Peptide MD

Learning Outcomes

•Students will be able to recognize the different types of intermolecular forces and identify them on amino acids.

•Students will be able to determine the types of interactions (intermolecular forces, disulfide bonds…) that different amino acids have based on chemical structure.

•Students will be able to summarize how proteins fold based upon hydrophobic collapse and formation of hydrogen bonds to make secondary structures.

•Students will be able to predict how the primary sequence structure of a protein (such as the M2 channel) affects its function.

•Students will be able to explain how computer simulations are applied to chemistry.

•Students will be able to describe the process by which a computer calculates molecular motion and structures.

•Students will be able to use 3D modeling software to identify different 2°, 3°, and 4° structures in proteins.

•Students will be able to use computational software to modify an existing protein and model the effects of these primary sequence on the 2° and 3° of the protein.

•Students will be able to examine the results of the simulation to compare them to their hypotheses.

MA State Standards Addressed

•9-12.DTC.a.1 Use digital tools to design and develop a significant digital artifact (e.g., multipage website, online portfolio, simulation).

•9-12.DTC.b.1 Communicate and publish key ideas and details to a variety of audiences using digital tools and media-rich resources.

•9-12.CT.e.1 Create models and simulations to help formulate, test, and refine hypotheses, individually and collaboratively.

•9-12.CT.e.2 Form a model from a hypothesis generated from research and run a simulation to collect and analyze data to test that hypothesis, individually and collaboratively.