IJCRR
Section: Healthcare
ISI Impact Factor
(2019-20): 1.628
IC Value (2019): 90.81
SJIF (2020) = 7.893

Copyright@IJCRR

Different Interaction Analysis of Receptors and Ligands in Suppressing Diabetics

Balasankar Karavadi¹, Premalatha J², Vinothkumar C², Rajasekar B³

¹Associate professor, School of Bio and Chemical Engineering, Sathyabama Institute of Science and Technology, Chennai, Tamilnadu-600 119, India; ²Assistant professor, School of Electrical and Electronics Engineering, Sathyabama Institute of Science and Technology, Chennai, Tamilnadu-600 119, India; ³Associate professor, School of Electrical and Electronics Engineering, Sathyabama Institute of Science and Technology, Chennai, Tamilnadu-600 119, India.

ABSTRACT

Introduction: Many recent studies are done on the efficiency of natural components for the treatment of diabetes, it has been found that many antioxidant components are present. Objective: The present study aims to study and identify the target sites which can be used as targets with appropriate ligands for diabetics.

Methods: Structure-based drug design was performed and protein docking was done with known ligands. Analyzing the receptor-ligand interaction between the active site of the protein and the chemical molecules was performed.

Results: All the compounds that satisfy the absorption, distribution, metabolism, excretion and toxicity (ADMET) properties are more favourable to bind with receptor. Discovery Studio tool was used to find the least energetic compound and based on the docking parameter against the receptor-ligand complex and which notified us of the acceptors and the donors in the analysis portion. From the study, we analysed that these components which contain bioactive compounds can be used in medical research. Nitenin showed a good dock score of 47.404 and can inhibit the overexpression of the CD62E gene.

Conclusion: The finalized complex of Nitenin compound can be used for further medical studies in the preparation of drug molecule against diabetes. The docking study reveals that the antioxidant components that are present can be used in the treatment of diabetes.

Key Words: ADMET, Diabetic, Ligand, Docking, Drug

INTRODUCTION

Diabetes is described by unusually significant levels of sugar (glucose) in the blood.¹ At the point when the measure of glucose in the blood increments, e.g., after supper, it triggers the arrival of the hormone insulin from the pancreas. Insulin invigorates muscle and fat cells to expel glucose from the blood and animates the liver to use glucose, causing the glucose level to diminish to ordinary levels.²

In individuals with diabetes, glucose levels stay high. This might be because insulin isn't being created by any means, isn't made at adequate levels, or isn't as compelling as it ought to be. The most well-known types of diabetes are type 1 diabetes (5%), which is an immune system issue, and type 2 diabetes (95%), which is related to stoutness. Gestational diabetes is a type of diabetes that happens in pregnancy, and different types of diabetes are extremely uncommon and are brought about by a solitary quality transformation.³

For a long time, researchers have been scanning for intimations in our hereditary cosmetics that may clarify why a few people are bound to get diabetes than others.⁴ The hereditary scene of diabetes presents a portion of the qualities that have been proposed to assume a job in the improvement of diabetes.⁵

As the incendiary reaction advances, chemokines discharged by harmed tissue enter the veins and initiate the moving leukocytes, which are presently ready to firmly tie to the endothelial surface and start advancing into the tissue. P-selectin has a comparable capacity, however is communicated on the endothelial cell surface inside minutes as it is put away inside the cell as opposed to delivered on request.⁶

ADMET screening is accomplished for the characteristic segments that are recovered from the database for testing their harmfulness and to locate the best lead particle that fulfils the ADMET parameter conditions (Figure 1).^{7,8} The AD-

Corresponding Author:

Balasankar Karavadi, Associate professor, School of Bio and Chemical Engineering, Sathyabama Institute of Science and Technology, Chennai, Tamilnadu-600 119, India; Email: balasankar.bioinfo@sathyabama.ac.in

ISSN: 2231-2196 (Print)

ISSN: 0975-5241 (Online)

Received: 09.09.2020

Revised: 12.11.2020

Accepted: 19.12.2020

Published: 12.04.2021

MET screening process is finished utilizing Disclosure STUDIO programming. The ligand particles for which the AMET must be done is downloaded from PUBMED then stacked in the revelation page and checked for ADMET results.

Figure 1: AMDET Point Plot for the antioxidant compounds.

Structure-based drug design is the method of performing docking using the known protein docking with known ligands. This has been the frequently used method of analyzing the receptor-ligand interaction between the active site of the protein and the chemical molecules.⁹

MATERIALS AND METHODS

The template structure was obtained from protein data bank.¹⁰ The modeled structures were validated using SAVS,

an online server.¹¹ The CASTp server was used to analyze binding sites of the protein molecules. Further, on the basis of high throughput method lead molecules having more affinity with the target proteins were obtained from DrugPort database.¹² Then the structurally similar compounds were obtained using PubChem database.³ Finally a dataset was created for potential ligands inhibiting the target proteins using vegaZZ software. Accelrys Discovery Studio 2.0 was used to analyze specific protein-ligand docked complexes and finally toxicity of the ligand molecules were analysed using ADMET descriptors.⁴

RESULTS AND DISCUSSION

Receptor Ligand Interaction: Ligand-Nitenin

Figure 2: Nitenin and receptor CD62E complex protein interaction.

Table 1: Result for interaction between nitenin ligand and cd62e receptor

S. NO	PUBCHEM CID	LigScore1_Dreiding	LigScore2_Dreiding	PMF	DOCK SCORE	LF_rotlbonds	MW	LIG_INTERNAL_ENERGY
1	44257187	2.14	4.19	8.7	47.404	6	328.24	-12.391
2	44257187	1.99	4.12	7.98	47.039	6	328.24	-12.391
3	44257187	1.63	3.87	6.09	45.108	6	328.24	-10.845
4	44257187	2.8	4.55	3.09	44.483	6	328.24	-10.106
5	44257187	1.62	4.19	6.43	44.155	6	328.24	-8.263
6	44257187	2.06	4.04	4.89	43.651	6	328.24	-9.422
7	44257187	2.79	4.55	5.19	43.635	6	328.24	-8.463
8	44257187	1.36	4.03	8.67	43.022	6	328.24	-9.983
9	44257187	2.1	4.07	4.47	42.988	6	328.24	-7.991
10	44257187	2.26	4.49	2.63	42.974	6	328.24	-7.277

The docking score of this interaction is 47.404 and LigScore1_Dreiding and LigScore2_Dreiding values are 2.14

and 4.19, -PMf value is 8.7 and the internal energy is 12.391 (Figure 2).

Ligand- Fulvinervin A

Figure 3: FulvinervinA and receptorCD62E complex protein intraction

Table 2: Interaction between fulvinervinA ligand and cd62e receptor

S. NO	PUBCHEM CID	LigScore1_Dreiding	LigScore2_Dreiding	PMF	DOCK_SCORE	LF_rotlbonds	LIG_INTERNAL_ENERGY	MWt
1	42607884	1.34	4.29	9.49	44.994	3	-8.699	364.27
2	42607884	1.46	4.3	6.57	44.248	3	-7.994	364.27
3	42607884	1.32	4.22	6.94	43.719	3	-7.359	364.27
4	42607884	1.54	4.23	11.35	42.906	3	-6.943	364.27
5	42607884	1.26	4.12	5.21	42.651	3	-7.674	364.27
6	42607884	1.29	4.07	5.05	42.588	3	-9.256	364.27
7	42607884	1.44	3.94	3.95	42.346	3	-8.625	364.27
8	42607884	1.33	4.07	3.9	42.096	3	-7.884	364.27
9	42607884	1.56	4.21	5.81	42.065	3	-6.41	364.27
10	42607884	1.68	4.2	9.48	41.759	3	-6.446	364.27

The docking score of this interaction is 44.994 and LigScore1 and LigScore2 values are 1.34 and 4.29, -PMF 9.49 value is and the internal energy is 364.27 (Figure 3).

Ligand- Emoroidenone

Figure 4: Emoroidenone and receptorCD62E complex protein.

Table 3: Result for interaction between moroidenone ligand and cd62e receptor

S. NO	PUBCHEM CID	LigScore 1	LigScore 2	PMF	DOCK_SCORE	LF	LIG_INTERNAL_ENERGY	MW
1	42607866	1.15	3.78	10.35	39.125	2	-7.686	316.23
2	42607866	1.21	3.82	12.47	38.828	2	-7.686	316.23
3	42607866	1.21	3.79	11.55	38.585	2	-7.63	316.23
4	42607866	1.16	3.76	12.33	37.832	2	-7.506	316.23
5	42607866	1.16	3.76	12.33	37.832	2	-7.506	316.23
6	42607866	1.2	3.73	10.1	37.8	2	-7.487	316.23
7	42607866	1.2	3.73	10.1	37.8	2	-7.487	316.23
8	42607866	1.16	3.77	11.89	37.787	2	-7.506	316.23
9	42607866	1.16	3.77	11.89	37.787	2	-7.506	316.23
10	42607866	1.08	3.71	9.75	37.555	2	-7.487	316.23

The docking score of this interaction is 39.125 and Lig-1Score 1.15, LigScore2 3.78 PMF value is 10.35 and the internal energy is -7.686 (Figure 4).

From the results obtained it is analyzed that the antioxidants present in Tephrosia play a major role in the treatment of diabetes. It is concluded that they can use the CD62e receptor which increases estrogen production and bone mineral density.

CONCLUSION

In this study, we have noticed that the compounds present in herbal medicinal can be used as a diabetes medicine. The anti-diabetes properties related to the compound which use as a ligand to show the interaction between receptor CD62E structure tells that the compound can inhibit the overexpression of CD62E receptor by binding in the active site cavity. Discovery Studio tool was used to find the least energetic compound and based on the docking parameter against the receptor-ligand complex and which notified us of the acceptors and the donors in the analysis portion. Finally, from the study, we can conclude that these components which contain bioactivity can be used in future medical research. Nitenin showed a good dock score of 47.404 and can inhibit the overexpression of the CD62E gene. The finalized complex of nitenin compound can be used for further medical studies in the preparation of drug molecule against diabetes.

ACKNOWLEDGMENT

The authors acknowledge the scholars whose articles are cited and included in references to this manuscript. The authors are also thankful to authors/ editors/publishers of all those articles, journals and books from where the literature for this article has been reviewed and discussed. We acknowledge

our institute management for their support.

Conflict of Interest: Nil

REFERENCES

1. Anderson DM, Maraskovsky E, Billingsley WL, Dougall WC, Tometsko ME, et al. Homologue of the TNF receptor and its ligand enhance T-cell growth and dendritic-cell function. *Nature* 1997;390:175–179.
2. Boyce BF, Xing L, Shakespeare W, Wang Y. Regulation of bone remodelling and emerging breakthrough drugs for osteoporosis and osteolytic bone metastases. *Kidney Int Suppl* 2003;12: 2–5.
3. Simonet WS, Lacey DL, Dunstan CR, Kelley M, Chang MS, Luthy R, et al. Osteoprotegerin: a novel secreted protein involved in the regulation of bone density. *Cell* 1997;89:309–319.
4. Ida Leida M, Ridwan M. Thaha, Andi SelviYusnitasari, Af-sahyana Effect of Sap Palm (*Borassus flabellifer*) on Blood Glucose Level in Pre-Diabetic Patients. *Int J Curr Res Rev* 2020;12(24):96-100.
5. Tolar J, Teitelbaum SL, Orchard PJ. Osteopetrosis. *N Engl J Med* 2004;351:2839–2849.
6. Breuil V, Schmid-Antomarchi H, Schmid-Alliana A, Rezzonico R, Euler-Ziegler L, Rossi B. The receptor activator of nuclear factor (NF)-kappaB ligand (RANKL) is a new chemotactic factor for human monocytes. *FASEB J* 2003;17:1751–1753.
7. Aswathy BK, Nisha H. Homology Modeling and Docking Studies to Identify the Targets in Pancreatic Cancer. *Res J Pharm Tech* 2017;10(7): 2032-2040.
8. Aswathy BK, Martina V. Insilico Analysis of Inhibitors Related to Aggressive Behavior in Human Beings. *Res J Pharm Tech* 2018;11(4):1436-1441.
9. Karavadi B, Suresh M. Homology modelling and molecular drug design approach in identifying drug targets of TIGR4 in *Streptococcus pneumoniae*. *Bio sci Biotechnol Res Asia* 2014;11:517-522.
10. Karavadi B, Suresh MX. In silicomodeling of capsular polysaccharidebiosynthesis protein and tyrosine kinase of G54 strain in *Streptococcus pneumoniae* and their ligand identification. *Int J Pharm Pharm Sci* 2014;6:547-550.
11. Karavadi B, Suresh MX. Receptor identification and lead the molecular discovery of a phage-encoded protein in TCH8431/19A

- strain of *Streptococcus pneumoniae*: A computational approach. *Int J Appl Pharm* 2014;6:6-10.
12. Karavadi B, Suresh XM. Homology modelling of polymerase and CPS biosynthesis proteins in CGSP14 strain of *Streptococcus pneumoniae* and its ligand identification: An in silico approach. *Asian J Pharm Clin Res* 2014;7:162-165.