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Computational docking studies of the Parkinson disease protein(parkinson disease protein 7(park7))

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Abstract

Parkinson's disease (PD) is a neurodegenerative and neurological disorder of the central nervous system due to accelerated loss of dopaminergic neurons in the midbrain and this area is responsible for the production of dopamine. Dopamine connects the stroma and the striatum to regulate muscle activity. Major realization in people with PD loss of more than 60% of dopamine-producing cells in the brain include rigidity, tremors, dyskinesia, parkinsonian gait, and unsteady posture. Parkinson disease protein 7(PARK7) is otherwise known as Protein deglycase (DJ-1).It has been identified as a gene responsible for hereditary recessive Parkinson's disease (PD). As a result, a complete understanding of DJ-1 function will aid in the understanding of the molecular mechanisms underlying Parkinson's disease pathogenesis. The Molecular docking was performed using Argus Lab Software version 4.0.1. Few Natural compounds were Curdione, coumaric acid, sinapic acid, and bisdemethoxycurcumin retrieved through Literature survey. Molecular docking was performed with Natural compounds against the target Parkinson disease protein 7(PARK7) and the results were discussed.

Keywords: Parkinson disease protein 7(PARK7), Argus lab, Molecular docking, Natural compounds.

Introduction

Parkinson's disease (PD) is a neurodegenerative and neurological disorder of the central nervous system due to accelerated loss of dopaminergic neurons in the midbrain and this area is accountable for the production of dopamine. Dopamine connects the stroma and the striatum to regulate muscle activity. PD(Parkinson Disease) is termed after Dr. James Parkinson; the surgeon first defined it as "tremor paralysis" in 1817. The incidence of Parkinson's disease increases with age, and in most European countries. The precise cause of loss of cell is unclear. Genetic and environmental influences include probable causes. Major manifestations in people with PD loss of more than 60% of dopamine-producing cells in the brain include rigidity, tremors, dyskinesia, parkinsonian gait, and unsteady posture.Although movement-related manifestations of PD are the main symptoms, gradual muscle function deterioration and continuing brain injury can guide to secondary symptoms dementia, memory loss, confusion, stress, anxiety, constipation, difficulty swallowing, depression, erectile dysfunction. PD is a condition that is often based on symptoms and signs. Observation of sustained response with the dopaminergic drug test (levodopa or dopamine agonist) is the most widely used diagnostically. Genetic markers are being tested to diagnose PD. A series of experiments have focused on the levels of cerebrospinal fluid proteins beta-amyloid and alpha-synuclein.[1]

Curcuma longa (turmeric) is a rhizomatous herbaceous perennial plant in the Zingiberaceae family. It is also known as kasturimanjaland has been used in Siddha medicine for over a thousand years in Asia to treat a variety of ailments such as skin diseases, pulmonary issues, aches and pains, wounds, sprains, and gastrointestinal system issues. It has also been used to treat stomach and liver diseases and it has a high antimicrobial potential. A curcuminoid is the active ingredient in C. longa extract. C. longa extract is known to have anti-inflammatory, antioxidant, and anti-depressant properties. Previous research has shown that C. longa extract is very effective against inflammation and Alzheimer's disease (Dose-dependent effect of Curcuma longa for Parkinson's disease treatment)[2].

Parkinson disease protein 7(PARK7) is otherwise known as Protein deglycase (DJ-1). It has been identified as a gene responsible for hereditary recessive Parkinson's disease (PD). As a result, a complete understanding of DJ-1 function will aid in the understanding of the molecular mechanisms underlying Parkinson's disease pathogenesis. However, because various and sometimes contradictory, roles for DJ-1 have been reported, the molecular function of DJ-1 remains debatable. Several papers have recently suggested that DJ-1 family proteins are involved in aldehyde detoxification[3].

Materials and Methods

Uniprot Database:

The UniProt Knowledgebase (UniProtKB) is the central repository for functional protein information, with accurate, consistent, and rich annotation[4]. The FASTA sequence was obtained from the Uniprot database, and the Uniprot ID is Q99497.PDB ID was retrieved from Uniprot database.

Protein Data Bank:

The Protein Data Bank (PDB) is a database of atomic coordinates and other information about proteins and other important biological macromolecules[5].PDB ID is 1P5F was retrieved from Uniprot Database and file download in PDB format.

Pubchem Database:

PubChem has one of the most comprehensive collections of publicly available chemical information. PubChem has quickly grown to become a key chemical information resource, serving scientific communities in a variety of fields such as cheminformatics, chemical biology, medicinal chemistry, and drug discovery[6].To obtain the 2D structure of the phytochemical

compounds(Curdione,coumaric acid, sinapic acid, and bisdemethoxycurcumin)are download in SDF file format.

QED:

Quantitative estimation of Drug-likeness is a drug-likeness index modelled using information available on marketed drugs. It is frequently used in current small-molecule drug development for computational approaches and to measure drug-like characteristics[7].The 2D structure was obtained from Pubchem Database and downloaded as SDF File Format and the Drug-likeness of the Natural compounds were analyzed.

Castp:

Computed Atlsas of Surface Topography of protein (Castp) web service intends to give a thorough and detailed quantitative analysis of protein interior gaps and surface pockets, which are significant concave regions typically involved with binding processes[8].This server is used for Active Site prediction of the protein and the PDB ID is 1P5F.

Pymol:

PyMOL, a crossplatform molecular graphics tool, is widely used for threedimensional (3D) visualisation of proteins, nucleic acids, small molecules, and electron transport chains [9]. Pymol is used to convert SDF file format to a MOL file format and also used for molecular visualization of the Ligand structure.

Argus Lab:

The primary computational technique used in the early stages of computer-aided drug discovery is molecular docking.The availability of free software for performing docking simulations of protein-ligand systems has resulted in an increase in the number of studies employing this technique[10].Argus lab software was used for docking purpose and to calculate the binding energy of the given protein and compounds.

Results

Molecular Docking:

Argus lab was used for molecular docking. Curdione[1],coumaric acid[1], sinapic acid[1], and bisdemethoxycurcumin[1] were the natural compounds used for docking procedure and the binding energy of these compounds are given below in the Table 1 and the figures are given below.

Table:1 Interaction of Parkinson disease protein 7 with Natural compound

Natural Compound	Binding energy Kcal/mol
curdione	-6.641 Kcal/mol.
coumaric acid	-8.57661 Kcal/mol.
sinapic acid	-6.89456 Kcal/mol.
bisdemethoxycurcumin	-12.9968 Kcal/mol.

Figure 1: Interaction of PARK7 with curdione is binding energy -6.641 Kcal/mol

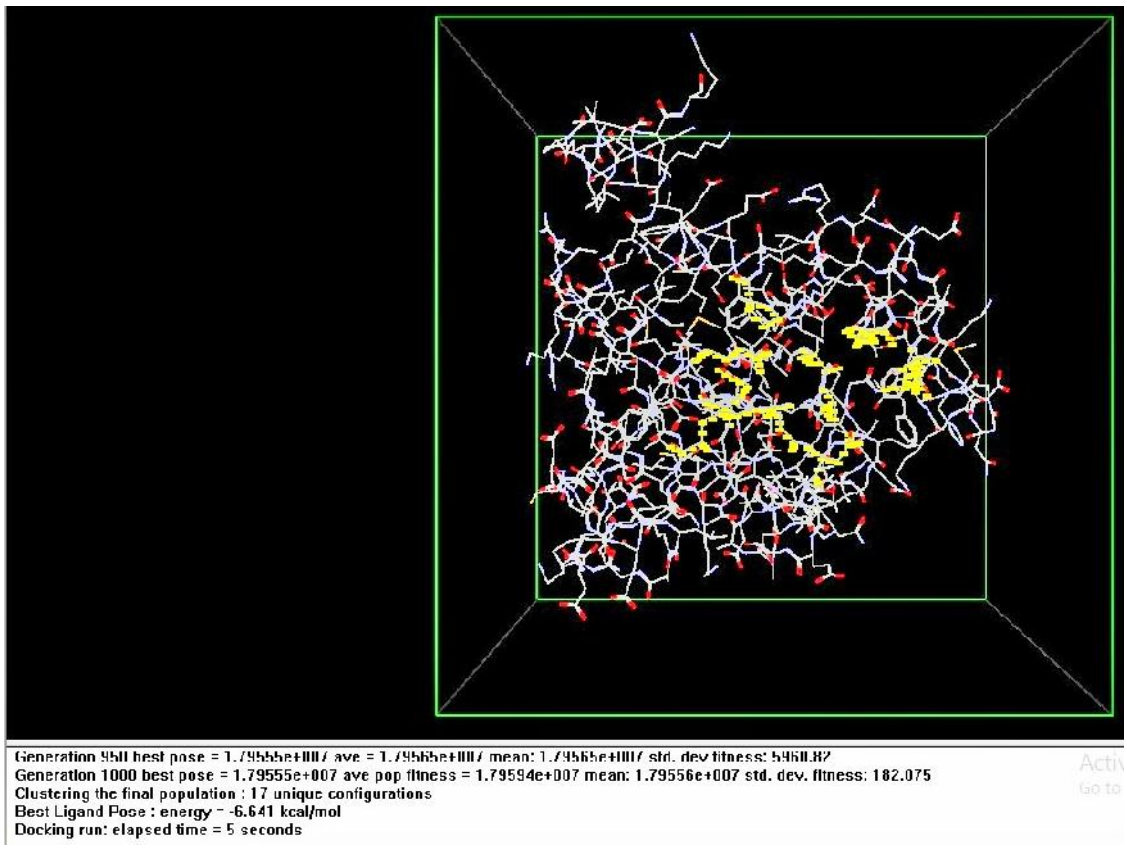


Figure 2: Interaction of PARK7 with coumaric acid is binding energy -8.57661 Kcal/mol.

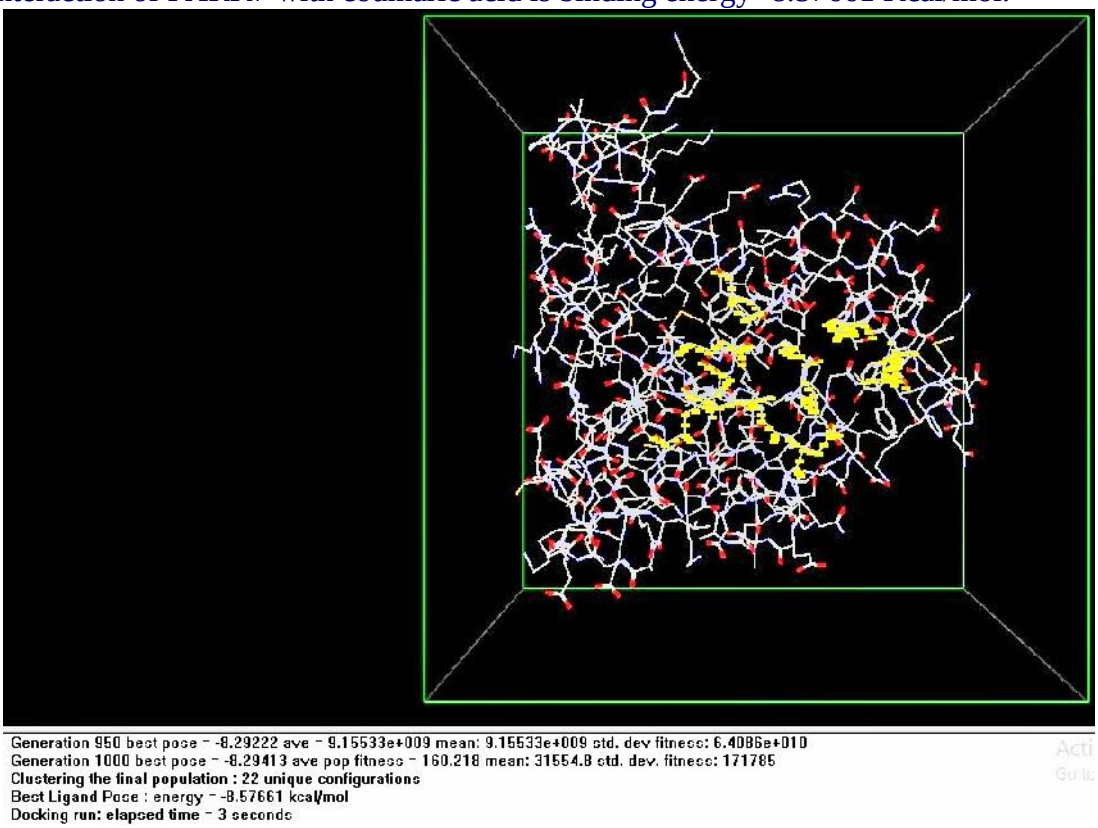


Figure 3: Interaction of PARK7 with sinapic acid is binding energy -6.89456 Kcal/mol.

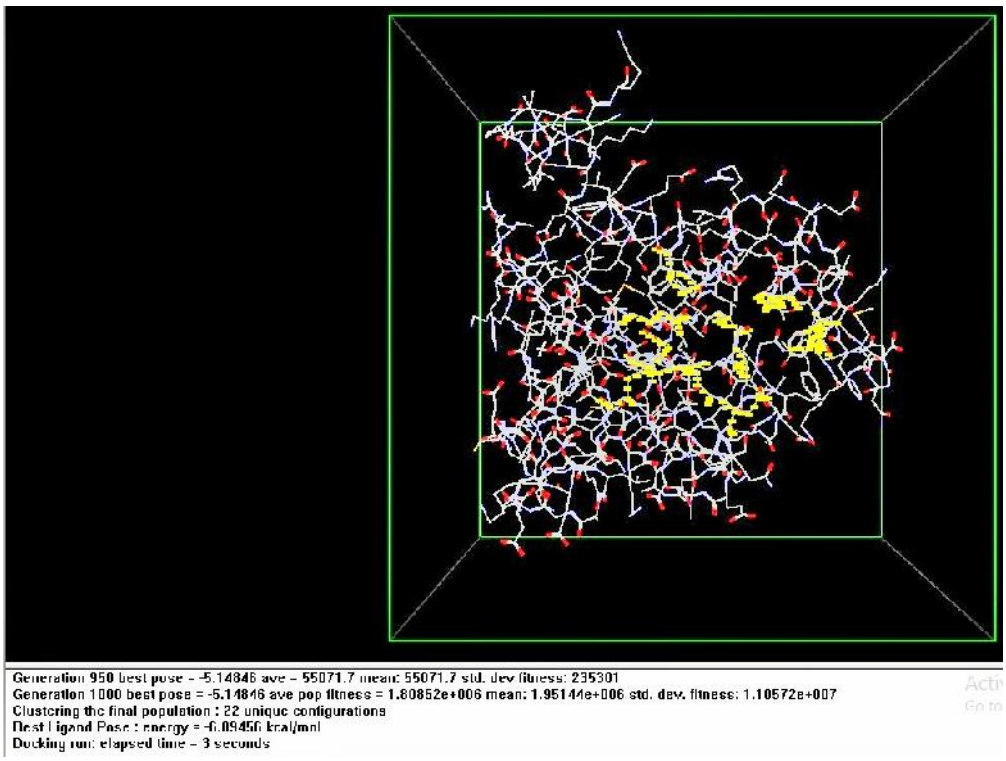
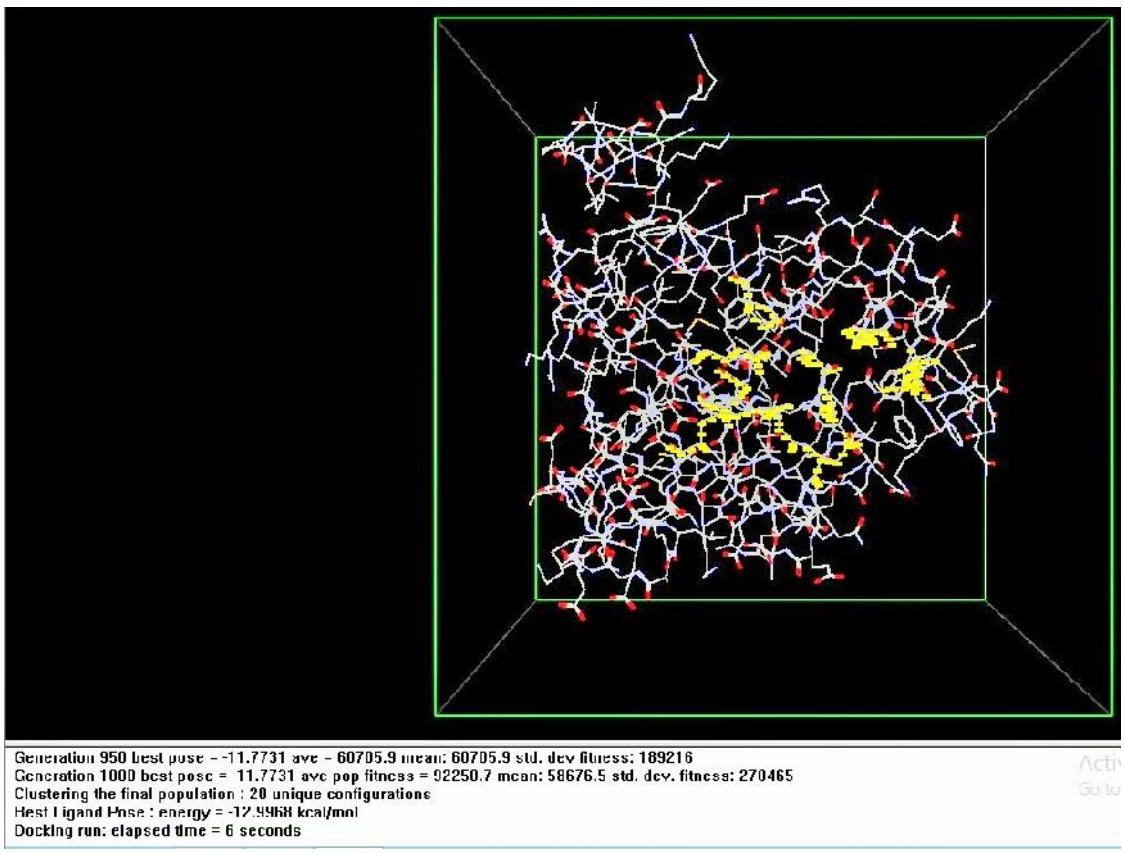


Figure 4: Interaction of PARK7 with bisdemethoxycurcumin compound is binding energy -12.9968 Kcal/mol.



Discussion

Parkinson disease is a neurological ailment that produces involuntary movements such as shaking, stiffness, and balance and coordination problems .Using Argus lab, Molecular Docking was performed for the Parkinson disease protein 7 with phytochemical compounds. The best binding interaction of the protein PARK7 with the bisdemethoxycurcumin compound was predicted to have the best binding energy -12.9968 Kcal/mol.

Conclusion

Parkinson disease protein 7(PARK7) is otherwise known as Protein deglycase (DJ-1).It has been identified as a gene responsible for hereditary recessive Parkinson's disease (PD). As a result, a complete understanding of DJ-1 function will aid in the understanding of the molecular mechanisms underlying Parkinson's disease pathogenesis. Few Natural compounds were docked with the Parkinson disease protein 7(PARK7) and the bisdemethoxycurcumin compound was predicted to have the best binding energy -12.9968 Kcal/mol which may be considered and used for further invitro studies.

Conflict of interest:

The authors declare they have no competing interests.

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Abbreviations:

UniProt: Knowledgebase (UniProtKB).
PDB:Protein data bank.
QED:Quantitative estimation of Drug-likeness
Castp:ComputedAtlsas of Surface Topography of protein

References

1. DeMaagd, G., & Philip, A. (2015). Parkinson's Disease and Its Management: Part 1: Disease Entity, Risk Factors, Pathophysiology, Clinical Presentation, and Diagnosis. *P &T : a peer-reviewed journal for formulary management*, *40*(8), 504–532.
2. A. jothilinsubitsha, sofiakhanam, and snehasabu. (2021-June-11). Plants as a promising source for the treatment of parkinson disease: a systemic review.;5(4):158–166
3. Ross Gibson, Sanika P. Dalvi, Prasad S. Dalvi,2021,DJ-1 and Parkinson's disease,BrainDisorders,Volume 3
4. The UniProt Consortium, UniProt: a worldwide hub of protein knowledge, *Nucleic Acids Research*, Volume 47, Issue D1, 08 January 2019, Pages D506–D515
5. Feng, H.B.J.W.Z. and Weissig, G.G.T.B.H., IN Shindyalov PE Bourne (2000). *Nucleic Acids Res*, *28*, pp.235-242.
6. Kim, S., Thiessen, P. A., Bolton, E. E., Chen, J., Fu, G., Gindulyte, A., Han, L., He, J., He, S., Shoemaker, B. A., Wang, J., Yu, B., Zhang, J., & Bryant, S. H. (2016). PubChem Substance and Compound databases. *Nucleic acids research*, *44*(D1), D1202–D1213.
7. Bickerton, G. R., Paolini, G. V., Besnard, J., Muresan, S., & Hopkins, A. L. (2012). Quantifying the chemical beauty of drugs. *Nature chemistry*, *4*(2), 90–98.
8. Wei Tian, Chang Chen, Xue Lei, Jieling Zhao, Jie Liang, CASTp 3.0: computed atlas of surface topography of proteins, *Nucleic Acids Research*, Volume 46, Issue W1, 2 July 2018, Pages W363–W367
9. Yuan, S., Chan, H.S. and Hu, Z., 2017. Using PyMOL as a platform for computational drug design. *Wiley Interdisciplinary Reviews: Computational Molecular Science*, *7*(2), p.e1298.

10. Bitencourt-Ferreira G, de Azevedo WF Jr. Molecular Docking Simulations with ArgusLab. Methods Mol Biol. 2019;2053:203-220. doi: 10.1007/978-1-4939-9752-7_13. PMID: 31452107.

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