International Journal of Science and Research (IJSR)
ISSN (Online): 2319-7064
Index Copernicus Value (2015): 78.96 | Impact Factor (2015): 6.391

Tau Protein: Neurological Associated with Parkinson's and Alzhiemer Disease, Study using Structural Prediction Methods (Homology Modeling and Secondary Prediction Methods)

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Abstract: ***Comparative study in Bioinformatics can be based on different aspects like function, structure and sequence which enhance the study. 3D Structure prediction is one of the exhaustive process in the field of Bioinformatics, once predicted will able to target the of molecule and can be comparatively analysed. For structure analysis tau protein has been targeted one of the protein that stabilizes microtubules. They are abundant in neurons of the central nervous system and are less commonly found on other region.***

Keywords: Structure prediction, Tau, GOR, Homology Modeling

1. Introduction

Tau proteins are proteins that stabilize microtubules. They are abundant in neurons of the central nervous system and are less common elsewhere, but are also expressed at very low levels in CNS astrocytes and oligodendrocytes. Pathologies and dementias of the nervous system such as Alzheimer's disease and Parkinson's disease are associated with tau proteins that have become defective and no longer stabilize microtubules properly. The tau proteins are the product of alternative splicing from a single gene that in humans is designated MAP (microtubule-associated protein tau) and is located on chromosome 17. The tau proteins were identified in 1975 as heat stable proteins essential for microtubule assembly and has since been characterized as an intrinsically disordered protein. Tau proteins are proteins that perform the function of stabilizing microtubules.

Figure 1

2. Programs

The Protein Data Bank (PDB) is a crystallographic database for the three-dimensional structural data of large biological molecules such as proteins and nucleic acids. The PDB is a key resource in areas of structural biology, such as structural genomics. Most major scientific journals, and some funding agencies, now require scientists to submit their structure data to the PDB. The file format initially used by the PDB was called the PDB file format. Swiss-Pdb Viewer (SPdbV) is an easy-to-use and powerful molecular modeling program. In addition to its many built in features, it is tightly linked to Swiss-Model.

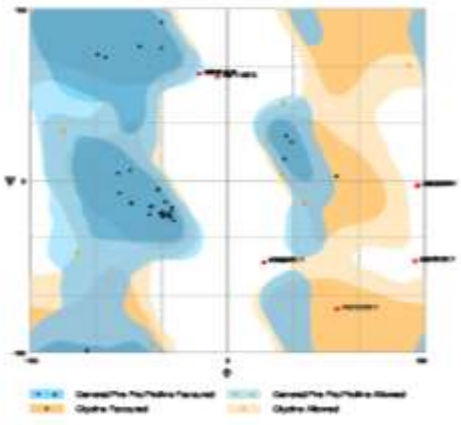

Figure 2

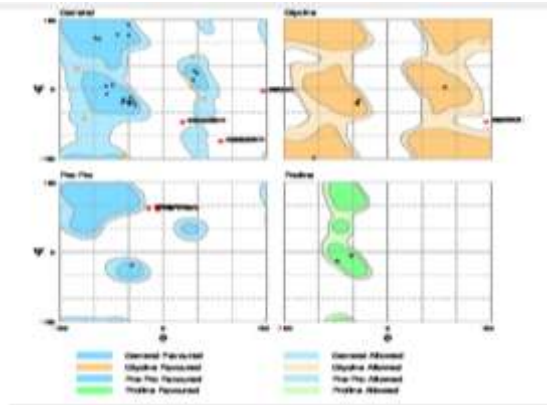

Figure 3

Homology modeling, also known as comparative modeling of protein, refers to constructing an atomic-resolution model of the "target" protein from its amino acid sequence and an experimental three-dimensional structure of a related homologous protein (the "template"). There are two ways of doing homology modelling: The "First Approach Mode" lets you paste a primary sequence, and if anything goes well, you will get a model. The "Project Mode" lets you provide your own manually improved alignment.

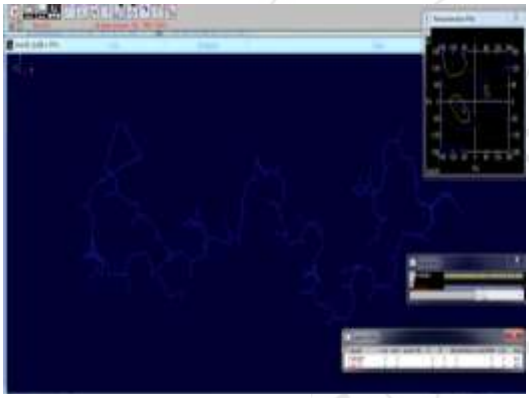

Figure 4

Information theory approaches are popular in secondary structure prediction, and are epitomized by the so-called GOR Method, which takes its name from the last names of the authors who originally developed it (Garnier, Osguthorpe, and Robson, 1978). The theory began as essentially a more rigorous method than calculating Chou-Fasman-like propensities for calculating the probability of a given amino acid assuming a given secondary structure element.

Figure 5

PDBsum is a database that provides an overview of the contents of each 3D macromolecular structure deposited in the Protein Data Bank. The original version of the database was developed around 1995 by Roman Laskowski and collaborators at University College London. As of 2014, PDBsum is maintained by Laskowski and collaborators in the laboratory of Janet Thornton at the European Bioinformatics Institute (EBI).

Figure 6

Figure 7

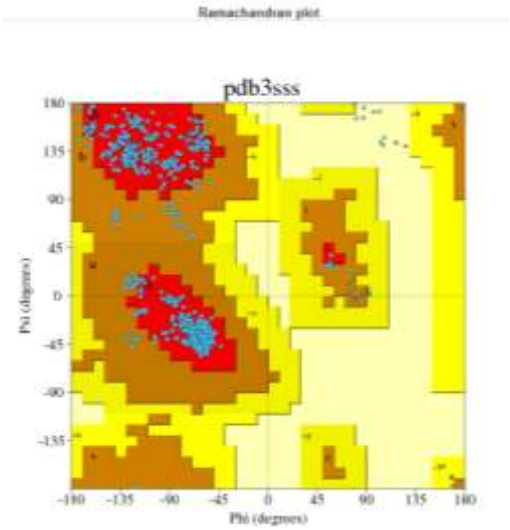

Figure 8

Table 1

Ramachandran Plot statistics		
	No. of residues	%
Most favoured regions [A,B,L]	494	91.70%
Additional allowed regions [a,b,l,p]	45	8.30%
Generously allowed regions [~a,~b,~l,~p	0	0
Disallowed regions [XX]	0	0
Non-glycine and non-proline residues	539	100%
End-residues (excl. Gly and Pro)	12	
Glycine residues	54	
Proline residues	18	
Total number of residues	623	

3. Conclusion

We tried to find the similar sequence and structure based on tau protein (controls the central nervous system), target was to find the exact fragments works like tau shown in fig 4.

Based on the result obtained by applying structure prediction methods and similarity finding 19 different fragments obtained which shows the similarity based on E-Value, and structure similarity based on homology modeling and implementing GOR (Garnier, osguthorpe, Robson method used for secondary structure elements presence and Ramachandran to examine the angles coordinates, of Phi and Psi which has been achieved and ramachandran plot statistics also shown in Table no.1.

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