ProtParam Protein Analysis Project

# Project Overview

This project demonstrates the use of ExPASy ProtParam for analyzing protein sequences. The repository contains example protein sequences, ProtParam analysis results, and detailed notes explaining ProtParam tool features for beginners.

## Repository Structure

ProtParam-Protein-Analysis/  
│── README.md  
│── data/  
│ └── sample\_sequence.fasta  
│── results/  
│ └── protparam\_output.txt  
│── docs/  
│ └── ProtParam\_Notes.md

# About ProtParam

ProtParam is an ExPASy (Expert Protein Analysis System) tool that allows users to calculate various physical and chemical parameters of proteins from their amino acid sequences.

# Key Features of ProtParam

* 1. Number of Amino Acids – Counts total residues in the protein.
* 2. Molecular Weight – Calculates the molecular mass of the protein.
* 3. Theoretical pI – Estimates the isoelectric point (pH at which the protein has no net charge).
* 4. Amino Acid Composition – Shows frequency of each residue in percentages.
* 5. Atomic Composition – Carbon, Hydrogen, Nitrogen, Oxygen, Sulfur counts.
* 6. Extinction Coefficient – Predicts absorbance at 280 nm.
* 7. Estimated Half-life – Predicts protein stability across organisms (mammals, yeast, E. coli).
* 8. Instability Index – Determines whether the protein is stable (<40 = stable).
* 9. Aliphatic Index – Measures thermostability based on aliphatic residues.
* 10. GRAVY (Hydropathicity) – Indicates overall hydrophobic or hydrophilic nature.

# Results: Normal vs Mutant Protein

Normal Protein:  
- Number of amino acids: 53  
- Molecular weight: 5339.12  
- Theoretical pI: 4.10  
- Negatively charged residues: 5  
- Positively charged residues: 2  
- Instability index: 25.75 (Stable)  
- Aliphatic index: 108.49  
- GRAVY: 0.628  
  
Mutant Protein:  
- Number of amino acids: 53  
- Molecular weight: 5324.10  
- Theoretical pI: 3.77  
- Negatively charged residues: 5  
- Positively charged residues: 1  
- Instability index: 27.35 (Stable)  
- Aliphatic index: 115.85  
- GRAVY: 0.774  
  
Key Observations:  
- Slight reduction in molecular weight in mutant.  
- pI shifted from 4.10 → 3.77.  
- Leucine count increased, Lysine reduced.  
- Protein remains stable despite mutation.

# Applications of ProtParam

* Protein property prediction before experimental work
* Mutation effect analysis
* Comparative proteomics
* Protein engineering & drug design