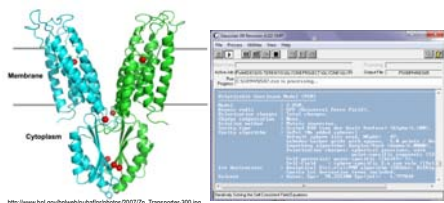


DFT Calculations of Amide I Vibrational Frequencies for a Model Peptide

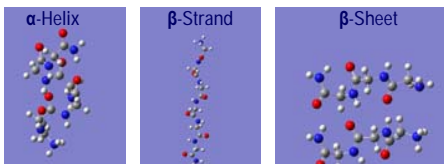
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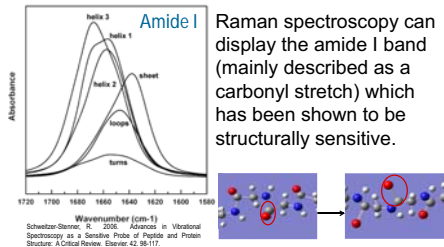
Introduction



- The local 3D arrangement of peptides and proteins made by hydrogen bonding defines secondary structure.



- Knowing the secondary structure of a peptide or a protein is important because it is a key determinant of their biological function.



- The rules that are used to interpret the secondary structure from the amide I band are:

- Alpha Helices $\rightarrow 1650 - 1655\text{cm}^{-1(13)}$
- Beta Sheets/Strands $\rightarrow 1665 - 1675\text{cm}^{-1(13)}$
- Random Coils $\rightarrow 1665\text{cm}^{-1(13)}$

- The goal of this study was to perform a detailed theoretical study of the correlation between peptide secondary structures and the amide I vibrational frequencies. This would test the validity of the rules for interpreting the secondary structure and for better predicting the secondary structure from the amide I band.

Method

- This study used a model peptide consisting of 6 glycine residues that was created on GaussView 5.0 (Figure A).
- The conformation of a peptide or protein can be broken up into its dihedral angles as indicated by Figure B.
 - Ψ is the angle that is made from nitrogen to nitrogen.
 - Φ is the angle that is made from carbonyl to carbonyl.
 - Ω is the angle that is made from carbon to carbon. This angle will be ignored for this study because it remains $\sim 180^\circ$.

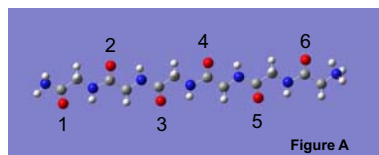


Figure A

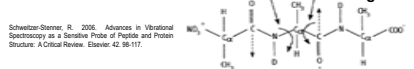


Figure B

- For the calculations the Ψ and Φ angles were changed in increments of five degrees for the β -strand/ β -sheet region and two degrees for the α -helix region according to the Ramachandran plot.

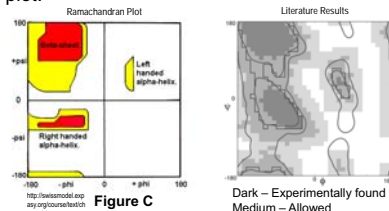


Figure D

- The model peptide was subjected to density functional theory (DFT) calculations on Gaussian 09. The entire calculation method was DFT/B3LYP/6-31G/d/p with a solvent model of CPCM in water.

Results*

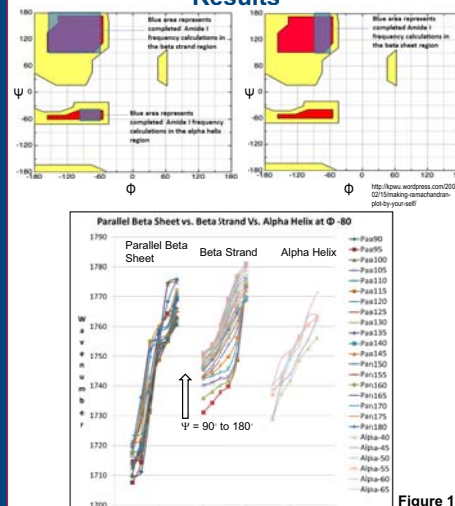


Figure 1

Amide I Ramachandran Frequency Plots

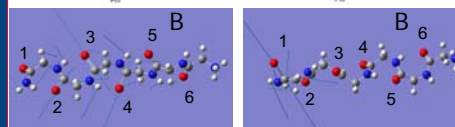
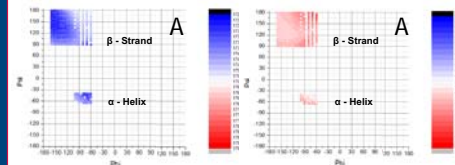


Figure 2. The frequency of the amide I mode shown in B is plotted in Ramachandran space shown in A.

Figure 3. The frequency of the amide I mode shown in B' is plotted in Ramachandran space shown in A.

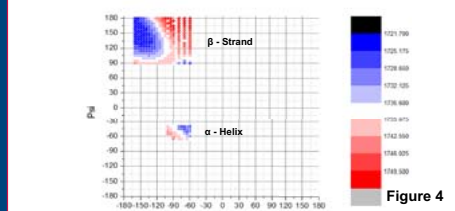


Figure 4

*All graphs in this section contain raw data. No scaling has been applied to them yet.

Discussion

- Figure 1 shows that in general the amide I frequencies of the alpha helix region are lower than those in the beta strand region, although there is much overlap. This does not agree with the experimental literature (see Introduction). Also, the amide I frequencies for beta sheet go much lower than for beta strand.
- There are six distinct amide I modes for this peptide, each characterized by different combinations of CO stretches. The amide I mode with mainly carbonyls 2, 3 and 4 stretching (Figure 2) is generally lower in frequency than the mode with mainly carbonyl 1 stretching (Figure 3). This is consistent with weaker H-bonding of terminal residue carbonyls versus non-terminal residue carbonyls.
- There is a generally good correlation between the most frequently observed dihedral angles in proteins measured experimentally (Figure D) and the trends in the amide I frequencies from our calculations (Figure 4), likely reflecting the importance of H-bonding both to the stability of protein secondary structure and for determining the frequency of the amide I mode.
- So far, this study shows that there is a correlation between secondary structure and the amide I vibrational frequencies. However, this correlation does not entirely agree with the rules that are commonly used to interpret the secondary structures from the amide I band.

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