Short summary of the activities

Here you can find a short description of the steps students take while experiencing each of this activities translated to English. You can reach the activities with clicking the links: 'CFTR PROTEIN' (the first activity), 'IPNS PROTEIN' (the second activity) and 'AFP PROTEIN' (the third activity) at the upper menu bar.

- The first activity entitled “Exploring the genotype–phenotype relations in Cystic Fibrosis” is a multistep "in-depth" activity composed from two tasks. The discovery of the human gene coding for the Cystic Fibrosis Trans-membrane Conductance Regulator (CFTR) (Riordan et al., 1989) represents a landmark accomplished in human genetics. The students first use the database of protein domains, families and functional sites in Prosite to determine what the functional motifs of CFTR protein are. Then they analyze how F508Del, the most common mutation worldwide responsible for CF, impairs on the protein sequence, structure, function and level. Furthermore, students learn how to test for the presence of CFTR F508Del mutation by utilizing Primer3Plus to design primers for a PCR amplification which is mutation-dependent. In this activity students connect between the micro (genotype: wild type vs. mutated gene and corresponding protein) and macro (phenotype) levels, as well as the relations between sequence, structure and function. They also apply findings of basic research to design diagnostic tool for medical use.
- The second activity entitled "Structure-function relationship in isopenicillin N synthase proteins". The multistep "in-depth" activity composed from four parts activity named “Screening for novel genes involved in antibiotic biosynthesis” and we translated only the fourth part of this activity, as a single step "in-depth" activity composed from one task. In this part the students are invited to use the free 3D molecule viewer Jmol to visualize the three-dimensional (3D) structure of a homologous enzyme (1QJE.pdb), and the related co-factor, substrate and product (Burzlaff et al., 1999). Although students do not discover a gene involved in the biosynthesis of a novel antibiotics, they are able to experience an authentic scientific process first hand.
- The third activity entitled "Structure–function relationship in antifreeze proteins” is a single step "in-depth" activity composed from one task. The students explore she structure-function of antifreeze proteins (following Garnham, Campbell, & Davies, 2011). Students use Jmol to view the crystal structure of antifreeze protein (AFP) from Marinomonas primoryenis, an Antarctic bacterium. They resolve the “anchored clathrate” mechanism by which AFP, which folds as a Ca^{2+}-bound parallel beta helix, irreversibly binds to ice, through contributions of both the hydrophobic effect and hydrogen bonding.

References:

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