cl25	120.3 (4)
C3—C2—H2	107.4	C17—C16—C15	120.1 (4)
S7—C2—H2	107.4	C17—C16—H16	120.0
O9—C3—C2	111.2 (3)	C15—C16—H16	120.0
O9—C3—C4	106.0 (3)	C16—C17—C12	120.3 (4)
C2—C3—C4	111.8 (3)	C16—C17—H17	119.8
O9—C3—H3	109.3	C12—C17—H17	119.8
C2—C3—H3	109.3	C14—C18—C19	117.7 (4)

C4—C3—H3	109.3	C14—C18—H18A	107.9
O10—C4—C3	109.8 (3)	C19—C18—H18A	107.9
O10—C4—C5	109.7 (3)	C14—C18—H18B	107.9
C3—C4—C5	112.0 (3)	C19—C18—H18B	107.9
O10—C4—H4	108.4	H18A—C18—H18B	107.2
C3—C4—H4	108.4	C20—C19—C24	117.3 (5)
C5—C4—H4	108.4	C20—C19—C18	124.7 (4)
O11—C5—C4	111.3 (3)	C24—C19—C18	117.9 (5)
O11—C5—C6	110.8 (3)	C19—C20—C21	121.6 (5)
C4—C5—C6	109.2 (3)	C19—C20—H20	119.2
O11—C5—H5	108.5	C21—C20—H20	119.2
C4—C5—H5	108.5	C22—C21—C20	119.7 (5)
C6—C5—H5	108.5	C22—C21—H21	120.1
O1—C6—C12	108.5 (3)	C20—C21—H21	120.1
O1—C6—C5	109.8 (3)	C23—C22—C21	119.3 (5)
C12—C6—C5	113.2 (3)	C23—C22—O26	115.7 (5)
O1—C6—H6	108.4	C21—C22—O26	125.0 (5)
C12—C6—H6	108.4	C24—C23—C22	120.3 (5)
C5—C6—H6	108.4	C24—C23—H23	119.9
C8—S7—C2	102.0 (3)	C22—C23—H23	119.9
S7—C8—H8A	109.5	C23—C24—C19	121.8 (5)
S7—C8—H8B	109.5	C23—C24—H24	119.1
H8A—C8—H8B	109.5	C19—C24—H24	119.1
S7—C8—H8C	109.5	C22—O26—C27	119.7 (5)
H8A—C8—H8C	109.5	O26—C27—C28	108.0 (7)
H8B—C8—H8C	109.5	O26—C27—H27A	110.1
C3—O9—H9	108 (4)	C28—C27—H27A	110.1
C4—O10—H10	108 (4)	O26—C27—H27B	110.1
C5—O11—H11	107 (4)	C28—C27—H27B	110.1
C17—C12—C13	119.1 (4)	H27A—C27—H27B	108.4
C17—C12—C6	120.3 (4)	C27—C28—H28A	109.5
C13—C12—C6	120.6 (4)	C27—C28—H28B	109.5
C14—C13—C12	121.6 (4)	H28A—C28—H28B	109.5
C14—C13—H13	119.2	C27—C28—H28C	109.5
C12—C13—H13	119.2	H28A—C28—H28C	109.5
C13—C14—C15	117.2 (4)	H28B—C28—H28C	109.5

C6—O1—C2—C3	63.6 (4)	C12—C13—C14—C15	0.6 (6)
C6—O1—C2—S7	−169.6 (3)	C12—C13—C14—C18	−175.5 (4)
O1—C2—C3—O9	−172.6 (3)	C13—C14—C15—C16	0.0 (6)
S7—C2—C3—O9	63.4 (4)	C18—C14—C15—C16	176.0 (4)
O1—C2—C3—C4	−54.4 (4)	C13—C14—C15—Cl25	−178.2 (4)
S7—C2—C3—C4	−178.4 (3)	C18—C14—C15—Cl25	−2.2 (6)
O9—C3—C4—O10	−68.1 (4)	C14—C15—C16—C17	−0.7 (7)
C2—C3—C4—O10	170.6 (3)	Cl25—C15—C16—C17	177.6 (4)
O9—C3—C4—C5	169.8 (3)	C15—C16—C17—C12	0.7 (6)
C2—C3—C4—C5	48.6 (4)	C13—C12—C17—C16	−0.1 (6)
O10—C4—C5—O11	66.0 (4)	C6—C12—C17—C16	−177.8 (4)

C3—C4—C5—O11	−171.9 (3)	C13—C14—C18—C19	−114.6 (6)
O10—C4—C5—C6	−171.3 (3)	C15—C14—C18—C19	69.4 (7)
C3—C4—C5—C6	−49.2 (4)	C14—C18—C19—C20	28.8 (9)
C2—O1—C6—C12	170.4 (3)	C14—C18—C19—C24	−153.5 (5)
C2—O1—C6—C5	−65.4 (4)	C24—C19—C20—C21	−1.4 (10)
O11—C5—C6—O1	179.9 (3)	C18—C19—C20—C21	176.3 (6)
C4—C5—C6—O1	56.9 (4)	C19—C20—C21—C22	−0.7 (10)
O11—C5—C6—C12	−58.7 (4)	C20—C21—C22—C23	1.7 (10)
C4—C5—C6—C12	178.3 (3)	C20—C21—C22—O26	−177.3 (6)
O1—C2—S7—C8	−63.5 (4)	C21—C22—C23—C24	−0.6 (10)
C3—C2—S7—C8	60.9 (4)	O26—C22—C23—C24	178.5 (6)
O1—C6—C12—C17	−130.3 (4)	C22—C23—C24—C19	−1.6 (10)
C5—C6—C12—C17	107.6 (4)	C20—C19—C24—C23	2.6 (10)
O1—C6—C12—C13	52.0 (5)	C18—C19—C24—C23	−175.3 (6)
C5—C6—C12—C13	−70.1 (5)	C23—C22—O26—C27	179.1 (6)
C17—C12—C13—C14	−0.6 (6)	C21—C22—O26—C27	−1.9 (10)
C6—C12—C13—C14	177.1 (4)	C22—O26—C27—C28	178.9 (7)

Hydrogen-bond geometry (Å, º)

D—H···*A*	*D*—H	H···*A*	*D*···*A*	*D*—H···*A*
O9—H9···O10^{i}	0.84 (1)	1.85 (2)	2.686 (4)	175 (5)
O10—H10···O11^{i}	0.84 (1)	2.23 (3)	2.970 (4)	147 (5)
O11—H11···O9^{ii}	0.84 (1)	2.01 (2)	2.837 (5)	170 (6)

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

(2*S*,3*R*,4*R*,5*S*,6*R*)-2-[4-Chloro-3-(4-ethoxybenzyl)phenyl]-6-(methylsulfanyl)tetrahydro-2*H*-pyran-3,4,5-triol monohydrate (II)

Crystal data

$C_{21}H_{25}ClO_5S·H_2O$
M_r = 442.93
Orthorhombic, $P2_12_12_1$
a = 4.4659 (3) Å
b = 9.8994 (8) Å
c = 48.073 (5) Å
V = 2125.3 (3) Å^3
Z = 4
F(000) = 936
D_x = 1.384 Mg m^{-3}
Cu *Kα* radiation, *λ* = 1.54184 Å
Cell parameters from 2038 reflections
θ = 4.6–67.2°
μ = 2.81 mm^{-1}
T = 173 K
Prism, colourless
0.08 × 0.08 × 0.05 mm

Data collection

Rigaku Xcalibur Ruby (Gemini ultra) diffractometer
Radiation source: fine-focus sealed X-ray tube, Enhance Ultra (Cu) X-ray Source
Mirror monochromator
Detector resolution: 10.3575 pixels mm^{-1}
ω scans
Absorption correction: multi-scan (CrysAlis PRO; Rigaku Oxford Diffraction, 2015)
T_{min} = 0.560, T_{max} = 1.000
11848 measured reflections
3737 independent reflections
3253 reflections with $I > 2\sigma(I)$
R_{int} = 0.083
θ_{max} = 67.6°, θ_{min} = 3.7°
h = −5→5
k = −7→11
l = −57→53

Refinement

Refinement on F^2
Least-squares matrix: full
$R[F^2 > 2\sigma(F^2)] = 0.073$
$wR(F^2) = 0.149$
$S = 1.35$
3737 reflections
279 parameters
8 restraints
Hydrogen site location: mixed
H atoms treated by a mixture of independent and constrained refinement

$w = 1/[\sigma^2(F_o^2) + (0.0183P)^2 + 2.0927P]$ where $P = (F_o^2 + 2F_c^2)/3$
$(\Delta/\sigma)_{max} < 0.001$
$\Delta\rho_{max} = 0.71$ e Å^{-3}
$\Delta\rho_{min} = -0.39$ e Å^{-3}
Absolute structure: Flack x determined using 1099 quotients [(I+)-(I-)]/[(I+)+(I-)] (Parsons, Flack and Wagner, Acta Cryst. B69 (2013) 249-259).
Absolute structure parameter: 0.02 (3)

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.

Fractional atomic coordinates and isotropic or equivalent isotropic displacement parameters (Å²)

	x	*y*	*z*	U_{iso}*/U_{eq}
O1	0.4138 (10)	0.2338 (4)	0.32594 (9)	0.0300 (10)
C2	0.2965 (17)	0.1227 (6)	0.31066 (14)	0.0292 (15)
H2	0.0739	0.1203	0.3129	0.035*
C3	0.3725 (15)	0.1378 (6)	0.27997 (13)	0.0273 (15)
H3	0.5946	0.1319	0.2776	0.033*
C4	0.2648 (16)	0.2740 (6)	0.26914 (12)	0.0282 (14)
H4	0.0427	0.2693	0.2666	0.034*
C5	0.3344 (17)	0.3897 (6)	0.28882 (14)	0.0296 (15)
H5	0.5530	0.4104	0.2874	0.036*
C6	0.2645 (17)	0.3581 (6)	0.31885 (13)	0.0277 (14)
H6	0.0435	0.3452	0.3209	0.033*
S7	0.4542 (4)	−0.02891 (17)	0.32496 (4)	0.0358 (4)
C8	0.282 (2)	−0.0248 (8)	0.35884 (14)	0.0448 (19)
H8A	0.3580	0.0531	0.3693	0.067*
H8B	0.3308	−0.1081	0.3689	0.067*
H8C	0.0646	−0.0172	0.3568	0.067*
O9	0.2341 (12)	0.0346 (4)	0.26364 (9)	0.0328 (11)
H9	0.361 (14)	−0.028 (6)	0.2639 (15)	0.039*
O10	0.3951 (12)	0.3081 (5)	0.24320 (10)	0.0342 (12)
H10	0.269 (8)	0.291 (8)	0.2308 (3)	0.041*
O11	0.1713 (13)	0.5085 (5)	0.28115 (10)	0.0392 (13)
H11	0.134 (17)	0.500 (4)	0.2640 (5)	0.047*
C12	0.3698 (15)	0.4589 (6)	0.34025 (13)	0.0260 (14)
C13	0.2978 (16)	0.4369 (7)	0.36771 (14)	0.0307 (15)
H13	0.1606	0.3664	0.3719	0.037*
C14	0.4143 (16)	0.5120 (7)	0.38983 (14)	0.0336 (16)
C15	0.6019 (17)	0.6201 (7)	0.38196 (15)	0.0330 (16)
C16	0.6726 (17)	0.6477 (7)	0.35477 (14)	0.0331 (16)

H16	0.7987	0.7219	0.3503	0.040*
C17	0.5577 (18)	0.5659 (6)	0.33381 (14)	0.0326 (16)
H17	0.6082	0.5835	0.3150	0.039*
C18	0.3475 (17)	0.4741 (7)	0.41914 (14)	0.0361 (16)
H18A	0.1416	0.4374	0.4201	0.043*
H18B	0.3543	0.5564	0.4308	0.043*
C19	0.5647 (18)	0.3699 (7)	0.43105 (15)	0.0354 (17)
C20	0.6680 (18)	0.2602 (7)	0.41556 (15)	0.0394 (18)
H20	0.6121	0.2528	0.3966	0.047*
C21	0.8488 (19)	0.1624 (8)	0.42711 (16)	0.0401 (19)
H21	0.9159	0.0886	0.4161	0.048*
C22	0.932 (2)	0.1719 (7)	0.45475 (15)	0.0407 (19)
C23	0.8321 (18)	0.2803 (8)	0.47028 (16)	0.0406 (18)
H23	0.8905	0.2885	0.4892	0.049*
C24	0.6489 (18)	0.3762 (7)	0.45862 (15)	0.0372 (18)
H24	0.5784	0.4486	0.4698	0.045*
Cl25	0.7588 (5)	0.72261 (18)	0.40774 (4)	0.0463 (5)
O26	1.1092 (13)	0.0793 (5)	0.46841 (11)	0.0449 (14)
C27	1.212 (2)	−0.0365 (8)	0.45391 (16)	0.049 (2)
H27A	1.3441	−0.0095	0.4384	0.059*
H27B	1.0398	−0.0874	0.4462	0.059*
C28	1.381 (3)	−0.1227 (9)	0.47430 (19)	0.066 (3)
H28A	1.5540	−0.0725	0.4813	0.099*
H28B	1.4491	−0.2053	0.4650	0.099*
H28C	1.2491	−0.1466	0.4899	0.099*
O1W	0.0159 (12)	0.2555 (5)	0.20304 (11)	0.0376 (12)
H1W	−0.104 (13)	0.314 (5)	0.1982 (17)	0.056*
H2W	−0.073 (15)	0.184 (4)	0.2055 (17)	0.056*

Atomic displacement parameters (Å²)

	U^{11}	U^{22}	U^{33}	U^{12}	U^{13}	U^{23}
O1	0.029 (3)	0.024 (2)	0.036 (2)	−0.001 (2)	−0.004 (2)	−0.0004 (19)
C2	0.023 (4)	0.019 (3)	0.046 (4)	−0.001 (3)	−0.007 (3)	0.000 (3)
C3	0.014 (3)	0.026 (3)	0.041 (4)	−0.001 (3)	−0.001 (3)	−0.005 (3)
C4	0.027 (4)	0.025 (3)	0.033 (3)	0.007 (3)	−0.001 (3)	0.000 (3)
C5	0.027 (4)	0.019 (3)	0.043 (4)	0.000 (3)	−0.003 (3)	−0.002 (3)
C6	0.024 (4)	0.022 (3)	0.038 (4)	0.001 (3)	0.000 (3)	−0.001 (2)
S7	0.0382 (11)	0.0249 (8)	0.0443 (10)	0.0028 (8)	−0.0045 (8)	0.0024 (7)
C8	0.058 (6)	0.038 (4)	0.038 (4)	0.001 (5)	−0.003 (4)	0.009 (3)
O9	0.032 (3)	0.025 (2)	0.041 (3)	0.001 (2)	−0.005 (2)	−0.005 (2)
O10	0.038 (3)	0.031 (3)	0.033 (3)	−0.005 (2)	−0.001 (2)	0.0011 (19)
O11	0.049 (3)	0.028 (3)	0.041 (3)	0.008 (2)	−0.006 (2)	−0.0025 (19)
C12	0.020 (3)	0.019 (3)	0.040 (4)	0.005 (3)	−0.004 (3)	−0.002 (3)
C13	0.020 (4)	0.028 (3)	0.045 (4)	0.008 (3)	−0.004 (3)	−0.005 (3)
C14	0.026 (4)	0.033 (4)	0.042 (4)	0.011 (3)	−0.002 (3)	−0.006 (3)
C15	0.026 (4)	0.028 (4)	0.045 (4)	0.000 (3)	−0.008 (3)	−0.013 (3)
C16	0.027 (4)	0.028 (4)	0.044 (4)	0.004 (3)	0.001 (3)	0.000 (3)

C17	0.032 (4)	0.027 (4)	0.039 (4)	0.009 (3)	−0.003 (3)	0.001 (3)
C18	0.030 (4)	0.038 (4)	0.040 (4)	0.002 (4)	0.001 (3)	−0.006 (3)
C19	0.033 (4)	0.031 (4)	0.043 (4)	−0.006 (3)	0.006 (3)	0.001 (3)
C20	0.039 (5)	0.043 (4)	0.036 (4)	−0.009 (4)	−0.001 (3)	−0.002 (3)
C21	0.038 (5)	0.037 (4)	0.046 (5)	−0.003 (4)	0.005 (3)	−0.003 (3)
C22	0.047 (5)	0.034 (4)	0.042 (4)	−0.002 (4)	0.000 (4)	0.001 (3)
C23	0.037 (5)	0.047 (4)	0.038 (4)	−0.003 (4)	0.003 (3)	0.000 (3)
C24	0.041 (5)	0.033 (4)	0.038 (4)	−0.004 (4)	0.004 (3)	−0.006 (3)
Cl25	0.0522 (12)	0.0413 (10)	0.0453 (10)	−0.0086 (10)	−0.0066 (9)	−0.0098 (8)
O26	0.049 (4)	0.038 (3)	0.048 (3)	0.007 (3)	−0.004 (2)	−0.003 (2)
C27	0.051 (6)	0.041 (4)	0.056 (5)	0.002 (5)	0.001 (4)	−0.001 (4)
C28	0.077 (8)	0.056 (5)	0.064 (6)	0.011 (6)	0.012 (5)	0.006 (4)
O1W	0.037 (3)	0.025 (2)	0.050 (3)	−0.002 (2)	−0.003 (2)	0.002 (2)

Geometric parameters (Å, º)

O1—C2	1.423 (8)	C15—C16	1.372 (10)
O1—C6	1.440 (8)	C15—Cl25	1.748 (6)
C2—C3	1.521 (10)	C16—C17	1.391 (10)
C2—S7	1.795 (6)	C16—H16	0.9500
C2—H2	1.0000	C17—H17	0.9500
C3—O9	1.428 (8)	C18—C19	1.528 (11)
C3—C4	1.524 (9)	C18—H18A	0.9900
C3—H3	1.0000	C18—H18B	0.9900
C4—O10	1.417 (8)	C19—C24	1.379 (10)
C4—C5	1.518 (9)	C19—C20	1.395 (10)
C4—H4	1.0000	C20—C21	1.377 (11)
C5—O11	1.431 (8)	C20—H20	0.9500
C5—C6	1.510 (9)	C21—C22	1.383 (11)
C5—H5	1.0000	C21—H21	0.9500
C6—C12	1.508 (9)	C22—O26	1.377 (9)
C6—H6	1.0000	C22—C23	1.382 (11)
S7—C8	1.801 (8)	C23—C24	1.373 (11)
C8—H8A	0.9800	C23—H23	0.9500
C8—H8B	0.9800	C24—H24	0.9500
C8—H8C	0.9800	O26—C27	1.417 (9)
O9—H9	0.837 (13)	C27—C28	1.503 (12)
O10—H10	0.836 (14)	C27—H27A	0.9900
O11—H11	0.843 (13)	C27—H27B	0.9900
C12—C13	1.376 (10)	C28—H28A	0.9800
C12—C17	1.387 (10)	C28—H28B	0.9800
C13—C14	1.398 (10)	C28—H28C	0.9800
C13—H13	0.9500	O1W—H1W	0.821 (13)
C14—C15	1.411 (10)	O1W—H2W	0.820 (14)
C14—C18	1.488 (10)		
C2—O1—C6	111.6 (5)	C15—C14—C18	124.3 (6)
O1—C2—C3	110.0 (5)	C16—C15—C14	122.9 (6)

O1—C2—S7	107.7 (4)	C16—C15—Cl25	117.9 (6)
C3—C2—S7	111.5 (5)	C14—C15—Cl25	119.2 (5)
O1—C2—H2	109.2	C15—C16—C17	119.3 (7)
C3—C2—H2	109.2	C15—C16—H16	120.3
S7—C2—H2	109.2	C17—C16—H16	120.3
O9—C3—C2	111.5 (5)	C12—C17—C16	120.4 (7)
O9—C3—C4	107.9 (5)	C12—C17—H17	119.8
C2—C3—C4	110.3 (5)	C16—C17—H17	119.8
O9—C3—H3	109.0	C14—C18—C19	113.4 (6)
C2—C3—H3	109.0	C14—C18—H18A	108.9
C4—C3—H3	109.0	C19—C18—H18A	108.9
O10—C4—C5	106.5 (5)	C14—C18—H18B	108.9
O10—C4—C3	112.4 (5)	C19—C18—H18B	108.9
C5—C4—C3	113.0 (5)	H18A—C18—H18B	107.7
O10—C4—H4	108.2	C24—C19—C20	117.3 (7)
C5—C4—H4	108.2	C24—C19—C18	120.2 (6)
C3—C4—H4	108.2	C20—C19—C18	122.4 (7)
O11—C5—C6	108.1 (5)	C21—C20—C19	121.7 (7)
O11—C5—C4	110.8 (5)	C21—C20—H20	119.1
C6—C5—C4	113.4 (5)	C19—C20—H20	119.1
O11—C5—H5	108.1	C20—C21—C22	119.8 (7)
C6—C5—H5	108.1	C20—C21—H21	120.1
C4—C5—H5	108.1	C22—C21—H21	120.1
O1—C6—C12	105.0 (5)	O26—C22—C23	116.4 (7)
O1—C6—C5	107.9 (5)	O26—C22—C21	124.6 (7)
C12—C6—C5	116.8 (5)	C23—C22—C21	119.0 (7)
O1—C6—H6	109.0	C24—C23—C22	120.6 (7)
C12—C6—H6	109.0	C24—C23—H23	119.7
C5—C6—H6	109.0	C22—C23—H23	119.7
C2—S7—C8	99.2 (3)	C23—C24—C19	121.6 (7)
S7—C8—H8A	109.5	C23—C24—H24	119.2
S7—C8—H8B	109.5	C19—C24—H24	119.2
H8A—C8—H8B	109.5	C22—O26—C27	119.3 (6)
S7—C8—H8C	109.5	O26—C27—C28	107.5 (7)
H8A—C8—H8C	109.5	O26—C27—H27A	110.2
H8B—C8—H8C	109.5	C28—C27—H27A	110.2
C3—O9—H9	103 (5)	O26—C27—H27B	110.2
C4—O10—H10	107.6 (17)	C28—C27—H27B	110.2
C5—O11—H11	105.9 (16)	H27A—C27—H27B	108.5
C13—C12—C17	118.5 (6)	C27—C28—H28A	109.5
C13—C12—C6	118.5 (6)	C27—C28—H28B	109.5
C17—C12—C6	122.8 (6)	H28A—C28—H28B	109.5
C12—C13—C14	124.0 (7)	C27—C28—H28C	109.5
C12—C13—H13	118.0	H28A—C28—H28C	109.5
C14—C13—H13	118.0	H28B—C28—H28C	109.5
C13—C14—C15	114.9 (6)	H1W—O1W—H2W	109 (2)
C13—C14—C18	120.8 (7)		

C6—O1—C2—C3	67.4 (7)	C12—C13—C14—C15	3.7 (10)
C6—O1—C2—S7	−170.9 (4)	C12—C13—C14—C18	−174.4 (6)
O1—C2—C3—O9	−174.5 (5)	C13—C14—C15—C16	−1.8 (10)
S7—C2—C3—O9	66.1 (6)	C18—C14—C15—C16	176.2 (7)
O1—C2—C3—C4	−54.6 (7)	C13—C14—C15—Cl25	179.4 (5)
S7—C2—C3—C4	−174.0 (5)	C18—C14—C15—Cl25	−2.6 (10)
O9—C3—C4—O10	−73.3 (7)	C14—C15—C16—C17	−0.4 (11)
C2—C3—C4—O10	164.7 (6)	Cl25—C15—C16—C17	178.4 (6)
O9—C3—C4—C5	166.1 (6)	C13—C12—C17—C16	0.8 (10)
C2—C3—C4—C5	44.1 (8)	C6—C12—C17—C16	−173.4 (6)
O10—C4—C5—O11	69.5 (7)	C15—C16—C17—C12	1.0 (10)
C3—C4—C5—O11	−166.6 (6)	C13—C14—C18—C19	87.0 (8)
O10—C4—C5—C6	−168.7 (6)	C15—C14—C18—C19	−90.9 (9)
C3—C4—C5—C6	−44.8 (8)	C14—C18—C19—C24	144.3 (7)
C2—O1—C6—C12	169.5 (5)	C14—C18—C19—C20	−40.6 (10)
C2—O1—C6—C5	−65.3 (7)	C24—C19—C20—C21	−0.6 (11)
O11—C5—C6—O1	176.4 (5)	C18—C19—C20—C21	−175.8 (7)
C4—C5—C6—O1	53.1 (8)	C19—C20—C21—C22	−0.1 (12)
O11—C5—C6—C12	−65.7 (8)	C20—C21—C22—O26	179.2 (8)
C4—C5—C6—C12	171.0 (6)	C20—C21—C22—C23	−0.1 (12)
O1—C2—S7—C8	66.4 (5)	O26—C22—C23—C24	−178.5 (7)
C3—C2—S7—C8	−172.8 (5)	C21—C22—C23—C24	0.9 (12)
O1—C6—C12—C13	−63.6 (8)	C22—C23—C24—C19	−1.6 (12)
C5—C6—C12—C13	176.9 (6)	C20—C19—C24—C23	1.4 (11)
O1—C6—C12—C17	110.6 (7)	C18—C19—C24—C23	176.8 (7)
C5—C6—C12—C17	−8.9 (10)	C23—C22—O26—C27	178.0 (7)
C17—C12—C13—C14	−3.3 (10)	C21—C22—O26—C27	−1.3 (12)
C6—C12—C13—C14	171.1 (7)	C22—O26—C27—C28	−176.5 (8)

Hydrogen-bond geometry (Å, º)

D—H···*A*	*D*—H	H···*A*	*D*···*A*	*D*—H···*A*
O9—H9···O10^{i}	0.84 (1)	1.99 (2)	2.807 (7)	166 (7)
O10—H10···O1*W*	0.84 (1)	1.79 (2)	2.621 (7)	177 (3)
O11—H11···O9^{ii}	0.84 (1)	2.14 (4)	2.825 (7)	138 (5)
O1*W*—H1*W*···S7^{ii}	0.82 (1)	2.47 (2)	3.282 (5)	170 (8)
O1*W*—H2*W*···O11^{iii}	0.82 (1)	1.90 (3)	2.694 (6)	162 (7)

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