



Synthesis and crystal structures of 3-hydroxy-2,4-dimethyl-2*H*-thiophen-5-one and 3-hydroxy-4-methyl-2*H*-thiophen-5-one

Asma Nashawi,^{a,b} Christopher P. Lawson,^a M. Omar Abdel-Sattar,^{b,c} Joop H. ter Horst,^d Geoffrey D. Coxon^{a*} and Alan R. Kennedy^e

Received 27 March 2020

Accepted 22 June 2020

Edited by A. J. Lough, University of Toronto, Canada

Keywords: crystal structure; hydroxy-thiophenone; hydrogen bonding.

CCDC references: 2011283; 2011284

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

^aStrathclyde Institute for Pharmacy and Biomedical Sciences, University of Strathclyde, 161 Cathedral Street, Glasgow G4 0RE, Scotland, ^bDepartment of Pharmaceutical Chemistry, King Abdul Aziz University, Jeddah, 21589, Saudi Arabia, ^cDepartment of Chemistry, Al-Azhar University, Cairo, 11884, Egypt, ^dEPSRC Future Manufacturing Research Hub for Continuous Manufacture and Advanced Crystallisation (CMAC), Technology and Innovation Centre, University of Strathclyde, 99 George Street, Glasgow G1 1RD, Scotland, and ^eWestchem, Department of Pure & Applied Chemistry, University of Strathclyde, 295 Cathedral Street, Glasgow G1 1XL, Scotland. *Correspondence e-mail: geoff.coxon@strath.ac.uk

The structures of two hydroxy-thiophenone derivatives related to the antibiotic thiolactomycin are presented. These are the racemic 3-hydroxy-2,4-dimethyl-2*H*-thiophen-5-one, C₆H₈O₂S, and 3-hydroxy-4-methyl-2*H*-thiophen-5-one, C₅H₆O₂S. The main structural feature of both compounds is C(6) hydrogen-bonded chains formed between the OH and C=O groups. In achiral C₅H₆O₂S, these chains propagate only by translation, corresponding to $x + 1, y, z + 1$. However, in contrast, for racemic C₆H₈O₂S the hydrogen-bonded chains propagate through a $-x + \frac{3}{2}, y + \frac{1}{2}, z$ operation, giving chains lying parallel to the crystallographic *b*-axis direction that are composed of alternate *R* and *S* enantiomers. The crystals of 3-hydroxy-4-methyl-2*H*-thiophen-5-one were found to be twinned by a 180° rotation about the reciprocal 001 direction. In the final refinement the twin ratio refined to 0.568 (2):0.432 (2).

1. Chemical context

Thiolactomycin (TLM) 1, (5*R*)-4-hydroxy-3,5-dimethyl-5-[(1*E*)-2-methylbuta-1,3-dienyl]thiophen-2-one, is a naturally occurring antibiotic isolated from *Nocardia spp* (Sasaki *et al.*, 1982). Over the last three decades, synthetic efforts towards the synthesis of the single enantiomer and analogues have provided relatively complex solutions. These have exploited asymmetric synthesis, diastomeric recrystallization or enzymatic resolution requiring between seven and eleven steps and thus have significantly restricted the development of this scaffold towards clinical application. For examples see Chambers & Thomas (1997), McFadden *et al.* (2002), Ohata & Terashima (2009), Kamal *et al.* (2008), Toyama *et al.* (2006) and Bommineni *et al.* (2016). Herein we present findings from our initial studies focused on the single-crystal determination of thiolactone analogues.

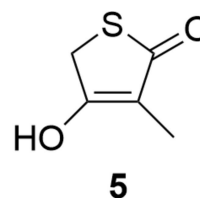
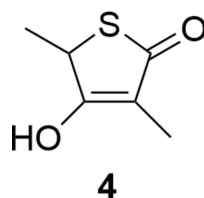
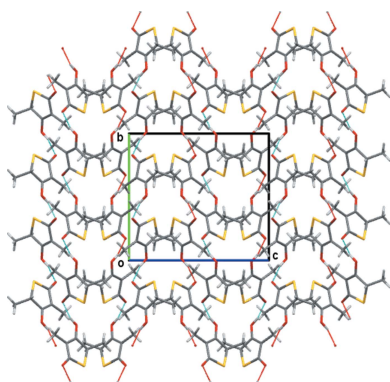


Table 1
 Selected geometric parameters (Å, °) for **4**.

S1—C1	1.778 (3)	C3—C2	1.351 (4)
S1—C4	1.816 (3)	C3—C4	1.507 (4)
O1—C1	1.238 (3)	C2—C1	1.434 (4)
O2—C3	1.326 (3)		
C1—S1—C4	92.62 (12)	C3—C2—C1	112.3 (2)
O2—C3—C4	113.4 (2)	C2—C1—S1	112.1 (2)
C2—C3—C4	117.8 (2)	C3—C4—S1	105.16 (18)

Table 2
 Selected geometric parameters (Å, °) for **5**.

S1—C1	1.775 (3)	C1—C2	1.440 (4)
S1—C4	1.799 (3)	C2—C3	1.347 (4)
O1—C1	1.231 (4)	C2—C5	1.502 (4)
O2—C3	1.332 (4)	C3—C4	1.499 (4)
C1—S1—C4	92.33 (15)	O2—C3—C4	119.7 (3)
C2—C1—S1	112.0 (2)	C2—C3—C4	117.2 (3)
C3—C2—C1	112.2 (3)	C3—C4—S1	106.2 (2)

2. Structural commentary

The molecular structures of compounds **4** and **5** are shown in Figs. 1 and 2, respectively. As can be seen from Tables 1 and 2, equivalent geometric parameters in the two structures are similar, with the largest difference in bond length being found for the S1—C4 values [1.816 (3) and 1.799 (3) Å]. A notable structural difference is the orientation of the hydroxy groups containing the O2 atoms. In both structures, this O atom is coplanar with the SC₄ ring, but in structure **4** the H atom points towards C5 and is eclipsed by the C2=C3 double bond whilst in structure **5** the H atom points towards the CH₂ group and is eclipsed by the C3—C4 single bond. This change in orientation is associated with a change in the bond angles involving O2 [compare C4—C3—O2 angles of 113.4 (2) and 119.7 (3)°]. A search of the Cambridge Structural Database (version 5.40; Groom *et al.*, 2016) found only three other structures with similar 4-hydroxy-thiophen-2-one cores. These are TLM itself (BIHKIM, Nawata *et al.*, 1989) and two other derivatives (FIVKEA, Chambers *et al.*, 1987; POXZOS,

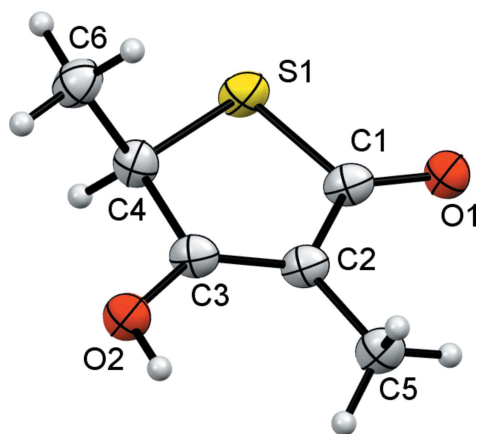
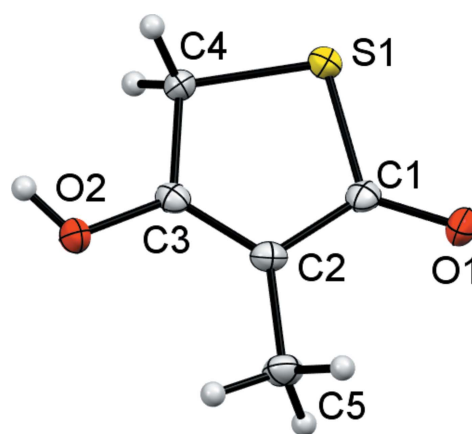

Figure 1
 The molecular structure of **4** with non-H atoms shown as 50% probability ellipsoids. H atoms are drawn as small spheres of arbitrary size.

Figure 2
 The molecular structure of **5** with non-H atoms shown as 50% probability ellipsoids. H atoms are drawn as small spheres of arbitrary size.

Table 3
 Hydrogen-bond geometry (Å, °) for **4**.

<i>D</i> —H··· <i>A</i>	<i>D</i> —H	H··· <i>A</i>	<i>D</i> ··· <i>A</i>	<i>D</i> —H··· <i>A</i>
O2—H1H···O1 ⁱ	0.88 (4)	1.77 (4)	2.621 (3)	164 (4)

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

Table 4
 Hydrogen-bond geometry (Å, °) for **5**.

<i>D</i> —H··· <i>A</i>	<i>D</i> —H	H··· <i>A</i>	<i>D</i> ··· <i>A</i>	<i>D</i> —H··· <i>A</i>
O2—H1H···O1 ⁱ	0.84 (5)	1.80 (5)	2.629 (3)	168 (5)
C4—H4B···O1 ⁱⁱ	0.99	2.58	3.552 (4)	169

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

Kikionis *et al.*, 2009). These have generally similar geometric parameters to those of **4** and **5**. Two of the database structures have the same hydroxy group orientation as **5**. Only POXZOS has the same hydroxy orientation as **4**, and here this orientation is predetermined by the OH group participating in an intramolecular six-membered hydrogen-bonded ring. As with structures **4** and **5**, in the database structures the orientation of the OH group is associated with systematic changes to the C—C—O bond angles involving OH.

3. Supramolecular features

The main supramolecular feature of both structures **4** and **5** is a one-dimensional C(6) hydrogen-bonded chain utilizing OH as the donor group and O1 as the acceptor group, see Tables 3 and 4. Behind these basic similarities there lies a great deal of difference in detail. In **5** the chains propagate by translations corresponding to $x + 1, y, z + 1$. This propagation by translation alone gives the repeating pattern shown in Fig. 3 where all of the SC₄ rings of the hydrogen-bonded unit are coplanar and all of the S atoms lie on the same side of the chain. When travelling along the *b*-axis direction, neighbouring chains bear their S atoms on different sides, giving the layered structure shown in Fig. 4. In contrast, for structure **4** the chain propagates through a $-x + \frac{3}{2}, y + \frac{1}{2}, z$ operation giving a chain lying

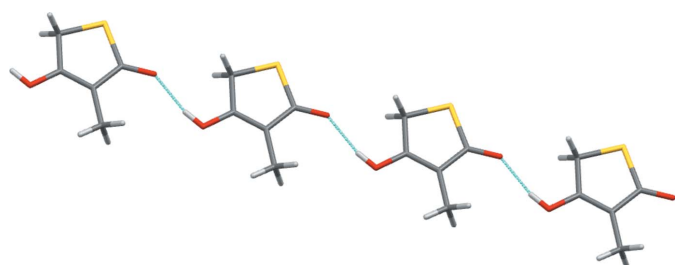


Figure 3
Part of the hydrogen-bonded chain motif present in the structure of **5**. The chain extends parallel to the [101] direction.

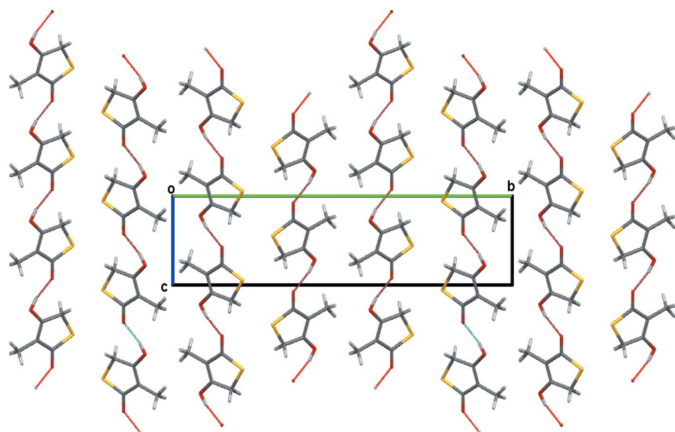


Figure 4
Packing diagram for compound **5** in a view down the *a* axis. Note the alternating Me...Me and S...S layers.

parallel to the crystallographic *b*-axis direction. As shown in Fig. 5, this results in the neighbouring *R* and *S* enantiomers of the racemic chain having perpendicular relationships between the planes of their SC₄ rings. This different chain geometry gives a very different packing arrangement from that of structure **5**, see Fig. 6. The only interchain contact significantly shorter than the sum of van der Waals radii in either structure occurs in structure **5**. This is a C—H...O contact between the CH₂ group and the ketone O atom. Of the 4-hydroxy-thiophen-2-one structures described in the literature, both those of FIVKEA and BIHKIM (TLM) display the same C(6) hydrogen-bonded chain motif as **4** and **5**. In both cases, the geometrical detail of the chain is similar to that found in **4**, with the difference that both literature examples are enantiopure. The final structure, POXZOS, contains additional

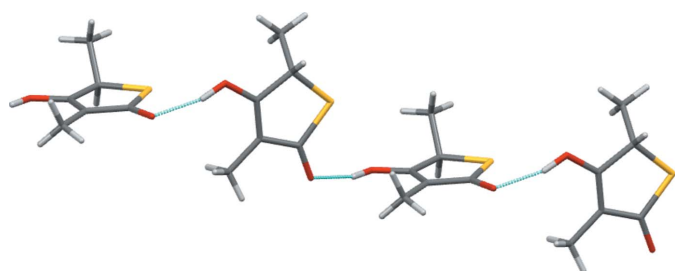
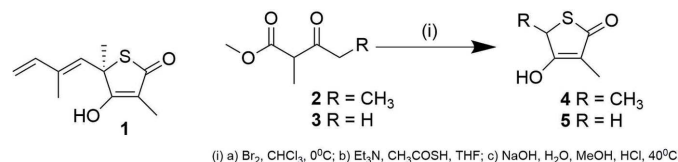


Figure 5
Part of the hydrogen-bonded chain motif present in the structure of **4**. The chain extends parallel to the crystallographic *b* axis.

carboxylic acid and carbonyl groups and these strong hydrogen-bonding groups dominate the intermolecular contacts formed and so stop the formation of the otherwise common C(6) motif.

4. Synthesis and crystallization

General synthesis of thiolactone analogues **4** and **5**:



Bromine (1.1 eq) was added to a stirring solution of the corresponding oxoester (1 eq.) dissolved in chloroform (50 ml) at 273 K. The mixtures were allowed to warm to ambient temperature and stirred for 20 h before removing the solvent under vacuum. The resulting crude mixtures were dissolved in THF (50 ml) before adding trimethylamine (1.1 eq.) and thioacetic acid (1.1 eq.) and stirring at ambient temperature for a further 18 h. The resulting mixtures were reduced under vacuum to give dark-orange oils that were vacuum filtered over silica using petrol (40/60) and diethyl ether (5:2) as eluent before removing the solvent. The mixtures were dissolved in ethanol (50 ml) before adding a solution of sodium hydroxide (2 eq.) dissolved in water (20 ml) and stirring for 24 h at 333 K. After cooling, HCl (0.1M) was added until the solutions reached pH 5 before washing with ethyl acetate (3 × 50 ml) and drying over anhydrous magnesium sulfate. The mixtures were reduced under vacuum and precipitated using petrol (40/60) and

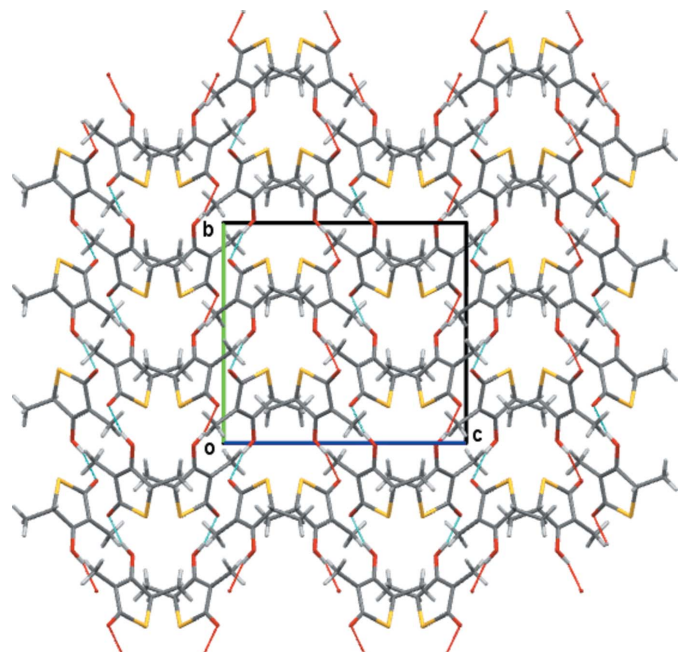


Figure 6
Packing diagram for compound **4** with a view down the *a* axis.

Table 5
Experimental details.

	4	5
Crystal data		
Chemical formula	C ₆ H ₈ O ₂ S	C ₅ H ₆ O ₂ S
<i>M_r</i>	144.18	130.16
Crystal system, space group	Orthorhombic, <i>Pbca</i>	Monoclinic, <i>P2₁/c</i>
Temperature (K)	123	100
<i>a</i> , <i>b</i> , <i>c</i> (Å)	9.286 (1), 11.4809 (8), 12.6469 (10)	4.1054 (3), 22.9727 (13), 6.1928 (5)
α , β , γ (°)	90, 90, 90	90, 103.728 (7), 90
<i>V</i> (Å ³)	1348.3 (2)	567.37 (7)
<i>Z</i>	8	4
Radiation type	Cu <i>K</i> α	Mo <i>K</i> α
μ (mm ⁻¹)	3.63	0.46
Crystal size (mm)	0.55 × 0.08 × 0.04	0.12 × 0.02 × 0.01
Data collection		
Diffractometer	Oxford Diffraction Gemini S	Rigaku XtaLAB AFC12
Absorption correction	Analytical (<i>CrysAlis PRO</i> ; Rigaku OD, 2019)	Multi-scan (<i>CrysAlis PRO</i> ; Rigaku OD, 2019)
<i>T_{min}</i> , <i>T_{max}</i>	0.323, 0.847	0.766, 1.000
No. of measured, independent and observed [<i>I</i> > 2 σ (<i>I</i>)] reflections	4293, 1323, 1115	2121, 2121, 1955
<i>R_{int}</i>	0.049	0.026
(<i>sin</i> θ / λ) _{max} (Å ⁻¹)	0.620	0.650
Refinement		
<i>R</i> [<i>F</i> ² > 2 σ (<i>F</i> ²)], <i>wR</i> (<i>F</i> ²), <i>S</i>	0.053, 0.148, 1.07	0.050, 0.113, 1.19
No. of reflections	1323	2121
No. of parameters	88	79
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)	0.67, -0.29	0.43, -0.33

Computer programs: *CrysAlis PRO* (Rigaku OD, 2019), *SIR92* (Altomare *et al.*, 1994), *SHELXL2014* (Sheldrick, 2015), *Mercury* (Macrae *et al.*, 2020) and *ORTEP-3 for Windows* (Farrugia, 2012).

diethyl ether to give the products as a solid. For **4**, crystals suitable for crystallographic analysis were grown from a THF solution. For **5**, crystals were grown from a toluene solution.

3-Hydroxy-2,4-dimethyl-2H-thiophen-5-one (4) Off-white solid (1.1 g, 22%); m.p. 408–409 K. ¹H NMR (CDCl₃) δ 4.12 (*dd*, *J* = 7.1, 1.3 Hz, 1H), 1.57 (*d*, *J* = 7.1 Hz, 4H). ¹³C NMR (CDCl₃) δ 197.16, 177.63, 111.32, 77.26, 77.21, 77.00, 76.75, 42.99, 18.80, 7.62.

3-Hydroxy-4-methyl-2H-thiophen-5-one (5)

Off-white solid (1.6 g, 18%); m.p. 397–398 K. ¹H NMR (CDCl₃) δ 3.94 (*s*, 2H), 1.68 (*s*, 3H). ¹³C NMR (CDCl₃) δ 195.1, 175.2, 111.2, 32.1, 7.2.

5. Refinement

Crystal data, data collection and structure refinement details are summarized in Table 5. For both structures, C-bound H atoms were placed in the expected geometric positions and treated in riding modes with C–H = 0.98, 0.99 and 1.00 Å for methyl, CH₂ and CH groups, respectively. *U*_{iso}(H) = 1.5*U*_{eq}(C) for methyl groups and 1.2*U*_{eq}(C) for the other CH groups. The H atoms of the hydroxy groups were refined isotropically. Data collection on **5** was carried out by the National Crystallography Service (Cole & Gale, 2012). The crystals of **5** were found to be twinned by a 180° rotation about the reciprocal 001 direction. This feature was accounted for by producing a hklf 5 formatted datafile during data processing.

In the final refinement the twin ratio refined to 0.568 (2):0.432 (2).

Acknowledgements

The authors wish to thank the National Crystallographic Service at the University of Southampton for data collection on **5**.

Funding information

The Saudi Arabia Universities External Joint Supervision Programme is thanked for funding a studentship (AN).

References

- Altomare, A., Cascarano, G., Giacovazzo, C., Guagliardi, A., Burla, M. C., Polidori, G. & Camalli, M. (1994). *J. Appl. Cryst.* **27**, 435.
- Bommineni, G. R., Kapilashrami, K., Cummings, J. E., Lu, Y., Knudson, S. E., Gu, C. D., Walker, S. G., Slayden, R. A. & Tonge, P. J. (2016). *J. Med. Chem.* **59**, 5377–5390.
- Chambers, M. S. & Thomas, E. J. (1997). *J. Chem. Soc. Perkin Trans. I*, pp. 417–432.
- Chambers, M. S., Thomas, E. J. & Williams, D. J. (1987). *J. Chem. Soc. Chem. Commun.* pp. 1228–1230.
- Coles, S. J. & Gale, P. A. (2012). *Chem. Sci.* **3**, 683–689.
- Farrugia, L. J. (2012). *J. Appl. Cryst.* **45**, 849–854.
- Groom, C. R., Bruno, I. J., Lightfoot, M. P. & Ward, S. C. (2016). *Acta Cryst.* **B72**, 171–179.
- Kamal, A., Azeeza, S., Malik, M. S., Shaik, A. A. & Rao, M. V. (2008). *J. Pharm. Pharm. Sci.* **11**, 56S–80S.
- Kikionis, S., McKee, V., Markopoulos, J. & Igglessi-Markopoulou, O. (2009). *Tetrahedron*, **65**, 3711–3716.

- Macrae, C. F., Sovago, I., Cottrell, S. J., Galek, P. T. A., McCabe, P., Pidcock, E., Platings, M., Shields, G. P., Stevens, J. S., Towler, M. & Wood, P. A. (2020). *J. Appl. Cryst.* **53**, 226–235.
- McFadden, J. M., Frehywot, G. L. & Townsend, C. A. (2002). *Org. Lett.* **4**, 3859–3862.
- Nawata, Y., Sasaki, H., Oishi, H., Suzuki, K., Sawada, M., Ando, K. & Iitaka, Y. (1989). *Acta Cryst. C* **45**, 978–979.
- Ohata, K. & Terashima, S. (2009). *Tetrahedron*, **65**, 2244–2253.
- Rigaku OD (2019). *CrysAlis PRO*. Rigaku Oxford Diffraction, Yarnton, Oxfordshire, England.
- Sasaki, H., Oishi, H., Hayashi, T., Matsuura, I., Ando, K. & Sawada, M. (1982). *J. Antibiot.* **35**, 396–400.
- Sheldrick, G. M. (2015). *Acta Cryst. C* **71**, 3–8.
- Toyama, K., Tauchi, T., Mase, N., Yoda, H. & Takabe, K. (2006). *Tetrahedron Lett.* **47**, 7163–7166.

supporting information

Acta Cryst. (2020). E76, 1158-1162 [https://doi.org/10.1107/S2056989020008269]

Synthesis and crystal structures of 3-hydroxy-2,4-dimethyl-2*H*-thiophen-5-one and 3-hydroxy-4-methyl-2*H*-thiophen-5-one

Asma Nashawi, Christopher P. Lawson, M. Omar Abdel-Sattar, Joop H. ter Horst, Geoffrey D. Coxon and Alan R. Kennedy

Computing details

For both structures, data collection: *CrysAlis PRO* (Rigaku OD, 2019); cell refinement: *CrysAlis PRO* (Rigaku OD, 2019); data reduction: *CrysAlis PRO* (Rigaku OD, 2019); program(s) used to solve structure: *SIR92* (Altomare *et al.*, 1994); program(s) used to refine structure: *SHELXL2014* (Sheldrick, 2015); molecular graphics: *Mercury* (Macrae *et al.*, 2020) and *ORTEP-3 for Windows* (Farrugia, 2012); software used to prepare material for publication: *SHELXL2014* (Sheldrick, 2015).

3-Hydroxy-2,4-dimethyl-2*H*-thiophen-5-one (4)

Crystal data

$C_6H_8O_2S$	$D_x = 1.421 \text{ Mg m}^{-3}$
$M_r = 144.18$	Cu $K\alpha$ radiation, $\lambda = 1.54184 \text{ \AA}$
Orthorhombic, <i>Pbca</i>	Cell parameters from 1393 reflections
$a = 9.286 (1) \text{ \AA}$	$\theta = 7.0\text{--}72.8^\circ$
$b = 11.4809 (8) \text{ \AA}$	$\mu = 3.63 \text{ mm}^{-1}$
$c = 12.6469 (10) \text{ \AA}$	$T = 123 \text{ K}$
$V = 1348.3 (2) \text{ \AA}^3$	Rod, colourless
$Z = 8$	$0.55 \times 0.08 \times 0.04 \text{ mm}$
$F(000) = 608$	

Data collection

Oxford Diffraction Gemini S diffractometer	1323 independent reflections
Radiation source: sealed tube	1115 reflections with $I > 2\sigma(I)$
ω scans	$R_{\text{int}} = 0.049$
Absorption correction: analytical (CrysAlisPro; Rigaku OD, 2019)	$\theta_{\text{max}} = 73.0^\circ$, $\theta_{\text{min}} = 7.0^\circ$
$T_{\text{min}} = 0.323$, $T_{\text{max}} = 0.847$	$h = -11 \rightarrow 11$
4293 measured reflections	$k = -13 \rightarrow 10$
	$l = -15 \rightarrow 12$

Refinement

Refinement on F^2	Hydrogen site location: mixed
Least-squares matrix: full	H atoms treated by a mixture of independent and constrained refinement
$R[F^2 > 2\sigma(F^2)] = 0.053$	$w = 1/[\sigma^2(F_o^2) + (0.081P)^2 + 0.8472P]$
$wR(F^2) = 0.148$	where $P = (F_o^2 + 2F_c^2)/3$
$S = 1.07$	$(\Delta/\sigma)_{\text{max}} < 0.001$
1323 reflections	$\Delta\rho_{\text{max}} = 0.67 \text{ e \AA}^{-3}$
88 parameters	$\Delta\rho_{\text{min}} = -0.29 \text{ e \AA}^{-3}$
0 restraints	

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 (\AA^2)

	<i>x</i>	<i>y</i>	<i>z</i>	$U_{\text{iso}}^*/U_{\text{eq}}$
S1	0.84281 (8)	0.16688 (5)	0.67914 (5)	0.0327 (3)
O1	0.6506 (2)	0.17209 (14)	0.52486 (16)	0.0311 (5)
O2	0.9490 (2)	0.48890 (16)	0.62458 (16)	0.0329 (5)
C3	0.8868 (3)	0.3850 (2)	0.6199 (2)	0.0283 (6)
C6	0.9207 (4)	0.3465 (3)	0.8144 (2)	0.0374 (7)
H6A	0.9733	0.4199	0.8231	0.056*
H6B	0.9571	0.2890	0.8651	0.056*
H6C	0.8179	0.3597	0.8271	0.056*
C2	0.7822 (3)	0.3476 (2)	0.5539 (2)	0.0272 (6)
C1	0.7427 (3)	0.2288 (2)	0.57332 (19)	0.0281 (6)
C5	0.7097 (3)	0.4157 (2)	0.4680 (2)	0.0330 (6)
H5A	0.6367	0.4670	0.4990	0.049*
H5B	0.6636	0.3619	0.4182	0.049*
H5C	0.7815	0.4627	0.4304	0.049*
C4	0.9423 (3)	0.3008 (2)	0.7017 (2)	0.0302 (6)
H4	1.0472	0.2864	0.6892	0.036*
H1H	0.914 (5)	0.542 (3)	0.581 (3)	0.053 (11)*

Atomic displacement parameters (\AA^2)

	U^{11}	U^{22}	U^{33}	U^{12}	U^{13}	U^{23}
S1	0.0477 (5)	0.0172 (4)	0.0332 (4)	0.0017 (2)	-0.0059 (3)	0.0025 (2)
O1	0.0410 (11)	0.0178 (9)	0.0344 (10)	-0.0013 (7)	-0.0046 (7)	-0.0024 (7)
O2	0.0438 (11)	0.0188 (9)	0.0360 (10)	-0.0026 (8)	-0.0046 (8)	-0.0005 (7)
C3	0.0383 (13)	0.0172 (11)	0.0294 (12)	0.0014 (10)	0.0030 (10)	-0.0021 (9)
C6	0.0475 (17)	0.0328 (14)	0.0318 (14)	-0.0009 (12)	-0.0047 (12)	-0.0014 (11)
C2	0.0377 (14)	0.0178 (12)	0.0262 (11)	0.0024 (10)	0.0017 (10)	-0.0022 (9)
C1	0.0389 (14)	0.0187 (12)	0.0266 (11)	0.0046 (10)	0.0025 (10)	-0.0012 (9)
C5	0.0473 (15)	0.0183 (13)	0.0334 (13)	-0.0006 (11)	-0.0048 (11)	0.0004 (9)
C4	0.0352 (13)	0.0208 (12)	0.0346 (13)	0.0014 (10)	-0.0035 (10)	-0.0018 (10)

Geometric parameters (\AA , $^\circ$)

S1—C1	1.778 (3)	C6—H6B	0.9800
S1—C4	1.816 (3)	C6—H6C	0.9800
O1—C1	1.238 (3)	C2—C1	1.434 (4)
O2—C3	1.326 (3)	C2—C5	1.498 (4)
O2—H1H	0.88 (4)	C5—H5A	0.9800
C3—C2	1.351 (4)	C5—H5B	0.9800

C3—C4	1.507 (4)	C5—H5C	0.9800
C6—C4	1.532 (4)	C4—H4	1.0000
C6—H6A	0.9800		
C1—S1—C4	92.62 (12)	O1—C1—S1	121.6 (2)
C3—O2—H1H	116 (3)	C2—C1—S1	112.1 (2)
O2—C3—C2	128.8 (2)	C2—C5—H5A	109.5
O2—C3—C4	113.4 (2)	C2—C5—H5B	109.5
C2—C3—C4	117.8 (2)	H5A—C5—H5B	109.5
C4—C6—H6A	109.5	C2—C5—H5C	109.5
C4—C6—H6B	109.5	H5A—C5—H5C	109.5
H6A—C6—H6B	109.5	H5B—C5—H5C	109.5
C4—C6—H6C	109.5	C3—C4—C6	112.0 (2)
H6A—C6—H6C	109.5	C3—C4—S1	105.16 (18)
H6B—C6—H6C	109.5	C6—C4—S1	111.7 (2)
C3—C2—C1	112.3 (2)	C3—C4—H4	109.3
C3—C2—C5	127.3 (2)	C6—C4—H4	109.3
C1—C2—C5	120.4 (2)	S1—C4—H4	109.3
O1—C1—C2	126.3 (2)		
O2—C3—C2—C1	-180.0 (2)	C4—S1—C1—O1	-179.6 (2)
C4—C3—C2—C1	-0.9 (3)	C4—S1—C1—C2	0.2 (2)
O2—C3—C2—C5	0.2 (5)	O2—C3—C4—C6	58.8 (3)
C4—C3—C2—C5	179.2 (2)	C2—C3—C4—C6	-120.4 (3)
C3—C2—C1—O1	-179.8 (3)	O2—C3—C4—S1	-179.77 (18)
C5—C2—C1—O1	0.0 (4)	C2—C3—C4—S1	1.0 (3)
C3—C2—C1—S1	0.4 (3)	C1—S1—C4—C3	-0.64 (19)
C5—C2—C1—S1	-179.8 (2)	C1—S1—C4—C6	121.0 (2)

Hydrogen-bond geometry (Å, °)

<i>D</i> —H... <i>A</i>	<i>D</i> —H	H... <i>A</i>	<i>D</i> ... <i>A</i>	<i>D</i> —H... <i>A</i>
O2—H1H...O1 ⁱ	0.88 (4)	1.77 (4)	2.621 (3)	164 (4)

Symmetry code: (i) $-x+3/2, y+1/2, z$.

3-Hydroxy-4-methyl-2H-thiophen-5-one (5)

Crystal data

C₅H₆O₂S
M_r = 130.16
 Monoclinic, *P*2₁/*c*
a = 4.1054 (3) Å
b = 22.9727 (13) Å
c = 6.1928 (5) Å
 β = 103.728 (7)°
V = 567.37 (7) Å³
Z = 4

F(000) = 272
D_x = 1.524 Mg m⁻³
 Mo *K*α radiation, λ = 0.71073 Å
 Cell parameters from 1968 reflections
 θ = 5.2–31.4°
 μ = 0.46 mm⁻¹
T = 100 K
 Needle, colourless
 0.12 × 0.02 × 0.01 mm

*Data collection*Rigaku XtaLAB AFC12
diffractometer

Radiation source: rotating anode

 ω scansAbsorption correction: multi-scan
(CrysAlisPro; Rigaku OD, 2019) $T_{\min} = 0.766$, $T_{\max} = 1.000$

2121 measured reflections

2121 independent reflections

1955 reflections with $I > 2\sigma(I)$ $R_{\text{int}} = 0.026$ $\theta_{\max} = 27.5^\circ$, $\theta_{\min} = 3.5^\circ$ $h = -5 \rightarrow 5$ $k = -29 \rightarrow 29$ $l = -8 \rightarrow 8$ *Refinement*Refinement on F^2

Least-squares matrix: full

 $R[F^2 > 2\sigma(F^2)] = 0.050$ $wR(F^2) = 0.113$ $S = 1.19$

2121 reflections

79 parameters

0 restraints

Hydrogen site location: mixed

H atoms treated by a mixture of independent
and constrained refinement $w = 1/[\sigma^2(F_o^2) + (0.0078P)^2 + 1.3568P]$ where $P = (F_o^2 + 2F_c^2)/3$ $(\Delta/\sigma)_{\max} < 0.001$ $\Delta\rho_{\max} = 0.43 \text{ e } \text{\AA}^{-3}$ $\Delta\rho_{\min} = -0.33 \text{ e } \text{\AA}^{-3}$ *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.

Refinement. Refined as a 2-component twin against a hklf 5 formatted datafile.

This datafile was created by CrysAlisPro for twinning by a 180 degree rotation about rec 001.

Matrix used -0.9970 -0.0004 0.0038 0.0195 -0.9997 0.0133 0.7232 0.0009 0.9991

BASF refined to 0.432 (2).

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

	<i>x</i>	<i>y</i>	<i>z</i>	$U_{\text{iso}}^*/U_{\text{eq}}$
S1	0.6910 (2)	0.70598 (3)	0.55558 (14)	0.0183 (2)
O1	0.8610 (6)	0.64486 (10)	0.9223 (4)	0.0231 (6)
O2	0.0808 (6)	0.58103 (10)	0.2795 (4)	0.0203 (5)
C1	0.6862 (8)	0.64503 (13)	0.7309 (5)	0.0164 (7)
C2	0.4606 (8)	0.60031 (13)	0.6216 (5)	0.0164 (7)
C3	0.3060 (8)	0.61502 (12)	0.4117 (5)	0.0155 (6)
C4	0.3963 (8)	0.67257 (13)	0.3276 (5)	0.0160 (6)
H4A	0.1943	0.6972	0.2798	0.019*
H4B	0.4987	0.6669	0.1996	0.019*
C5	0.4138 (10)	0.54539 (13)	0.7423 (6)	0.0213 (7)
H5A	0.2293	0.5227	0.6513	0.032*
H5B	0.3611	0.5553	0.8842	0.032*
H5C	0.6206	0.5224	0.7701	0.032*
H1H	0.003 (12)	0.597 (2)	0.156 (8)	0.045 (14)*

Atomic displacement parameters (\AA^2)

	U^{11}	U^{22}	U^{33}	U^{12}	U^{13}	U^{23}
S1	0.0204 (4)	0.0149 (3)	0.0183 (4)	-0.0017 (3)	0.0021 (3)	0.0002 (3)

O1	0.0287 (15)	0.0240 (11)	0.0138 (11)	0.0028 (10)	-0.0005 (10)	0.0007 (9)
O2	0.0211 (13)	0.0178 (10)	0.0187 (12)	-0.0034 (10)	-0.0017 (10)	0.0002 (9)
C1	0.0161 (17)	0.0162 (14)	0.0172 (15)	0.0052 (13)	0.0043 (12)	0.0002 (12)
C2	0.0182 (17)	0.0133 (13)	0.0189 (15)	0.0015 (12)	0.0067 (13)	0.0016 (12)
C3	0.0126 (14)	0.0138 (13)	0.0202 (16)	0.0013 (12)	0.0041 (13)	-0.0011 (12)
C4	0.0177 (16)	0.0146 (13)	0.0146 (14)	0.0001 (13)	0.0020 (12)	0.0012 (11)
C5	0.0261 (19)	0.0157 (14)	0.0226 (16)	-0.0006 (14)	0.0070 (15)	0.0044 (13)

Geometric parameters (Å, °)

S1—C1	1.775 (3)	C2—C5	1.502 (4)
S1—C4	1.799 (3)	C3—C4	1.499 (4)
O1—C1	1.231 (4)	C4—H4A	0.9900
O2—C3	1.332 (4)	C4—H4B	0.9900
O2—H1H	0.84 (5)	C5—H5A	0.9800
C1—C2	1.440 (4)	C5—H5B	0.9800
C2—C3	1.347 (4)	C5—H5C	0.9800
C1—S1—C4	92.33 (15)	C3—C4—H4A	110.5
C3—O2—H1H	111 (3)	S1—C4—H4A	110.5
O1—C1—C2	127.8 (3)	C3—C4—H4B	110.5
O1—C1—S1	120.2 (3)	S1—C4—H4B	110.5
C2—C1—S1	112.0 (2)	H4A—C4—H4B	108.7
C3—C2—C1	112.2 (3)	C2—C5—H5A	109.5
C3—C2—C5	127.2 (3)	C2—C5—H5B	109.5
C1—C2—C5	120.6 (3)	H5A—C5—H5B	109.5
O2—C3—C2	123.0 (3)	C2—C5—H5C	109.5
O2—C3—C4	119.7 (3)	H5A—C5—H5C	109.5
C2—C3—C4	117.2 (3)	H5B—C5—H5C	109.5
C3—C4—S1	106.2 (2)		
C4—S1—C1—O1	179.5 (3)	C5—C2—C3—O2	0.3 (5)
C4—S1—C1—C2	-1.2 (3)	C1—C2—C3—C4	1.4 (4)
O1—C1—C2—C3	179.4 (3)	C5—C2—C3—C4	-179.8 (3)
S1—C1—C2—C3	0.1 (4)	O2—C3—C4—S1	177.8 (3)
O1—C1—C2—C5	0.5 (5)	C2—C3—C4—S1	-2.1 (4)
S1—C1—C2—C5	-178.8 (3)	C1—S1—C4—C3	1.7 (2)
C1—C2—C3—O2	-178.6 (3)		

Hydrogen-bond geometry (Å, °)

<i>D</i> —H \cdots <i>A</i>	<i>D</i> —H	H \cdots <i>A</i>	<i>D</i> \cdots <i>A</i>	<i>D</i> —H \cdots <i>A</i>
O2—H1H \cdots O1 ⁱ	0.84 (5)	1.80 (5)	2.629 (3)	168 (5)
C4—H4B \cdots O1 ⁱⁱ	0.99	2.58	3.552 (4)	169

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