

T = 120 K

 $0.36 \times 0.28 \times 0.24$ mm



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Crystal structure of diisopropylaminium dichloroacetate

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In the title compound, $C_6H_{16}N^+ \cdot C_2HCl_2O_2^-$, the cation exhibits non-crystallographic C_2 symmetry. In the crystal, the components are linked by N-H···O and C-H···O hydrogen bonds into chains propagating along [010].

Keywords: crystal structure; diisopropylamine dichlorocacetate; hydrogen bonding.

CCDC reference: 1060114

1. Related literature

For the background to the biological activity of the title compound, see: Gelernt & Herbert (2009); Yamane et al. (2014); Liu et al. (2015). For a related structure, see: Yu & Qian (2009).



2. Experimental

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2.1. Crystal data	
$C_6H_{16}N^+ \cdot C_2HCl_2O_2^-$	b = 9.04914 (17) Å
$M_r = 230.13$	c = 13.6496 (3) Å
Monoclinic, $P2_1/c$	$\beta = 106.433 \ (2)^{\circ}$
a = 10.0272 (2) Å	V = 1187.94 (4) Å ³

Z = 4Cu Ka radiation $\mu = 4.71 \text{ mm}^{-1}$

2.2. Data collection

Agilent Xcalibur Atlas Gemini ultra	11039 measured reflections
diffractometer	2107 independent reflections
Absorption correction: multi-scan	1911 reflections with $I > 2\sigma(I)$
(CrysAlis PRO; Agilent, 2014)	$R_{\rm int} = 0.026$
$T_{\min} = 0.662, T_{\max} = 1.000$	

2.3. Refinement

 $R[F^2 > 2\sigma(F^2)] = 0.038$ $wR(F^2) = 0.092$ S = 1.032107 reflections

122 parameters H-atom parameters constrained $\Delta \rho_{\rm max} = 0.81 \text{ e } \text{\AA}^{-3}$ $\Delta \rho_{\rm min} = -0.85 \text{ e } \text{\AA}^{-3}$

Table 1 Hydrogen-bond geometry (Å, °).

$D - H \cdot \cdot \cdot A$	D-H	$H \cdot \cdot \cdot A$	$D \cdot \cdot \cdot A$	$D - \mathbf{H} \cdot \cdot \cdot A$
$N1-H1A\cdotsO1^{i}$ $N1-H1B\cdotsO2^{ii}$ $C6-H6\cdotsO1^{iii}$	0.92	1.87	2.788 (2)	177
	0.92	1.90	2.757 (2)	154
	1.00	2.38	3.258 (2)	146

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

Data collection: CrysAlis PRO (Agilent, 2014); cell refinement: CrysAlis PRO; data reduction: CrysAlis PRO; program(s) used to solve structure: SHELXS97 (Sheldrick, 2008); program(s) used to refine structure: SHELXL97 (Sheldrick, 2008); molecular graphics: SHELXTL (Sheldrick, 2008); software used to prepare material for publication: OLEX2 (Dolomanov et al., 2009), SHELXTL, PLATON (Spek, 2009) and publCIF (Westrip, 2010).

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Supporting information for this paper is available from the IUCr electronic archives (Reference: GK2629).

References

- Agilent (2014). CrysAlis PRO. Agilent Technologies, Yarnton, England.
- Dolomanov, O. V., Bourhis, L. J., Gildea, R. J., Howard, J. A. K. & Puschmann,
- H. (2009). J. Appl. Cryst. 42, 339-341. Gelernt, M. D. & Herbert, V. (1982). Nutr. Cancer, 3, 129-133.
- Liu, D.-X., Wang, F.-F., Yue, J., Jing, X.-B. & Huang, Y.-B. (2015). Drug Deliv.
- 22, 136-143.
- Sheldrick, G. M. (2008). Acta Cryst. A64, 112-122.
- Spek, A. L. (2009). Acta Cryst. D65, 148-155.
- Westrip, S. P. (2010). J. Appl. Cryst. 43, 920-925.
- Yamane, K., Indalao, I.-L., Chida, J., Yamamoto, Y., Hanawa, M. & Kido, H. (2014). PLos ONE, 9, e98032.
- Yu, Y.-H. & Qian, K. (2009). Acta Cryst. E65, o1278.

supporting information

Acta Cryst. (2015). E71, o361 [doi:10.1107/S2056989015007586]

Crystal structure of diisopropylaminium dichloroacetate

Wei Sun and Guangzhi Shan

S1. Comment

Diisopropylaminium dichlorocacetate (DADA) is the effective constituent of Vitamin B15 (Gelernt *et al.*, 2009). Recently, DADA has been found as a potential PDK4 inhibitor for treatment of severe influenza (Yamane *et al.*, 2014). Moreover the desirable therapeutic effects of colorectal cancer in mat is shown (Liu *et al.*, 2015). No data about the crystal structure of diisopropylaminium dichlorocacetate has been reported so far.

The title molecule is shown in Fig. 1. The asymmetric unit contains one diisopropylaminium cation and one dichloroacetate anion. In the crystal structure, the cations and anions are linked by intermolecular N—H…O and C—H…O hydrogen bonds (Table 1, Fig.2) to form chains propagating along [010].

S2. Experimental

Single crystals suitable for X-ray analysis were obtained by slow solvent evaporation from a solution of the title compound in a dichloromethane/cyclohexane mixture (1:1 v/v) at room temperature.

S3. Refinement

All H atoms were positioned geometrically and constrained to ride on the parent atoms, with N—H = 0.92 Å and C—H = 0.98–1.00 Å, and with $U_{iso}(H) = 1.5U_{eq}(methyl C)$ or $1.2U_{eq}(C, N)$ for other H atoms.



Figure 1

The molecular structure of the title compound. The displacement parameters are shown at the 30% probability level.



Figure 2

Crystal packing of the title compound, viewed down the b direction. Dashed lines indicate hydrogen bonds.

Bis(propan-2-yl)azanium 2,2-dichloroacetate

Crystal data

C₆H₁₆N⁺·C₂HCl₂O₂⁻ $M_r = 230.13$ Monoclinic, $P2_1/c$ a = 10.0272 (2) Å b = 9.04914 (17) Å c = 13.6496 (3) Å $\beta = 106.433$ (2)° V = 1187.94 (4) Å³ Z = 4

Data collection

Agilent Xcalibur Atlas Gemini ultra diffractometer Radiation source: sealed X-ray tube, Enhance Ultra (Cu) X-ray Source Mirror monochromator Detector resolution: 10.4674 pixels mm⁻¹ ω scans Absorption correction: multi-scan (*CrysAlis PRO*; Agilent, 2014)

Refinement

Refinement on F^2 Least-squares matrix: full $R[F^2 > 2\sigma(F^2)] = 0.038$ $wR(F^2) = 0.092$ S = 1.032107 reflections 122 parameters 0 restraints F(000) = 488 $D_x = 1.287 \text{ Mg m}^{-3}$ Cu K\alpha radiation, \lambda = 1.54184 \rangle A Cell parameters from 5039 reflections $\theta = 4.6-66.9^{\circ}$ $\mu = 4.71 \text{ mm}^{-1}$ T = 120 KBlock, colourless $0.36 \times 0.28 \times 0.24 \text{ mm}$

 $T_{\min} = 0.662, T_{\max} = 1.000$ 11039 measured reflections 2107 independent reflections 1911 reflections with $I > 2\sigma(I)$ $R_{int} = 0.026$ $\theta_{\max} = 66.9^{\circ}, \theta_{\min} = 4.6^{\circ}$ $h = -11 \rightarrow 11$ $k = -7 \rightarrow 10$ $l = -16 \rightarrow 16$

Primary atom site location: structure-invariant direct methods Secondary atom site location: difference Fourier map Hydrogen site location: inferred from neighbouring sites H-atom parameters constrained $w = 1/[\sigma^2(F_o^2) + (0.0344P)^2 + 1.3398P]$ where $P = (F_o^2 + 2F_c^2)/3$ $(\Delta/\sigma)_{\text{max}} < 0.001$ $\begin{array}{l} \Delta\rho_{\rm max}=0.81~{\rm e}~{\rm \AA}^{-3}\\ \Delta\rho_{\rm min}=-0.85~{\rm e}~{\rm \AA}^{-3} \end{array}$

Special details

Experimental. The crystal was placed in the cold stream of an Oxford Cryosystems open-flow nitrogen cryostat with a nominal stability of 0.1 K. .

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

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

	X	У	Ζ	$U_{ m iso}$ */ $U_{ m eq}$	
Cl1	0.53986 (5)	0.16195 (6)	0.60806 (5)	0.04006 (18)	
Cl2	0.62278 (7)	-0.05527 (9)	0.76920 (6)	0.0651 (3)	
01	0.86608 (14)	-0.08510 (15)	0.66082 (12)	0.0292 (3)	
O2	0.84614 (15)	0.15792 (15)	0.68081 (12)	0.0308 (3)	
N1	0.15036 (16)	-0.05351 (17)	0.75375 (12)	0.0202 (3)	
H1A	0.0563	-0.0607	0.7230	0.024*	
H1B	0.1801	-0.1441	0.7822	0.024*	
C2	0.80092 (19)	0.0312 (2)	0.66498 (14)	0.0216 (4)	
C3	0.2208 (2)	-0.0234 (2)	0.67193 (15)	0.0268 (4)	
H3	0.3218	-0.0050	0.7050	0.032*	
C6	0.1729 (2)	0.0574 (2)	0.83878 (15)	0.0256 (4)	
H6	0.1401	0.1563	0.8087	0.031*	
C4	0.1577 (2)	0.1123 (3)	0.61147 (17)	0.0331 (5)	
H4A	0.0568	0.0998	0.5855	0.050*	
H4B	0.1972	0.1253	0.5540	0.050*	
H4C	0.1785	0.1995	0.6558	0.050*	
C1	0.6441 (2)	0.0036 (2)	0.65013 (17)	0.0291 (5)	
H1	0.6122	-0.0772	0.5989	0.035*	
C7	0.0847 (3)	0.0110 (3)	0.90727 (17)	0.0362 (5)	
H7A	-0.0130	0.0049	0.8669	0.054*	
H7B	0.0943	0.0840	0.9619	0.054*	
H7C	0.1158	-0.0858	0.9373	0.054*	
C5	0.2054 (3)	-0.1610 (3)	0.60590 (18)	0.0421 (6)	
H5A	0.2486	-0.2451	0.6483	0.063*	
H5B	0.2513	-0.1450	0.5522	0.063*	
H5C	0.1065	-0.1815	0.5747	0.063*	
C8	0.3249 (2)	0.0689 (3)	0.8971 (2)	0.0436 (6)	
H8A	0.3593	-0.0283	0.9247	0.065*	
H8B	0.3363	0.1395	0.9533	0.065*	
H8C	0.3779	0.1029	0.8511	0.065*	

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

	U^{11}	U^{22}	U^{33}	U^{12}	U^{13}	U^{23}
Cl1	0.0265 (3)	0.0351 (3)	0.0558 (4)	0.0130 (2)	0.0072 (2)	0.0078 (2)
Cl2	0.0341 (3)	0.0849 (5)	0.0860 (5)	0.0143 (3)	0.0328 (3)	0.0510 (4)
01	0.0201 (7)	0.0203 (7)	0.0470 (9)	0.0020 (6)	0.0090 (6)	-0.0021 (6)
02	0.0266 (7)	0.0206 (7)	0.0473 (9)	-0.0036 (6)	0.0139 (6)	-0.0056 (6)
N1	0.0162 (7)	0.0192 (8)	0.0250 (8)	0.0001 (6)	0.0055 (6)	0.0007 (6)
C2	0.0188 (9)	0.0231 (10)	0.0229 (9)	0.0003 (8)	0.0056 (7)	0.0012 (7)
C3	0.0173 (9)	0.0376 (12)	0.0271 (10)	-0.0007 (8)	0.0091 (8)	0.0046 (9)
C6	0.0270 (10)	0.0204 (10)	0.0292 (10)	0.0020 (8)	0.0078 (8)	-0.0026 (8)
C4	0.0333 (12)	0.0334 (12)	0.0334 (11)	-0.0038 (9)	0.0106 (9)	0.0076 (9)
C1	0.0187 (10)	0.0231 (10)	0.0434 (12)	0.0032 (8)	0.0053 (9)	0.0030 (9)
C7	0.0416 (13)	0.0394 (13)	0.0313 (11)	0.0023 (10)	0.0161 (10)	-0.0025 (10)
C5	0.0558 (15)	0.0426 (14)	0.0327 (12)	0.0147 (12)	0.0201 (11)	0.0021 (10)
C8	0.0314 (12)	0.0473 (14)	0.0466 (14)	-0.0040(11)	0.0020 (10)	-0.0203(12)

Atomic displacement parameters $(Å^2)$

Geometric parameters (Å, °)

Cl1—C1	1.771 (2)	C6—C8	1.511 (3)	
Cl2—C1	1.780 (2)	C4—H4A	0.9800	
O1—C2	1.248 (2)	C4—H4B	0.9800	
O2—C2	1.230 (2)	C4—H4C	0.9800	
N1—H1A	0.9200	C1—H1	1.0000	
N1—H1B	0.9200	C7—H7A	0.9800	
N1—C3	1.505 (2)	С7—Н7В	0.9800	
N1—C6	1.503 (2)	С7—Н7С	0.9800	
C2—C1	1.548 (3)	C5—H5A	0.9800	
С3—Н3	1.0000	С5—Н5В	0.9800	
C3—C4	1.514 (3)	С5—Н5С	0.9800	
С3—С5	1.519 (3)	C8—H8A	0.9800	
С6—Н6	1.0000	C8—H8B	0.9800	
С6—С7	1.516 (3)	C8—H8C	0.9800	
H1A—N1—H1B	107.3	H4B—C4—H4C	109.5	
C3—N1—H1A	108.1	Cl1—C1—Cl2	109.02 (12)	
C3—N1—H1B	108.1	Cl1—C1—H1	108.8	
C6—N1—H1A	108.1	Cl2—C1—H1	108.8	
C6—N1—H1B	108.1	C2—C1—Cl1	113.38 (14)	
C6—N1—C3	116.92 (15)	C2—C1—Cl2	107.99 (14)	
O1—C2—C1	112.56 (16)	C2—C1—H1	108.8	
O2—C2—O1	128.50 (18)	С6—С7—Н7А	109.5	
O2—C2—C1	118.92 (17)	С6—С7—Н7В	109.5	
N1—C3—H3	108.9	С6—С7—Н7С	109.5	
N1—C3—C4	109.89 (16)	H7A—C7—H7B	109.5	
N1—C3—C5	107.58 (17)	H7A—C7—H7C	109.5	
С4—С3—Н3	108.9	H7B—C7—H7C	109.5	
C4—C3—C5	112.62 (18)	С3—С5—Н5А	109.5	

С5—С3—Н3	108.9	С3—С5—Н5В	109.5
N1—C6—H6	108.7	С3—С5—Н5С	109.5
N1—C6—C7	107.75 (16)	H5A—C5—H5B	109.5
N1—C6—C8	111.19 (16)	H5A—C5—H5C	109.5
С7—С6—Н6	108.7	H5B—C5—H5C	109.5
С8—С6—Н6	108.7	С6—С8—Н8А	109.5
C8—C6—C7	111.81 (19)	C6—C8—H8B	109.5
C3—C4—H4A	109.5	C6—C8—H8C	109.5
C3—C4—H4B	109.5	H8A—C8—H8B	109.5
C3—C4—H4C	109.5	H8A—C8—H8C	109.5
H4A—C4—H4B	109.5	H8B—C8—H8C	109.5
H4A—C4—H4C	109.5		
01—C2—C1—Cl1	-157.58 (15)	C3—N1—C6—C7	175.93 (16)
O1—C2—C1—Cl2	81.51 (19)	C3—N1—C6—C8	-61.2 (2)
O2—C2—C1—Cl1	23.8 (2)	C6—N1—C3—C4	-67.1 (2)
O2—C2—C1—Cl2	-97.11 (19)	C6—N1—C3—C5	169.99 (17)

Hydrogen-bond geometry (Å, °)

D—H···A	D—H	H···A	D····A	D—H···A	
N1—H1A···O1 ⁱ	0.92	1.87	2.788 (2)	177	
N1—H1 <i>B</i> ···O2 ⁱⁱ	0.92	1.90	2.757 (2)	154	
C6—H6····O1 ⁱⁱⁱ	1.00	2.38	3.258 (2)	146	

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