module developed to teach protein structure fundamentals while supporting ongoing research in enzyme discovery. It can be readily implemented in both entry-level and upper-division college biochemistry or biophysics courses. Pre-activity lectures introduced fundamentals of protein secondary structure and provided context for the research projects, while a homework assignment familiarized students with 3D visualization of biomolecules using UCSF Chimera, a free protein structure viewer. The activity is an online survey in which students compare structure elements in papain, a well-characterized cysteine protease from Carica papaya to novel homologous proteases identified from the genomes of an extremophilic microbe (Halanaerobium praevalens) and two carnivorous plants (Drosera capensis and Cephalotus follicularis). Students were then able to identify, with varying levels of accuracy, a number of structural features in cysteine proteases that could expedite the identification of novel or biochemically interesting cysteine proteases for experimental validation in a university laboratory. Student responses to a post-activity survey were largely positive and constructive, describing points in the activity that could be improved and indicating that the activity helped them learn about protein structure.

2646-Pos

Using structure to predict function in protein biochemistry: a combined computational and wet lab approach

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We have developed an undergraduate biochemistry lab curriculum based on authentic inquiry. The Biochemistry Authentic Scientific Inquiry Lab (BASIL) uses a combined computational and wet lab approach to study proteins of known structure but unknown function. There are over 3800 structures in the Protein Data Bank (PDB) that have unknown function. Students use a combination of sequence and structure alignment tools to study these structures with the goal of identifying possible enzymes. They then use molecular docking to predict what model substrates fit near a proposed active site. Students can produce the target enzymes in the lab using standard wet-lab biochemistry techniques for expression and purification, and they then perform kinetic assays with model substrates selected from their docking studies. We assess their learning as students and their growth as scientists in terms of research methods, visualization, biological context, and mechanisms of protein function. We have successfully used this curriculum in biochemistry lab courses for majors and non-majors. The curriculum is modular and can be used as a whole or individual parts may be incorporated into an existing course - either lecture or lab. The course modules are available for no charge via GitHub. We welcome new collaborators who are interested in adopting the curriculum in full or in part. We can offer synchronous support via virtual meetings and asynchronous support via Slack. This project is supported in part by NSF IUSE 1709355.

2647-Pos

Single-molecule kinetics of annexin V membrane binding in an undergraduate physical biochemistry lab course

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Single-molecule microscopy methods represent one of the great advances in biophysics over the last 40 years but are rarely taught in undergraduate laboratory courses due to instrumentation costs. Single-molecule measurements also offer a direct glimpse into the stochastic nature of events underlying physical and biochemical processes. We have developed and implemented two modules for teaching total internal reflection fluorescence (TIRF) microscopy and single-molecule analysis into an undergraduate physical biochemistry lab course at the University of Colorado Denver. The experiments use a student-level microscope that was purchased in part with institutional funds for instructional lab equipment. In the first module, students learn about laser safety, develop hands-on familiarity with the microscope, and use fluorescent microbeads to measure the critical illumination angle for TIRF. In the second module, students image a commercially available fluorescent protein, annexin V, binding reversibly to supported lipid bilayers prepared by the instructor or teaching assistant. Using freely available particle tracking software, students estimate on- and off-rates from single-molecule data that they acquire in a single lab period. Measurements taken by students in the course yield reasonably consistent k_{off} and k_{on} values that reproduce those of more rigorous measurements performed by our research group. Surprisingly, the ratio of these rate constants differs by a factor of $\sim$1000 from the equilibrium dissociation constant toward liposomes that students determine in a separate bulk titration experiment, suggesting that the affinity of this membrane remodeling protein depends strongly on the geometry of the lipid bilayer. Through these experiments, biochemistry students gain experience using advanced microscopy instrumentation and learn how to analyze single-molecule data to characterize protein-membrane interactions.

2648-Pos

Biomechanical study of glioblastoma cells cultured on 2D and in 3D, analyzed by single-cell traction force microscopy

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All living cells experience and integrate a multitude of mechanical and physical cues within their 3D microenvironment to adapt to organismal development. In turn, they respond by exerting forces, regulating their shape, internal cytoskeletal tension, and elastic modulus. Disruption of the cellular forces, as well as variations in subcellular mechanical properties, can lead to altered pathophysiological conditions and the onset of diseases e.g., cancer. Diseases like cancer i.e., brain cancer (glioblastoma) are characterized by dramatic changes in cell and tissue mechanics, and dysregulation of forces at the cell and tissue level can activate mechanosignaling to compromise tissue integrity and function and promote disease progression. Cells can move by exerting traction forces to their environment. These forces can be assessed by using microfabricated substrates and improved computational approaches, by characterizing the biomechanical forces generated by single cells cultured in defined microenvironments. It provides a valuable insight into the malignancy of cancer cells. This preliminary research focuses on the traction forces induced by single glioblastoma cells in two-dimensional (2D) and three-dimensional (3D) tumor-inspired models. The dimensionality of cell culture i.e., 2D and 3D cell culture influences cancer cell motility and cellular interaction with the surrounding cells and ECM. However, cells grown in 2D adapt to this artificial environment and may no longer display characteristics of the original tumor. An attempt to develop (3D) tumor-inspired models and their functionality in unraveling the role of the microenvironment on tumor cell behaviors has been done. Characterizing the cues involved in glioblastoma cell migration could enable the scientific and medical community to develop better strategies to understand and treat brain cancer.

2649-Pos

Clinical biophysics: complex genetic diseases—inheritance, influence, and occurrence mechanisms of polygenic multifactorial diseases

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Complex Genetic Diseases such as Diabetes Mellitus (DM, Type II Diabetes), Cancer, Hypertension, Cardiovascular Diseases (CVD), Multiple Sclerosis, Schizophrenia, Depression, Epilepsy, Parkinson's Disease, Alzheimer, Lupus Erythematosus, Inflammatory Bowel Diseases are Polygenic Multifactorial Diseases. Polygenic means, more than one (many) genes are responsible. Multifactorial means, influenced by environmental factors, in other term by life quality. Many environmental factors are effective on such disorders. Life quality may be figured out by cigarette smoking, stress, nutrition status, sport-exercises, sleep quality, life style, inhabitance-residental area, envinronmental hygiene, food-water hygiene and healthiness, GMO nutrition, working style and conditions, concomitant disease etc. Genetics creates predisposition in complex genetic diseases. The influence of environmental factors is absolutely necessary for the emergence of the disease. Environmental factors affect both the onset and prognosis of the disease. The severity of the genetic predisposition is important, but even if there is a genetic predisposition, in a quality life, the disease may not occur at all, it may occur at a later age or its course is mild. In a poor life quality, the complex genetic diseases may apper in earlier age with poor prognosis. It is known that these diseases, especialiy in demyelinating neurological diseases progress obviously with episodes between temporary recovery and poor prognosis, related to the life quality. In the complex interaction, the fact that the proteins work in groups, as machineries will play an important role. On the other hand, oxydative stress is a major molecular mechanism underlying all diseases. Epigenetic mechanisms are known important in posttranslational modifications of proteins to be functional. Even single nucleotide polymorphisms (SNPs) in multiple genes interact in complex manner to predispose a Complex Genetic Disease. Remains genomic imprinting, ion channels and transporter disorders and other mechanisms needed to be elucidated. In this presentation, we will focus on and discuss the inheritance, influence and occurence mechanisms of Polygenic Multifactorial Diseases.

2650-Pos

Learning biophysics via modeling and simulation: a course for science and engineering undergraduates

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Undergraduate physical-science curricula are often rooted in pencil-and-paper calculation, despite the fact that most research is done with computers.