Contributions to Design 2 Data (D2D) took place over the Fall 2021 and Spring 2022 semesters at Truckee Meadows Community College. This project introduced students to biotechnological laboratory methods, while assisting a national project in gathering data on protein folding and assisting the predictability of protein folding software algorithms. The overarching goal of this national project is to test the accuracy of protein modeling software predictability in measuring an enzyme's catalytic efficiency (how well the enzyme works) when a single amino acid is substituted with another amino acid and to provide an authentic research experience in the classroom.

In Fall 2021 and Spring 2022, we performed the build and test stages of the D2D project. Novel mutants of Beta-Glucosidase B (BglB) were modeled within a protein folding software called FoldIt and then wet lab procedures were performed. DNA Oligos were ordered after designing mutants in FoldIt. The mutants were built through kunkel mutagenesis and *E. coli* were chemically transformed with the plasmids containing BglB Mutants. The optimization of miniprep helped to increase DNA concentration around twofold and likelihood of confirmed mutations.

BglB proteins were expressed and purified after DNA concentration. Enzyme activity results for our mutant, E406W, suggested that the mutation stopped expression; the other mutants, W325Y and W409N, had lower enzymatic activity (lower catalytic efficiency of 20 vs. 100 mM^{-1} min^{-1} [k_{cat}/K_M] for mutants vs. WT). Protein folding software such as FoldIt are invaluable as they can be used to advance medical or agricultural research such as drug development. This research streamlined the D2D workflow in the classroom, which provides an authentic research experience.