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COMPARATIVE STUDY OF APP PROTEIN ASSOCIATED WITH ALZHEIMER'S DISEASE IN DIFFERENT ORGANISMS USING STRUCTURE PREDICTION METHOD (HOMOLOGY MODELING) AND ANALYSIS OF THEIR NETWORK PATHWAYS

[1]Sumedh Choukidar, [1]*Prasad Choukidar and [2]Dr. Sanjay Harke

[1]Institute of Biosciences and Technology, MGM Campus, Aurangabad.(M.S) 431001.
[2]MGM's G.Y Pathrikar college of C.S and I.T., MGM Campus, Aurangabad.(M.S) 431001.

***Corresponding Author: Prasad Choukidar**

Institute of Biosciences and Technology, MGM Campus, Aurangabad.(M.S) 431001.

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ABSTRACT

Comparative study in Bioinformatics is based on different aspects like sequence, structure and function which enhance the study. Protein structure prediction refers to generating 3 dimensional models from Amino acid sequence using computational algorithms. for structure analysis App protein has been targeted, plays a central role in the pathophysiology of Alzheimer's disease. Further, we studied the network of 'App'(Amyloid precursor protein) using STRING database as a study we took Different organism samples like Rattus norvegicus, Xenopus tropicalis, Mus Musculus and Homo sapiens. The aim of this paper to find the common protein associated with 'App' protein.

KEYWORDS: App protein, Structure prediction, STRING Database.

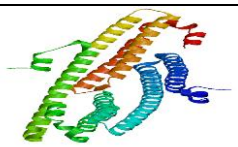
INTRODUCTION

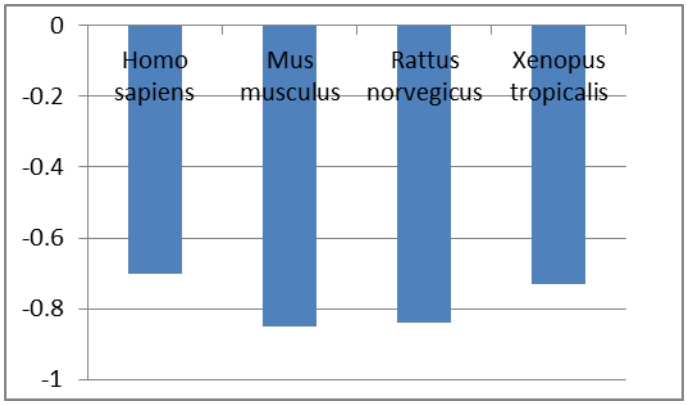
APP gene makes a protein called amyloid precursor protein, it helps in the movement of nerve cells during development this protein is found in the central nervous system. APP is a type 1 transmembrane protein whose proteolysis gives amyloid ß (Aß) peptides. generally ß-secretes and y-secretes increase the levels of Aß. The ß amyloid precursor protein gene located on chromosome 21 the rare mutations in APP gene cause Alzheimer Disease. The present study revealed that proteins: presenilin-1 (chromosome 21), presenilin-2 (chromosome-2) and amyloid precursor protein play a significant role in the pathogenesis of Alzheimer's Disease.

Programs: Bioinformatics provides the Different softwares through which the target sequences are obtained in a specific file format using the biological Database (ncbi). Obtained sequences are processed for to predict the structure of the sequence for homology modeling using the Swiss model server. The neural network pathways are created using STRING Database.

Structure prediction: protein tertiary structure prediction by Homology modelling is a knowledge based method, it predicts the new protein structure from its sequence. Protein structure prediction is most important for making new drugs and novel enzymes. The Q-Mean & Z- score provides the structural features of the model the Q-Mean & Z- score around zero (0) indicates good Quality of structure[Graph:1].

Table 1: Showing Predicted structure of 'App' protein with it's Q-mean score.

Sr.no	Organism name	NCBI accession	Protein structure	Q-mean Score
1	Homo sapiens	AAH65529.1		-0.70
2	Mus musculus	AAH70409.1		-0.85
3	Rattus norvegicus	NP_062161.1		-0.84
4	Xenopus tropicalis	AAH75266.1		-0.73



GRAPH: 1

STRING Database: the STRING (search tool for the retrieval of interacting genes/proteins), it is freely accessible database, contains information from many sources including computational prediction methods and public text collections. it is the database of known and predicted protein-protein interactions. protein-protein interactions are characterized as transient or stable and both types of interactions can be strong or weak. protein-protein interaction plays a key role in a variety of cellular functions including signal transduction, cycle progression and metabolic pathways.

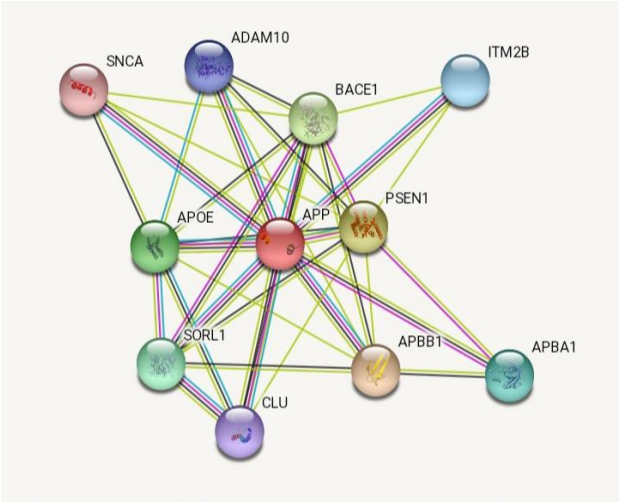


Fig: Neural network pathway of APP protein (Homo Sapiens).

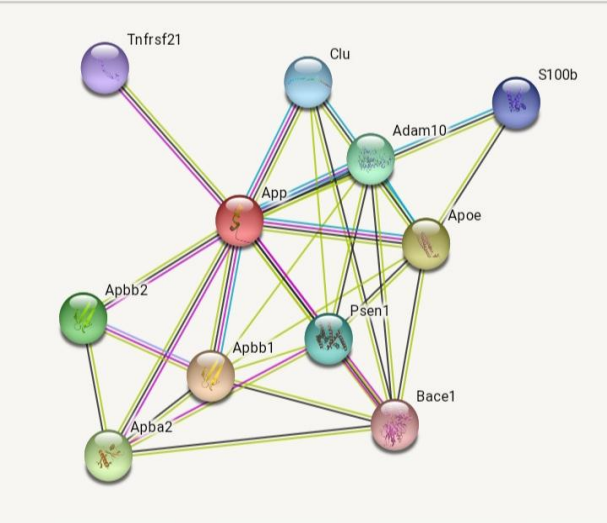


Fig: Neural network pathway of APP protein (Mus Musculus).

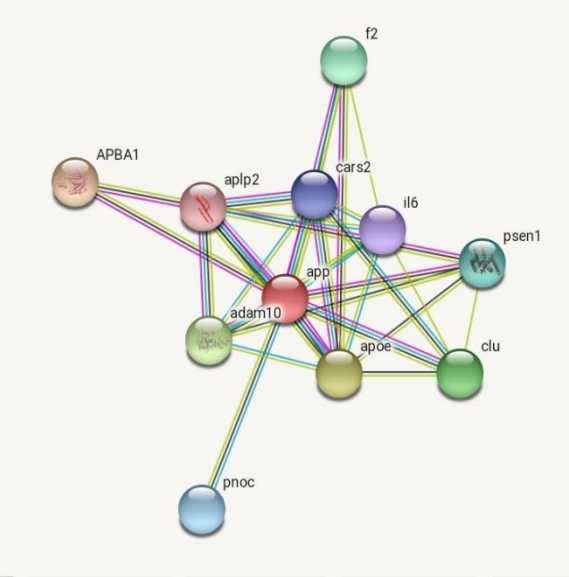


Fig: Neural network pathway of APP protein (Xenopus tropicalis).

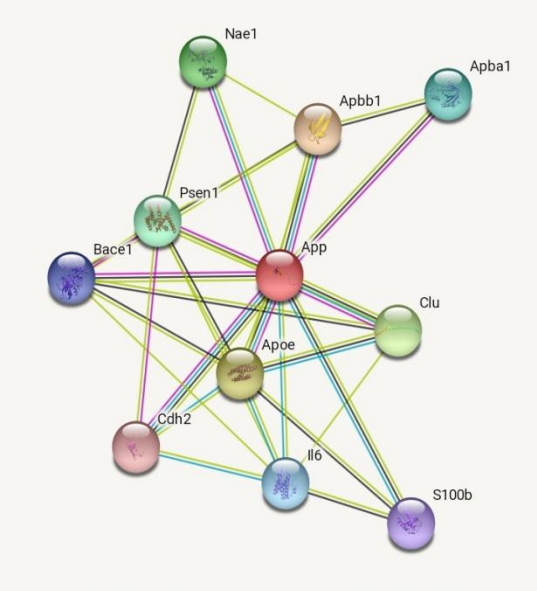


Fig: Neural network pathway of APP protein (Rattus norvegicus).

RESULT AND CONCLUSION

We tried to find the network of four pathways associated with Alzheimer disease in Homo sapiens, Mus Musculus, Rattus norvegicus and Xenopus tropicalis obtained from STRING Database. Results are shown in the above figures, the protein Apoe and psen1 is a common protein in the pathways of Mus Musculus, Homo sapiens, Xenopus tropicalis and Rattus norvegicus.

Hence, if Apoe and psen1 protein considerd as a target protein and it potential inhibitors could be found it will lead to inhibit or cure the Alzheimer Disease.

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