

ORIGINAL ARTICLE

**Metabolites of Docosahexaenoic Acid Produced by Probiotic *Bacillus cereus* able to Inhibit 2BX4 and 6LU7 Receptors of SARS-CoV-2**

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ABSTRACT

*Inflammatory properties of omega-3 fatty acids have been shown to play a pivotal role in attenuation of uncontrolled immune response in the lungs secondary to bacterial or viral infections which could be useful against COVID-19. In this study, metabolites of docosahexaenoic acid were evaluated against SARS-CoV-2 Main protease (Mpro). GC-MS analysis of docosahexaenoic acid shown that 51 compounds produced by Bacillus cereus. They were docked against three SARS-CoV-2 proteins (receptors), namely Mpro using Epic, LigPrep and Glide module of Schrödinger. Among 51 compounds, Hexadecanoic acid, 2-hydroxy-1 (hydroxymethyl) ethyl ester (MW-330.5g/ mol), Monoelaidin (MW-356.5g/ mol), (Z)-3-(Heptadec-10-en-1-yl) phenol (MW-330.5g/ mol), Decanedioic acid, bis(2-ethylhexyl) ester.1 (MW-426.7g/ mol), Glycidyl palmitate (MW-312.5g/ mol) and Phenol,2,4-Bis(1,1-Dimethylethyl) (MW-278.5) were found to have an ability to bind with both the candidate receptor proteins, 2BX4 and 6LU7. Thus, these compounds could be chosen for further research and assessment in the context of targeted medicinal therapy approach for the virulent SARS-CoV-2 virus.*

**Keywords:** Docosahexaenoic acid, Bioconversion, Metabolites, Molecular docking, SARS-CoV-2.

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**INTRODUCTION**

Several notable viral diseases, including influenza, chikunguniya, Nipah, Zika, and Ebola, have caused global outbreaks in recent decades [1,2]. The sudden emergence of COVID-19 has become a life-threatening threat for millions of people throughout the world. The upsurge of COVID-19 caused by SARS-CoV-2 had put the world on a standstill, within a short span of time. The epidemic had its repercussions on every walk of life, affecting the global economy, transportation and healthcare systems. Besides, there are difference in opinion about the credibility and safety of the drugs available in the market [3]. Discovering the immunizing agent, the community of researchers uses different strategies focusing to develop an anti-viral drug by targeting either of many structural and non-structural proteins with an agenda for developing inhibitors (i) to impede infectious agent passage into the host cells, and (ii) to forestall infectious agent replication [4]. Several drugs are being repurposed to treat COVID-19, including ritonavir, lopinavir, hydroxychloroquine, chloroquine, azithromycin, remdesivir and clinical trials are underway [5]. However, a potential COVID-19 medication has still a long way to come. In this context, it is

a timely requisite that we should consider natural compounds as a substitute for the synthetic molecules for tackling this disease.

Several SARS-CoV-2 macromolecules have been chosen for designing and developing anti-Covid-19 medicines, including 3-chymotrypsin-like protease (3CL pro), endoribonuclease, RNA-dependent RNA polymerase, and 2-O methyltransferase. 3CLpro protein is involved in all stages of the virus life cycle, including viral entry, viral protein maturation, and viral infection pathogenesis [6]. (3CLpro/Mpro), the viral 3 C-like protease or major protease encoded by Non-Structural Protein, is one of the best-characterized therapeutic targets among Covid and it produces NSPs such as RNA dependent RNA polymerase and helicase which play an essential role in viral replication, and its inhibition interrupts the viral life cycle [7]. The 3CLpro/Mpro or main proteases namely, M<sup>Cov1</sup>Pro (PDB code 2BX4) from SARS-CoV and M<sup>Cov2</sup>Pro (PDB code 6LU7) from SARS-CoV-2 were used in this study.

Now-a-days, *in-silico* techniques have become an inevitable part in the domain of drug discovery, especially when we arrive at the question of target identification [8,9]. For short-listing the probable hits from the huge data of candidate molecules and identification of the lead compound, computational tools are a boon, since they save the cost both in terms of time and money. Target identification is the first step in any drug designing process [10]. Cellular structures, especially proteins which are suspected to play a pivotal role in the pathogenicity of the microbe are identified as the target for drug delivery [8,10]. An ideal target should be effective, safe and should be specific to the selected ligand/drug molecule. Lead identification and optimization is the next phase in the hierarchy of drug development [10]. Optimized lead molecule will then go through pre-clinical trials to test its safety and efficacy [9,11].

In this study, we are employing *in-silico* drug designing techniques by focusing on structure-based computational modeling of ligand-receptor interactions, to identify potential targets for SARS-CoV-2. Molecular docking is a widely used technique in the domain of drug designing [12]. It helps in understanding how macromolecules, usually proteins interact with small molecules called ligands to form a stable complex [8,10]. The particulars we could gain from the favoured orientations could be used to predict the best pose/conformer of the ligand-receptor interactions [12,13]. This could be achieved from the scoring function of the molecular docking software [14]. Through docking, we aim to arrive at a confirmation of ligand-receptor complex with minimum free energy and maximum stability [13]. If we could figure out the general principles underlying the stability and energy of the ligand-receptor complex formation, we might be able to forecast the variables that influence the docking of the molecules [12]. Docking could also be employed to understand protein-protein interactions [8,14], binding site identification [14], hit identification [14] and lead optimization [10] in the drug discovery process [14,15]. In the case of protein-ligand interaction, molecular docking techniques provide us with distinct docked conformers and orientation of ligand molecule, so as to be compatible with the active site of the receptor protein [14]. The prospective candidate compounds capable of reducing viral replication, infection and thus acting as an effective treatment against SARS-CoV-2 may be identified based on the affinity shown by the ligands.

DHA (Docosahexaenoic acid) is a vital component for immunity and critical life stages (such as postpartum) and it's crucial during pregnancy and childhood because it's play important role in brain development [16,17]. DHA makes up approximately 90% of the omega-3 fatty acids in the human brain, as well as up to 25% of the total fat content. It is largely found in cell membranes, where it enhances membrane fluidity and cell-to-cell gaps. This makes it easier for nerve cells to send and receive electrical impulses [18]. In addition to its documented antimicrobial and antiviral properties, DHA possesses anti-inflammatory activity and inhibit tumorigenesis [19,20,5,21]. The microbicidal activity of selected Long Chain Unsaturated Fattyacid's and their derivatives has been reported on various enveloped viruses, parasites and pathogenic bacteria such as *Pseudomonas aeruginosa*, *Bacillus subtilis*, *Listeria monocytogenes*, *Helicobacter pylori*, *Staphylococcus aureus* and *Neisseria gonorrhoea* [19,22]. Fish oil inhibits tumor cell proliferation, whereas arachidonic acid, a long-chain n-6 fatty acid, promotes cancer cell proliferation [23]. Bristrian has suggested using parenteral supplementation of fish-oil emulsions containing significant levels of EPA (Eicosapentaenoic acid) and DHA (4-6 gram/day) to treat patients with severe SARS-CoV-2 in order to limit cytokine release and moderate the inflammatory response [24]. In our study, we focused on structure-based computational modelling of ligand-receptor interactions and deals with the *in-silico* study of various bioconverted docosahexaenoic acid metabolites as potential bioactive components (to be used as drugs) against COVID-19 enzyme (A) M<sup>Cov1</sup>Pro (PDB code 2BX4) from SARS-CoV and (B) M<sup>Cov2</sup>Pro (PDB code 6LU7) from SARS-CoV-2 as the receptors.

**MATERIAL AND METHODS****BIOCONVERSION OF DHA USING PROBIOTIC *BACILLUS CEREBUS***

Bioconversion was described previously [22] and carried out in five set of 50 mL SM broth with supplement of 200mg of DHA were added to 24 hrs old culture of *Bacillus cereus* to the five set of SM broth individually and followed by continued incubation for an 24 hrs to 120 hrs at 37°C and bioconversion was allowed to proceed.

**EXTRACTION OF FATTYACIDS FROM BIOCONVERTED BROTH**

Bio-converted broth were suspended in 3mL of 4 mol<sup>-1</sup> sodium hydroxide, and incubated at 90°C for 90 min. After cooling, the pH of the sample was adjusted to 2 with hydrochloric acid. Fatty acids were then extracted by adding 2 mL anhydrous diethyl ether and separated by centrifugation at 5500×g for 10 min. The upper phase was removed and dehydrated by adding anhydrous sodium sulfate. The dehydrated fatty acids were collected and dried under a stream of nitrogen. Next, 50 µL bistrimethylsilyltrifluoroacetamide (BSTFA) was added, and the mixture was incubated at 70°C for 30 min and dried under a stream of nitrogen. The fatty acids were dissolved in 100 µL hexane for GC/MS analysis [25].

**CHARACTERIZATION OF BIOCONVERTED METABOLITES BY GC-MS ANALYSIS**

Fatty acid composition analysis was performed on the Shimadzu GCMS QP 2020 that employed a fused silica column, packed with SH-Rxi-%Sil MS (30 m × 0.25 mm ID × 250µm<sup>2</sup>) and the components were separated using Helium as carrier gas at a constant flow of 1 ml/min. The injector temperature was set at 280°C during the chromatographic run. 1µL of extract sample injected into the instrument the oven temperature was as follows: 40°C (2 min); followed by 280°C at the rate of 10°C min<sup>-1</sup> and 280°C, where it was held for 3 min. The mass detector conditions were: transfer line temperature 280°C; ion source temperature 230°C; and ionization mode electron impact at 70 eV, a scan time 0.2 s and scan interval of 0.1 s, fragments from 40 to 550 Da. The spectrums of the components were compared with the database of spectrum of known components stored in the GC-MS NIST (2017) library.

**LIGAND PREPARATION**

From the GC-MS analysis, 53 compounds were downloaded in SDF (Spatial Data File) two-dimensional (2D) format from the PubChem database (<https://pubchem.ncbi.nlm.nih.gov/>, accessed on March 2021). Ligand was prepared using LigPrep tool of Maestro v 11.1. The pH 7.0 ± 2.0 was used for the generation of ionization states of the compounds with Epik 2.2 (Force field: OPLS4) in Schrödinger ver.11.1. Up to 32 possible stereoisomers per ligand were retained.

**PROTEIN PREPARATION**

The three-dimensional (3D) structure of the (A) M<sup>Cov1</sup>Pro (PDB code 2BX4) from SARS-CoV and (B) M<sup>Cov2</sup>Pro (PDB code 6LU7) from SARS-CoV-2 were retrieved from the RCSB Protein Data Bank (<https://www.rcsb.org/structure/>, accessed on 12 March 2021) in PDB format. The Protein Preparation Wizard (Schrödinger ver.11.1) was used to prepare the 6LU7 and 2BX4 receptor using the following processes: optimization, removal of water molecules, and minimization (Force field: OPLS4).

**RECEPTOR GRID GENERATION AND GLIDE BASED MOLECULAR DOCKING**

The grid generation (Schrödinger Maestro ver.11.1) for the selected receptor was performed using the default parameters (Force field: OPLS4). Receptor grids were calculated for the prepared proteins for the observation of poses by various ligands bound within the active predicted site during the docking procedure. The vander Waals radius scaling factor and the partial atomic charge were 1.00 and 0.25, respectively. A cubic box of specific dimensions centered on the centroid of the active site residues was obtained for the receptor. The bounding box was set to 14 × 14 × 14 Å for docking experiments. Ligand docking was followed by the flexible standard precision (Schrödinger ver.11.1), and the docking score and the interactions of the receptor-ligand docking were recorded using Glide.

**RESULTS AND DISCUSSION**

Coronaviruses are single stranded RNA viruses with a length of about 26,000-32,000 base pairs [26]. As of now, 39 coronavirus species have been identified in 27 sub-genera, 5 genera and 2 sub-families that belong to the family Coronaviridae of the order Nidovirales [27]. Even though the rate of mutation of SARS-CoV-2 has been estimated to be about 1-2 mutations per month, the mode of infection and transmission still remains unchanged [28]. This makes it prone to drug ability. By focusing on its mode of entry into the host system, it is possible to sort out the proteins that are crucial for its virulence and thus effective anti-viral drugs could be developed against this fatal disease.

In the present study, structure-based computational modeling of ligand-receptor interactions has been performed, focusing on the ligand molecules which were derived from the bioconversion of DHA. A total of 82 compounds were identified from the bioconverted DHA using GC-MS, which are listed in (Fig.1-5)

and (Table S1-S6) along with their medicinal properties. The total ionic chromatogram (TIC) is shown in (Fig 1-5). Fifty-one compounds were selected for molecular docking analyses based on their medicinal properties. DHA has been shown to possess anti-viral, anti-cancerous and anti-microbial properties [29,30]. It has also demonstrated therapeutic effect in reducing cardio metabolic risk factors [31]. Besides, independent studies by researchers substantiates the role of DHA in inhibiting viral replication and infection [32,33]. One of the best-characterized and distinguished drug targets among CoVs is 3CLpro also called Mpro, a viral 3 C-like protease or main protease. 3CLpro along with PLpro (papain-like protease) cleaves the polyprotein pp1ab and pp1a to produce non-structural proteins (NSPs) such as RNA dependent RNA polymerase and helicase [34, 35, 36]. They play an essential role in viral replication and hence its inhibition interrupts the viral life cycle. Mpro is highly conserved among CoVs, sharing over 90% sequence identity, differing only 12 residues between M<sup>Cov1</sup>Pro from SARS-CoV and M<sup>Cov2</sup>Pro from SARS-CoV-2 [7]. The crystal structure of SARS-CoV-2 main protease in complex with an inhibitor N3 (PDB ID 6LU7) and the crystal structure of SARS Coronavirus Main Proteinase (P21212) (PDB ID 2BX4) were considered as the receptors for the present study. Nelfinavir, a protease inhibitor (PI) [37] has been used as the control for molecular docking throughout our experiment. It is widely used in the treatment of HIV (human immunodeficiency virus) infection and the AIDS (acquired immunodeficiency syndrome) [38]. Nelfinavir selectively binds to the HIV protease and inhibits it by interfering in its replication machinery [38]. Both experimental and computational evidences suggest the ability of nelfinavir in inhibiting the cytopathic effect caused by SARS-CoV-2 [39].

Molecular Docking was carried out using bioconverted DHA metabolites against COVID-19 enzyme receptors, 6LU7 and 2BX4 with Nelfinavir as the control. Docking was done using Glide module (Maestro software) of Schrodinger ver.11.1. The strength of the receptor-ligand interactions was determined based on the Glide score. The higher the Glide score value in the negative scale, the better the interaction between the protein and the ligand [40]. In other words, the lower the Glide scores the better the affinity between the protein and the ligand. Potential ligands were shortlisted based on the ligand efficiency, Glide score and docking score. The receptors, 2BX4 and 6LU7 were docked with 51 ligands which were derived from the bioconversion of DHA, whose results are displayed in (Table 1-2) respectively. In the docking experiment, four ligands were shown to possess considerable docking score against 2BX4 (Table-1). Among them, Hexadecanoic acid, 2-hydroxy-1 (hydroxymethyl) ethyl ester displayed the highest predicted binding affinity with a Glide score of -5.118. The next in line was Monoelaidin (Gscore: -4.515), (Z)-3-(Heptadec-10-en-1-yl) phenol (Gscore: -4.376) and Decanedioic acid, bis(2-ethylhexyl) ester.1(Gscore: -4.085). In the case of 6LU7, two ligands exhibited appreciable binding efficiency (Table-2). They were (Z)-3-(Heptadec-10-en-1-yl) phenol with a Glide score of -3.872 and Phenol, 2,4-Bis(1,1-Dimethylethyl), Oxime with a Gscore of -3.672.

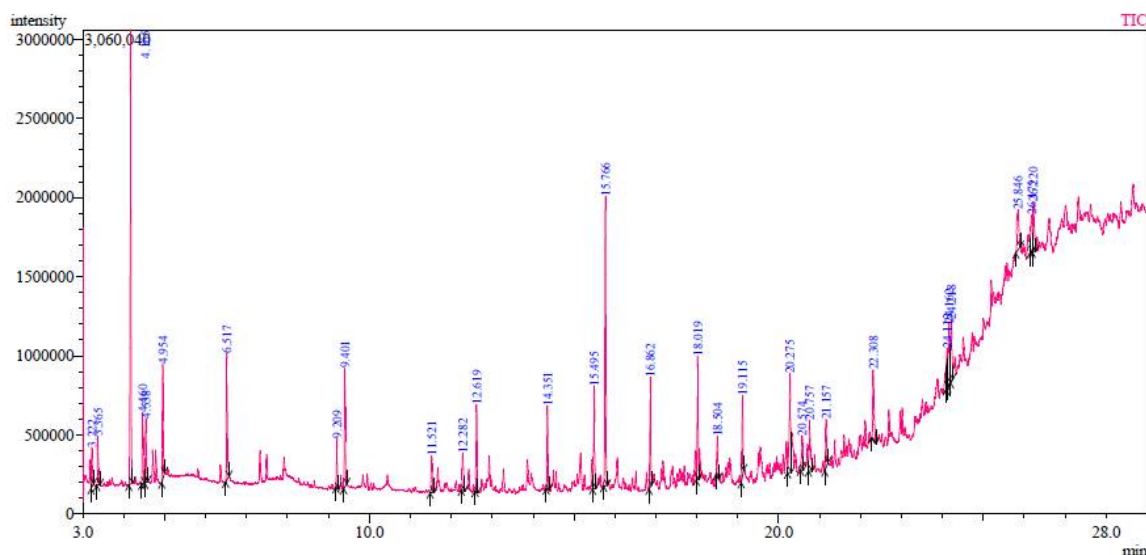
The docking interaction between the control and 2BX4 was appreciably high with a Glide score of -4.687. Molecular docking revealed that 3 ligand atoms of the control, interacted with various amino acid residues of the protein at position 108(proline), 110(glutamine) and 294 (phenylalanine) respectively. Proline made a hydrophobic interaction with the 'OH' atom of nelfinavir, whereas glutamine made a polar hydrogen bond interaction with the functional group, 'NH' and phenylalanine made a hydrophobic interaction with 'N+H' group of the ligand (Fig.6a). 51 metabolites derived from the bioconversion of DHA were docked against 2BX4. Among them, Hexadecanoic acid, 2-hydroxy-1 (hydroxymethyl) ethyl ester displayed the highest binding efficiency with a Glide score of -5.118. Docking results revealed that 2 ligand atoms of Hexadecanoic acid, 2-hydroxy-1 (hydroxymethyl) ethyl, interacted with amino acid residues of the protein at positions 111 and 295 with threonine and aspartic acid respectively. Threonine makes a polar hydrogen bond interaction with the 'OH' atom of the ligand, whereas aspartic acid makes a negatively charged hydrogen bond interaction with OH (Fig.6b). The next interacting molecule with 2BX4 with a higher Glide score was monoelaidin (Gscore: -4.515). Monoelaidin made an OH bond interaction with threonine and aspartate at positions 111 and 295 respectively, similar to that of hexadecanoic acid, 2-hydroxy-1 (hydroxymethyl) ethyl ester (Fig.6c). (Z)-3-(Heptadec-10-en-1-yl) phenol comes in the next position with a Glide score of -4.376. It made an OH bond interaction with asparagine at 203th position (Fig.6D). Decanedioic acid, bis(2-ethylhexyl) ester.1(Gscore: -4.085) interacted with the histidine amino acid residue of 2BX4 at 246th position. It made a polar hydrogen bond interaction with the 'O' atom of the protein (Fig.6e).

6LU7 is a key enzyme in SARS-Cov-2, which was illustrated as playing a crucial role in the viral replication and infection [5].The docking interaction between the control (nelfinavir) and 6LU7 was considerably high with a Glide score of -4.009, as in the case of 2BX4. Molecular docking revealed that 4 ligand atoms of the control, interacted with different amino acid residues of 2BX4 at positions 105,110 and 294 with arginine, glutamine and phenylalanine respectively (Fig.7a). Arginine made a positively charged hydrogen

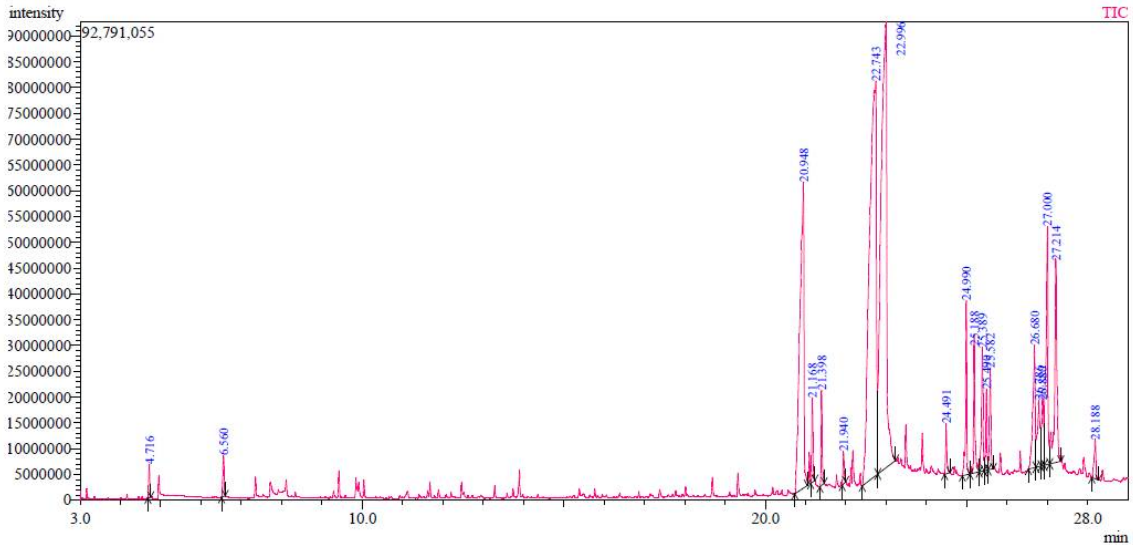
bond interaction with the 'OH' atom of nelfinavir, whereas glutamine made hydrogen bond interactions with the functional groups, 'NH' and 'OH'. Phenylalanine made a hydrophobic pi-pi stacking with the benzene ring as shown in (Fig.7a). 51 bioconverted metabolites of DHA were docked against 6LU7 and the docking images and the bonding interactions were analysed. In the case of 6LU7, two ligands exhibited appreciable binding efficiency (Table-2). They were (Z)-3-(Heptadec-10-en-1-yl) phenol with a Gscore of -3.872 and phenol, 2,4-Bis(1,1-Dimethylethyl) with a Gscore of -3.672. Docking results revealed that 2 ligand atoms of (Z)-3-(Heptadec-10-en-1-yl) phenol, interacted with the amino acid residues of the protein at position 108 and 246 with proline and histidine respectively. Proline made a hydrophobic interaction with 'OH' atom of the ligand, whereas histidine makes a polar pi-pi stacking with the benzene ring as shown in (Fig.7b). In the case of phenol, 2,4-Bis(1,1-Dimethylethyl), 2 ligand atoms interacted with the amino acid residues of 6LU7 at position 110 and 294 with glutamine and phenyl alanine respectively. Glutamine made a polar hydrogen bonding interaction with the 'OH' atom of the ligand, whereas phenylalanine made a hydrophobic pi-pi stacking with the benzene ring (Fig.7c).

Thus, in this study, the SARS-CoV-2 proteins namely, 6LU7 and 2BX4 were considered as targets to screen the bioconverted metabolites of DHA and identify potential drugs against SARS-CoV-2 that have appreciable binding affinity towards these receptor proteins which play essential role in viral replication. In the docking experiments, four ligands showed considerable docking score against 2BX4 (Table-1). Among them, Hexadecanoic acid, 2-hydroxy-1 (hydroxymethyl) ethyl ester displayed the highest Glide score (-5.118), greater than even that of the control (nelfinavir) (Gscore: -4.687). Hence, Hexadecanoic acid, 2-hydroxy-1 (hydroxymethyl) ethyl ester is proposed to possess better inhibitory property towards 2BX4 than that of the control. Thus, Hexadecanoic acid, 2-hydroxy-1 (hydroxymethyl) ethyl ester is strongly recommended as a potential drug candidate for SARS-CoV-2 (M<sup>Cov1</sup>Pro). Interestingly, in the case of 6LU7, the standard inhibitor, nelfinavir (Gscore: -4.009) showed the highest docking score compared to the analysed compounds. Next in line was (Z)-3-(Heptadec-10-en-1-yl) phenol, which depicted a Glide score of -3.872. Hence, (Z)-3-(Heptadec-10-en-1-yl) phenol could also be considered as a drug candidate for SARS-CoV-2 (M<sup>Cov2</sup>Pro). This study recommended that Hexadecanoic acid, 2-hydroxy-1 (hydroxymethyl) ethyl ester (MW-330.5g/mol), Monoelaidin (MW-356.5g/mol), (Z)-3-(Heptadec-10-en-1-yl) phenol (MW-330.5g/mol), Decanedioic acid, bis(2-ethylhexyl) ester.1 (MW-426.7g/mol), Glycidyl palmitate (MW-312.5g/mol) and Phenol,2,4-Bis(1,1-Dimethylethyl) (MW-278.5) have the ability to bind to both the candidate receptor proteins, 2BX4 and 6LU7 (Table-3). Hence, these identified compounds could be selected for further study and evaluation with respect to the targeted drug treatment approach for the noxious SARS-CoV-2.

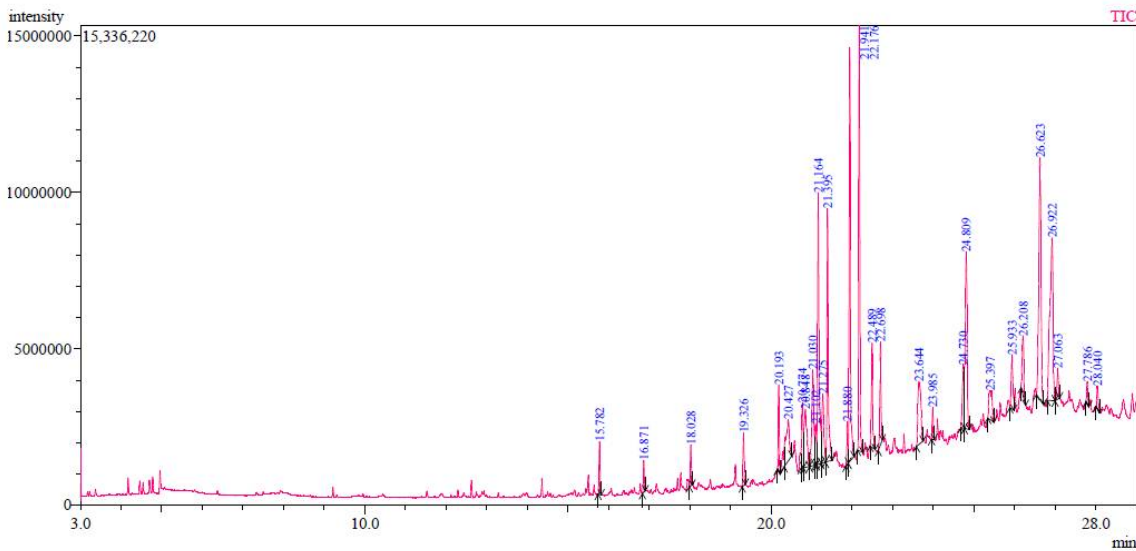
**Fig. 1. GC-MS Chromatogram of Docosahexaenoic acid bioconverted metabolites at 24 hrs**



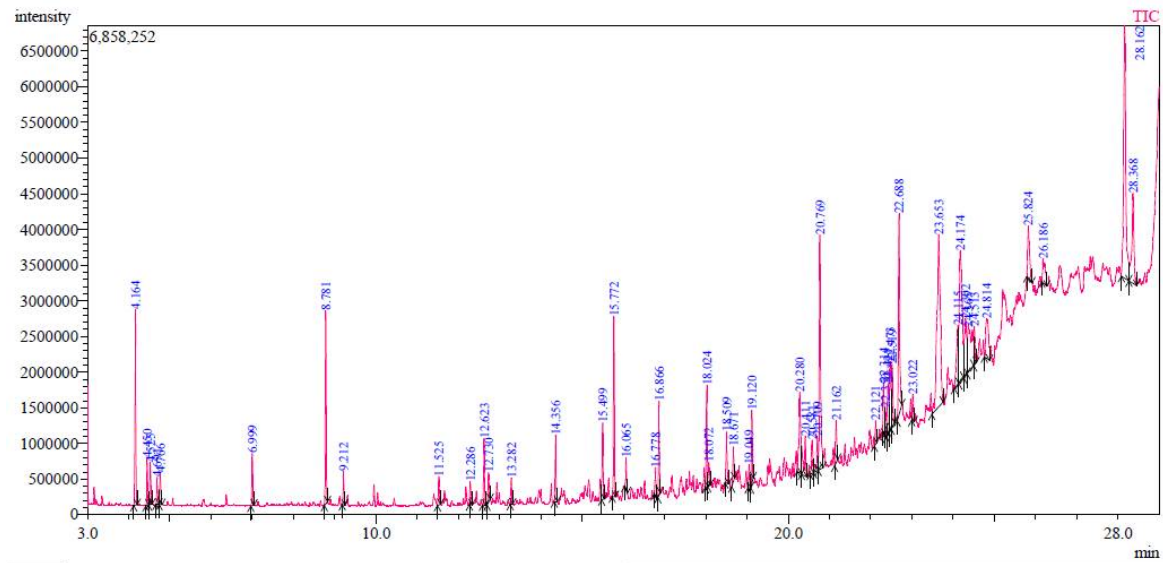
**Fig. 2. GC-MS Chromatogram of Docosahexaenoic acid bioconverted metabolites at 48 hrs**



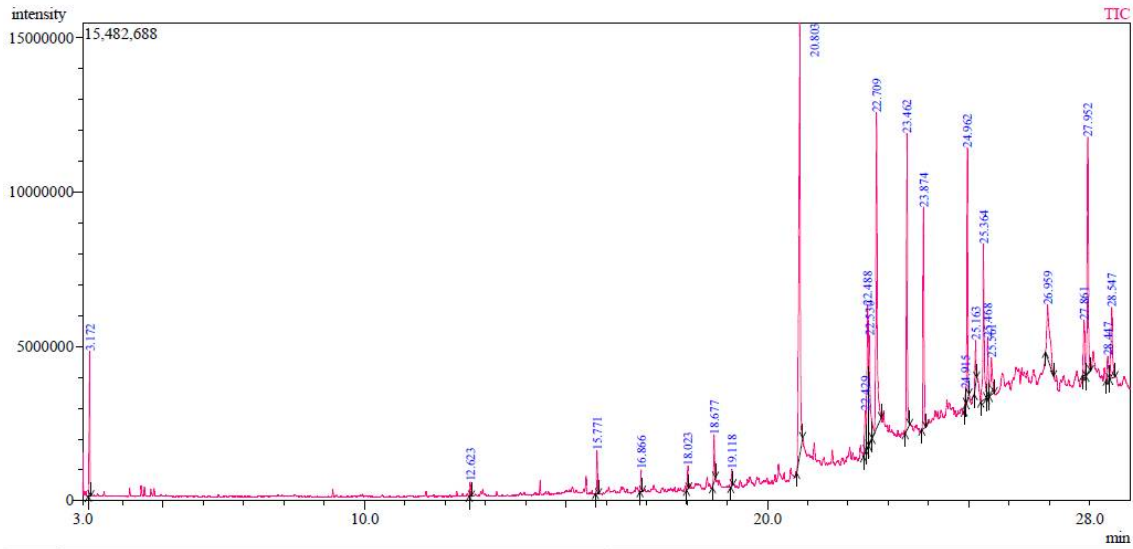
**Fig. 3. GC-MS Chromatogram of Docosahexaenoic acid bioconverted metabolites at 72 hrs**



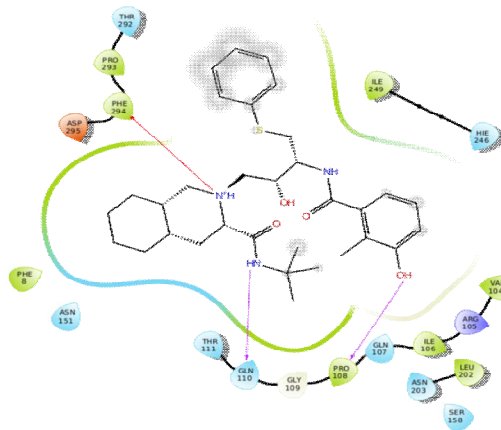
**Fig. 4. GC-MS Chromatogram of Docosahexaenoic acid bioconverted metabolites at 96 hrs**



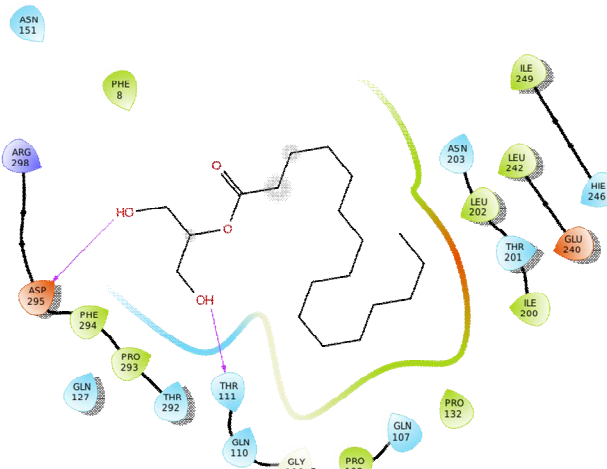
**Fig. 5. GC-MS Chromatogram of Docosahexaenoic acid bioconverted metabolites at 120 hrs**



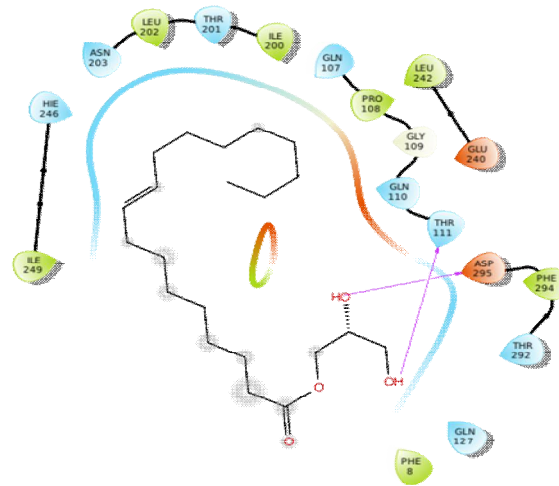
**Fig. 6. Interaction diagram with H-bonds and other interactions of a 2BX4 with (a) Nelfinavir, with (b) Hexadecanoic acid 2-hydroxy-1-(hydroxymethyl)ethyl ester, with (c) Monoelaidin, (d) (Z)-3-(Heptadec-10-en-1-yl)phenol, with (e) Decanedioic acid, bis(2-ethylhexyl) ester, and with (f) Glycidyl palmitate showing different polar and non-polar interactions and bonds**



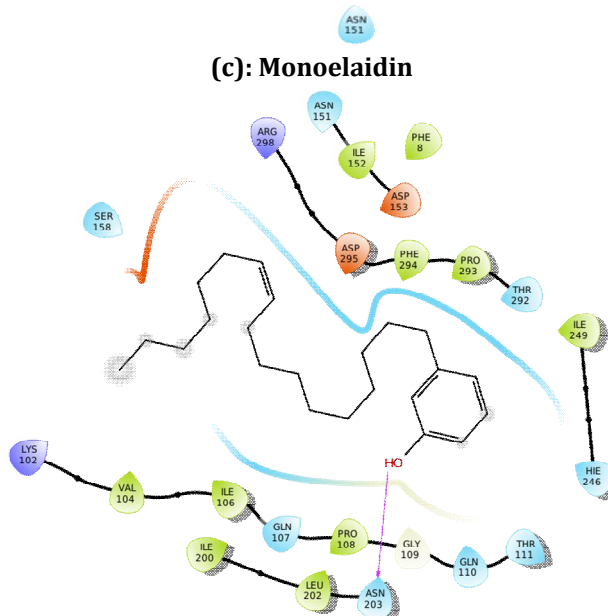
**(a): Nelfinavir (Control)**



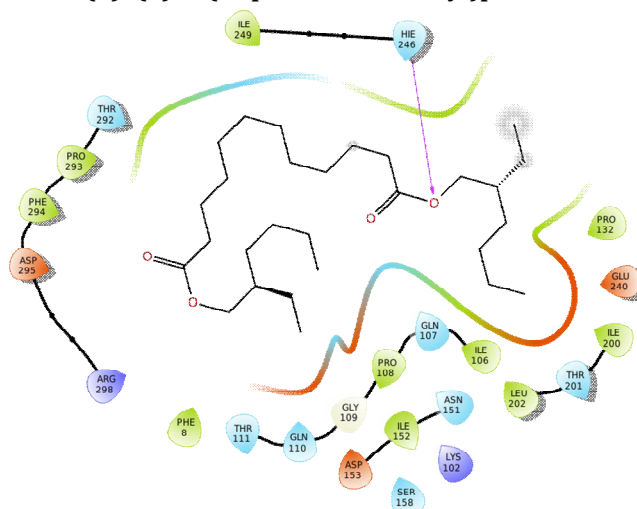
**(b): Hexadecanoic acid, 2-hydroxy-1-(hydroxymethyl)ethyl ester**



**(c): Monoelaidin**



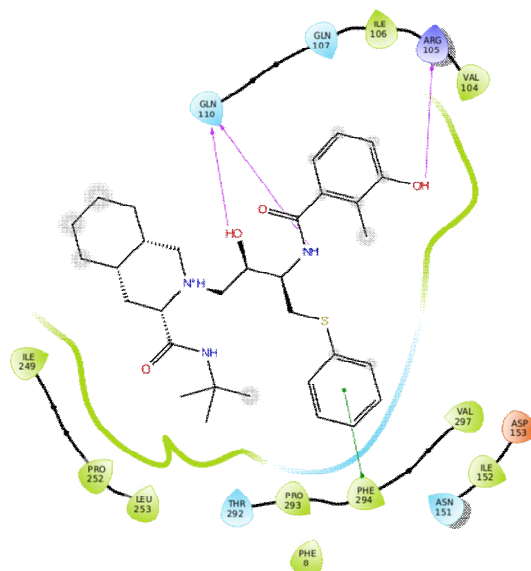
**(d): (Z)-3-(Heptadec-10-en-1-yl)phenol**



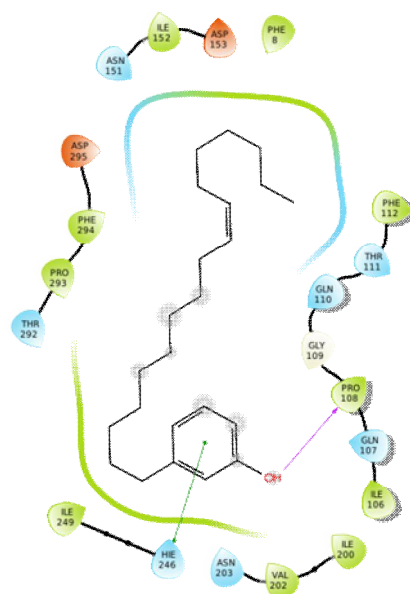
**(e): Decanedioic acid, bis(2-ethylhexyl) ester**



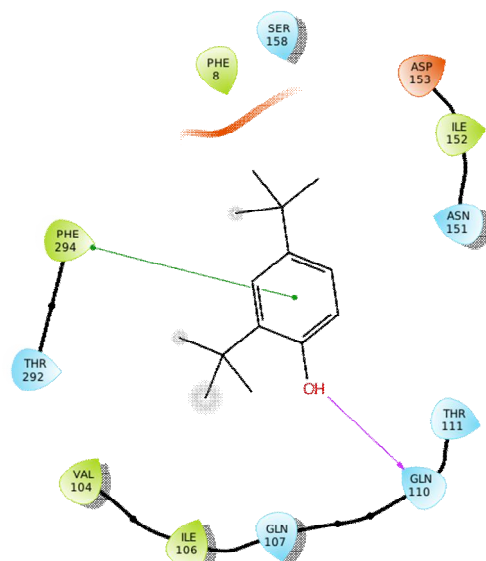
**Fig. 7. Interaction diagram with H-bonds and other interactions of a 6LU7 with (a) Nelfinavir, with (b) (Z)-3-(Heptadec-10-en-1-yl)phenol, with (c) Phenol, 2,4-Bis(1,1-Dimethylethyl)-, (d) Oxime-, methoxy-phenyl- (3), (e) with Hexadecanoic acid, 2-hydroxy-1-(hydroxymethyl) ethyl ester (f) 9-Octadecenoic Acid (9Z)-, Oxiranylmethyl Ester, (g) Decanedioic Acid, Bis(2-Ethylhexyl) Ester, (h) Squalene, (i) 2-Pentacosanone, (j) Z,Z-6,27-Hexatriactontadien-2-One, (k) Glycidyl Palmitate, (l) Propyl Stearate, (m) Benzene, 1,3-Bis(1,1-Dimethylethyl)-, (n) Monoelaidin, (o) 1-Hexanol, 2-Ethyl-, (p) Z,Z-6,28-Heptatriactontadien-2-One, (q) Arachidic Acid showing diferent polar and non-polar interactions and bonds**



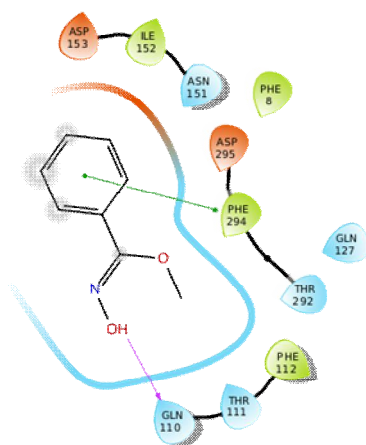
**(a): Nelfinavir (Control)**



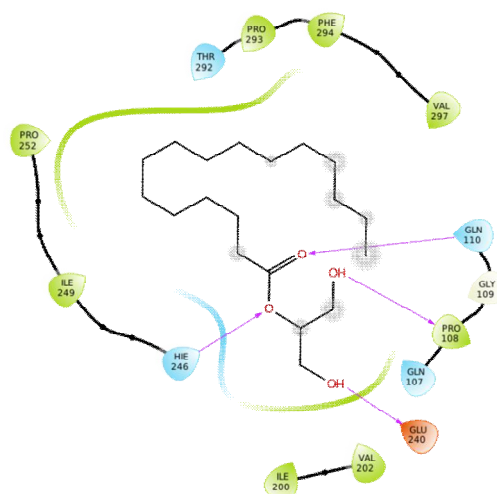
**(b): (Z)-3-(Heptadec-10-en-1-yl)phenol**



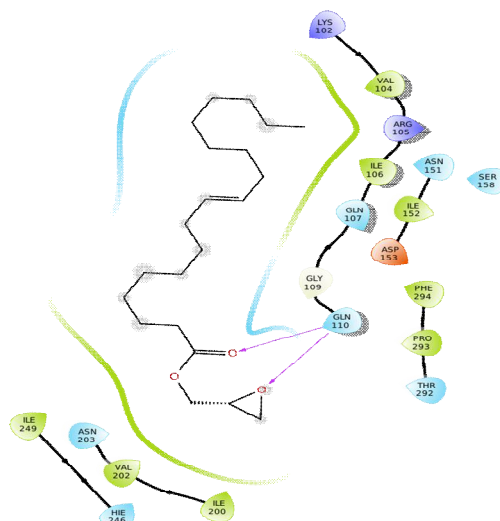
**(c): Phenol, 2,4-Bis(1,1-Dimethylethyl)-**



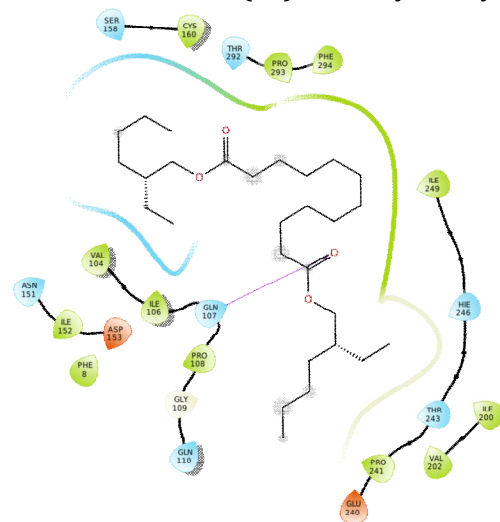
**(d): Oxime-, methoxy-phenyl- (3)**



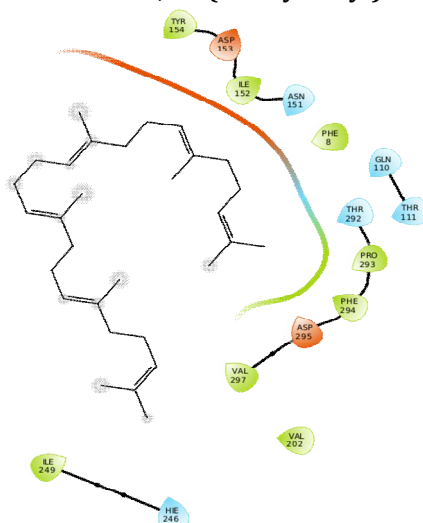
**(e): Hexadecanoic acid, 2-hydroxy-1-(hydroxymethyl)ethyl ester**



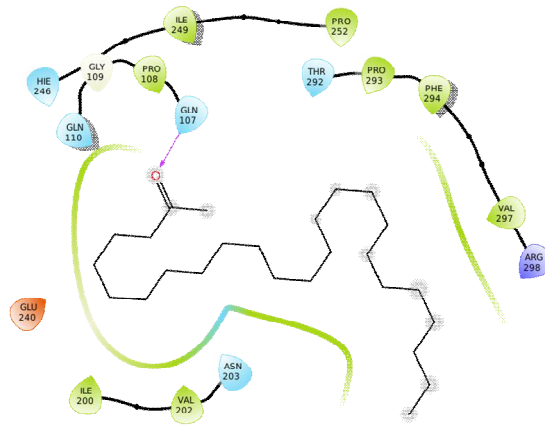
**(f): 9-Octadecenoic acid (9Z)-, oxiranylmethyl ester**



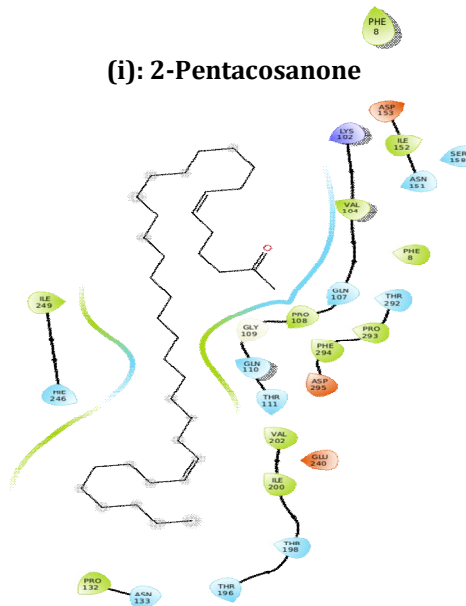
**(g): Decanedioic acid, bis(2-ethylhexyl) ester**



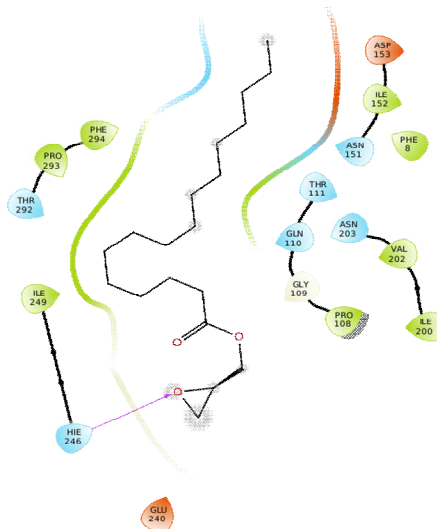
**(h): Squalene**



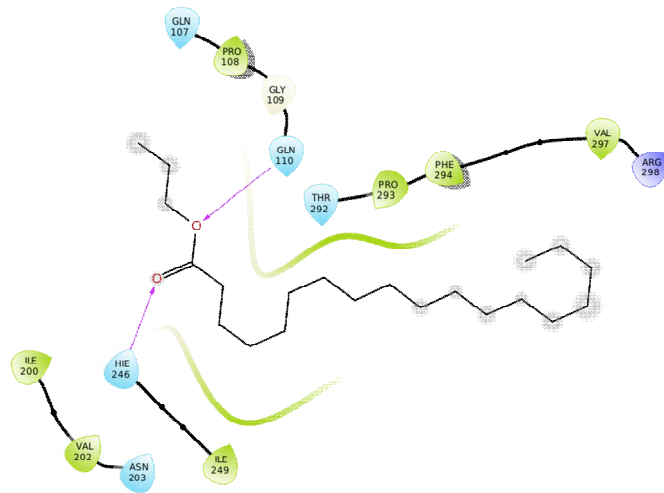
**(i): 2-Pentacosanone**



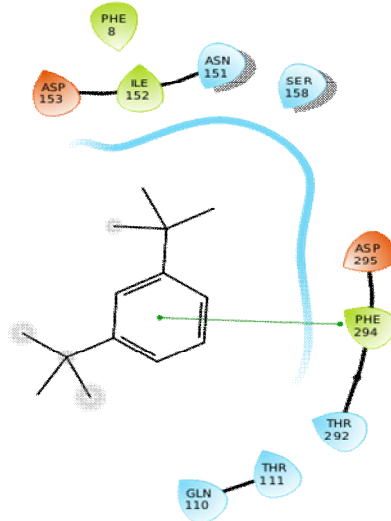
**(j): Z,Z-6,27-Hexatriactontadien-2-one**



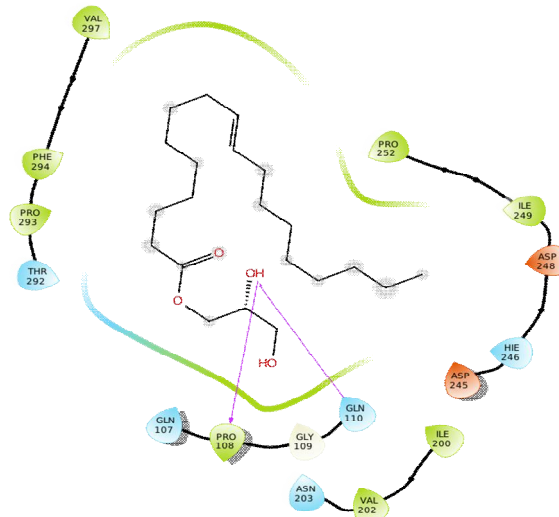
**(k): Glycidyl palmitate**



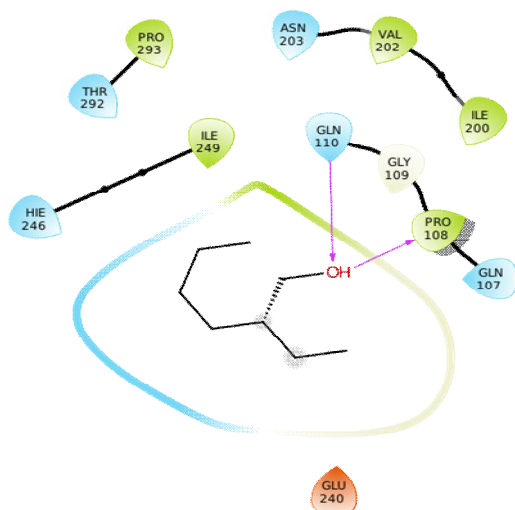
(l): Propyl stearate



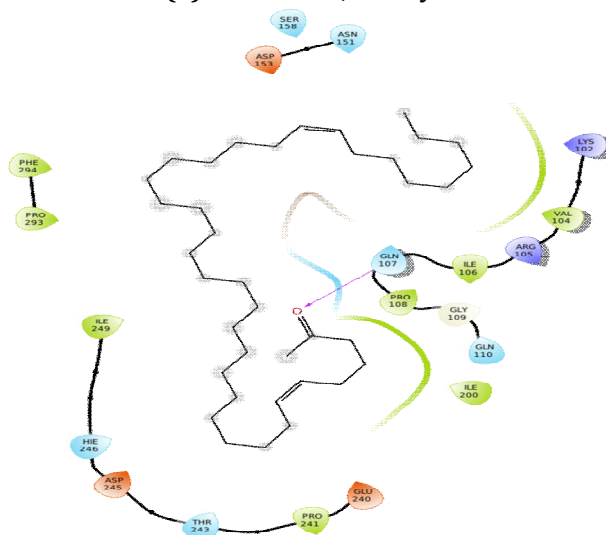
(m): Benzene, 1,3-Bis(1,1-Dimethylethyl)-



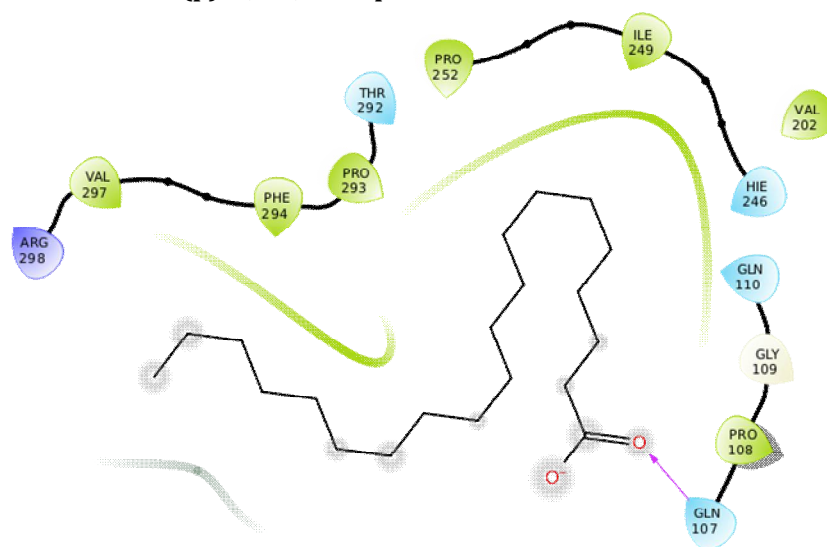
(n): Monoelaidin



**(o): 1-Hexanol, 2-Ethyl-**



**(p): Z,Z-6,28-Heptatriactontadien-2-one**



**(q): Arachidic acid**

**Table 1 - Result of the docking experiment performed between the receptor (2BX4) and the ligands (Compounds)**

S.N	Receptor	Ligand	Glide Ligand Efficiency	Docking Score	Glide G score	RMSD
1	The 3CLpro/ Mpro or mains proteases (PDB code 6LU7) from SARS-CoV	Nelfinavir (Control)	-0.1	-3.995	-4.009	1.4
2		(Z)-3-(Heptadec-10-En-1-Yl)Phenol	-0.161	-3.871	-3.872	1.6
3		Phenol, 2,4-Bis(1,1-Dimethylethyl)-	-0.245	-3.672	-3.672	0.6
4		Oxime-, Methoxy-Phenyl- (3)	-0.303	-3.334	-3.334	0.4
5		Hexadecanoic Acid, 2-Hydroxy-1-(Hydroxymethyl)Ethyl Ester	-0.144	-3.314	-3.314	-
6		9-Octadecenoic Acid (9Z)-, Oxiranylmethyl Ester	-0.136	-3.272	-3.272	-
7		Decanedioic Acid, Bis(2-Ethylhexyl) Ester	-0.1	-3.206	-3.206	-
8		Squalene	-0.104	-3.133	-3.133	1.8
9		2-Pentacosanone	-0.12	-3.124	-3.124	-
10		Z,Z-6,27-Hexatriactontadien-2-One	-0.084	-3.119	-3.119	-
11		Glycidyl Palmitate	-0.14	-3.09	-3.09	-
12		Propyl Stearate	-0.127	-2.922	-2.922	-
13		Benzene, 1,3-Bis(1,1-Dimethylethyl)-	-0.207	-2.891	-2.891	0.6
14		Monoelaidin	-0.11	-2.746	-2.746	-
15		1-Hexanol, 2-Ethyl-	-0.289	-2.604	-2.604	0.6
16		Z,Z-6,28-Heptatriactontadien-2-One	-0.067	-2.556	-2.556	-
17		Arachidic Acid	-0.114	-2.518	-2.521	-
18		Stigmast-5-En-3-Ol,Oleate	-0.047	-2.286	-2.286	-
19		Stigmasta-5,22-Dien-3-Ol, Acetat, (3-Beta,2	-0.069	-2.276	-2.276	-
20		Ergosta-5,7,9(11),22-Tetraen-3-Ol, (3.Beta.,22E)-	-0.077	-2.235	-2.235	0.8
21		Furan, Tetrahydro-2,5-Dimethyl-	-0.263	-1.844	-1.844	0.4
22		Hexamethylcyclotrisiloxane	-0.148	-1.776	-1.776	0.4
23		2,3-Diacetoxypropyl Stearate	-0.054	-1.665	-1.665	-
24		Octane, 6-Ethyl-2-Methyl-	-0.146	-1.604	-1.604	0.6
25		Hexanal	-0.225	-1.573	-1.573	0.6
26		2,6,11-Trimethyldodecane	-0.099	-1.491	-1.491	0.8
27		9,17-Octadecadienal, (Z)-	-0.078	-1.474	-1.474	1.4
28		4-Pentyl-Cyclohexanecarboxylic Acid	-0.077	-1.377	-1.377	0.8
29		3-Hexanone	-0.077	-1.377	-1.377	0.4
30		(8Z,11Z)-Heptadecadienal	-0.077	-1.377	-1.377	1.2
31		Oleic Acid	-0.066	-1.325	-1.329	1.4
32		1-Propene, 3,3-Dichloro-	-0.259	-1.297	-1.297	0.4
33		Butyl Isodecyl Phthalate	-0.05	-1.291	-1.291	1.2
34		Cyclodecasiloxane, Eicosamethyl-	-0.029	-1.179	-1.179	0.8
35		10(E),12(Z)-Conjugated Linoleic Acid	-0.059	-1.171	-1.174	1.4
36		Hexadecane, 2,6,10,14-Tetramethyl-	-0.058	-1.162	-1.162	1.6
37		2 Nonadecanone	-0.051	-1.028	-1.028	-
38		Heneicosane	-0.041	-0.858	-0.858	-
39		Stearic Acid	-0.041	-0.815	-0.819	-
40		Palmitic Acid	-0.029	-0.522	-0.526	1.4
41		Hexadecanal	-0.028	-0.479	-0.479	1.2
42		Cis-9-Hexadecenal	-0.02	-0.344	-0.344	1.2
43		2-Heptodecanone	-0.011	-0.207	-0.207	1.4
44		9-Heptadecanone	-0.01	-0.173	-0.173	1.4
45		1-Cyclohexyldimethylsilyloxybutane	0	0.007	0.007	0.6
46		Icosanal	0.005	0.097	0.097	-
47		Hexadecane	0.006	0.1	0.1	1.4
48		Dodecane	0.027	0.319	0.319	0.8
49		Eicosane	0.034	0.677	0.677	-
50		8-Octadecanone	0.038	0.725	0.725	1.4
51		Dotriacontane	0.08	2.575	2.575	-

**Table 2 - Result of the docking experiment performed between the receptor (6LU7) and the ligands (Compounds)**

S.No	Receptor	Ligand	Docking Score	Glide Ligand Efficiency	Glide G score	RMSD
1	The 3CLpro/M pro or mains proteases: M <sup>Cov2</sup> Pro (PDB code 6LU7) 7) from SARS-CoV-2.	Nelfinavir (Control)	-4.673	-0.117	-4.687	1.4
2		Hexadecanoic acid, 2-hydroxy-1-(hydroxymethyl)ethyl ester	-5.118	-0.223	-5.118	-
3		Monoelaidin	-4.515	-0.181	-4.515	-
4		(Z)-3-(Heptadec-10-en-1-yl)phenol	-4.375	-0.182	-4.376	1.6
5		Decanedioic acid, bis(2-ethylhexyl) ester	-4.085	-0.128	-4.085	-
6		Glycidyl palmitate	-3.837	-0.174	-3.837	-
7		Phenol, 2,4-Bis(1,1-Dimethylethyl)-	-3.754	-0.25	-3.754	0.6
8		Squalene	-3.747	-0.125	-3.747	1.8
9		Butyl isodecyl phthalate	-3.741	-0.144	-3.741	-
10		Propyl stearate	-3.611	-0.157	-3.611	-
11		Oxime-, methoxy-phenyl- (3)	-3.561	-0.324	-3.562	0.4
12		9-Octadecenoic acid (9Z)-, oxiranylmethyl ester	-3.512	-0.146	-3.512	-
13		Ergosta-5,7,9(11),22-tetraen-3-ol, (3.beta.,22E)-	-3.282	-0.113	-3.282	0.8
14		Furan, tetrahydro-2,5-dimethyl-1	-3.268	-0.467	-3.268	0.4
15		4-Pentyl-Cyclohexanecarboxylic Acid	-3.239	-0.231	-3.242	0.8
16		Stigmasta-5,22-Dien-3-Ol, Acetat, (3-Beta,2	-3.201	-0.097	-3.201	-
17		2 Nonadecanone	-3.161	-0.158	-3.161	-
18		Z,Z-6,27-Hexatriactontadien-2-one	-3.104	-0.084	-3.104	-
19		2-Pentacosanone	-3.039	-0.117	-3.039	-
20		1-Hexanol, 2-Ethyl-	-2.885	-0.321	-2.885	0.6
21		Octane, 6-Ethyl-2-Methyl-	-2.794	-0.254	-2.794	0.6
22		Oleic acid	-2.776	-0.139	-2.78	1.4
23		9,17-Octadecadienal, (Z)-	-2.759	-0.145	-2.759	1.4
24		1-Cyclohexyldimethylsilyloxybutane	-2.756	-0.197	-2.756	0.6
25		3-Hexanone	-2.728	-0.39	-2.728	0.4
26		Benzene, 1,3-Bis(1,1-Dimethylethyl)-	-2.503	-0.179	-2.503	0.6
27		Hexanal	-2.442	-0.349	-2.442	0.6
28		Hexadecane, 2,6,10,14-Tetramethyl-	-2.42	-0.121	-2.42	1.6
29		10(E),12(Z)-Conjugated linoleic acid	-2.318	-0.116	-2.321	1.4
30		Z,Z-6,28-Heptatriactontadien-2-one	-2.252	-0.059	-2.252	-
31		Arachidic acid	-2.236	-0.102	-2.239	-
32		cis-9-hexadecenal	-2.218	-0.13	-2.218	1.2
33		Icosanal	-2.211	-0.105	-2.211	-
34		Hexadecanal	-2.131	-0.125	-2.131	1.2
35		2-Heptodecanone	-2.121	-0.118	-2.121	1.4
36		(8Z,11Z)-Heptadecadienal	-2.024	-0.112	-2.024	1.2
37		2,6,11-Trimethyldodecane	-1.999	-0.133	-1.999	0.8
38		Hexamethylcyclotrisiloxane	-1.992	-0.166	-1.992	0.4
39		9-Heptadecanone	-1.982	-0.11	-1.982	1.4
40		Stearic acid	-1.97	-0.098	-1.973	-
41		Palmitic acid	-1.71	-0.095	-1.714	1.4
42		2,3-Diacetoxypopyl stearate	-1.669	-0.054	-1.669	-
43		8-Octadecanone	-1.559	-0.082	-1.559	1.4
44		1-Propene, 3,3-Dichloro-	-1.5	-0.3	-1.5	0.4
45		Cyclodecasiloxane, eicosamethyl-	-1.289	-0.032	-1.289	0.8
46		Heneicosane	-1.284	-0.061	-1.284	-
47		Tetradecane	-1.125	-0.08	-1.125	1.2
48		Eicosane	-0.831	-0.042	-0.831	-
49		Hexadecane	-0.751	-0.047	-0.751	1.4
50		Dodecane	-0.62	-0.052	-0.62	0.8
51		Stigmast-5-en-3-ol,oleate	-0.27	-0.006	-0.27	-



**Table 3 - Potential candidates for targeted drug treatment approach for SARS-CoV-2 (M<sup>Cov1</sup><sub>Pro</sub> and M<sup>Cov2</sup><sub>Pro</sub>)**

S. No.	Compound	G score with 2BX4	G score with 6LU7
1	Hexadecanoic acid, 2-hydroxy-1 (hydroxymethyl) ethyl ester	-5.118	-3.314
2	Monoelaidin	-4.515	-2.746
3	(Z)-3-(Heptadec-10-en-1-yl) phenol	-4.376	-3.872
4	Decanedioic acid, bis(2-ethylhexyl) ester.1	-4.085	-3.206
5	Glycidyl palmitate	-3.837	-3.09
6	Phenol,2,4-Bis(1,1-Dimethylethyl)	-3.754	-3.672

**Table S1 - Metabolites from bioconverted Docosahexaenoic acid at 24 hrs**

S. No.	Retention Time (min)	Percentage (%)	Compound Name	Medicinal Properties
1	22.176	13.27	2-Nonadecanone	Anti-depression Anti-bacterial Anti-tumor
2	21.941	12.91	Z,Z-6,27-Hexatriactontadien-2-one	-
3	21.164	8.47	cis-9-Hexadecenal	Anti-biofilm Anti-melanogenic Anti-fungal
4	21.395	7.89	Eicosanal-	Anti-depressant Anxiolytic effect Anti-oxidant
5	26.623	7.54	Stigmast-5-En-3-Ol, Oleat	Anti-obesity
6	26.922	5.07	Tetrapentacontane	Anti-microbial Anti-Oxidant
7	22.489	3.26	Oleic Acid	Anti-tumor Anti-Microbial
8	22.698	3.20	Octadecanoic acid	Anti-bacterial Anti-oxidant
9	21.275	2.15	(Z)-3-(Heptadec-10-en-1-yl)phenol	Anti-bacterial Anti-diarrheal Anti-oxidant
10	20.193	2.69	2-Heptadecanone	
11	20.774	2.05	n-Hexadecanoic acid	Anti-bacterial Anti-fungal Anti-biofilm Anti-cancer
12	24.730	1.95	Heneicosane	Anti-inflammatory
13	15.782	1.65	Phenol, 2,4-Bis(1,1-Dimethylethyl)-	Anti-fungal Anti-oxidant
14	19.326	1.64	Hexadecanal	-
15	21.880	1.34	8,11-Heptadecadienal, (8Z,11Z)-	-
16	21.102	1.28	9,17-Octadecadienal, (Z)-	Antimicrobial
17	23.985	0.99	2-Pentacosanone	-
18	16.871	0.99	Hexadecane	-
19	27.063	0.97	8-Octadecanone	Antimicrobial
20	25.397	0.89	Stigmasta-5,22-Dien-3-Ol, Acetat, (3-Beta,2	Antimicrobial
21	28.040	0.72	9-Heptadecanone	-
22	27.786	0.70	Z,Z-6,28-Heptatriactontadien-2-one	Alpha-amylase Inhibition Antioxidant Activity

**Table S2 - Metabolites from bioconverted Docosahexaenoic acid at 48 hrs**

S. No.	Retention Time (min)	Percentage (%)	Compound Name	Medicinal Properties
1	22.996	15.86	Octadecanoic acid	Anti-bacterial Anti-oxidant
2	22.743	13.93	6-Octadecenoic acid	Anti-bacterial
3	20.948	10.92	n-Hexadecanoic acid	Anti-bacterial Anti-fungal Anti-biofilm Anti-cancer
4	27.000	8.34	9-Octadecenoic acid (Z)-, 2,3-dihydroxypropyl ester	Anti-microbial Anti-Fungal
5	27.214	7.11	Octadecanoic acid, 2,3-dihydroxypropyl ester	Anti-microbial Anti-oxidant
6	25.389	4.40	9-Octadecenoic acid (Z)-, oxiranylmethyl ester	-
7	26.680	4.30	n-Propyl 9-octadecenoate	-
8	25.582	3.50	Glycidyl palmitate	Anti-staphylococcal activity
9	21.398	11.29	Eicosanal-	Anti-depressant Anxiolytic effect Anti-oxidant
10	21.168	3.01	cis-9-Hexadecenal	Anti-biofilm Anti-melanogenic Anti-fungal
11	25.490	2.83	Hexadecanoic acid, 2-hydroxy-1-(hydroxymethyl)ethy	Anti-fungal Anti-microbial
12	26.786	2.31	1-Cyclohexyldimethylsilyloxybutane	-
13	26.880	2.26	Octadecanoic acid, propyl ester	-
14	24.491	1.75	Eicosanoic acid	Anti-bacterial
15	6.560	1.43	Oxime-, methoxy-phenyl-	Pancreatic lipase inhibitory activity
16	28.188	1.41	Dotriacontane	Anti-fungal
17	4.716	1.18	Hexanal	Anti-fungal
18	21.940	1.15	Z,Z-6,27-Hexatriacontadien-2-one	-

**Table S3 - Metabolites from bioconverted Docosahexaenoic acid at 72 hrs**

S. No.	Retention Time (min)	Percentage (%)	Compound Name	Medicinal Properties
1	4.165	17.03	Benzene, Methyl-	-
2	15.766	10.84	Phenol, 2,4-Bis(1,1-Dimethylethyl	Anti-fungal Anti-oxidant
3	6.517	4.75	Oxime-, methoxy-phenyl-	Pancreatic lipase inhibitory activity
4	18.019	4.61	Eicosane	Anti-microbial
5	9.401	4.43	Cyclotrisiloxane, hexamethyl-	Anti-oxidant Anti-biofilm
6	16.862	4.11	Hexadecane	-
7	12.619	3.28	Dodecane, 2,6,11-trimethyl-	Anti-microbial Anti-oxidant
8	14.351	3.12	Tetradecane	-
9	19.115	3.03	Heneicosane	Anti-inflammatory
10	4.460	2.65	3-Hexanone	-
11	22.308	2.62	Octadecane	-
12	4.538	2.39	2-Hexanone	-
13	24.218	2.32	1H,5H-Cyclopropa[G][1,2,4]Triazolo[1,2-A]	-
14	24.162	2.31	Hexatriacontane	Anti-oxidant Anti-microbial
15	20.757	1.90	1-Butyl 2-(8-Methylnonyl) Phthalate #	-
16	26.220	1.90	Silikonfett Se30 (Grevels)	-
17	9.209	1.86	Octane, 6-Ethyl-2-Methyl-	-
18	3.365	1.82	Furan, tetrahydro-2,5-dimethyl-	-
19	24.112	1.50	Cyclodecasiloxane, eicosamethyl-	Immunotherapeutic agent
20	25.846	1.48	Tetrapentacontane	Anti-microbial Anti-Oxidant
21	12.282	1.41	Benzene, 1,3-Bis(1,1-Dimethylethyl)-	Anti-cancer
22	11.521	1.38	Dodecane	-
23	20.574	1.29	4-Pentyl-Cyclohexanecarboxylic Acid	-

**Table S4 - Metabolites from bioconverted Docosahexaenoic acid at 96 hrs**

S. No.	Retention Time (min)	Percentage (%)	Compound Name	Medicinal Properties
1	28.162	7.18	Decanedioic acid, bis(2-ethylhexyl) ester	Anti-fungal
2	20.769	6.67	n-Hexadecanoic acid	Anti-bacterial Anti-fungal Anti-biofilm Anti-cancer
3	22.688	5.70	Octadecanoic acid	Anti-bacterial Anti-oxidant
4	4.164	5.56	Benzene, Methyl-	-
5	8.781	5.49	1-Hexanol, 2-Ethyl-	-
6	15.772	5.11	Phenol, 2,4-Bis(1,1-Dimethylethyl)-	Anti-fungal Anti-oxidant
7	23.653	4.90	Ergosta-5,7,9(11),22-tetraen-3-ol, (3.β.,22E)-	-
8	24.174	3.72	Tetrapentacontane	Anti-microbial Antioxidant
9	18.024	2.88	Eicosane	Anti-microbial
10	16.866	2.68	Hexadecane	-
11	28.368	2.56	Squalene	-
12	15.499	2.17	Hexadecane, 2,6,10,14-Tetramethyl-	-
13	19.120	2.06	Heneicosane	Anti-inflammatory
14	22.473	1.96	Oleic Acid	Anti-tumor Anti-microbial
15	12.623	1.90	Dodecane, 2,6,11-trimethyl-	Anti-microbial Anti-oxidant
16	14.356	1.88	Tetradecane	-
17	24.115	1.67	Cyclodecasiloxane, eicosamethyl-	Immunotherapeutic agent
18	6.999	1.48	1-Propene, 3,3-Dichloro-	-
19	25.824	1.48	Bis(2-ethylhexyl) phthalate	-
20	22.314	1.44	Hexatriacontane	Anti-microbial
21	22.421	1.44	10(E),12(Z)-Conjugated linoleic acid	Anti-carcinogen Anti-inflammatory
22	4.450	1.36	3-Hexanone	Anti-microbial Anti-oxidant
23	4.525	1.20	2-Hexanone	-
24	20.411	1.15	Hexadecanoic acid, methyl ester	Anti-oxidant
25	24.814	1.13	1,16-Dibromohexadecane	-
26	18.671	0.99	Tetradecanoic acid	Anti-oxidant Anti-bacterial
27	20.709	0.98	2,6,10,15,19,23-Hexamethyltetracosane	-
28	9.212	0.95	Octane, 6-Ethyl-2-Methyl-	Anti-cancer
29	20.581	0.94	4-Pentyl-Cyclohexanecarboxylic Acid	-
30	4.766	0.90	2-Hexanol	Antimicrobial Anti-inflammatory
31	16.065	0.88	Hexadecane, 2,6,10,14-Tetramethyl	-
32	12.730	0.85	4-Propylbenzaldehyde	-
33	11.525	0.81	Dodecane	-
34	16.778	0.81	1-Hexadecanol	-
35	4.691	0.76	3-Hexanol	Anti-bacterial
36	13.282	0.75	Dodecane, 4,6-dimethyl-	-

**Table S5 - Metabolites from bioconverted Docosahexaenoic acid at 120 hrs**

S. No.	Retention Time (min)	Percentage (%)	Compound Name	Medicinal Properties
1	20.803	15.04	n-Hexadecanoic acid	Anti-bacterial Anti-fungal Anti-biofilm Anti-cancer
2	22.709	10.97	Octadecanoic acid	Anti-bacterial Anti-oxidant
3	23.462	10.31	Palmitoyl chloride	-
4	24.962	8.77	9-Octadecenoic acid (Z)-, 2,3-dihydroxypropyl ester	Anti-microbial Anti-fungal
5	27.952	10.69	Butyl 4,7,10,13,16,19-docosahexaenoate	-
6	23.874	7.70	Glycidyl palmitate	-
7	25.364	5.43	9-Octadecenoic acid (Z)-, oxiranylmethyl ester	-
8	3.172	5.02	Heptane	-
9	22.488	8.71	Oleic Acid	Anti-tumor Anti-microbial
10	25.468	2.07	Hexadecanoic acid, 2-hydroxy-1-(hydroxymethyl)ethyl	Anti-fungal Anti-microbial
11	27.861	2.73	Methyl 4,7,10,13,16-docosapentaenoate	-
12	26.959	1.87	cis-10-Pentadecenoic acid, isobutyl ester	-
13	18.677	1.65	Tetradecanoic acid	Anti-oxidant Anti-bacterial
14	25.163	1.59	Octadecanoic acid, 2,3-dihydroxypropyl ester	Anti-microbial Anti-oxidant
15	15.771	1.50	Phenol, 2,4-Bis(1,1-Dimethylethyl)-	Anti-fungal Anti-oxidant
16	22.429	1.46	9,12-Octadecadienoic Acid (Z,Z)-	Anti-bacterial
17	25.561	1.28	Myristic acid glycidyl ester	-
19	18.023	0.80	Eicosane	Anti-microbial
20	16.866	0.75	Hexadecane	-
21	24.915	0.61	3-([2-(4-Fluorophenyl)Ethyl]Amino)Methyl	-
22	19.118	0.59	Heneicosane	Anti-inflammatory
23	12.623	0.48	Dodecane, 4,6-dimethyl-	-

**Table S6 - Metabolites from bioconverted Docosahexaenoic acid using *Bacillus cereus***

S. No.	Retention Time (min)	Percentage (%)	Compound Name	Medicinal Properties
1	22.176	13.27	2-Nonadecanone	Anti-depression Anti-bacterial Anti-tumor
2	21.941	12.91	Z,Z-6,27-Hexatriactontadien-2-one	-
3	43.881	11.48	cis-9-Hexadecenal	Anti-biofilm Anti-melanogenic Anti-fungal
4	21.395	7.89	Eicosanal-	Anti-depressant Anxiolytic effect Anti-oxidant
5	26.623	7.54	Stigmast-5-En-3-Ol, Oleat	Anti-obesity
6	26.922	10.27	Tetrapentacontane	Anti-microbial Anti-oxidant
7	22.489	13.93	Oleic Acid	Anti-tumor Anti-microbial
8	22.698	32.53	Octadecanoic acid	Anti-bacterial Anti-oxidant
9	21.275	2.15	(Z)-3-(Heptadec-10-en-1-yl)phenol	Anti-bacterial Anti-diarrheal Anti-oxidant
10	20.193	2.69	2-Heptadecanone	-
11	20.774	34.68	n-Hexadecanoic acid	Anti-bacterial Anti-fungal

				Anti-biofilm Anti-cancer
12	24.730	7.63	Heneicosane	Anti-inflammatory
13	15.782	31.59	Phenol, 2,4-Bis(1,1-Dimethylethyl)-	Anti-fungal Anti-oxidant
14	19.326	1.64	Hexadecanal	-
15	21.880	1.34	8,11-Heptadecadienal, (8Z,11Z)-	-
16	21.102	1.28	9,17-Octadecadienal, (Z)-	Antimicrobial agent
17	23.985	0.99	2-Pentacosanone	-
18	16.871	8.53	Hexadecane	-
19	27.063	0.97	8-Octadecanone	Antimicrobial metabolite
20	25.397	0.89	Stigmasta-5,22-Dien-3-Ol, Acetat, (3-Beta,2	Antimicrobial
21	28.040	0.72	9-Heptadecanone	-
22	27.786	0.70	Z,Z-6,28-Heptatriactontadien-2-one	Alpha-amylase inhibition Antioxidant activity
23	27.000	17.11	9-Octadecenoic acid (Z)-, 2,3-dihydroxypropyl ester	Anti-microbial Anti-fungal
24	27.214	8.7	Octadecanoic acid, 2,3-dihydroxypropyl ester	Anti-microbial Anti-oxidant
25	25.389	9.83	9-Octadecenoic acid (Z)-, oxiranylmethyl ester	-
26	26.680	4.30	n-Propyl 9-octadecenoate	-
27	25.582	3.50	Glycidyl palmitate	Anti-staphylococcal activity
28	25.490	4.9	Hexadecanoic acid, 2-hydroxy-1-(hydroxymethyl)ethy	Anti-fungal Anti-microbial
29	26.786	2.31	1-Cyclohexyldimethylsilyloxybutane	-
30	26.880	2.26	Octadecanoic acid, propyl ester	-
31	24.491	1.75	Eicosanoic acid	Anti-bacterial
32	6.560	6.18	Oxime-, methoxy-phenyl-	Pancreatic lipase inhibitory activity
33	28.188	1.41	Dotriacontane	Anti-fungal
34	4.716	1.18	Hexanal	Anti-fungal
35	4.165	22.59	Benzene, Methyl-	-
36	18.019	8.29	Eicosane	Anti-microbial
37	9.401	4.43	Cyclotrisiloxane, hexamethyl-	Anti-oxidant Anti-biofilm
38	12.619	5.18	Dodecane, 2,6,11-trimethyl-	Anti-microbial Anti-oxidant
39	14.351	5.0	Tetradecane	-
40	4.460	4.01	3-Hexanone	Anti-microbial Anti-oxidant
41	22.308	2.62	Octadecane	-
42	4.538	3.59	2-Hexanone	-
43	24.218	2.32	1H,5H-Cyclopropa[G][1,2,4]Triazolo[1,2-A]	-
44	24.162	3.75	Hexatriacontane	Anti-oxidant Anti-microbial
45	20.757	1.90	1-Butyl 2-(8-Methylnonyl) Phthalate #	-
46	26.220	1.90	Silikonfett Se30 (Grevels)	-
47	9.209	1.86	Octane, 6-Ethyl-2-Methyl-	-
48	3.365	1.82	Furan, tetrahydro-2,5-dimethyl-	-
49	24.112	1.50	Cyclodocasiloxane, eicosamethyl-	Immunotherapeutic agent
50	12.282	1.41	Benzene, 1,3-Bis(1,1-Dimethylethyl)-	Anti-cancer
51	11.521	2.19	Dodecane	-
52	20.574	1.29	4-Pentyl-Cyclohexanecarboxylic Acid	-
53	28.162	7.18	Decanedioic acid, bis(2-ethylhexyl) ester	Anti-fungal
54	8.781	5.49	1-Hexanol, 2-Ethyl-	-
55	23.653	4.90	Ergosta-5,7,9(11),22-tetraen-3-ol, (3.beta.,22E)-	-
56	28.368	2.56	Squalene	-
57	15.499	3.05	Hexadecane, 2,6,10,14-Tetramethyl-	-

58	24.115	1.67	Cyclodecasiloxane, eicosamethyl-	Immunotherapeutic agent
59	6.999	1.48	1-Propene, 3,3-Dichloro-	-
60	25.824	1.48	Bis(2-ethylhexyl) phthalate	-
61	22.421	1.44	10(E),12(Z)-Conjugated linoleic acid	Anti-carcinogen Anti-inflammatory
62	20.411	1.15	Hexadecanoic acid, methyl ester	Anti-oxidant
63	24.814	1.13	1,16-Dibromohexadecane	-
64	18.671	5.89	Tetradecanoic acid	Anti-oxidant Anti-bacterial
65	20.709	0.98	2,6,10,15,19,23-Hexamethyltetracosane	-
66	9.212	0.95	Octane, 6-Ethyl-2-Methyl-	Anti-cancer
67	20.581	0.94	4-Pentyl-Cyclohexanecarboxylic Acid	-
68	4.766	0.90	2-Hexanol	Anti-microbial Anti-inflammatory
69	12.730	0.85	4-Propylbenzaldehyde	-
70	16.778	0.81	1-Hexadecanol	-
71	4.691	0.76	3-Hexanol	Anti-bacterial
72	13.282	0.75	Dodecane, 4,6-dimethyl-	-
73	23.462	10.31	Palmitoyl chloride	-
74	27.952	10.69	Butyl 4,7,10,13,16,19-docosahexaenoate	-
75	23.874	7.70	Glycidyl palmitate	-
76	3.172	5.02	Heptane	-
77	27.861	2.73	Methyl 4,7,10,13,16-docosapentaenoate	-
78	26.959	1.87	cis-10-Pentadecenoic acid, isobutyl ester	-
79	22.429	1.46	9,12-Octadecadienoic Acid (Z,Z)-	Anti-bacterial
80	25.561	1.28	Myristic acid glycidyl ester	-
81	24.915	0.61	3-([2-(4-Fluorophenyl)Ethyl]Amino)Methyl	-
82	12.623	0.48	Dodecane, 4,6-dimethyl-	-

**Table S7 - Result of the docking experiment performed between the receptor (2BX4) and the ligands (Compounds)**

S. No.	Ligands	Glide Ligand Efficiency	Docking Score	Glide Score	Amino acid	Amino acid Residue position	Type of Interactions
1.	Nelfinavir (Control)	-0.117	-4.673	-4.687	Phenylalanine	Phe 8	Hydrophobic
					Valine	Val 104	Hydrophobic
					Arginine	Arg 105	Positively charged
					Isoleucine	Ile 106	Hydrophobic
					Glutamine	Gln 107	Polar
					Proline	Pro 108	Hydrophobic Hydrogen Bond with "OH"
					Glycine	Gly 109	Glycine
					Glutamine	Gln 110	Polar Hydrogen Bond with "NH"
					Threonine	Thr 111	Polar
					Asparagine	Asx 151	Polar
					Histidine	His 246	Polar
					Isoleucine	Ile 249	Hydrophobic
					Threonine	Thr 292	Polar
					Proline	Pro 293	Hydrophobic
Phenylalanine	Phe 294	Hydrophobic Hydrogen bond with "N·H"					
Aspartate	Asp 295	Negatively charged					
2.	Hexadecanoic acid, 2-hydroxy-1-(hydroxymethyl)ethyl ester	-0.223	-5.118	-5.118	Phenylalanine	Phe 8	Hydrophobic
					Glutamine	Gln 107	Polar
					Proline	Pro 108	Hydrophobic
					Glycine	Gly 109	Glycine
					Glutamine	Gln 110	Polar

					Threonine	Thr 111	Polar <b>Hydrogen Bond with "OH" (Distance-2.05)</b>
					Glutamine	Gln 127	Polar
					Proline	Pro 132	Hydrophobic
					Asparagine	Asn 151	Polar
					Isoleucine	Ile 200	Hydrophobic
					Threonine	Thr 201	Polar
					Leucine	Leu 202	Hydrophobic
					Asparagine	Asn 203	Polar
					Glutamate	Glu 240	Negatively charged
					Leucine	Leu 242	Hydrophobic
					Histidine	His 246	Polar
					Isoleucine	Ile 249	Hydrophobic
					Threonine	Thr 292	Polar
					Proline	Pro 293	Hydrophobic
					Phenylalanine	Phe 294	Hydrophobic
					Aspartate	Asp 295	Negatively charged <b>Hydrogen Bond with "OH" (Distance-1.72)</b>
					Arginine	Arg 298	Positively charged
3.	Monoelaidin	-4.515	-0.181	-4.515	Phenylalanine	Phe 8	Hydrophobic
					Glutamine	Gln 107	Polar
					Proline	Pro 108	Proline
					Glycine	Gly 109	Glycine
					Glutamine	Gln 110	Polar
					Threonine	Thr 111	Polar Hydrogen Bond with "OH" (Distance-1.84)
					Glutamine	Gln 127	Polar
					Asparagine	Asn 151	Polar
					Isoleucine	Ile 200	Hydrophobic
					Threonine	Thr 201	Polar
					Leucine	Leu 202	Hydrophobic
					Asparagine	Asn 203	Polar
					Glutamate	Glu 240	Negatively charged
					Leucine	Leu 242	Hydrophobic
					Histidine	His 246	Polar
					Isoleucine	Ile 249	Hydrophobic
					Threonine	Thr 292	Polar
					Phenylalanine	Phe 294	Hydrophobic
					Aspartate	Asp 295	Negatively charged Hydrogen Bond with "OH" (Distance-1.72)
4.	(Z)-3-(Heptadec-10-en-1-yl)phenol	-0.182	-4.375	-4.376	Phenylalanine	Phe 8	Hydrophobic
					Lysine	Lys 102	Positively charged
					Valine	Val 104	Hydrophobic
					Isoleucine	Ile 106	Hydrophobic
					Glutamine	Gln 107	Polar
					Proline	Pro 108	Hydrophobic
					Glycine	Gly 109	Glycine
					Glutamine	Gln 110	Polar
					Threonine	Thr 111	Polar
					Asparagine	Asn 151	Polar
					Isoleucine	Ile 152	Hydrophobic
					Aspartate	Asp 153	Negatively

							charged
					Serine	Ser 158	Polar
					Isoleucine	Ile 200	Hydrophobic
					Leucine	Leu 202	Hydrophobic
					Asparagine	Asn 203	Polar Hydrogen Bond with "OH"(Distance- 2.01)
					Histidine	His 246	Polar
					Isoleucine	Ile 249	Hydrophobic
					Threonine	Thr 292	Polar
					Proline	Pro 293	Hydrophobic
					Phenylalanine	Phe 294	Hydrophobic
					Aspartate	Asp 295	Negatively charged
					Arginine	Arg 298	Positively charged
5.	Decanedioic acid, bis(2-ethylhexyl) ester.1	-0.128	-4.085	-4.085	Phenylalanine	Phe 8	Hydrophobic
					Lysine	Lys 102	Positively charged
					Isoleucine	Ile 106	Hydrophobic
					Glutamine	Gln 107	Polar
					Proline	Pro 108	Hydrophobic
					Glycine	Gly 109	Glycine
					Glutamine	Gln 110	Polar
					Threonine	Thr 111	Polar
					Proline	Pro 132	Hydrophobic
					Asparagine	Asn 151	Polar
					Isoleucine	Ile 152	Hydrophobic
					Aspartate	Asp 153	Negatively charged
					Serine	Ser 158	Polar
					Isoleucine	Ile 200	Hydrophobic
					Threonine	Thr 201	Polar
					Leucine	Leu 202	Hydrophobic
					Glutamate	Glu 240	Negatively charged
					Histidine	His 246	Polar Hydrogen Bond with"O"(Distance- 2.51)
					Isoleucine	Ile 249	Hydrophobic
					Threonine	Thr 292	Polar
					Proline	Pro 293	Hydrophobic
					Phenylalanine	Phe 294	Hydrophobic
					Aspartate	Asp 295	Negatively charged
					Arginine	Arg 298	Positively charged
6.	Glycidyl palmitate	-0.174	-3.837	-3.837	Phenylalanine	Phe 8	Hydrophobic
					Lysine	Lys 102	Positively charged
					Isoleucine	Ile 106	Hydrophobic
					Glutamine	Gln 107	Polar
					Proline	Pro 108	Hydrophobic
					Glycine	Gly 109	Glycine
					Glutamine	Gln 110	Polar
					Threonine	Thr 111	Polar
					Proline	Pro 132	Hydrophobic
					Asparagine	Asn 151	Polar
					Isoleucine	Ile 152	Hydrophobic
					Aspartate	Asp 153	Negatively charged
					Serine	Ser 158	Polar
					Isoleucine	Ile 200	Hydrophobic
					Threonine	Thr 201	Polar
					Leucine	Leu 202	Hydrophobic Hydrogen Bond with



							"O"(Distance-2.18)
					Asparagine	Asn 203	Polar
					Glutamate	Glu 240	Negatively charged
					Leucine	Leu 242	Hydrophobic
					Histidine	His 246	Polar
					Threonine	Thr 292	Polar
					Proline	Pro 293	Hydrophobic
					Phenylalanine	Phe 294	Hydrophobic

**Table S8 - Result of the docking experiment performed between the receptor (6LU7) and the ligands (Compounds)**

S.No	Ligands	Glide Ligand Efficiency	Docking Score	Glide Score	Amino acid	Amino acid Residue	Type of Interactions
1.	Nelfinavir (Control)	-0.1	-3.995	-4.009	Phenylalanine	Phe 8	Hydrophobic
					Valine	Val 104	Hydrophobic
					Arginine	Arg 105	Positively charged Hydrogen Bond with OH(Distance-2.43)
					Isoleucine	Ile 106	Hydrophobic
					Glutamine	Gln 107	Polar
					Glutamine	Gln 110	Hydrogen Bonding with NH(Distance-1.85) and OH(Distance-2.07)
					Asparagine	Asn 151	Polar
					Isoleucine	Ile 152	Hydrophobic
					Aspartate	Asp 153	Negatively Charged
					Isoleucine	Ile 249	Hydrophobic
					Proline	Pro 252	Hydrophobic
					Leucine	Leu 253	Hydrophobic
					Threonine	Thr 292	Polar
					Proline	Pro 293	Hydrophobic
Phenylalanine	Phe 294	Hydrophobic Pi-Pi Stacking (Distance-3.75)					
2.	(Z)-3-(Heptadec-10-en-1-yl)phenol	-0.161	-3.871	-3.872	Phenylalanine	Phe 8	Hydrophobic
					Isoleucine	Ile 106	Hydrophobic
					Glutamine	Gln 107	Polar
					Proline	Pro 108	Hydrophobic Hydrogen Bond with OH(Distance-1.84)
					Glycine	Gly 109	Glycine
					Glutamine	Gln 110	Polar
					Threonine	Thr 111	Polar
					Phenylalanine	Phe 112	Hydrophobic
					Asparagine	Asn 151	Polar
					Isoleucine	Ile 152	Hydrophobic
					Aspartate	Asp 153	Negatively Charged
					Isoleucine	Ile 200	Hydrophobic
					Valine	Val 202	Hydrophobic
					Asparagine	Asn 203	Polar
Histidine	His 246	Polar Pi-Pi Stacking (Distance-5.19)					
Isoleucine	Ile 249	Hydrophobic					
Threonine	Thr 292	Polar					
Proline	Pro 293	Hydrophobic					

					Phenylalanine	Phe 294	Hydrophobic
					Aspartate	Asp 295	Negatively charged
3.	Phenol, 2,4-Bis(1,1-Dimethylethyl)-	-0.245	-3.672	-3.672	Phenylalanine	Phe 8	Hydrophobic
					Valine	Val 104	Hydrophobic
					Isoleucine	Ile 106	Hydrophobic
					Glutamine	Gln 107	Polar
					Glutamine	Gln 110	Polar Hydrogen Bond with OH (Distance-1.70)
					Threonine	Thr 111	Polar
					Asparagine	Asn 151	Polar
					Isoleucine	Ile 152	Hydrophobic
					Aspartate	Asp 153	Negatively charged
					Serine	Ser 158	Polar
					Threonine	Thr 292	Polar
					Phenylalanine	Phe 294	Hydrophobic Pi-Pi stacking (Distance-4.99)
4.	Oxime-, methoxy-phenyl- (3)	-0.303	-3.334	-3.334	Phenylalanine	Phe 8	Hydrophobic
					Asparagine	Asn 151	Polar
					Isoleucine	Ile 152	Hydrophobic
					Aspartate	Asp 153	Negatively charged
					Glutamine	Gln 110	Polar Hydrogen Bond (Distance-1.59)
					Threonine	Thr 111	Polar
					Phenylalanine	Phe 112	Hydrophobic
					Glutamine	Gln 127	Polar
					Threonine	Thr 292	Polar
					Phenylalanine	Phe 294	Hydrophobic Pi-Pi stacking (Distance-3.95)
					Aspartate	Asp 295	Negatively charged
5.	Hexadecanoic acid, 2-hydroxy-1-(hydroxymethyl) ethyl ester	-0.144	-3.314	-3.314			
					Glutamine	Gln 107	Polar
					Proline	Pro 108	Hydrophobic Hydrogen Bond with OH (Distance-1.81)
					Glycine	Gly 109	Glycine
					Glutamine	Gln 110	Polar Hydrogen Bond with O (Distance-2.64)
					Isoleucine	Ile 200	Hydrophobic
					Valine	Val 202	Hydrophobic
					Glutamate	Glu 240	Negatively charged Hydrogen Bond with OH (Distance-1.78)
					Histidine	His 246	Polar Hydrogen Bond with O (Distance-1.94)
					Isoleucine	Ile 249	Hydrophobic
					Proline	Pro 252	Hydrophobic
					Threonine	Thr 292	Polar
					Proline	Pro 293	Hydrophobic
					Phenylalanine	Phe 294	Hydrophobic
					Valine	Val 297	Hydrophobic
6.	9-Octadecenoic acid	-0.136	-3.272	-	Lysine	Lys 102	Positively charged

	(9Z)-, oxiranylmethyl ester			3.272	Valine	Val 104	Hydrophobic
					Arginine	Arg 105	Positively charged
					Isoleucine	Ile 106	Hydrophobic
					Glutamine	Gln 107	Polar
					Glycine	Gly 109	Glycine
					Glutamine	Gln 110	Polar Hydrogen Bond with O (Distance-2.00) and O (Distance-2.05)
					Asparagine	Asn 151	Polar
					Isoleucine	Ile 152	Hydrophobic
					Aspartate	Asp 153	Negatively charged
					Serine	Ser 158	Polar
					Isoleucine	Ile 200	Hydrophobic
					Valine	Val 202	Hydrophobic
					Asparagine	Asn 203	Polar
					Histidine	His 246	Polar
					Isoleucine	Ile 249	Hydrophobic
Threonine	Thr 292	Polar					
Proline	Pro 293	Hydrophobic					
Phenylalanine	Phe 294	Hydrophobic					
7.	Decanedioic acid, bis(2-ethylhexyl) ester	-0.1	-3.206	-3.206	Phenylalanine	Phe 8	Hydrophobic
					Valine	Val 104	Hydrophobic
					Isoleucine	Ile 106	Hydrophobic
					Glutamine	Gln 107	Polar Hydrogen Bonding with O (Distance-1.78)
					Proline	Pro 108	Hydrophobic
					Glycine	Gly 109	Glycine
					Glutamine	Gln 110	Polar
					Asparagine	Asn 151	Polar
					Isoleucine	Ile 152	Hydrophobic
					Aspartate	Asp 153	Negatively charged
					Serine	Ser 158	Polar
					Cysteine	Cys 160	Hydrophobic
					Isoleucine	Ile 200	Hydrophobic
					Valine	Val 202	Hydrophobic
					Glutamate	Glu 240	Negatively charged
					Proline	Pro 241	Hydrophobic
					Threonine	Thr 243	Polar
					Histidine	His 246	Polar
					Isoleucine	Ile 249	Hydrophobic
					Threonine	Thr 292	Polar
Proline	Pro 293	Hydrophobic					
Phenylalanine	Phe 294	Hydrophobic					
8.	Squalene	-0.104	-3.133	-3.133	Phenylalanine	Phe 8	Hydrophobic
					Glutamine	Gln 110	Polar
					Threonine	Thr 111	Polar
					Asparagine	Asn 151	Polar
					Isoleucine	Ile 152	Hydrophobic
					Aspartate	Asp 153	Negatively charged
					Tyrosine	Tyr 154	Hydrophobic
					Valine	Val 202	Hydrophobic
					Threonine	Thr 292	Polar
					Proline	Pro 293	Hydrophobic
					Phenylalanine	Phe 294	Hydrophobic
					Aspartate	Asp 295	Negatively charged
Valine	Val 297	Hydrophobic					

					Histidine	His 246	Polar
					Isoleucine	Ile 249	Hydrophobic
9.	2-Pentacosanone	-0.12	-3.124	-3.124	Phenylalanine	Phe 8	Hydrophobic
					Glutamine	Gln 107	Polar Hydrogen Bond with "O"(Distance- 1.79)
					Proline	Pro 108	Hydrophobic
					Glycine	Gly 109	Glycine
					Glutamine	Glu 110	Polar
					Isoleucine	Ile 200	Hydrophobic
					Valine	Val 202	Hydrophobic
					Asparagine	Asn 203	Polar
					Glutamate	Glu 240	Negatively charged
					Histidine	His 246	Polar
					Isoleucine	Ile 249	Hydrophobic
					Proline	Pro 252	Hydrophobic
					Threonine	Thr 292	Polar
					Proline	Pro 293	Hydrophobic
					Phenylalanine	Phe 294	Hydrophobic
					Valine	Val 297	Hydrophobic
					Arginine	Arg 298	Positively charged
10.	Z,Z-6,27-Hexatriactontadien-2-one	-0.084	-3.119	-3.119	Phenylalanine	Phe 8	Hydrophobic
					Lysine	Lys 102	Positively charged
					Valine	Val 104	Hydrophobic
					Glutamine	Gln 107	Polar
					Proline	Pro 108	Hydrophobic
					Glycine	Gly 109	Glycine
					Glutamine	Gln 110	
					Threonine	Thr 111	Polar
					Proline	Pro 132	Hydrophobic
					Asparagine	Asn 133	Polar
					Asparagine	Asn 151	Polar
					Aspartate	Asp 153	Negatively charged
					Serine	Ser 158	Polar
					Threonine	Thr 196	Polar
					Threonine	Thr 198	Polar
					Isoleucine	Ile 200	Hydrophobic
					Valine	Val 202	Hydrophobic
					Glutamate	Glu 240	Negatively charged
					Histidine	His 246	Polar
					Isoleucine	Ile 249	Hydrophobic
					Threonine	Thr 292	Polar
					Proline	Pro 293	Hydrophobic
					Phenylalanine	Phe 294	Hydrophobic
					Aspartate	Asp 295	Negatively charged
11.	Glycidyl palmitate	-0.14	-3.09	-3.09	Phenylalanine	Phe 8	Hydrophobic
					Proline	Pro 108	Hydrophobic
					Glycine	Gly 109	Glycine
					Glutamine	Gln 110	Polar
					Threonine	Thr 111	Polar
					Asparagine	Asn 151	Polar
					Isoleucine	Ile 152	Hydrophobic
					Aspartate	Asp 153	Negatively charged
					Isoleucine	Ile 200	Hydrophobic
					Valine	Val 202	Hydrophobic
					Asparagine	Asn 203	Polar
					Glutamate	Glu 240	Negatively charged
					Histidine	His 246	Polar Hydrogen Bond with "O"(Distance- 2.24)

					Isoleucine	Ile 249	Hydrophobic
					Threonine	Thr 292	Polar
					Proline	Pro 293	Hydrophobic
					Phenylalanine	Phe 294	Hydrophobic
12.	Propyl stearate	-0.127	-2.922	-2.922	Glutamine	Gln 107	Polar
					Proline	Pro 108	Hydrophobic
					Glycine	Gly 109	Glycine
					Glutamine	Gln 110	Polar Hydrogen Bond with "O"(Distance- 2.73)
					Isoleucine	Ile 200	Hydrophobic
					Valine	Val 202	Hydrophobic
					Asparagine	Asn 203	Polar
					Histidine	His 246	Polar Hydrogen Bond with "O"(Distance- 1.97)
					Isoleucine	Ile 249	Hydrophobic
					Threonine	Thr 292	Polar
					Proline	Pro 293	Hydrophobic
					Phenylalanine	Phe 294	Hydrophobic
					Valine	Val 297	Hydrophobic
					Arginine	Arg 298	Positively charged
13.	Benzene, 1,3-Bis(1,1-Dimethylethyl)-	-0.207	-2.891	-2.891	Phenylalanine	Phe 8	Hydrophobic
					Glutamine	Gln 110	Polar
					Threonine	Thr 111	Polar
					Asparagine	Asn 151	Polar
					Isoleucine	Ile 152	Hydrophobic
					Aspartate	Asp 153	Negatively charged
					Serine	Ser 158	Polar
					Threonine	Thr 292	Polar
					Phenylalanine	Phe 294	Hydrophobic Pi-Pi stacking <b>(Distance-3.93)</b>
					Asparagine	Asn 295	Negatively charged
14.	Monoelaidin	-0.11	-2.746	-2.746	Glutamine	Gln 107	Polar
					Proline	Pro 108	Hydrophobic Hydrogen Bond with "OH" <b>(Distance- 1.82)</b>
					Glycine	Gly 109	Glycine
					Glutamine	Gln 110	Polar Hydrogen Bond with "OH" <b>(Distance- 1.90)</b>
					Isoleucine	Ile 200	Hydrophobic
					Valine	Val 202	Hydrophobic
					Asparagine	Asn 203	Polar
					Aspartate	Asp 245	Negatively charged
					Histidine	His 246	Polar
					Aspartate	Asp 248	Negatively charged
					Isoleucine	Ile 249	Hydrophobic
					Proline	Pro 252	Hydrophobic
					Threonine	Thr 292	Polar
					Proline	Pro 293	Hydrophobic
					Phenylalanine	Phe 294	Hydrophobic
					Valine	Val 297	Hydrophobic
15.	1-Hexanol, 2-Ethyl-	-0.289	-2.604	-2.604	Glutamine	Gln 107	Polar
					Proline	Pro 108	Hydrophobic

						Hydrogen Bond with "OH" <b>(Distance-1.98)</b>
					Glycine	Gly 109
					Glutamine	Gln 110
						Polar Hydrogen Bond with "OH" <b>(Distance-1.96)</b>
					Isoleucine	Ile 200
					Valine	Val 202
					Asparagine	Asn 203
					Glutamate	Glu 240
					Histidine	His 246
					Isoleucine	Ile 249
					Threonine	Thr 292
					Proline	Pro 293
16.	Z,Z-6,28-Heptatriactontadien-2-one	-0.067	-2.556	-2.556	Lysine	Lys 102
					Valine	Val 104
					Arginine	Arg 105
					Isoleucine	Ile 106
					Glutamine	Glu 107
						Polar Hydrogen Bond with "O" <b>(Distance-2.22)</b>
					Proline	Pro 108
					Glycine	Gly 109
					Glutamine	Gln 110
					Asparagine	Arg 151
					Aspartate	Asp 153
					Serine	Ser 158
					Isoleucine	Ile 200
					Glutamate	Glu 240
					Proline	Pro 241
					Threonine	Thr 243
					Aspartate	Asp 245
					Histidine	His 246
					Isoleucine	Ile 249
					Proline	Pro 293
					Phenylalanine	Phe 294
17.	Arachidic acid	-0.114	-2.518	-2.521	Glutamine	Gln 107
						Polar Hydrogen Bond with "O" <b>(Distance-1.78)</b>
					Proline	Pro 108
					Glycine	Gly 109
					Glutamine	Gln 110
					Valine	Val 202
					Histidine	His 246
					Isoleucine	Ile 249
					Proline	Pro 252
					Threonine	Thr 292
					Proline	Pro 293
					Phenylalanine	Phe 294
					Valine	Val 297
					Arginine	Arg 298

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**AUTHORSHIP**

Visali Kannan and Murugan Athiappan Conceived and designed the study, conduct the research and wrote the first draft of the manuscript. Usha Singaravelu wrote the molecular docking result part of the

manuscript. Rubavathi Anandan, Dinesh Kumar Sudalaimani, Neginah Vijayasingh, Subathra Lavan and Shantkriti Srinivasan were revised the manuscript for important intellectual content. All authors contributed to and approved the final draft of the manuscript.

## COMPETING INTERESTS

The authors have declared that no competing interest exists.

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