

Identification Of Calcium Signaling Proteins involved in the AD by In-silico Approach and Confirmation through Precise Animal Model.

Kesavan Swaminathan Jayachandran

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Bioinformatics, Bharathidasan University, Tiruchirappalli, India.

This research poster shows the application of Bioinformatics tools for the accurate prediction of our target proteins in the multiple signaling pathways, which reduces the time, cost and labor significantly. Many of our research communities still follow the conventional way of reaching the target proteins through several wet lab experiments, which may be used for the confirmation instead of prescreening as presented here.

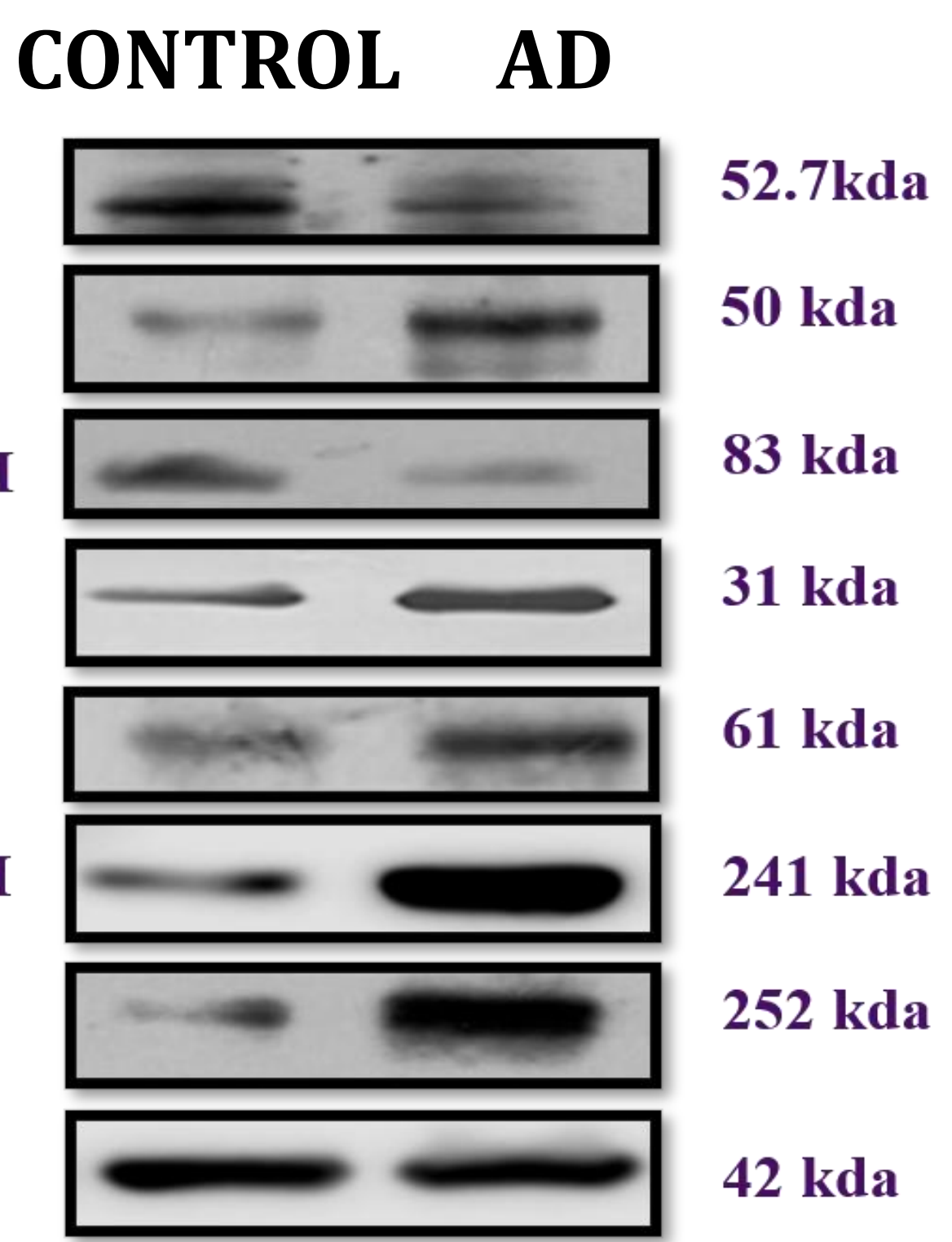
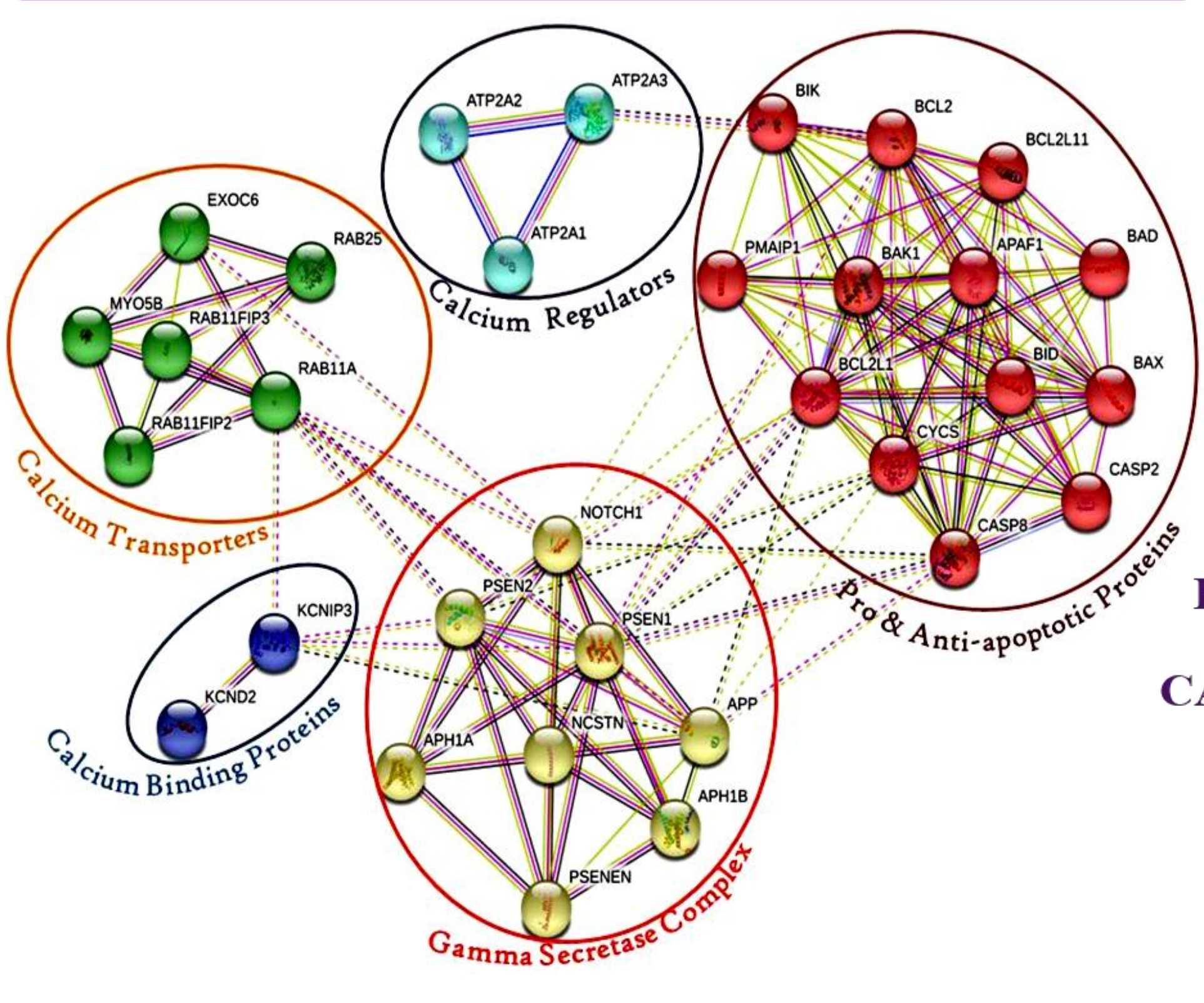
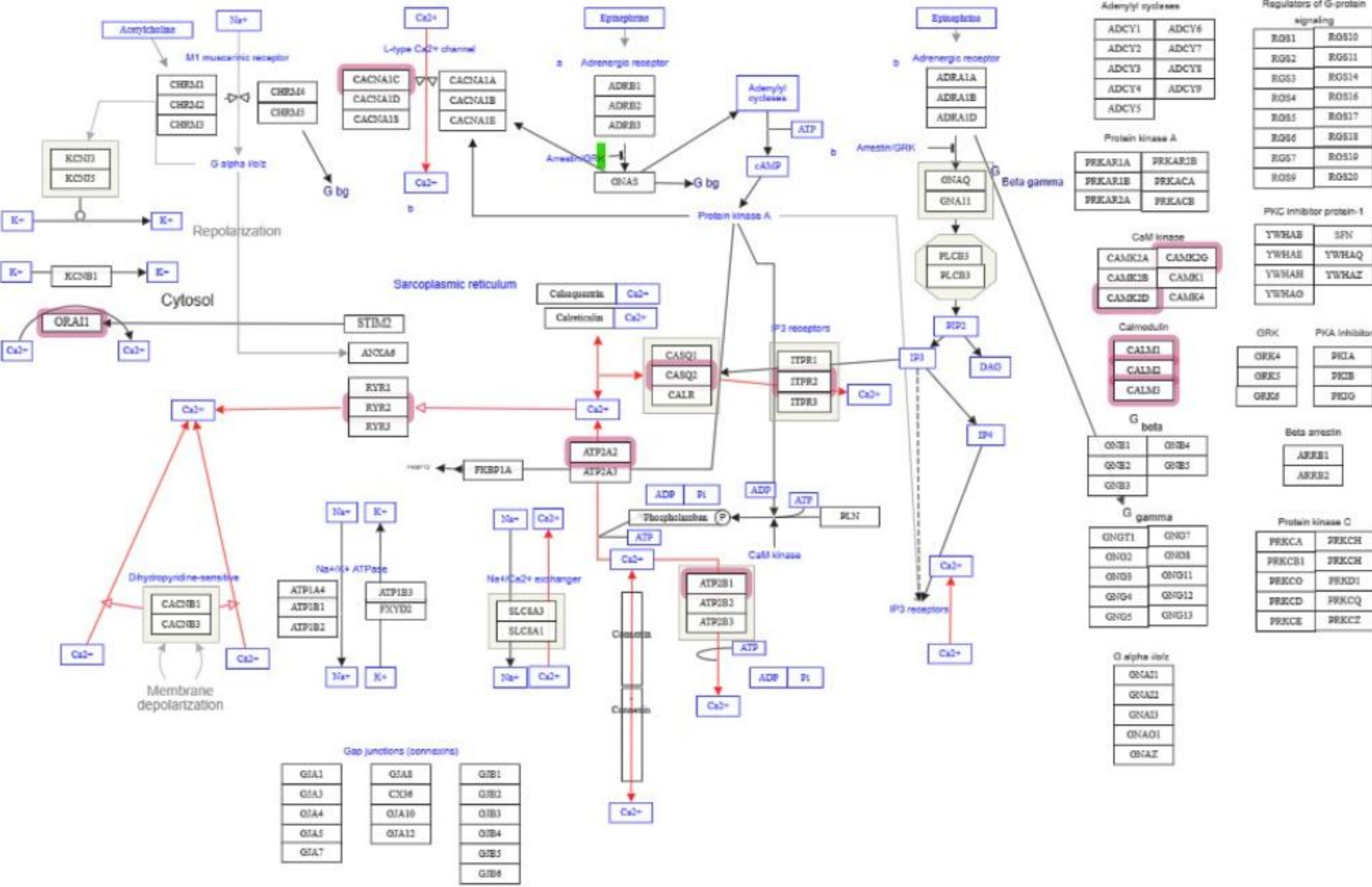
INTRODUCTION

- Alzheimer’s disease is the major cause of memory loss in the aged population.
- Two known mechanism namely tau phosphorylation and amyloid plaque formations are considered as a broad categories of AD investigations.
- In both conditions, calcium signalling imbalance plays a important role, which needs to be explored in order to understand the mechanism of AD development.
- Keeping the above fact in mind, the work is designed to explore the calcium imbalance in the combined in-silico and *in-vivo* AD induced model experimental rat model. give image for this

METHODOLOGY



RESULTS



List of Identified 24 Proteins through Bioinformatics approach.

Protein	Protein
•ATP2A2	•TRPC3/6
•RYSR2	•ITPR2
•CACNA1C	•ATP2B1
•SLC8A1	•VDAC1
•CAMK2D	•CACNA1H
•CAMK2G	•MCU
•CALM1,2,3	•NOS2
•PPP3CA	•NOS3
•PLCB4	•PLCB2
•PDGFD	•AMK2
•ORAI1	•FGF16
•CASQ2	•FGF23

CONCLUSION

- The above calcium signaling protein levels were significantly upregulated with PS2 overexpression compared to PS1, which raises several questions regarding the correlation between calcium imbalance and PS2 overexpression. Several reports suggest that PS2 expression is highly correlated with apoptosis, and Alzheimer’s disease is also associated with the loss of several active neurons in the brain through apoptosis. A detailed study is in progress to clearly understand the association between PS2 overexpression and calcium imbalance.
- Conclusion: The data obtained shows that there is a significant probability of getting reliable results while using the in-silico model for accurate predictions.

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CONTACT DETAIL

Dr. K.S. JAYACHANDRAN
Assistant Professor
Department of Bioinformatics
Bharathidasan University
Tiruchirappalli-620024, India.
Phone(Mobile) :+918667618604
Mail ID: s.jayachandran@bdu.ac.in

