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IN SILICO DRUG DESIGN IN HUMAN APOPTOSIS INDUCING FACTOR (AIF) IN LUNG CANCER

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ABSTRACT

The malignant condition known as lung cancer is characterized by unchecked growth in the lung's tissues or cells. This aberrant growth develops into a tumour known as a carcinoma. If it is not appropriately or quickly treated, it may metastasize to other areas of the body. In multicellular organisms, apoptosis is a process of programmed cell death in which the cell goes through a sequence of biochemical events that promote cell development, eliminate undesirable cells, preserve tissue integrity, and stop the spread of cancer. It is the cell's method of carrying out a controlled suicide. The cell shrinks, develops blebs, and breaks apart its DNA during apoptosis. Apoptotic cell mutations can result in tissue damage, tumour growth, unchecked cell division, and neurodegenerative diseases. causing apoptosis. Mutations in apoptotic cells can lead to uncontrolled cell proliferation, tumor development, tissue damage, and neurodegenerative disorders. Apoptosis-inducing factor (AIF) is a mitochondrial protein involved in both caspase-dependent and caspase-independent apoptosis pathways. AIF was initially characterized as a cell death mediator and plays an important role in lung cancer. Coiled-Coil-Helix, domain containing Protein 4, or CHCHD4, is involved in oxidative stress regulation and mitochondrial health maintenance. CHCHD4 plays a role in the cellular reaction to damage by interacting with proteins in the inner membrane of the mitochondria. CHCHD4 may have an impact on lung cancer cell survival, particularly in the presence of oxidative stress, which is typical of cancer cells. Computer-aided drug design (CADD), also known as in silico drug design, is a computational method that uses bioinformatics tools to find molecules that resemble drugs. The biological and physicochemical characteristics of possible drug candidates are analysed and predicted with the aid of these tools. Because it offers tools and techniques for analyzing vast amounts of biological data, forecasting drug-target interactions, modelling protein structures, and simulating molecular interactions, bioinformatics is essential to in-silico drug design. This research could pave the way for more effective therapies targeting mitochondrial functions and cell death pathways in cancer, bridging the gap between theoretical research and practical application in drug discovery to improve patient outcomes.

Keywords: - Lung cancer, Apoptosis inducing factor, In-Silico drug design, Molecular Docking, Structure Analysis

I.INTRODUCTION

For many years, lung cancer has been a remarkable public health concern. Around the world, lung cancer is a major cause of death. According to the International Agency for Research on Cancer's (IARC) GLOBOCAN 2020 evaluation of cancer incidence and mortality, lung cancer continues to be the primary cause of cancer-related deaths, accounting for an estimated 1.8 million deaths (18%) in 2020. [1] Lung Cancer is a disease which is caused by uncontrol growth in the abnormal cells or tissues of lung. When this abnormal growth is not treated properly or timely they spread other parts of body by the process of metastasis. Lung cancer causes major death in all other cancers. Lung cancer devolved by the genetic damage in DNA of cell in the airways, mostly caused by inhaling harmful chemicals of cigarette smoke. There are two type of lung cancer small cell lung cancer and non-small cell lung cancer.[9] non-small cell lung cancer is very common type of cancer, adenocarcinoma, squamous cell carcinoma and large cell carcinoma are also common in lung cancer. General symptoms of lung cancer are persistent cough, chest pain, shortness of breath other symptoms are related to location and size of tumour. Lung cancer diagnose by imagining test and biopsy of tumour. Lung cancer mostly diagnosed in later state or advanced state for that reason treatment possible limited.[2]

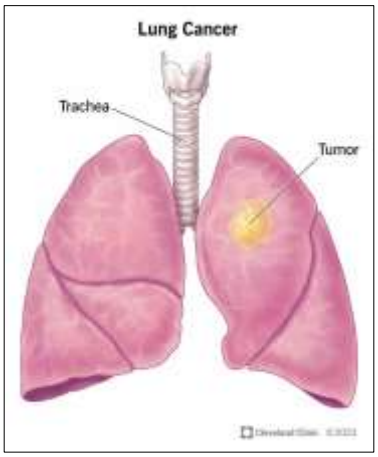

Figure 1: lung cancer

Lung cancer treatments are based on the type of cancer, how much it has spread, and the person's medical history. Early detection of lung cancer conducts better treatments and outcomes.[2]

Treatments include:

- Surgery
- Immunotherapy
- Chemotherapy
- Radiotherapy
- And targeted therapy

Apoptosis is a programmed cell death that found in multicellular cells, where the cell undergoes a series of biochemical events leading to cell development, eliminating unwanted cells, maintaining tissue health and preventing cancer growth it's like a cell committing suicide in controlled manner. In the process of apoptosis the cell shrinks, making blebs and cell DNA is fragmented. After this the cell waste contain are packed into small packets of membrane by immune cell for garbage collection. It is a highly regulated process that can be triggered by internal cell stress or external signals from other cells. Apoptosis activates caspases, enzyme that degrades protein that leading to cell death. Apoptosis is essential process for normal cell development and preventing human body from harmful disease like cancer. If there is mutation in apoptotic cell this led to uncontrolled cell proliferation and tumour development and it can also cause tissue damage and neurodegenerative disorders. The normal average adult human loses 50 to 70 billion cells each day due to apoptosis, while children between 8 and 14 years old, the approximate loss is 20 to 30 billion cells each day.[3]

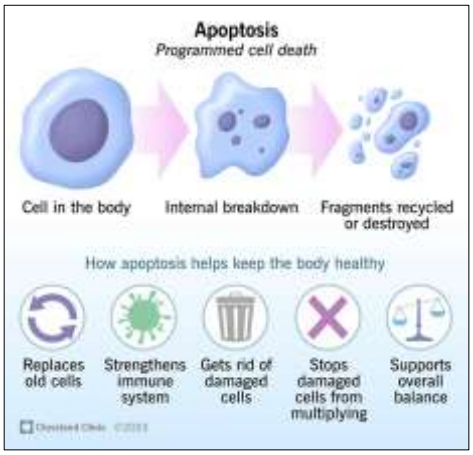

Figure 2: - Apoptosis a programmed cell death

Apoptosis is triggered by a variety of factors through intrinsic and extrinsic pathways. The Intrinsic Pathway of apoptosis trigger sensed stress in cell, DNA damage, Biochemical stress or imbalance of cell chemicals, required growth signals and Mitochondrial dysfunction of cell initiates apoptosis in the cell. Other side Extrinsic pathways of apoptosis triggers receive signal from binding of extracellular ligands of cell surface death receptors and virus infection also trigger cell apoptosis. Sometime Radiation, Hypoxia, Increased Intracellular Calcium amount, Chemotherapy, excess heat exposure, Ethanol, high salt, and UV irradiation can induce an Apoptosis process in the cell.[3]

Apoptosis-inducing factor (AIF) is a mitochondrial protein that plays an important role in both caspase-dependent and caspase-independent apoptosis pathways. AIF was initially characterized as a cell death mediator. In lung cancer, apoptosis-inducing factors play an important part. AIFs play a double role in lung cancer they come up with cell death pathways as well as occupy an essential function of housekeeping inside the mitochondrial cell. In the cell, it determines the rate of oxidative phosphorylation. This oxidative phosphorylation drives the progression of lung cancer. The High amount of AIF expression in non-small cell lung cancer patients associated with low prognosis in this cancer form cell shows high expression of AIFs. While normal cell shows a low expression of AIFs. With the help of, AIF it is easy to target cells with radio chemo therapies because it plays the potential role of prognostic biomarker. Many Studies have shown that AIF may have anti-tumor activity However, some more recent research suggests AIF can also promote cancer cell survival. Although AIF's role can depend on its specific context within the tumor cell microenvironment. CHCHD4 (Coiled-Coil-Helix-Coiled-Coil-Helix Domain Containing Protein 4) is involved in mitochondrial function. It regulates oxidative stress and maintains mitochondrial health. CHCHD4 is also thought to interact with proteins involved in the mitochondrial inner membrane and contribute to cellular response to damage. In the context of lung cancer, CHCHD4 affects cell survival, particularly under conditions of oxidative stress, which is common in cancer cells. [4,5]

The crystal structure of the sample discloses how AIF interacts with the fused N-terminal domain of CHCHD4. This detailed molecular interaction is crucial because it shows the binding sites, structural changes, and potential conformational shifts when the two proteins bind together. By understanding this structure, researchers can identify whether these interactions are critical for cell survival or apoptotic regulation in cancer cells, especially those resistant to traditional treatments like chemotherapy and radiation. The interaction between AIF and CHCHD4 might be a new therapeutic target. If AIF is involved in promoting cancer cell survival or resistance to treatment in lung cancer, disrupting its interaction with CHCHD4 could sensitize cancer cells to apoptosis. By inhibiting this binding or blocking the activity of AIF in the context of CHCHD4, it might be possible to trigger apoptosis in chemo-resistant lung cancer cells, making them more susceptible to treatment. Since both AIF and CHCHD4 are involved in mitochondrial function and stress response, understanding how they work together could reveal how lung cancer cells adapt to metabolic stress and survive in harsh tumor microenvironments. If the interaction between AIF and CHCHD4 is found to be upregulated in lung cancer cells, this could indicate a potential biomarker for cancer progression or resistance to therapy. Targeting the AIF-CHCHD4 complex could be a novel approach in lung cancer treatment, either by directly disrupting this interaction or by modulating the proteins' activities to promote cancer cell death and overcome therapy resistance. [4,5]

Computer-aided drug design (CADD), also known as in silico drug design, is a computational method that uses bioinformatics tools to find molecules that resemble drugs. It aids in the analysis and forecasting of potential drug candidates' biological and physicochemical qualities. A novel approach to cutting the expense, time, and labour needed in the drug discovery process is the use of in silico methods. CADD has grown to be a crucial component of modern drug discovery techniques in order to guide and expedite the process. Knowing the chemical structure of active small molecules (ligand-based) or the target receptor structure (protein-based) is the basis for in silico tools. They are used for discovering and optimizing hit or lead compounds of pharmaceutical interest. [6,7] Computer-aided molecular design is a quality approach which that is implemented in major pharmaceutical and biotechnological research companies.

Two categories of in-silico drug design techniques exist. The process of creating new medications based on the three-dimensional structure of a targeted protein linked to particular illnesses is known as structure-based drug design, or SBDD. In this procedure, a therapeutic target and active ligand are chosen in order to ascertain the target protein's three-dimensional structure. Small molecules are then docked into the binding cavity, synthesized, and its biological properties are optimized. In the Ligand-Based Drug Design approach, ligands that bind to proteins are found by designing molecules with comparable properties. Large databases of compounds are screened by in silico drug design tools to find possible drug candidates. These tools also optimize the structure of promising drug candidates to increase their binding affinity, safety, and effectiveness. Drug compounds to treat a variety of illnesses, such as cancer, diabetes, and bacterial and viral infections, are successfully designed and identified using in silico tools. [8,9]

Because it provides potential tools and techniques for analyzing large biological data, predicting drug-target interactions, modeling protein structures, and simulating molecular interactions, bioinformatics plays a significant role in in-silico drug design. In order to gather and examine the vast amount of biological data, it integrates statistics, computer science, and biology. Researchers can more easily handle large datasets, comprehend their biological processes, and create more accurate and precise drug designs thanks to this multifaceted field. The main applications of bioinformatics include figuring out the structure and function of biomolecules, forecasting drug-target interactions using a variety of computational algorithms, data mining techniques, molecular modeling methods, and in-silico drug development techniques that include target identification, molecular simulation, validation, prioritization, and compound function prediction. In-silico methods used to development of drugs through prediction of compound function, target identification, molecular simulation, validation, and prioritization.

The primary use of in silico drug design is virtual screening, which finds promising drug candidates by using computational screening and large chemical libraries. Drug binding affinity and activity against the target protein are predicted by computational models, including molecular docking, molecular dynamics simulations, and machine learning techniques. By forecasting activity, toxicity, and pharmacokinetics, bioinformatics tools are also utilized in predictive modeling and QSAR (Quantitative Structure-Activity Relationship) analysis. These analyses, which are produced by combining bioinformatics tools with machine learning techniques, enhance compound selection and optimization. [8]

II.MATERIAL AND METHODS

The structural and functional analysis of human apoptosis inducing factor in lung cancer was conducted using combined approach of bioinformatic tools and In-Silico drug design technique. The Crystal structure of human apoptosis-inducing factor (AIF) bound to the fused N-terminal domain of CHCHD4 was retrieved from the Protein Data Bank (PDB ID:8VGY). In molecular graphic programme which is used to visualize three-dimensional structure of protein and nucleic acid. We used this tool to visualize the structure, function and interactions of our target protein molecules, which assist us to design drug**.** Basic Local Alignment Search Tool is an important tool in bioinformatics which is commonly used in drug discovery with sequence analysis. With the help of this tool, we identify drug targets, sequence analysis, protein analysis and understanding evolutionary relationship of our protein sample. Molecular visualization programme tools are a potential tool in bioinformatics to display more accurate and clear 3D structures images of biological targets. We used this tool to visualize structure images, identifying binding sites, analyse drug target interaction of our target protein sample. Web server designed for protein ligand blind docking which is useful method for examine the binding site of ligand and receptors. By the help of web server, we predict binding regions between our target protein and ligand, calculate their centres and size of cavity-by-cavity detection approach, execute docking with open-source docking programme. [10,11,12] Multiple sequence alignment tool used to align protein structure, analyse ligand binding sites, active domain, predicted protein-protein interaction in drug designing process. It is a versatile tool. With the help of this tool, we can identify target and validated it. We also align protein structure and predict protein-protein interaction of our sample. Amino Acid Structural descriptor tool is use to identifies all cavities in our target protein score them based on their physiochemical properties of functional groups that present in the cavities. With the help of this tool, we investigate therapeutic potential of existing drugs. This all tools we used in our research. [13,14,15]

III.RESULT

To performed In-silico drug design and molecular docking, target data was obtained from the National Center for Biotechnology Information (NCBI) database, including the PDB ID (8VGY). The three-dimensional structure of the target was downloaded in PDB format from the Protein Data Bank (PDB) database. The sample which is in PDB format, was ship into the molecular graphic programme software. This was extremely helpful for the structural analysis of 8VGY and understanding its molecular composition. Furthermore, the hydrogen bonds in the molecules were visualized using various features available in the software.

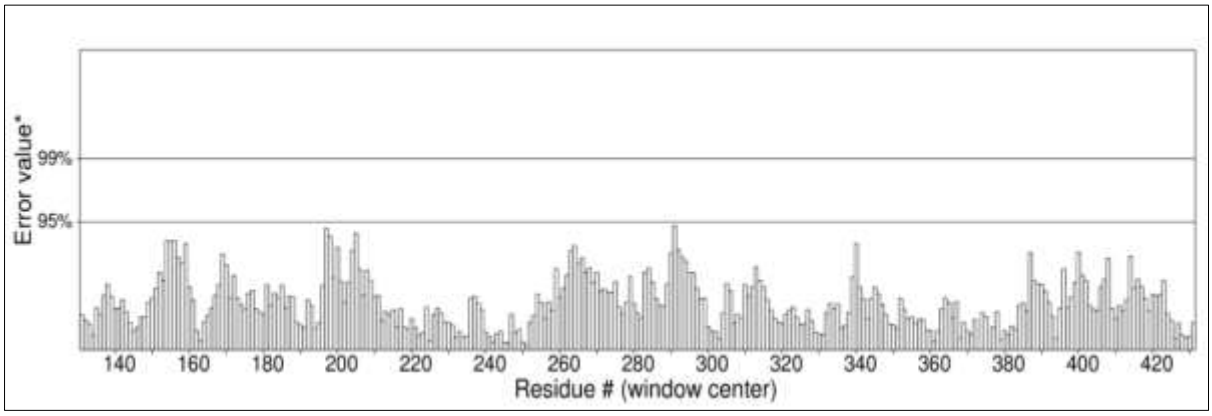

Figure 3: -Structure validation of human lung cancer with score 99.23%

(Structure validation for the sample 8VGY was carried out using the structure validation server, and the overall quality factor of the sample was found to be 99.23%.)

Biological Sequence

sequence (8vgy) human apoptosis-inducing factor (AIF) bound to the fused N-terminal domain of CHCHD4

MLTPEQKQKKAALSASEGEEVPQDKAPSHVPFLLIGGGTAAFAAARSIRARDPGARVLIV
SEDPELPYMRPPLSKELWFSDDPNVTKTLRFKQANGKERSIYFQPPSFYVSAQDLPHIEN
GGVAVLTGKKVVQLDVRDNMVKLNDGSQITYEKCLIATGGTPRSLSAIDRAGAEVKSRTT
LFRKIGDFRSLEKISREVKSITIIGGGFLGSELACALGRKARALGTEVIQLFPEKGNMGK
ILPEYLSNWTMEKVRREGVKVMPNAIVQSVGVSSGKLLIKLKDGRKVETDHIVAAVGLEP
NVELAKTGGLEIDSDFGGFRVNAELQARSNIWVAGDAACFYDIKLGRRRVEHHDHAVVSG
RLAGENMTGAAKPYWHQSMFWSDLGPDVGYEAIGLVDSSLPTVGVFAKATAQDNPKSATE
QSGTGIRSESETESEASEITIPPSTPAVPQAPVQGEDYGKGVIFYLRDKVVVGIVLWNIF
NRMPIARKIIKDGEQHEDLNEVAKLFNIHEDSGSGPGSGSMSYCRQEGKDRIIFVTKEDH
ETPSSAELVADDPNDPYEEHGLILPLEVLFQ
Progressive alignment progress: 50 % (1 out of 2)

Progressive alignment progress: 100 % (2 out of 2)

Red part indicates highly conserved positions and blue indicates lower conservation. In multiple sequence Alignment Analysis facilitating the alignment and comparison of protein sequence, identification of critical region and mutation that may contribute to cancer development

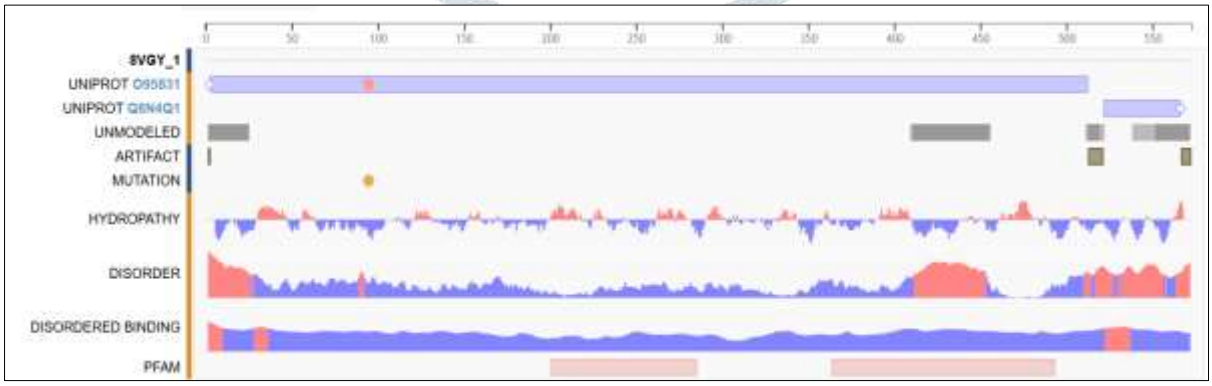

Figure 4: - Sequence annotation of human lung cancer (8VGY)

Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
Chain A, Apoptosis-inducing factor 1, mitochondrial Mitochondrial intermembrane space import and asse...	Homo sapiens	1172	1172	100%	0.0	100.00%	571	6VGY_A
Chain A, Apoptosis-inducing factor 1, mitochondrial [Homo sapiens]	Homo sapiens	1045	1045	89%	0.0	100.00%	543	5KVH_A
Chain A, Apoptosis-inducing factor 1, mitochondrial [Homo sapiens]	Homo sapiens	1041	1041	89%	0.0	99.80%	543	8D3J_A
apoptosis-inducing factor 1, mitochondrial isoform AIF-exB precursor [Homo sapiens]	Homo sapiens	1041	1041	89%	0.0	99.80%	609	NP_665811.1
apoptosis-inducing factor 1, mitochondrial isoform AIF precursor [Homo sapiens]	Homo sapiens	1041	1041	89%	0.0	99.80%	613	NP_004199.1
Chain A, Apoptosis-inducing factor 1, mitochondrial [Homo sapiens]	Homo sapiens	1040	1040	89%	0.0	99.80%	543	8D3G_A
Chain A, APOPTOSIS INDUCING FACTOR 1, MITOCHONDRIAL [Homo sapiens]	Homo sapiens	1040	1040	89%	0.0	99.80%	511	4BUR_A
Chain B, Apoptosis-inducing factor 1, mitochondrial [Homo sapiens]	Homo sapiens	1040	1040	89%	0.0	99.80%	543	8D3I_B

Figure 5: - Sequence similarity search for human lung cancer

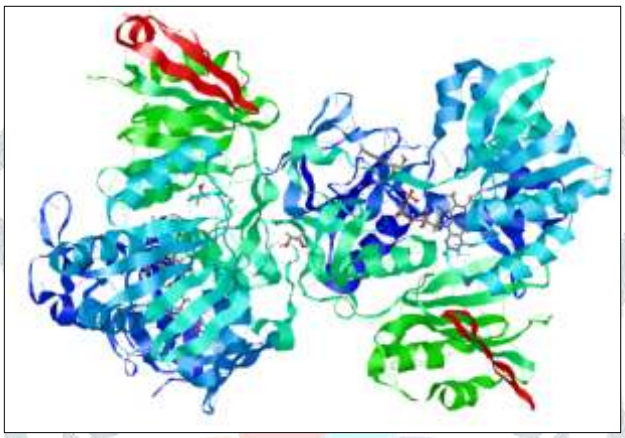

Figure 6: - Hydrogen bond analysis (structure-function relationship)

Figure 7: - Representation of Secondary structure Alpha helix magenta beta sheet yellow

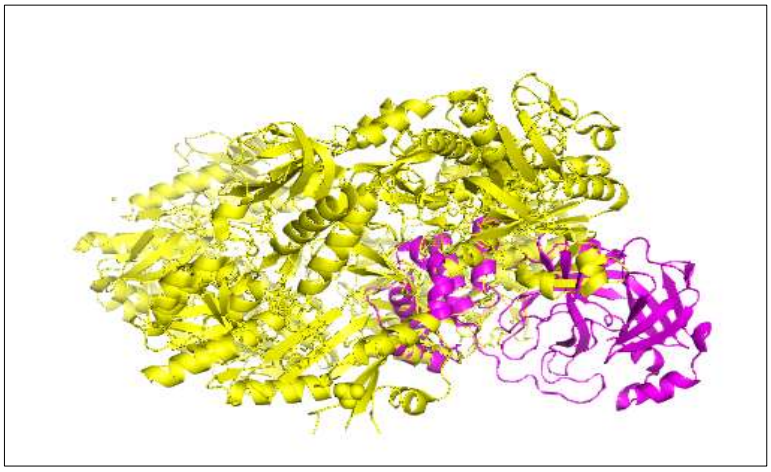

Figure 8: - Protein- protein docking to check similarities between identical structure

Computational prediction RMSD value of 0.9 Å (angstroms) indicates a high degree of structural similarity between the two protein conformations being compared in terms of their atomic positions. It showing in analysis Conformational Consistency in protein dynamics, such as during molecular dynamics simulations, an RMSD of 0.9 Å shows the stable conformation with only minor fluctuations in between Alignment.

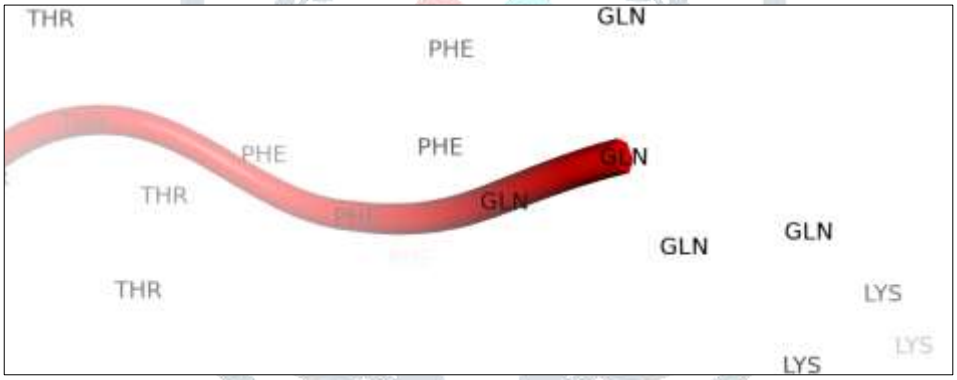

Figure 9: -Residue representing B-Factor analysis (GLN, LYS, PHE)

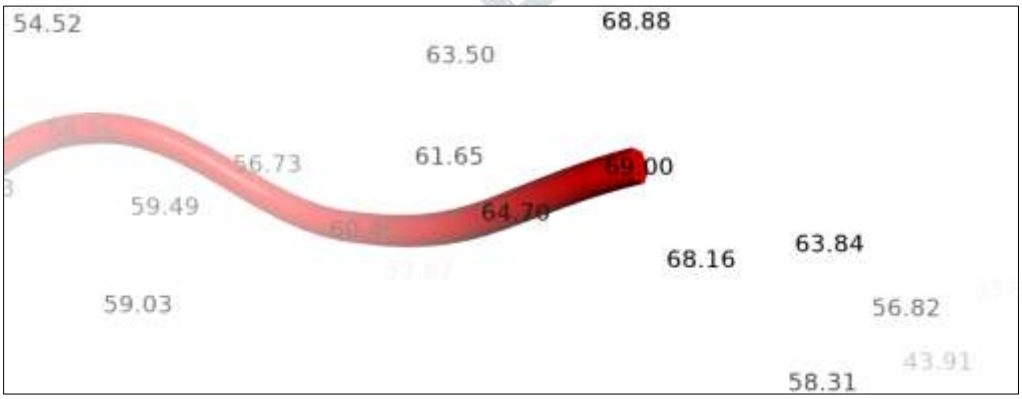

Figure 10: - B- factor analysis in pymol score 69 red loop c terminal

In computational analysis GLN, PHE, LYS are essential for normal cellular function, due to altered metabolism in lung cancer makes them harmful, these amino acid act as a fuel for tumor growth that alter immune response and disordered

of protein sample. In structure analysis of atoms, bond interaction analysis of 8VGY by three-dimensional visualization tool, Glutamine, Phenylalanine and lysine can potentially contribute to the progression of lung cancer making them

harmful. Increase in glutamine metabolism it is support tumor growth and proliferation. Elevated Phenylalanine level in lung cancer may fuel aggressive tumor behaviour. Dysregulated lysine modifications can activate oncogenes or silence tumor suppressor gene, promoting lung cancer progression. They responsible for metabolic reprogramming and Tumour Microenvironment. In 3D structure red loop indicates high B-factors (high flexibility or disorder).

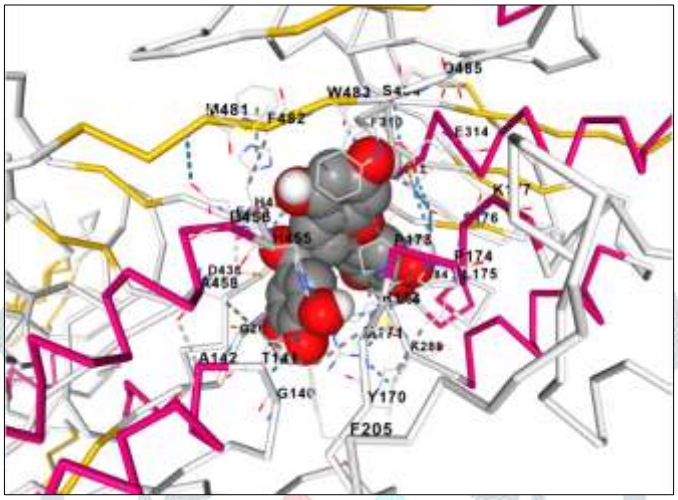

Figure 11: - Protein ligand (Epigallocatechin Gallate) interaction molecular docking score -10.4

Table 1: Molecular Docking Table

Sr number	PDB file name	Drug name	Autodock vina score	Binding affinity
1	8VGY	Epigallocatechin Gallate	-10.4	Excellent strong binding affinity
2	8VGY	Berberine	-8.2	Strong binding affinity
3	8VGY	B-caroten	8.3	Weak binding affinity

In docking score analysis score is -10 that is excellent one (Stable binding) indicate a strong binding affinity between ligand and receptor. In ligand Berberine Score -8.1 indicate strong interaction between the ligand and binding site of receptor.

Cavities	
cavity_1_TVIGNSRPACDEFLHMWKYQ	cavity_2_WHDTAPMSGRYFQVELINCK
cavity_3_KVNLITGEPSDAYRFH	cavity_4_YTSEGRDAVPKHIFLN
cavity_5_NASQMDREKLVPTGWIYHF	cavity_6_EIVNPGSTCDFRLKHAMQ
cavity_7_RQFAPGTYVHSDMKELWNI	cavity_8_AKHVRWDQIEPYSMLTGFNC
cavity_9_IAVRKLDNQTEPGYWSF	cavity_10_NVREIFGAYDSCPKLH
cavity_11_KNRQAPFIMHVEDLTWGSY	cavity_12_TARGIKLNYVEDFPSC
cavity_13_WKMSQDYIHFAGRLVEPTC	cavity_14_KARNFQSPYEIMHVWDLTG
cavity_15_RTAPGEHMNKYDWSFQL	cavity_16_FEHRVLMPGNSTKIDA

Figure 12:In molecular docking cavity identification on a proteomic sample (8vgy,4BUR)

Active Site Prediction Analysis (Cavity point identification)

```
File Name       =  cavity_1_TVIGNSRPACDEFLHMWKYQ
Cavity point -8.080 18.948  -50.555
Volume of the Cavity = 2062

1       THR     488     HB      -19.633 13.976  -62.781
2       THR     488     1HG2    -18.425 11.977  -63.456
3       ARG     519     HE      -18.027 19.417  -64.145
4       ARG     519     2HB     -14.259 17.613  -65.253
5       ARG     519     3HB     -13.854 18.893  -66.104
6       PRO     520     3HD     -13.732 15.072  -65.393
7       PRO     520     3HG     -11.923 14.192  -64.362
8       PRO     520     3HB     -10.087 13.654  -65.541
9       PRO     520     HA      -10.442 15.878  -65.905
10      SER     523     3HB     -7.590  20.027  -66.503
11      LYS     524     3HZ     -6.706  15.193  -64.859
12      THR     607     O       -23.069 22.433  -59.412
13      GLY     609     2HA     -19.937 24.147  -57.256
14      GLY     609     O       -18.816 24.402  -60.079
```

Figure 13: - Cavity point identification in cavity 1

When we interpretated cavity point -19 kcal/mol shows very strong binding interaction between the ligand and cavity point this is fit well (favourable binding region). On the other side Binding Affinity Interpretated +7 kcal/mol positive value suggest very weak and no binding (unfavourable binding site).

IV.CONCULISON

The crystal structure of AIF bound to CHCHD4 offers an important tool for understanding the molecular mechanisms that allow lung cancer cells to survive and evade apoptosis. By take a look at the functional relationship between these two proteins, researchers can potentially develop new therapeutic strategies to enhance apoptosis in lung cancer cells, especially those resistant to traditional treatments. Drug discovery in modern drug discovery, helping to bridge the gap between theoretical research and practical application in developing new effective medication for patient's outcomes. This research could pave the way for more effective therapies targeting mitochondrial functions and cell death pathways in cancer.

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REFERENCES

1. Lemjabbar-Alaoui H, Hassan OU, Yang YW, Buchanan P. Lung cancer: Biology and treatment options. Biochim Biophys Acta. 2015 Dec;1856(2):189-210. doi: 10.1016/j.bbcan.2015.08.002. Epub 2015 Aug 19. PMID: 26297204; PMCID: PMC4663145.
2. Leiter, A., Veluswamy, R.R. & Wisnivesky, J.P. The global burden of lung cancer: current status and future trends. *Nat Rev Clin Oncol* 20, 624–639 (2023). https://doi.org/10.1038/s41571-023-00798-3
3. Sevrioukova IF. Apoptosis-inducing factor: structure, function, and redox regulation. Antioxid Redox Signal. 2011 Jun 15;14(12):2545-79. doi: 10.1089/ars.2010.3445. Epub 2011 Mar 10. PMID: 20868295; PMCID: PMC3096518.
4. Daniele Bano, Jochen H.M. Prehn, Apoptosis-Inducing Factor (AIF) in Physiology and Disease: The Tale of a Repented Natural Born Killer, eBioMedicine, Volume 30,2018, Pages 29-37, ISSN 2352-3964, https://doi.org/10.1016/j.ebiom.2018.03.016.
5. Wong RS. Apoptosis in cancer: from pathogenesis to treatment. J Exp Clin Cancer Res. 2011 Sep 26;30(1):87. doi: 10.1186/1756-9966-30-87. PMID: 21943236; PMCID: PMC3197541.
6. Zhang X, Wu F, Yang N, Zhan X, Liao J, Mai S, Huang Z. In silico Methods for Identification of Potential Therapeutic Targets. Interdiscip Sci. 2022 Jun;14(2):285-310. doi: 10.1007/s12539-021-00491-y. Epub 2021 Nov 26. PMID: 34826045; PMCID: PMC8616973.
7. Kumari, Uma & Gupta, Taneya & Gupta, Chaitanya & Virk, Navjot. (2023). INSILICO Analysis of CADD Approach for Alzheimer Disease Caused by Heavy Metals in Humans. International Journal for Research in Applied Science and Engineering Technology. 11. 1368-1373. 10.22214/ijraset.2023.54875.
8. Chang Y, Hawkins BA, Du JJ, Groundwater PW, Hibbs DE, Lai F. A Guide to In Silico Drug Design. Pharmaceutics. 2022 Dec 23;15(1):49. doi: 10.3390/pharmaceutics15010049. PMID: 36678678; PMCID: PMC9867171.
9. Agamah FE, Mazandu GK, Hassan R, Bope CD, Thomford NE, Ghansah A, Chimusa ER. Computational/in silico methods in drug target and lead prediction. Brief Bioinform. 2020 Sep 25;21(5):1663-1675. doi: 10.1093/bib/bbz103. PMID: 31711157; PMCID: PMC7673338.
10. Kumari, Uma & Tripathi, Kartik. (2023). Computational Analysis and Molecular Docking Approach for Liver Cancer. International Journal for Research in Applied Science and Engineering Technology. 11. 1828 to 1633. 10.22214/ijraset.2023.54927.
11. Meng XY, Zhang HX, Mezei M, Cui M. Molecular docking: a powerful approach for structure-based drug discovery. Curr Comput Aided Drug Des. 2011 Jun;7(2):146-57. doi: 10.2174/157340911795677602. PMID: 21534921; PMCID: PMC3151162.
12. Rosignoli S, Paiardini A. Boosting the Full Potential of PyMOL with Structural Biology Plugins. Biomolecules. 2022 Nov 27;12(12):1764. doi: 10.3390/biom12121764. PMID: 36551192; PMCID: PMC9775141.
13. Kumari, Uma & Agrawal, Nidhi. (2023). NGS and Mutational Profile Analysis of Non-Small-Cell Lung Carcinoma (NSCLC). International Journal for Research in Applied Science and Engineering Technology. 11. 3090-3094. 10.22214/ijraset.2023.50880.
14. Kumari, Uma & Gupta, Shruti. (2023). NGS and Sequence Analysis with Biopython for Prospective Brain Cancer Therapeutic Studies. International Journal for Research in Applied Science and Engineering Technology. 11. 10.22214/ijraset.2023.50885.
15. Uma Kumari, Vineeta Johri, Swarali Dhopate, Tijil Jha Structure Based Drug Designing for the prediction of epitope for targeting Malignant brain Tumor, 2024 JETIR July 2024, Volume 11, Issue 7 www.jetir.org (ISSN-2349-5162)