Melting of a β-Hairpin Peptide Using Isotope-Edited 2D IR Spectroscopy and Simulations

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Isotope-edited two-dimensional infrared spectroscopy has been used to characterize the conformational heterogeneity of the β-hairpin peptide TrpZip2 (TZ2) across its thermal unfolding transition. Four isotopologues were synthesized to probe hydrogen bonding and solvent exposure of the β-turn (K8), the N-terminus (S1), and the midstrand region (T10 and T3T10). Isotope-shifts, 2D lineshapes, and other spectral changes to the amide I 2D IR spectra of labeled TZ2 isotopologues were observed as a function of temperature. Data were interpreted on the basis of structure-based spectroscopic modeling of conformers obtained from extensive molecular dynamics simulations. The K8 spectra reveal two unique turn geometries, the type I′ β-turn observed in the NMR structure, and a less populated disordered or bulged loop. The data indicate that structures at low temperature resemble the folded NMR structure with typical cross-strand hydrogen bonds, although with a subpopulation of misformed turns. As the temperature is raised from 25 to 85 °C, the fraction of population with a type I′ turn increases, but the termini also fray. Hydrogen bonding contacts in the midstrand region remain at all temperatures although with increasing thermal disorder. Our data show no evidence of an extended chain or random coil state for the TZ2 peptide at any temperature. The methods demonstrated here offer an approach to characterizing conformational variation within the folded or unfolded states of proteins and peptides.

Introduction

Protein conformational dynamics lie at the heart of numerous biophysical processes, including protein folding, substrate binding, molecular recognition, and self-assembly. Historically, such processes were often conceived in terms of rigid protein molecules with minimal conformational degrees of freedom. However, structure formation in such processes involves a complex interplay between the favorable energy of contact formation and conformational entropy. Protein flexibility and conformational heterogeneity are intrinsic to all systems, but this disorder and its role in biophysical processes remains difficult to study and describe experimentally. This stems from a paucity of methods that can explore these questions. Conformational dynamics occur over picosecond and longer time-scales, and atomistic structural resolution in solution is only routinely available from computer simulations. The most detailed experimental observations have emerged from magnetic resonance spin relaxation rate measurements that characterize inherently disordered proteins,1 residue-level protein folding,2 transient protein–protein complexes,3,4 and microsecond structural fluctuations.5–8

Two-dimensional infrared spectroscopy (2D IR) is an emerging method that is being used to directly measure structure and conformational dynamics in proteins and peptides.9–14 Analogous to multidimensional NMR, 2D IR observes structure-sensitive vibrational couplings through cross peaks in a 2D spectrum.15 In addition, 2D lineshapes provide information on molecular flexibility and solvent exposure through their peak frequency and ellipticity. Time-dependent changes to cross peaks and lineshapes reveal chemical exchange processes and fluctuations. Since the measurement time scale for vibrational spectroscopy is in the picosecond range, such studies provide an avenue to characterize conformational variation and ultrafast fluctuations. The technique has been used to measure protein structure and dynamics with particular focus on the amide I vibrations, which are sensitive to secondary structure and local hydrogen bonding geometry of the peptide groups.9–12,16–20

This paper describes our investigation of the structure of a β-hairpin peptide using isotope-edited 2D IR to site-specifically investigate the conformation of its backbone as a function of temperature. In this mode, the isotope-shifted amide I band can
The trpzip peptides were engineered with four tryptophan residues arranged with two side chains on each of the opposing -strands that lead to a remarkably stable system through the favorable perpendicular stacking of the indole rings. Our spectroscopic model that draws on molecular dynamics simulations of the two states is unclear. 54

Experimental amide I site frequencies are mapped onto the amide I Hamiltonian that describes the amide I frequency shifts for these Markov states. Spectra are calculated using the local spectroscopic model that draws on molecular dynamics simulations of the two states is unclear. 54

be used to infer local structure and dynamics through variations in its vibrational frequency or couplings to other vibrations. Our approach combines 2D IR spectroscopy on a series of peptide isotopologues with spectroscopic modeling of the peptide’s conformers. This pair of tools is used to develop a picture of conformational heterogeneity across the thermal unfolding transition.

The system that is studied is a 12-residue hairpin peptide trpzip2 (TZ2) designed by Cochran et al. 21 It has received significant attention in the literature, with multiple experimental studies and numerous theoretical treatments. 17,22–27 Within the last several years, TZ2 has become a benchmark system which is now used in the development of new simulation techniques. 22,26,28–30

The trpzip peptides were engineered with four tryptophan residues arranged with two side chains on each of the opposing -strands that lead to a remarkably stable system through the favorable perpendicular stacking of the indole rings. 21 Our interest in this system is motivated by unsolved questions regarding the folding of these peptides. Single-domain peptides like -hairpins display conformational dynamics that mirror the folding of larger globular proteins. 31,32 Discussion of hairpin folding mechanisms are often guided by two simple pictures: (1) the kinetic zipper model, in which nucleation of the -turn is followed by “zipping” of cross-strand backbone contacts, 33–35 and (2) hydrophobic collapse, in which initial clustering by a core of hydrophobic side chains precedes formation of native backbone contacts. 36,37 Extensive fluorescence 38–40 and IR absorption 41–43 measurements have monitored the kinetics of hairpin unfolding on 1–10 µs time scales but have not reached agreement on which model best describes the folding. 41,43,44

Often, folding of this peptide is described within the framework of a two-state folding model, although its validity and the nature of the two states is unclear. 5

Molecular dynamics (MD) simulations of TZ2 folding have provided intricate details that enrich and challenge these two models, such as partial hydrophobic collapse, fraying of the terminal residues, ordering of backbone hydrogen bonds, salt bridging, and rearrangements of the hydrophobic core. 30,45,46 To date, however, the complex set of possible folding pathways observed by simulations have not led to a consensus view of the folding mechanism. Experimental evidence has substantiated this complexity and supports a rough free energy landscape in which there are a number of populated minima. 30 To date, the structural details of this heterogeneity have not been experimentally observed, particularly in the peptide backbone. The key information missing from these studies is specific details of hydrogen bond and side chain contact formation at a level of detail that can distinguish conformers.

To obtain residue-level structural insight in the thermal denaturation of TZ2, we use amide I 2D IR in combination with 13C and 18O-isotope-labeling methods. 11,18–20,47–52 Inserting these labels into the peptide amide group red shifts the amide I vibrational frequency away from the main band and provides a spectroscopic probe of the labeled site. Four isotopologues are used to probe cross-strand contacts and isolate peptide units in the turn, termini, and central region of the folded structure (see Figure 1).

In the first isotopologue, S1, an 18O isotope is introduced into the N-terminal serine to probe the stability and fraying of the terminal peptide groups. In the second, T10, an 18O label is placed on the T10 site to monitor the midstrand contacts. The third, TT, also monitors midstrand contacts using 13C isotopologues at threonines T3 and T10 of the peptide. The two labeled amides of TT are hydrogen bound across the -strands in the folded structure, and vibrational coupling between these sites provides sensitivity to the interstrand contacts in this region. 53 Finally, the isotopologue K8 has a 13C label incorporated into the lysine-8 residue to probe the thermal disordering of the -turn.

The interpretation of 2D IR spectra uses a structure-based spectroscopic model that draws on molecular dynamics simulations of the TZ2 peptide in water. Our spectral simulations make use of the extensive set of TZ2 conformers obtained from the molecular dynamics simulations of Swope and co-workers, 30,46 and accompanying Markov state analysis of Chodera et al. 29 Experimental amide I frequency shifts and 2D lineshapes are assigned and interpreted on the basis of calculated 2D spectra for these Markov states. Spectra are calculated using the local amide I Hamiltonian that describes the amide I frequency shifts of the peptide groups and vibrational couplings between these groups. 34–57 The amide I site frequencies are mapped onto the local molecular electric field. 55,56,58,59 This describes the red-
shifting of the amide I frequency upon hydrogen bonding to the peptide unit.

The disorder and local fluctuations of each conformer is reflected in the 2D line shape of the labeled site.\textsuperscript{17,60} The diagonal line width of the 2D IR peak is sensitive to the degree of conformational disorder, whereas the antidiagonal width reflects the fluctuations and time scale of interchange. Therefore the ellipticity of the line shape is inversely related to the time scale over which the vibration samples the possible configurations. A large value of the ellipticity indicates significant disorder in the corresponding local structure. Fast fluctuations in structure and hydrogen bonded solvent lead to round peaks.\textsuperscript{61}

This study establishes a detailed picture of the conformational changes upon temperature-induced unfolding of TT2. The isotopologues provide evidence that the termini disorder as the temperature is raised, and the central region retains cross-strand contacts. Further we find explicit evidence for distinct conformers of the turn, and that the population of the expected type I' turn increases with temperature. Taken together, these observations reveal a temperature varying heterogeneous ensemble, whose conformers all experience thermally induced fraying, but do not unfold into a random coil structure. In addition to this agreement with previous results, the work shown here gives a level of detail unattainable with other methods. Isotope-editing provides structural detail at the level of individual amide groups with higher spectral resolution than FTIR spectroscopy, while resolving picosecond dynamics that report on peptide flexibility and solvent exposure.

### Material and Methods

**Peptide Samples.** For experimental studies, the unlabeled peptide, UL, was prepared using Fmoc-based solid phase peptide synthesis on a PS3 peptide synthesizer (Protein Technologies Inc.). Each TT2 isotopologue was prepared as a C-terminal amide, which is consistent with previous experimental work. The solid support was a Rink Amide MBHA resin (01-64-0037, Novabiochem), and Fmoc-protected amino acids were obtained from PTI Instruments in prepackaged cartridges at four molar excess HBTU activator and amino acid. The primary reaction solvent was DMF (EM-DX1732; EMD Chemicals; 99.9% purity). Removal of the Fmoc groups at each step was done with 20% piperidine in DMF (PTI Instruments), and the coupling reaction was carried out in 0.4 M N-methylmorpholine/DMF activator solution (PTI Instruments). A cleavage cocktail of 95% TFA and 5% TIPS was used to remove the peptide from the resin and the acid-labile protecting groups from the side chains. Purification was performed with a C18 HPLC column and two-phase buffer gradient: (buffer A) 0.1% TFA in H2O and (buffer B) 80% acetonitrile, 0.085% TFA in H2O. The mass spectrum of synthesized K8 is provided in the Supporting Information.

The midstrand isotope-labeled compound, TT, was prepared with an 18O label in the carbonyl oxygen (identified as $\dagger$) of the S1 residue (S*WTWENKWTWK). Labeled serine was synthesized directly from Fmoc-serine-OH (Novabiochem) using acid catalyzed hydrolysis. Anhydrous HCl gas was bubbled through Fmoc-Ser-OH in H3O\textsubscript{2}O-acetonitrile (approximately 1:4 by volume), and then heated at 80 °C for four weeks. MALDI mass spectrometry of the amino acid was used to verify that the substitution was successful, with an approximately 75% isotopic enrichment of the carbonyl oxygen atoms. For use in peptide synthesis, the serine hydroxyl group was protected by a sililation reaction using N-methyl-N-(tert-butyldimethylsilyl)-trifluoroacetamide (MTBSTFA) in the procedure of Madson et al.\textsuperscript{63} Specifically, 139 mg of 18O labeled serine was dissolved in 15 mL of DMF and 3 mL of MTBSTFA, where it silinates both the side chain hydroxyl group and the carboxylic acid. The reaction solution was lyophilized and the remaining peptide was then suspended in hexane (20 mL). Ethanol (1.1 mol excess relative to Ser) was added to selectively desilylate the carboxylic acid. The resulting amino acid was used in an Fmoc-SPPS synthesis identical to that of UL. MALDI-TOF mass spectrometry of the labeled TT2-S1 verified the mass of the isotope-labeled peptide indicating that the isotope-labeled serine was incorporated into the peptide (Supporting Information).

The midstrand label, T10, was prepared with an 18O label in the carbonyl oxygen using the same method as described above for the N-terminal18O S1 label.

For infrared studies, residual TFA was removed from each peptide by lyophilizing against 20 mM DCI in D2O repeated at least three times. This also served to exchange the labile protons for deuterons. For FTIR spectra, each peptide was dissolved in pure D2O, and the pH was adjusted to 2.5 by adding 0.5–1.5 µL of 25 mM DCI. The low pH was chosen to avoid aggregation while measurements are being taken at high temperatures. Final peptide concentrations were between 10 and 12 mg/mL. The 2D IR spectra of UL, S1, and K8 were taken in a phosphate-buffered pH 7.0 solution at similar concentrations.

**Spectroscopic Methods.** Temperature dependent infrared absorption spectra of each peptide isotopologue were collected from 5 to 95 °C in 5 °C increments. The sample cell used in these measurements consists of ~25 µL of the peptide solution sandwiched between two 1 mm thick CaF\textsubscript{2} windows that are separated by a 50 µm Teflon spacer. For temperature control, the cell was mounted in a brass housing whose temperature was regulated with water from a recirculating chiller. Spectra were acquired on a Nicolet 380 FTIR spectrometer at 1.0 cm\textsuperscript{-1} spectral resolution by averaging 64 one-second scans.

2D IR spectra were collected as described in previous publications,\textsuperscript{15} with $\tau_w = 100$ fs and the polarization geometry all parallel (ZZZZ) unless otherwise noted. The evolution time, $\tau_w$, was scanned to 1.5 ps for the nonrephasing spectrum and 2.0 ps for the rephasing spectrum at 4 fs time steps, and a rectangular window function was used for the Fourier transform.

**Simulation and Modeling.** To simulate 2D IR spectra, five kinetically metastable macrostates were chosen from the decomposition made by Chodera et al.\textsuperscript{29} Their work distilled the 3.23 µs of trpzip2 simulation data by Pitera et al.\textsuperscript{46} into 40 Markov states that displayed patterns in backbone hydrogen bonds and side chain packing. Each macrostate, which was
All molecular dynamics simulations were performed with GROMACS 3.3.1.\textsuperscript{54,65} The simulations of Pitera et al.\textsuperscript{46} considered the unblocked peptide, which was fully protonated here (+3 charge) with chloride counterions. Each of the atomistic structures comprising the macrostate was subjected to \( \sim 5000 \) steps of a steepest descent energy minimization to conform to the OPLS/AA force field\textsuperscript{66–72} using the particle mesh Ewald method to treat long-range electrostatics.\textsuperscript{73} The peptides were solvated in a box of rigid SPC/E water\textsuperscript{74} that extended 1.5 nm from the solute, and the water was allowed to equilibrate for 10 ps in the NPT ensemble (300 K, 1 atm) while the peptide was fixed.\textsuperscript{75–78} The simulation was continued with no constraints, except on the bond lengths, for 1 ns of equilibration and 100 ps of data acquisition. Structures were saved every 20 fs to yield 5000 frame trajectories.

For each frame, a Hamiltonian was constructed using the ab initio based models given in refs 57 and 58

\[
H_S = \sum_i \left( \omega_i B_i^\dagger B_i - \frac{1}{2} \Delta_i \right) + \sum_{i,j} J_{ij} B_i^\dagger B_j
\]

where \( B_i^\dagger \) and \( B_i \) are bosonic creation and annihilation operators for a vibration at site \( i \). The frequency of each site and the coupling between sites are given by \( \omega_i \) and \( J_{ij} \) respectively. The anharmonicity, \( \Delta_i \), lowers the energy for double excitation of site \( i \), and was fixed at 16 cm\(^{-1}\). The frequencies and coupling values were calculated as previously described.\textsuperscript{55,58} The transition dipoles for each site had a unit magnitude and were oriented 20° off the CO bond vector in the CN direction. Where applicable, the sites were isotope-labeled by shifting their frequency 41 cm\(^{-1}\) to the red.

The 2DIR spectra were calculated using the numerical integration of the Schrödinger equation (NISE) scheme.\textsuperscript{79,80} In this procedure the time-evolution matrices needed in the nonlinear response functions that govern the 2DIR spectra are calculated by solving the time-dependent Schrödinger equation. This is done numerically by dividing time into small intervals during which the Hamiltonian can safely be assumed to be constant. The time-evolution matrix for the time-independent Schrödinger equation can then be found for each interval and the time-evolution matrices for longer time periods are found by multiplying the matrices for the small intervals in a time ordered fashion. The resulting spectra were summed over each structure in the macrostate to produce spectra that reflected the disordered ensembles.

Results

Amide I’ FTIR Spectroscopy. FTIR spectra of the TZ2 isotopologues at 25 °C are shown in Figure 2. The peak maximum of the UL amide I’ band is 1636 cm\(^{-1}\), and there is a prominent shoulder at 1674 cm\(^{-1}\). On the basis of the NMR structure, these bands have previously been assigned to \( \nu_1 \) and \( \nu_\parallel \) excitonic transitions, delocalized vibrations of the amide backbone in which cross-strand peptide bonds oscillate in-phase or out-of-phase with one another.\textsuperscript{53,62} Twisting of the \( \beta \)-strands leads to two nearly degenerate \( \nu_1 \) vibrations located at the turn and midstrand regions of the peptide, while the \( \nu_\parallel \) vibration is largely localized at the turn. Because the spectra shown are taken at pH 2.5, the glutamic acid side chain carbonyl stretch contributes at 1710 cm\(^{-1}\).\textsuperscript{81}

![Figure 2](image)

Changes to the IR spectrum upon isotope substitution are also plotted in Figure 2 for K8, T10, TT and S1. Isotope-labeling leads to small shifts in intensity and frequency of the \( \nu_1 \) and \( \nu_\parallel \) bands, and an increase of amplitude to the red of the bands from the isotope-labeled peptide carbonyl. As seen in difference spectra relative to UL, K8 has a broad (~35 cm\(^{-1}\)) increase in intensity from \( \nu_{K8} = 1585–1615 \) cm\(^{-1}\), indicating significant structural heterogeneity at this site. The \( \nu_1 \) band of K8 narrows and shifts slightly to the blue (1638 cm\(^{-1}\)), suggesting that isotopic substitution significantly rearranges the underlying \( \nu_1 \) eigenstate composition.

In addition to a drop of intensity in the \( \nu_\parallel \) band, the T10 spectrum shows a pronounced shoulder at 1627 cm\(^{-1}\) due to the labeled peptide group. This is a relatively high frequency, indicative of a single moderately strong hydrogen bond to the oxygen as expected from the NMR structure. Upon labeling both threonines (TT), spectral loss is observed at 1640 and 1675 cm\(^{-1}\), and a broad absorbance gain is observed at \( \nu_{TT} = 1610 \) cm\(^{-1}\). The additional red shift of \( \nu_{TT} \) relative to \( \nu_{T10} \) reflects the strength of coupling between the cross-strand labeled oscillators of the \( \nu_{TT} \) band. Labeling both of the threonine residues red-shifts the midstrand \( \nu_1 \) vibration and also perturbs the high frequency, \( \nu_{\parallel} \). A similar but narrower band was observed at 1608 cm\(^{-1}\) for the TZ2 mutant TZ2-T3A*T10A*.\textsuperscript{25}

The FTIR spectrum of S1 is qualitatively similar to the UL spectrum. The peak absorption frequency is red-shifted by 2 cm\(^{-1}\) relative to UL, and the difference spectrum reveals a slight
The spectra show on and off-diagonal features in the amide I band. Positive features arise from fundamental (ν = 0→1) vibrational transitions, whereas negative features arise from ν = 1→2 transitions. As described previously, the UL spectrum shows the Z-shaped contour profiles of the excitonic amide I′ bands expected for antiparallel contacts between two strands. The ν⊥ band is resolved as a separate peak rather than a shoulder as in FTIR, and the peak splitting between ν∥ and ν⊥ peaks is 37 cm⁻¹ in the ω1 dimension. Coupling between ν∥ and ν⊥ vibrations is observed in the off-diagonal region as ridges that extend along ω1 = 1630 and 1674 cm⁻¹.

For K8, the most striking feature in the 2D IR spectrum is the observation that the νK8 band is composed of two distinct diagonal peaks: one at 1593 cm⁻¹ (νK8−1) and the other at 1611 cm⁻¹ (νK8−2), with no detectable cross peak between them. (See also Figure 6.) Also, the diagonal line width of νK8−1 (σ = 6.9 cm⁻¹) is broader than νK8−2 (σ = 4.5 cm⁻¹). Strong coupling of the νK8−2 to the ν∥ band is observed as a ridge extending to ω1 = 1612 cm⁻¹ and ω2 = 1650 cm⁻¹ (Figure 6). The presence of two shifted peaks for a single K8 isotope-label is an indication of two structurally distinct subensembles. The 18 cm⁻¹ peak splitting between these features indicates that the conformers differ considerably in hydrogen bonding configuration to the K8 peptide oxygen. The relatively high frequency of νK8−2 indicates a single hydrogen bond to oxygen. The most reasonable explanation for this observation is that the νK8−2 peak originates in a properly folded type I’ turn in which the labeled oxygen has a single cross-strand hydrogen bond. The νK8−1 peak frequency is characteristic of a peptide group with two or more hydrogen bonds and a higher degree of configurational freedom. This suggests a solvent exposed carbonyl that might be present in a disordered or bulged turn.

For T10, the main excitonic band retains the Z-shaped contours of UL, but an additional sharp peak from the labeled site is observed at ω1 = ω2 = 1630 cm⁻¹. Like νK8−2 this high frequency is suggestive of a single hydrogen bond to oxygen as seen in the NMR structure. In the 2D IR spectrum of the double labeled species, TT, the ν∥ band is well-resolved at 1602 cm⁻¹, and the splitting between ν∥ and ν⊥ in the ω1 dimension is 28 cm⁻¹. The additional red-shift relative to T10 arises from strong coupling between the Thr3 and Thr10 amides forming a midstrand ν⊥-like mode. Changes to the 2D IR ν∥ band relative to the other isotopologues are dramatic, including loss of off-diagonal structure and a diagonal line width increase of approximately 21 cm⁻¹. This line width change suggests that the eigenstate distribution of TZ2-TT is much more heterogeneous than in the other peptides.

The 2D IR spectrum of S1 does not show a peak corresponding to the 18O label in the serine group; however, there are changes relative to UL along the diagonal. The ν∥ band of the S1 2D IR spectrum, which has a resolvable peak at 1674 cm⁻¹ in the UL spectrum, now appears as a diagonal ridge to the blue of the ν∥ band. In addition there is a 2 cm⁻¹ red-shift to 1634 cm⁻¹ and line-narrowing of the ν∥ peak. These observations indicate that the frequency of the UL S1 site energy is relatively high (~1675 cm⁻¹) and that labeling moves the oscillator into resonance with the ν∥ exciton band. This would also explain the lack of both a resolvable peak and interstrand coupling observed between labeled residues in the TZ2 mutant TZ2-S1A*,T10A*.

Temperature-Dependent Spectra. Temperature-dependent amide I′ FTIR spectra of each isotope-labeled hairpin are shown in Figure 4. Each spectrum shows similar trends with temperature, including the loss of amplitude in the ν∥ region and rise of amplitude in the 1660 cm⁻¹ region commonly attributed to disordered chains. To characterize the overall melting behavior, singular value decomposition (SVD) of the entire amide I′ band is carried out for each data set. For each isotopologue, the data is well described with the first two spectral components. Spectral changes with temperature are characterized by the second SVD component, and are shown as melting curves in Figure 5. The melting curves are nearly identical and each show slight curvature without a distinct cooperative unfolding transition.

Figure 3. 2D IR Spectra of TZ2 isotopologues at 25 (top) and 75 ºC (bottom).
The $^{12}$C peak intensities are obtained from the absorbance within 5 cm$^{-1}$ of the amide I peak maximum. The integration regions for other traces are $v_{K8-1}$, 1588–1598 cm$^{-1}$; $v_{K8-2}$, 1612–1619 cm$^{-1}$; $v_{TT}$, 1603–1611 cm$^{-1}$. Traces are scaled to overlap between 70 and 95 °C.

This data is consistent with previous IR, fluorescence, and UV-CD measurements\textsuperscript{17,23,24,82} and is identical to the earlier UL data at pH 7.62

In addition to SVD characterization, it is also useful to observe specific spectral regions within the band. The relative intensities of the isotope-shifted peaks of K8, T10 and TT are compared with the $v_1$ peak of UL in Figure 5. Intensities are obtained by averaging the absorbance around the peak positions ($v = \pm \sim 5$ cm$^{-1}$), and are compared by overlaying the curves between 70–95 °C. This demonstrates that the melting behavior follows the same trends for all spectroscopic features between 55 and 95 °C. The melting curves for $v_1$ peak intensities of all isotopologues have profiles matching the second SVD component melting curves within 10%. Similarly, the intensity of the T10 and TT labels both track the SVD melting curves, suggesting that these curves report on the interstrand contacts in the central region of the peptide. For K8, the $v_{K8-1}$ region changes quasi-linearly with increasing temperature. In contrast, the $v_{K8-2}$ region is largely unchanged for temperatures $<40$ °C. This melting behavior suggests that the $v_{K8-2}$ peak reports on peptides with a natively structured turn, while the $v_{K8-1}$ peak reports on non-native turn configurations that show a melting curve similar to that expected for a less-stable or disordered peptide. The high apparent melting temperature of the $v_{K8-2}$ peak suggests that the natively structured turn region is in fact more stable than the rest of the peptide and could account for the residual backbone structure previously reported over similar temperatures.

Temperature-dependent changes to the 2D IR spectra of each isotopologue can be seen by comparing the 25 and 75 °C spectra shown in Figure 3. Along the diagonal axis ($\omega_1 = \omega_2$), spectral shifts track those observed in the FTIR data, and spectral features broaden along the antidiagonal axis with increasing temperature. In our analysis, we concentrate on the center frequency, amplitude, and 2D lineshapes of the isotope-labeled features. The line shape can be characterized by their widths parallel and perpendicular to the diagonal axis. The diagonal line width ($\sigma$) reflects inhomogeneous broadening that originates in static structural disorder on the time scale of the experiment ($\sim 2$ ps). Antidiagonal widths ($\Gamma$) report on rapid frequency shifts that originate in subpicosecond peptide-solvent interactions and structural fluctuations. The relative magnitudes of these linewidths, or ellipticity $E = (\sigma^2 - \Gamma^2)/(\sigma^2 + \Gamma^2)$,\textsuperscript{51,83} measured as a function of temperature can be used to interpret changes from static disorder to dynamic disorder due to increasing structural flexibility and solvent exposure.\textsuperscript{61}

Spectral changes to the UL 2D IR data are similar to those reported earlier at pH 7, which were interpreted as fraying of the termini and an intact turn at all temperatures. The antidiagonal line width grows with temperature for both of the $\beta$-sheet modes in the 2D IR spectrum (data not shown). The full width at half-maximum (FWHM) of the $v_1$ band is only $\sim 2.0$ cm$^{-1}$ larger than that of the $v_1$ band at 15 °C, but the slope of the line width increase versus temperature of $v_1$ is twice that of the $v_1$ band.

Thermally induced spectral changes to the $v_{K8}$ peaks can be seen more clearly in Figure 5. As the temperature of the system increases, the spectrum responds both to structural rearrangements and shifting populations between native and misfolded ensembles. The center frequency of the $v_{K8-1}$ and $v_{K8-2}$ bands does not change with temperature, but the amplitudes of both peaks decrease. In addition, the $v_{K8-1}$ intensity decreases with respect to the $v_{K8-2}$ peak, indicating that the native turn is more stable than the disordered turn. Linewidth changes to the TZ2-K8 spectra are consistent with those of the unlabeled hairpin (Figure 7). The slope of the line fit to the FWHM of the $^{12}$C $v_1$ band (0.058 ± 0.012 cm$^{-1}$/°C) is twice as large as the corresponding slope of TZ2-UL (0.020 ± 0.006 cm$^{-1}$/°C). For the $v_{K8-1}$ and $v_{K8-2}$ peaks, the FWHM measurement is noisier
due to lower signal strength. However, the line width of the high frequency peak, $\nu_{K8-2}$, does not display a significant slope with temperature, indicating that the homogeneous broadening does not increase significantly with temperature. The limited resolution of the $\nu_{K8}$ peaks prevents a quantitative description of the diagonal line width. However, in the spectra shown in Figure 6 there does not seem to be any clear sign of diagonal peak broadening with temperature.

Together, these observations support the idea that two bands are reporting on subensembles of peptides for which the relative population shifts with temperature, but the line width properties remain relatively constant. The presence of two isotope-shifted peaks in the turn may reflect two distinct conformational states of the peptide; however, from the $K8$ measurement alone one cannot rule out additional states that have the same type of solvent exposure in the turn. Of course, conformational dynamics will be present that interconvert these turn structures. Not surprisingly, if a two state analysis is applied to this exchange of conformers (K8-1 to K8-2), one finds that the temperature-dependence does not follow van’t Hoff behavior (Figure 7). However, on average the frequency of the $\nu_{TT}$ peak and magnitude of cross-strand coupling remains unchanged from lower temperatures. These disordering pathways are consistent with the fraying transition described in previous hairpin simulations.30,84,85

**Simulation Results.** To better interpret how the observed amide I spectral features report on peptide conformation, structure-based modeling of 2D IR spectra was applied to five sets of TZ2 conformers drawn from the Markov state analysis of Chodera et al.29 Each configuration chosen for the spectral simulations should be viewed as an ansatz from which structural features can be identified that play an important role in determining the spectroscopy. One representative structure from each Markov state chosen is shown at the top of Figure 8, but conformational disorder varies for each of these states, as shown in the Supporting Information. Specifically, we focused on the following five conformational ensembles:

- “Folded” (FO, 250851) is a well-ordered ensemble that has an average of four backbone hydrogen bonds, which correspond to those in the NMR structure.21 The S1, T3, K8, and T10 carbonyls are all oriented for cross strand hydrogen bonds, and all four tryptophan side chains are packed to one face of the peptide.
• “Bulged Turn” (BT, 214369) is a compact coiled structure with a well-solvated, bulged turn region and an average of one cross-strand hydrogen bond that appears near the strand termini. This state contains S1, T3, K8, and T10 peptide carbonyls that are solvent exposed, and tryptophan side chains make rare contacts.

• “Disordered” (SR, 271154) is a disordered ensemble whose common feature is a bulged turn and an average of one backbone hydrogen bond with a misaligned registry near the C terminus. Tryptophans are poorly organized.

• “Frayed” (FR, 11131) has a compact properly formed type I’ turn region with an average of two backbone hydrogen bonds,
but disordered strand termini. The T3 and T10 are oriented toward the opposite strand, and tryptophan side chains are disordered.

**“Extended Disorder”** (ED, 64336) is an extended and well-solvated state with substantial disorder and rare backbone hydrogen bonds.

Here the number identifying each state refers to the designation in Supporting Information for ref 28.

As a first point of contact to experiment, we used electric field mapping to calculate histograms of amide I site energies for the 11 peptide units of the backbone. The red-shift is primarily sensitive to hydrogen bonding to the oxygen site. Histograms for sites S1, T3, K8, and T10 are shown in Figure 9, with the remainder in the Supporting Information. It is apparent that the distribution of site energies for site T3 and K8 vary in such a way that the mean frequency is unique for the FO and BT conformers. On the other hand, S1 and T10 appear to be insensitive to conformation. Time-correlation functions for the site energy showed biphasic behavior, with a picosecond component attributed to solvent induced dephasing, and a longer component assigned to sampling of backbone configurations. The longer decay time varied from ~50 ps for S1, T3, and T10 to >200 ps for W4 and K8.

Our modeling of all conformers provides a general relationship between the amide I site frequency and the hydrogen bonds it participates in. We find that a hydrogen bond (HB) of an amide carbonyl to protein gives about the same red shift as a hydrogen bond to water. (For our purposes, in simulations a hydrogen bond to water involves a hydrogen bond number and red-shift is mild ($\rho = 0.53$). Therefore the solvent-exposed K8 conformers should exhibit an additional red shift relative to FO, but the conformational disorder and fluctuations in peptide backbone and water hydrogen bonds will also lead to a larger inhomogeneous width. Based on these observations, we conclude that the $v_{K8-1}$ peak represents peptides with non-native turns, and the high frequency $v_{K8-2}$ peak reports on structures with native type $\Gamma'$ -turns.

During simulations of the IR spectra for the NMR structure at pH 2.5, a correlation between the K8 site frequency and two distinct E5 side chain configurations was observed. Specifically, fully solvated by water, it has the ability to form multiple HBs, giving a larger average red shift. From analysis of both types of HBs, we find that on average, one HB leads to an 11 cm$^{-1}$ red shift, however the dispersion in this relationship ($\sigma = 25$ cm$^{-1}$) leads only to a modest correlation ($\rho = -0.50$). These results can be compared with the results of ab initio calculations on isolated clusters, which reveal a 20 cm$^{-1}$ red-shift for each HB to oxygen and an additional 10 cm$^{-1}$ red shift for hydrogen bonds donated by the peptide N$-{H}$.86

For each of these five conformers, we simulated the infrared spectroscopy of the five isotopologues studied here. Simulated FTIR and FTIR difference spectra for each structure are shown in the Supporting Information section. In general we find that qualitative similarities exist between several of the experimental and simulated spectra, which we discuss in terms of peak positions, amplitudes, linewidths, and lineshapes. The simulated 2D IR spectra of the unlabeled peptide for FO, BT, and FR conformers each display two diagonal peaks and Z-shaped contours that resemble the experiment at low temperatures. For the disordered SR state, two bands are also resolved although in this case, the high-frequency band carries most of the intensity. Limiting the simulation only to a specific structure with +1C slipped registry and 4 hydrogen bonds leads to a spectrum similar to BT (see the Supporting Information). For the disordered ED state, the amide I band has little structure and reflects the diagonally stretched resonance of an inhomogeneous line shape.

As expected, each of the five K8 simulations gives rise to one resonance for the labeled site, although the peak position and line width vary with conformation. In particular, we see a correlation between the orientation and solvent exposure of the K8 amide group and the frequency of the isotope-shifted peak. In the case of FO and FR states each have a K8 amide group oriented so that its carbonyl oxygen forms a cross-strand hydrogen bond with the W4 amide proton, as expected for a type $\Gamma'$ -turn. In their calculated spectra, the $v_{K8}$ peak is split from the amide I maximum by 25–30 cm$^{-1}$, and the diagonal line width is a compact 5–6 cm$^{-1}$. In addition, a distinct cross-peak is observed between the $v_{K8}$ and $v_1$ bands in the calculated spectra for these states. For each of the other structures (SR, BT, and ED) the K8 oxygen has higher water exposure on average, although with higher variance in hydrogen bonds formed. The $v_{K8} - v_1$ amide I peak splitting for each of the corresponding spectra is 30–36 cm$^{-1}$, and the label resonance has distinctly broader diagonal linewidths of 10–14 cm$^{-1}$. The calculated BT spectrum shows the largest shift and line width. The observed differences can be attributed to variation in hydrogen bonding to the K8 carbonyl. Fully solvated carbonyls will on average participate in two hydrogen bonds to water, as opposed to one cross-strand hydrogen bond in the case of properly folded $\beta$ turns. For the K8 carbonyl, we find that each hydrogen bond contributes on average a 16 cm$^{-1}$ red shift in amide I frequency; however, the correlation between hydrogen bond number and red-shift is mild ($\rho = -0.53$). Therefore the solvent-exposed K8 conformers should exhibit an additional red shift relative to FO, but the conformational disorder and fluctuations in peptide backbone and water hydrogen bonds will also lead to a larger inhomogeneous width. Based on these observations, we conclude that the $v_{K8-1}$ peak represents peptides with non-native turns, and the high frequency $v_{K8-2}$ peak reports on structures with native type $\Gamma'$ -turns.

Figure 9. (Top) Isotope-labeled TZ2 amide I site energy distributions for the five Markov states. (Bottom) Distribution of calculated amide I site energies grouped by number of hydrogen bonds. A linear fit to the mean value gives $\omega = 1645.7$ cm$^{-1} - 16.3 \times$ (no. of CO H-bonds).
two configurations of the glutamic acid side chain and backbone
dihedrals that differed in O(K8)······O(C(E5)) separation by 6.1
and 6.8 Å were predicted to be observed with frequency splitting
of 12 cm⁻¹. The observation of these two conformers required a
protonated form of the glutamic acid (pKₐ 4.6). We ruled this
out as an explanation of the two K8 peaks in experiments
because the amide I resonances in FTIR and 2D IR spectra
exhibit no pH dependence between pH 2.5 and 7.

The T10 peptide carbonyl adopts a variety of conformations
in the Markov states simulated. In the case of the FO and FR
states it is oriented for a cross-strand hydrogen bond, for BT it
is entirely solvent exposed, and for SR and ED it samples a
variety of configurations. In simulated spectra we note that a
conformer with solvent exposed T10 carbonyl gives rise to a
structured excitonic spectrum and a red-shifted and spectrally
distinct T10 peak, whereas the internally hydrogen bonded site
gives a peak merged with the excitonic band, as observed in
experiment. For the SR and ED states, the intensity of the
labeled transition is greatly diminished over the intense band
seen in the completely water-exposed state. Of all simulations,
the FR state corresponds best to the low temperature experi-
mental spectra. These observations demonstrate that the T10
experimental spectra provide evidence of a T10 carbonyl that
participates in a single cross-strand hydrogen bond over the
temperature range sampled.

For 2D simulations of TT, we find that all conformers except
ED have a resolvable red-shifted peak arising from the TT label.
In the case of the disordered states SR and ED, there is little
change in the spectrum between the T10 and TT simulations,
which reflects the limited correlation between the positions of
their T3 and T10 peptide units. For the FO and FR conformers,
which have close T3-T10 contacts, a distinct νTT peak is
observed although the T10 spectrum showed no distinct T10
isotope-shifted feature. This is a result of the additional red-
shift of the νTT band as a result of T3-T10 amide Γ coupling,
which varies between 6−7 cm⁻¹ for the FO conformers and
leads to a νTT − ν⊥ splitting of ≥30 cm⁻¹. Comparing the T10
and TT 2D spectra for the BT state shows few differences
besides additional inhomogeneous broadening of the νTT transition.
Each of the simulated spectra containing proximal T3 and
T10 sites bear similarity to the experimental spectra, but those
that compare favorably to the calculated T10 and TT spectra
are FR and FO. Finally, we note that the intensity of the
simulated νTT feature scales with the strength of coupling
between the two threonine sites. From these observations,
we conclude that contacts between strands in the central region of
the peptide exist throughout the temperature range studied. We
also conclude that out-of-registry structure is not significantly
populated in the equilibrium conditions observed here.

Simulations of the S1 spectrum were used to address the lack of
a distinct peak for the 18O peptide site, and the shifts in intensity
and line shape seen in FTIR and 2D IR spectra. In general, for the
Markov states studied, the S1 site is protected from the solvent,
because the serine side chain and terminal
-NH₃⁺ both prefer to be oriented to the solvent, and because
tryptophan side chains interfere with water penetration to the
S1 carbonyl. Thus, the S1 site energies are generally high-regardless of conformation. The FO state has many intact
S1−W11 hydrogen bonds, the SR has S1 carbonyls that
experience a range of solvent and side chain environments, and
the FR is the most solvent exposed.

The experimental (S1-UL) FTIR difference spectrum indicates
that intensity is lost at 1675 and 1640 cm⁻¹ upon S1 labeling.
Simulations of this spectrum for various conformers shows that
this characteristic double peak loss feature matches those
observed in the FO state, whereas other states show a single
loss feature (see Supporting Information). Cross-strand hydrogen
bonding between the S1 and W11 in the FO state lead to strong
coupling across the β-strand and a low frequency ν1-like mode
which is decoupled from the rest of the band and shifts upon
18O isotope-labeling. However, the high frequency loss features
in FTIR and 2D IR are also present in BT, SR, and FR, which
have high site energies and weak coupling to the remaining
peptide units. 18O labeling shifts the S1 vibrational frequency
for each system from very high energies (≥1700 cm⁻¹) in the
unlabeled spectrum to frequencies just to the blue of the ν1.
The distribution of S1 configurations available in these con-
formers suggests that the S1 site is generally disordered at all

**Discussion and Conclusions**

Spectral changes to the amide I band of TZ2, using four
isotopic substitutions to probe the β-turn (K8), the N-terminus
(S1), and the midstrand region (T10 and TT) of the hairpin
structure, provide a site-specific description of the thermal
denaturation of this β hairpin. The [13C] label at K8 reveals two
unique turn geometries, the type I′/β-turn observed in the NMR
structure (νK8−2), and a less populated disordered or bulged loop
(νK8−1). Structural disorder within the νK8−2 band does not
increase significantly with temperature, from which we conclude
that the β-turn structures remain well-ordered. The νK8−1
population in contrast does decay with temperature, indicating
a relatively unstable loop. The hairpin retains interstrand contacts
in the midstrand T3-T10 region over the entire temperature range
studied as evidenced by the consistently high frequency of the
T10 resonance and coupling-shifted TT resonance. Unlike νK8−2,
the 2νTT line shape changes from a heterogeneously broadened
peak to a more symmetric homogeneously broadened peak,
indicating that this region experiences an increase in the
magnitude of picosecond fluctuations in the peptide, its internal
contacts, and immediate surroundings. Spectroscopy of the
N-terminal serine group amide group puts constraints on the
possible conformations of the termini. From our observations,
we believe that S1 is free to explore a large configurational
space, relative to the other labeled residues. These vary from
structures in which the S1 amides are hydrogen bonded to the
W11 amide to structures in which there is no interaction with the
other peptide amides.

Additional information on the TZ2 turn is available from
recent experiments on turn labeled TZ2-G7* and spectroscopic
simulations based on the NMR structure. An isotopic shifted peak
was well-resolved in the room temperature 2D IR spectrum,
and shown to be consistent with a solvent exposed
amide groups. In addition, 1 ps waiting-time 2D IR data revealed
cross peak structure to the G7* site that was attributed to
different solute−solvent substates. These observations are
consistent with our assignments, and can be explained with our
conformer simulations. The dominant isotope-shifted peak is at
1595 cm⁻¹, reflecting the high degree of solvent exposure of the
G7 carbonyl observed in the FO structure. Other conformers
studied have lower solvent exposure and considerable disorder,
leading to higher transition frequencies, as observed in experiment.

The picture that emerges from these data provides a detailed
view of a heterogeneous thermal fraying process. The 25 °C
state includes roughly 60% conformers that retain most of the
cross-strand contacts seen in the NMR structure, whereas others
have midstrand hydrogen bonding contacts and a bulged loop.
As temperature is raised, the ends fray for all molecules,
becoming more solvent exposed, and introducing more disorder into the central contacts of the hairpin. Contacts remain within the central region of the hairpin, but on average the turn is more ordered. No idealized unfolded state with fully solvated backbone is observed. These results add structural insight to the building body of evidence that TZ2 folding is heterogeneous.\textsuperscript{30,38,88} Further, these data provide a point of reference for testing the conformational variation and energy landscape observed by TZ2 molecular dynamics simulations.\textsuperscript{26,29,30,39,46}

These results also provide insight into the kinetics observed in temperature-jump unfolding experiments.\textsuperscript{16} We have evidence of different compact conformers and that the extended state is never realized under the conditions studied here. Therefore T-jump experiments do not characterize an idealized transition from folded to random coil structure. Instead such experiments characterize the shifting distribution of conformational substates, and changes in thermal disorder within those minima. In the future, transient T-jump 2D IR experiments will provide an avenue to more directly follow the evolution of conformational distributions.\textsuperscript{16,89} Such experiments could use folding rates to test for a correspondence of our K8 conformers with the Trp fluorescence wavelength changes in the potential of the method to unravel systems with conformational heterogeneity.\textsuperscript{45,93} Explains the varying experimental views that both the nature of the turn and the hydrophobic packing\textsuperscript{23} are critical to hairpin folding.

Curiously, the type I’ turn appears to be favorable at high temperature. One can rationalize the origin of this apparent annealing by comparison of Markov states. The frayed state provides the possibility of packing W4 and W9 side chains about the turn which is not possible with the bulged turn. As such it appears that the desolvation entropy for water about tryptophans plays a key role in determining the relative stability of these conformers. This counterintuitive shift of turn stability could be compared with cold-denaturing transitions attributed to hydrophobic hydration.\textsuperscript{30}

What can we say about the TZ2 and the folding pathways of $\beta$ hairpins? While it was originally assumed that there is a choice to be made between zipping\textsuperscript{40} and hydrophobic collapse,\textsuperscript{91} it appears that both of these processes play crucial roles for the folding of TZ2. For TZ2, the simulations seem to be in agreement that folding proceeds from the turn to the termini, but that this “zip-out” process involves both contacts between W4 and W9 and turn hydrogen bonding contacts.\textsuperscript{28,39,92} This hybrid zipper type model\textsuperscript{45,93} explains the varying experimental views that both the nature of the turn and the hydrophobic packing\textsuperscript{23} are critical to hairpin folding.

Our observations closely match those of Gao and co-workers,\textsuperscript{22,94} who recently performed MD simulations of the sequence dependent temperature-dependence of $\beta$ hairpin folding. Temperature-dependent studies of TZ2 unfolding indicated that there was a propensity for the HB closest to the turn (E5-G7) to form as the temperature is raised, even though other HB tended to rupture. These authors used clustering analysis of states during TZ2 folding to argue that the folding mechanism from an extended state is dominated by a zip-out mechanism in which the turn forms first, although they do identify bulged configurations along the folding path.\textsuperscript{22,94} Hydrophobic clustering and cross-strand HBs were favorable at low temperature in the central region, whereas the frayed state was favored at high temperature.

Recently there have been several studies of peptide structure with isotope-labeled 2D IR spectroscopy that demonstrate the capabilities of this method for insight into backbone conformation and hydrogen bonding environment.\textsuperscript{11,19,20,51} This work indicates the potential of the method to unravel systems with conformational heterogeneity and disorder. With an appropriately large set of trial conformers and increased improvements in spectroscopic modeling, one should be able to use self-consistent modeling of multiple isotopologues to provide a detailed picture of the global range of conformations adopted by the peptide. Experimentally, one can also imagine that for cases such as TZ2, 3D IR spectroscopy on multiply labeled peptides can provide a higher level of conformational detail by correlating the local structural environment between multiple sites of the same peptide. Such experiments provide an avenue to characterize conformational heterogeneity of rapidly exchanging conformers of proteins and peptides in folded and disordered states.

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Supporting Information Available: Details on the synthesis and calculations including (1) mass spectra of the synthesized peptides, (2) temperature dependent trends in FTIR and 2DIR spectra of TZ2 isotopologues, (3) table of spectral features in peptides, (2) temperature dependent trends in FTIR and 2DIR spectra of TZ2 isotopologues, (4) visualization of Markov states, (5) histograms of TZ2 site energies from simulations, (6) analysis of site frequency shifts as a function of hydrogen bonding, and (7) spectral simulations for single structures. This material is available free of charge via the Internet at http://pubs.acs.org.

References and Notes

