International Journal of Current Trends in Engineering & Technology
www.ijctet.org, ISSN: 2395-3152
Volume: 04, Issue: 01 (January -February, 2018)

IN SILICO SCREENING OF COMPOUNDS FROM TURMERIC (Curcuma longa L.) AGAINST CANCER CAUSING PROTEINS

*DSVGK Kaladhar[1, *], Tejaswani Banjara[2], Shri Kant[3], Shraddha Tiwari Mishra[4], Santosh Kumari Dupplala[5]*
[1,2,4,5]Department of Microbiology and Bioinformatics, UTD, Bilaspur University, Bilaspur (CG)
[3]Computational structural Biology laboratory, IIT, Kharagpur
*Corresponding author- Dr. DSVGK Kaladhar, dkaladhar@gmail.com 9885827025

ABSTRACT :- *Turmeric (Curcuma longa L) has an extensive history of use in Ayurvedic medicine in the treatment of inflammatory conditions. Several pharmacological activities, including antioxidant and antimicrobial properties, have been attributed due to presence of secondary metabolite, curcumin. Present article focuses on in silico anti-cancer properties of phytocompounds present in turmeric. Based on the present studies, in-silico screening approaches suggests that anti-cancer properties of different compounds from turmeric compounds like 1-(4-hydroxy-3-methoxyphenyl)-5-(4-hydroxyphenyl)-1, 4-pentadiene-3-one, curcumin and 1,5-bis(4-hydroxy-3-methoxyphenyl)-penta-(1E,4E)-1,4-dien-3-one shows the better anti-cancer activities against cervical cancer (CRAS), lung cancer (SOX 2), CPL1 and BRCA1 related proteins respectively.*

Keywords:- in silico, anticancer activity, turmeric.

INTRODUCTION

Cancer is a cellular disease that originates from malignantly transformed normal human cell. Although cancer is common in humans, cancer is a rare cellular event with a risk of 1/10000 billion for a normal cell to become a cancer cell. Turmeric is common spice in an Indian food derived from the rhizomes of the plant (*Curcuma longa*) and has an ancient history of use in Ayurvedic and Chinese medicine as a treatment for inflammatory conditions [1,2]. *C. longa* is a perennial member of the Zingiberaceae family and is cultivated in India and other parts of Southeast Asia. Curcumin is the yellow pigment isolated from the rhizome of perennial herb *Curcuma longa* [3]. Curcumin, a primary active constituent of turmeric and the one responsible for its vibrant yellow color, the chemical structure of curcumin was elucidated in 1910 by Lampe and Milobedzka [1] and it was reported to be a derivative of methane substituted by 2-ferulic acid residues. It has been commonly used as spice and medicine, the traditional use of turmeric as food additives and to impart yellow color in textile and pharmaceutical industries. Moreover, turmeric medicinal properties are well known for its anti-inflammatory, topical remedy in skin care and various kind of cancer treatment. The role of curcumin, one of the most studied chemopreventive agents, on anti-inflammatory and cancer activity has been well appreciated. Curcuminoids have shown different activities based on the structural and functional positions of elements present in compounds that were isolated from turmeric. A recent study suggested that curcumin had the relative higher potency for suppression of tumor necrosis factor (TNF)-induced nuclear factor-kB (NF-kB) activation than that of demethoxycurcumin and bisdemethoxycurcumin, while tetra hydro-curcumin without the conjugated bonds in the central seven-carbon chain was completely inactive. The results suggest that the methoxy groups on the phenyl ring have critical role but conjugated bonds in the central seven-carbon chain also important for curcuminoids' NF-kB activity [9]. However, the suppression of proliferation of various tumor cell lines by curcumin [(1,2,7)], emethoxycurcumin, and bisdemethoxycurcumin was found to be comparable; indicating the methoxy groups play the minimum role in the antiproliferative effects of curcuminoids. It has long been realized that immunohistochemistry can add an important new level of information on top of morphology and that protein expression patterns in a cancer may yield crucial diagnostic and prognostic information. About 708 spots of tissues and cells has been analyzed previously in each antibody and the resulting data and images have been presented in the Human Protein Atlas [10].

Table 1. Compounds from *Curcuma longa*

No.	Compound Name	Compound Type	Ref.
1	curcumin (curcumin I)	Diarylheptanoid	[4,5]
2	demethoxycurcumin (curcumin II)	Diarylheptanoid	[4,5]
3	1-(4-hydroxy-3-methoxyphenyl)-7-(3, 4-dihydroxyphenyl)-1, 6-heptadiene-3, 5-dione	Diarylheptanoid	[6]
4	1-(4-hydroxyphenyl)-7-(3, 4-dihydroxyphenyl)-1, 6-heptadiene-3, 5-dione	Diarylheptanoid	[6]
5	bisdemethoxycurcumin (curcumin III)	Diarylheptanoid	[4]
6	Tetrahydroxycurcumin	Diarylheptanoid	[4]

7	5-hydroxyl-1-(4-hydroxy-3-methoxyphenyl)-7-(4-hydroxyphenyl)-4,6-heptadiene-3-one	Diarylheptanoid	[7]
8	5-hydroxyl-1,7-bis(4-hydroxy-3-methoxyphenyl)-4,6-heptadiene-3-one	Diarylheptanoid	[7,8]
9	1,7-bis(4-hydroxyphenyl)-1-heptene-3,5-dione	Diarylheptanoid	[7]
10	5-hydroxyl-7-(4-hydroxy-3-methoxyphenyl)-1-(4-hydroxyphenyl)-4,6-heptadiene-3-one	Diarylheptanoid	[7]
11	3-hydroxy-1,7-bis-(4-hydroxyphenyl)-6-heptene-1,5-dione	Diarylheptanoid	[6]
12	1,5-dihydroxy-1-(4-hydroxy-3-methoxyphenyl)-7-(4-hydroxyphenyl)-4,6-heptadiene-3-one	Diarylheptanoid	[6]
13	1,5-dihydroxy-1-(4-hydroxyphenyl)-7-(4-hydroxy-3-methoxyphenyl)-4,6-heptadiene-3-one	Diarylheptanoid	[6]
14	1,5-dihydroxy-1,7-bis(4-hydroxy-3-methoxyphenyl)-4,6-heptadiene-3-one	Diarylheptanoid	[6]
15	1,5-dihydroxy-1,7-bis(4-hydroxyphenyl)-4,6-heptadiene-3-one	Diarylheptanoid	[6]
16	1,5-epoxy-3-carbonyl-1,7-bis(4-hydroxyphenyl)-4,6-heptadiene	Diarylheptanoid	[3]
17	Cyclocurcumin	Diarylheptanoid	[8,9]
18	1,7-bis(4-hydroxy-3-methoxyphenyl)-1,4,6-heptatrien-3-one	Diarylheptanoid	[8]
19	1,7-bis-(4-hydroxyphenyl)-1,4,6-heptatrien-3-one	Diarylheptanoid	[6-8]
20	1,5-bis(4-hydroxyphenyl)-penta-(1E,4E)-1,4-dien-3-one	Diarylheptanoid	[4,6,7]
21	1-(4-hydroxy-3-methoxyphenyl)-5-(4-hydroxyphenyl)-1, 4-pentadiene-3-one	Diarylheptanoid	[6]
22	1,5-bis(4-hydroxy-3-methoxyphenyl)-penta-(1*E*,4*E*)-1,4-dien-3-one	Diarylheptanoid	[4,6]
23	4"-(4"'-hydroxyphenyl)-2"-oxo-3"-butenyl-3-(4'-hydroxyphenyl-3'-methoxy)-propenoate	Phenylpropene	[3,6,7]
24	4"-(4"'-hydroxyphenyl-3-methoxy)-2"-oxo-3"-butenyl-3-(4'-hydroxyphenyl)-propenoate	Phenylpropene	[4,6]
25	calebin-A	Phenylpropene	[4]
26	(*E*)-4-(4-hydroxy-3-methoxyphenyl)but-3-en-2-one	Phenylpropene	[6,7]
27	(*E*)-ferulic acid	Phenylpropene	[3,6]
28	(*Z*)-ferulic acid	Phenylpropene	[4,6,8]
29	vanillic acid	Phenolic	6
30	Vanillin	Phenolic	[6,8]

MATERIALS AND METHODS

System properties

Intel (R)Core (TM)2Duo CPU, 2GHz Processor with 4 GB RAM and 32 bit System

ChemSW

Various phytochemical compounds present in curcuma longa structure was taken from various journals and literature, after the literature survey. 3D structure of ligands was designed using ChemSW tool, and all 3D structure obtained from ChemSW was saved in .pdb format.

The Human Protein Atlas: Cancer target selection

Many genes showing diverse normal functions leading to abnormality within the system are involved in human cancer. More than 500 genes have been identified as strongly implicated in the process of transforming normal cells to cancer cells. The expression of these genes in normal cells contributes to normal growth, survival and function, whereas dysregulated expression, including overexpression, loss of expression or expression of a defect protein, in cancer cells contributes to ungoverned tumor growth. Altered gene expression can be caused by coarse structural and numerical chromosomal rearrangements, specific gene amplifications, silencing of transcription through methylation and mutations, e.g. point mutations with single base substitutions and small inserts or deletions, that lead to loss or gain of function of the corresponding protein [11]. Cancer proteins were selected from the cancer proteome (http://www.proteinatlas.org/humanproteome/cancer). Important cancer target protein was taken from The Human Protein Atlas. And selected target molecules were designed based on Swiss model (https://swissmodel.expasy.org/).

Protein Data Bank

Archiving of 3D protein structures from Protein Data

Bank (PDB) is a single worldwide repository of protein information related to large biological molecules, including proteins and few nucleic acids. These are the molecules of life that are found in all organisms including bacteria, yeast, plants, flies, other animals, and humans. Understanding the shape of a molecule deduce a structure's role in human health and disease, and in drug development [12].

Table 2. The pdb molecules are constructed using Swissmodel

Types of cancer	Gene associated with cancer	NCBI Accession Number
Colorectal cancer	Apc	AAA03586
brcal cancer	Cpl-1	KTF28416
Breast cancer	ERBB2	CCD83327
cervical cancer	JUN	NP_000413
ovarian cancer	MYC	Q969H0
Pancreatic cancer	pik3ca	P31749
human lung cancer	sox2	AAH13923
Colorectal cancer	CRAS	P01116

The structures in the archive range from tiny proteins and bits of DNA to complex molecular machines like the ribosome. The PDB archive is available at no cost to users. The PDB archive is updated weekly. PDB files format were used to save the ligands as well as cancer causing protein after modeling. Indeed, most of the docking servers and tools requires the .pdb format.

String database

STRING is a database of known and predicted protein-protein interactions The interactions include direct (physical) and indirect (functional) associations; they stem from computational prediction, from knowledge transfer between organisms, and from interactions aggregated from other (primary) databases [(12,13]. Network biology approaches was adopted for the identification of important protein-protein interactions, important for the cross-talk between different selected cancer types. Namely APC, cpl-1, ERBB2, JUN, MYC pilc3ca, CRAS and SOX 2 selected cancer proteins-protein interaction study was done using String Database (https://string-db.org/).

Protein-ligand docking

Protein ligand docking was carried out to screen the phytochemical compounds present in turmeric, to identify the potential anti-cancer activity in selected cancers type proteins are Apc, cpl-1, ERBB2, JUN, MYC, pilc3ca SOX 2 and CRAS respectively. iGEMDOCK, A Graphical Environment for Recognizing Pharmacological Interactions and Virtual Screening Hence *in silico* identification of potential compounds were conducted by docking method using iGEMDOCK v1.6 [(14-16)].

RESULTS AND DISCUSIONS

Ligand molecules structure elucidation

The designing and optimization of compounds selected for screening (Figure 1)

Network profiling of potential cancer targets

Network analysis of the all seven-cancer target proteins were constructed using string database tool and network analysis was done (Figure 2).

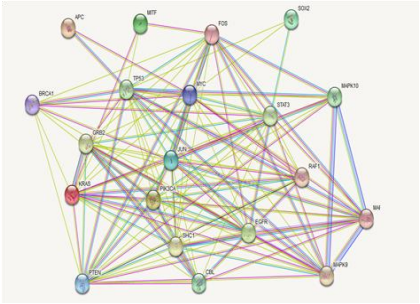
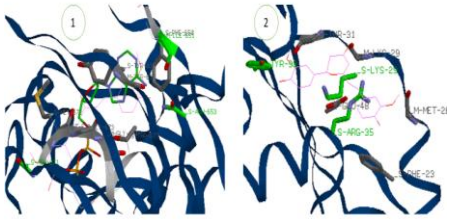
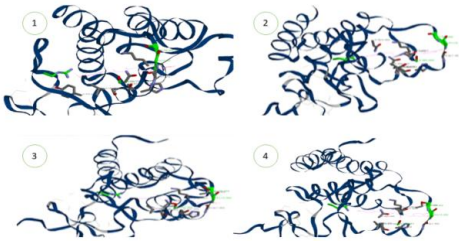


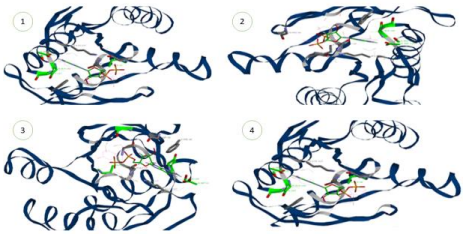
Figure 2. Network construction for proteins causing cancer using String



Best conformations of CPL 1 BRCA 1 related protein shown as ribbon models blue in color, ligand as green and red in color (stick model colored by atom type)



Best conformations of SOX 2 protein shown as ribbon models blue in color, ligand as green and red in color (stick model colored by atom type)



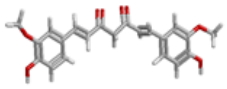
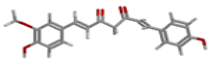
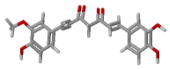
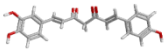
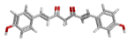
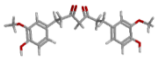
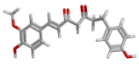
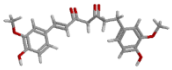
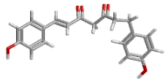
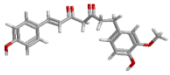
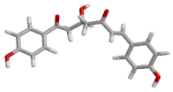
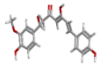
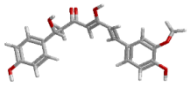
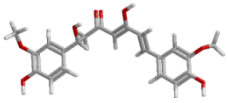
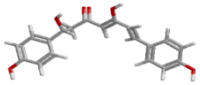
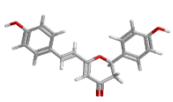
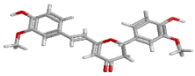
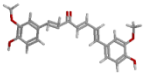
Best conformations of CRAS protein shown as ribbon models blue in color, ligand (stick model colored by atom type).

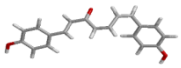
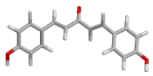
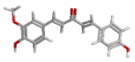
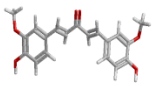
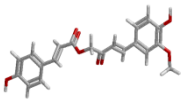
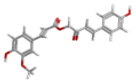
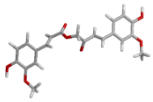
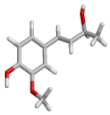
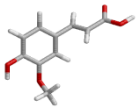
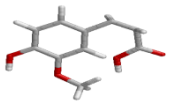
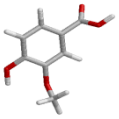
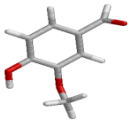
Figure 5. Docking reports shown docking results of diseased proteins (Cancer) with ligands.

Discussions

In-silico approaches to elucidate the anticancer activity of thirty (30) different compounds with different 7 types of cancer target proteins was done with the help of iGEMDOCK. Different anti-cancer targets were selected from "The Human Protein Altus", then after series of computation tools were utilized to In-silico screen the anticancer ligand from turmeric. Several *in silico* docking studies has proved good results with wet lab technologies with docking softwares in cancer studies [(17-20)]

Figure 1. Designed compounds using ChemSW

1. Curcumin (curcumin I) 	2. Demethoxycurcumin (curcumin II) 	3. 1-(4-hydroxy-3-methoxyphenyl)-7-(3, 4-dihydroxyphenyl)-1, 6-heptadiene-3,  5-dione
4. 1-(4-hydroxyphenyl)-7-(3, 4-dihydroxyphenyl)-1, 6-heptadiene-3, 5-dione 	5. Bisdemethoxycurcumin (curcumin III) 	6. Tetrahydroxycurcumin 
7. 5-hydroxyl-1-(4-hydroxy-3-methoxyphenyl)-7-(4-hydroxyphenyl)-4,6-heptadiene-  3-one	8. 5-hydroxyl-1,7-bis(4-hydroxy-3-methoxyphenyl)-4,6-heptadiene-3-one 	9. 1,7-bis(4-hydroxyphenyl)-1-heptene-3,5-dione 
10. 5-hydroxyl-7-(4-hydroxy-3-methoxyphenyl)-1-(4-hydroxyphenyl)-4,6-heptadiene-3-one 	11. 3-hydroxy-1,7-bis-(4-hydroxyphenyl)-6-heptene-1,5-dione 	12. 1,5-dihydroxy-1-(4-hydroxy-3-methoxyphenyl)-7-(4-hydroxyphenyl)-4,6-heptadiene-3-one 
13. 1,5-dihydroxy-1-(4-hydroxyphenyl)-7-(4-hydroxy-3-methoxyphenyl)-4,6-heptadiene-3-one 	14. 1,5-dihydroxy-1,7-bis(4-hydroxy-3-methoxyphenyl)-4,6-  heptadiene-3-one	15. 1,5-dihydroxy-1,7-bis(4-hydroxyphenyl)-4,6-heptadiene-3-one 
16. 1,5-epoxy-3-carbonyl-1,7-bis(4-hydroxyphenyl)-4,6-heptadiene 	17. cyclocurcumin 	18. 1,7-bis(4-hydroxy-3-methoxyphenyl)-1,4,6-heptatrien-3-one 

19. 1,7-bis-(4-hydroxyphenyl)-1,4,6-heptatrien-3-one 	20. 1,5-bis(4-hydroxyphenyl)-penta-(1E,4E)-1,4-dien-3-one 	21. -(4-hydroxy-3-methoxyphenyl)-5-(4-hydroxyphenyl)-1, 4-pentadiene-3-one 
22. 1,5-bis(4-hydroxy-3-methoxyphenyl)-penta-(1*E*,4*E*)-1,4-dien-3-one 	23. 4"-(4"'-hydroxyphenyl)-2"-oxo-3"-butenyl-3-(4'-hydroxyphenyl-3'-methoxy)-propenoate 	24. 4"-(4"'-hydroxyphenyl-3-methoxy)-2"-oxo-3"-butenyl-3-(4'-hydroxyphenyl)-propenoate 
25. calebin-A 	26. (*E*)-4-(4-hydroxy-3-methoxyphenyl) but-3-en-2-one 	27. (*E*)-ferulic acid 
28. (*Z*)-ferulic acid 	29. vanillic acid 	30. vanillin 

Docking of various types of cancer causing proteins with the important phytochemical presents in *curcuma longa* using iGEMDOCK, with normal mode setting were utilized (Table 3)

Table 3. Docking scores obtained from iGEMDOCK

Ligand Name	CPL1 (BRCA1 related)	ERBB2	SOX 2	PIK3CA	JUN	CRAS	MYC
curcumin (curcumin I)	-94.08	-75.81	-115.94	-88.36	-79.53	-94.78	-84.9
demethoxycurcumin (curcumin II)	-95.72	-79.87	-105.13	-81.24	-79.49	-87.45	-82.77
1-(4-hydroxy-3-methoxyphenyl)-7-(3, 4-dihydroxyphenyl)-1, 6-heptadiene-3, 5-dione	-96.74	-75.33	-108.89	-85.65	-77.83	-90.43	-90.52
1-(4-hydroxyphenyl)-7-(3, 4-dihydroxyphenyl)-1, 6-heptadiene-3, 5-dione	-87.05	-68.57	-106.13	-76.56	-78.8	-89.51	-84.64
bisdemethoxycurcumin (curcumin III)	-82.87	-69.44	-95.85	-70.29	-78.5	-85.89	-84.53
Tetrahydroxycurcumin	-92.05	-72.33	-92.74	-86.11	-81.16	-95.68	-87.87
5-hydroxyl-1-(4-hydroxy-3-methoxyphenyl) -7-(4-hydroxyphenyl)-4,6-heptadiene-3-one	-97.29	-72.16	-90.52	-84.11	-76.17	-100.7	-85.56

5-hydroxyl-1,7-bis (4-hydroxy-3-methoxyphenyl) -4,6-heptadiene-3-one	-93.32	-69.42	-97.58	-93.98	-74.28	-98.75	-91.53
1,7-bis(4-hydroxyphenyl) -1-heptene-3,5-dione	-86.61	-66.67	-89.36	-80.76	-69.05	-107.64	-83.44
5-hydroxyl-7- (4-hydroxy-3-methoxyphenyl) -1-(4-hydroxyphenyl)-4,6-heptadiene-3-one	-82.63	-66.03	-84.24	-87.18	-73.97	-88.06	-83.67
3-hydroxy-1,7-bis-(4-hydroxyphenyl) -6-heptene-1,5-dione	-91.04	-67.96	-97.03	-85.48	-72.59	-114.35	-93.74
1,5-dihydroxy-1- (4-hydroxy-3-methoxyphenyl) -7-(4-hydroxyphenyl)-4,6-heptadiene-3-one	-94.12	-74.49	-84.95	-82.83	-86.23	-115.85	-84.03
1,5-dihydroxy-1-(4-hydroxyphenyl) -7-(4-hydroxy-3-methoxyphenyl)-4, 6-heptadiene-3-one	-97.64	-66.73	-93.88	-88.01	-83.57	-88.14	-82.32
1,5-dihydroxy-1,7-bis (4-hydroxy-3-methoxyphenyl)-4, 6-heptadiene-3-one	-94.91	-70.73	-92.14	-85.14	-79.73	-91.97	-84.75
1,5-dihydroxy-1,7-bis(4-hydroxyphenyl)-4, 6-heptadiene-3-one	-95.12	-64.67	-82.04	-80.37	-79.73	-109.11	-87.86
1,5-epoxy-3-carbonyl-1, 7-bis(4-hydroxyphenyl)-4,6-heptadiene	-94.12	-63.91	-89.39	-80.99	-70.9	-111.89	-91.77
Cyclocurcumin	-99	-64.74	-86.91	-89.88	-90.9	-106.75	-98.17
1,7-bis(4-hydroxy-3-methoxyphenyl)-1, 4,6-heptatrien-3-one	-83.74	-66.16	-78.21	-83.04	-83.73	-97.22	-86.97
1,7-bis-(4-hydroxyphenyl)-1, 4,6-heptatrien-3-one	-90.09	-60.21	-84.39	-76.01	-73.22	-103.96	-82.96
1,5-bis(4-hydroxyphenyl) -penta-(1E,4E)-1,4-dien-3-one	-91.19	-57.52	-80.95	-73.71	-69.49	-109.01	-85.61
1-(4-hydroxy-3-methoxyphenyl) -5-(4-hydroxyphenyl)-1, 4-pentadiene-3-one	-96.55	-67.78	-84.02	-77.41	-73.02	-121.48	-85.21
1,5-bis(4-hydroxy-3-methoxyphenyl) -penta-(1*E*,4*E*)-1,4-dien-3-one	-103	-68.37	-87.36	-82.41	-80.37	-103.69	-94.91
4"-(4"'-hydroxyphenyl)-2"-oxo-3" -butenyl-3-(4'-hydroxyphenyl-3'-methoxy) -propenoate	-88.44	-76.28	-91.09	-85.34	-84.34	-102.56	-87.82
4"-(4"'-hydroxyphenyl-3-methoxy)-2" -oxo-3"-butenyl-3-(4'-hydroxyphenyl) -propenoate	-91.87	-76.57	-89.12	-76.83	-73.93	-94.43	-85.05
calebin-A	-86.27	-76.08	-87.92	-82.23	-83.7	-69.77	-99.16
(*E*)-4-(4-hydroxy-3-methoxyphenyl) but-3-en-2-one	-67.92	-51.72	-68.63	-59.85	-59.55	-70.59	-80.46
(*E*)-ferulic acid	-67	-52.08	-69.28	-54.67	-59.7	-82.1	-71.06
(*Z*)-ferulic acid	-81.99	-56.36	-74.26	-55.58	-61.31	-76.88	-83.49

vanillic acid*	-76.29	-54.95	-76.53	-59.06	-50.87	-82.89	-75.51
Vanillin	-68.72	-52.13	-64.3	-51.77	-53.75	-67.63	-75.01

Docking studies were carried out using iGEMDOCK v 1.6 in Personnel computer. Docking results from iGEMDOCK, was ranked based on the lowest binding energy (negative delta G). Docking scores scheme was made in two different range for the identification of the potential interaction between ligands and target proteins; 1) > -75 to -100: represented yellow in color, 2) From -100 to -125: depicted in dark green in color (showed in table 3). The binding energy range 2 was taken as most potential interaction in between hydrogen atoms of ligands and interacting atoms. Analysis of docked complex of "**1-(4-hydroxy-3-methoxyphenyl)-5-(4-hydroxyphenyl)-1, 4-pentadiene-3-one"** with Cervical cancer (CRAS) protein found highest interaction as compared to all other protein ligand-docking studies were carried out. And some important amino acid residues **Lys-16**, **Asp-119**, **Ser-145**, **Ala-146** and **Lys-147** were identified with highest binding energy -121.5 Kcal/mol^{-1}, those amino acid residues play key role in the hydrogen bonding and other kind of protein-ligand interactions (eg. Hydrophobic, electrostatic, ionic etc.) that is may require for the regulation of anti-cancer activity of "1-(4-hydroxy-3-methoxyphenyl)-5-(4-hydroxyphenyl)-1, 4-pentadiene-3-one" in the cervical cancer.

Docking study of **curcumin** from turmeric with cancer causing protein, human lungs cancer (SOX 2) docking result analysis showed the highest binding energy 115.94 Kcal/mol^{-1}, as compared with other phytochemical present in turmeric. Some key amino acid residues were identified are as follow **Arg-932**, **Ser-949**, **Lys-953** and **Thr-954**.

CPL 1 BRCA 1 related protein shows the higher affinity with ligand **"1,5-bis(4-hydroxy-3-methoxyphenyl)-penta-(1*E*,4*E*)-1,4-dien-3-one"** and the binding energy -103 Kcal/mol^{-1} was observed. From the protein-ligand interaction analysis shows some key residues which interacts with ligand are **Ile-651**, **Asn654**, and **Asn671**.

CONCLUSION

In-silico approaches towards the screening of potent anti-cancer compound from the turmeric was performed for selected cancer types. The anti-cancer activity of "1-(4-hydroxy-3-methoxyphenyl)-5-(4-hydroxyphenyl)-1, 4-pentadiene-3-one" in cervical cancer was observed optimum as compared to other phytochemical screened from turmeric. In case of curcumin anti-cancer activity in lung cancer was optimal and the compound "1,5-bis(4-hydroxy-3-methoxyphenyl)-penta-(1*E*,4*E*)-1,4-dien-3-one", shows the best anti-cancer activity in CPL 1 BRCA 1 related protein. Other phytochemicals screened for anti-cancer activity in different types of cancerous cell shows least affinity as compared to following compounds "1-(4-hydroxy-3-methoxyphenyl)-5-(4-hydroxyphenyl)-1, 4-pentadiene-3-one", curcumin and "1,5-bis(4-hydroxy-3-methoxyphenyl)-penta-(1*E*,4*E*)-1,4-dien-3-one" respectively.

ACKNOWLEDGEMENT

Author would like to thank management and staff of Bilaspur University, Bilaspur (CG), India for their kind support in bringing out the above literature and providing lab facilities.

REFERENCES

[1]. Jurenka, Julie S. "Anti-inflammatory properties of curcumin, a major constituent of Curcuma longa: a review of preclinical and clinical research." *Alternative medicine review* 14.2 (2009).

[2]. Yang, Cheng-Liang, et al. "Curcumin blocks small cell lung cancer cells migration, invasion, angiogenesis, cell cycle and neoplasia through Janus kinase-STAT3 signalling pathway." *PloS one* 7.5 (2012): e37960.

[3]. Chavalittumrong, Pranee, and Warunee Jirawattanapong. "Variation of active constituents of Curcuma domestica rhizomes at different ages." *Thai J Pharm Sci* 16.2 (1992): 165-174.

[4]. Park, Byeoung-Soo, et al. "Curcuma longa L. constituents inhibit sortase A and Staphylococcus aureus cell adhesion to fibronectin." *Journal of agricultural and food chemistry* 53.23 (2005): 9005-9009.

[5]. Roth, Geoffrey N., Amitabh Chandra, and Muraleedharan G. Nair. "Novel bioactivities of Curcuma longa constituents." *Journal of natural products* 61.4 (1998): 542-545.

[6]. Li, Wei, et al. "Structure elucidation and NMR assignments for curcuminoids from the rhizomes of Curcuma longa." *Magnetic Resonance in Chemistry*47.10 (2009): 902-908.

[7]. Kita, Tomoko, et al. "Isolation of dihydrocurcuminoids from cell clumps and their distribution in various parts of turmeric (Curcuma longa)." *Bioscience, biotechnology, and biochemistry* 73.5 (2009): 1113-1117.

[8]. Park, So-Young, and Darrick SHL Kim. "Discovery of Natural Products from Curcuma l onga that Protect Cells from Beta-Amyloid Insult: A Drug Discovery Effort against Alzheimer's Disease." *Journal of natural products*65.9 (2002): 1227-1231.

[9]. D'Acquisto, Fulvio, Michael J. May, and Sankar Ghosh. "Inhibition of nuclear factor kappa B (NF-B)." *Molecular interventions* 2.1 (2002): 22.

[10]. Stein, Lincoln D., et al. "The generic genome browser: a building block for a model organism system database." *Genome research* 12.10 (2002): 1599-1610.

[11]. Uhlen, Mathias, et al. "Towards a knowledge-based human protein atlas." *Nature biotechnology* 28.12 (2010): 1248-1250.

[12]. T. Panduranga Vital, G.S.V. Prasada Raju and D.S.V.G.K. Kaladhar. "Understanding of Protein-Ligand Interaction for Breast and Lung Cancer Compounds Using Docking Method." *WJPPS*, 4.1, (2015): 945-966.

[13]. Kaladhar SVGK Dowluru, Govinda Rao Duddukuri, Ramesh K, Varahalarao Vadlapudi, Nagendra Sastry Yarla. "In Vitro Protease Inhibition, Modulation of PLA2 Activity and Protein Interaction Studies on Calotropis gigantea." *Journal of Clinical & Cellular Immunology*, 4, (2013): 165.

[14]. Dowluru SVGK Kaladhar, Nagendra Sastry Yarla and N. Anusha. "Functional Analysis and Molecular Docking studies of Medicinal Compounds for AChE and BChE in Alzheimer's Disease and Type 2 Diabetes Mellitus." *Aging and Disease*, 4.4, (2013): 186-200.

[15]. DSVGK Kaladhar, P Chandra Sai, PV Nageswara Rao, A Krishna chaitanya, Govinda Rao D, V. Varahala Rao, P Suresh, E Rajeshwara Reddy, S Vijaya kumar, Vinod Kumar D and G Bhaskar Reddy, "Protein interaction networks in MetalloProteins and Docking approaches of Metallic Compounds with TIMP and MMP in Control of MAPK Pathway." *LDDD*, 10.1, (2013): 49-55.

[16]. DSVGK Kaladhar, N Anusha, V Varahala Rao, Ch Surekha, Sudhakar M, "Regulation of Metabolic Syndromes by means of controlling diseased Ache and Bche with Multitarget Inhibitors through *in silico* techniques." *Journal of Computational Methods in Molecular Design*, 2.4, (2012):122-17.

[17]. Sudhakar Meesala, Satyanarayana Rentala, DSVGK Kaladhar, "Dna Laddering, Rt-Pcr and in Silico Interaction Studies for Aqueous Leaf Extracts of Ipomoea Sepiaria as Anticancer Agents Towards Pc-3 Cell Lines." *IJRSB*, 5.9, (2017): *11-15*

[18]. Nagendra sastry Yarla, Koduri Satyakumar, Duppalapudi Srinivasu, **Kaladhar DSVGK,** Gjumrakch Aliev, Gangappa Dharmapuri, Goutham Raju SP, Swathi Putta, Srinivas Jagarlapoodi, Govinda Rao Duddukuri, "Phospholipase A2: A Potential Therapeutic Target in Inflammation and Cancer (In silico, In vitro, In vivo and Clinical Approach)." *J Cancer Sci Ther*., 7, (2015): 8

[19]. Nagendra Sastry Yarlaa, Rajaram. A, Mahaboob Basha, Abdul Rajack, D. S. V. G. K. Kaladhar,Bharat Kumar Allam, Rajeswara Rao. P, Krishna Nand Singh, Sunanda Kumari K, Reddanna P, Umadevi Parimi, Anupam Bishayee, Govinda Rao. D, "5-Lipoxygenase and Cyclooxygenase Inhibitory Dammarane Triterpenoid 1 from Borassus flabellifer Seed Coat Inhibits Tumor Necrosis Factor-α Secretion in LPSInduced THP-1 Human Monocytes and Induces Apoptosis in MIA PaCa-2 Pancreatic Cancer Cells." *Anti-Cancer Agents in Medicinal Chemistry, **15**.8, (2015): 1066-1077.*

[20]. Bharat Kumar Bugata, Kaladhar DSVGK. "QSAR and Docking Studies of Synthesized Diarylsulfonylurea Chalcone Hybrids as Anti-Inflammatory Agents." *Int. J. Pharm. Sci. Rev. Res.,* 24.2, (2014):144-149