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Crystal structure of zymonic acid and a redetermination of its precursor, pyruvic acid

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The structure of zymonic acid (systematic name: 4-hydroxy-2-methyl-5-oxo-2,5-dihydrofuran-2-carboxylic acid), C₆H₆O₅, which had previously eluded crystallographic determination, is presented here for the first time. It forms by intramolecular condensation of parapyruvic acid, which is the product of aldol condensation of pyruvic acid. A redetermination of the crystal structure of pyruvic acid (systematic name: 2-oxopropanoic acid), C₃H₄O₃, at low temperature (90 K) and with increased precision, is also presented [for the previous structure, see: Harata et al. (1977). Acta Cryst. B33, 210–212]. In zymonic acid, the hydroxylactone ring is close to planar (r.m.s. deviation = 0.0108 Å) and the dihedral angle between the ring and the plane formed by the bonds of the methyl and carboxylic acid carbon atoms to the ring is 88.68 (7)°. The torsion angle of the carboxylic acid group relative to the ring is 12.04 (16)°. The pyruvic acid molecule is almost planar, having a dihedral angle between the carboxylic acid and methyl-ketone groups of 3.95 (6)°. Intermolecular interactions in both crystal structures are dominated by hydrogen bonding. The common R²(8) hydrogen-bonding motif links carboxylic acid groups on adjacent molecules in both structures. In zymonic acid, this results in dimers about a crystallographic twofold of space group C2/c, which forces the carboxylic acid group to be disordered exactly 50:50, which scrambles the carbonyl and hydroxyl groups and gives an apparent equalization of the C—O bond lengths [1.2568 (16) and 1.2602 (16) Å]. The other hydrogen bonds in zymonic acid (O—H···O and weak C—H···O), link molecules across a 2₁-screw axis, and generate an R²(9) motif. These hydrogen-bonding interactions propagate to form extended pleated sheets in the ab plane. Stacking of these zigzag sheets along c involves only van der Waals contacts. In pyruvic acid, inversion-related molecules are linked into R²(8) dimers, with van der Waals interactions between dimers as the only other intermolecular contacts.

1. Chemical context

The Human Metabolome Database (Wishart et al., 2007, 2009, 2013, 2018) lists the compound 4-hydroxy-2-methyl-5-oxo-furan-2-carboxylic acid (C₆H₆O₅), commonly named zymonic acid, with the metabocard HMDB0031210. Zymonic acid is used as a flavor constituent for confectionery and tobacco products (Yannai, 2004). The generation of zymonic acid can proceed by condensation of parapyruvic acid, which itself forms by aldol condensation of pyruvic acid (IUPAC name 2-oxopropanoic acid, C₃H₄O₃; Bloomer et al., 1970). Therefore, zymonic acid is directly derived from pyruvic acid, and is thus related to the compounds present in the tricarboxylic acid (Krebs) cycle (Nelson & Cox, 2004) and its reductive version (Guzman, 2011; Guzman & Martin, 2008; Zhou & Guzman, 2016). As an intermediate in central metabolism, zymonic acid
is produced in the cytoplasm at very low concentration, from where it can be excreted to the extracellular region.

The electron-impact mass spectrum (MS) and electrospray ionization fragmentation of zymonic acid following gas and liquid chromatography, respectively, have been reported (Allen et al., 2015, 2016). The use of \(^{13}\)C-zymonic acid has enabled mapping of pH changes, independently of concentration, in mammalian organs and tumors via hyperpolarized magnetic resonance (Düwel et al., 2017). Thus, zymonic acid is a non-invasive extracellular imaging sensor to localize and quantify pH \textit{in vivo} (Düwel et al., 2017; Hundshammer et al., 2017), with many possible applications in medical diagnosis (Schilling et al., 2016). As part of the process resulting in the aforementioned invention, the detailed \(^1\)H and \(^{13}\)C NMR spectra of pure zymonic acid have been reported (Hundshammer et al., 2017). Herein, we contribute new information to characterize zymonic acid by reporting for the first time its crystal structure, along with a low-temperature redetermination of pyruvic acid.

2. Structural commentary

Aside from the effects on the geometry of the carboxylic acid group in zymonic acid that stem from disorder about the twofold axis (see below), there are no unusual bond lengths or angles in either compound.

In zymonic acid (Fig. 1), the hydroxylactone ring is essentially planar (r.m.s. deviation = 0.0108 Å), with the largest deviation from planarity [0.0171 (8) Å] for the ring oxygen atom, O3. The plane defined by the ring carbon atom C4, the methyl carbon atom C6, and the carboxylic acid carbon atom C5, is almost perpendicular to the mean plane of the ring atoms [dihedral angle = 88.68 (7)°]. Lastly, the orientation of the carboxylic acid group relative to the ring, as defined by the torsion angle O4—C5—C4—O3, is 12.04 (16)°. For the carboxylic acid group, disorder about the crystallographic twofold axis effectively averages the C—O double and C—O single bonds, rendering them equivalent [the C5—O4 and C5—O5 distances are 1.2568 (16) and 1.2602 (16) Å, respectively], and requires modeling of half-occupancy hydrogens (H4O and H5O) on each.

In spite of increased precision resulting from much lower temperature (90 K versus 266 K) and data collection on modern equipment, the redetermined structure of pyruvic acid (Fig. 2) is largely unchanged from that reported by Harata et al. (1977). For example, the dihedral angle between the planes defined by atoms C1/C2/C3/O3 and C1/C2/O1/O2 is 3.95 (6)° at 90.00 (2) K versus 3.5° at 266 (1) K.

3. Supramolecular features

The main intermolecular interactions in the crystals of both zymonic and pyruvic acids are hydrogen bonds. In zymonic acid, the carboxylic acid groups of adjacent molecules are related by a crystallographic twofold axis to form hydrogen bonds \([O4—H4O···O4ii \text{ and } O5—H5O···O5ii]\); symmetry code: (ii) \(-x+y+\frac{1}{2}, -z+\frac{1}{2}\) giving \(R_2(8)\) dimer motifs (Table 1). This common supramolecular construct in carboxylic acids usually occurs between inversion-related or symmetry-independent molecules. Here, the orientation of the dimer relative to the crystallographic twofold axis forces the average struc-
ture to be statistically disordered (Fig. 3). Another pair of hydrogen bonds [O2—H2/C1/C1/C1O1i and C3—H3/C1/C1/C1O2i; symmetry code: (i) 3x + 1, 1/2 + y, 3/2] link molecules related by a 21-screw axis, into \( R_2^2(9) \) motifs (Fig. 4). These hydrogen-bonding interactions combine to form extended pleated sheets that propagate in the \( ab \) plane (Fig. 5), which in turn, stack along the \( c \)-axis direction. In pyruvic acid, inversion-related molecules form the common \( R_2^2(8) \) dimer motif (Fig. 6).

4. Database survey
A search of the Cambridge Crystal Structure Database (Version 5.40, Nov. 2018; Groom et al., 2016) for zymonic acid gave no hits for searches on either ‘zymonic’ or on the structural formula. A search on the structural formula of pyruvic acid gave two hits. CSD entry PRUVAC (Harata et al., 1977) describes the pure compound at 266 K, and is similar to the present pyruvic acid structure (after transformation to a common cell setting). CSD entry FAFGUR (Prohens et al., 2016) describes a co-crystal of pyruvic acid with the drug agomelatine. The CSD does contain structures for derivatives of both zymonic and pyruvic acids, but none of these have features that are especially relevant to the current work.

5. Synthesis and crystallization
Vacuum distillation of pyruvic acid (Sigma–Aldrich, 98.5%) was used for purification (Eugene & Guzman, 2017a,b). Freshly distilled pyruvic acid was crystallized in a closed vial in a freezer at 253 K. The tail of this distillation, a viscous yellowish residue enriched in parapyruvic and zymonic acids, was isolated in a vial, and the headspace filled with \( \text{N}_2(\text{g}) \) before sealing it with a cap. Crystals of zymonic acid were produced slowly from this isolated residue kept at 275 K inside a refrigerator. The easily identifiable transparent crystals of zymonic acid appear above the level of the viscous solution within two weeks. Pyruvic acid crystals are deliquescent in air, even at 263 K (Harata et al., 1977), so they had to be kept cold, with minimal exposure to ambient air. Thus, throughout all experimental stages from initial inspection through data collection, special techniques for crystal handling at low temperature (Parkin & Hope, 1998) were employed.

Table 2
Hydrogen-bond geometry (\( \AA \), °) for pyruvic acid.

| D—H—A | D—H | H—A | D—A | D—H···A |
|--------|------|-----|------|---------|
| O1—H1···O2i | 0.913 (14) | 1.742 (14) | 2.6536 (8) | 175.5 (12) |

Symmetry code: (i) \( x + 1, y + 1, z + 1 \).

Table 2. In accordance with the work of Harata et al. (1977), there are no other noteworthy intermolecular interactions.
6. Refinement

Crystal data, data collection, and structure refinement details are summarized in Table 3. Non-disordered hydrogen atoms were found in difference Fourier maps. For pyruvic acid, the hydroxyl hydrogen-atom coordinates were refined freely, while methyl hydrogen C—H distances used a riding model. Hydroxyl hydrogen-atom coordinates were refined freely, while methyl hydrogen C—H distances used a riding model. Hydroxyl hydrogen-atom coordinates were refined freely, while methyl hydrogen C—H distances used a riding model. Hydroxyl hydrogen-atom coordinates were refined freely, while methyl hydrogen C—H distances used a riding model.

| Crystal data | zymonic acid | pyruvic acid |
|--------------|--------------|--------------|
| Chemical formula | C₆H₆O₅ | C₃H₄O₃ |
| Mᵣ | 158.11 | 88.06 |
| Crystal system, space group | Monoclinic, C2/c | Monoclinic, P2₁/c |
| Temperature (K) | 90 | 90 |
| a, b, c (Å) | 24.145 (3), 6.6523 (7), 8.6201 (7) | 10.7486 (3), 5.1925 (2), 6.8302 (2) |
| β (°) | 95.169 (4) | 99.063 (1) |
| V (Å³) | 1378.9 (3) | 376.45 (2) |
| Z | 8 | 4 |
| Radiation type | Mo Kα | Mo Kα |
| μ (mm⁻¹) | 0.14 | 0.14 |
| Crystal size (mm) | 0.30 × 0.25 × 0.02 | 0.26 × 0.22 × 0.18 |

| Data collection | zymonic acid | pyruvic acid |
|-----------------|--------------|--------------|
| Diffractometer | Bruker D8 Venture dual source | Bruker D8 Venture dual source |
| Absorption correction | Multi-scan (SADABS; Krause et al., 2015) | Multi-scan (SADABS; Krause et al., 2015) |
| Tmin, Tmax | 0.721, 0.959 | 0.809, 0.971 |
| No. of measured, independent and observed | 18595, 1856, 1392 | 10479, 1425, 1242 |
| Rint | 0.062 | 0.025 |
| (sin θ/λ)max (Å⁻¹) | 0.650 | 0.796 |
| Refinement | | |
| R[F² > 2σ(F²)], wR(F²), S | 0.037, 0.100, 1.09 | 0.031, 0.082, 1.08 |
| No. of reflections | 1586 | 1425 |
| No. of parameters | 104 | 60 |
| 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 |
| Δρmax, Δρmin (e Å⁻³) | 0.36, –0.24 | 0.40, –0.21 |

6. Refinement

Crystal data, data collection, and structure refinement details are summarized in Table 3. Non-disordered hydrogen atoms were found in difference Fourier maps. For pyruvic acid, the hydroxyl hydrogen-atom coordinates were refined freely, while methyl hydrogen C—H distances used a riding model that allowed the C—H distance to refine. For zymonic acid, riding models were used for all hydrogen atoms apart from those disordered about the twofold axis, which were modeled in accordance with the recommendations of Fäbry (2018). Uiso(H) parameters of non-disordered hydrogens were set to either 1.2Ueq or 1.5Ueq (for the methyl and hydroxyl groups, respectively) of the attached atom. To ensure stable refinement of disordered groups in the zymonic acid structure, constraints (SHELXL command EADP) were used to equalize displacement parameters of superimposed atoms.

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References

Allen, F., Greiner, R. & Wishart, D. (2015). Metabolomics, 11, 98–110.
Allen, F., Pon, A., Greiner, R. & Wishart, D. (2016). Anal. Chem. 88, 7689–7697.
Bloomer, J. L., Gross, M. A., Kappler, F. E. & Pandey, G. N. (1970). J. Chem. Soc. D, p. 1030a.
Brunner (2016). APEX3: Bruker AXS Inc., Madison, Wisconsin, USA.
Düwel, S., Hundshammer, C., Gersch, M., Feuerecker, B., Steiger, K., Buck, A., Walch, A., Haase, A., Glaser, S. J., Schwaiger, M. & Schilling, F. (2017). Nat. Commun. 8, 15126.
Eugene, A. J. & Guzman, M. I. (2017a). J. Phys. Chem. A, 121, 2924–2935.
Eugene, A. J. & Guzman, M. I. (2017b). J. Phys. Chem. A, 121, 8741–8744.
Fäbry, J. (2018). Acta Cryst. E74, 1344–1357.
Groom, C. R., Bruno, I. J., Lightfoot, M. P. & Ward, S. C. (2016). Acta Cryst. B72, 171–179.
Guzman, M. I. (2011). Origins of Life: The Primal Self-Organization, edited by R. Egel, D.-H. Lankena & A. Y. Mulikdianjan, pp. 85–105: Springer Berlin Heidelberg.
Guzman, M. I. & Martin, S. T. (2008). Int. J. Astrobiology, 7, 271–278.
Harata, K., Sakabe, N. & Tanaka, J. (1977). Acta Cryst. B33, 210–212.
Hundshammer, C., Düwel, S., Köcher, S. S., Gersch, M., Feuerecker, B., Scheurer, C., Haase, A., Glaser, S. J., Schwaiger, M. & Schilling, F. (2017). ChemPhysChem, 18, 2422–2425.
Krause, L., Herbst-Irmer, R., Sheldrick, G. M. & Stalke, D. (2015). J. Appl. Cryst. 48, 3–10.
Nelson, D. L. & Cox, M. (2004). Lehninger Principles of Biochemistry, 4th ed. New York: W. H. Freeman.
Parkin, S. (2013). CIFFIX, https://xray.uky.edu/Resources/scripts/ciffix

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Parkin, S. & Hope, H. (1998). *J. Appl. Cryst.* **31**, 945–953.

Prohens, R., Barbas, R., Portell, A., Font-Bardia, M., Alcobé, X. & Puigjaner, C. (2016). *Cryst. Growth Des.* **16**, 1063–1070.

Schilling, F., Glaser, S., Düwel, S. & Gersch, M. (2016). *pH-Biosensors Based on Compounds Produced From Pyruvic Acid For Magnetic Resonance Imaging and Spectroscopy and Their Uses*. Google Patents.

Sheldrick, G. M. (2008). *Acta Cryst.* **A64**, 112–122.

Sheldrick, G. M. (2015a). *Acta Cryst.* **A71**, 3–8.

Sheldrick, G. M. (2015b). *Acta Cryst.* **C71**, 3–8.

Wishart, D. S., Feunang, Y. D., Marcu, A., Guo, A. C., Liang, K., Vázquez-Fresno, R., Sajed, T., Johnson, D., Li, C., Karu, N., Sayeeda, Z., Lo, E., Assempour, N., Berjanskii, M., Singhal, S., Arndt, D., Liang, Y., Badran, H., Grant, J., Serra-Cayuela, A., Liu, Y., Mandal, R., Neveu, V., Pon, A., Knox, C., Wilson, M., Manach, C. & Scalbert, A. (2018). *Nucleic Acids Res.* **46**, D608–D617.

Wishart, D. S., Jewison, T., Guo, A. C., Wilson, M., Knox, C., Liu, Y., Djoumbou, Y., Mandal, R., Aziat, F., Dong, E., Bouatra, S., Sinelnikov, I., Arndt, D., Xia, J., Liu, P., Yallou, F., Bjorndahl, T., Perez-Pineiro, R., Eisner, R., Allen, Neveu, V., Greiner, R. & Scalbert, A. (2013). *Nucleic Acids Res.* **41**, D801–D807.

Yannai, S. (2004). *Dictionary of food compounds with CD-ROM: Additives, flavors, and ingredients*. Boca Raton: Chapman and Hall/CRC.

Zhou, R. & Guzman, M. I. (2016). *J. Phys. Chem. C* **120**, 7349–7357.
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Computing details
For both structures, data collection: APEX3 (Bruker, 2016); cell refinement: APEX3 (Bruker, 2016); data reduction: APEX3 (Bruker, 2016); program(s) used to solve structure: SHELXT (Sheldrick, 2015a). Program(s) used to refine structure: SHELXL2018/3 (Sheldrick, 2015b) for zymonic; SHELXL2018 (Sheldrick, 2015b) for pyruvic. For both structures, molecular graphics: XP in SHELXTL (Sheldrick, 2008); software used to prepare material for publication: SHELXL (Sheldrick, 2008) and CIFFIX (Parkin, 2013).

4-Hydroxy-2-methyl-5-oxo-2,5-dihydrofuran-2-carboxylic acid (zymonic)

Crystal data
C₆H₆O₅
Mr = 158.11
Monoclinic, C2/c
a = 24.145 (3) Å
b = 6.6523 (7) Å
c = 8.6201 (7) Å
β = 95.169 (4)°
V = 1378.9 (3) Å³
Z = 8

F(000) = 656
Dₐ = 1.523 Mg m⁻³
Mo Kα radiation, λ = 0.71073 Å
Cell parameters from 9925 reflections
θ = 3.2–27.5°
μ = 0.14 mm⁻¹
T = 90 K
Thin plate, colourless
0.30 × 0.25 × 0.02 mm

Data collection
Bruker D8 Venture dual source diffractometer
Radiation source: microsource
Detector resolution: 5.6 pixels mm⁻¹
φ and ω scans
Absorption correction: multi-scan
(SADABS; Krause et al., 2015)
T_max = 0.721, T_min = 0.959
18595 measured reflections
1586 independent reflections
1392 reflections with I > 2σ(I)
R_{int} = 0.062
θ_max = 27.5°, θ_min = 3.2°
k = −31→31
l = −11→10

Refinement
Refinement on F²
Least-squares matrix: full
R[F² > 2σ(F²)] = 0.037
wR(F²) = 0.100
S = 1.09
1586 reflections
104 parameters
0 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/[σ²(Fo²) + (0.0428P)² + 1.4377P]
where P = (Fo² + 2Fc²)/3
Extended Details

Experimental. The crystal was mounted using polyisobutene oil on the tip of a fine glass fibre, which was fastened in a copper mounting pin with electrical solder. It was placed directly into the cold gas stream of a liquid-nitrogen based cryostat (Hope, 1994; Parkin & Hope, 1998). Diffraction data were collected with the crystal at 90K, which is standard practice in this laboratory for the majority of flash-cooled crystals.

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. Refinement progress was checked using Platon (Spek, 2009) and by an R-tensor (Parkin, 2000). The final model was further checked with the IUCr utility checkCIF.

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

|    | x     | y     | z     | Uiso*/Ueq | Occ. (<1) |
|----|-------|-------|-------|-----------|-----------|
| C1 | 0.67036 (5) | 0.40914 (19) | 0.56905 (14) | 0.0170 (3) |
| O1 | 0.68738 (4) | 0.24154 (14) | 0.54864 (11) | 0.0209 (2) |
| C2 | 0.69378 (5) | 0.5659 (2) | 0.67706 (14) | 0.0178 (3) |
| O2 | 0.74026 (4) | 0.51656 (15) | 0.76588 (12) | 0.0240 (3) |
| H2 | 0.752557 | 0.618162 | 0.815574 | 0.036* |
| C3 | 0.66149 (5) | 0.7275 (2) | 0.66335 (15) | 0.0182 (3) |
| H3 | 0.667502 | 0.849554 | 0.719574 | 0.022* |
| O3 | 0.62412 (4) | 0.48283 (13) | 0.48901 (11) | 0.0188 (2) |
| C4 | 0.61371 (5) | 0.68442 (19) | 0.54353 (15) | 0.0186 (3) |
| O4 | 0.54061 (4) | 0.51162 (15) | 0.66013 (12) | 0.0249 (3) |
| C5 | 0.507244 | 0.517998 | 0.736346 | 0.109 (14)* 0.5 |
| O5 | 0.54177 (4) | 0.84824 (16) | 0.66262 (14) | 0.0303 (3) |
| H5O | 0.509866 | 0.849228 | 0.727610 | 0.109 (14)* 0.5 |
| C6 | 0.56056 (5) | 0.67919 (19) | 0.62725 (15) | 0.0188 (3) |
| H6A | 0.65945 (7) | 0.8285 (2) | 0.40645 (17) | 0.0257 (3) |
| H6B | 0.644218 | 0.825746 | 0.355945 | 0.039* |
| H6C | 0.578557 | 0.787894 | 0.331471 | 0.039* |

Atomic displacement parameters (Å²)

|    | U¹¹ | U²² | U³³ | U¹² | U¹³ | U²³ |
|----|-----|-----|-----|-----|-----|-----|
| C1 | 0.0184 (6) | 0.0180 (6) | 0.0151 (6) | −0.0007 (5) | 0.0038 (5) | 0.0010 (5) |
| O1 | 0.0238 (5) | 0.0173 (5) | 0.0213 (5) | 0.0015 (4) | 0.0010 (4) | −0.0013 (4) |
| C2 | 0.0165 (6) | 0.0204 (6) | 0.0165 (6) | −0.0023 (5) | 0.0016 (5) | −0.0020 (5) |
| O2 | 0.0186 (5) | 0.0249 (5) | 0.0274 (5) | 0.0035 (4) | −0.0050 (4) | −0.0073 (4) |
| C3 | 0.0168 (6) | 0.0190 (6) | 0.0190 (6) | −0.0032 (5) | 0.0020 (5) | −0.0036 (5) |
| O3 | 0.0213 (5) | 0.0155 (5) | 0.0192 (5) | 0.0003 (3) | −0.0013 (4) | −0.0027 (3) |
| C4 | 0.0205 (6) | 0.0135 (6) | 0.0212 (6) | −0.0007 (5) | −0.0012 (5) | −0.0018 (5) |
### Geometric parameters (Å, °)

| Bond/Angle | Value            | Bond/Angle | Value            |
|------------|------------------|------------|------------------|
| C1—O1      | 1.2067 (16)      | C4—C6      | 1.5179 (19)      |
| C1—O3      | 1.3505 (15)      | C4—C5      | 1.5282 (19)      |
| C1—C2      | 1.4763 (18)      | O4—C5      | 1.2568 (16)      |
| C2—C3      | 1.3268 (18)      | C4—H4O     | 1.0854           |
| C2—O2      | 1.3411 (16)      | O5—C5      | 1.2602 (16)      |
| O2—H2      | 0.8400           | O5—H5O     | 0.9926           |
| C3—C4      | 1.5051 (17)      | C6—H6A     | 0.9800           |
| C3—H3      | 0.9500           | C6—H6B     | 0.9800           |
| O3—C4      | 1.4505 (15)      | C6—H6C     | 0.9800           |
| C1—O1—O3   | 122.52 (12)      | O3—C4—C5  | 108.03 (10)      |
| O1—C1—C2  | 128.95 (12)      | C3—C4—C5  | 112.41 (11)      |
| O3—C1—C2  | 108.53 (11)      | C6—C4—C5  | 115.0            |
| C3—C2—O2  | 134.75 (12)      | C5—O4—H4O | 117.2            |
| C3—C2—C1  | 109.12 (11)      | C5—O5—H5O | 125.69 (13)      |
| O2—C2—C1  | 116.12 (11)      | O4—C5—O5  | 118.80 (11)      |
| C2—C3—C4  | 108.35 (11)      | O5—C5—C4  | 115.45 (11)      |
| C2—C3—H3  | 125.8            | C4—C6—H6A | 109.5            |
| C4—C3—H3  | 125.8            | C4—C6—H6B | 109.5            |
| C1—O3—C4  | 109.24 (10)      | H6B—C6—H6C| 109.5            |
| O3—C4—C3  | 104.7 (11)       | H6A—C6—H6B| 109.5            |
| O3—C4—C6  | 109.47 (11)      | H6B—C6—H6C| 109.5            |
| C3—C4—C6  | 114.07 (11)      | H6B—C6—H6C| 109.5            |
| O1—C1—C2—C3 | -179.25 (13)   | C1—O3—C4—C5 | -112.19 (11) |
| O3—C1—C2—C3 | 1.17 (15)       | C2—C3—C4—O3 | -1.69 (14)   |
| O1—C1—C2—O2 | -0.3 (2)        | C2—C3—C4—C6 | -121.33 (13) |
| O3—C1—C2—O2 | -179.92 (10)   | C2—C3—C4—C5 | 113.14 (12)   |
| O2—C2—C3—C4 | -178.23 (14)   | O3—C4—C5—O4 | 12.04 (16)   |
| C1—C2—C3—C4 | 0.39 (15)       | C3—C4—C5—O4 | -100.56 (13) |
| O1—C1—O3—C4 | 178.13 (12)   | C6—C4—C5—O4 | 132.92 (13)   |
| C2—C1—O3—C4 | -2.26 (13)    | O3—C4—C5—O5 | -170.61 (11) |
| C1—O3—C4—C3 | 2.43 (13)      | C3—C4—C5—O5 | 76.79 (14)    |
| C1—O3—C4—C6 | 125.11 (12)   | C6—C4—C5—O5 | -49.72 (16)   |
O4—H4O···O4ii 1.09 1.52 2.607 (2) 176
O5—H5O···O5ii 0.99 1.63 2.624 (2) 179

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

2-Oxopropanoic acid (pyruvic)

Crystal data

\[\text{C}_3\text{H}_4\text{O}_3\frac{}{}\]

\[M_r = 88.06\]

Monoclinic, \(P2_1/c\)

\[a = 10.7486 (3) \text{Å}\]

\[b = 5.1925 (2) \text{Å}\]

\[c = 6.8302 (2) \text{Å}\]

\[\beta = 99.063 (1)^\circ\]

\[V = 376.45 (2) \text{Å}^3\]

\[Z = 4\]

\(F(000) = 184\)

\(D_\text{x} = 1.554 \text{Mg m}^{-3}\)

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

Cell parameters from 6955 reflections

\[\theta = 3.8–34.3^\circ\]

\[\mu = 0.14 \text{mm}^{-1}\]

\(T = 90 \text{K}\)

Well-faceted block, colourless

0.26 \(\times\) 0.22 \(\times\) 0.18 mm

Data collection

Bruker D8 Venture dual source diffractometer

Radiation source: microsource

Detector resolution: 5.6 pixels mm\(^{-1}\)

\(\phi\) and \(\omega\) scans

Absorption correction: multi-scan (\textit{SADABS}; Krause \textit{et al.}, 2015)

\(T_{\text{min}} = 0.890, T_{\text{max}} = 0.971\)

10479 measured reflections

1425 independent reflections

1242 reflections with \(I > 2\sigma(I)\)

\(R_{\text{int}} = 0.025\)

\(\theta_{\text{max}} = 34.5^\circ, \theta_{\text{min}} = 3.8^\circ\)

\(h = -16\rightarrow16\)

\(k = -7\rightarrow8\)

\(l = -10\rightarrow10\)

Refinement

Refinement on \(F^2\)

Least-squares matrix: full

\[R(F^2 > 2\sigma(F^2)) = 0.031\]

\[wR(F^2) = 0.082\]

\[S = 1.08\]

1425 reflections

60 parameters

0 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

\(w = 1/[(\sigma(F^2) + (0.0299P)^2 + 0.1264P)]\)

where \(P = (F^2 + 2F_c^2)/3\)

\((\Delta/\sigma)_{\text{max}} < 0.001\)

\(\Delta\rho_{\text{max}} = 0.40 \text{ e Å}^{-3}\)

\(\Delta\rho_{\text{min}} = -0.21 \text{ e Å}^{-3}\)

Special details

Experimental. The crystal was mounted using polyisobutene oil on the tip of a fine glass fibre, which was fastened in a copper mounting pin with electrical solder. It was placed directly into the cold gas stream of a liquid-nitrogen based cryostat (Parkin & Hope, 1998).

Diffraction data were collected with the crystal at 90K, which is standard practice in this laboratory for the majority of flash-cooled crystals.

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. Refinement progress was checked using \textit{Platon} (Spek, 2009) and by an \(R\)-tensor (Parkin, 2000). The final model was further checked with the IUCr utility \textit{checkCIF}.  

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

|   | x       | y         | z         | Uiso*/Ueq |
|---|---------|-----------|-----------|-----------|
| O1| 0.41673 (5) | 0.30370 (12) | 0.30191 (9) | 0.01968 (14) |
| H1| 0.4903 (13) | 0.320 (3)    | 0.3883 (19) | 0.030*     |
| C1| 0.33963 (6)  | 0.48448 (14) | 0.34005 (11) | 0.01316 (14) |
| O2| 0.36317 (5)  | 0.65673 (11) | 0.46175 (8)  | 0.01589 (13) |
| C2| 0.20853 (6)  | 0.46732 (14) | 0.21028 (10) | 0.01271 (14) |
| C3| 0.11464 (7)  | 0.65949 (15) | 0.25725 (11) | 0.01520 (15) |
| H3A| 0.1499 (3)   | 0.8314 (12)  | 0.255 (1)    | 0.023*     |
| H3B| 0.0940 (5)   | 0.6245 (9)   | 0.388 (1)    | 0.023*     |
| H3C| 0.0389 (6)   | 0.6478 (9)   | 0.1594 (9)   | 0.023*     |
| O3| 0.18824 (5)  | 0.30508 (11) | 0.08250 (9)  | 0.01774 (14) |

Atomic displacement parameters (Å²)

|   | U₁¹  | U₂²  | U₃³  | U₁₂  | U₁₃  | U₂₃  |
|---|------|------|------|------|------|------|
| O1| 0.0132 (2) | 0.0218 (3) | 0.0222 (3) | 0.0041 (2) | −0.0027 (2) | −0.0084 (2) |
| C1| 0.0121 (3) | 0.0138 (3) | 0.0136 (3) | −0.0002 (2) | 0.0018 (2)  | 0.0003 (2)  |
| O2| 0.0135 (2) | 0.0155 (3) | 0.0176 (3) | −0.00038 (19) | −0.00071 (19) | −0.0034 (2) |
| C2| 0.0119 (3) | 0.0139 (3) | 0.0121 (3) | −0.0011 (2) | 0.0010 (2)  | 0.0009 (2)  |
| C3| 0.0140 (3) | 0.0163 (3) | 0.0148 (3) | 0.0023 (2)  | 0.0008 (2)  | −0.0013 (3) |
| O3| 0.0167 (3) | 0.0181 (3) | 0.0173 (3) | −0.0002 (2) | −0.0008 (2) | −0.0049 (2) |

Geometric parameters (Å, °)

|   |   |   |   |   |   |   |
|---|---|---|---|---|---|---|
| O1—C1 | 1.3053 (9) | C2—C3 | 1.4896 (10) |
| O1—H1 | 0.913 (14) | C3—H3A | 0.971 (6) |
| C1—O2 | 1.2201 (9) | C3—H3B | 0.971 (6) |
| C1—C2 | 1.5446 (10) | C3—H3C | 0.971 (6) |
| C2—O3 | 1.2079 (9) |   |   |   |   |   |

|   |   |   |   |   |   |   |
|---|---|---|---|---|---|---|
| O1—O1—H1 | 108.4 (8) | C2—C3—H3A | 109.5 |
| O2—C1—O1 | 126.37 (7) | C2—C3—H3B | 109.5 |
| O2—C1—C2 | 120.38 (6) | H3A—C3—H3B | 109.5 |
| O1—C1—C2 | 113.24 (6) | C2—C3—H3C | 109.5 |
| O3—C2—C3 | 124.85 (7) | H3A—C3—H3C | 109.5 |
| O3—C2—C1 | 119.96 (7) | H3B—C3—H3C | 109.5 |
| C3—C2—C1 | 115.19 (6) |   |   |   |   |   |

|   |   |   |   |   |   |   |
|---|---|---|---|---|---|---|
| O2—C1—C2—O3 | 175.81 (7) | O2—C1—C2—C3 | −4.59 (10) |
| O1—C1—C2—O3 | −3.34 (10) | O1—C1—C2—C3 | 176.26 (6) |

Hydrogen-bond geometry (Å, °)

| D—H···A | D—H | H···A | D···A | D—H···A |
|---------|-----|------|-------|--------|
| O1—H1···O2i | 0.913 (14) | 1.742 (14) | 2.6536 (8) | 175.5 (12) |
Symmetry code: (i) −x+1, −y+1, −z+1.