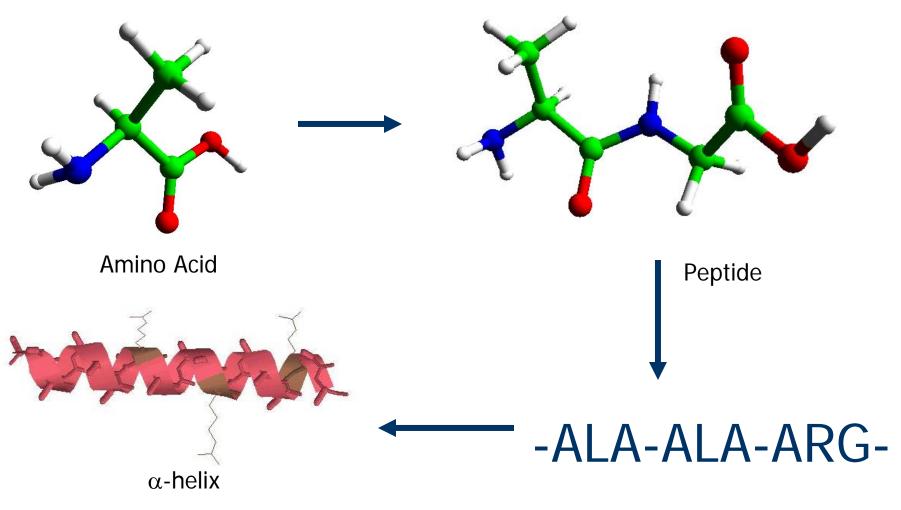
Protein Stability of a 21 Residue Alanine Based Peptide

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Biochemistry Background

- Genes are used to make amino acids
 - The human genome is 3 billion DNA base pairs
 - Estimated 20,000-25,000 genes
- Amino acids are the basic building blocks of proteins
- Two major angles that biochemists are concerned with
 - <u>_</u> Ф
 - <u> </u>Ψ

Protein Construction



Polypeptide

The Problem

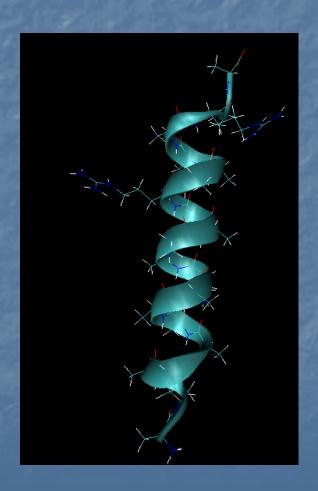
- The central dogma of biochemistry
 - How do proteins fold
 - How do external variants affect protein folding/stability
- Methods
 - Computational
 - X-ray crystallography
 - NMR spectroscopy
 - UV Raman
 - Fluorescence

Protein Folding/Stability

- Affected inter-molecular interactions
 - Amino acid hydrophobicity
 - Salt bridges
 - van der Waals forces
 - Ion-ion interactions
 - Hydrogen bonding
- Observed behaviors in salt solutions
 - Chloride destabilizes α-helices
 - Perchlorate stabilizes α-helices
 - Sulfate destabilizes α-helices

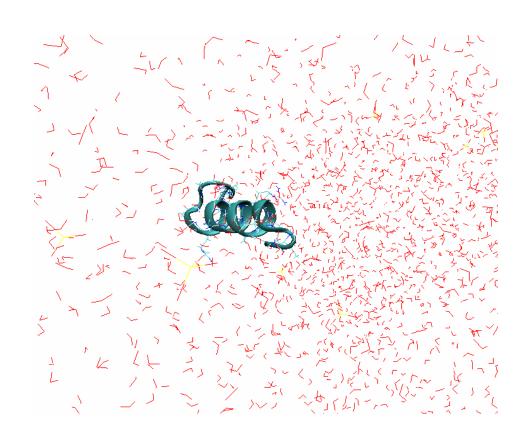
The peptide

- α-helical in structure
- Melting temperature
 - **303K**

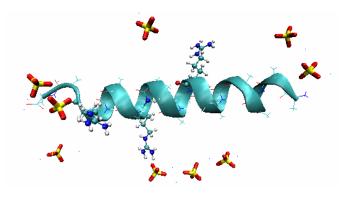


Molecular Dynamics

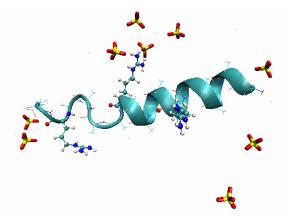
- Used AMBER 9
- System
 - 15 Sodiums added
 - 9 Sulfates added
 - 2338 molecules of Water
 - Temperature of 300K
 - Simulations ran for 70 ns
- Hardware
 - 8 Xeon processor cluster
 - 1 ns of simulation took12 hours of clocktime torun



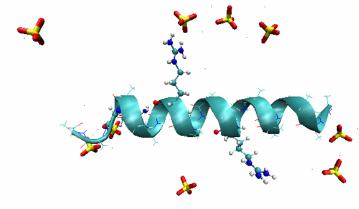
Preliminary Results



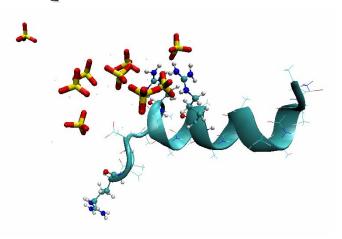
Initial helix



During Simulation



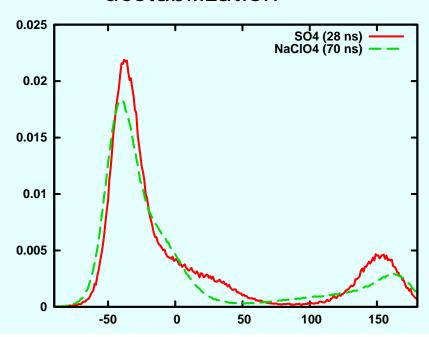
Equilibration



After 28 ns

Preliminary Conclusions

- Sodium Sulfate
 - Already unfolding after the equilibrations
 - Strong indicator of destabilization



- Phosphate and Acetate
 - Not unfolding after the equilibrations
 - Strong indicator of stabilization

Summary

- These simulations support previous experimental results
- They also support the trend of the Hoffmeister effect
- Based on results not discussed here, the change in solvent activity is the reason for stabilization

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Questions