ZIBELINE INTERNATIONAL™ PUBLISHING

ISSN: 2521-0807 (Print)
ISSN: 2521-0424 (Online)
CODEN: MSMAGK

Matrix Science Medica (MSM)

DOI: http://doi.org/10.26480/msm.01.2026.10.18

RESEARCH ARTICLE

SECONDARY METABOLITES IN *SENNA OBTUSIFOLIA* AS POTENTIAL DRUG CANDIDATE FOR TREATMENT OF AFLATOXIN SYNTHESIS

Zacchaeus S. Ololade[a,b], Oluwafemi A. Ojo[b,d], Richard A. Oyero[b], Olayinka F. Onifade[c] and Olawumi T. Oyebanji[b]

[a] *Department of Pharmaceutical and Medicinal Chemistry, Faculty of Pharmacy, University of Medical Sciences, Ondo, Nigeria*
[b] *Department of Chemistry, Medicinal and Organic Chemistry Unit, University of Medical Sciences, Ondo, Nigeria*
[c] *Department of Chemical and Food Sciences, Biochemistry Unit, Bells University of Technology, Ota, Nigeria*
[d] *Nigeria Agricultural Quarantine Service, Post Entry Quarantine Diagnostic and Surveillance Station, Moore Plantation, Ibadan, Nigeria*
Corresponding author email: sololade@unimed.edu.ng

ARTICLE DETAILS

Article History:

Received 12 January 2026
Revised 20 February 2026
Accepted 28 March 2026
Available online 30 April 2026

ABSTRACT

Senna obtusifolia is a medicinal plant traditionally used to treat diseases in Africa. This study was undertaken to investigate the potential of the phytochemicals in *S. obtusifolia* as drug candidate for treatment of aflatoxin synthesis. 20 compounds through a GC-MS analysis and their 2D structures were extracted from Pubchem server. The 3D structure of polyketide synthase A, a poisonous and carcinogenic chemical substance, produced by *Aspergillus flavus* and *Aspergillus parasiticus*, which is the target protein was obtained from RCSB PDB server, and were utilized for analysis of molecular binding affinity of the drug-like compounds. Bioavailability radar was used for a rapid assessment of drug-likeness in which physicochemical properties such as: lipophilicity, size, polarity, solubility, flexibility and saturation were taken into consideration. The result showed inhibition of the target protein – polyketide synthase A. The molecular interactions and *in silico* pharmacokinetics profiling of the best binding five compounds from the molecular docking process were assessed. The docking results showed that *cis*-oleic acid, methyllinolelaidate, stearic acid, methyl-11-octadecenoate, and methyl-n-octadecanoate, showed superior inhibitory potential through their respective docking scores: -9.214, -9.213, -8.688, -8.343 and -8.303 kcal/mol, in addition to good pharmacokinetics profiles compared to palmitic acid –a natural substrate which has a docking score of -8.097. In bioavailability radar, physicochemical range on each axis was depicted as a pink area in which the radar plot of the molecule has to fall entirely to be considered drug-like. This study showed that *S. obtusifolia* can serve as phytotherapy in treatment of health problems caused by aflatoxin.

KEYWORDS

Senna obtusifolia, phytotherapy, aflatoxin, pharmacokinetic.

1. INTRODUCTION

Natural products from medicinal plants are good reserved sources of natural preservative and antimicrobial agents. Medicinal plants are embedded with diverse of secondary metabolites that are useful in drug design and development (Adesina et al., 2022; Ololade et al., 2022). Mycotoxins, especially aflatoxins, are complex molecules with intricate interactions at the molecular level. Aflatoxins, being toxic compounds, pose significant health risks, and understanding how they can be neutralized or inhibited is of paramount importance (Kibugu et al., 2024; Nazareth et al., 2024).

Aflatoxins are potent carcinogens that can contaminate a variety of crops, especially cereals. In developing nations, where agricultural produce are consumed raw or not thoroughly treated or screened before eating, the risk posed by aflatoxin contamination is not just a health concern but also an economic and social one. Contaminated crops can lead to significant economic losses for farmers and traders, and the health implications for consumers, including liver cancer and immune suppression, can be dire (Kumar et al., 2022; Ololade et al., 2024). The contamination of the aflatoxin poses a serious health challenge to humans, and due to the unaffordable cost of drugs to address the consequences of this toxin (Ajmal et al., 2022; Shabeer et al., 2022). Phytoremediation as a potential treatment of aflatoxin contamination could open new avenues for less cost, available, natural, and eco-friend. Senna obtusifolia is a medicinal plant traditionally used to treat anti-inflammatory, anti-oxidative, anti-pyretic, pains, skin and gastrointestinal disorder among Africans (Alao et al., 2018; Mujeeb et al., 2023). To the best of our knowledge, there is paucity information on the use of Senna obtusifolia for the treatment of aflatoxin. Therefore, the present study was undertaken to investigate the molecular drug design using phytochemicals in Senna obtusifolia as drug candidate for treatment of aflatoxin synthesis.

2. MATERIALS AND METHODS

2.1 Collection of Plant Sample

The plant samples were collected in Ondo, Nigeria. The plant specimen was authenticated at the UNIMED herbarium as Senna obtusifolia.

2.2 Preparation of the Extract

The extraction from the plant materials was performed by maceration using methanol/ethylacetate (2:1) according to method used (Ololade et al., 2021).

2.3 GC-MS Analysis

The conditions for the analyses were set as previously reported (Ololade and Anuoluwa, 2022; Adesina et al., 2022).

2.4 In Silico (molecular docking) Assays

Quick Response Code	Access this article online	
	Website: www.matrixscmedica.com	DOI: 10.26480/msm.01.2026.10.18

Cite The Article: Zacchaeus S. Ololade, Oluwafemi A. Ojo, Richard A. Oyero, Olayinka F. Onifade and Olawumi T. Oyebanji (2026). Secondary Metabolites In *Senna Obtusifolia* As Potential Drug Candidate For Treatment Of Aflatoxin Synthesis. *Matrix Science Medica (MSM),* 10 (1): 10-18.

2.4.1 Ligand molecule preparation

A molecular docking study to identify potent compounds of the 20 compounds generated through GC-MS was conducted. The 2D chemical structures were extracted from the PubChem database (https://pubchem.ncbi.nlm.nih.gov/compound/). Subsequently, 2D and geometry optimizations, including energy minimization of the ligands, were carried out using algorithms in Schrödinger Maestro v 12.5. The LigPrep module (Schrödinger, LLC, NY, USA, 2009) within the Maestro builder panel was utilized to prepare the ligands. This preparation involved adding hydrogen atoms, eliminating salt and ionization effects at a pH range of 7.0 ± 2.0, under the influence of the OPLS_2003 force field for energy minimization. The resulting low-energy ligand isomer was generated with an RMSD cutoff of 0.01 Å.

2.4.2 Preparation of protein structures and grid generation.

To address the research objectives concerning polyketide synthase A, we opted for the protein structure with the PDB ID 3HRQ, which displayed favorable attributes, including a resolution of less than 2 Å, an R-value free lower than 0.30, and an R-value Work below 0.25. These specific structural data were sourced from the Protein Data Bank (http://www.rcsb.org) (Labib et al., 2020). We harnessed the capabilities of the Protein Preparation Wizard within the Maestro's task panel to prepare the protein target. This procedure encompassed the assignment of bond orders to the protein, the addition of hydrogen atoms, and the removal of water molecules situated within a 3 Å radius of hetero groups (Burger et al., 2024). Following this, we conducted structural minimization of the protein using the OPLS-2003 force field, as per Schrödinger LLC's methodologies (NY, USA, 2009). To facilitate molecular docking studies, receptor grid boxes was generated through the "Glide's Receptor Grid Generation" module. These grid boxes were centered precisely on the active site, employing a 20 Å radius around the crystal structure of the co-crystallized ligand. The computational cubic box dimensions were configured to be 10 Å x 10 Å x 10 Å for this purpose.

2.5 Molecular docking

Molecular docking is a method employed in structure-based drug design, aimed at identifying crucial amino acid interactions between a chosen protein and synthesized ligands possessing low-energy conformations. The primary objective is to determine the ligands' interactions with the receptor, with a focus on minimizing the energy interactions. This is accomplished using a scoring function, which is employed to predict the binding affinity between the ligands and the receptor. The docking process began with Glide Standard Precision (SP) docking for drug-like bioactive compounds.

This allowed us to evaluate the potential binding of the ligands to the target protein. These compounds were further subjected to more accurate extra-precision (XP) docking, which employs an exhaustive search approach and a sophisticated scoring function emphasizing ligand-receptor complementarity to reduce false positive and provides enhanced accuracy in predicting binding affinity and assesses the ligand's efficiency as an inhibitor of the polyketide synthase target.

2.6 The Binding free energy (MMGBSA)

The analysis after docking focused on assessing the stability of the formed complex i.e. (protein-ligand complex) by calculating the binding free energy. This calculation was performed using the Prime MMGBSA module available in Maestro. MMGBSA combines molecular mechanics with Poisson-Boltzmann or generalized Born and surface area continuum solvation to estimate the free energy of the ligand binding to the macromolecule. In the Prime MMGBSA method, the free energy difference is computed between the minimized protein-ligand complex and the unbound protein and ligand. This calculation is expressed as follows:

E_minimized complex = E_minimized protein – E_minimized ligand

The molecules were subjected to minimization using the OPLS3 force field, and the VSGB (Variable dielectric Solvent Generalized Born) solvation model was employed in this process.

3. Results and Discussion

3.1 Chemical Composition of the Extract of Senna obtusifolia

Chemical constituents of the extract of Senna obtusifolia analyzed using GC-MS. A total of twenty-seven (27) chemical components were identified accounting for about 97.50% of the total components in the extract, the constituents with higher estimated percentage composition were: cis-oleic acid (20.0%), palmitic acid (13.0%), stearic acid (11.0%), 1,E-8,Z-10-pentadecatriene (10.0%), 1,E-11,Z-13-octadecatriene (10%), ethyl iso-allocholate (5.0%) and undec-10-enoic acid (4.5%) as shown in Table 1.

Table 1: Chemical Composition of the Aerial Extract of Senna obtusifolia

Compound	Percentage Composition
1-heptatriacotanol	3.0
longborneol (juniperol)	2.0
ethyl iso-allocholate	5.0
pentadecanoic acid	1.0
cis-1-chloro-9-octadecene	1.0
2-dodecen-1-yl (-) succinic anhydride	1.0
z-9-octadecenal	1.0
octadecanoic acid	1.0
γ-butyrolactone	0.5
1-pyrrolidinylacetic acid	0.5
3,5-dihydroxy-6-methyl-2,3-dihydro-4H-pyran-4-one	0.5
α-pipecolinic acid	0.2
p-vinylguaiacol	0.3
undec-10-enoic acid	4.5
1,*E*-8,*Z*-10-pentadecatriene	10.0
lauric acid	1.0
Z-9-tetradecenal	1.0
myristic acid	0.5
methyl-14-methylpentadecanoate	2.0
1,*E*-11,*Z*-13-octadecatriene	10.0
palmitic acid	13.0
methyl-n-octadecanoate	1.0
methyl-11-octadecenoate	3.0
methyllinolelaidate	3.0
stearic acid	11.0
cis-oleic acid	20.0
glycerol-1-palmitate	0.50
Percentage Total	97.5

3.2 In Silico (Ligand Structure Based Drug Design)

3.2.1 Molecular Docking

Molecular docking is a computational method used to predict and analyze the interactions between ligands (small molecules) and target protein to understand their binding mode and affinity (Challapa-Mamani et al., 2023). The higher the negativity of the binding scores the stronger the inhibitory potential against the target (3HRQ domain). In comparison to the natural substrate palmitic acid (PLM) which has a docking score of -8.097 as indicated in Table 2 below, 5 compounds regarded as the chosen/hit compounds have more negative docking scores (Table 3).

However, it is important to highlight that all the chosen hit compounds exhibited superior inhibitory potential as demonstrated by their respective docking scores: -9.214, -9.213, -8.688, -8.343, and -8.307 kcal/mol. These scores surpass the inhibitory potential of PLM, which is an established natural substrate employed in repressing the expression of polyketide synthase A gene, with a docking score of -8.131 kcal/mol, respectively. This comparative analysis indicate that 5 of the given 20 compounds showed greater binding affinity to the target protein than the natural substrate PLM.

3.3 Molecular Interactions of Compounds within the Active Site of Polyketide Synthase A

Structural-based design relies on the three-dimensional structure of a target protein to design and optimize molecules by identifying binding sites, simulating interactions, and improving their effectiveness for drug discovery (Chang et al., 2022). The interaction which contributes significantly to the inhibition of the 3HRQ protein in this study is shown in Figure 1 below. The 2D interaction, shown in Fig. 1 and described in Table 3, showed that all the selected five lead compounds interacted similarly

with the natural substrate PLM, having hydrophobic interaction with similar residues His 1345, Val 1347, Leu 1630, Phe 1551, Asp 1509, Leu 1352, Leu 1508, Asn 1554, Gly 1550, Tyr 1492, Met 1498, Phe 1501, Ala 1499, Met 1495, among others thus, contributing to the greater binding affinity of the compounds to the target protein domain. His 1345 does not only form a hydrophobic bond with the PLM but also interacts using a salt bridge interaction. The significance of hydrophobic interactions in drug development emphasizes that increasing the number of hydrophobic atoms in a drug can enhance its binding affinity with the target mediator, leading to greater drug effectiveness (Lou and Martin, 2021). Furthermore, these hydrophobic interactions can complement hydrogen bonding, and the presence of water in hydrophobic areas as shown in the figures below, is crucial for preserving flexibility. In summary, a strategic augmentation of hydrophobic interactions within the specific active core site of drug-target complexes can result in enhanced biological inhibition activity of the drug.

Table 2: Molecular Docking Score (kcal/mol) of Docked Compounds against Polyketide Synthase A.

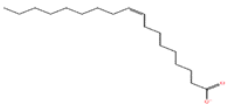
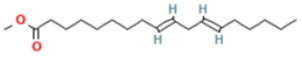
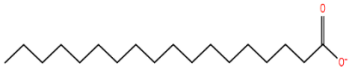
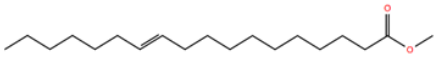
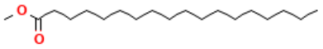
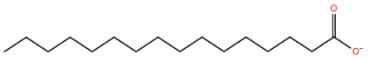
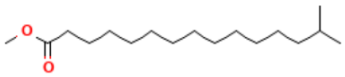
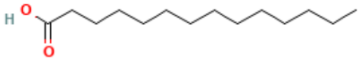
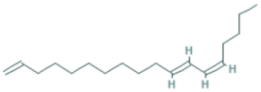
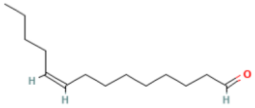
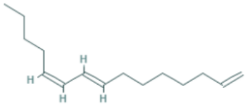
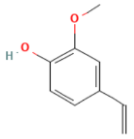
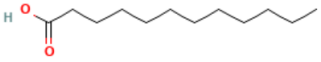
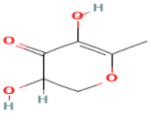
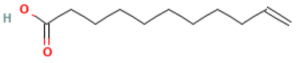
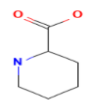
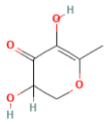
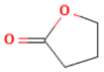
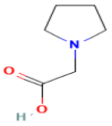
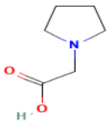
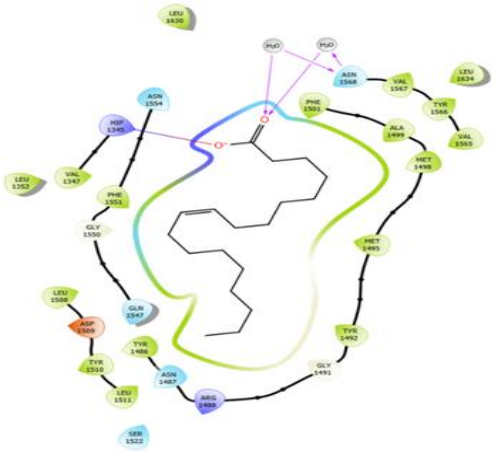
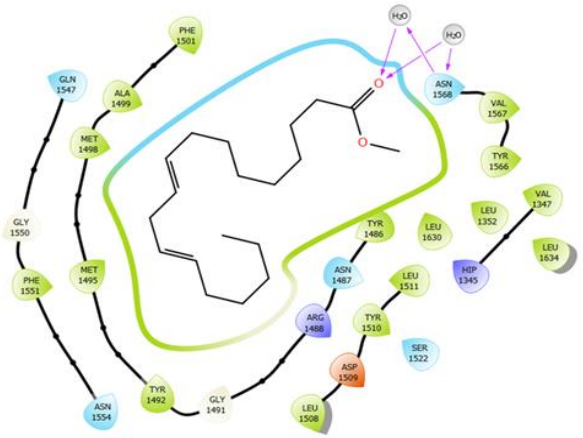
SN	Compound Pubchem ID	compound name	Binding Energy (kcal/mol)	Compound structure
1.	445639	cis-oleic acid	-9.214	
2.	5362793	methyllinolelaidate	-9.213	
3.	5281	stearic acid	-8.688	
4.	5364432	methyl-11-octadecenoate	-8.343	
5.	8201	methyl-n-octadecanoate	-8.307	
6.	985	Palmitic acid.	-8.097	
7.	21205	methyl-14-methylpentadecanoate	-7.585	
8.	11005	myristic acid	-6.551	
9.	5365585	1,E-11,Z-13-octadecatriene	-6.323	
10.	5364471	Z-9-tetradecenal	-6.134	
11.	5365582	1,E-8,Z-10-pentadecatriene	-5.739	
12.	332	p-vinylguaiacol	-5.503	
13.	3893	lauric acid	-5.408	
14.	119838	3,5-dihydroxy-6-methyl-2,3-dihydro-4H-pyran-4-one	-4.512	
15.	5634	undec-10-enoic acid	-4.305	

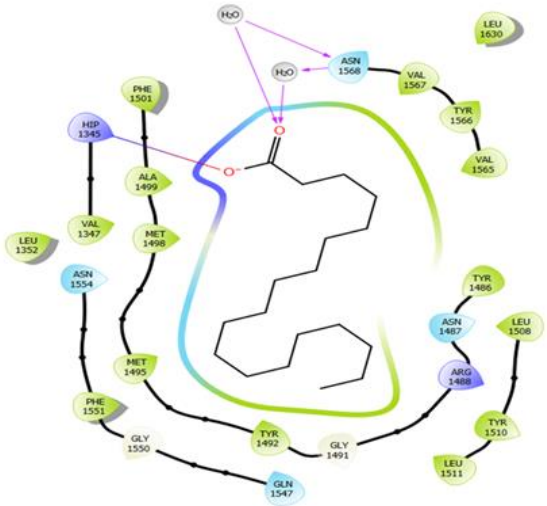
Table 2 (Cont): Molecular Docking Score (kcal/mol) of Docked Compounds against Polyketide Synthase A.				
SN	**Compound Pubchem ID**	**compound name**	**Binding Energy (kcal/mol)**	**Compound structure**
16.	348274231	α-pipecolinic acid	-4.205	
17.	119838	3,5-dihydroxy-6-methyl-2,3-dihydro-4H-pyran-4-one	-4.077	
18.	198960514	γ-butyrolactone	-3.839	
19.	414564	1-pyrrolidinylacetic acid	-3.38	
20.	414564	1-pyrrolidinylacetic acid	-1.362	



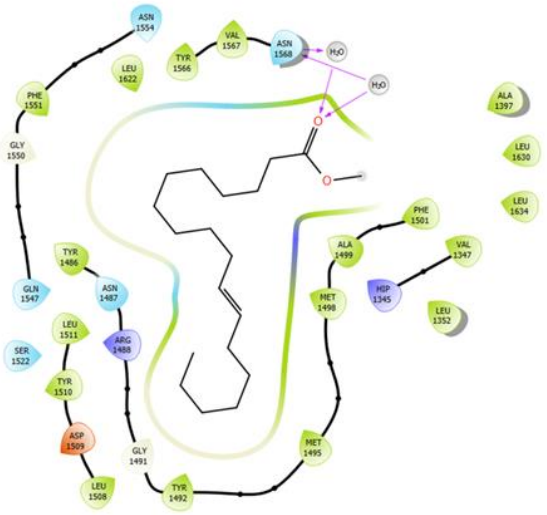
(a)



(b)



(c)



(d)

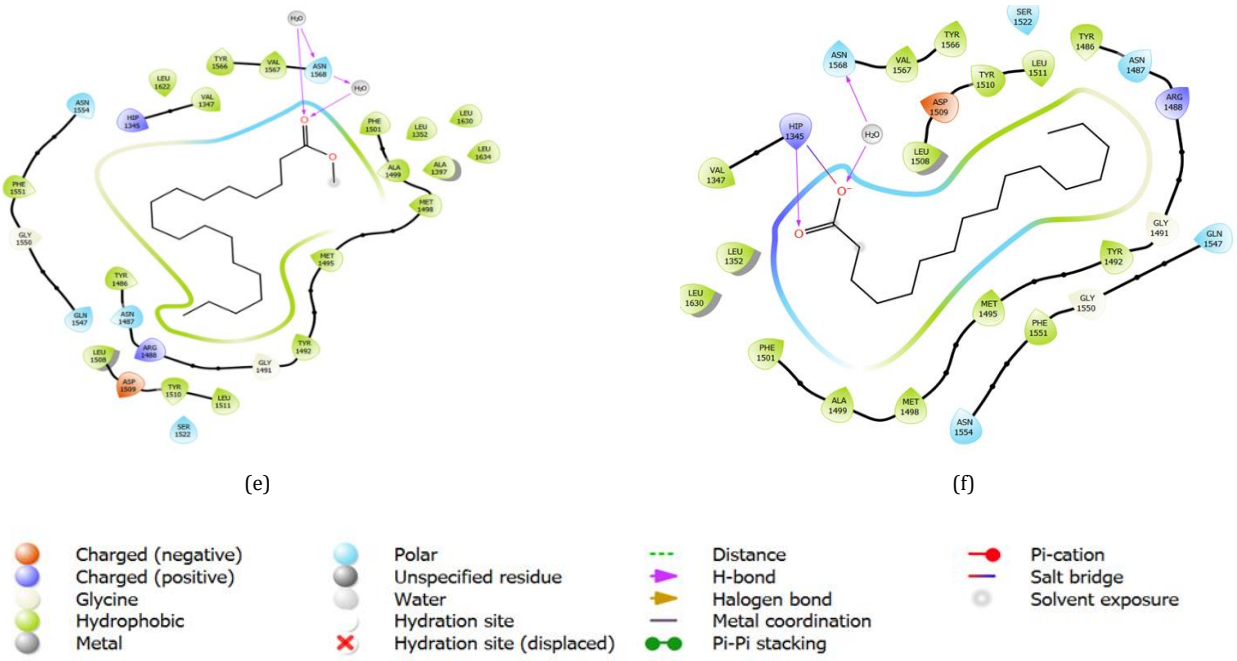
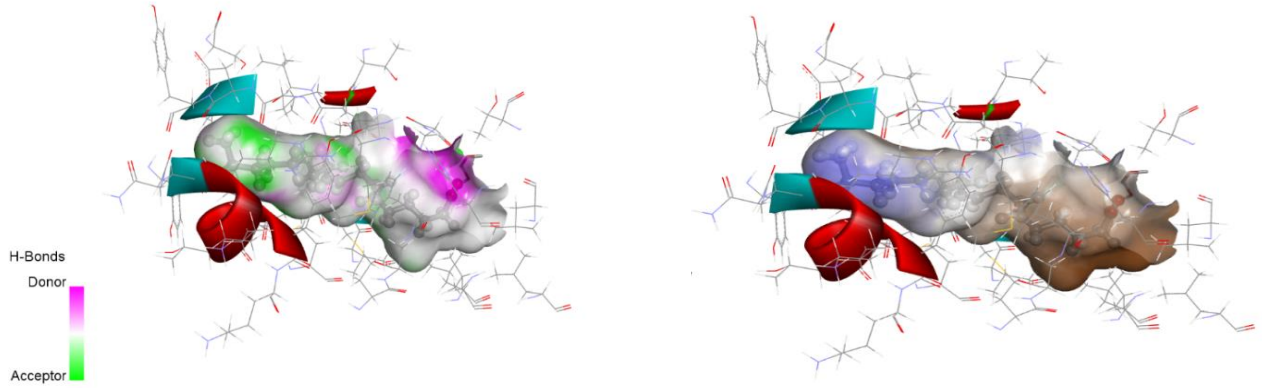
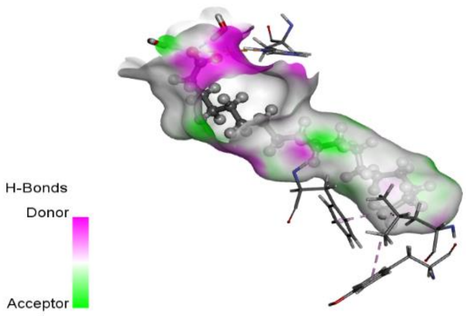


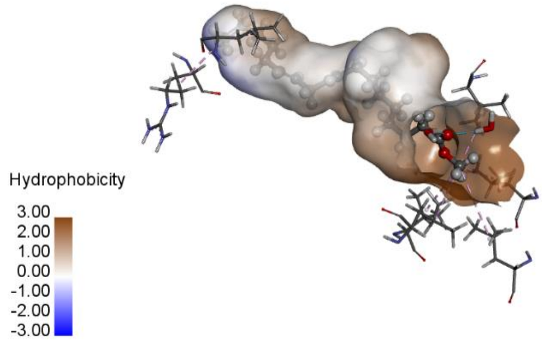
Figure 1: Interaction of the five hit compounds including palmitic acid (natural substrate) with polyketide synthase amino residues. (a) cis-oleic acid (b) methyllinolelaidate (c) stearic acid (d) methyl-11-octadecenoate (e) methyl-n-octadecanoate (f) palmitic acid

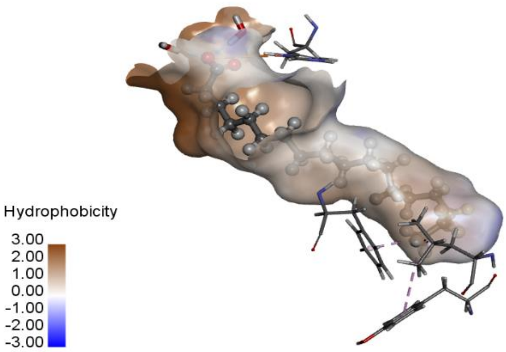
Table 3: Showing Interactions of all Ligands' Atoms with Amino Acid Residues in the Binding Site of Polyketide Synthase after Molecular Docking

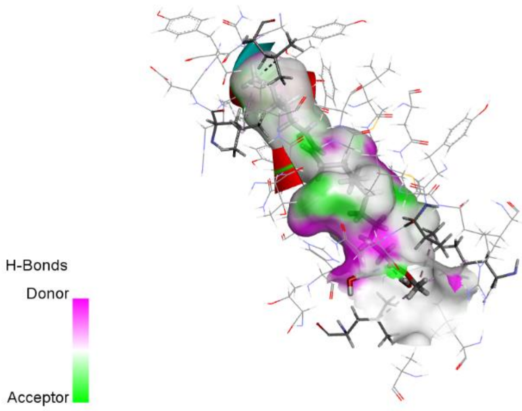
Compound Name	H-Bond	Hydrophobic Interactions	Other Interactions
cis-oleic acid	-	Leu 1630, Asn 1568, Val 1567, Tyr 1566, Val 1565, Phe 1501, Ala 1499, Met 1498, Met 1495, Tyr 1492, Gly 1491, Arg 1488, Asn 1487, Tyr 1486, Gln 1547, Gly 1550, Phe 1551, Asn 1554, Leu 1634, His 1345, Val 1347, Leu 1352, Leu 1508, Asp 1509, Tyr 1510, Leu 1511, Ser 1522.	Salt bridge with His 1345.
methyllinolelaidate	-	Leu 1352, Val 1347, His 1345, Asn 1568, Val 1567, Tyr 1566, Phe 1501, Ala 1499, Met 1498, Met 1495, Tyr 1492, Gly 1491, Arg 1488, Asn 1487, Tyr 1486, Leu 1630, Leu 1634, Leu 1508, Asp 1509, Ser 1522, Tyr 1510, Leu 1511, Glu 1547, Gly 1550, Phe 1551, Asn 1554.	-
stearic acid	-	Asn 1568, Val 1567, Tyr 1566, Asn 1554, Phe 1551, Gly 1550, Gln 1547, Tyr 1486, Asn 1487, Arg 1488, Leu 1511, Tyr 1510, Leu 1508, Gly 1491, Tyr 1492, Met 1495, Met 1498, Ala 1499, Phe 1501, Val 1347, His 1345, Ala 1397, Leu 1352, Leu 1630.	Salt bridge with His 1345.
methyl-11-octadecenoate	-	Asn 1554, Phe 1551, Gly 1550, Tyr 1566, Val 1567, Asn 1568, Phe 1501, Ala 1499, Met 1498, Leu 1634, Leu 1630, His 1345, Val 1347, Leu 1352, Met 1495, Tyr 1492, Ser 1522, Gly 1491, Arg 1488, Asn 1487, Tyr 1486, Thr 1546, Gln 1547, Leu 1511, Tyr 1510, Asp 1509, Leu 1508, Ala 1397.	-
methyl-n-octadecanoate	-	Leu 1511, Tyr 1510, Asp 1509, Ser 1522, Leu 1508, Tyr 1486, Asn 1487, Arg 1488, Gly 1495, Tyr 1492, Met 1495, Met 1498, Ala 1499, Phe 1501, Gln 1547, Gly 1550, Phe 1551, Asn 1554, His 1345, Val 1347, Tyr 1566, Val 1567, Asn 1568, Leu 1352, Leu 1634, Leu 1630, Val 1394, Ala 1397.	-
palmitic acid	His 1345	Val 1347, Leu 1352, Leu 1630, Phe 1501, Ala 1499, Met 1498, Met 1495, Tyr 1492, Gly 1491, Glu 1547, Gly 1550, Phe 1551, Asn 1554, Arg 1488, Asn 1487, Tyr 1486, Ser 1522, Leu 1511, Tyr 1550, Asp 1509, Leu 1508, Tyr 1566, Val 1567, Asn 1568.	Salt bridge with His 1345.

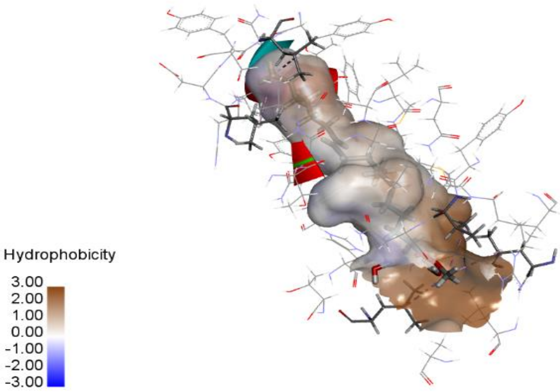


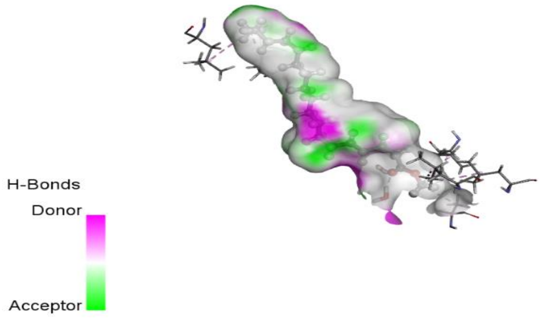

H-Bonds
Donor
Acceptor

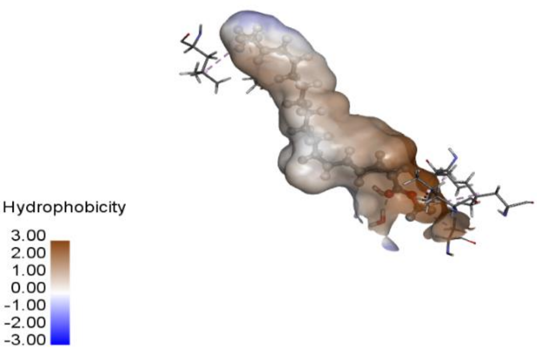

Hydrophobicity
3.00
2.00
1.00
0.00
-1.00
-2.00
-3.00

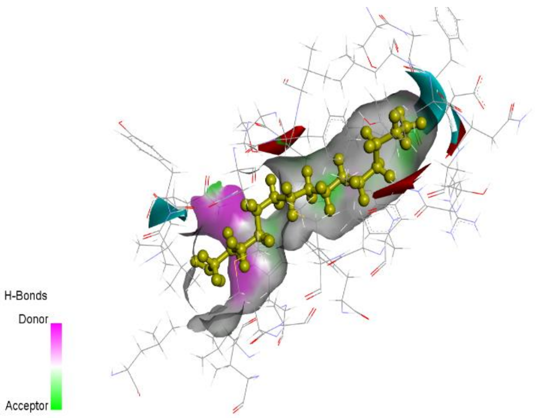

Hydrophobicity
3.00
2.00
1.00
0.00
-1.00
-2.00
-3.00


H-Bonds
Donor
Acceptor


Hydrophobicity
3.00
2.00
1.00
0.00
-1.00
-2.00
-3.00


H-Bonds
Donor
Acceptor


Hydrophobicity
3.00
2.00
1.00
0.00
-1.00
-2.00
-3.00


H-Bonds
Donor
Acceptor

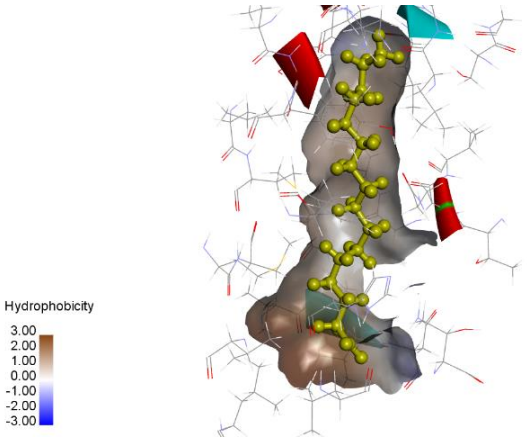


Figure 2: Hydrogen bonds (A) and hydrophobic interactions (B) maps between PKS and five chosen inhibitors and palmitic acid (yellow ball and stick). 1) cis-oleic acid. 2) methyllinolelaidate. 3) stearic acid 4) methyl-11-octadecenoate. 5) methyl-n-octadecanoate 6) Palmitic acid. Ligands are presented in ball and stick while amino acid residues of PKS are in lines executed in BIOVIA's Discovery Studio 2016.

It was established in the figure 2 shown above that, the chemical interactions, hydrogen bonds, and hydrophobic regions between the 5 chosen hit compounds and the target protein showed the binding efficiency which lead to greater drug efficacy. Discovery studio was utilized for analyzing the hydrophobic and H -bond interactions between the ligands and domain complexes after being visualized in 2D using PyMOL to get interactions complex of each ligand and 3HRQ domain to define binding efficiency (Ravikumar et al., 2023).

3.4 MM-GBSA Analysis

The MM-GBSA technique is a computational method used for estimating the binding free energies of bio molecular complexes, providing insights into molecular interactions in biological systems (Forouzesh et al., 2020). It stands as a promising strategy to enhance virtual screening outcomes, with a negative ΔG value indicating the stability of generated complexes within the binding pocket of the target. All lead compounds exhibit a negative ΔG value, as depicted in Table 4, with binding free energies for the docked complexes measuring at -65.50, -69.04, -66.67, -72.52, and -78.93 kcal/mol for methyl-n-octadecanoate, methyl-11-octadecenoate, methyllinolelaidate, stearic acid, cis-oleic acid, and palmitic acid respectively.

This indicates that all the selected compounds are more stable within the target's binding pocket compared to the standard substrate (PLM), which exhibits a binding free energy of -54.14 kcal/mol. Methyl-n-octadecanoate which has the highest binding energy also has the highest binding free energy also has the highest binding free energy.

Table 4: The MM-GBSA Binding Free Energy using Prime MMGBSA module in Maestro 12.5

SN	Compound ID	Compound Name	MMGBSA ΔG Bind
1.	8201	methyl-n-octadecanoate	-78.93
2.	5364432	methyl-11-octadecenoate	-72.52
3.	5362793	methyllinolelaidate	-69.04
4.	5281	stearic acid	-66.67
5.	445639	cis-oleic acid	-65.50
6.	985	Palmitic acid.	-54.14.

3.5 ADMET Properties and Drug-Likeness

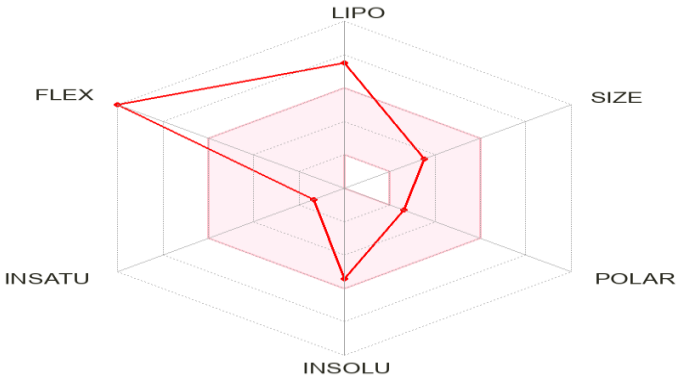
The properties of the candidate inhibitors were assessed, and all components were evaluated for toxicity and drug-likeness using SWISS-ADME. As shown in Table 5, the selected candidates exhibited favorable characteristics, including Gastrointestinal (GI) absorption, pharmacokinetic profiles (drug-likeness), Cytochrome P450 isoform inhibition, and bioavailability scores (Ononamadu et al., 2021; Rai et al., 2023; Ololade et al., 2025). Membrane permeability and bioavailability of the compounds in the results showed that none of the five lead (chosen) compounds including the PLM, violated the Lipinski's rule. Molecular weight (MW), or counts of hydrogen bond acceptors and donors in the molecules, are the physicochemical features that authenticate Lipinski rule of 5 (Ro5) –one of the rules that determines drug efficacy (Giménez et al., 2010; Kralj et al., 2023).

All the hit compounds are not blood–brain barrier permeant, only the PLM (natural substrate) is predicted to permeate the Blood-Brain Barrier (BBB). Cytochrome P450 (CYP) is a family of enzymes that catalyze the phase 1 metabolism of xenobiotic at large (Kuban and Daniel, 2021; Durairaj and Liu, 2025). Any compound that inhibits selected isoforms would induce a drug–drug interaction. The entire compounds show different inhibitions to the various isoforms of Cytochrome P450 (CYP), indicated in Table 5 below and bioavailability score show decent values. They are all moderately soluble and have high GI absorption.P-glycoprotein (P-gp), the most extensively studied ATP-binding cassette transporter, functions as a biological barrier by extruding toxic substances and xenobiotic out of cells serving to protect the integrity of tissues and cellular environments.

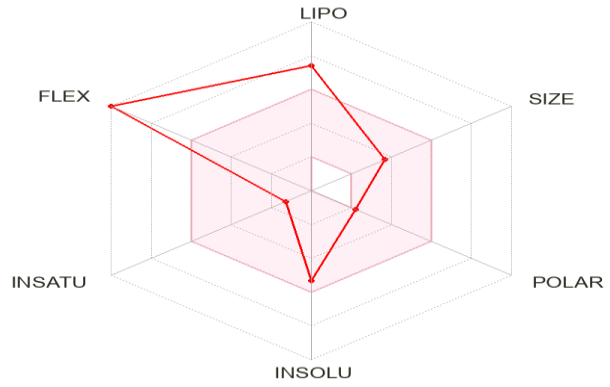
The result also showed that all the chosen compounds are non-substrate of P-gp. Bioavailability Radar (Figure 3) was used for a rapid assessment of drug-likeness in which six physicochemical properties were taken into account: lipophilicity, size, polarity, solubility, flexibility and saturation. A physicochemical range on each axis was depicted as a pink area in which the radar plot of the molecule has to fall entirely to be considered drug-like, physicochemical properties, physicochemical descriptors like molecular weight (MW), molecular refractivity (MR), count of specific atom types and polar surface area (PSA) were computed because these were proven useful descriptors in many models and rules to quickly estimate some ADME properties (Sherin et al., 2021; Murad et al., 2022; Ololade et al., 2025).

Table 5: ADMET profile and Drug Likeness of the Five Hit Compounds including the Natural Substrate using SWISS-ADME Server

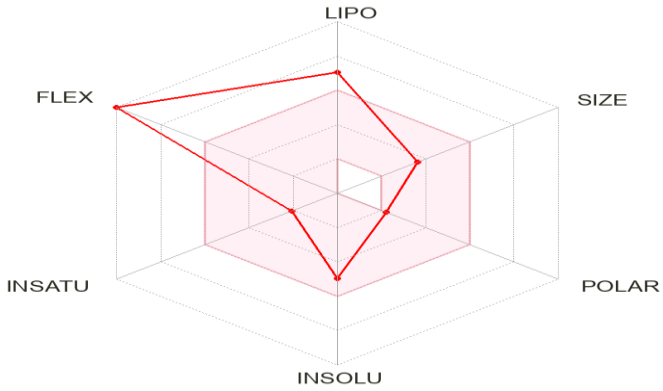
Molecule	GI absorption	BBB permeant	Pgp substrate	CYP1A2 inhibitor	CYP2C19 inhibitor	CYP2C9 inhibitor	CYP2D6 inhibitor	CYP3A4 inhibitor	log Kp (cm/s)	Lipinski #violations	Bioavailability Score
cis-oleic acid	High	No	No	Yes	No	Yes	No	No	-2.6	1	0.85
methyllinolelaidate	High	No	No	Yes	No	Yes	No	No	-3.25	1	0.55
stearic acid	High	No	No	Yes	No	No	No	No	-2.19	1	0.85
methyl-11-octadecenoate	High	No	No	Yes	No	No	No	No	-2.82	1	0.55
methyl-n-octadecanoate	High	No	No	Yes	No	No	No	No	-2.19	1	0.55
Palmitic acid.	High	Yes	No	Yes	No	Yes	No	No	-2.77	1	0.85



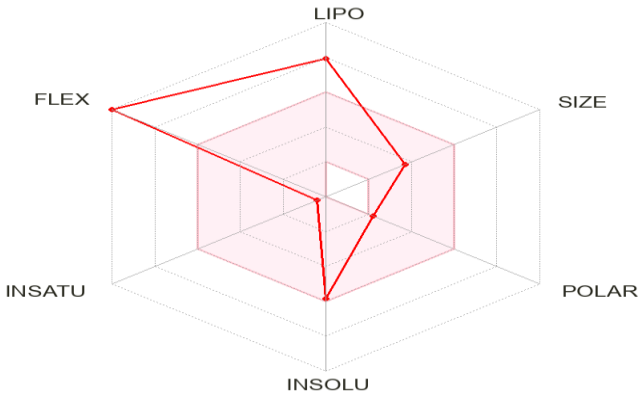
Molecule 1: *cis*-oleic acid



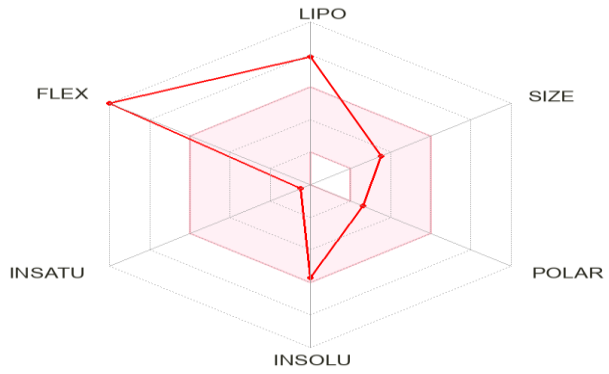
Molecule 2: methyl-11-octadecenoate



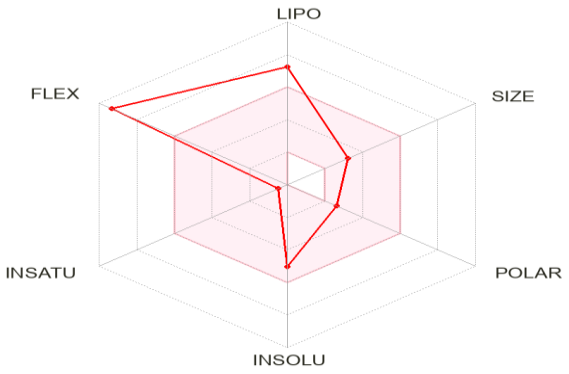
Molecule 3: methyllinolelaidate



Molecule 4: methyl-n-octadecanoate



Molecule 5: stearic acid



Molecule 6: Palmitic acid.

Figure 3: The bioavailability radar of the small molecules evaluated using swissADME web tool.

Cis-oleic acid (Molecule 1), methyl-11-octadecenoate (Molecule 2), methyllinolelaidate (Molecule 3), methyl-n-octadecanoate (Molecule 4), stearic acid (Molecule 5) and Palmitic acid (Molecule 6). (Lipophilicity (LIPO): XLOGP3 between -0.7 and +5.0, Molecular weight (SIZE): MW between 150 and 500 g/mol, Polarity (POLAR) TPSA between 20 and 130 Å 2 , Solubility (INSOLU): log S not higher than 6, Saturation (INSATU): fraction of carbons in the sp3 hybridization not less than 0.25, and Flexibility (FLEX): no more than 9 rotatable bonds.

4. Conclusion

This study showed that the phytochemicals in S. obtusifolia are medicinally active. The secondary metabolites in the sample exhibited combinatorial potential for drug development. All lead compounds exhibit a negative ΔG value with binding free energies for the docked complexes. The selected candidates exhibited favorable characteristics, including gastrointestinal (GI) absorption, pharmacokinetic profiles (drug-likeness), cytochrome P450 isoform inhibition, and bioavailability scores. The use of natural plants can serve as an alternative therapy to synthetic drug which are far expensive with adverse side effect in treatment of food poisons caused by aflatoxin. This is due to the presence of abundant terpenoids and polyphenolic compounds in medicinal plants when used in the appropriate doses.

Conflict of interest: We have no conflict of interest.

Data Availability Statement: The authors confirm that the data supporting the findings of this study are available within the article.

References

Adesina, A.R., Kajihausa, O.E., Sobukola, O.P., Ololade, Z.S. 2022. Some Quality Attributes of Gluten Free Fried Products from Defatted Peanut Flour and Starches of Common Tropical Roots, International Journal of Agricultural Science and Food Technology, 8(4), 265-272.

Adesina, A.R., Ogunmoyela, O.A.B., Arisa, N.U. and Ololade, Z.S. 2022.

Optimization of the production of local cheese from cow milk processed with the seed of Moringa oleifera, Journal of Food Processing and Preservation, 46(1), e16189.

Ajmal, M., Bedale, W., Akram, A. and Yu, J.H. 2022. Comprehensive Review of Aflatoxin Contamination, Impact on Health and Food Security, and Management Strategies in Pakistan. Toxins, 14(12), 845. https://doi.org/10.3390/toxins14120845

Alao, F.O., Ololade, Z.S. and Nkeonye, C.V. 2018. Phytochemicals and Antibacterial Potentials of Senna tora Leaf and Seed Extracts on Some Clinically Isolated Bacteria, Journal of Bacteriology and Parasitology, 9(3), 1-4.

Burger P.B., Hu X., Balabin I., Muller M., Stanley M., Joubert F., Kaiser T.M. 2024. FEP Augmentation as a Means to Solve Data Paucity Problems for Machine Learning in Chemical Biology. J Chem Inf Model, 64(9), 3812-3825. doi: 10.1021/acs.jcim.4c00071.

Challapa-Mamani M.R., Tomás-Alvarado E., Espinoza-Baigorria A., León-Figueroa D.A., Sah R., Rodriguez-Morales A.J., Barboza J.J. 2023. Molecular Docking and Molecular Dynamics Simulations in Related to Leishmania donovani: An Update and Literature Review. Trop Med Infect Dis., 8(10), 457. doi: 10.3390/tropicalmed8100457.

Chang Y., Hawkins B.A., Du J.J., Groundwater P.W., Hibbs D.E., Lai F. 2022. A Guide to In Silico Drug Design. Pharmaceutics, 15(1), 49. doi: 10.3390/pharmaceutics15010049.

Durairaj, P., and Liu, Z.L., 2025. Brain Cytochrome P450: Navigating Neurological Health and Metabolic Regulation. Journal of Xenobiotics, 15(2), 44. https://doi.org/10.3390/jox15020044

Forouzesh N., Onufriev A.V., 2020. MMGB/SA Consensus Estimate of the Binding Free Energy Between the Novel Coronavirus Spike Protein to the Human ACE2 Receptor. bioRxiv [Preprint]. 2020; 2020.08.25.267625. doi: 10.1101/2020.08.25.267625.

Gbenga-Fabusiwa, F.J., Jeff-Agboola, Y.A., Ololade, Z.S., Akinrinmade, R. and Agbaje, D.O. 2022. Waste-to-wealth; nutritional potential of five selected fruit peels and their health benefits: A review, African Journal of Food Science, 16(7), 172-183.

Giménez B.G., Santos M.S., Ferrarini M., Fernandes J.P., 2010. Evaluation of blockbuster drugs under the rule-of-five. Pharmazie., 65(2), 148-52.

Kibugu J., Munga L., Mburu D., Maloba F., Auma J.E., Grace D., Lindahl J.F., 2024. Dietary Mycotoxins: An Overview on Toxicokinetics, Toxicodynamics, Toxicity, Epidemiology, Detection, and Their Mitigation with Special Emphasis on Aflatoxicosis in Humans and Animals. Toxins (Basel)., 16(11), Pp. 483. doi: 10.3390/toxins16110483.

Kralj, S., Jukič, M. and Bren, U. 2023. Molecular Filters in Medicinal Chemistry. Encyclopedia, 3(2), 501-511. https://doi.org/10.3390/encyclopedia3020035

Kuban W., Daniel W.A. 2021. Cytochrome P450 expression and regulation in the brain. Drug Metab Rev., 53(1), 1-29.

Kumar P., Gupta A., Mahato D.K., Pandhi S., Pandey A.K., Kargwal R., Mishra S., Suhag R., Sharma N., Saurabh V., Paul V., Kumar M., Selvakumar R., Gamlath S., Kamle M., Enshasy H.A.E., Mokhtar J.A., Harakeh S., 2022. Aflatoxins in Cereals and Cereal-Based Products: Occurrence, Toxicity, Impact on Human Health, and Their Detoxification and Management Strategies. Toxins (Basel), 14(10), Pp. 687.

Labib M.M., Amin M.K., Alzohairy A.M., Elashtokhy M.M.A., Samir O., Saleh I., Arif I.A., Osman G.H., Hassanein S.E., 2020. In silico Targeting, inhibition and analysis of polyketide synthase enzyme in Aspergillus ssp. Saudi J Biol Sci., 27(12), 3187-3198.

Lou L.L., Martin J.C., 2021. Selected Thoughts on Hydrophobicity in Drug Design. Molecules. 26(4), Pp. 875. doi: 10.3390/molecules26040875.

Mujeeb A., Abideen Z., Aziz I., Sharif N., Hussain M.I., Qureshi A.S., Yang H.H. 2023. Phytoremediation of Potentially Toxic Elements from Contaminated Saline Soils Using Salvadora persica L.: Seasonal Evaluation. Plants (Basel). 12(3), 598. doi: 10.3390/plants12030598.

Murad H.A.S., Alqurashi T.M.A., Hussien M.A. 2022. Interactions of selected cardiovascular active natural compounds with CXCR4 and CXCR7 receptors: a molecular docking, molecular dynamics, and pharmacokinetic/toxicity prediction study. BMC Complement Med Ther., 22(1), 35. doi: 10.1186/s12906-021-03488-8.

Nazareth T.M., Soriano Pérez E., Luz C., Meca G., Quiles J.M., 2024. Comprehensive Review of Aflatoxin and Ochratoxin A Dynamics: Emergence, Toxicological Impact, and Advanced Control Strategies. Foods, 13(12), 1920. doi: 10.3390/foods13121920.

Ololade Z.S., Anuoluwa I.A., Adejuyitan J.A.and Uyaboerigha D.I. 2021. Black Velvet Tamarind: Phytochemical Analysis, Antiradical and Antimicrobial Properties of the Seed Extract for Human Therapeutic and Health Benefits. The Journal of Phytopharmacology, 10(4), 249-255.

Ololade, Z.S. and Olawore, N.O. 2021. Health Benefits of the Fruit Essential Oil of Eucalyptus citriodora: Secondary Metabolites, Radical Scavenging, Antioxidant, Antiinflamatory, Analgesic, Antimicrobial Potential, International Journal of Drug Development and Research, 13(4), 1-7.

Ololade, Z.S., Anuoluwa, I.A., Adeyemi A.F. and Uyaboerigha D.I. 2021. Synergistic Efficacy of Phytochemical, Antioxidant and Bactericidal Properties of the Aerial Essential Oil of Laggera crispate, Pharmacognosy Journal, 13(5), 1304-1311.

Ololade, Z.S., Anuoluwa, I.A., Onifade, O.F., Adeagbo, A.I., Oyebanji, O.T., Asaju, A.O., and Eze, J.C. 2025a. Evaluation of Annona muricata for Hepatoprotection, Hematological Assessment and Inhibitor of TGFβR1 in Liver Diseases, Archives of Physiology and Biochemistry; The Journal of Metabolic Diseases. 131(2), 1-18. doi.org/10.1080/13813455.2025.2499840.

Ololade, Z.S., Lajide, L., Onifade, O.F., Eze, J.C., Tommy B.E., Orodepo, G.O., Idowu, O.O., Oyebanji, O.T. and Olaniran, A.C. 2023. Exploration of Secondary Metabolites in Flower-Petal Annona muricata as Agonists for Peroxisome Proliferator-Activated Receptor-Alpha (PPARα) for Liver Function, The Journal of Phytopharmacology, 12(6), 411-420. doi: 10.31254/phyto.2023.12607

Ololade, Z.S., Ojo, O.A., Onifade, O.F., Akinnawo, C.A, Orodepo, G.O., Oyebanji, O.T., Tommy, B.E. and Azeez-Olaleye, L.D. (2024). Chemoinformatic Study on Phytochemicals from Melissa officinalis for Ligand Based Drug Design Inhibition of Aflatoxins Synthesis, Toxin Reviews, 43(2), 1-17. doi: 10.1080/15569543.2024.2344472.

Ononamadu C.J., Ibrahim A. 2021. Molecular docking and prediction of ADME/drug-likeness properties of potentially active antidiabetic compounds isolated from aqueous-methanol extracts of Gymnema sylvestre and Combretum micranthum. BioTechnologia (Pozn). 102(1), 85-99. doi: 10.5114/bta.2021.103765.

Rai M., Singh A.V., Paudel N., Kanase A., Falletta E., Kerkar P., Heyda J., Barghash R.F., Pratap Singh S., Soos M. 2023. Herbal concoction Unveiled: A computational analysis of phytochemicals' pharmacokinetic and toxicological profiles using novel approach methodologies (NAMs). Curr Res Toxicol., 5:100118.

Ravikumar Y., Koonyosying P., Srichairatanakool S., Ponpandian L.N., Kumaravelu J, Srichairatanakool S. 2023. In Silico Molecular Docking and Dynamics Simulation Analysis of Potential Histone Lysine Methyl Transferase Inhibitors for Managing β-Thalassemia. Molecules, 28(21), 7266. doi: 10.3390/molecules28217266.

Shabeer S., Asad S., Jamal A., Ali A., 2022. Aflatoxin Contamination, Its Impact and Management Strategies: An Updated Review. Toxins (Basel)., 14(5), 307. doi: 10.3390/toxins14050307.

Sherin D.R., Sharanya N., Manojkumar T.K., 2021. Potential drug leads for SARS-CoV2 from phytochemicals of Aerva lanata: a Machine Learning approach. Virusdisease. 32(4), 757-765.