

Docking

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 explain the factors that are used to design drug molecules for a protein target.
- 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 give examples of 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 model the effects of mutation on protein function and drug effectiveness.
- Students will be able to analyze binding affinity to determine whether or not a drug will be effective.

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.