PROTEIN EXPRESSION ANALYSIS OF THE [*PSI*+] and [*psi*-] YEAST STRAINS USING 2-D GEL ELECTROPHORESIS. ***Saiful Effendi Syafruddin***, *Margaret Barlow, Irene Evans*[1], and Thomas Kim*[2] Department of Biological Sciences[1], Department of chemistry[2], College of Science, Rochester Institute of Technology, sxs8836@rit.edu, mlb6932@rit.edu, imesbi@rit.edu, tdksch@rit.edu.*

DNA microarray and Quantitative Real Time Polymerase Chain Reaction (QRT-PCR) were used in previous projects to study changes in the gene expression between two yeast strains, [*PSI*+] and [*psi*-]. The [*PSI*+] strain contains the prion form of the *SUP35* protein, and this protein exists in a different conformation compared to the normal *SUP35* protein. The *SUP35* protein serves as the elongation release factor (eRF3) which functions to terminate the newly synthesized polypeptide chain. Since the protein is expressed in a different conformation (prion conformation) in the [*PSI*+] strain, the translation termination is no longer functional or successful and the read-through of stop codons occurs. The purpose of doing the DNA microarray was to determine whether the protein conformational change in the [*PSI*+] strain has any significant effects and causes differences in the gene expressions between these two strains. The microarray results showed that over 100 genes were over or under-expressed in [*PSI*+] and [*psi*-] strains. The results obtained from the microarray were validated by using the QRT-PCR technique; where every single gene found to be over or under-expressed was analyzed. Now, a yeast gene database containing the results from both studies along with the function of each gene has been generated. Therefore the purpose of this study is to determine whether there are significant differences in protein expression between these two strains. The central dogma of biology is DNA → RNA→protein. Hence, if there are differences in the gene expression between these [*PSI*+] and [*psi*-] strains, there should also be disparity in the proteins produced by these strains. In order to detect protein differences, 2-dimensional gel electrophoresis is used to analyze the protein harvested from both strains. In the first dimension or isoelectric focusing (IEF), the proteins are separated according to their isoelectric points (PI). Following the IEF is the equilibration step where the sulfhydryl group is reduced and alkylated. After being separated according to their PI, the proteins are then separated according to their molecular weight in the second dimension. The results from this project will be compared with the yeast gene changes found earlier to see if gene expression changes translate into similar protein expression changes.