Prediction and calculation of physiochemical properties using structural bioinformatics and ASAP tools

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ABSTRACT

Amino acids are very small bio-molecules with various properties. Predicting the physiochemical properties of protein and interpreting its function is of great importance in the field of medicine and life science. ASAP calculates various physiochemical properties that are needed for *invitro* experiments. ASAP uses normalization values that increase the sensitivity of the tool.

KEYWORDS: Amino acids, antigenicity, normalization and Protein modeling.

1. INTRODUCTION

Amino acids are very small biomolecules which compromise buiding blocks for proteins. It may be decoded by messanger RNA with its biochemical properties and codes for enzyme or proteins Immunodiagnnosis mainly possess conformational epitope with its functional molecule. And recognize physical stability by homology modelling, which can act with anti-protein anti-bodies. In clinical research number of vaccines have been identified which binds to protein-ligand interactions and antigenic protein may be highly effective for treating cancerous cells.

2. MATERIALS AND METHODS

Python: Python is a high-level language. Python is product oriented programming language. It has many object oriented and structural oriented language and also used in medical informatics for hospital management information system. It also produces errors when a complex product is identified and can be used in many research oriented applications. It can also be used in amino acid fractions and used to compare side chain interaction.

3. RESULTS

Python command prompt:



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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Figure.4. Antigenicity Prediction

Figure.3. Homepage of ASAP

DISCUSSION

Protein is the building blocks of the body. As pI was one of the major factor affecting the protein interactions, a clear view of pI for a particular protein should be known. Aliphatic index is calculated by ASAP. Tertitary structure

Tool start

BOTEIN SEQUENCE

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folding is based on the secondary structure. Hence secondary structure are the major structural elements in proteins. The ASAP predicts the secondary structure of the protein using chou Fasman algorithm.

4. 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. The tabular output for primary structure analysis show the physiochemical properties of the protein. It is an efficient tool for genomics and proteomics and has its application sin system biology.

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