



**CALIFORNIA STATE SCIENCE FAIR  
2006 PROJECT SUMMARY**

<b>Name(s)</b> Vasilios A. Morikis	<b>Project Number</b> <b>S0415</b>
<b>Project Title</b> <b>The Effect of Charged Amino Acids on the Formation of Alpha-helical Structures: Year 2</b>	
<p style="text-align: center;"><b>Abstract</b></p> <p><b>Objectives/Goals</b> Alpha helical secondary structures in proteins are formed by backbone (i,i+4) hydrogen bonds. My goal is to evaluate the effect of salt bridges between oppositely charged amino acid side chains at positions (i,i+4) on the stability of alpha-helices. I constructed, with my computer, models of peptides with repeated pentapeptide amino acid blocks with variable charge properties. I used energy minimization computational methods to evaluate peptide stability. This project addresses protein folding at the secondary structure level, an important question in biochemistry.</p> <p><b>Methods/Materials</b> Structural stability can be evaluated using minimization of the internal potential energies of proteins and peptides. I used the program Deep View to visualize the peptide models and to perform 500 steps of steepest decent followed by 500 steps of conjugate gradient energy minimizations. The peptides I examined are (DAAAK)<sub>n</sub>, (DAAAR)<sub>n</sub>, (EAAAK)<sub>n</sub>, and (EAAAR)<sub>n</sub> as well as their reverse-order sequences (KAAAD)<sub>n</sub>, (RAAAD)<sub>n</sub>, (KAAAE)<sub>n</sub>, and (RAAAE)<sub>n</sub>, where n=1-4. D and E are negatively charged acids, K and R are positively charged bases, and A is a neutral amino acid. I also used the following control peptides composed of the same type of amino acids (AAAAA)<sub>n</sub>, (KKKKK)<sub>n</sub>, (RRRRR)<sub>n</sub>, (DDDDD)<sub>n</sub>, (EEEEEE)<sub>n</sub>.</p> <p><b>Results</b> In all cases, I found that the peptide stability increases with n, the number of pentapeptide blocks. For direct peptides I observed the following stabilities: (DAAAR)<sub>n</sub> ~ (EAAAR)<sub>n</sub> &gt; (DAAAK)<sub>n</sub> ~ (EAAAK)<sub>n</sub>. For the reverse peptides I found: (RAAAD)<sub>n</sub> ~ (RAAAE)<sub>n</sub> &gt; (KAAAD)<sub>n</sub> ~ (KAAAE)<sub>n</sub>. For the control peptides I found: (RRRRR)<sub>n</sub> &gt; (KKKKK)<sub>n</sub> &gt; (DDDDD)<sub>n</sub> &gt; (EEEEEE)<sub>n</sub> &gt; (AAAAA)<sub>n</sub>.</p> <p><b>Conclusions/Discussion</b> Combinations of R with D or E are more stable than combinations of K with D or E. The sequence order has a negligible effect on stability. In the control peptides, R has higher effect on stability, followed by K, D, E, A in that order. Surprisingly, the most stable peptide was the control (RRRRR)<sub>n</sub> and expectedly the least stable peptide was (AAAAA)<sub>n</sub>. Detailed examination of the data suggests that the increased stability is owed to van der Waals and electrostatic interactions. In peptides containing R electrostatic interactions are dominant. In the remaining peptides van der Waals interactions are dominant. Electrostatic interactions involve charged side chains and backbone atoms with small contributions from salt bridge interactions between side chains.</p>	
<b>Summary Statement</b> My project aimed to determine the effect of charge on the stability of alpha-helical secondary structures using model peptides and energy minimization methods.	
<b>Help Received</b> Dr. Morikis for guidance and my mother for helping me glue the panels to the board.	