ABSTRACT

α-Synuclein (αsyn) is one of the major protein responsible for various lewy body diseases such as Parkinson's disease, lewy body formation, that leads to neurodegradation mostly observed in aged individuals.The mechanism of formation of aggregates and the intermediate protofibrils from the seed α syn and its impact in the neuronal damage is still not clear. Observing the importance of α syn in aggregation which effect the wide range of LBs associated diseases in majority of population worldwide, this study focus on the conformational structures of various mutant forms of α syn (A30P, E476K and A53T) and binding efficiency of each mutant type against each other and wild type using molecular simulation studies. Knowing the different forms of α syn in forming toxic oligomers and aggregation,strategies can be applied to inhibit the aggregation by some known molecules.