

## Prevalence and In-Silico Analysis of Cardiac Enzyme Profile and Serum Lipid Profile in Patients to Find Out Acute Coronary Syndromes (ACS)

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### Abstract

The objective of this research is to study the Prevalence and *in-silico* analysis of lipid and cardiac enzymes in acute coronary syndrome (ACS) patients. For this purpose, a total of 213 (137 males and 76 female) blood samples were collected from cardiac patients. Afterwards, analysis was done on collected blood samples to check the biomarker level of all cardiac and lipid enzymes in all patients to find out the ACS. Statistical descriptive analysis of prevalence results was done by using statistical software SPSS 21 and *in-silico* analysis was also performed. Statistical analysis correlation shows a relationship of lipid, cardiac enzymes, walk and exercise with significant level  $P < 0.05$ ,  $0.01$ . Regression analysis shows Creatine Phosphokinase (CPK), Creatine Kinase Muscle and Brain (CK-MB), Lactates Dehydrogenate (LDH), Very Low-Density Lipoprotein (V.L.D.L) positively and significantly related to smoking. Cholesterol, triglyceride, Aspartate Aminotransferase (AST) are negatively and significantly related with smoking which shows that F has 17.602% and R has .339% variation with smoking. *In silico* analysis showed that Selenocysteine, Asparagine, and lysine are binding residues for thrombospondin-1human (THBS1) and Tetrahydroisoquinoline (TIQ) ligand in molecular docking. Ligand and protein, have -5.7 is the lowest energy and distance between is 3.137 to 5.829. It was found that more exercise could reduce the ACS problems in cardiac patients.

**Keywords:** Acute Coronary Syndrome (ACS), Cardiac Disease, Lipid Profile, Thrombospondin-1 Human (TSP1), Tetrahydroisoquinoline (TIQ).

### 1. Introduction

Acute Coronary Syndrome is very common all over the world and thousands of people are dying due to ACS. ACS causes infection in the heart which is present in the down chest, chest pain is singling of ACS and those patients who have ACS and have a serious condition need proper medical care at that time (Canto *et al.*, 2000). Among all chest pain patients, few patients experience heart problems like blockage of heart veins, cardiac enzymes. Creatine Phosphokinase (CPK), Lactates Dehydrogenate (LDH), Triglyceride, Very Low-Density Lipoprotein (V.L.D.L) are those enzymes that cause heart problems and cause severe heart injury between the wall of the heart, sometimes these enzymes don't work properly and heart attacks occurred., Troponin T-tests is used to diagnoses the ACS in patients describe the heart condition of ACS patient (Zhang *et al.*, 2016). In ACS patients, the left shoulder pain, nausea, sweating, and chest pain are the common symptoms (Goodacre *et al.*, 2009). In chest pain patients, when cardiac and lipid enzyme doesn't work due to any reason then the blood flow is reduced in coronary arteries and the heart doesn't work properly which caused ACS (Amsterdam *et al.*, 2014). These are common symptoms of acute coronary symptoms, but three main clinical symptoms which commonly associated with the ACS, the first one is chest pain, secondly enzyme e.g. combinations of CK in blood level, thirdly use the electrocardiogram (ECG) machine which changes the Q waves and show the condition of the enzyme (Lange & Hillis, 2011). Electrocardiograms give a sound when the heart is contracting and relaxed, the contraction and relaxation completed one cycle (Torres & Moayed, 2007).

Creatinephosphokinase (CPK), and creatine kinase muscle and brain (CK-MB), are present in Cardiac tissue or skeletal muscles. If the CK enzyme doesn't work properly in acute coronary syndrome patients, it will damage cardiac tissues (Zhao, Ma, Bai, & Wang, 2018). Skeletal muscles and cardiac muscles have CPK enzymes in the human body that can produce energy and is the primary phosphorylase in a healthy person. If the CPK enzyme doesn't work properly cardiac and skeletal muscle is damaged and ACS occurred in patients (Jaye *et al.*, 2009). CPK and lactate dehydrogenate (LDH) combination play a very important role in ACS patients. In the heart, kidney, skeletal muscle and brain, aspartate aminotransferase (AST) enzyme is used as a primary cardiac biomarker. Aspartate aminotransferase is present in cardiomyocytes and the liver, when serum AST concentration is increased tissue is broken and has a high risk of acute coronary syndrome (Faloppi *et al.*, 2016).

Lipids play a very crucial role in ACS patients. Lipids have many biomarkers like cholesterol, triglyceride, and Very Low-Density Lipoprotein (V.L.D.L). High triglyceride levels in people increases the thickness in the artery of the heart wall and cause heart stroke, heart attack, and many other heart diseases are called ACS. Many biomarkers are used to reduce the ACS like high levels of LDL reduce the risk of cardiovascular diseases, very low-density lipoprotein is also used to reduce the health risk of cardiac patients. These biomarkers reduce the hardness of arteries and solve cardiac issues (Lin & Schuur, 2014). For this purpose, the level of cholesterol could be controlled in blood to reduce the ACS. If the cholesterol level is high in blood, it will block the arteries and result in cardiac diseases (Zhao *et al.*, 2018). We collected the samples of blood of ACS patients to analyse cardiac and lipid biomarkers to find better results by using Beckman analyser.

## **2. Material and Methods**

### **2.1 Sample Collection**

We collected 213 blood samples of ACS patients among them 137 were male and 76 were females. Various types of data were collected from the patients.

### **2.2 Questionnaire fill-up**

For this purpose, a questioner was designed for the collection of data of different variables e.g. age, gender, patient's disease history, address, exercise, walk time, smoking history, hypertension and heart disorder etc. of ACS patients by considering two options, yes or no

### **2.3 Methodology**

A volume of 0.5ml blood sample of an ACS patient was collected with the help of a syringe and shifted to a yellow tube containing a gel. The collected samples were centrifuged at 3200rpm for 2-3 minutes, to separate the serum from blood and poured it into the tube and put it into the serum rack. Then put this rack into BECKMAN COULTER AU480 for analytical ultracentrifugation and run the setup to analyse the biomarker. After that, the result was displayed on a computer and collected in printed form.

### **2.4 Statistical Analysis**

The obtained results were analysed to find significance level of cardiac enzyme profile and lipid profile. The frequencies, percentage, correlation and regression analysis were determined using statistically SPSS 21 software.

### **2.5 Molecular and Structural analysis**

For the prediction of the 3-dimensional protein structure of ACS were bioinformatics programs including I-TASSER tool Docking, Batch CD, Scanprosite, Expasy protpharam, Sosui Server, Deep Loc, coach, etc.

### 2.5.1 SEQUENCE RETRIEVAL

Nucleotide sequence of human Thrombospondin-1 was retrieved through NCBI (The National Centre for Biotechnology Information) [www.ncbi.nlm.nih.gov](http://www.ncbi.nlm.nih.gov).

### 2.5.2 IDENTIFICATIONS OF CODED PROTEIN

#### Conserved Domain Prediction

To study protein at the molecular level different online tools such as Batch CD and Scanprosite were applied to study the conserved domains.

#### Batch CD

A web-based tool Batch CD <https://www.ncbi.nlm.nih.gov/Structure/bwrpsb/bwrpsb.cgi> was applied to study the structural and functional domains in the protein sequence. This tool is available on NCBI's web page which is applied to search out the conserved domains in protein sequence (Lu *et al.*, 2019).

#### Scanprosite

Scanprosite <https://prosite.expasy.org/scanprosite/> was applied to search out the functional domains of the protein and family of the protein by this prediction helps out in the characterization of our desired protein (de Castro *et al.*, 2006).

### 2.5.3 PREDICTIONS OF PHYSICOCHEMICAL PROPERTIES

#### ExpasyProtParam

ProtParam is a tool that permits the calculus of diverse physical and chemical frameworks for a specific protein for a customer set foot in the protein sequence (<https://www.expasy.org/>). The computed framework incorporates the molecular influence, approximate half-life, unreliability indicator, aliphatic index, and a prime Gaverage of hydrophobicity (GRAVY).

#### Sosui Server

SOSUI sever to predict nature and cellular location of Protein. It is to calculate the hydrophobicity of protein ([http://harrier.nagahama-i-bio.ac.jp/sosui/sosui\\_submit.html](http://harrier.nagahama-i-bio.ac.jp/sosui/sosui_submit.html)) (Imai *et al.*, 2008).

#### DeepLoc

DeepLoc-1.0 predicts the subcellular localization of eukaryotic proteins. <https://services.healthtech.dtu.dk/service.php?DeepLoc-1.0>. Its vessel differentiates between 10 in the middle of localizations after that reticulum, Lysosome/Vacuole, and Peroxisome, Golgi apparatus, Cell membrane, Nucleus, Cytoplasm, Endoplasmic Chloroplast, Extracellular, Mitochondrion, Cell membrane (Almagro Armenteros, S nderby, S nderby, Nielsen, & Winther, 2017).

#### Target P Server

Target P 1.1 predicted the location of eukaryotic proteins. It is open with the URL <http://www.cbs.dtu.dk/services/>. Its location is based on the presence of any N- terminal forecast: Secretory pathway single peptide OR mitochondrial select peptide (Mtp) (Emanuelsson, Brunak, Von Heijne, & Nielsen, 2007).

### 2.5.4 PREDICTION OF PROTEIN-PROTEIN INTERACTIONS

#### String

The aim of this database (<http://string-db.org>) is to provide information related to interaction between different proteins, it includes physical as well as functional association. The latest version of this bioinformatics tool can give results about 2000 species and more (Szkarczyk *et al.*, 2015).

### 2.5.5 STRUCTURAL ANALYSIS OF PROTEIN

#### I-Tasser

I-TASSER tool is used for the prediction of the three-dimensional structure of protein and solves the computational structure of biology. This tool is freely available at given link

<https://zhanglab.ccmb.med.umich.edu/I-TASSER/>. It is based on a secondary structure with modelling of hierarchical protein which enhances the iterative implementation of TASSER and profile-profile threading Alignment program (Y. Zhang, 2008).

### Docking

Docking is a computational tool used to predict structure-based drug design for small molecule ligands in strength and single type procedure. Small molecules are used as the target sites. This method was done by using the Auto Dock vina Tool. Using docking, hundreds of procedures are performed using ligand, protein, and drug docking which is performed in different functions like a prediction of the active site and binding site of docking.

Molecular docking was performed using ligand and protein structure. The protein structure of thrombospondin-1 human (TSP1) was taken from the I-Tasser best model ligand of Tetrahydroisoquinoline (TIQ) was taken from Pub-chem <https://pubchem.ncbi.nlm.nih.gov/com>. 3D structure of ligand and protein was optimized using discovery studio 3.5 and saved it. Docking was done using auto dock-vina 1.5.6 (Choi *et al.*, 2013).

### 2.5.6 LIGAND BINDING SITE PREDICTION

#### Coach

COACH is used for the prediction of protein ligand-binding sites. It is freely available at this link <https://zhanglab.ccmb.med.umich.edu/COACH/>. For the prediction of the binding site, two methods have been used S-SITE and TM-SITE which is used as a template in ligand binding site from the specific sequence and structural comparison from Bio Lip protein (Yang, Roy, & Zhang, 2013).

## 3. Results

### 3.1 Statistical Analysis

#### Correlation within a Walk, Exercise, Smoking, Lipid and Cardiac

Two-tailed correlation tests among five variables were conducted. All variables checked with significant level 0.01 and 0.05 to show the relationship among all variables. Exercise and walking show a strong positive relationship with a significant  $p < 0.01$  level, smoking shows a negative relationship with walking and exercise. Cardiac has a positive relationship with walking and smoking, and strongly positive with exercise at a significant level  $p < 0.05$ . The lipid test shows a positive relationship with walk  $r = 0.74$  and in cardiac  $r = 0.01$  and shows a negative relationship with exercise and smoking. Results show that variables have different relationships with different variables. So, the direction with variables has been the same as predictable in bases of hypothesis which is based on empirical and theoretical findings shown in Table 1.

**Table 1:** Correlation Analysis between Walk, Exercise, Smoking, Cardiac, Lipid

	1	2	3	4	5
1 Walk	1				
2 Exercise	.321**	1			
3 Smoking	-.099	-.130	1		
4 Cardiac	.67	.166*	.031	1	
5 Lipid	.074	.013	.125	.001	1

\*\* Correlation is significant at the 0.01 level (2-tailed)

\* Correlation is significant at the 0.05 level (2-tailed)

### 3.2 REGRESSION ANALYSIS

#### Regression analysis of Smoking with Cholesterol, Triglyceride, V.L.D.L, LDH, CPK, C.K.M.B, and AST

Cholesterol negatively and significantly predicted with smoking and standardized beta value ( $\beta = .127$ ,  $P < 0.05$ ), triglyceride is also negative and significant with smoking and standardized beta ( $\beta = .065$ ,  $P < 0.05$ ), V.L.D.L is positively and significantly with standardized beta ( $\beta = .000$ ,  $P < 0.05$ ), LDH is positive and significant with smoking with standardizes beta value ( $\beta = .066$ ,  $P < 0.05$ ), CPK is positive and significant with smoking with standardized beta value ( $\beta = .013$ ,  $P < 0.05$ ), C.K.M.B is also positively and significantly with smoking with beta value ( $\beta = .041$ ,  $P < 0.05$ ), AST predicted negatively and significantly with smoking beta value ( $\beta = .106$ ,  $P < 0.05$ ). This modern summary has shown that R2 has a .339% variation and factors have shown a 17.602% variation in smoking its significant level and other statically test F-test value, adjust R2, standard deviation, the standard error shows its goodness of fit model in table 2.

**Table 2:** Regression Analysis of AST with Cholesterol, Triglyceride, V.L.D.L, L.D.H, CPK, and C.K.M.B

Model	Unstandardized Beta (B)	Standard Error (SE)	Standardized beta ( $\beta$ )	t-test (t)	Significant values
(Constant)	-143.840	96.341		-1.493	.013
cholesterol	-.619	0276	-.141	-2.246	.026
triglyceride	.585	.313	.128	1.869	.063
V.L.D.H	.896	.830	.074	1.080	.281
LDH	.647	.065	.695	9.954	.000
CPK	-.055	.56	-.062	-.989	.032
C.K.M. B	-1.884	.434	-.321	-4.338	0.000

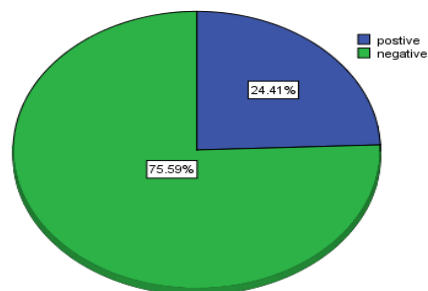
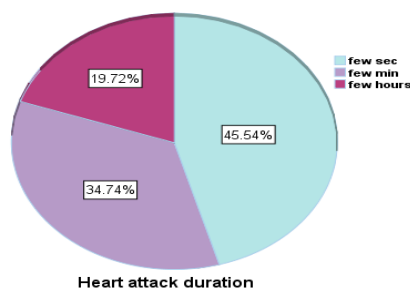
F= 17.602; Std. dev = 0.986; R2= .339

#### Heart attack duration in ACS Patients

Figure 1 shows the mean age of ACS patients who have heart attack pain duration, in green colour shown that 45.54% of patients have few sec pain duration, purple colour shows that 34.74% of patients have few minutes' pain duration, pink colour shows that 19.72% patients have few hours' pain duration during a heart attack.

#### Troponin Test

Troponin test blue colour showed 24.41% of positive results, and the green colour showed 75.59% of patients have negative results shown in figure 2.



**Figure 1:** Percentage of Heart attack duration **Figure 2:** Percentage of Troponin test

### 3.3 COMPUTATIONAL TOOL

#### Sequences Retrieval

>sp|P07996.2|TSP1\_HUMAN RecName: Full=Thrombospondin-1; Altname: Full=Glycoprotein G; Flags: Precursor

#### Conserved Domain Prediction

##### Scanprosite

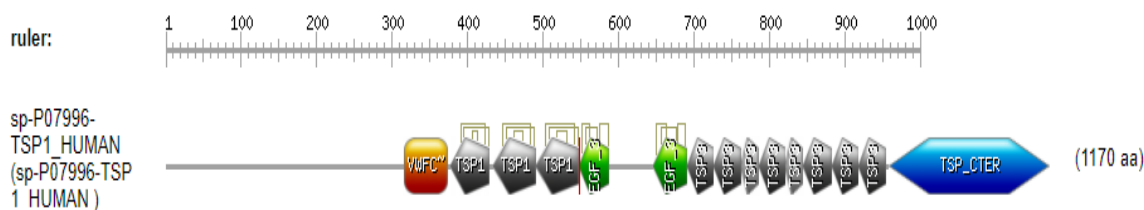
Scanprosite predicted 1 VWFC having an active site and 3 TSP-1, 2-EGF, 8-TSP3 1-TSP-TER and disulphide bridges as shown in the figure 1 it is an ACS domain (1170) with a score and its amino acids length. They are divided into two subfamilies, A and B, according to their overall molecular organization. The subgroup A proteins TSP-1 and -2 contain an N-terminal domain, a VWFC domain 316-337: score 13.465, three TSP1 C1, C2, C3 repeats have tsp-1 C1 (domain 379-429, score = 12.845), second TSP-1 C2 (domain 435-490, score = 14.831), third TSP-1 C3 (domain 492-547, score = 14.403). three EGF-like domains 547-587: score = 9.234, TSP3 repeats have eight pathways C4, C5, C6, C7, C8, C9, C10, C11, C4(domain 691-726: score = 13.113), C5(727-762: score = 17.948), C6(763-785: score = 11.836), C7(786-821: score = 16.452), C8(822-844, score = 12.305), C9(845-882: score = 14.147), C10(883-918: score = 18.075) C11(919-954: score = 16.330) and a C-terminal domain. TSP\_CTER (958-1170: score = 99.261) show in figure 3.

##### Legend:



hits by profiles: [15 hits (by 5 distinct profiles) on 1 sequence]

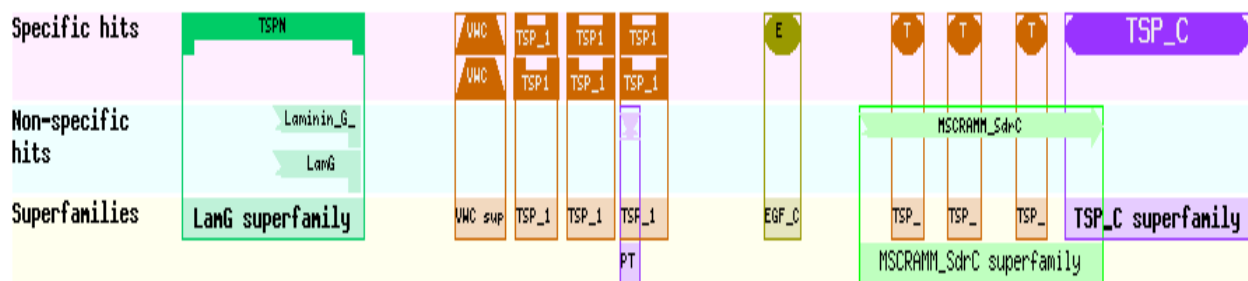
Upper case represents match positions, lower case insert positions, and the '-' symbol represents deletions relative to the matching profile.



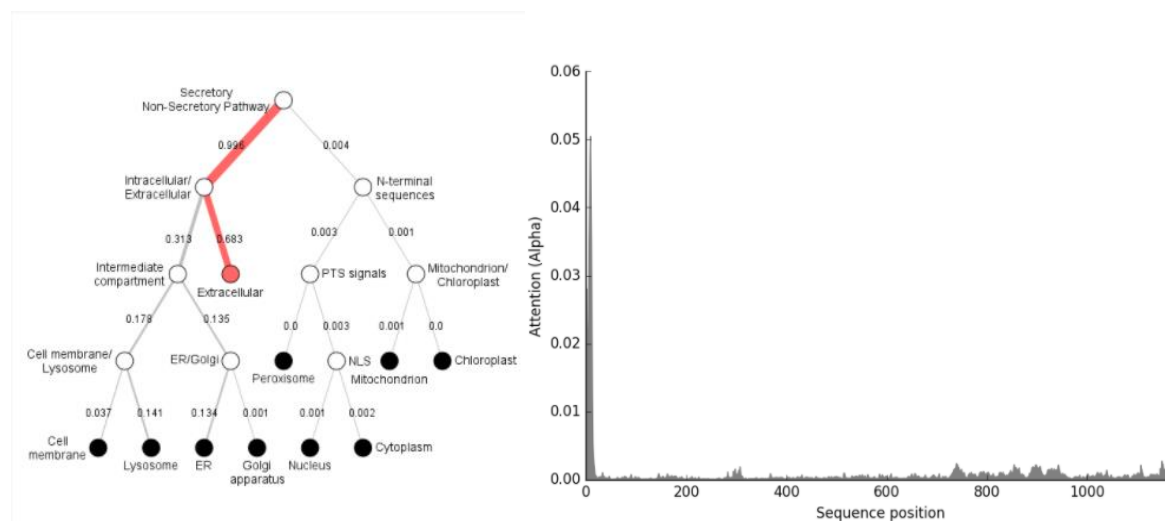
**Figure 3: Graphical representation domain of TSP1 using Scanprosite**

#### Batch CD

By performing the Batch CD TOOLS, it gives the specific hits with the Bit score 410.867 and E- values are  $3.752226 \times 10^{-136}$  its query sequence ranges from, accession pfam05735 the specific hit TSNP, VWC, TSP-1, E, T, TSP-C, and nonspecific hits are Laminin-G-, LamG, VWC sup, EGF-C, TSP-C superfamily, and total domain area 14 as shown in the figure 4 a, b, c.



**Figure 4: (a) Graphical representation of thrombospondin-1 human (TSP) protein by using the Batch CD**



**Figure 4: (b) Presence of protein in different location (c) Graphical representation of TSP1 protein**

### 3.4 PREDICTIONS OF PHYSICOCHEMICAL PROPERTIES

#### ExpasyProtparam

The sequence id of thrombospondin-1 human (TSP1-HUM) is P07996.2 and the total number of amino acids is 1170. The molecular weight of thrombospondin (THBS) is 129382.67 and PI value is 4.71 and composed and the no of amino acid is that negatively charged in Glu and Asp is 182 and the complete no of positive functions of the residue is Lys and Arg is 115. So, the EC value of the average of hydropathicity (GRAVY) is -0.719. The total number of atoms is 17513. The half-life of thrombospondin (THBS) is 30 Hours for mammalian reticulocytes, in vitro and less than 20 hours in yeast and has been Vivo and also less than 10 hours the function of the E. coli, has been in vivo. So, the N terminal has been residue the originates from the observation that has been recognizing the thrombospondin-1 human (TSP1-HUM) and has the major role in determining the experiment that blows up the different major functions of the N-terminal amino acid arranged by major mutagenesis as shown in that is given below table 3.

**Table 3:** Physio-chemical Properties using EXPASY PROTPARAM

Query ID	
<b>Number of AC</b>	P07996.2
<b>Protein</b>	Thrombospondin-1
<b>Gene</b>	Thrombospondin-1 (THBS1)
	Synonym: TSP, TSP1
<b>Organism</b>	Homo sapiens (Human)
<b>Weight</b>	129382.67
<b>Theoretical pI</b>	4.71
<b>Signal peptide</b>	1-18
<b>Chain</b>	1-1170
<b>Amino acid</b>	1170
<b>Amino acidic composition</b>	52,(A) 60,(R) 81,(N) 131,(D) 70,(C) 50,(Q) 51,(E) 105,(G) 27,(H) 45,(I) 64,(L) 55,(K) 14,(M) 35,(F) 70,(P) 74,(S) 61,(T) 22,(W) 31,(Y) 72,(V) 0,(O) 0,(U) 0,(B) 0,(Z) 0,(X)
<b>Negatively charged residues</b>	(Asp, Glu): 182
<b>Positively charged residues</b>	(Arg, Lys): 115
<b>Half-life</b>	30 Hours (mammalian reticulocytes, in vitro) >20 hours (yeast, in vivo) >10 hours (E. coli, in vivo)
<b>Instability index</b>	42.03
<b>Aliphatic index</b>	58.62
<b>GRAVY</b>	-0.719
<b>Composition</b>	
Carbon	5517
Hydrogen	8468
Nitrogen	1612
Oxygen	1832
Sulfur	84
<b>Formula</b>	C <sub>5517</sub> H <sub>8468</sub> N <sub>1612</sub> O <sub>1832</sub> S <sub>84</sub>
<b>Atoms</b>	17513

**Sosui Server**

The total length was 1170A and the Average of hydrophobicity was -0.718890. This amino acid sequence is of a MEMBRANE PROTEIN which has 1 Tran's membrane helix. In this helix, the N terminal is 1 and the Trans-membrane region MGLAWGLGVFLMHVCGTNR IPE and C terminal 23, and its type is the primary and total length of helices is 1 as shown in Table 4.

**Table 4:** Regions of *Thrombospondin-1 Human (TSP)* Protein using Sosui Server

No.	N-Terminal	Transmembrane region	C-Terminal	Type	Length
1	1	MGLAWGLGVFLMHVCGTNR IPE	23	PRIMARY	23



### DeepLoc

thrombospondin-1 human (TSP1) is present in 10 different locations like extracellular 0.5431, lysosome /vacuole 0.1193, cell membrane 0.0193, endoplasmic reticulum 0.3158, plastid 0.0001, cytoplasm 0.0006, mitochondria 0.0005, peroxisome 0, Golgi apparatus 0.0009, and in nucleus 0.0003 as shown in table 5.

**Table 5:** Location ofThrombospondin-1 Human (TSP1) Protein using DEEP LOC Tool

Localization	values
Extracellular	0.5431
Lysosome/vacuole	0.1193
Cell membrane	0.0193
Endoplasmic reticulum	0.3158
Plastid	0.0001
Cytoplasm	0.0006
Mitochondria	0.0005
Peroxisome	0
Golgi apparatus	0.0009
Nucleus	0.0003
Type	Likelihood
Soluble	0.9808
Membrane	0.0398

### Target Server

By performing the target P server, the ascension no. Sp-07996.2- thrombospondin-1 human (TSP1) has the length of 1170 amino acid sequence and final score on which the final prediction is based on the Loc (S), however, the highest location with the highest score is the most likely target and shows the location between the score of mTP, SP, RC. Mitochondria targeting peptide (mTP) contain 0.031 scores, single peptide contains 0.835 scores, and the other peptide contains 0.153 scores and reliability class (RC) is 2 which shows in Table 6.

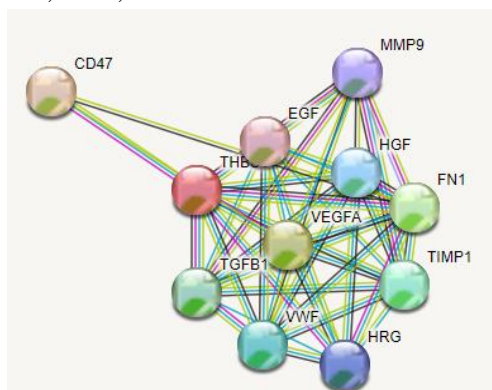
**Table 6: Prediction of thrombospondin-1 human (TSP) Protein using Target P Server**

Name	Length	Mtp	SP	Other	Loc	RC
Sp-07996.2-TSP1-HUM	1170	0.031	0.835	0.153	S	2
Cut-off	0.000	0.000	0.000			

### 3.5 PREDICTION OF PROTEIN-PROTEIN INTERACTIONS STRING

Figure 5 shows the network of nodes that explains the interaction of thrombospondin-1 human (TSP1) with other protein domains. There is a total number of nodes is 11n and the number of edges is 47. The average node degree is 8.55. The average local clustering coefficient is 0.939. The expected number of edges is 19 and the ppl enrichment p-value is 2.49e-08. In this model, the nodes which are connected by 5 different colour lines show the type of interaction evidence. The strength of the data report is indicated by

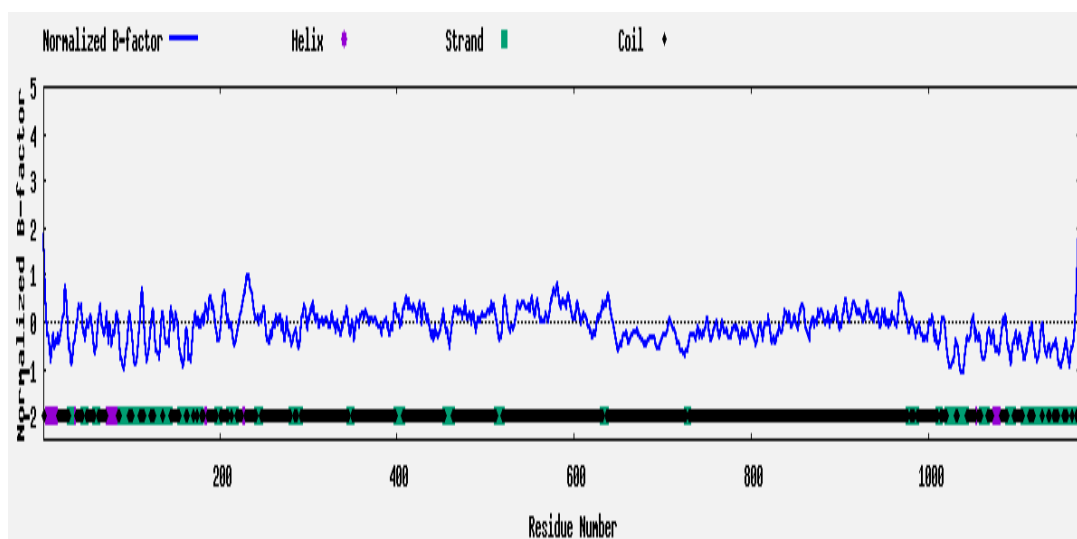
three-line thickness and molecular action is indicated by nodes that are connected by two lines. Here the green-coloured node in the middle is the query protein which is thrombospondin-1 human (TSP1) and this is the first shell of interactors and pink and blue nodes are the second shells. The green colour shows gene fusions whereas green and pink showing gene co-occurrence and the blue colour lines show gene neighbourhood and these all show the predicted interactions. Text mining, protein homology, and co-expression is shown by yellow, sky blue, and black lines respectively. The input protein is thrombospondin-1 human (TSP1) and its functional partners predicted by string are CD47, VEGFA, FN1, TGFB1, VWF, HGF, HRG, MMP9, EGF, and TIMP 1.



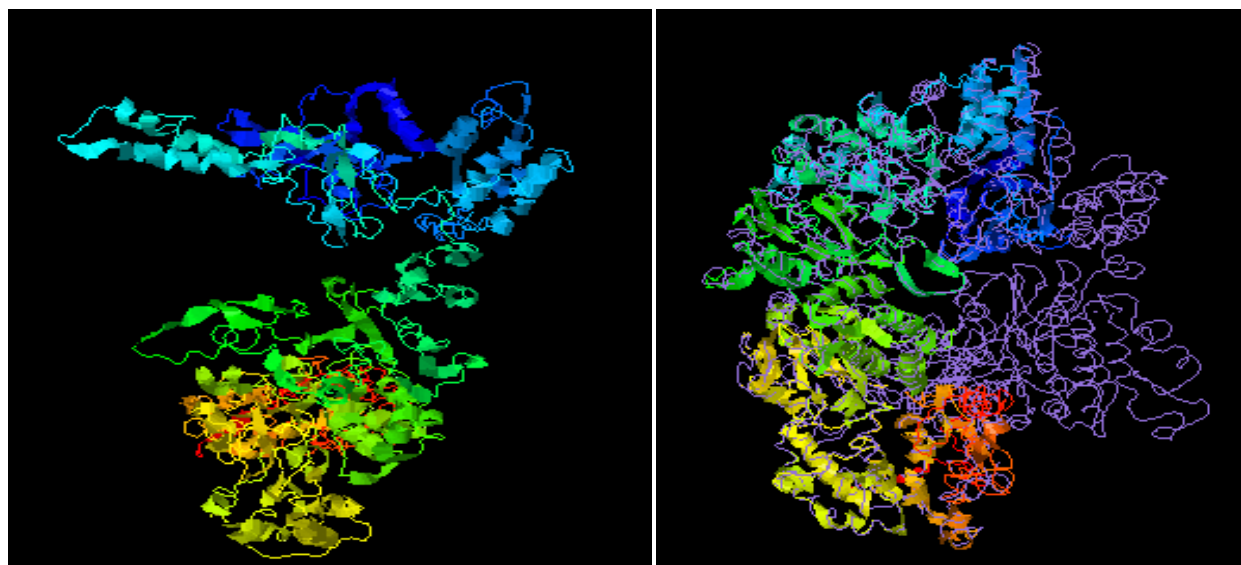
**Figure 5:** Interaction of TSP protein with another domain

### I-Tasser

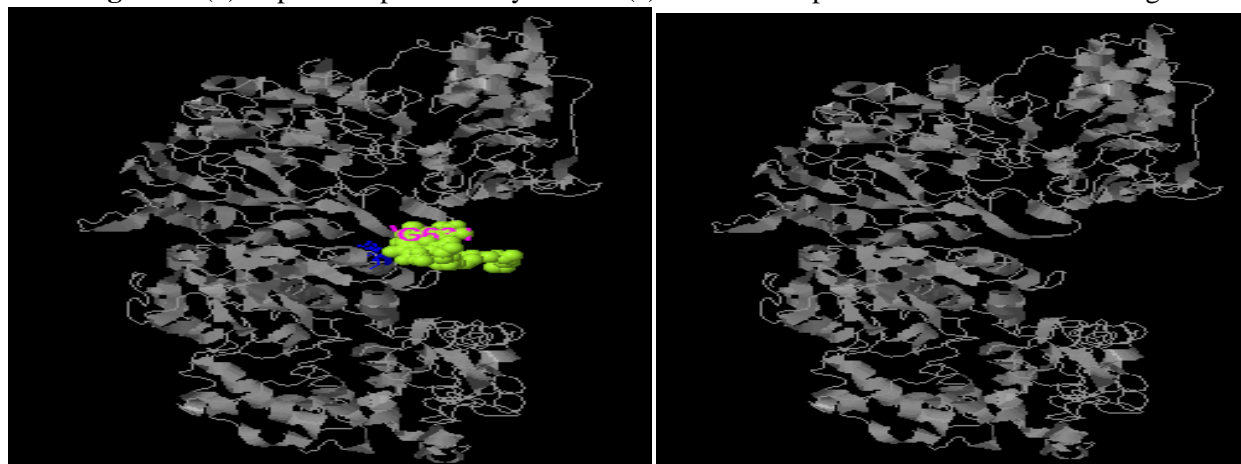
Predicted normalized B-factor as shown in figure 6(a) and the model predicted by I-TASSER as shown in Figure 6(b). Proteins are structurally close to the target in the PDB as identified by TM-align using I-TASSER as shown in figure 6(c). The ligand-binding site is shown in figure 6(d) shows enzyme commission number (EC) and active site are shown in figure 6(e).



**Figure 6:** (a) Predicted normalized B-factor



**Figure 6:** (b) Top model predicted by I-Tasser (c) Structure of protein close to PDB TM align



**Figure 6:** (d) ligand binding site (e) Enzyme commission number and active site

### Docking

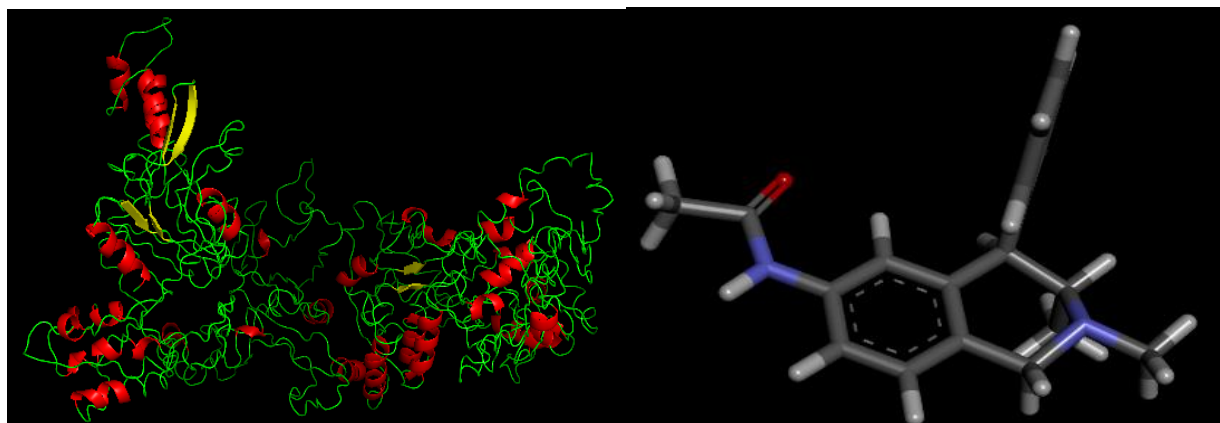
As a result, opening the configuration file shows the axis of X= 100.813, Y= 100.828, and Z= 101.710 set the grid at 26 using different tools like discovery studio and auto dock vinato determine Interaction of thrombospondin-1 human(TSP1) protein and Tetrahydroisoquinoline (TIQ) ligand. Protein structure is determined from the I-Tasser best C-Score model. This is shown in figure 7(a) and the ligand is determined from Pub Cam which shows in figure 7(b).

### Docking with Thrombospondin-1 (TSP1) and Tetrahydroisoquinoline (TIQ)

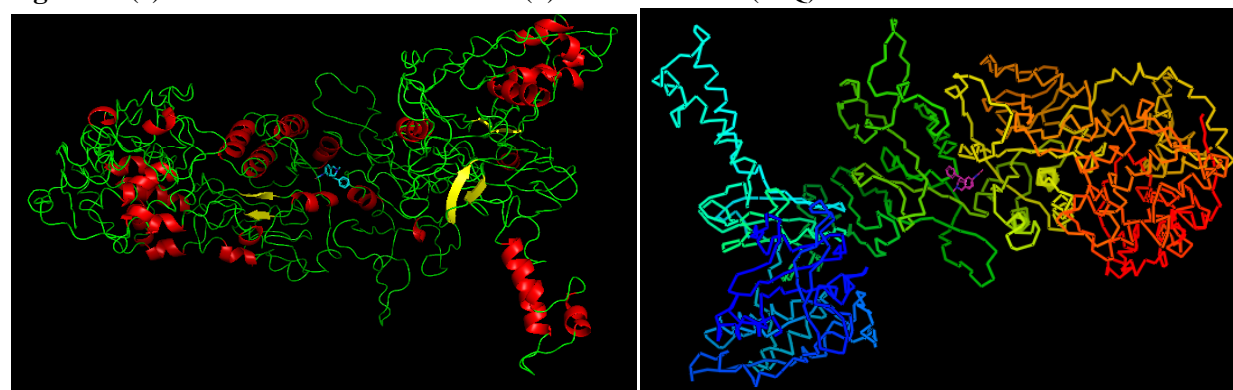
Selenocysteine, Asparagine, and lysine are binding residues involved in thrombospondin-1 human (TSP1) and Tetrahydroisoquinoline (TIQ) ligand. Ligand is in blue and protein is in red is a helix, green colour is a loop, and yellow colour shows the sheets which are involved thrombospondin-1 human (TSP) and Tetrahydroisoquinoline (TIQ) interaction figure 7(c).

### Docking Surfaces

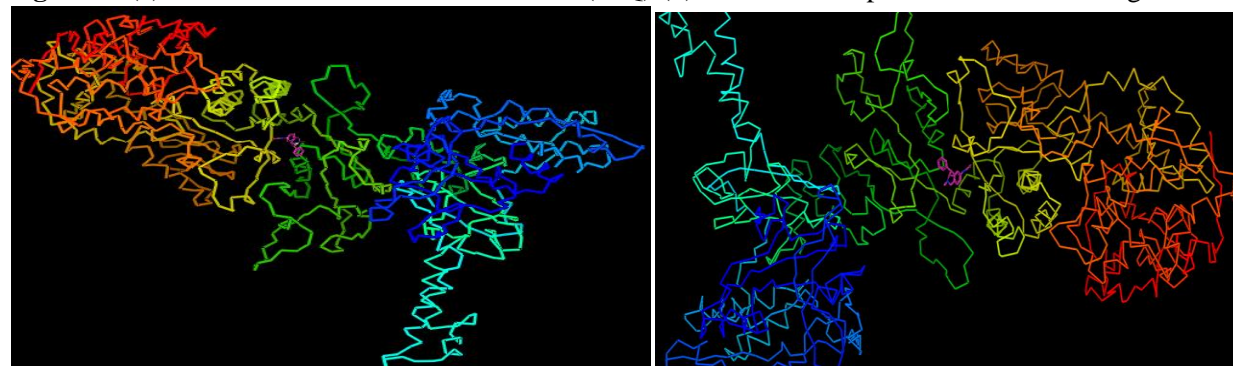
Different types of surfaces are present in molecular docking here we will explain four surfaces of molecular docking mesh, transparent, and solid surface which shows in figure 7 (d,e,f).



**Figure 7:** (a) 3D structure of TSP1-Human (b) 3D structure of (TIQ)



**Figure 7:** (c) Attraction between TSP1-hum and (TIQ) (d) Mesh surface predicted from docking



**Figure 7:** (e) Transparent surface predicted from docking (f) Solid surface predicted from docking

### The Affinity of Molecular Docking

The lowest energy shows the best result which describes the novel interaction between the ligand and protein, here -5.7 is the lowest energy, and the distance between ligand and protein is 3.137 to 5.829 and considered the best energy which shows in table 7.

**Table 7: Affinity of Molecular Docking**

Mode	Affinity (kcal/mol)	dist. from best mode rmsd l. b	dist. from best mode rmsdu. b.
1.	-7.1	0.000	0.000
2.	-7.0	3.818	5.763
3.	-6.9	3.192	5.586
4.	-6.9	2.868	5.488
5.	-6.8	3.057	4.810
6.	-6.7	3.634	5.300
7.	-6.6	2.446	4.943
8.	-6.1	3.230	6.373
9.	-5.7	3.137	5.829

#### 4. Discussion

A significant study was associated which shows lipid abnormalities with cardiovascular disease risk Framingham heart study (Lin & Schuur, 2014). In this study, many variables are used to find out accurate results about the ACS patients. For this purpose we collected their clinical information like diabetes, cholesterol level, smoking time, smoking level and blood pressure physical activity. The result of acute coronary syndrome shows many trials for every cardiac and lipid risk factor, especially elevated creatine kinase muscle and brain, creatine kinase, and lactate dehydrogenase. A study was done to check the Helsinki heart disease in which dyslipidaemia men age forty to fifty-five, who did not cardiovascular heart disease and major problems such as hypertension or diabetes. The subject of this study showed that males and employed by specific companies. It decreased the frequency of cardiovascular heart diseases, such as myocardial infarction and cardiac death by thirty-four percent, which has not decreased mortality in all cases. Lipid panels are also responsible for the decrease in coronary heart disease. It shows the proportional hazards model which indicates the changes of 8% positive in high-density lipoprotein-cholesterol and negatively 7% in low-density lipoprotein which reduces cardiac disease (C. C. Chen, Lu, Wu, & Chang, 2001). Our study shows that cardiac and lipid shows a positive relationship with significant value  $P > 0.05$  variables vary in a different relationship so, these variables are predicted based on hypothesis. Results of regression show that CPK has positively and significantly predicted with smoking, and smoking hurts cholesterol and AST along with another statistical test including adjusted F test, R square, unstandardized beta, t-test, and standard error values shown the significance  $P > 0.05$  goodness of fit model. The acute coronary syndrome. Study was observed in males and females treated with cardiac and lipid biomarkers. Level of V.L.D.L, cholesterol, creatine kinase, phosphokinase, and lactate dehydrogenase of Acute Coronary Syndrome. Sleeping time of ACS patients. In ACS patients 58.7% do walk and 41.3% do not walk daily. 23.5% of patients do exercise and 75.5% of patients don't take exercise. Diet told of ACS patients 37.6% patients eat vegetable, 2.3% people eat meat, 60% people eat mix vegetables. Pain the duration of ACS patients, 31.0% of patients have many years of heat pain, 34.3% of patients have some weeks of pain, 34.7% patients have some days of pain in the shoulder, back, or arm pain. The network of protein-protein interaction based on protein homology in functional conservation. Many studies show that protein interaction is very limited in domain interaction (Itzhaki, Akiva, Altuvia, & Margalit, 2006) domains of the protein shows that is functional, evolutionary, and functionally unit of protein (Vogel, Bashton, Kerrison, Chothia, & Teichmann, 2004) (Ren *et al.*, 2009). Our study shows that thrombospondin-1 human (TSP1) is the multi-domain glycoprotein that performs

many functions like maintaining the cell surface and extracellular Matrix. In molecular organization overall it will be divided into categories A, and B. Group proteins contain the N-Terminal domain and B is contain the C-Terminal domain. The study shows that T4HNR partners with s. Macrospores have the highest level with fatty acid synthase. Our study shows that strings have a network of nodes which shows the interaction with other domains of the protein and have a P-Value of 2.49. Conservation of domain prediction shows VWFC domain has 316-337 and has a score of 9.234. In computational analysis, docking has a 37-energy score in all pathogens which evaluates their efficacy. It has maximum energy in Kcal/mol and has an active site that is prominent. Docking has many tools and servers to give better results like his target site, docking score (Y.-C. Chen, 2015). This study showed the interaction between Tetrahydroisoquinoline (TIQ) ligand and thrombospondin-1 human (TSP1) as a -5.7 lowest energy which considers the best energy source. UNK amino acids are involved in the interaction of this and Tetrahydroisoquinoline (TIQ) as a binding residue.

## 5. Conclusion

The acute coronary syndrome study in ACS males and females showed various risk factors for ACS, including age, blood pressure, smoking and drinking habits, lipid levels, and exercise, were controlled by applying the regression and correlation, all biomarkers were significantly associated with the decline in ACS incidence within the cardiac and lipid group. Our study demonstrated that Docking has a novel interaction between thrombospondin-1 human (TSP1) and Tetrahydroisoquinoline (TIQ) ligand as the lowest score of -5.7 and shows the better distance between protein and ligand interaction which consider the best energy score. Our results may provide a very solid background and useful information for future research on the acute coronary syndrome. Nevertheless, further research is necessary to disprove the possibility that the release of cardiac troponins may also occur in the setting of reversible ACS resulting from cellular ischemia.

## 6. References

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