

# P<sup>3</sup>-Protein Property Predictor

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**Abstract-** Proteins are the most flexible macro molecules in living frameworks and serve critical capacities in basically all natural procedures. The main reason to develop this predictor is to provide raw data of the advanced protein properties in very less time. I got this idea of developing this protein property predictor while doing my academic project where I have spent a lot of time in collecting the raw data, analyzing and tabulating it. By using this protein property predictor we can reduce the time of collecting the raw data. This predictor provides numerical data in very less time. The users also provided with the script form of the data upon request. It provides access to a variety of databases and analytical tools dedicated to proteins and proteomics. ExPASy databases include SWISSPROT and TrEMBL, SWISS-2DPAGE, PROSITE, ENZYME and the SWISS-MODEL repository. Analysis tools are available for specific tasks relevant to proteomics, similarity searches, pattern and profile searches, post-translational modification prediction, topology prediction, primary, secondary and tertiary structure analysis and sequence alignment. A good user interface, that is intuitive yet powerful, is essential when configuring and managing network security components. A browser based Web User Interface (WUI) represents a good way to provide this. Administrators and users already know how to use a web browser to access services. Providing network device configuration in this way builds on this experience and gives them a familiar, yet rich, way to configure and manage network resources. The Web user interface is the easiest type of management to use.

## I. INTRODUCTION

Because of its simple point-and-select nature, it gives the end user a jumpstart into the management of the Juniper firewall. The interface is very straightforward. On the left-hand side of the browser is the menu column. From here you can choose from the various configuration options. This menu can be either Dynamic Hypertext Markup Language (DHTML) based, the default, or Java based. The functionality is the same, but the look and feel is slightly different. By default, the WebUI is configured to work over only the Hypertext Transfer Protocol (HTTP). It can, however, be configured to work over Hypertext Transfer Protocol Secure (HTTPS). This provides a mechanism to secure your Web management traffic. Most of the popular Web browsers such as Internet Explorer, or Firefox work well with it. User interface design isn't just about buttons and menus.

**Keywords-** Bioinformatics, Protein Properties, Numerical-data Script-data, Less-time.

## II. MODE OF USAGE

1. If the user needs the limited properties (less than 5) then click on the button named "**MANDATORY DOCUMENT FOR LIMITED PROPERTIES**" and fill the document
2. If the user needs the entire properties then click on the button named "**MANDATORY DOCUMENT FOR ENTIRE PROPERTIES**" and fill the document
3. Select the **FASTA -SEQUENCE** from NCBI and provide the sequence in the space provided
4. Select the properties and send your information to authors gmail p3.useraccess@gmail.com
5. For doubts and clarifications please send your query to authors personal gmail divya181001@gcu.ac.in

## III. LINK TO ACCESS

P<sup>3</sup> computes various physico-chemical properties that can be deduced from a protein sequence. No additional information is required about the protein under consideration. The protein can either be specified as a Swiss-Prot/TrEMBL accession number or ID, or in form of a raw sequence. White space and numbers are ignored. If you provide the accession number of a Swiss-Prot/TrEMBL entry, you will be prompted with an intermediary page that allows you to select the portion of the sequence on which you would like to perform the analysis. The choice includes a selection of mature chains or peptides and domains from the Swiss-Prot feature table (which can be chosen by clicking on the positions), as well as the possibility to enter start and end position in two boxes. By default (i.e. if you leave the two boxes empty) the complete sequence will be analyzed.

**Note: It is not possible to specify post-translational modification for your protein, nor will ProtParam know whether your mature protein forms dimers or multimers. If you do know that your protein forms a dimer, you may just duplicate your sequence (i.e. append a second copy of the sequence to the first), as all computations performed by P<sup>3</sup> are based on either compositional data, or on the N-terminal amino acid. Follow this link to access (<https://divyap3.htmlsave.net>). The Example output can be seen in this link (<https://sendeyo.com/en/2d43b27f95>)**

## IV. IMPORTANT TERMS

S.no	Name of the Property	Description
01	SAP.estme	Solvent Affordability of the protein(0%,95%,5%,25%)
02	MCR.estme	Membrane Connecting regions
03	UNEXPOSE.estme	Percentage proportion of the Buried residues (90-95%)
04	MFBR.estme	Molar fraction of the buried residues
05	PropTFA.estme	Percentage probability in Trifluoroacetic acid
06	INDEX3.4.estme	Significance of protein at pH 3.4
07	rcHPLC.estme	Retention coefficient in HPLC at pH 2.1
08	MOB.estme	Mobility of the amino acids
09	CONS.estme	Constants from HPLC peptide retention
10	HP.estme	Hydration potential at 25°C
11	CONTACT.estme	Contact energy derived from three dimensional data
12	HYDRO.estme	Hydrophaticity
13	RF.estme	Identified/Recognised factors
14	P.estme	Polarity
15	BULK.estme	Massiveness of the protein
16	PSSP.estme	Protein Secondary Structure Prediction
17	PSA.estme	Peptide signal analyser
18	CPTP.estme	Concurrent protein topology predictor
19	DBC.estme	Disulphide bond connectivity
20	BCAD.estme	B-cell antigen determinants
21	PA.estme	Protein Antigenicity
22	SSP.estme	Similarity score prediction
23	AWt.HE-estme	Atomic weight ratio of the hetero elements
24	AFL.estme	Average flexibility index
25	CPBS.estme	Conformational parameter for beta sheet
26	CPaH.estme	Conformational parameter for alpha helix
27	MWt.estme	Molecular weight of the protein
28	PHF.estme	Protein helices forecasting
29	IMPP.estme	Integral membrane prediction of the protein
30	ASIMP.estme	Analysis situs of the integral membrane protein

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