Optional Final Project

Version 1.6

1. Write a report on the protein that has been assigned to you. The report can include essentially any information on your protein that you find interesting.
2. The report should four pages maximum, in 11 point, Calibri font, 1.5 line spacing. Figures and tables should be included as appendices, and should be called in the main text, and do not count in the page limit. Figures should be numbered, with clear figure legends. See [this paper](https://ww2.chemistry.gatech.edu/~lw26/publications/LDW_144.pdf) for examples of figure legends.
3. Use Kegg, the NCBI and other online sources to describe the organism that contains your protein and to broadly characterize the role of your protein in biochemistry and in metabolism and, if relevant, in technology or medicine.
4. Draw out the chemical reaction catalyzed by your protein (do not copy and paste an image from the web). Show all chemical structures and indicate the reaction mechanism.
5. Give the protein sequence of your protein in fasta format.
6. Use Blast to determine the distribution of your protein over phylogeny.
7. Use Jane Richardson’s Molprobity page to determine the quality of the 3D structure of your protein and to construct a phi/psi map of your protein. What does the phi/psi map tell you about your protein?
8. Construct a hydropathy plot for your protein. What does the hydrophathy plot tell you about your protein?
9. Construct a Pymol script that illustrates important structural and functional aspects of your protein and its mutants and phylogenetic variants. Analyze the molecular interactions of functional regions such as the catalytic site or protein-ligand interface, or protein-protein interface.
10. [Omit this] Use the 3D structure of your protein to design some mutants should inactivate your protein. These mutations would change the interactions of your protein with the substrate or the transition state of the reaction catalyzed by your protein
11. [Omit this] Fold your mutants using swiss pdb viewer or alpha fold and visualize the mutant structures in Pymol.
12. [Omit this] Use SNAPGene to design a construct to overexpress your protein in *E. coli*, fused to a hexa-his tag, or some other tag of your choice.
13. References. Use Endnote to format the citations in your report (Use PNAS format). Endnote can be downloaded from OIT.