

Solvent-induced conformational changes in cyclic peptides: a vibrational circular dichroism study†

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The three-dimensional structure of a peptide is strongly influenced by its solvent environment. In the present study, we study three cyclic tetrapeptides which serve as model peptides for β -turns. They are of the general structure cyclo(Boc-Cys-Pro-X-Cys-OMe) with the amino acid X being either glycine (**1**), or L- or D-leucine (L- or D-**2**). Using vibrational circular dichroism (VCD) spectroscopy, we confirm previous NMR results which showed that D-**2** adopts predominantly a β_{II} turn structure in apolar and polar solvents. Our results for L-**2** indicate a preference for a β_I structure over β_{II} . With increasing solvent polarity, the preference for **1** is shifted from β_{II} towards β_I . This conformational change goes along with the breaking of an intramolecular hydrogen bond which stabilizes the β_{II} conformation. Instead, a hydrogen bond with a solvent molecule can stabilize the β_I turn conformation.

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Introduction

Besides periodic secondary structures like α -helices and β -sheets, turns are the most common structural motifs in peptides and as such they establish the directional reversal in peptide strands. Most attention in studies on turns has been paid to the tight β -turns which link the strands of antiparallel β -sheet structures. They are also exposed to the environment of peptides, *i.e.* the solvent, ions, and substrates. β -Turns consist of four amino acid residues linked by three amide bonds and show a high structural flexibility. Initially, β -turns were assumed to form a hydrogen bond between the carbonyl group of the first (position i) and the amide N-H of the fourth amino acid residue (position $i + 3$).¹ However, it was later shown that β -turns without this hydrogen bond exist as well.² Nowadays, eight different tight β -turns are distinguished and characterized mainly by the dihedral angles adopted by the amino acid residues $i + 1$ and $i + 2$.³ The amino acid sequences and its peptidic and non-peptidic environments determine which β -turn conformation is adopted under certain conditions.

The most common experimental techniques used to study peptide conformations are infrared and Raman spectroscopy,³ electronic circular dichroism (ECD) and two-dimensional NMR spectroscopy. The chiroptical versions of infrared and Raman

spectroscopy, vibrational circular dichroism (VCD) spectroscopy and Raman optical activity (ROA), which measure vibrational optical activity (VOA),⁴ have also become well-known and powerful techniques to study peptides, proteins^{5–8} and carbohydrates⁹ as well as other chiral molecules in solution.^{10–17}

Small peptides can serve as structural model systems for examining the influence of the peptide environment on the conformations of turns. They can easily be synthesized and studied in much greater detail using spectroscopic and theoretical methods. In many cases, small peptides have also been used to establish structure–spectra relationships. For instance, the CD spectra of pure β_I and β_{II} turns have been determined by Perczel *et al.* in their studies on cyclic hexapeptides¹⁸ confirming the theoretical predictions by Woody.^{19,20} Diem *et al.* used cyclic tri-, tetra-, and pentapeptides to establish the VCD spectral pattern of the amide I vibrations of β -turns.^{21–23}

Recently, we introduced the model peptide cyclo(Boc-Cys-Pro-Gly-Cys-OMe) **1** (Fig. 1),²⁴ a cyclic disulfide-bridged tetrapeptide of which the two derivatives cyclo(Cys-Pro-Gly-Cys)²³ (**1a**) and cyclo(Boc-Cys-Pro-Gly-Cys-NHMe)²⁵ (**1b**) have been studied before. For the unprotected form **1a** of the tetrapeptide, Diem *et al.* assumed a mixture of β_I and β_{II} turn structures in DMSO. This assignment was based on a comparison of the amide I VCD pattern with the ones measured for cyclo(Cys-Pro-Phe-Cys) and cyclo(Cys-Pro-D-Phe-Cys) in DMSO and DMSO/CDBr₃, which contain mainly either β_I or β_{II} turn structures, respectively. The cyclo(Boc-Cys-Pro-Gly-Cys-NHMe) derivative **1b**, on the other hand, was assigned to a β_I structure based on the lack of experimental evidence for nuclear Overhauser effects (NOE) between the Pro-C²H and Gly-NH.

In contrast to these previously studied derivatives, **1** is highly soluble in non-polar chloroform as well as in polar solvents

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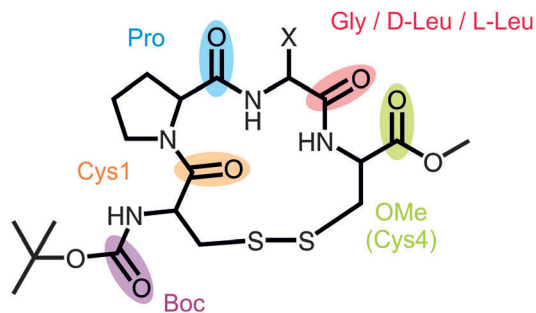


Fig. 1 General structure of the investigated cyclic tetrapeptides with X = H for **1** and X = iso-butyl for **D-** and **L-2**.

such as acetonitrile and DMSO. This allowed us to investigate the effect of solvents and temperature on the turn conformation with different techniques such as 2D-NMR, IR, and CD spectroscopy, as well as Car-Parrinello molecular dynamics.²⁴ It has been shown that **1** adopts a β_{II} structure in solution and in the solid state and that a hydrogen bond between Cys1-C=O and Cys4-NH stabilizes the turn conformation of the cyclic peptide. While Cys1-C=O forms another hydrogen bond with the NH-bond of Gly of the neighboring molecule in solid state, in solution, however, the carbonyl group competes with solvent molecules for the hydrogen bonding donor.

The present work complements this initial investigation by applying VCD spectroscopy to investigate the preferred conformations of the cyclic peptide **1** in solvents of different polarities, *i.e.* chloroform, acetonitrile and DMSO. Additionally, two related peptides (**L-2** and **D-2**) with *L*- or *D*-leucine instead of glycine are studied here. Unlike NMR and ECD, VCD spectroscopy can be used to compare the peptides in all three solvents. For instance, the peaks of some NH protons could not be resolved in the reported NMR spectra of **1** in chloroform. The UV and ECD bands of the peptides were also masked by bands from chloroform or DMSO.

In this paper, the VCD analysis of the three tetrapeptides is carried out first without making any assumptions based on the previous studies (except the crystal structure of **1**). Afterwards, the obtained results are compared to the NMR experiments and molecular dynamics simulations. Our VCD analysis thus provides new evidence to establish more conclusively the β -turn structures of **1** and **2** in acetonitrile and the role of the solvent on the conformation of the peptides.

Experimental and computational details

The synthesis procedures of **1**, **L-2**, and **D-2** were reported elsewhere.^{24,26} Deuterated solvents were purchased from Sigma-Aldrich and Cambridge Isotopes.

The IR and VCD spectra of **1**, **L-2**, and **D-2** were measured at a resolution of 4 cm^{-1} in the fingerprint region (1800–1100 cm^{-1}) using a Bruker Vertex 70 FTIR spectrometer equipped with a PMA50 module for polarization modulated measurements. The photoelastic modulator was set to an optimum working frequency

of 1500 cm^{-1} . The spectra were recorded in the solvents CDCl_3 , CD_3CN , and DMSO-d_6 under otherwise identical conditions, *i.e.* a concentration of 45 mg ml^{-1} (~ 0.1 mM), a path length of 100 μm , and an accumulation time of 4 hours ($\sim 25\text{k}$ scans). Background-correction by subtracting solvent spectra has been carried out for the IR spectra while the VCD spectra are shown as obtained.

Geometry optimizations and spectra calculations were performed at the B3LYP/6-311++G(2d,p) level of theory using the Gaussian 09 (Rev. C.01) software package.²⁷ Dispersion-correction has been taken into account at the DFT-D level using the iop(3/124 = 3) setting; however, the correction did not significantly affect the calculated VCD pattern in the amide I and amide II regions. Implicit solvation effects have been accounted for by using the polarizable continuum model (IEFPCM) for chloroform and acetonitrile.^{28–30} The normal mode frequencies obtained were scaled by a factor of 0.98 for a better visual comparison with the experimental spectra. Line broadening has been taken into account by assigning a Lorentzian band shape with a half-width at half-height of 8 cm^{-1} to the calculated dipole and rotational strengths.

The dynamical behaviour of **1** in acetonitrile was investigated by Replica Exchange Molecular Dynamics (REMD) simulations carried out for 60 ns using the Gromacs4.6 code^{31–33} and the OPLSA force field.³⁴ The temperature range was 290–400 K and the temperature distribution was established according to the Patriksson and van der Spoel approach.³⁵ Although originally intended for water, this approach allowed for a good exchange ratio between replicas in acetonitrile too (see the ESI† for replica exchange statistics). The reported crystal structure of **1**²⁴ was used as the starting point for the simulations. For the treatment of electrostatic and van der Waals interactions the PME method³⁶ and a twin range cut-off³⁷ were used, respectively, with cut-off distances of 1.2 nm in both cases. The exchange of replicas was attempted every 1 ps. The time step for all simulations was 2 fs. Bonds containing hydrogen atoms were kept fixed using the LINCS algorithm.³⁸ The cluster analysis of the results was performed using the Gromos method.³⁹

Results and discussion

Experimental IR and VCD spectra

The fingerprint region of the infrared spectrum of a peptide can be divided into the carbonyl/amide I region (1800–1600 cm^{-1}), the amide II region (1600–1480 cm^{-1}) which is characterized by N–H bending and C–N stretching vibrations, and the region below 1480 cm^{-1} which contains the amide III region (1350–1250 cm^{-1}) and arises from complex peptide backbone as well as side group vibrations. For the present study, we focus on the amide I and amide II regions since they are very characteristic for the hydrogen bonding network of the peptide, and comment only briefly on the region below 1480 cm^{-1} .

Fig. 2 compares the experimental IR and VCD spectra of **1**, **L-2**, and **D-2** measured in the three different solvents CDCl_3 , CD_3CN , and DMSO-d_6 . Direct comparisons for the IR spectra of **1** and **D-2** are provided in the supporting information (Fig. S1, ESI†).



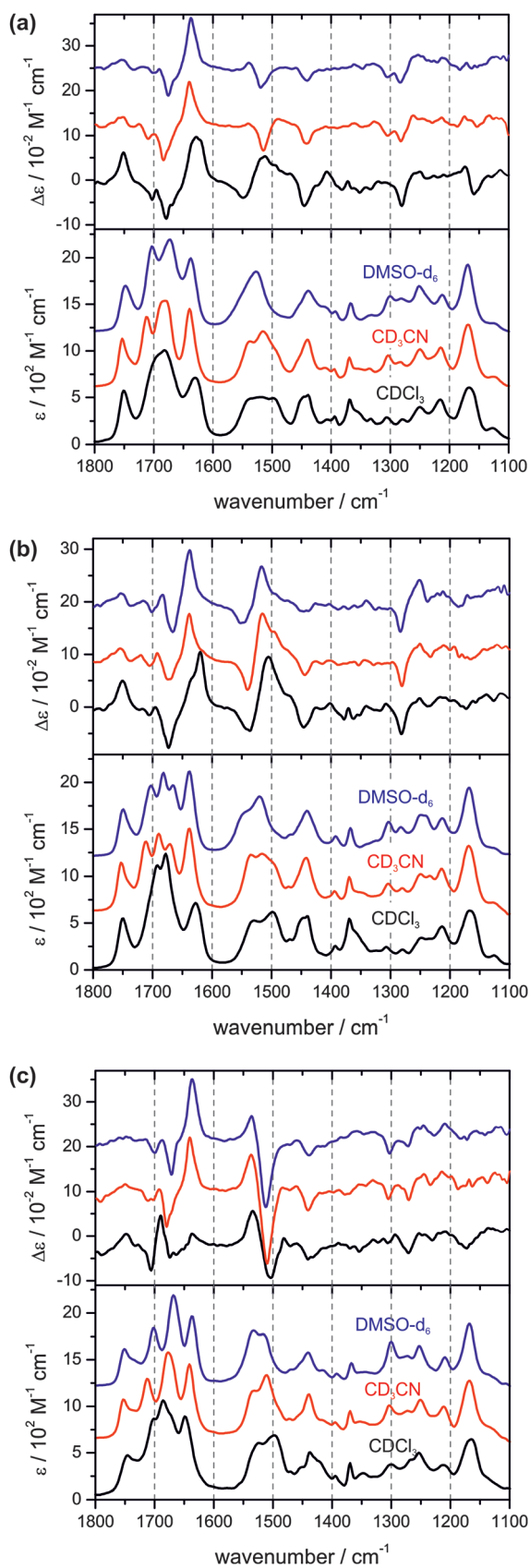


Fig. 2 Experimental VA and VCD spectra of **1** (top), **D-2** (middle), and **L-2** (bottom) in CDCl_3 , CD_3CN , and DMSO-d_6 .

Table 1 Vibrational band positions for **1**, **D-2**, and **L-2** in the amide I and II regions in CDCl_3 (A), CD_3CN (B), and DMSO-d_6 (C). Wavenumbers are given in cm^{-1}

	1 (X = Gly)			D-2 (X = D-Leu)			L-2 (X = L-Leu)		
	A	B	C	A	B	C	A	B	C
Ester C=O	1751	1753	1747	1749	1753	1749	1745	1753	1751
Boc C=O	1703	1711	1703	1706	1711	1703	1703	1713	1701
Amide I X				1691	1689	1682	1686		
Amide I Pro	1682	1680	1672	1678	1670	1666	1672	1676	1668
Amide I Cys1	1630	1639	1637	1628	1637	1637	1649	1641	1637
Amide II	1548	1537	1539	1529	1535	1544	1524	1534	1534
	1512	1515	1520	1505	1516	1520		1514	1519
	1496	1491		1498	1494		1496		

For the spectra of **1**, it has been ensured that the spectral pattern did not show any concentration dependence. For all three peptides, distinct changes in the amide I and II regions of the IR spectra can be observed when the solvent is changed from non-polar chloroform to either of the polar solvents. The band assignments discussed below are summarized in Table 1.

First, we examine the amide I regions of the IR spectra of the peptides and the solvent-induced changes. The carbonyl vibration of the methyl ester group of Cys(4) appears to be unaffected by the different solvents and is found to be at 1750 cm^{-1} in all spectra. The carbonyl vibration of Cys(1) observed at 1627 cm^{-1} in chloroform- d_1 is blue-shifted by about 10 cm^{-1} in the polar solvents and is slightly narrower. The most prominent changes occur in the region $1750\text{--}1650 \text{ cm}^{-1}$. In the spectrum of **1** in chloroform- d_1 , this region is dominated by a broad band with an intensity maximum at 1680 cm^{-1} and shoulders at the higher wavenumber side. In acetonitrile- d_3 , a sharp feature at 1712 cm^{-1} separates from the broad band which is still found to be centred at 1680 cm^{-1} (1703 and 1672 cm^{-1} in DMSO-d_6). The amide I region of **L-2** behaves quite similarly. For peptide **D-2**, an intense band with two maxima at 1678 and 1691 cm^{-1} and a shoulder at the higher wavenumber side is observed in chloroform which splits into three bands found at 1670 , 1689 , and 1711 cm^{-1} in the spectra measured in acetonitrile- d_3 (1666 , 1682 , and 1703 cm^{-1} in DMSO-d_6). From higher to lower wavenumbers, these three bands are assigned to the carbonyl vibration of the Boc-group, Pro, and the amino acid Gly respectively **D/L-Leu**.

Second, we consider the VCD spectra of the amide I region of the three peptides. The experimental spectra taken in chloroform feature a strong positive band for the carbonyl vibration of the methyl ester group of Cys(4) which becomes weaker in polar solvents. For the Cys(1) carbonyl vibration, a strong positive VCD is observed for **1** and **D-2** which shows as two closely spaced positive bands in chloroform. For **L-2**, the intensity of the VCD of Cys(1) in chloroform is much weaker and becomes stronger in polar solvents. The VCD pattern in the $1750\text{--}1650 \text{ cm}^{-1}$ region is rather complex. The VCD band assigned to the carbonyl vibration of the variable amino acid residue, Gly or Leu, is in all cases negative. However, for **1** the negative band at 1678 cm^{-1} features a small negative shoulder at 1669 cm^{-1} . For the carbonyl vibration of the Boc-group, a weak negative VCD is observed, while the VCD band of the carbonyl vibration of Pro



can only be clearly identified as the positive band in the spectra of **1-2**.

For the amide I region, it can be concluded that the IR and VCD spectra do not show clear evidence for significant conformational changes due to solute-solvent interactions. Furthermore, a direct comparison with the amide I VCD spectra reported by Diem *et al.* for the unprotected version **1a** is difficult because of the unknown influence of the Boc-group on the amide I vibrations.

Therefore, we now turn to the amide II region which features three vibrational modes assigned to the Cys(4), the variable amino acid residue Gly respectively *D/L*-Leu, and Cys(1). In all sets of IR spectra, the amide II vibrations are found to blend into one very broad band. However, a clear blue-shift of the bands can be observed when going from CDCl₃ over CD₃CN towards DMSO-*d*₆. The corresponding VCD spectra of the amide II vibrations show very significant changes upon substitution of the solvent. The region features a dominant $-/+$ pattern in all spectra of peptide **D-2**, and a $+/-$ pattern for **1-2**. The spectral pattern of peptide **1**, however, clearly changes from $-/+$ in chloroform-*d*₁ to $+/-/+$ in the two polar solvents. This observation is a strong indicator for a solvent-induced conformational change of the tetrapeptide's cyclic backbone which is only possible for **1** but not for **D-** or **1-2**.

Below 1480 cm⁻¹, no significant changes can be observed in the IR spectra. In light of the above mentioned spectral changes of **1**, it is noteworthy that the amide III region of **1** is similar to that of **1-2**. The VCD pattern found that the 1385–1330 cm⁻¹ region of the chloroform measurements of **1** and **2** compared to the lack of VCD bands in polar solvents could carry further interesting structural information which, however, we will not address any further in this study.

Our experimental spectra thus suggest that the conformational equilibria in **D-** and **1-2** are much less sensitive to solvent-induced conformational changes than in **1**. By contrast, we can clearly establish that the conformational preferences of **1** very much depend on the solvent environment.

Conformational analysis

In order to further interpret the experimental VCD spectra, density functional theory (DFT) based spectra calculations were carried out.^{40–42} Since VCD spectroscopy is very sensitive to conformational changes, a thorough conformational analysis of **1** and subsequent spectra calculations were performed.

The starting point for the analysis was the crystal structure of **1**,²⁴ which has been optimized at the B3LYP-D/6-311++G(2d,p) level of theory in the gas phase. The obtained optimized geometry, denoted r1–c1, is shown in Fig. 3. As the comparison of the ϕ and ψ angles in Table 2 shows, a β_{II} turn structure is adopted in the solid state and in the optimized geometry. The hydrogen bond between Cys(1)-CO and Cys(4)-NH which has been found in the crystal structure is also found in the optimized geometry. Additionally, the gas phase optimized structure features a hydrogen bond between Cys(1)-CO and Gly-NH.

For the first step of the conformational analysis, the ring conformation was kept essentially unchanged, while the relative conformations of the terminating Boc and OMe ester groups

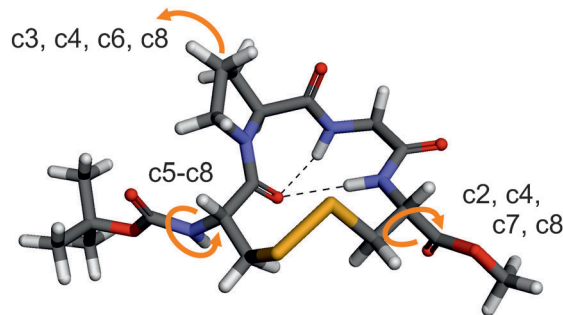


Fig. 3 Optimized geometry of **1** in the gas phase (r1–c1). The arrows indicate conformational changes in the side group conformers c2 to c8.

Table 2 β -turn structures in the gas phase optimized ring conformations. Angles are in degrees

Structure	$\phi(i+1)$	$\psi(i+1)$	$\phi(i+2)$	$\psi(i+2)$
β_I ideal	-60	-30	-90	0
β_{II} ideal	-60	120	80	0
1 crystal	-62.1	135.6	60.4	29.4
β_{II} r1–c1 ($g^{(-)}g^{(-)}t$)	-77.7	103.0	78.5	9.6
β_{II} r7–c1 ($g^{(-)}g^{(+)}g^{(+)}$)	-75.6	105.4	113.1	-16.8
β_{II} r6–c1 ($tg^{(+)}g^{(+)}$)	-83.3	81.3	125.9	-6.7
β_I r2–c1 ($g^{(-)}g^{(-)}t$)	-85.7	-6.7	-116.5	26.6
β_I r4–c1 ($tg^{(+)}g^{(+)}$)	-83.1	-3.8	-107.2	10.0

as well as the proline ring were modified. This procedure yielded a total of eight different side group conformations (denoted c1 to c8, shown in Fig. S3 of the ESI[†]). In all but conformers c1 and c2, the hydrogen bond between Cys(1)-CO and Gly-NH was found to be cleaved.

Raman measurements of **1** and **D-2** indicate that the S–S bridge adopts different conformations (*cf.* ESI[†]). The conformation of disulfide bridges are typically described by the three torsional angles of the C ^{α} –C–S–S–C–C ^{α} unit as *gauche-gauche-gauche* (*ggg*), *trans-gauche-gauche* (*tgg* or *ggt*), and *trans-gauche-trans* (*tgt*). In its crystal structure and in the optimized gas phase structure (Fig. 3), the tetrapeptide **1** adopts a $g^{(-)}g^{(-)}t$ conformation. For **1** with a β_{II} turn structure and the side groups adopting conformation c1, additional ring conformations with $g^{(+)}g^{(-)}t$, $g^{(+)}g^{(-)}g^{(+)}$, $g^{(-)}g^{(+)}g^{(+)}$, $tg^{(+)}g^{(+)}$, $tg^{(-)}g^{(+)}$ geometries of the disulfide bridge were generated (Fig. S4, ESI[†]).

For two of the SS bridge conformations, namely the $g^{(-)}g^{(-)}t$, and the $tg^{(+)}g^{(+)}$ conformations, the β_{II} has been changed to a β_I turn structure (Table 2 and Fig. S5, ESI[†]). For both β_I -*tgg* conformations, the effects of conformational changes of the side groups have been evaluated as well by generating all eight side group conformations.

After this comprehensive conformational analysis, implicit solvation effects of chloroform and acetonitrile have been taken into account by repeating the geometry optimizations for the β_{II} ring geometries r1 and r6 as well as for the corresponding β_I structures r2 and r4, applying the integral equation formalism of the polarizable continuum model (IEFPCM).^{28–30} Unlike for the gas phase structures, the hydrogen bond between Cys(1)-CO and Gly-NH was found to be cleaved for the r1–c1 conformer (Fig. S6, ESI[†]).



For all the obtained optimized structures, IR and VCD spectra calculations were carried out.

A conformational analysis of the highly flexible molecule **1** based on static structures certainly cannot cover all possible conformations. Furthermore, explicit solute–solvent interactions, especially with the polar solvents, will also influence the relative population of the conformers and completely change energetic preferences. Therefore, the calculated energy differences between the conformers are of low significance, although some trends can be derived. For instance, the side-group conformations c5–c8 are typically far less favoured than the first four. All energy differences are given in the ESI† (Table S1). Therefore, instead of the analysis of the VCD spectra of **1** based on energetic differences, we focus on similarities between the experimental and calculated spectral patterns.

Fig. 4 exemplifies the clear trend in the calculated VCD spectral pattern for the β_{II} structures r1–c1 and r6–c1 and their corresponding β_I structures r2–c1 and r4–c1. The complete set of calculated VCD spectra is shown in Fig. S7–S9 of the ESI†. In general, the amide I region (1800–1600 cm^{-1}) is found to be much more sensitive to conformational changes of the side group than the amide II region (1600–1480 cm^{-1}) which contains mostly contributions of the terminal Boc and methyl ester groups.

Overall, most of the calculated VCD spectra resemble the strong experimental $-/+$ VCD couplet found in the amide I region reasonably well. However, there are no obvious characteristics in the spectra which could be assigned to either β_{II} or β_I turn structures. On the other hand, a significant and more characteristic change is observed for the amide II region when comparing β_{II} and β_I structures. The amide II of the β_{II} structures features a $-/+ (+)$ pattern which resembles the experimentally observed amide II region of **1** in chloroform and **D-2** in all three solvents. In contrast, the amide II pattern is inverted for β_I structures showing a $+/- (-)$ or $+/- (+)$ pattern. This pattern is very similar to the experimental amide II of **L-2** and of **1** in polar solvents. This comparison of spectral patterns suggests that **D-2** adopts predominantly a β_{II} turn structure, while **L-2** preferably resides in a β_I turn. For peptide **1**, significant contributions of both β_I and β_{II}

type structures to the overall conformational equilibrium in polar solvents has to be assumed.

Explicit solute–solvent interactions can affect not only the energetic preferences of certain conformers, but, in general, also influence the calculated IR and VCD intensities. Therefore, we briefly considered explicit solvation for r1–c1 and r2–c1. One acetonitrile molecule was placed in a hydrogen bond with the Gly–NH in r1–c1 and r2–c1. This, however, only affected the negative VCD band of the amide II region of the β_I structure, so that the spectra obtained look very similar to those without solvent molecules. The corresponding calculated spectra are shown in the ESI† (Fig. S11).

Replica exchange MD of **1**

In our initial study on **1**, we only carried out short MD calculations (500 ps) without replica exchange.²⁴ The study on **D-2** and **L-2**, however, showed that REMD can help to ensure that the calculations do not get trapped in the local energy minimum of the β_{II} turn structure.²⁶ Therefore, we carried out additional REMD simulations on **1** for the present study. Starting from a crystal structure like β_{II} conformation, the simulations show that the β_{II} motif is basically conserved for **1** in acetonitrile, not only at 300 K but also at higher temperatures (Table 3). A small contribution of β_I structures was found representing only 7% of the total number of structures in the 300 K simulation and about 14% in the 400 K runs. These conformers rapidly converted back to the preferred β_{II} motif. This was corroborated by additional simulations with a β_I structure as starting point (Fig. S14, ESI†). This observation proves that the energy barrier for the conversion from β_{II} to β_I is much higher than in the opposite direction. Furthermore, the new REMD simulations show that **1** does indeed adopt the β_I turn structure, although only to a very small extent. On the other hand, this small amount of β_I structures in **1** may increase with longer simulation times.

Comparison with NMR results and MD data

For the tetrapeptide **D-2**, the VCD analysis points to a predominant β_{II} turn structure. This is consistent with the previous experimental findings from 2D-NMR studies and theoretical REMD simulations.²⁶ For the peptide **L-2**, the interpretation of the VCD spectra suggests a dominant β_I turn conformation, while in 2D-NMR the presence of both β_{II} and β_I turns was observed,²⁶ although it was not possible to use the NMR data to quantify the relative preferences of the turn structures.

For the glycine-containing peptide **1**, the previous 2D-NMR of **1** in CD_3CN showed some clear indications for a β_{II} turn, while the cross-peaks, characteristic for β_I turns, were unfortunately

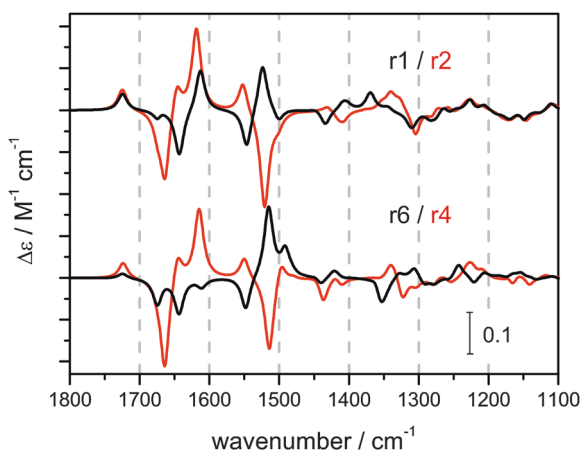


Fig. 4 Calculated VCD spectra of the β_{II} structures r1–c1 and r6–c1 and the corresponding β_I structures r2–c1 and r4–c1 (IEFPCM acetonitrile).

Table 3 Backbone angles ϕ and ψ calculated for representative structures obtained using cluster analysis at 300 K and 400 K and averaged over the trajectory (REMD simulation, 300 K trajectory). Angles are in degrees and distances in Å

	$\phi (i + 1)$	$\psi (i + 1)$	$\phi (i + 2)$	$\psi (i + 2)$	$C_{\text{Cys1}}^{\alpha} - C_{\text{Cys2}}^{\alpha}$
300 K	−79	102	110	−16	5.77
400 K	−75	92	116	−9	5.63
REMD	-76 ± 8	103 ± 16	106 ± 10	-11 ± 15	5.7 ± 0.2
Ideal β_{II}	−60	120	80	0	<7.0



overlapping with other signals.²⁴ Therefore, the presence or absence of β_I could not be proven experimentally with NMR spectroscopy.

It is noted that the VCD band of **1** in the amide II region is relatively weak in comparison to those of **D**- and **L**-**2**. Furthermore, the VCD spectrum resulting from a simple average of the experimental VCD spectra of **D**- and **L**-**2** in either polar solvent is remarkably similar to the spectrum of **1** in the same solvent (cf. Fig. S2, ESI†). These two observations are important since they allow us to conclude that **1** indeed adopts a β_I structure to a certain extent in polar solvents although this preference for β_I is estimated to be only half as much as for **L**-**2**. In chloroform, the conformational equilibrium of **1** is slightly shifted towards β_{II} .

The REMD simulations also qualitatively support these conclusions. The relative trend – **L**-**2** prefers the β_I turn twice as much as **1** – is also established.

Conclusions

In the present work, we apply VCD spectroscopy to study the β -turn conformations of three cyclic tetrapeptides:^{24,26} **1**, **D**-, and **L**-**2**, in the three different solvents, namely chloroform- d_1 , acetonitrile- d_3 , and DMSO- d_6 . The comparison of experimental and theoretical VCD spectra supports the previous finding^{24,26} that **D**-**2** preferably features a β_{II} turn structure. For **L**-**2**, the VCD analysis clearly identifies the β_I turn as the major conformation. This advances the previous studies where evidence for both β_{II} and β_I turn structures was reported although no relative preferences could be quantified. The most important and surprising finding in the present study, however, is that peptide **1** preferably adopts a β_I structure in polar solvents, whereas previous NMR evidence for β_I was obscured. The current study further demonstrates that this equilibrium between β_{II} and β_I turns for **1** depends on the polarity of the solvent. These results therefore reveal a high flexibility of the peptide **1**.

In summary, this study shows that not only can the chirality of a single amino acid change conformational preferences from β_{II} to β_I , but also solvent polarity can have significant effects. Furthermore, VCD spectroscopy can provide characteristic spectral patterns of β_{II} and β_I turns to complement NMR studies of secondary structural preferences, especially when unresolved or overlapping NMR peaks prevent one from reaching a conclusion.

In future work, we plan to investigate other cyclic tetrapeptides in order to establish a generalized correlation between the VCD spectral pattern and the adopted secondary structure. We will further study the solvent-dependence of the conformational preferences and also the structural changes caused by ring opening reactions.

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