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anti-Ethyl acetohydroximate

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Key indicators: single-crystal X-ray study; T = 100 K; mean σ (C–C) = 0.002 Å; R factor = 0.034; wR factor = 0.098; data-to-parameter ratio = 14.1.

In the crystal structure of the title compound, $C_4H_9NO_2$, the O-H···N hydrogen bonds link the molecules into supramolecular chains extending along the *b*-axis direction. The conformation of the NOH group in the nearly planar (r.m.s. deviation = 0.0546 Å) ethyl acetohydroximate molecule is trans to N=C.

Related literature

For related structures, see: Kjaer et al. (1977); Larsen (1971). For studies of the IR spectra of hydrogen bonding in oxime derivatives, see: Flakus et al. (2012). For typical bond distances, see: Allen et al. (1987). For hydrogen-bond motifs, see: Bernstein et al. (1995); Etter et al. (1990).



Experimental

Crystal data

C₄H₉NO₂ $M_r = 103.12$ Monoclinic, C2/c a = 19.9481 (9) Åb = 4.4138(1) Å c = 13.3277 (5) Å $\beta = 109.027 \ (4)^{\circ}$

V = 1109.35 (7) Å³ Z = 8Mo Ka radiation $\mu = 0.10 \text{ mm}^{-1}$ T = 100 K $0.52\,\times\,0.18\,\times\,0.14$ mm



Data collection

Refinement

 $R[F^2 > 2\sigma(F^2)] = 0.034$ H atoms treated by a mixture of $wR(F^2) = 0.098$ independent and constrained S = 1.08refinement $\Delta \rho_{\text{max}} = 0.22 \text{ e} \text{ Å}^{-3}$ 970 reflections $\Delta \rho_{\rm min} = -0.22 \text{ e } \text{\AA}^{-3}$ 69 parameters

Diffraction, 2006)

 $R_{\rm int} = 0.025$

 $T_{\min} = 0.505, \ T_{\max} = 1.000$ 6699 measured reflections

970 independent reflections 868 reflections with $I > 2\sigma(I)$

Table 1

Hydrogen-bond geometry (Å, °).

$D - H \cdot \cdot \cdot A$	D-H	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - \mathbf{H} \cdot \cdot \cdot A$
$O1 - H1 \cdots N1^i$	0.871 (19)	1.954 (19)	2.8196 (14)	172.4 (16)
Symmetry code: (i	$-x + \frac{1}{2}, y + \frac{1}{2}, -x$	$z + \frac{3}{2}$.		

Data collection: CrysAlis CCD (Oxford Diffraction, 2006); cell refinement: CrysAlis CCD; data reduction: CrysAlis RED (Oxford Diffraction, 2006); program(s) used to solve structure: SHELXS97 (Sheldrick, 2008); program(s) used to refine structure: SHELXL97 (Sheldrick, 2008); molecular graphics: Mercury (Macrae et al., 2006); software used to prepare material for publication: publCIF (Westrip, 2010).

Supplementary data and figures for this paper are available from the IUCr electronic archives (Reference: FF2116).

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anti-Ethyl acetohydroximate

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S1. Comment

Anti-ethyl acetohydroximate [systematic name: ethyl *N*-hydroxyacetimidate], (I), was investigated in a continuation of our studies of the IR spectra of hydrogen bonding in oxime derivatives (Flakus *et al.*, 2012). In order to study interactions occurring *via* hydrogen bonds and molecular packing in this compound, we have now determined the structure of (I) using diffraction data collected at 100 K. Until now, the structures of *syn*-methyl acetohydroximate and *syn*- and *anti*-ethyl benzohydroximate were determined (Kjaer *et al.*, 1977; Larsen *et al.*, 1971). The crystal structure of *syn*-methyl acetohydroximate is composed of layers of molecules, which form cyclic, hydrogen-bonded trimers, whereas the crystals of *syn*- and *anti*-ethyl benzohydroximate are composed of dimers formed by pairs of O—H…N hydrogen- bonded molecules.

The molecule of (I) is nearly planar (r.m.s. deviations 0.0546 Å for all non-H atoms). The lengths of the bonds C=N (1.2771 (17) Å) and N—O (1.4286 (13) Å) in (I) are comparable to the mean values found in other oximes (C=N 1.281 Å; N—O 1.394 Å) (Allen *et al.*, 1987). The conformation of the NOH group in the planar ethyl acetohydroximate molecule is *trans* to N=C. In the crystal, O—H···N are observed forming infinite chains along the *b* axis (Fig. 2) with a graph-set motif of *C*(3) (Etter *et al.*, 1990; Bernstein *et al.*, 1995).

S2. Experimental

Ethyl acetohydroximate was purchased from Aldrich-Sigma. Crystals of title compound, suitable for X-ray diffraction, were selected directly from purchased sample.

S3. Refinement

The H atoms were introduced in geometrically idealized positions with C—H distances of 0.99 Å and $U_{iso}(H)$ values set at $1.2U_{eq}(C)$ for methylene group or 0.98 Å and with $U_{iso}(H)$ values set at $1.5U_{eq}(C)$ for methyl groups. The H atom which takes part in hydrogen bonding was located in a difference Fourier map and was refined with $U_{iso}(H)$ value set at $1.5U_{eq}(O)$.



Figure 1

The asymmetric unit of (I), with the atom-numbering scheme, showing 50% probability displacement ellipsoids. H atoms are shown as small spheres of arbitrary radius.



Figure 2

Part of the crystal structure of (I), showing the C(3) chains. The red lines indicate the hydrogen-bonding interactions. For the sake of clarity, all H atoms bonded to C atoms were omitted.

Ethyl N-hydroxyethanecarboximidate

Crystal data

C₄H₉NO₂ $M_r = 103.12$ Monoclinic, C2/c Hall symbol: -C 2yc a = 19.9481 (9) Å b = 4.4138 (1) Å c = 13.3277 (5) Å $\beta = 109.027$ (4)° V = 1109.35 (7) Å³ Z = 8

Data collection

Oxford Diffraction Xcalibur	6699 measured reflections
diffractometer with a Sapphire3 detector	970 independent reflections
Radiation source: fine-focus sealed tube	868 reflections with $I > 2\sigma(I)$
Graphite monochromator	$R_{\rm int} = 0.025$
Detector resolution: 16.0328 pixels mm ⁻¹	$\theta_{\rm max} = 25.1^\circ, \ \theta_{\rm min} = 3.2^\circ$
ω–scan	$h = -22 \rightarrow 23$
Absorption correction: multi-scan	$k = -2 \rightarrow 5$
(CrysAlis RED; Oxford Diffraction, 2006)	$l = -15 \rightarrow 15$
$T_{\min} = 0.505, \ T_{\max} = 1.000$	
Refinement	
Refinement on F^2	Secondary atom site location: difference Fourier
Least-squares matrix: full	map

 $R[F^2 > 2\sigma(F^2)] = 0.034$ Hydrogen site location: inferred from $wR(F^2) = 0.098$ neighbouring sites S = 1.08H atoms treated by a mixture of independent 970 reflections and constrained refinement 69 parameters $w = 1/[\sigma^2(F_o^2) + (0.0616P)^2 + 0.5949P]$ where $P = (F_0^2 + 2F_c^2)/3$ 0 restraints Primary atom site location: structure-invariant $(\Delta/\sigma)_{\rm max} < 0.001$ direct methods $\Delta \rho_{\rm max} = 0.22 \text{ e} \text{ Å}^{-3}$ $\Delta \rho_{\rm min} = -0.22 \ {\rm e} \ {\rm \AA}^{-3}$

Special details

Geometry. All e.s.d.'s (except the e.s.d. in the dihedral angle between two l.s. planes) are estimated using the full covariance matrix. The cell e.s.d.'s are taken into account individually in the estimation of e.s.d.'s in distances, angles and torsion angles; correlations between e.s.d.'s in cell parameters are only used when they are defined by crystal symmetry. An approximate (isotropic) treatment of cell e.s.d.'s is used for estimating e.s.d.'s involving l.s. planes.

F(000) = 448

 $\theta = 3.1 - 34.4^{\circ}$

 $\mu = 0.10 \text{ mm}^{-1}$

Needle, colourless

 $0.52 \times 0.18 \times 0.14 \text{ mm}$

T = 100 K

 $D_{\rm x} = 1.235 {\rm Mg} {\rm m}^{-3}$

Melting point = 296-298 K

Mo *K* α radiation, $\lambda = 0.71073$ Å

Cell parameters from 6376 reflections

Refinement. Refinement of F^2 against ALL reflections. The weighted *R*-factor *wR* and goodness of fit *S* are based on F^2 , conventional *R*-factors *R* are based on *F*, with *F* set to zero for negative F^2 . The threshold expression of $F^2 > \sigma(F^2)$ is used only for calculating *R*-factors(gt) *etc.* and is not relevant to the choice of reflections for refinement. *R*-factors based on F^2 are statistically about twice as large as those based on *F*, and *R*- factors based on ALL data will be even larger.

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

	x	у	Ζ	$U_{ m iso}$ */ $U_{ m eq}$	
01	0.31644 (5)	0.6668 (2)	0.82875 (7)	0.0201 (3)	
O2	0.39491 (4)	0.1706 (2)	0.69431 (7)	0.0185 (3)	
N1	0.31725 (5)	0.4501 (2)	0.74954 (8)	0.0165 (3)	

C1	0.38102 (7)	0.3704 (3)	0.76216 (10)	0.0158 (3)
C2	0.44623 (7)	0.4799 (3)	0.84598 (10)	0.0215 (3)
H2A	0.4568	0.6871	0.8294	0.032*
H2B	0.4862	0.3472	0.8486	0.032*
H2C	0.4385	0.4774	0.9149	0.032*
C3	0.33586 (7)	0.0728 (3)	0.60358 (10)	0.0187 (3)
H3A	0.3103	0.2503	0.5636	0.022*
H3B	0.3022	-0.0497	0.6271	0.022*
C4	0.36699 (8)	-0.1145 (3)	0.53500 (11)	0.0235 (3)
H4A	0.3987	0.0118	0.5100	0.035*
H4B	0.3287	-0.1929	0.4739	0.035*
H4C	0.3938	-0.2843	0.5765	0.035*
H1	0.2735 (10)	0.740 (4)	0.8065 (13)	0.035*

Atomic displacement parameters (\mathring{A}^2)

	U^{11}	U^{22}	U^{33}	U^{12}	U^{13}	U^{23}
01	0.0168 (5)	0.0243 (5)	0.0190 (5)	0.0038 (4)	0.0054 (4)	-0.0041 (4)
O2	0.0153 (5)	0.0230 (5)	0.0163 (5)	0.0012 (3)	0.0041 (4)	-0.0017 (4)
N1	0.0170 (6)	0.0172 (6)	0.0154 (6)	-0.0001 (4)	0.0052 (4)	0.0006 (4)
C1	0.0167 (7)	0.0174 (6)	0.0140 (6)	0.0000 (5)	0.0062 (5)	0.0034 (5)
C2	0.0152 (7)	0.0290 (7)	0.0193 (7)	0.0011 (5)	0.0042 (5)	-0.0014 (6)
C3	0.0175 (7)	0.0201 (7)	0.0164 (7)	-0.0019 (5)	0.0026 (5)	0.0002 (5)
C4	0.0282 (7)	0.0241 (7)	0.0188 (7)	-0.0025 (6)	0.0086 (6)	-0.0006 (5)

Geometric parameters (Å, °)

01—N1	1.4286 (13)	C2—H2C	0.9800
01—H1	0.871 (19)	C3—C4	1.5082 (17)
O2—C1	1.3547 (15)	С3—НЗА	0.9900
O2—C3	1.4517 (15)	С3—Н3В	0.9900
N1C1	1.2771 (17)	C4—H4A	0.9800
C1—C2	1.4922 (17)	C4—H4B	0.9800
C2—H2A	0.9800	C4—H4C	0.9800
C2—H2B	0.9800		
N1—O1—H1	104.1 (11)	O2—C3—C4	106.57 (10)
C1—O2—C3	117.55 (9)	O2—C3—H3A	110.4
C1-N1-01	109.76 (10)	C4—C3—H3A	110.4
N1-C1-O2	120.21 (12)	O2—C3—H3B	110.4
N1-C1-C2	126.66 (12)	C4—C3—H3B	110.4
O2—C1—C2	113.11 (10)	НЗА—СЗ—НЗВ	108.6
C1—C2—H2A	109.5	C3—C4—H4A	109.5
C1—C2—H2B	109.5	C3—C4—H4B	109.5
H2A—C2—H2B	109.5	H4A—C4—H4B	109.5
C1—C2—H2C	109.5	C3—C4—H4C	109.5
H2A—C2—H2C	109.5	H4A—C4—H4C	109.5
H2B—C2—H2C	109.5	H4B—C4—H4C	109.5

01—N1—C1—O2	-178.49 (9)	C3—O2—C1—C2	-174.04 (10)
O1—N1—C1—C2	0.24 (17)	C1—O2—C3—C4	173.10 (10)
C3—O2—C1—N1	4.85 (16)		

Hydrogen-bond geometry (Å, °)

D—H···A	D—H	H···A	D····A	D—H···A
O1—H1…N1 ⁱ	0.871 (19)	1.954 (19)	2.8196 (14)	172.4 (16)

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