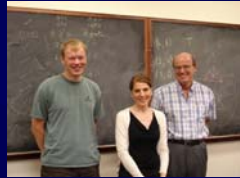


# Center for Biological Physics\*

Jeff Toller, Mohave High School  
Bullhead City, Arizona

Tracy Blondis, Westwood High School  
Mesa, Arizona

## Summary of Research Group Work



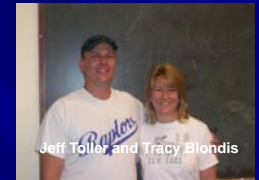
van der Vaart - Ozkan - Thorpe

**Arjan van der Vaart** – studying the conformational changes of proteins as they interact with other molecules  
**Banu Ozkan** – studying the mechanism of protein folding  
**Michael Thorpe** – studying geometric conformation changes based on flexibility and rigidity of biological molecules

\* Supported by Science Foundation Arizona, National Science Foundation, and Arizona State University

## General Overview of Our Students

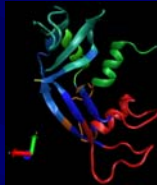
- ◆ Title I School – 75% qualify for free or reduced lunch/breakfast
- ◆ A Minority Majority School
  - 45% Hispanic
  - 40% Caucasian
  - 8% African-American
  - 5% Native American
  - 2% Other
- ◆ Transient School



Jeff Toller and Tracy Blondis

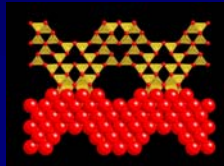
## Selected Research in Laboratory

- ◆ Identify fundamental structure of proteins to analyze protein folding. Concerned primarily with chemical interaction of amino acid side chains.
- ◆ Recognize areas of rigidity and flexibility in proteins. Flexible areas interact with other molecules to undergo chemical reactions. Great potential for combating disease as proteins could be manufactured for use.
- ◆ Use of computer simulations in analyzing data and parameters. Protein folding occurs within picoseconds. Computer modeling allows for time manipulations when analyzing data.



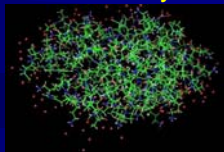
## Dr. Mike Thorpe, ASU Department of Physics

- ◆ Dr. Thorpe's research is diverse and includes an emphasis in the theory of flexibility and mobility in glassy networks. During our MSTF summer program, Dr. Thorpe introduced the concept of flexible regions in proteins that is determined by x-ray crystallography.



## Dr. Arjan van der Vaart, Dept. of Chemistry & Biochemistry

- ◆ Dr. van der Vaart's research is to better understand the fundamental principles that govern conformational behavior in computational simulations. He hopes to build predictive models for explaining how biological molecules interact.



## Dr. Banu Ozkan, ASU Dept. of Physics

- ◆ Dr. Ozkan's research focuses on how amino acid sequence encodes for the specific function and structure of proteins. Banu also hopes to find how proteins fold and assemble into macromolecules.



Special Thanks to  
 Dr. Mike Thorpe  
 Dr. Arjan van der Vaart  
 Dr. Banu Ozkan

Organizations that made this possible  
 Science Foundation of Arizona  
 National Science Foundation  
 Arizona State University

*"This Summer 2007 Math and Science Teaching Fellows has given us an insight into the rapidly changing method of conducting scientific research. What an awesome opportunity to learn cutting edge research and then have the ability to share it with our students."*

– Tracy Blondis and Jeff Toller

## Our Curricular Tasks and Methods of Proposed Instructional Delivery

- ◆ Introduce students to the four orders of protein structure
  - Primary Structure – amino acid sequence
  - Secondary Structure –  $\alpha$  and  $\beta$  helices
  - Tertiary Structure – folding
  - Quaternary Structure – compacted subunits

*To do this, a PowerPoint presentation will be provided with integrated computer simulations and embedded short videos*
- ◆ Have students evaluate regions of protein flexibility and rigidity by examining computer models
  - Students will use critical thinking to determine areas of flexibility and rigidity in molecules by analyzing video simulations of proteins. Students will assemble in small groups to brainstorm possibilities and support their conclusions. Then as a class, ideas will be written on white boards. Similar ideas between groups will be emphasized in the hopes that students will lead themselves to the correct answers.*
- ◆ Students will determine properties of chemical bonding between amino side chains based on hydrophilic and hydrophobic regions.
  - Plastic interactive models will be fabricated that students can hold and manipulate. These models will have painted regions indicating hydrophobic and hydrophilic areas. Students will be asked to find a logical method for chemical bonding. Emphasis will be given on size of their molecule where a smaller size indicates a smaller energy state.*
- ◆ Have students understand the mechanism of protein folding by using a modified protein modeling software

*TEALsim, a free protein software designed for low level understanding of protein folding, will be demonstrated to students. This software includes a few basic proteins that students can manipulate to determine the known properties of protein folding.*