Name of Experiment: Secondary and Tertiary Structure prediction of protein / Nucleotides.

Experiment No: 5

Date: 10/1/24

Experiment Result:

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Aim:- To predict the secondary & tertiary Structure of protein using relavant software tools.

Introduction:-

Some of the important secondary & tertiary Structure prediction tools available at EXPASY.org

AGADIR:- An algorithm to predict the helical contents of peptides.

APSSP:- Advanced protein secondary structure prediction server.

CFSSP:- Chan and amp : Fasman secondary Structure prediction server.

HNN:- Heirarchial Neural Network method (Quemeur, 1997).

GOR:- Garnier at 1996.

HTMSRAP:- Helical Transmembrane segment rotational angle predictio

Jpred:- A conesenses method for the protein secondary structure at university of Dundee.

PSI pred:- Various protein structure prediction method at bloomsbury center for bioinformatics.

SOPMA:- Geourjan and Delage, 1995.

→ The PSI pred protein Structure prediction server aggregates several of our structure sequence, perform the predition of their choice and receive the results of the prediction vice e mail. You may

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- detect one of three prediction methods. to apply to your sequences.

PSI pred :- A highly accurate method for the protein secondary structure prediction.

MEMSAT and MEMSATSVM :- widely used transmem -brane topology prediction method and one of GENTHREADAR.

PGENTHREADAR, and PDOMTHREADAR - sequence profile based fold recognition methods.

*) Query :- Fibrinogen

*) URL :- Jpred → Compbio.dundee.ac.uk/jpred/ (secondary structure prediction)

Alphafold :- https://alphafold.ebi.ac.uk/

Procedure :-

i) Jpred

*) Log on to NCBI and retrieve a protein sequence in FASTA format.

*) Log on to compbio.dundee.ac.uk/pred/

*) paste the retrieved protein sequences.

*) Click on make prediction button.

*) Hits of the given query with respect to is obtained Click on continue option.

*) Result will be displayed.

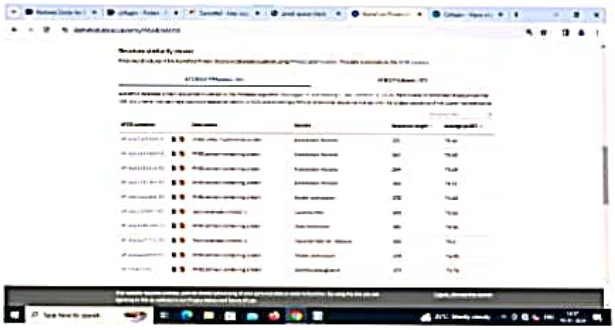
* In this annotation indicates that THEI jury was involved to rationalize significantly different primary prediction.
* (-) → other type of secondary structure.
* THEI. conf → the confidence estimate for prediction Lupus 14 & 18 coded prediction sequence. these are binary prediction for each location.

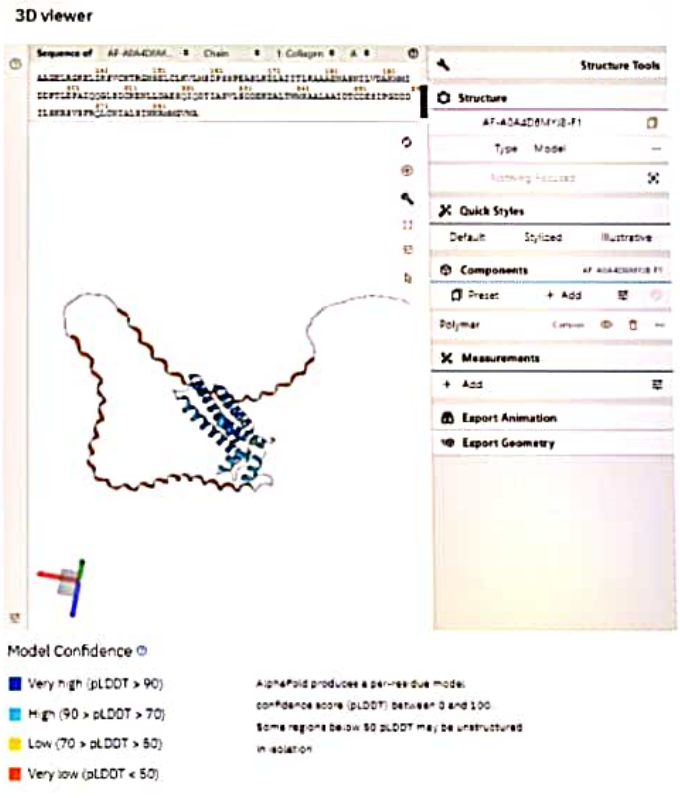
b. Alpha fold:-

* It is AI system predicts protein 3D structure from it the tool contains 200 million entries with broad coverage of uniport & pdb the alpha fold is able to produce highly accurate side chain when backbone is accurate, considerably improves over template even when strong template are available.
→ The plDDT measure of confidence is obtained on a scale of 0-100 it's a measure of per residue estimate of its confidence.

P - 10
C - 10
V - 10
R - 15

45




## keratin, partial [Paralichthys olivaceus]

GenBank: BAB16373.1

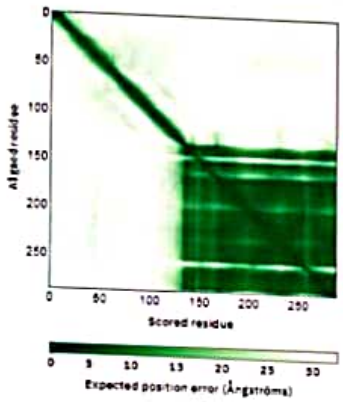
GenPept Identical Proteins Graphics

>BAB16373.1 keratin, partial [Paralichthys olivaceus]

KNQRELEAWLQTQSESLSKEVAVKTEVLQTTKAEISDLRRTMQNLEIELQSQLSMKAALEGTLSDTECRY

SMQLQSLQIQVTSLEEQLMQLRADMERQNQEYNILLDIKTRLEMEIAEY

**Predicted aligned error (PAE)**




Click and drag a box on the PAE viewer to select regions of the structure and highlight them on the 3D viewer.

PAE data is useful for assessing inter-domain accuracy – go to Help section below for more information.

[redacted]

# Jpred 4

Incorporating Jnet

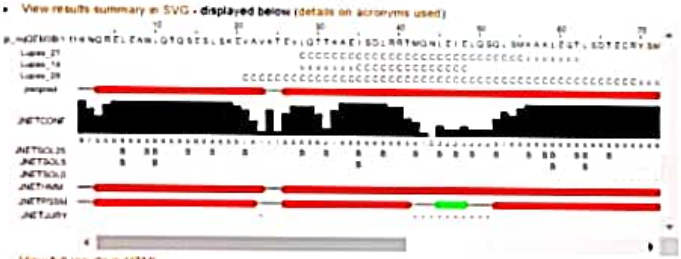
## A Protein Secondary Structure Prediction Server

Home | REST API | About | FAQ | Help & Tutorials | Monitoring | Contact | Publications

## Results

**After much trouble and strife Bob the scheduling penguin has retrieved your results! Rejoice. For your pleasure the following viewing options are available. You may bookmark this page for future reference although data is not kept on the server for more than two days**

- View results summary in SVG - **displayed below** (details on acronyms used)



- View full results in HTML
- View simple results in HTML
- View results in PDF
- View results in Jalview (**Link to a separate page with the Jalview Java Desktop application**)
- View everything in a results directory (**details on data each file contains are available through** README file)
- Get all files in TAR.GZ archive