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Integrative Network Pharmacology and Structure-Based Molecular Docking for the Computational Identification of CHEK2-Targeting Phytochemicals in Triple-Negative Breast Cancer

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Abstract

Triple-negative breast cancer (TNBC) is one of the most aggressive forms of breast cancer and it is very difficult to treat because it lacks the common hormone receptors which is used in targeted therapies. The main aim of this study was identifying an important target gene involved in TNBC and to evaluate the potential of selected natural compounds using computational approaches. Genes related to TNBC they were collected from the Gene Cards database, and the most relevant genes were selected for further analysis. A protein-protein interaction (PPI) network was then constructed and analysed using Cytoscape software. Based on network parameters such as degree and betweenness centrality, CHEK2 (Checkpoint kinase 2) was identified as a main target gene because of its strong interactions with other associated genes. Five phytochemicals-curcumin, piperine, cinnamaldehyde, 6-gingerol, and allicin were selected from previously published studies for further investigation. The three-dimensional structure of the CHEK2 protein was obtained using PDB database and evaluated before docking analysis. Molecular docking was then performed using the Dock Thor with a blind docking approach to study the interaction of these compounds with the target protein. The docking results showed that all phytochemicals exhibited stable binding with the protein. Among them, curcumin demonstrated the highest binding affinity (−9.386 kcal/mol), followed by piperine (−8.847 kcal/mol), cinnamaldehyde (−8.12 kcal/mol), 6-gingerol (−7.933 kcal/mol), and allicin (−7.855 kcal/mol). These results indicates that curcumin may have stronger interaction potential with the CHEK2 protein. In conclusion, the study highlights the importance of network-based target identification and it supports the potential role of natural phytochemicals, particularly curcumin, in TNBC treatment. Further experimental validation is required to confirm these findings.

Keywords: TNBC, CHEK2, molecular docking, phytochemicals, network pharmacology, curcumin.

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1. Introduction

Breast cancer is the most common global malignancy and the main cause of cancer deaths. (Katsura et al., 2022). During the recent years, many different therapies have emerged in the era of breast cancer. Breast cancer is a heterogeneous disease in which genetic and environmental factors are mainly involved (Barzaman et al., 2020). The alarming increase in rate of breast cancer cases emphasizes the management of disease at multiple levels. (Kashyap et al., 2022) Several observational studies have reported a strong association between breast density and breast cancer risk. Women with extremely dense breast tissue (BI-RADS category D) have been found to have nearly twice the risk of developing breast cancer compared to those with lower breast density. This association remains statistically significant even after adjusting for factors such as age and body mass index (BMI) (Bodewes et al., 2022).

Triple-negative breast cancer (TNBC) is a type of breast cancer. These cancers vary in how they look under the microscope, their genetic makeup, and how they interact with the immune system. It does not have three common receptors which are estrogen, progesterone, and HER2 that are usually present in other types of breast cancer (Derakhshan & Reis-Filho, 2022). TNBC can vary from one patient to another, which is making its treatment more challenging. Some tumors may also grow and spread quickly, while others may respond differently to treatment. Because of this, researchers are trying to better understand the molecular characteristics of TNBC in order to develop more targeted and effective therapies in the future (Li et al., 2022). Reports suggest that TNBC accounted for nearly 12% of breast cancer cases diagnosed in the United States between 2012 and 2016, and its five-year survival rate was lower compared to hormone receptor-positive breast cancer. Despite this, most prevention and screening strategies are still mainly designed for less aggressive types like luminal breast cancers. (Howard & Olopade, 2021) Since TNBC does not respond to hormone therapy or HER2-targeted treatments, doctors have limited and less reliable options to manage it. Also, there is no single standard treatment that works for every patient, that makes treatment more challenging. And because of this, there is a growing need to explore better and more effective ways to treat TNBC. Current approaches include the use of different drugs and therapies, and researchers are also studying newer treatment options, especially targeted therapies, to improve patient outcomes. (Yin et al., 2020)

Around 6% of breast cancer cases in women are linked to inherited genetic factors. Among the genes that increase the risk, CHEK2 is one of the most commonly found. Changes or mutations in this gene can affect how cells repair DNA, which may increase the chances of cancer development. (Conde, 2024) CHEK2 is a gene involved in the DNA damage response and it helps in maintaining genomic stability. Mutations in this gene are among the commonly identified inherited changes which are associated with an increased risk of breast cancer. These variants can impair normal DNA repair processes, therefore it contributes to cancer development. (Stolarova et al., 2020). CHEK2 is a gene that performs an important role in the DNA damage response, especially when there are serious breakage in DNA strands. It produces a protein called CHK2 kinase, which helps in cell recognizing the damage and activate repair mechanisms. By doing this, it helps maintain the stability of the cell's genetic material. If CHEK2 is not working properly due to mutations, the DNA repair process can be affected, which might lead to the accumulation of damage and increase the risk of cancer development. (Qian et al., 2024) Phytochemicals which are derived from medicinal plants are getting attention as potential anticancer agents because to their natural origin and relatively lower toxicity compared to other treatments. These compounds can act on multiple targets in cancer cells, which makes them promising for safer and more effective therapies. Network pharmacology is an approach which helps in understanding how these phytochemicals interact with other multiple genes, proteins, and pathways involved in a disease, rather than focusing on just a single target. (Khan et al., 2020) Molecular docking is a computational method which is used in drug discovery in understanding how a small molecule like a drug or phytochemical binds to a target protein. It helps predict the interaction between the compound and the target at the molecular level. (Pinzi & Rastelli, 2019)

Therefore for identifying the potential drug targets of Triple negative breast cancer, first one should understand

the mechanism of disease pathogenesis. With the emergence of network biology, it has become easier to understand the whole disease mechanism at the system level by constructing a network-based computational model for the disease. Exploring these networks will provide valuable information about the functional association of genes/proteins in the network that will help in identifying the most potential drug target for disease among the wide range of genes/proteins in the network. The current in-silico study was performed to study the underlying disease mechanism of triple negative breast cancer and to identify the most potential drug target for disease. A further drug discovery approach was used to identify novel lead molecules for the disease.

2. Methodology

2.1 Data collection

Data collection was done using the Gene Cards database, from which we collected 15 disease-associated genes. These genes were selected based on their relevance scores to maintain a disease-specific focus, and the top 15 most relevant genes were included for further analysis and it is shown in table 1.

Table 1: List of all the genes

Symbol	Description	Category	UniProt ID	GeneCards ID	Score
BRCA2	BRCA2 DNA Repair Associated	Protein Coding	P51587	GC13P032315	705.01
BRCA1	BRCA1 DNA Repair Associated	Protein Coding	P38398	GC17M043044	672.29
ATM	ATM Serine/Threonine Kinase	Protein Coding	Q13315	GC11P108222	565.68
PALB2	Partner and Localizer of BRCA2	Protein Coding	Q86YC2	GC16M023603	502.57
CHEK2	Checkpoint Kinase 2	Protein Coding	O96017	GC22M028687	457.28
BRIP1	BRCA1 Interacting DNA Helicase 1	Protein Coding	Q9BX63	GC17M061679	448.72
BARD1	BRCA1 Associated RING Domain 1	Protein Coding	Q99728	GC02M214725	413.35
TP53	Tumor Protein P53	Protein Coding	P04637	GC17M007661	356.42
CDH1	Cadherin 1	Protein Coding	P12830	GC16P068737	349.76
C11orf65	Chromosome 11 Open Reading Frame 65	Protein Coding	Q8NCR3	GC11M108308	347.07
ERBB2	Erb-B2 Receptor Tyrosine Kinase 2	Protein Coding	P04626	GC17P039687	318.83

EGFR	Epidermal Growth Factor Receptor	Protein Coding	P00533	GC07P055019	287.83
MSH2	Mut S Homolog 2	Protein Coding	P43246	GC02P047403	274.96
MSH6	Mut S Homolog 6	Protein Coding	P52701	GC02P047695	273.81
MLH1	Mut L Homolog 1	Protein Coding	P40692	GC03P036993	269.14

2.2 Construction of PPI Network

STRING (Von Mering et al., 2005) allows a study of network interaction by providing several features. PPI network constructed using of STRING (Search Tool for the Retrieval of Interacting Genes) (Aoki & Kanehisa, 2005) by 15 genes for triple negative breast cancer as input and the confidence score was taken 0.75. further PPI Network was analysed and visualized by Cytoscape 3.3.0 (Srivastava et al., 2018)

2.3 Analysis of PPI Network

Analysis of the protein–protein interaction (PPI) network was carried out using Cytoscape (version 3.3.0). The Network Analyzer tool in Cytoscape was used to evaluate key parameters such as node degree and betweenness centrality (BC). In the network, each node represents a gene, while the edges represent interactions between them. The number of edges connected to a node indicates its degree, reflecting how many interactions that gene has with others. (Saito et al., 2012) Betweenness centrality explains the significance of the node primarily based on the quantity of the shortest ways that undergo every node. In the study, the PPI network was analysed based on these parameters.

2.4 Ligand identification

Phytochemical identification was carried out by selecting the top 5 phytochemicals based on literature review. These compounds were chosen due to their reported biological relevance in previous studies. The chemical structures of the selected phytochemicals were then retrieved from the PubChem database (Kim, 2016) for further analysis and is shown in Table 2.

Table 2: List of Phytochemicals

S. No.	*Phytochemical Name*	*Plant Name*	*Plant Part Used*
1	*Curcumin*	*Turmeric (Curcuma longa)*	*Rhizome*
2	*Piperine*	*Black Pepper (Piper nigrum)*	*Fruit*
3	*6-Gingerol*	*Ginger (Zingiber officinale)*	*Rhizome*
4	*Allicin*	*Garlic (Allium sativum)*	*Bulb*
5	*Cinnamaldehyde*	*Cinnamon (Cinnamomum verum)*	*Bark*

2.5 Molecular Docking

Blind molecular docking was done using the Dock Thor to study how the selected ligands bind with the target protein. The results were analysed based on binding affinity (kcal/mol), in which lower value shows better and more stable binding. Along with this, different energy values like total energy, van der Waals energy, and electrostatic energy were also observed to understand the interaction in more detail. The ligand

showing the most favourable binding energy was considered as the best protein–ligand complex.

3. Results and Discussions

3.1 Network Analysis and Identification of Target

The PPI Network was constructed shown in figure 1 inputting 15 genes for Triple Negative Breast Cancer using the STRING Database. Retrieved network was analysed and visualized using Cytoscape 3.3.0 plug-in Network based on 12 topological parametres. Among which figure 2, 3 and 4 shows the interaction of the degree centrality, betweenness centrality and closeness centrality parameter. CHEK2 (Checkpoint kinase 2) was selected as a key drug target based on its highest betweenness centrality (BC) value and degree node in the protein-protein interaction (PPI) network. This indicates that CHEK2 has a central position in the network and is strongly linked with other genes, which is making it an important target for further study. CHEK2 is also associated with hereditary breast cancer and works as a tumor suppressor gene. If one copy of this gene is inherited in a mutated form, it can increase the chances of developing cancer. According to the two-hit model, cancer may develop when the second copy of the gene also gets lost or becomes inactive during the early stages. (Kenemans et al., 2004)

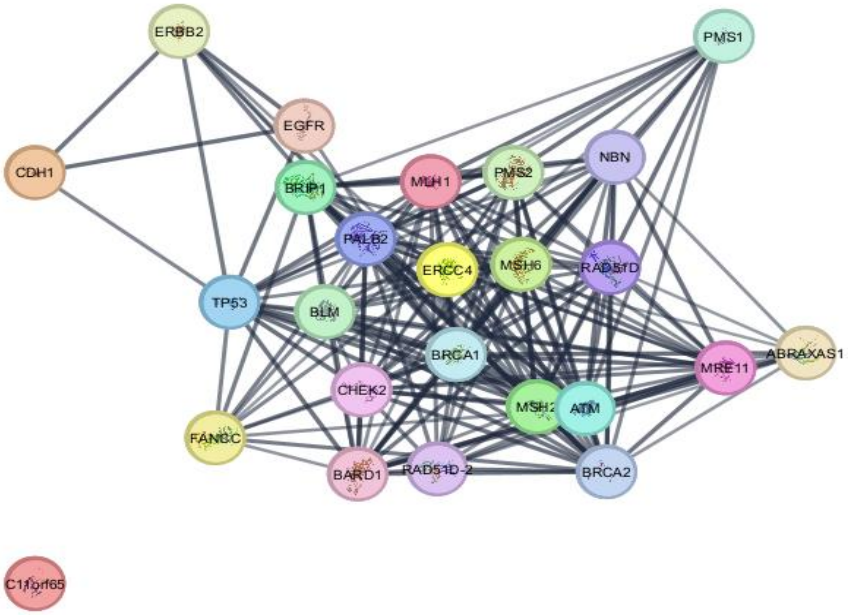

Figure 1. *PPI network of genes related to triple-negative breast cancer*

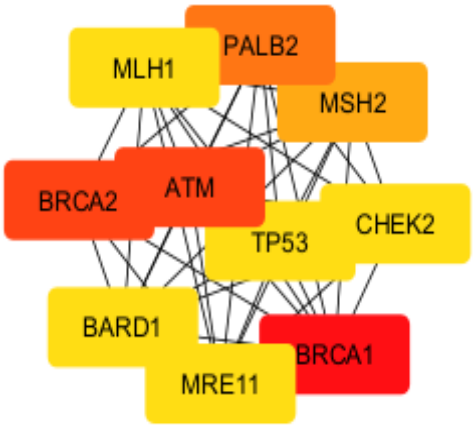

Figure 2. *Degree centrality network showing the number of direct connections for each gene*

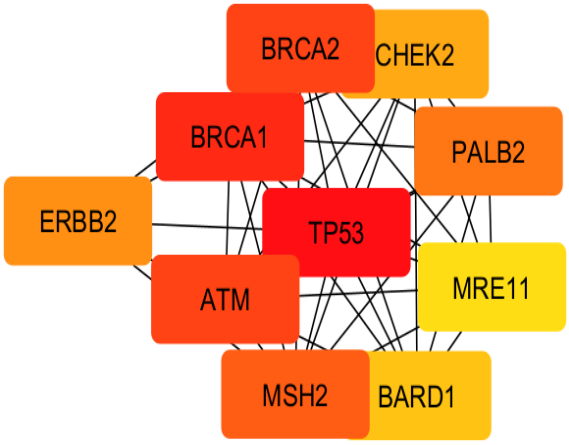

Figure 3. *Betweenness centrality network showing which genes connect different parts of the network.*

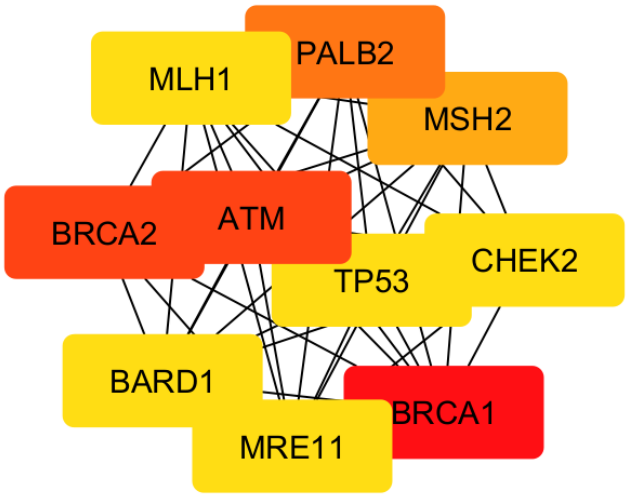

Figure 4. *Closeness centrality network showing how easily each gene can reach others in the network.*

MCC	DMNC	MNC	DEGREE	EPC	BOTTLENECK	EcCENTRICITY	CLOSENESS	RADIALITY	BETWEENNESS	STRESS	CLUSTERING COEFFECIENT
BRCA2	RAD51D	BRCA2	BRCA2	BRCA2	BRIP1	BRCA2	BRCA2	BRCA2	BRCA2	ATM	RAD51D
ATM	PMS2	ATM	ATM	ATM	BRCA2	ATM	ATM	ATM	ATM	BARD1	ABRAXAS1
MRE11	ERCC4	MRE11	MRE11	MRE11	ATM	BLM	MRE11	MRE11	MRE11	BRCA1	ERCC4
MSH6	BLM	TP53	TP53	TP53	ERCC4	MRE11	TP53	TP53	TP53	BRCA2	BLM
MLH1	NBN	MLH1	MLH1	MLH1	MRE11	TP53	MLH1	MLH1	PALB2	CHEK2	NBN
PALB2	MRE11	PALB2	PALB2	PALB2	TP53	PMS1	PALB2	PALB2	MSH2	MRE11	MSH6
MSH2	MSH6	MSH2	MSH2	MSH2	MSH6	MSH2	MSH2	MSH2	BARD1	MSH2	CDH1
BARD1	MLH1	BARD1	BARD1	BARD1	PMS1	FANCC	BARD1	BARD1	BRCA1	PALB2	RAD51D-2
BRCA1	BARD1	BRCA1	BRCA1	BRCA1	BRCA1	BRCA1	BRCA1	BRCA1	CHEK2	PMS2	PMS1
CHEK2	CHEK2	CHEK2	CHEK2	CHEK2	CHEK2	CHEK2	CHEK2	CHEK2	ERBB2	TP53	FANCC

Figure 5. *Identification of the Primary Hub Gene in Triple Negative Breast Cancer Based on Occurrence Across 12 Centrality Parameters.*

CHEK2	11
MRE11	11
BRCA2	10
BRCA1	10
ATM	10
MSH2	9
BARD1	9
TP53	9
PALB2	8
MLH1	7
MSH6	4
BLM	3
ERCC4	3
PMS1	3

***Figure 6**. hub gene frequency in Triple Negative Breast Cancer across 12 centrality parameters.*

3.2 Protein Structure and Validation

The 3D structure of the selected protein was taken from the PDB database and then checked using its validation report to see if the structure is reliable. The R-free value (0.263) is within an acceptable range, which suggests that the structure is fairly reliable. The clash score and Ramachandran outliers were also low, indicating that there are very few structural issues and the overall geometry of the protein is good. However, a slightly higher percentage of sidechain outliers (16.1%) was observed, which may indicate minor deviations in side chain conformations. The RSRZ outliers were also within an acceptable range, supporting the overall quality of the structure. Overall, the validation results suggest that the protein structure is of satisfactory quality and suitable for further molecular docking studies. Figure 7 is showing the structure validation report of CHEK2 Protein retrieved from PDB.

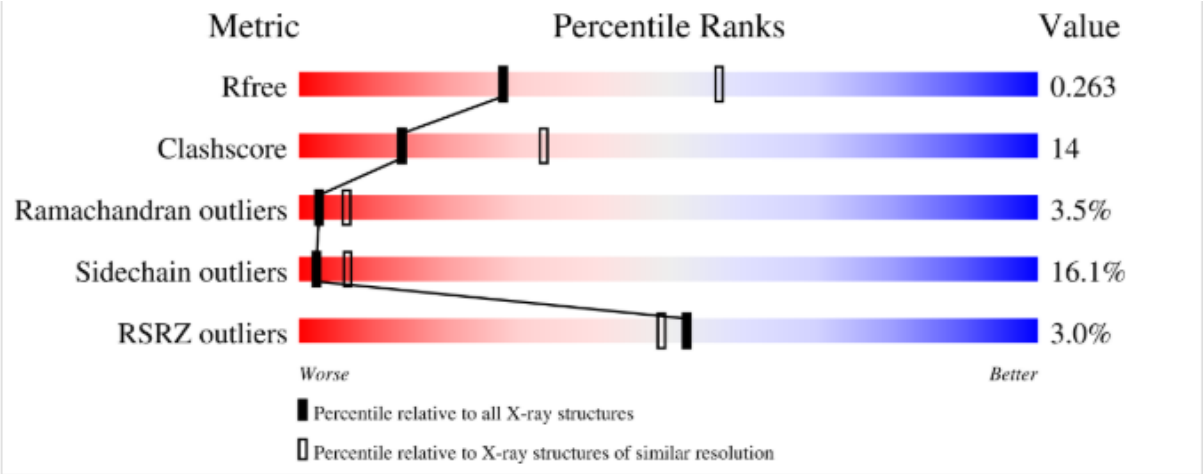

***Figure 7.** Structural validation report of CHEK2 protein retrieved from PDB (PDB ID: 2CN8), showing quality assessment parameters.*

Additionally, a 3D image of the validated protein structure was visualized and included to support structural interpretation in figure 8 and figure 9.

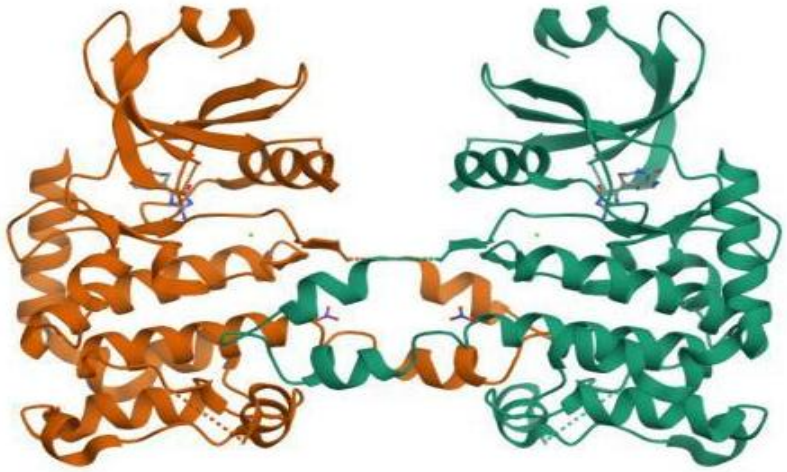

Figure 8. 3D structure of the CHEK2 protein obtained from the PDB database.

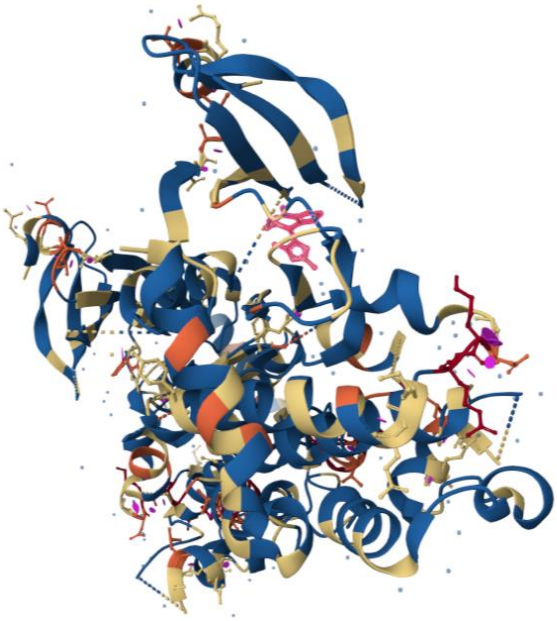

Figure 9. 3D structure of CHEK2 protein used for molecular docking analysis

3.3 Molecular docking Analysis

The molecular docking analysis is the probably most suitable way in identifying best-fit interaction between protein and ligand. Protein-ligand interaction plays a key role in drug discovery. Docking uses the computational simulation to identify the preferred orientation of ligand to a receptor when interacted with each other to form a higher stability complex. Molecular docking was performed using five phytochemicals selected based on literature review. These compounds were docked with the target protein using blind docking on the Dock Thor. All the selected compounds showed stable binding with the protein based on their binding affinity values.

Among them, curcumin showed the highest binding affinity (−9.386 kcal/mol), indicating the strongest interaction the image of the interaction is attatched in figure 10. Other compounds also showed good binding, with piperine (−8.847 kcal/mol), cinnamaldehyde (−8.12 kcal/mol), 6-gingerol (−7.933 kcal/mol), and allicin (−7.855 kcal/mol) demonstrating comparatively stable

interactions. The table 3 is attatched below which shows the docking results. Curcumin is a natural compound which is found in turmeric (*Curcuma longa),* and is widely used as a spice and also in traditional medicine. In recent years, it has attracted attention in cancer research due to its potential anticancer properties. Studies indicates that curcumin may help slow the growth of cancer cells, promote cell death, and reduce inflammation. These effects are believed to occur through its interaction with different pathways involved in cancer development (Unlu et al., 2016).

Table 3*: Docking scores of top five phytochemicals with CHEK 2 protein.*

Ligand Name	*Binding Affinity (kcal/mol)*
Curcumin	*-9.386*
Piperine	*-8.847*
Cinnamaldehyde	*-8.120*
6-Gingerol	*-7.933*
Allicin	*-7.855*

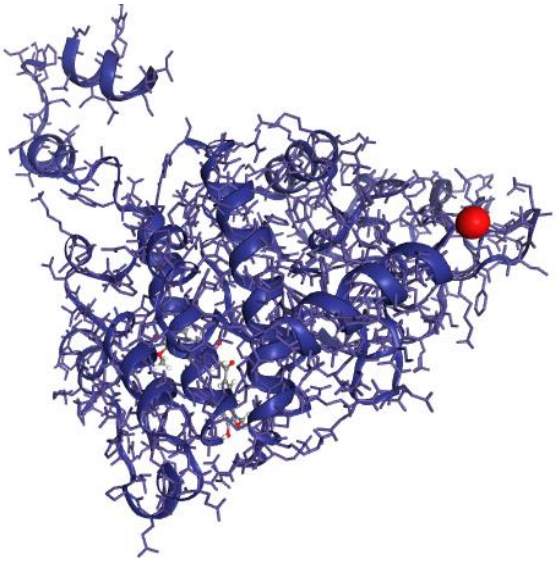

Figure 10. Molecular docking result of Curcumin with CHEK 2 protein showing best binding pose.

4.0 Conclusion

In this study, we tried to explore possible treatment options for breast cancer by using the network analysis and molecular docking approach. From the PPI network analysis, CHEK2 was identified as one of the important genes because it plays a role in DNA damage repair and also helps in controlling the cell cycle. Because of its strong connection with other genes, it can be considered as a potential target, but still there are more detailed studies that are required to fully understand its role.

After that, five phytochemicals like curcumin, piperine, cinnamaldehyde, 6-gingerol and allicin were selected based on previous studies. And these compounds were then docked with the target protein to see how well they are interacting. All of the compounds showed some level of binding with the protein, which means they may have some potential. But among them, curcumin showed the highest binding affinity, so it can be said that it interacts more strongly as compared to others. This kind of indicates that natural compounds might also be useful in cancer treatment, at least at some level.

But at the same time, it is very important to mention that all the results in this study are based on in silico methods. These computational methods provide useful preliminary insights, but they are also not sufficient to confirm the effectiveness of the compounds completely. Therefore, further experimental studies such as in-vitro and in-vivo analyses are required to evaluate their actual therapeutic potential and safety. Overall, the present study suggests that computational approaches can help in identifying very important target proteins and potential drug candidates. It also indicates that plant-based compounds may have potential as alternative therapeutic agents, although more detailed research is still needed before their clinical application.

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Conflict of Interest and Ethical Compliance: All authors confirm that:
i. Any potential conflicts of interest, whether financial or non-financial, have been fully disclosed. – Yes / Not Applicable
ii. All sources of funding and financial support received for the conduct of the study have been appropriately acknowledged, including any updates made during revision. – Yes / Not Applicable
iii. Necessary ethical approvals have been obtained from the relevant institutional or regulatory bodies for studies involving human participants, animals, or sensitive data, wherever applicable, and are clearly stated in the manuscript. – Yes / Not Applicable

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