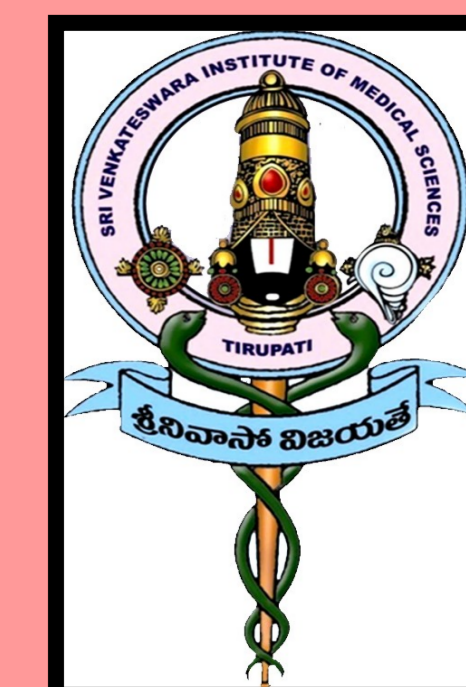




Docking studies to explore novel inhibitors against human beta-site APP cleaving enzyme (BACE-1) involved in Alzheimer's disease



¹S.Anjum Mobeen*, ²Manne Munikumar, ²Amineni Umamaheswari**

¹ Dept. of Biotechnology & Bioinformatics, Yogi Vemana University, Kadapa- 516001. ²Bioinformatics Centre, Department of Bioinformatics, SVIMS University, Tirupati -517507.

*Presenting Author, ** Corresponding Author, Email: svims.btisnet@nic.in

- K**
E
Y
P
O
I
N
T
S
- ⇒ Alzheimer's disease is an intractable neurodegenerative disorder, characterized by the formation of senile plaques and neurofibrillary tangles (NFTs) which are the pathological hallmarks of the disease particularly in elder persons of age 65 and above.
 - ⇒ Beta-site APP cleaving enzyme (BACE-1) is an aspartyl protease, which initiates the processing of amyloidogenic pathway and is responsible for the formation of Senile plaques, a causative agent of the disease.
 - ⇒ Elevated level of BACE-1 causes the accumulation of insoluble form of A β peptides.
 - ⇒ Five published inhibitors of BACE-1 such as thiazolidinediones, rosiglitazone, pioglitazone, Sc7 and tartaric acid are available with poor pharmacological properties. Therefore, a computational approach was undertaken to design novel inhibitors against human BACE-1 with good pharmacological properties.

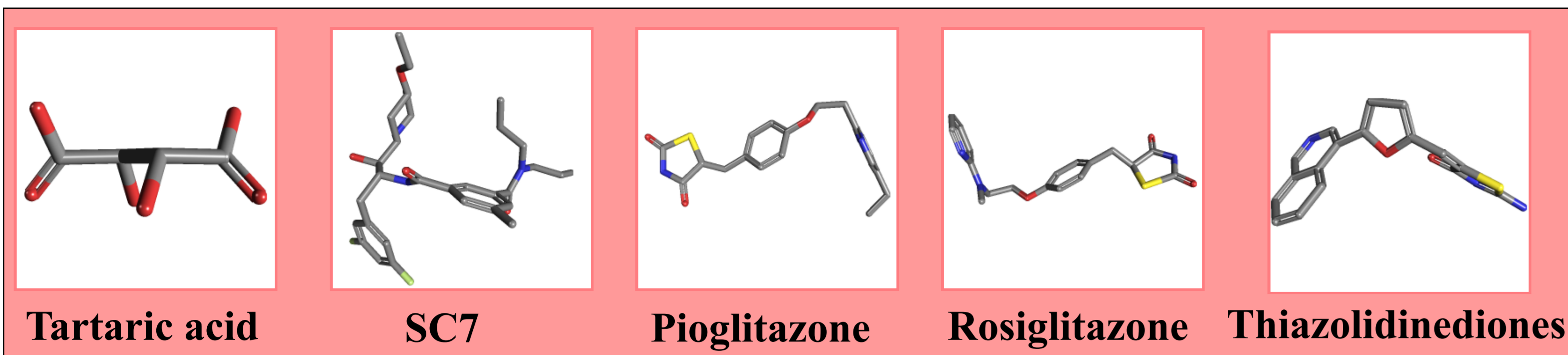
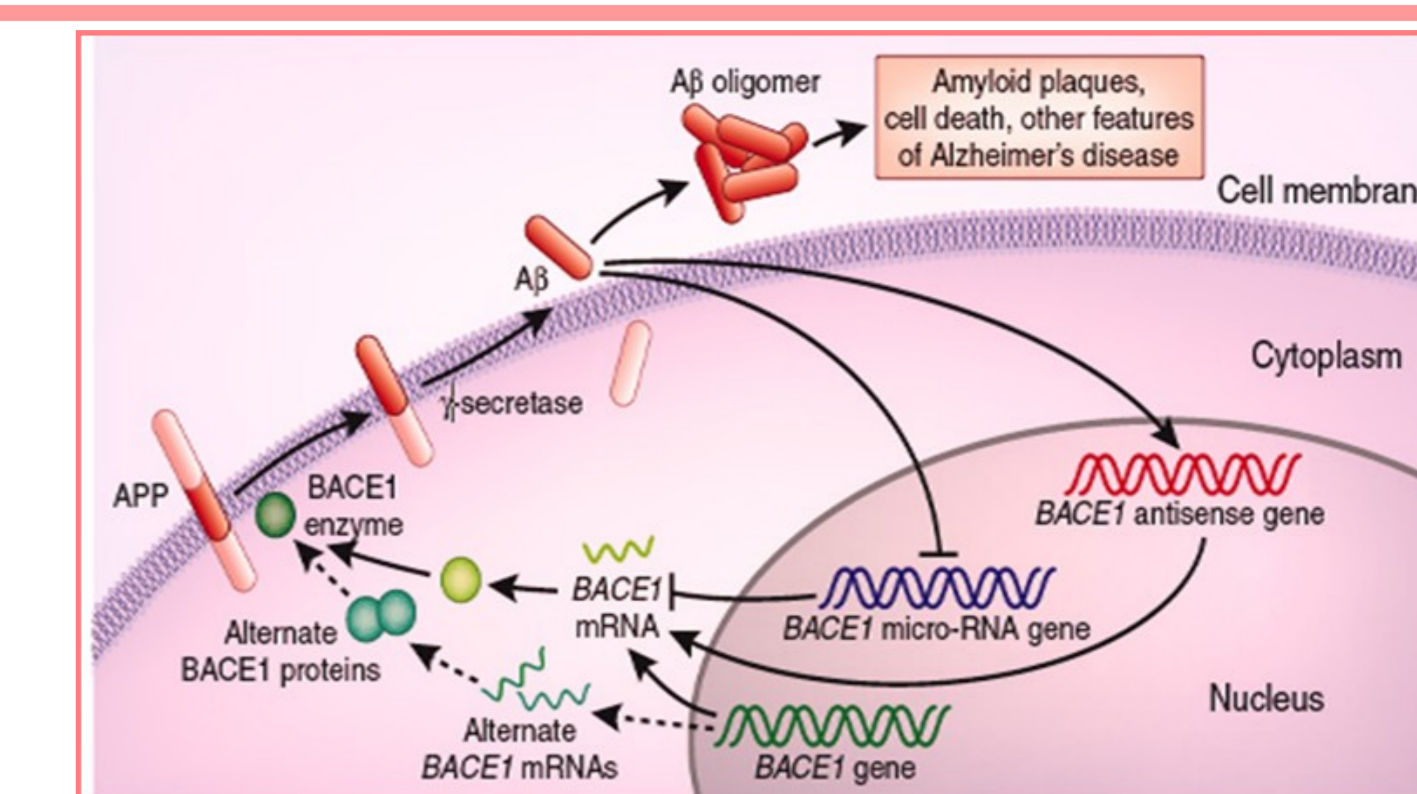


Figure: 1 Five existing inhibitors of human BACE-1.

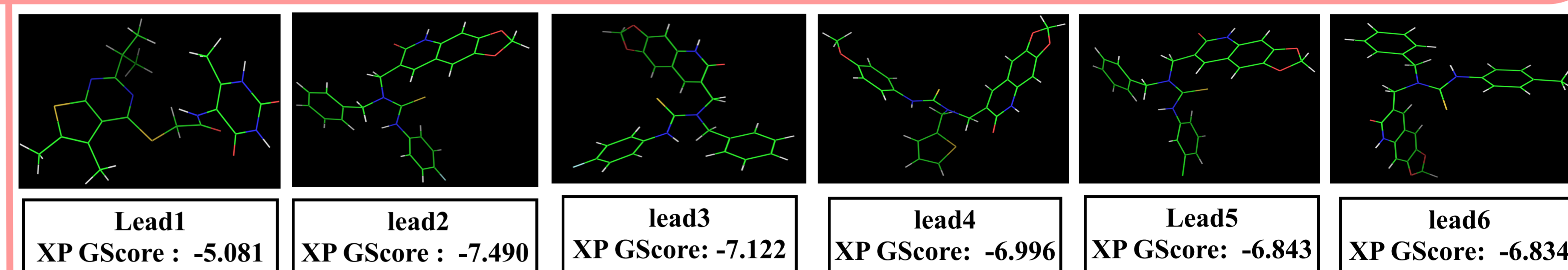
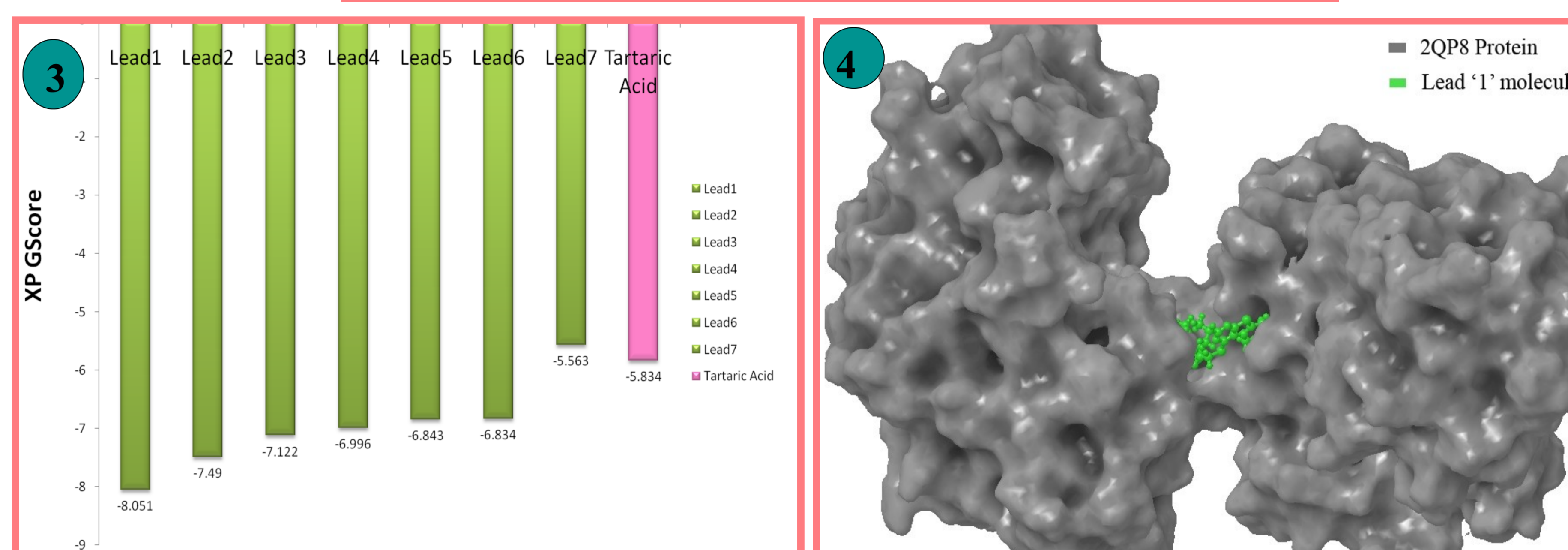


Figure: 2 Six proposed leads for human BACE-1



MATERIAL AND METHODS

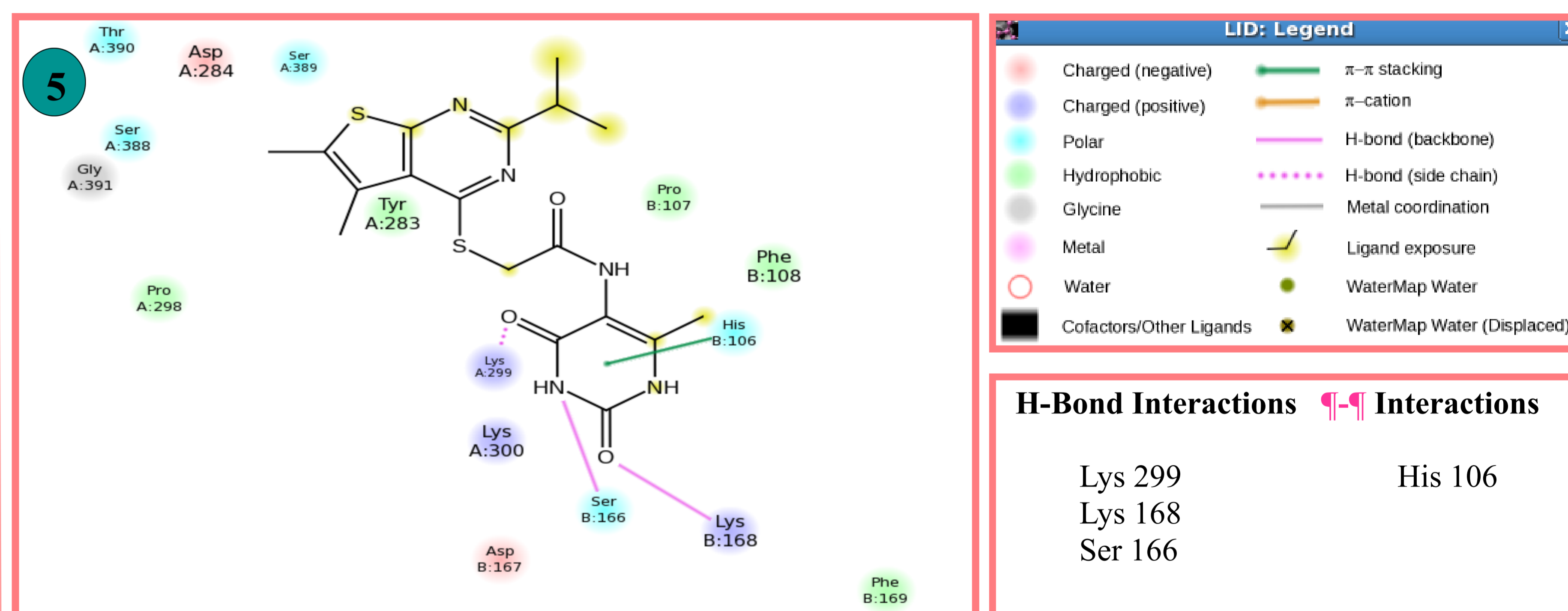
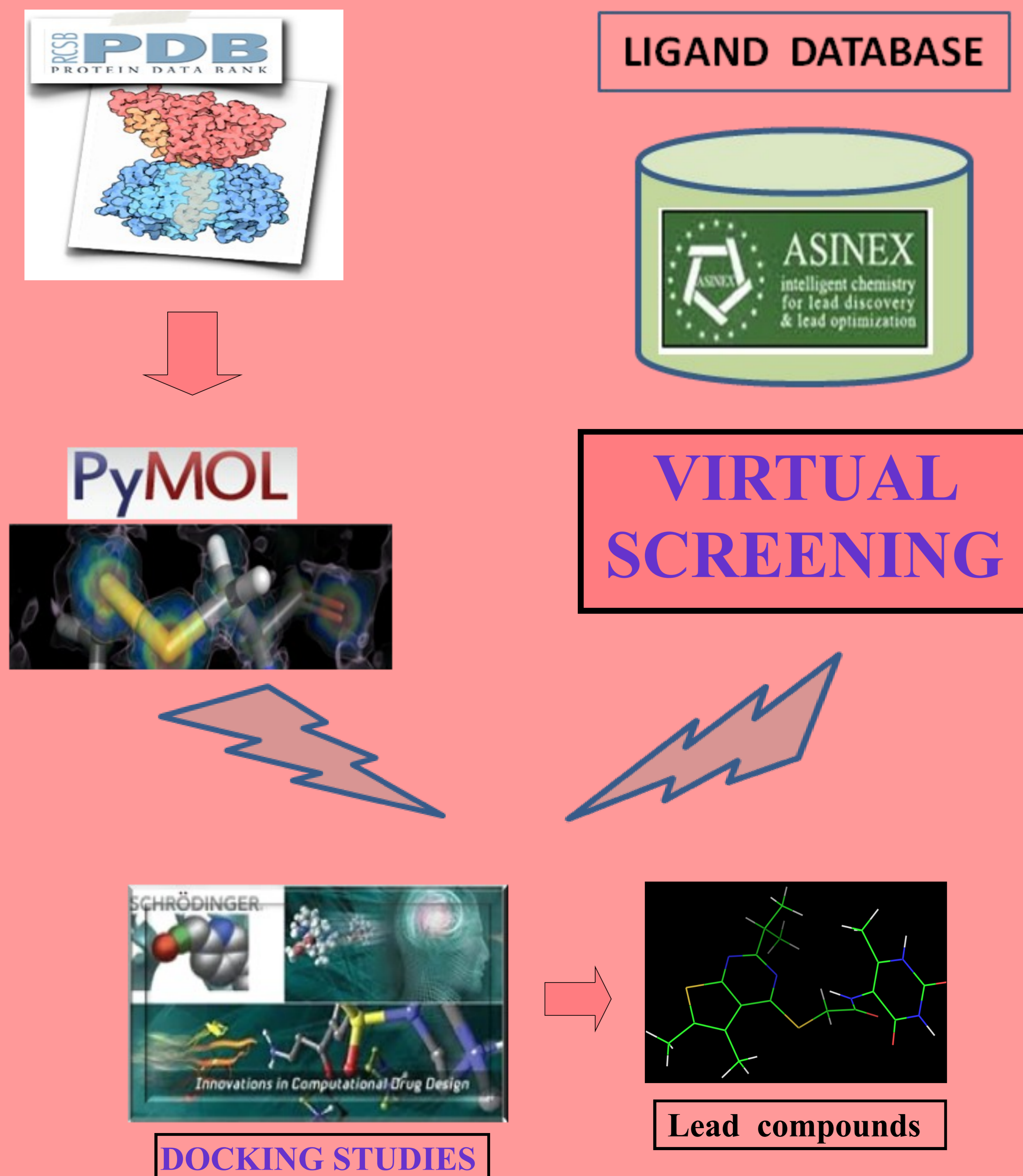


Figure:3 Comparison of XP GScore between leads and published inhibitor.

Figure:4 Docking complex of lead '1' with human BACE-1.

Figure:5 Interactions of lead '1' with human BACE-1 protein.

CONCLUSION

Seven leads were obtained and among them, six were proposed as potential leads based on XP GScore with better binding affinity and good pharmacological properties compared with existing inhibitors.

Lead 1 with XP GScore -8.051Kcal/mol, would be intriguing for rational drug design against Alzheimer's disease and would be highly encouraging for future Alzheimer's therapy if tested in animal models.

ACKNOWLEDGEMENT

I am indebted to honorable Dr.A.Umaheswari, Associate professor, Coordinator of BIF & Head of the Department, Bioinformatics, SVIMS, Tirupati for providing me an opportunity to carry out the project and helping me with unstined support and cooperation.

I want to express my deep sense of gratitude to Dr. V. Ramakrishna, Dr. C.Madhava Reddy, Dr. K.Riazunnisa and Dr. Prasanthi Dass Assistant Professors of Yogi Vemana University, KADAPA for their constant encouragement and sustained support.