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Hydrogen bonding in *N*,*N*′-bis[(1*S*)-2-azido-1-(2-methylpropyl)ethyl]oxalamide: twofold symmetry of $R_2^2(10)$ hydrogen-bonded dimers connected into an α-network

Zoran Štefanić,[a] Biserka Kojić-Prodić,[a]* Zoran Džolić,[a] Darinka Katalenić,[a] Mladen Žinić[a] and Anton Meden[b]

[a]Rudjer Bošković Institute, PO Box 180, HR-10002 Zagreb, Croatia, and [b]Faculty of Chemistry and Chemical Technology, University of Ljubljana, POB 537, 1001 Ljubljana, Slovenia
Correspondence e-mail: kojic@rudjer.irb.hr

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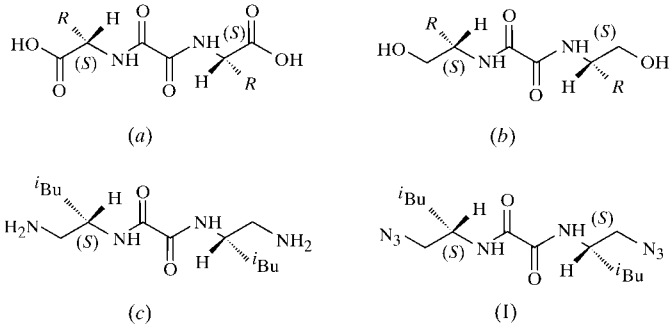
The title compound, $C_{14}H_{26}N_8O_2$, belongs to a class of retropeptides with an oxalamide unit (–NH–CO–CO–NH–), and is a precursor for the synthesis of an amine-terminal gelator. The compound is a good synthon for one-dimensional hydrogen bonding. The crystal structure reveals a hydrogen-bonded cyclic dimer with unusual twofold rotation symmetry.

Comment

The present structure determination is part of a systematic study related to the hydrogen bonding and gelation properties of bis(amino acid) (Makanević *et al.*, 2001; *a* in *Scheme*) and bis(amino alcohol) oxalamide derivatives (Makarević *et al.*, 2003; *b* in *Scheme*). A number of compounds of this class have been designed and synthesized to introduce the proton donor/acceptor functionalities required for one- or two-dimensional hydrogen-bonded assemblies, in order to investigate the delicate interplay of structure, non-covalent interactions and gelating properties (Jokić *et al.*, 1995; Perić, Makarević *et al.*, 2001; Perić, Kojić-Prodić *et al.*, 2001). The oxalamide moiety was selected as a good structural unit for the design of molecular solids (Coe *et al.*, 1997; Nguyen *et al.*, 1998). Coe *et al.* (1997) studied centrosymmetric oxalamide with terminal substituted carboxyl groups. In this group of compounds, there are two distinctive hydrogen-bonding patterns, both generating a two-dimensional β-network, *viz.* (i) N—H···O hydrogen bonds between oxalamide units and O—H···O hydrogen bonds between terminal carboxyl groups (forming polymorph *A*), and (ii) O—H···O hydrogen bonds between oxalamide and carboxyl groups (forming polymorph *B*). Pattern (i) is composed of an α-network generated by hydrogen bonding within oxalamide groups that are self-assembled into a β-network *via* hydrogen bonds between carboxyl groups, including centrosymmetric cyclic carboxylic acid dimers. The title compound, (I), served as a precursor of a novel amine-terminal oxalamide gelator (*c* in *Scheme*). The substitution of azide groups precludes hydrogen bonding at the terminal sides of the molecule. However, the oxalamide groups are available for the intermolecular N—H···O hydrogen bonds that generate the α-network.



An *ORTEP*III (Burnett & Johnson, 1996) drawing of (I) (Fig. 1) reveals two molecules, denoted *A* and *B*, in the asymmetric unit. The overall conformational differences between *A* and *B* are illustrated in Fig. 2. The (*S*)-leucyl residues are positioned on the same side of the central oxalamide unit, with similar conformations (Fig. 2 and Table 1). Torsion angles ω, ω', φ, φ', ψ, ψ', χ and χ' are labelled according to the literature (IUPAC-IUB Commission on Biochemical Nomenclature, http://www.chem.qmul.ac.uk/iupac/misc/ppep1.html; Karle *et al.*, 1994). A significantly different conformation is associated with ψ' of molecule *A* because of the unique conformation of the N21/N31/N41 azide group. Among the four azide groups, three are perpendicular to the plane of the oxalamide units, whereas the N21/N31/N41 group is parallel to this plane (Table 2). The average bond

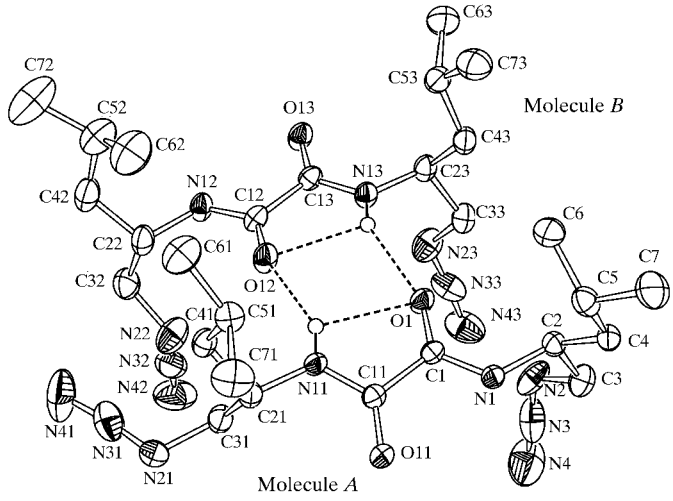


Figure 1
The molecular structure of (I), showing the two molecules, denoted *A* and *B*, in the asymmetric unit. Displacement ellipsoids are shown at the 50% probability level. Intramolecular N—H···O hydrogen bonds form a pseudo-C_5 type, typical of retropeptides, whereas intermolecular hydrogen bonds between *A* and *B* form a dimer.

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lengths for the azide groups are 1.146 (4) and 1.173 (5) Å for N—N bonds and 1.517 (4) Å for N—C bonds, with a bonding angle of 173.0 (4)°. This observation is based on an analysis of bond-geometry parameters with their corresponding standard deviations larger than 3σ. The crystal packing is defined as the α-network (Coe *et al.*, 1997) realized by N—H···O hydrogen bonds between oxalamide groups (Table 2 and Fig. 3), including different dimers. The two crystallographically independent molecules, *A* and *B*, are connected by a pair of N—H···O hydrogen bonds to form a dimer with approximate twofold rotational symmetry. The crystallographic twofold axis generates hydrogen-bonded dimers of types *A*···*A* and *B*···*B*, defined by graph-set notation as $R_2^2(10)$ (Bernstein *et al.*, 1995). An inspection of the Cambridge Structural Database (Version 5.24 of November 2002; Allen, 2002), using the oxalamide fragment, revealed 33 structures, among which a single example of a hydrogen-bonded dimer with twofold symmetry was found. The structure of *N*-hydroxyoxamide (Larsen, 1980) crystallizes in the space group *C*2/*c*. However, the three-dimensional hydrogen-bonded network of *N*-hydroxyoxamide cannot be compared with the one-dimensional network of (I). Dimers are connected in the sequence *BBAABB*... in the direction of the *c* axis. A ladder pattern (Fig. 3 and Table 2) formed in this way is based on intramolecular N—H···O hydrogen bonds with a pseudo-C_5 arrangement that is typical of retropeptides exhibiting intermolecular hydrogen bonds (Karle *et al.*, 1994). In this type of hydrogen bonding, each amide H atom acts as a double donor (three-centred or bifurcated hydrogen bond).

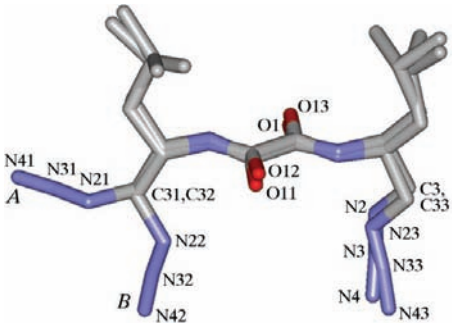

Figure 2
An overlap diagram of molecules *A* and *B*, illustrating the different conformations of the leucyl and azide groups (a least-squares fit through the oxalamide bridges was used). In molecule *A*, an approximate twofold axis bisects the C—C bond of the oxalamide group, whereas molecule *B* exhibits no symmetry.

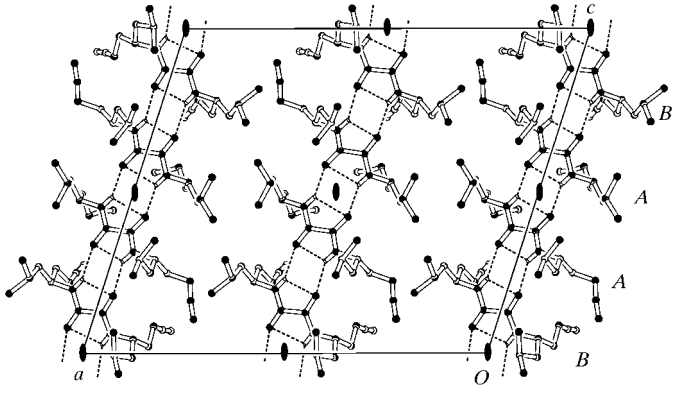

Figure 3
The crystal packing of (I). Inter- and intramolecular hydrogen bonds between oxalamide groups generate an α-network ladder pattern with the molecular sequence *AB–BA–AB–BA*. A twofold axis relates dimers *A*···*A* and *B*···*B*, whereas the *A*···*B* dimer reveals an approximate twofold symmetry. For clarity, only those H atoms that act as hydrogen-bond donors are shown.

Experimental

To a solution of the diol (*b*) (see *Scheme*; *R* is isobutyl) in dry pyridine (1.12 g, 3.88 mmol in 20 ml), *p*-TsCl (Ts is tosyl; 1.77 g, 9.28 mmol) was added, and the reaction mixture was stirred for 2 d at room temperature. When the reaction was complete (thin-layer chromatography), the solvent was evaporated under reduced pressure, and the residue was dissolved in CH_2Cl_2 (20 ml) and washed with H_2O, HOAc (5%) and H_2O. The organic phase was dried (Na_2SO_4) and evaporated. The crude tosylate was used in the next step without further purification. The tosylate was reacted with sodium azide (0.60 g, 9.23 mmol) in *N*,*N*-dimethylformamide (30 ml). The reaction mixture was heated for 1 h at 373 K and stirred overnight at room temperature. The salt was removed by filtration and the filtrate was evaporated under reduced pressure. The remaining solid was purified by flash chromatography using petroleum ether/ethyl acetate (5:2) as eluant. Compound (I) was obtained as a white solid (0.96 g, 73.1% total yield; m.p. 380–381 K). Single crystals suitable for X-ray analysis were obtained by slow evaporation of a dilute ethanol solution of (I). Spectroscopic analysis: $[\alpha]_D^{20} = -90$ ($c = 1$ in CH_2Cl_2); ^{1}H NMR ($CDCl_3$, 300 MHz, p.p.m.): δ 7.53 (*d*, $J = 9.1$ Hz, 2H, NH), 4.13 (*dt*, $J = 9.5$ Hz, $J' = 4.7$ Hz, 2H, CH_α), 3.46 (*m*, 4H, CH_2), 1.65–1.39 (*m*, 6H, CH_γ and CH_β), 0.95/0.94 (2*d*, $J = 5.1$ Hz, 6H each, CH_3); ^{13}C NMR ($CDCl_3$, 75 MHz, p.p.m.): δ 159.3 (CONH), 54.6 (CH_2), 47.8 (CH_α), 40.8 (CH_β), 24.7 (CH_γ), 23.0 and 22.0 (CH_3); IR (KBr, ν_{max}, cm^{-1}): 3295 (NH), 2099 (azide), 1654 (amide 1), 1522 (amide 2).

Crystal data

$C_{14}H_{26}N_8O_2$
$M_r = 338.43$
Monoclinic, *C*2
$a = 24.0235$ (5) Å
$b = 7.9361$ (2) Å
$c = 20.2167$ (5) Å
$\beta = 107.824$ (1)°
$V = 3669.37$ (15) Å^3
$Z = 8$
$D_x = 1.225$ Mg m^{-3}
Mo $K\alpha$ radiation
Cell parameters from 4035 reflections
$\theta = 2.9$–27.1°
$\mu = 0.09$ mm^{-1}
$T = 150$ (1) K
Prism, colourless
0.25 × 0.25 × 0.12 mm

Data collection

Nonius KappaCCD diffractometer
CCD rotation images, thick-slice scans
7645 measured reflections
7645 independent reflections
5889 reflections with $I > 2\sigma(I)$
$\theta_{max} = 27.1°$
$h = -30 \rightarrow 30$
$k = -10 \rightarrow 10$
$l = -25 \rightarrow 25$

Refinement

Refinement on F^2
$R(F) = 0.054$
$wR(F^2) = 0.129$
$S = 1.03$
7645 reflections
449 parameters
H-atoms treated by a mixture of constrained and independent refinement
$w = 1/[\sigma^2(F_o^2) + (0.0475P)^2 + 3.5690P]$ where $P = (F_o^2 + F_c^2)/3$
$(\Delta/\sigma)_{max} = 0.001$
$\Delta\rho_{max} = 0.21$ e Å^{-3}
$\Delta\rho_{min} = -0.29$ e Å^{-3}

Table 1
Selected torsion angles (°).

C2—N1—C1—C11	178.8 (2)	C23—N13—C13—C12	176.9 (2)
C1—N1—C2—C3	−105.1 (3)	C12—N12—C22—C32	−108.8 (3)
N1—C2—C3—N2	62.8 (3)	N12—C22—C32—N22	69.4 (3)
N1—C2—C4—C5	−54.1 (3)	N12—C22—C42—C52	−47.4 (4)
C21—N11—C11—C1	−179.6 (2)	C22—N12—C12—C13	−179.2 (2)
C11—N11—C21—C31	−95.9 (3)	C13—N13—C23—C33	−117.3 (3)
N11—C21—C31—N21	178.0 (2)	N13—C23—C33—N23	56.8 (3)
C51—C41—C21—N11	−64.1 (3)	N13—C23—C43—C53	−67.8 (3)

Table 2
Hydrogen-bonding geometry (Å, °).

D—H···*A*	*D*—H	H···*A*	*D*···*A*	*D*—H···*A*
N11—H11N···O12	0.84 (3)	2.15 (3)	2.893 (3)	147 (2)
N1—H1N···O11^{i}	0.84 (3)	2.11 (3)	2.879 (3)	153 (2)
N13—H13N···O1	0.81 (3)	2.21 (3)	2.948 (3)	152 (2)
N13—H13N···O12	0.81 (3)	2.28 (3)	2.673 (3)	110 (2)
N12—H12N···O13^{ii}	0.82 (3)	2.23 (3)	2.978 (3)	152 (2)
N1—H1N···O11	0.84 (3)	2.38 (3)	2.748 (3)	108 (2)
N12—H12N···O13	0.82 (3)	2.38 (3)	2.734 (4)	107 (2)
N11—H11N···O1	0.84 (3)	2.31 (3)	2.708 (3)	109 (2)

Symmetry codes: (i) $2-x, y, 1-z$; (ii) $2-x, y, 2-z$.

The atomic scattering factors included in *SHELXL*97 (Sheldrick, 1997) were used. H atoms were calculated geometrically; those attached to C atoms were refined as riding (C—H = 0.96–0.98 Å) and those attached to N atoms were refined freely (see Table 2 for distances).

Data collection: *COLLECT* (Nonius, 1997–2000); cell refinement: *HKL SCALEPACK* (Otwinowski & Minor, 1997); data reduction: *HKL DENZO* (Otwinowski & Minor, 1997) and *SCALEPACK*; program(s) used to solve structure: *SHELXS*97 (Sheldrick, 1997); program(s) used to refine structure: *SHELXL*97 (Sheldrick, 1997); molecular graphics: *ORTEP*-3 *for Windows* (Farrugia, 1997); software used to prepare material for publication: *WinGX* (Farrugia, 1999) and *PLATON* (Spek, 2003).

The crystallographic data set was collected on the Nonius KappaCCD diffractometer at the Laboratory of Inorganic Chemistry, Faculty of Chemistry and Chemical Technology, University of Ljubljana, Slovenia. We acknowledge with thanks the financial contribution of the Ministry of Science and Technology, Republic of Slovenia, through grants No. X-2000 and No. PS-511-102, which made the purchase of the apparatus possible.

Supplementary data for this paper are available from the IUCr electronic archives (Reference: GD1245). Services for accessing these data are described at the back of the journal.

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