

In silico analysis and immunodiagnosis of different amino acids using homology modeling

T. Jayalakshmi*, K. N. Vardhan, R. Priya, K. Vijayalakshmi

ABSTRACT

Introduction: Amino acids are very small biomolecules with various properties. Predicting the physiochemical properties of protein and interpreting its function are of great importance in the field of medicine and life science. **Materials and Methods:** Python is a high-level language. Python is product-oriented programming language. ASAP calculates various physiochemical properties that are needed for *in vitro* experiments. ASAP uses normalization values that increase the sensitivity of the tool. **Results and Discussion:** Protein is the building blocks of the body. As pI was one of the major factor affecting the protein interactions, a clear view for a particular protein should be known. Aliphatic index is calculated by ASAP. **Conclusion:** It is an efficient tool for genomics and proteomics and has its applications in system biology.

KEY WORDS: Amino acids, Antigenicity, Normalization and protein modeling

INTRODUCTION

Amino acids are very small biomolecules which compromise building blocks for proteins. It may be decoded by messenger RNA with its biochemical properties and codes for enzyme or proteins.^[5] Immunodiagnosis mainly possesses conformational epitope with its functional molecule^[3] and recognizes physical stability by homology modeling,^[4] which can act with anti-protein antibodies. In clinical research, the number of vaccines has been identified which binds to protein-ligand interactions and antigenic protein may be highly effective for treating cancerous cells.^[3]

MATERIALS AND METHODS

Python

Python is a high-level language. Python is product-oriented programming language.^[12]

It has many object-oriented and structural-oriented language^[1] and also used in medical informatics for hospital management information system.^[2]

It also produces errors when a complex product is identified and can be used in many research-

oriented applications.^[6] It can also be used in amino acid fractions and used to compare side chain interaction.^[7,8]

RESULTS

Python Command Prompt

The result shows the presence of user and database.

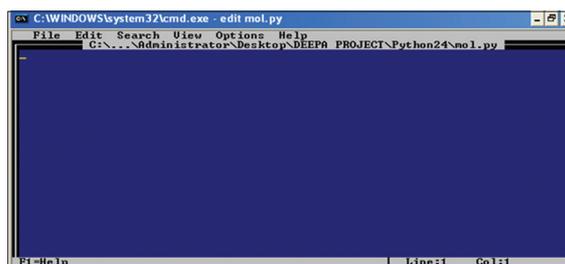


Figure 1: Command mode of python

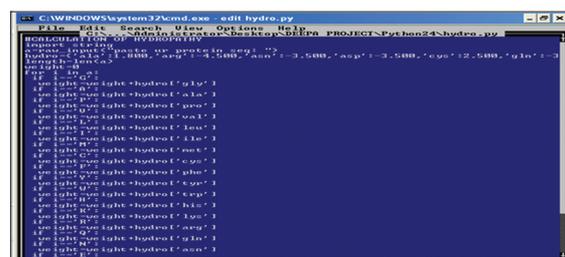


Figure 2: Parameter value for each amino acid and calculates the GRAVY value of the protein

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Department of Bioinformatics, Bharath University, Chennai, Tamil Nadu, India

*Corresponding author: T. Jayalakshmi, Department of Bioinformatics, Bharath University, Chennai, Tamil Nadu, India. Phone: +91-9940096229. E-mail: jayamaniraja07@gmail.com

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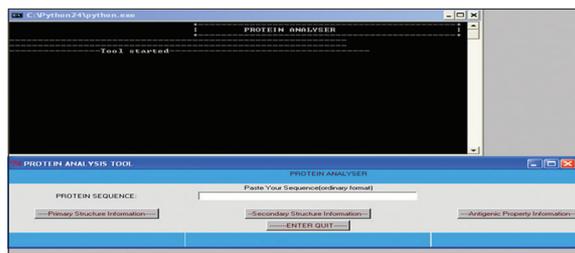


Figure 3: Homepage of ASAP

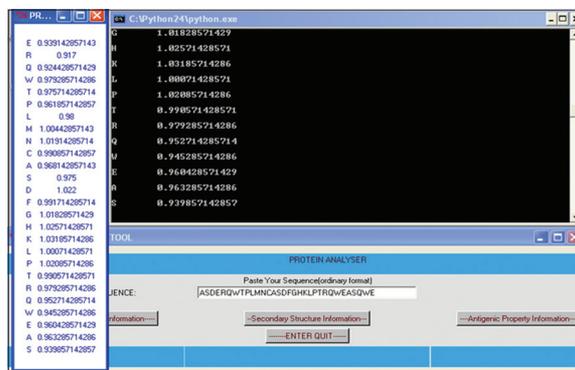


Figure 4: Antigenicity prediction

The Figures 1-4 represents the target protein and amino acid residue proteins.

DISCUSSION

Protein is the building blocks of the body. As pI was one of the major factors affecting the protein interactions, a clear view of pI for a particular protein should be known.^[10] Aliphatic index is calculated by ASAP. Tertiary structure folding is based on the secondary structure. Hence, the secondary structure is the major structural elements in proteins. The ASAP predicts the secondary structure of the protein using Chou–Fasman algorithm.^[9,10]

CONCLUSION

The Tool ASAP allows the user to predict the primary structural properties and the epitope prediction for the given protein sequence. It presents the output in the tabular frame.^[9] The tabular output for primary structure analysis shows the physiochemical properties of the protein. It is an efficient tool for genomics and proteomics and has its applications in system biology.

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