

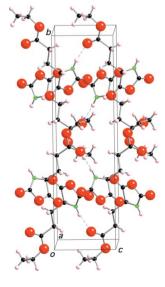
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Crystal structure of *γ***-ethyl-L-glutamate** *N***-carboxy anhydride**

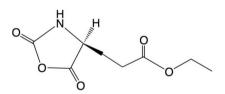
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In the title compound (alternative name *N*-carboxy-L-glutamic anhydride γ -ethyl ester), C₈H₁₁NO₅, the oxazolidine ring is essentially planar, with a maximum deviation of 0.019 (2) Å. In the crystal, molecules are linked by N-H···O hydrogen bonds between the imino group and the carbonyl O atom in the ethyl ester group, forming a tape structure along the *c*-axis direction. The oxazolidine rings of adjacent tapes are arranged into a layer parallel to the *ac* plane. This arrangement is favourable for the polymerization of the title compound in the solid state.

1. Chemical context

N-Carboxy anhydrides (NCAs) of amino acids are extensively used as monomers in the preparation of high molecular weight polypeptides (Kricheldorf, 2006). Amino acid NCAs are easily soluble but the resulting polypeptides are not soluble in general organic solvents. Only a few amino acid ester NCAs such as γ -benzyl-L-glutamate NCA and β -benzyl-L-aspartate NCA can be polymerized in solutions, because the resulting polypeptides are soluble in them. Thus, the polymerization of these amino acid ester NCAs has been investigated by many researchers. We found that every amino acid NCA crystal is polymerized in the solid state in hexane by the initiation of amines, and have studied the solid-state polymerization of amino acid NCAs with reference to the crystal structures (Kanazawa, 1992; Kanazawa & Magoshi, 2003; Kanazawa *et al.*, 2006).



The title compound, γ -ethyl-L-glutamate NCA (ELG NCA) is polymerized both in dioxane solution and in the solid state in hexane, using butylamine as initiator. However, ELG NCA is very reactive in the solid state in hexane using the same initiator. Therefore, it is important to determine the crystal structure in order to consider the difference in the reactivity of ELG NCA in solution and in the solid state.

2. Structural commentary

The molecular structure of the title compound is shown in Fig. 1. The oxazolidine ring is essentially planar, with a maximum deviation of 0.019 (2) Å for atom C1. The side chain



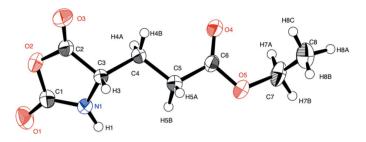


Figure 1

The molecular structure of the title compound showing atom labels and 50% probability displacement ellipsoids for non-H atoms.

has an extended conformation with the torsion angles C3-C4-C5-C6 and C4-C5-C6-O5 being 177.65 (13) and -172.05 (13)°, respectively.

3. Supramolecular features

In the crystal, ELG NCA molecules are linked by N1– $H1\cdots O4$ hydrogen bonds along the *c* axis (Table 1 and Fig. 2). The five-membered oxazolidine rings are packed in a layer and the $-CH_2CH_2COOCH_2CH_3$ groups are packed in another layer; these two different layers are stacked alternately. This

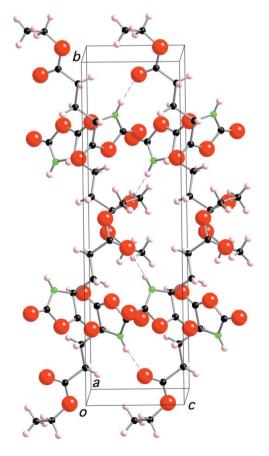


Figure 2

A crystal packing diagram of the title compound, viewed approximately along the *a* axis, showing the hydrogen bonds as dashed lines (see Table 1 for details).

Table 1		
Hydrogen-bond geometry	(Å	°)

riyarogen bona geometry (ri,).					
$D - H \cdots A$	D-H	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - H \cdot \cdot \cdot A$	
$N1-H1\cdots O4^i$	0.76 (2)	2.13 (2)	2.8766 (17)	170 (2)	

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

sandwich structure is one of the important requirements for high reactivity in the solid state, because the five-membered rings can react with each other in the layer.

4. Database survey

A search of the Cambridge Structural Database (Version 5.35, May 2014; Groom & Allen, 2014) revealed the presence of 20 hits for 4-methyloxazolidine-2,5-dione derivatives. A number of these compounds involve amino acid sides chains (amino acid NCAs). These include two polymorphs of a compound involving L-aspartate, namely N-carboxy- β -benzyl-L-aspartate anhydride (SOHRIQ: Kanazawa, 1998; no coordinates were deposited) and (SOHRIQ01: Kanazawa & Magoshi, 2003). Two other compounds involving L-glutamate have also been reported. They are very similar to the title compound and are polymorphs of N-carboxy- γ -benzyl-L-glutamate anhydride (ANCBGL; Kanazawa et al., 1978) and (WIPDUV; Kanazawa et al., 2006). For the latter, unfortunately no coordinates have been deposited. The structural overlay of the title compound and ANCBGL indicates that the N-carboxy-L-glutamate anhydride moieties have very similar conformations (Fig. 3).

5. Synthesis and crystallization

The synthesis of γ -ethyl-L-glutamate (ELG) was carried out by the reaction of L-glutamic acid with ethanol in a manner similar to that of γ -benzyl-L-glutamate (BLG) (Kanazawa, 1992). The title compound was obtained by the reaction of γ -ethyl-L-glutamate with trichloromethyl chloroformate or triphosgene in tetrahydrofuran, as reported previously for β -benzyl-L-aspartate (BLA) NCA (Kanazawa & Magoshi, 2003). The reaction product was recrystallized in a mixture of ethyl acetate and hexane (1:50 ν/ν), avoiding moisture contamination.



Figure 3 A view of the structural overlay of the title compound (blue) and ANCBGL (red; Kanazawa *et al.*, 1978).

research communications

Table 2Experimental details.

nbic, $P2_12_12$
, 20.581 (5), 5.8405 (14)
$\theta \times 0.14$
aLAB mini
(REQAB; Rigaku,
4
, 2042
1, 1.03
eated by a mixture of dent and constrained ent
-)

Computer programs: CrystalClear (Rigaku, 2009), SIR2004 (Burla et al., 2005), SHELXL97 (Sheldrick, 2008), CrystalStructure (Rigaku, 2010) and Mercury (Macrae et al., 2008).

6. Refinement details

Crystal data, data collection and structure refinement details are summarized in Table 2. The N-bound H atom was found in a difference Fourier map and its position was refined with $U_{\rm iso}({\rm H}) = 1.5U_{\rm eq}({\rm N})$. C-bound H atoms were positioned geometrically (C-H = 0.96–0.98 Å) and treated as riding with $U_{\rm iso}({\rm H}) = 1.2U_{\rm eq}({\rm C})$.

Acknowledgements

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supporting information

Acta Cryst. (2015). E71, 110-112 [https://doi.org/10.1107/S2056989014027170]

Crystal structure of γ -ethyl-L-glutamate N-carboxy anhydride

Hitoshi Kanazawa and Aya Inada

Computing details

Data collection: CrystalClear (Rigaku, 2009); cell refinement: CrystalClear (Rigaku, 2009); data reduction: CrystalClear (Rigaku, 2009); program(s) used to solve structure: SIR2004 (Burla et al., 2005); program(s) used to refine structure: SHELXL97 (Sheldrick, 2008); molecular graphics: CrystalStructure (Rigaku, 2010) and Mercury (Macrae et al., 2008); software used to prepare material for publication: CrystalStructure (Rigaku, 2010).

(S)-4-[2-(Ethoxycarbonyl)ethyl]-1,3-oxazolidine-2,5-dione

Crystal data	
$C_8H_{11}NO_5$	F(000) = 424
$M_r = 201.18$	$D_{\rm x} = 1.401 {\rm Mg} {\rm m}^{-3}$
Orthorhombic, $P2_12_12$	Mo <i>K</i> α radiation, $\lambda = 0.71069$ Å
Hall symbol: P 2 2ab	$\theta = 3.2 - 27.5^{\circ}$
a = 7.9337 (19) Å	$\mu=0.12~\mathrm{mm^{-1}}$
b = 20.581 (5) Å	T = 293 K
c = 5.8405 (14) Å	Prism, colorless
$V = 953.7 (4) \text{ Å}^3$	$0.66 \times 0.39 \times 0.14 \text{ mm}$
Z = 4	
Data collection	
Rigaku XtaLAB mini	9982 measured reflections
diffractometer	2190 independent reflections
Radiation source: fine-focus sealed tube	2042 reflections with $I > 2\sigma(I)$
Graphite monochromator	$R_{\rm int} = 0.024$
Detector resolution: 6.827 pixels mm ⁻¹	$\theta_{\rm max} = 27.5^{\circ}, \ \theta_{\rm min} = 3.2^{\circ}$
ω scans	$h = -10 \rightarrow 10$
Absorption correction: multi-scan	$k = -26 \rightarrow 26$
(<i>REQAB</i> ; Rigaku, 1998)	$l = -7 \rightarrow 7$
$T_{\min} = 0.926, \ T_{\max} = 0.984$	
Refinement	
Refinement on F^2	Secondary atom site location: dif
Least-squares matrix: full	map
$R[F^2 > 2\sigma(F^2)] = 0.034$	Hydrogen site location: inferred

 $wR(F^2) = 0.081$ *S* = 1.03 2190 reflections 131 parameters 0 restraints Primary atom site location: structure-invariant direct methods

ary atom site location: difference Fourier gen site location: inferred from neighbouring sites H atoms treated by a mixture of independent and constrained refinement $w = 1/[\sigma^2(F_o^2) + (0.0385P)^2 + 0.167P]$ where $P = (F_0^2 + 2F_c^2)/3$ $(\Delta/\sigma)_{\rm max} = 0.010$ $\Delta \rho_{\rm max} = 0.16 \text{ e} \text{ Å}^{-3}$ $\Delta \rho_{\rm min} = -0.16 \text{ e} \text{ Å}^{-3}$

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.

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	$U_{ m iso}$ */ $U_{ m eq}$
01	-0.02731 (16)	0.77067 (6)	-0.0480 (2)	0.0538 (4)
02	0.10460 (14)	0.72562 (4)	0.25649 (18)	0.0385 (3)
03	0.27691 (18)	0.70878 (5)	0.5536 (2)	0.0548 (4)
04	0.19733 (14)	0.94889 (5)	0.93375 (19)	0.0417 (3)
05	0.26952 (18)	1.03085 (5)	0.7069 (2)	0.0539 (4)
N1	0.15491 (17)	0.82887 (6)	0.1795 (2)	0.0344 (3)
C1	0.06782 (19)	0.77729 (7)	0.1092 (3)	0.0355 (3)
C2	0.22322 (19)	0.74470 (6)	0.4126 (3)	0.0340 (3)
С3	0.26475 (17)	0.81536 (6)	0.3704 (2)	0.0283 (3)
C4	0.23203 (19)	0.85660 (6)	0.5828 (3)	0.0318 (3)
25	0.2829 (3)	0.92684 (7)	0.5461 (3)	0.0425 (4)
C6	0.24451 (18)	0.96852 (6)	0.7513 (3)	0.0336 (3)
C 7	0.2257 (3)	1.07707 (7)	0.8886 (4)	0.0504 (5)
C8	0.3640 (3)	1.08564 (9)	1.0556 (4)	0.0575 (5)
H1	0.156 (3)	0.8596 (10)	0.108 (4)	0.0517*
H3	0.3827	0.8197	0.3231	0.0339*
H4A	0.1132	0.8547	0.6210	0.0381*
H4B	0.2950	0.8389	0.7108	0.0381*
H5A	0.4027	0.9288	0.5139	0.0509*
H5B	0.2234	0.9439	0.4140	0.0509*
H7A	0.1261	1.0617	0.9682	0.0604*
17B	0.1990	1.1188	0.8204	0.0604*
H8A	0.4623	1.1017	0.9782	0.0689*
H8B	0.3895	1.0446	1.1259	0.0689*
H8C	0.3301	1.1161	1.1711	0.0689*

Fractional atomic coordinates and isotropic or equivalent isotropic displacement parameters (\hat{A}^2)

Atomic displacement parameters $(Å^2)$

	U^{11}	U^{22}	U^{33}	U^{12}	U^{13}	U^{23}
01	0.0582 (7)	0.0549 (7)	0.0482 (7)	-0.0087 (6)	-0.0192 (6)	-0.0092 (6)
02	0.0425 (6)	0.0261 (4)	0.0470 (6)	-0.0067 (4)	-0.0017 (5)	-0.0028 (5)
03	0.0817 (9)	0.0355 (5)	0.0473 (6)	0.0005 (6)	-0.0118 (7)	0.0098 (5)
O4	0.0598 (7)	0.0274 (4)	0.0380 (6)	-0.0052 (5)	0.0094 (6)	-0.0030 (4)
O5	0.0899 (9)	0.0257 (5)	0.0461 (6)	-0.0118 (6)	0.0003 (7)	0.0003 (5)
N1	0.0486 (7)	0.0267 (5)	0.0280 (5)	-0.0060(5)	-0.0048 (5)	0.0024 (5)
C1	0.0387 (7)	0.0328 (7)	0.0349 (7)	-0.0035 (6)	-0.0014 (6)	-0.0044 (6)

supporting information

C2	0.0431 (7)	0.0275 (6)	0.0313 (7)	-0.0004 (6)	0.0049 (7)	-0.0027 (6)	
C3	0.0323 (6)	0.0269 (6)	0.0256 (6)	-0.0043 (5)	0.0016 (5)	-0.0021 (5)	
C4	0.0411 (7)	0.0278 (6)	0.0264 (6)	-0.0037 (5)	0.0040 (6)	-0.0032 (5)	
C5	0.0633 (10)	0.0333 (7)	0.0308 (7)	-0.0130 (7)	0.0052 (8)	-0.0035 (6)	
C6	0.0402 (7)	0.0245 (6)	0.0361 (7)	-0.0054(5)	-0.0046 (6)	0.0002 (5)	
C7 C8	0.0536 (9) 0.0606 (10)	0.0243 (6) 0.0450 (9)	0.0732 (11) 0.0668 (12)	0.0023 (7) 0.0006 (8)	-0.0051 (9) -0.0007 (10)	-0.0090(7) -0.0164(9)	

Geometric parameters (Å, °)

1	· /		
01—C1	1.1964 (18)	C4—C5	1.5159 (18)
O2—C2	1.3677 (18)	C4—H4A	0.9700
O2—C1	1.3985 (18)	C4—H4B	0.9700
O3—C2	1.1861 (17)	C5—C6	1.505 (2)
O4—C6	1.1997 (18)	С5—Н5А	0.9700
O5—C6	1.3237 (15)	C5—H5B	0.9700
O5—C7	1.467 (2)	C7—C8	1.478 (3)
N1-C1	1.3314 (18)	С7—Н7А	0.9700
N1—C3	1.4423 (18)	С7—Н7В	0.9700
N1—H1	0.76 (2)	C8—H8A	0.9600
С2—С3	1.5113 (17)	C8—H8B	0.9600
C3—C4	1.5251 (17)	C8—H8C	0.9600
С3—Н3	0.9800		
C2—O2—C1	109.58 (10)	H4A—C4—H4B	107.9
C6—O5—C7	116.82 (14)	C6—C5—C4	112.17 (12)
C1—N1—C3	113.46 (12)	C6—C5—H5A	109.2
C1—N1—H1	119.9 (15)	C4—C5—H5A	109.2
C3—N1—H1	125.7 (15)	C6—C5—H5B	109.2
01—C1—N1	130.91 (15)	C4—C5—H5B	109.2
01—C1—O2	121.12 (13)	H5A—C5—H5B	107.9
N1-C1-O2	107.97 (12)	O4—C6—O5	123.17 (14)
O3—C2—O2	122.09 (13)	O4—C6—C5	125.34 (12)
O3—C2—C3	129.38 (14)	O5—C6—C5	111.49 (13)
O2—C2—C3	108.53 (11)	O5—C7—C8	112.25 (14)
N1—C3—C2	100.35 (11)	O5—C7—H7A	109.2
N1—C3—C4	114.75 (11)	C8—C7—H7A	109.2
C2—C3—C4	111.48 (11)	O5—C7—H7B	109.2
N1—C3—H3	110.0	С8—С7—Н7В	109.2
С2—С3—Н3	110.0	H7A—C7—H7B	107.9
С4—С3—Н3	110.0	C7—C8—H8A	109.5
C5—C4—C3	111.76 (11)	C7—C8—H8B	109.5
C5—C4—H4A	109.3	H8A—C8—H8B	109.5
C3—C4—H4A	109.3	C7—C8—H8C	109.5
C5—C4—H4B	109.3	H8A—C8—H8C	109.5
C3—C4—H4B	109.3	Н8В—С8—Н8С	109.5
C3—N1—C1—O1	-176.31 (16)	O3—C2—C3—C4	-57.2 (2)

supporting information

C3—N1—C1—O2	3.49 (17)	O2—C2—C3—C4	122.05 (12)
C2	176.53 (14)	N1—C3—C4—C5	-70.08 (16)
C2—O2—C1—N1	-3.30 (16)	C2—C3—C4—C5	176.72 (13)
C1—O2—C2—O3	-178.76 (14)	C3—C4—C5—C6	177.65 (13)
C1—O2—C2—C3	1.89 (15)	C7—O5—C6—O4	-4.1 (2)
C1—N1—C3—C2	-2.23 (15)	C7—O5—C6—C5	176.04 (14)
C1—N1—C3—C4	-121.83 (14)	C4—C5—C6—O4	8.0 (2)
O3—C2—C3—N1	-179.18 (16)	C4—C5—C6—O5	-172.05 (13)
O2—C2—C3—N1	0.11 (14)	C6—O5—C7—C8	84.9 (2)
02 - C2 - C3 - N1	0.11 (14)	C6—O5—C7—C8	84.9 (2)

Hydrogen-bond geometry (Å, °)

D—H···A	D—H	Н…А	D····A	<i>D</i> —H··· <i>A</i>
N1—H1···O4 ⁱ	0.76 (2)	2.13 (2)	2.8766 (17)	170 (2)

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