WORLD JOURNAL OF PHARMACEUTICAL RESEARCH
Coden USA: WJPRAP Impact Factor 8.63
Volume 15, Issue 9, 907-922. Research Article ISSN 2277–7105

WRIGHTIA TINCTORIA (ROXB.) R.BR. A PLANT CONTAINS PHYTOCHEMICALS SHOWING ANTIVENOM PROPERTY BY EXPLORING ELAPID AND VIPER VENOM NEUTRALIZATION POTENTIAL BASED ON MOLECULAR DOCKING. AN IN SILICO APPROACH.

S. Sivaraj[*1], K. Alageswari[1], S. Rangaraj[2], A. Suguna[3]

[*1]Drugs Testing Laboratory, Melakuilkudi, Madurai-625 019, Tamilnadu, India.

[2]Department of Anesthesiology, Government Medical College, Kallakurichi - 606213, Tamilnadu, India.

[3]Department of Obstetrics and Gynaecology, Government Medical College, Kallakurichi - 606213, Tamilnadu, India.

Article Received on 31 March 2026,
Article Revised on 20 April 2026,
Article Published on 01 May 2026,

https://doi.org/10.5281/zenodo.19877733

***Corresponding Author**

S. Sivaraj

Drugs Testing Laboratory, Melakuilkudi, Madurai-625 019, Tamilnadu, India.

How to cite this Article: S. Sivaraj*1, K. Alageswari1, S. Rangaraj2, A. Suguna3 (2026). Wrightia Tinctoria (Roxb.) R.Br. A Plant Contains Phytochemicals Showing Antivenom Property By Exploring Elapid And Viper Venom Neutralization Potential Based On Molecular Docking. An In Silico Approach.. World Journal of Pharmaceutical Research, 15(9), 907–922.

ABSTRACT

Snakebite envenomation listed as a neglected tropical disease by World health Organisation (WHO). In the current study, we employed an in silico approach to assess bioactive compounds from *Wrightia tinctoria* (Roxb.) R.Br. as potential antivenom agents using key venom target protein phospholipase A_2 (6Q42) and metalloproteases (2E3X). All the selected bioactive molecules showed very good binding energy than the positive control varespladib (-8.54 kcal/mol) and marimastat (-6.09 kcal/mol) except chlorogenic acid, ruitin and tryptanthrin. It was found that the ligand ursolic acid scored more negative binding energy -9.16 kcal/mol, -13.94 kcal/mol towards phospholipase A_2 (6Q42) and metalloproteases (2E3X) respectively. The bioavailablity score reveals that the selected bioactive molecules have ideal oral bioavailablity except ruitin and chlorogenic acid.

KEYWORDS: ●Wrightia tinctoria (Roxb.) R.Br. ● Phospholipase A2 (6Q42) ● Metalloproteases (2E3X) ● Antivenom, ●Elapids, ●Viper.

INTRODUCTION

Snakebite envenomation is a major threat in public health which causing severe tissue damage, neurotoxicity, kidney failure and death. World health Organisation (WHO) reported snake bite envenoming as a Neglected tropical disease. Antivenom administration is the only choice of treatment for snakebite envenomation which has limitations in terms of cost, availability and accessibility.[1] Being the snake venom is a complex protein mixture of different enzymes, it is tough to identify the toxicity profile which creates challenges in timely administration of antivenom.[2] To complement conventional antivenom therapy, recent investigations focus towards identifying herbal bioactive molecules as potential antidotes due to the lower risk of adverse effects.[3] Earthen hemisphere is blessed with huge number of medicinal plants. Among them, *Wrightia tinctoria* (Figure.1) is an important medicinal plant used in various systems of indian medicine especially in siddha medicine. This plant is inexpensive, easily available, and have pharmacological significance such as antiviral, anti-inflammatory, cytotoxic, hepatoprotective, wound healing, post coital interceptive, anthelmintic, antinociceptive, antioxidant, antiviral, antifungal, antibacterial, antidandruff and antipsoriatic activity.[4] Molecular docking is an in silico approach provides information about behavior of small molecules, when it binds with receptor target. The main aim of ligand-protein docking is to identify the predominant binding model(s) and understand the interactions of a ligand with amino acid residues of target.[5]

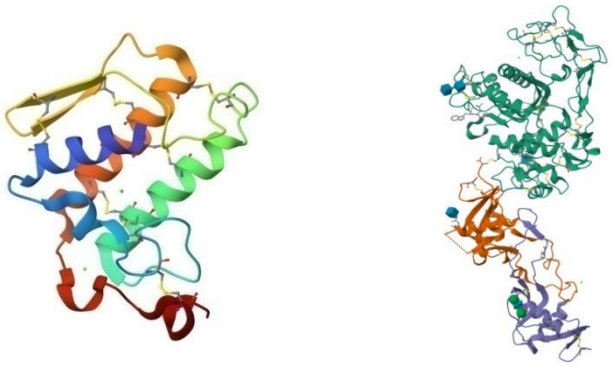
Figure 1: *Wrightia tinctoria* Plant.

MATERIALS AND METHODS

Proteins/Macromolecules

Atractaspidae (69 species), Elapidae (360 species) and Viperidae (340 species) are considered as medically significant venomous snake. Phospholipase A_2, metalloproteases, Serine

proteases and three finger toxins are identified as four main protein families of elapid and viper venom. Among them, phospholipase A_2 and metalloproteases are the two dominant protein families of elapid and viper venom.[6] To explore the antivenom property of bioactive molecules, phospholipase A_2 and metalloproteases are considered as ideal target. Three dimensional protein structure of PDB ID 6Q42 and PDB ID 2E3X (Figure.2) corresponding to human pancreatic phospholipase A_2 and Russell's viper venom Metalloproteases are downloaded from PDB (https://www.rcsb.org/), in .pdb format.

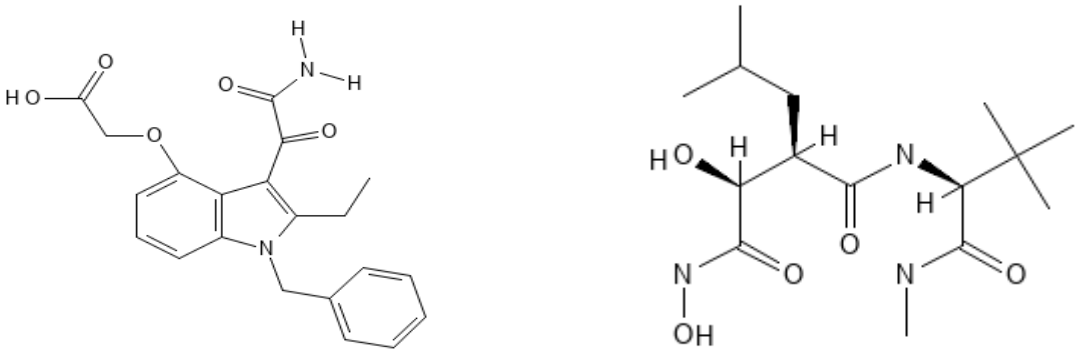


PDB ID:6Q42 **PDB ID:2E3X**

Figure 2: Protein Structure of 6Q42 and 2E3X.

Lead Molecule

Anandie le Roux et. al. reported varespladib and marimastat as potential inhibitors of snake venom phospholipase A_2 and metalloproteases.[7] So, varespladib and marimastat are considered as positive control (Standard) for Phospholipase A_2 (6Q42) and Metalloproteases (2E3X) respectively and the structure of the same is given in Figure 3.

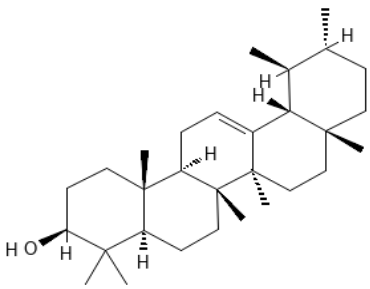


Varespladib **Marimastat**

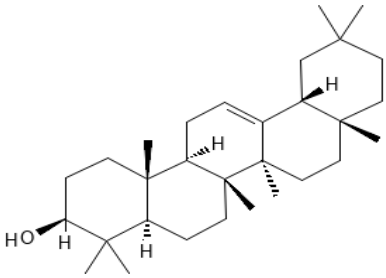
Figure 3: Chemical structures of Varespladib and Marimastat.

Selection of ligands and optimization of the geometry

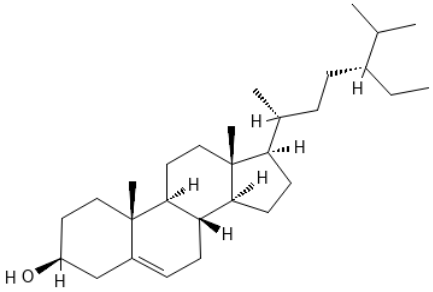
The plant *Wrightia tinctoria* (Figure.1) contains a large number of chemical constituents like steroids, triterpenoids, saponins, tannins, phenols, flavonoids, glycosides, carbohydrates, alkaloids and polyphenols with pharmacological significance.[8] Among them, fourteen reported phytochemical constituents are selected as ligands. The three dimensional (3D) structures of the selected ligands are downloaded from the https://pubchem.ncbi.nlm.nih.gov/ website in the .SDF format and optimized using the Avogadro version 1.2, with Force Field type MMFF94, and saved in .pdb format.[9] The two dimensional (2D) structures of selected ligands are given in Figure.4.



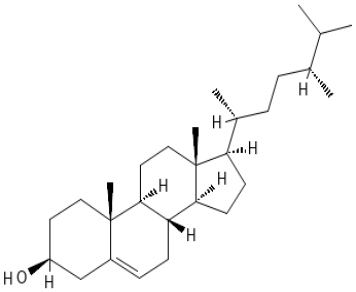
Alpha amyrin



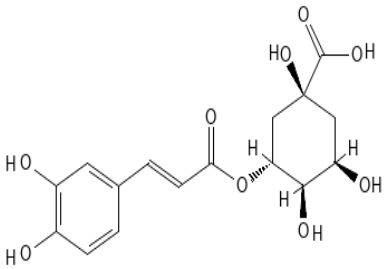
Beta amyrin



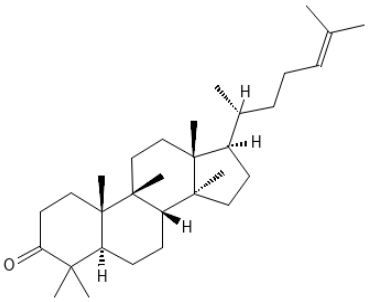
Beta sitosterol



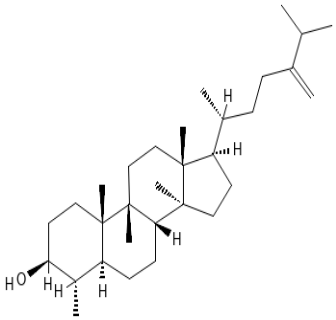
Campesterol



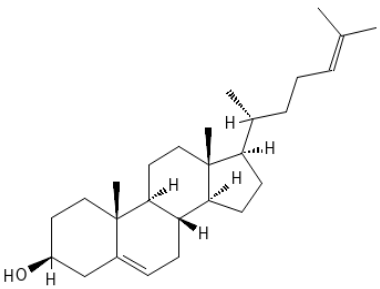
Chlorogenic acid



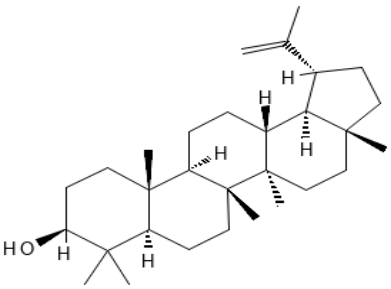
Cycloartenone



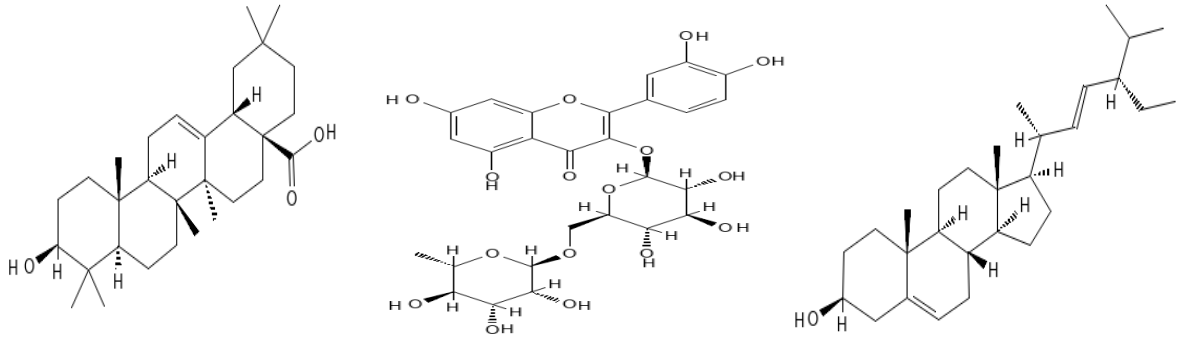
Cycloeucalenol



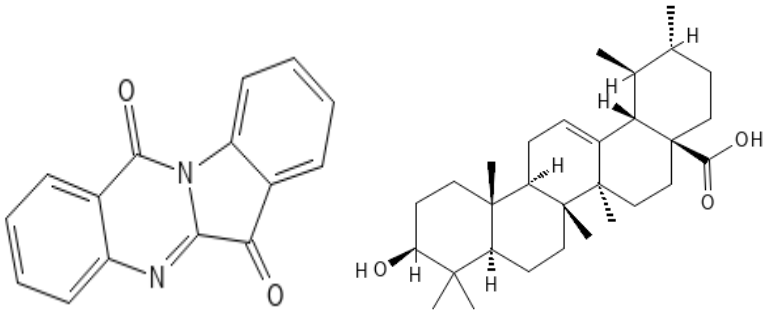
Desmosterol



Lupeol



Oleanolic acid **Ruitin** **stigmasterol**



Tryptanthrin **Ursolic acid**

Figure 4: 2D structures of selected ligands.

Molecular Docking

AutoDock program (version 4.2) was used to perform molecular docking study. All water molecules, heteroatoms, ligand, co-crystallized solvent and inhibitors are removed from the target protein 6Q42 and 2E3X. Polar hydrogens and partial charges were added to the target 6Q42 and 2E3X using Autodock tools (ADT) version 1.5.6.[10] The binding site region of target proteins 6Q42 and 2E3X are identified using PRANK Web 4.[11] Grid box was generated in such a way that covers the entire binding site region using suitable X, Y, Z coordinates and the binding affinity was calculated using AutoDock 4.2. The docking score of selected ligands with the target phospholipase A_2 (6Q42) and metalloproteases (2E3X) are listed in Table.1 and Table.2 respectively.

Table 1: Summary of the molecular docking studies of the selected ligands against phospholipase A2 (PDB: 6Q42).

Name	Estimated Free Energy of Binding (Kcal/mol)	Estimated Inhibition Constant (Ki)	Van der waals, Hydrogen bonding and desolvation enery Energy (Kcal/mol)	Total Intermolecular Energy (kcal/mol)
Varespladib (Standard)	-8.54	548.94 nM	-10.24	-11.23
Alpha amyrin	-8.73	396.04 nM	-8.96	-9.03
Beta amyrin	-8.71	412.88 nM	-9.02	-9.01
Beta sitosterol	-8.52	569.85 nM	-10.63	-10.61
Campesterol	-9.01	246.92 nM	-10.79	-10.80
Chlorogenic acid	-7.73	2.17 uM	-7.18	-11.01
Cycloartenone	-8.89	302.60 nM	-10.16	-10.09
Cycloeucalenol	-8.90	301.87 nM	-10.70	-10.68
Desmosterol	-8.69	426.70 nM	-10.18	-10.18
Lupeol	-8.20	968.84 nM	-8.76	-8.80
Oleanolic acid	-9.14	200.80 nM	-5.06	-10.03
Ruitin	-5.86	50.29 uM	-10.32	-10.64
Stigmasterol	-9.54	101.81 nM	-11.29	-11.33
Tryptanthrin	-7.65	2.46 uM	-7.57	-7.65
Ursolic acid	-9.16	192.60nM	-5.66	-10.06

Table 2: Summary of the molecular docking studies of the selected ligands against metalloproteases (PDB: 2E3X).

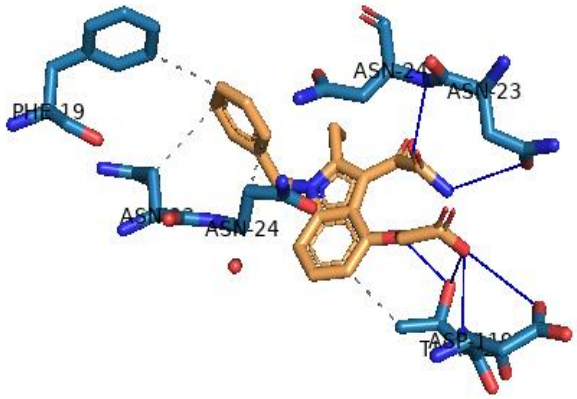
Name	Estimated Free Energy of Binding (Kcal/mol)	Estimated Inhibition Constant (Ki)	Van der waals, Hydrogen bonding and desolvation enery Energy (Kcal/mol)	Total Intermolecular Energy (kcal/mol)
Marimastat (Standard)	-6.09	34.48 uM	-8.45	-9.07
Alpha amyrin	-10.64	15.86 nM	-10.49	-10.94
Beta amyrin	-10.67	15.06 nM	-11.01	-10.97
Beta sitosterol	-10.39	24.41 nM	-12.39	-12.47
Campesterol	-10.20	33.38 nM	-11.91	-11.99
Chlorogenic acid	-9.77	69.49 nM	-7.32	-13.05
Cycloartenone	-10.53	19.21 nM	-11.74	-11.72
Cycloeucalenol	-10.45	21.98 nM	-12.18	-12.24
Desmosterol	-9.93	52.23 nM	-11.42	-11.43
Lupeol	-10.30	28.37 nM	-10.79	-10.89
Oleanolic acid	-13.18	218.45 pM	-9.87	-14.07
Ruitin	-6.01	39.30 uM	-9.98	-10.78
Stigmasterol	-10.24	30.94 nM	-12.03	-12.03
Tryptanthrin	-7.55	2.94 uM	-7.55	-7.55
Ursolic acid	-13.94	60.15 pM	-10.07	-14.84

Analysis of ligand interaction with amino acid residues of target phospholipase A_2 (6Q42) and metalloproteases (2E3X) done by using PLIP (Protein-Ligand interaction profiler) Web tool.[12] The summary of ligand interaction with aminoacid residues of phospholipase A_2 (6Q42) and metalloproteases (2E3X) are listed in Table.3 and Table.4 respectively. The detailed view of interaction of five top scored ligands between phospholipase A_2 (6Q42) and metalloproteases (2E3X) are illustrated in Figure.5 and Figure.6.

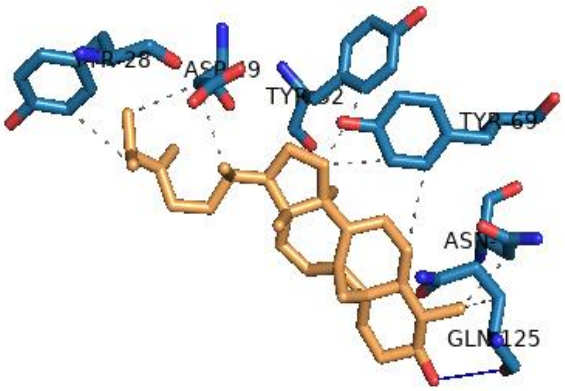
Table 3: Summary of ligand interaction with amino acid residues of target phospholipase A2 (PDB: 6Q42).

Name	Hydrophobic bonds	Distance (Å)	Hydrogen bonds	Distance (Å)	Salt Bridge	Distance (Å)
Varespladib (Standard)	PHE19B, ASN23B, ASN24B, THR120B	3.19, 3.8, 3.59, 3.07	ASN23A, ASN24A, ASP119B, THR120B, THR120B, THR120B	3.05, 2.29, 3.01, 2.1, 2.39, 2.0	-	-
Alpha amyrin	LEU31B, ASP49B, TYR52B, TYR69B	3.25, 3.35, 3.03, 3.34	ASN50B	1.92	-	-
Beta amyrin	TYR52B, LYS56B, ASP66B, PRO68B, TYR69B	3.15, 3.61, 3.49, 3.9, 3.19	-	-	-	-
Beta sitosterol	LEU31B, TYR52B, LYS56B, PRO68B, TYR69B	3.34, 3.37, 3.74, 3.86, 3.22	SER126A	3.36	-	-
Campesterol	-	-	-	-	-	-
Chlorogenic acid	PHE19B, PHE19B, PHE19B, LEU118A, ASP119A	3.25, 3.32, 3.97, 3.52, 3.34	ARG6B, ASP17B, ASP17B, PHE19B, LYS116A, LYS116A	2.45, 3.48, 2.47, 2.33, 2.34, 1.84	ARG6B, LYS122A, LYS122A	4.55, 3.36, 3.59
Cycloartenone	TYR28B, GLN46B, ASP49B, ASP49B, TYR52B, ASP53B, LYS56B, ASN67B,	3.17 , 3.77 3.18, 3.46, 3.92, 3.42, 3.41, 3.85, 3.64	-	-	-	-

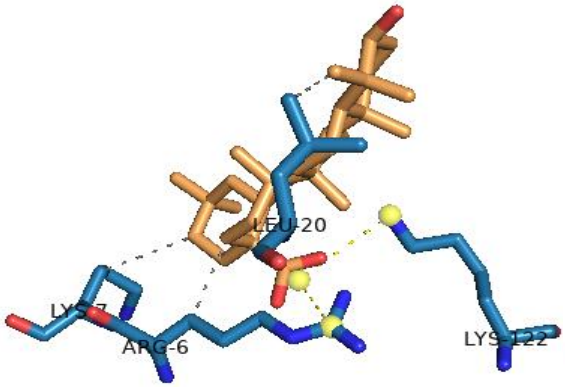
	PRO68B					
Cycloeucalenol	TYR28B, ASP49B, ASP49B, TYR52B, ASN67B, TYR69B, TYR69B, GLN125A,	3.34, 3.26, 3.32, 3.6, 3.35, 3.18, 3.63, 3.39,	GLN125A	3.55	-	-
Desmosterol	TYR28B, LEU31B, ASP49B, TYR52B, TYR52B, ASP53B, PRO68B, TYR69B, TYR69B,	3.39, 3.83, 3.19, 2.95, 3.43, 3.36, 3.46, 3.23, 3.83,	GLN125A	3.29	-	-
Lupeol	TYR52B, LYS56B, ASP66B, ASN67B, TYR69B	3.88, 3.15, 3.98, 3.35, 3.14	ASP49B	2.13	-	-
Oleanolic acid	ARG6B, LYS7B, LEU20B	3.22, 3.97, 3.22	-	-	ARG6B, LYS122 A	3.7, 3.92
Ruitin	LEU31B, LEU31B, LEU31B, TYR52B, LYS56B, PRO68B	3.71, 2.97, 3.94, 3.93, 3.19, 3.86	LEU31A, GLY32B, GLY33A, GLY33B, GLY33B, GLY33B, TYR69B, TYR69B, GLN125A,	2.01, 1.99, 2.7, 2.21, 3.65, 2.48, 2.18, 1.7, 1.96	-	-
Stigmasterol	ASN24B, LEU31B, THR120B, THR120B	3.34, 3.47, 3.48, 3.63	GLY26B, LEU118B	1.88, 2.43	-	-
Tryptanthrin	-	-	GLY33A	1.78	-	-
Ursolic acid	TRP3B, ARG6B, PHE19B, LEU20B	3.41, 3.29, 3.43, 3.2	-	-	ARG6B, LYS122 A	3.82, 3.76



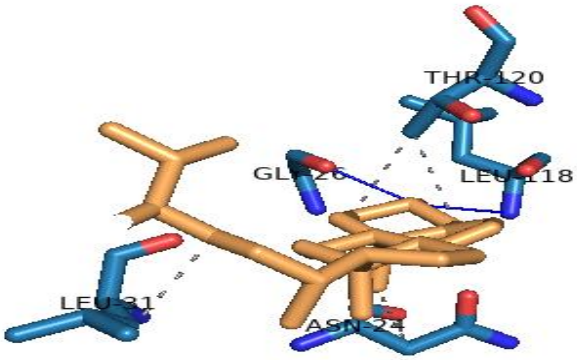
Varespladib (Standard)



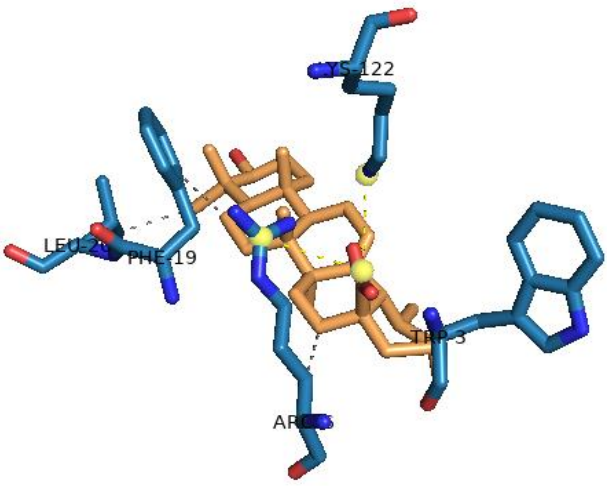
Cycloeucalenol



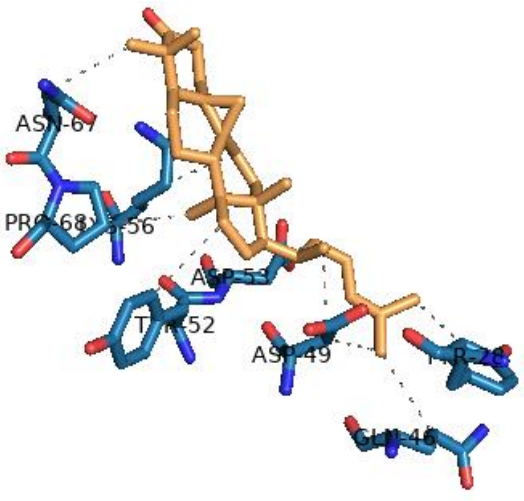
Oleanolic acid



Stigmasterol



Ursolic acid



Cycloartenone

Figure 5: 3D images of five top scored ligands with phospholipase A_2 (6Q42).

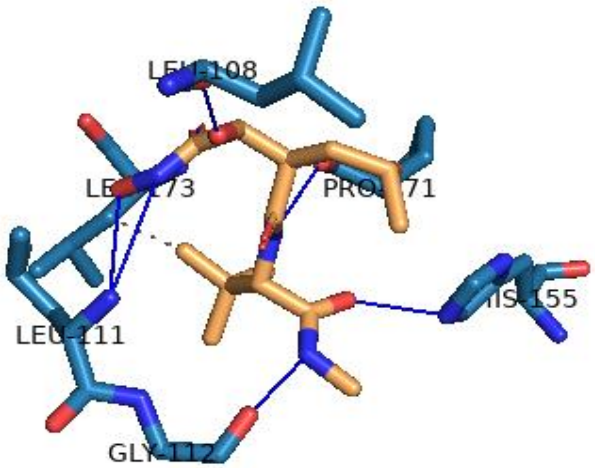
----- Hydrophobic bond -----Hydrogen bond -------Salt bridge interactions

Table 4: Summary of ligand interaction with amino acid residues of target metalloproteases (PDB: 2E3X).

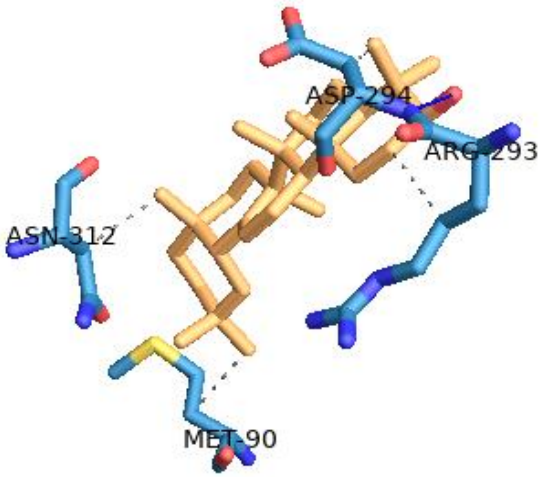
Name	Hydrophobic bonds	Distance (Å)	Hydrogen bonds	Distance (Å)	Salt Bridge	Distance (Å)
Marimastat (Standard)	LEU173A	3.46	LEU108A, LEU111A,LEU111A, GLY112A, HIS155A, PRO171A, LEU173A	2.07, 3.11, 3.29,2.11, 1.91, 2.24, 3.14	-	-
Alpha amyrin	ASP96A, PHE202A, ASN203A, ARG275A, LEU296A, LEU296A, ASN312A	3.73, 3.38, 3.9, 3.24, 3.36, 3.34, 3.04	ASN203A	2.11	-	-
Beta amyrin	MET90A, ARG293A, ASP294A, ASN312A	3.55, 3.82, 2.84, 3.52	ASP294A	2.27	-	-
Betasitosterol	ASP294A, LEU296A, LEU296A	3.58, 3.02, 3.27	HIS95A, HIS95A, HIS95A	2.23, 2.4, 2.08	-	-
Campesterol	ILE113A, ILE113A, VAL141A, ILE142A, ILE142A, HIS145A, LEU173A, MET390A	3.17, 3.25, 3.79, 3.72, 3.4, 3.62, 3.23, 3.84	MET390A	1.96	-	-
Chlorogenic acid	LYS199A	3.12	CYS120A, ASN203A, ASP294A, ASP294A, ASP314A	2.81, 2.2, 1.96, 1.97, 3.5	LYS199A, ARG275A	4.77, 2.59
Cycloartenone	ASN109A, THR110A, LEU111A, LEU111A, ILE113A, THR114A, HIS149A, VAL172A, LEU173A	3.84, 3.68, 3.83, 3.28, 3.36, 3.78, 3.65, 3.78, 3.35	-	-	-	-
Cycloeucalenol	THR110A,LEU	3.86, 3.81,	THR114A	1.83	-	-

	111A, LEU111A, LEU111A, ILE142A, HIS145A, LEU173A, LEU173A	3.49, 3.84, 3.33, 3.53, 3.14, 3.59				
Desmosterol	TYR311A, TYR311A	3.11, 3.25	PRO399A	2.49	-	-
Lupeol	LYS10A, LYS10A, PHE12A, PHE202A, PHE202A, PRO204A, TRP221A, TRP221A, LEU257A, LEU257A, GLU290A	3.02, 3.66, 3.01, 3.81, 2.99, 3.26, 3.78, 3.51, 2.78, 3.49, 2.9	GLU290A, CYS291A, CYS291A	3.56, 2.14, 2.23	-	-
Oleanolic acid	ILE142A, VAL172A, LEU173A	3.18, 3.23, 3.85	ASN109A, PRO171A	2.36, 1.97	HIS145A, HIS155A	4.72, 3.74
Ruitin	-	-	CYS120A, CYS120A, CYS120A, CYS120A, GLN121A, SER125A, LYS199A, LYS199A, CYS200A, ARG293A, ASN312A, ASP314A, ASP314A	2.29, 2.27, 1.7, 2.08, 3.09, 2.95, 1.84, 3.26, 2.57, 3.42, 2.69, 3.34, 2.51	-	-
Stigmasterol	ASN9A, LYS10A, LYS10A, PHE12A, PHE12A, PHE202A, PRO204A, PRO204A, PRO204A, ILE210A, ILE220A, TRP221A, TRP221A,	3.63, 3.48, 3.6, 3.54, 4, 3.71, 3.06, 3.12, 3.47, 3.35, 3.17, 3.4, 3.18, 3.62, 3.9	ASN9A	2.1	-	-

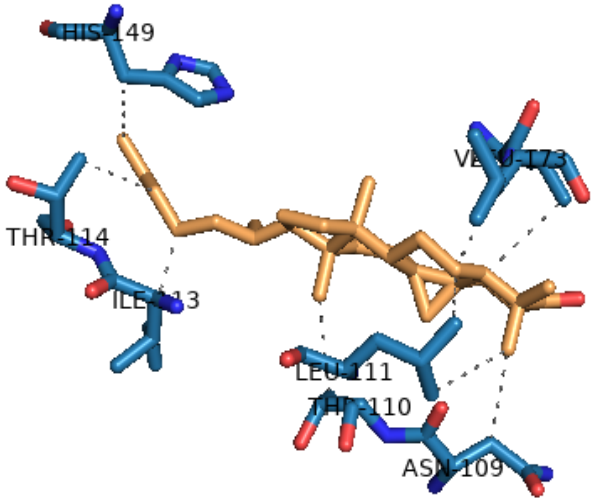
	ASN255A, LEU257A					
Tryptanthrin	PRO204A, TRP221A, ASN255A, GLU290A	3.75, 3.25, 3.18, 3.33	TRP221A, LEU257A, GLU290A	2.81, 2.77, 2.53	-	-
Ursolic acid	ILE57A, ASN203A, PRO205A, ASP209A	3.17, 3.55, 3.37, 3.03	LYS199A, ASP209A	1.99, 2.53	ARG293 A	3.68



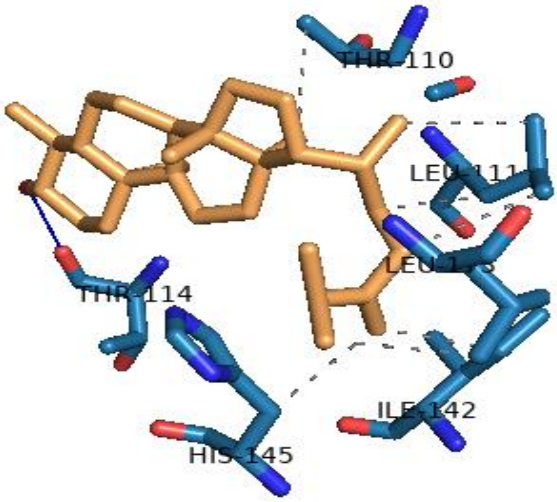
Marimastat (Standard)



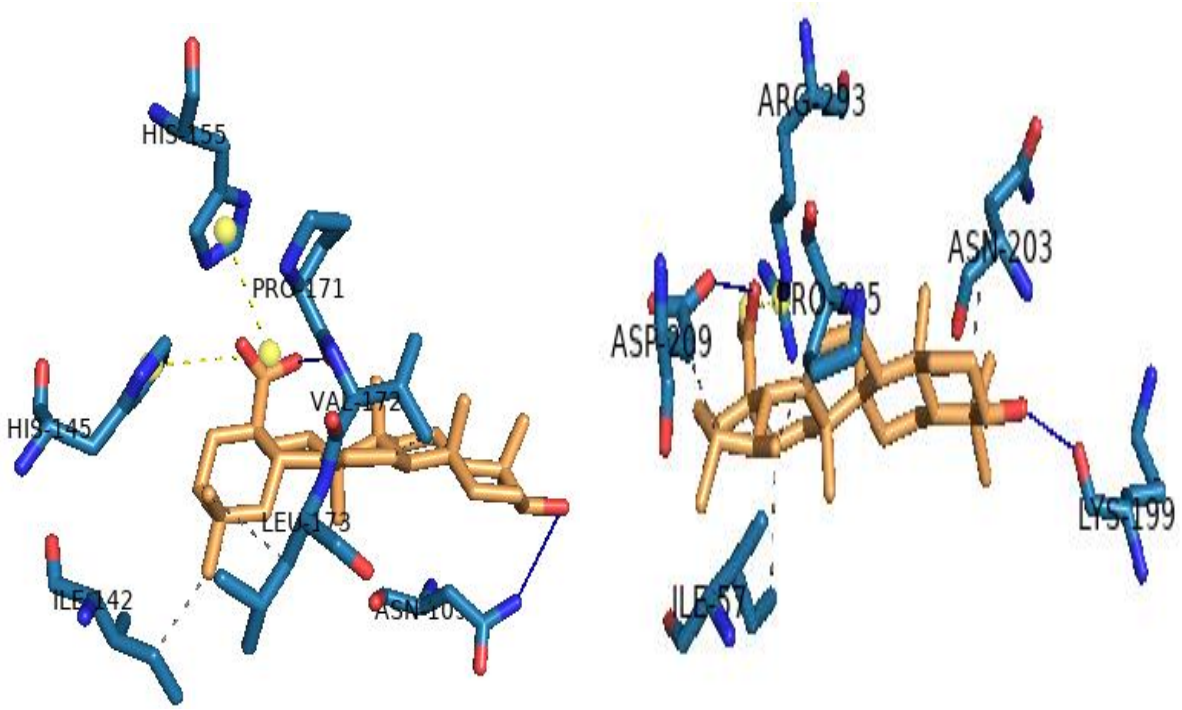
Beta amyrin



Cycloartenone



Cycloeucalenol



Oleanolic acid **Ursolic acid**

Figure.6: 3D images of five top scored ligands with metalloproteases (2E3X).

----- Hydrophobic bond -----Hydrogen bond -------Salt bridge interactions

Drug - likeness and Bioavailability score of selected Ligands

Drug - likeness assessment is very important due to the fact that many herbal drugs are administered via the oral route. Lipinski's rule of five clearly provides information about the oral bioavailablity of the drug using physiochemical parameters like molecular weight (≤ 500), number of hydrogen bond donors (≤ 5), octanol/water partition coefficient (LogP≤ 5) and number of hydrogen bond acceptors (≤ 10).[13] Based on this rule, for a drug molecule to be orally bioavailable, it must not violate more than one of aforesaid parameters. The number of violation of Lipinski's rule and oral bioavailablity (BA) score were predicted using SWISS ADME online tool and the results are given in the table.5.[14]

Table 5: Bioavilablity (BA) scores of selected ligands.

Name	Number of violation on Lipinski rule of five	Fraction Csp3	MW (g/mol)	TPSA (Å^2)	XLOGP3	Number of Rotatable bonds	BA score
Varespladib (Standard)	0	0.19	380.39	111.62	2.75	8	0.56
Marimastat (Stamdard)	0	0.80	331.41	127.76	0.51	11	0.55
Alpha amyrin	1	0.93	426.72	20.23	9.01	0	0.55
Beta amyrin	1	0.93	426.72	20.23	9.15	0	0.55
Beta sitosterol	1	0.93	414.71	20.23	9.34	6	0.55
Campesterol	1	0.93	400.68	20.23	8.80	5	0.55
Chlorogenic acid	1	0.38	354.31	164.75	-0.42	5	0.11
Cycloartenone	1	0.90	424.70	17.07	9.46	4	0.55
Cycloeucalenol	1	0.93	426.72	20.23	9.91	5	0.55
Desmosterol	1	0.85	384.64	20.23	8.27	4	0.55
Lupeol	1	0.93	426.72	20.23	9.87	1	0.55
Oleanolic acid	1	0.90	456.70	57.53	7.49	1	0.85
Ruitin	3	0.44	610.52	269.43	-0.33	6	0.17
Stigmasterol	1	0.86	412.69	20.23	8.56	5	0.55
Tryptanthrin	0	0.00	248.24	51.96	2.05	0	0.55
Ursolic acid	1	0.90	456.70	57.53	7.34	1	0.85

RESULTS AND DISCUSSION

Based on the outcome of docking analysis, out of fourteen selected bioactive compounds, except ruitin, all the compounds showed very good binding energy towards the target protein phospholipase A_2 (6Q42) and metalloproteases (2E3X). Except chlorogenic acid, ruitin and tryptanthrin, all other ligands showed about similar and more negative binding energy towards the target phospholipase A_2 (6Q42) than the positive control varespladib (-8.54 kcal/mol). In case of the target metalloproteases (2E3X), other than ruitin, all the selected ligands showed more negative binding energy than the positive control marimastat (-6.09 kcal/mol). The aforesaid results clearly indicate that most of the selected ligands form strong and stable complex with the target protein phospholipase A_2 (6Q42) and metalloproteases (2E3X). The ligand ursolic acid scored more negative binding energy -9.16 kcal/mol, -13.94 kcal/mol towards phospholipase A_2 (6Q42) and metalloproteases (2E3X) respectively. Moreover, The bioavailablity score of selected ligand clearly reveals that, all the ligands have ideal oral bioavilablity based on theoretical foundation except ruitin and chlorogenic acid. The ligand ursolic acid and oleanolic acid showed higher bioavailablity score of 0.85 than the positive control varespladib (0.56) and marimastat (0.55).

CONCLUSION

This study employed an in silico approach to assess bioactive compounds from *Wrightia tinctoria* (Roxb.) R.Br. as potential antivenom agents. To our best knowledge, we are reporting first the antivenom potential of bioactive compounds from this species using molecular docking analysis. The results suggest that the plant *Wrightia tinctoria* (Roxb.) R.Br. have many bioactive molecules with antivenom potential based on molecular docking. The Phytoconstituent ursolic acid is predicted to exhibit stable and high affinity interaction with key venom proteins. Further in vitro and in vivo evaluations are required to confirm the therapeutic efficacy. The outcome of the present study will provide new opportunities to allopathic and other alternative system of medicines for creating innovative treatments of venomous bites.

REFERENCES

1. Guilherme H M Salvador, Antoniel A S Gomes, Wendy Bryan Quiros, Julian fernandez, Matthew R Lewin, Jose María Gutierrez, Bruno Lomonte, Marcos R M fonts. Structural basis for phospholipase A-like toxin inhibition by the synthetic compound Varespladib (LY315920). Sci. Rep, 2019; 9: 17203.
2. Adewunmi Rofiat Funmilola, Gidado Abubakar, Zanna Hassan. Molecular Docking in Drug Discovery: A Review on Anti-snake Venom Development. International Journal of Biochemistry Research & Review, 2020; 29(3): 42-49.
3. Karthik Nagarajan S, Siva Annamalai, Bharath Christian CBS, Rajamaheswari K, Lavanya A, Arunachalam K. Molecular docking analysis of bioactive molecules from herbs with snakevenom phospholipase A2. Bioinformation, 2025; 21(3): 290-296.
4. Sangeetha S, Akhil Hari, Sijo Pattam, Nihal P, Athira A. An Updated Review on Wrightia tinctoria (Roxb). R Br. Journal of Pharmaceutical Research International, 2021; 33(56A): 234-244.
5. VivekSrivastava, SatyaPrakash Gupta, Mohd. Imran Siddiqi, BhartenduNath Mishra. Molecular docking studies on quinazolineantifolate derivatives as human thymidylate synthase inhibitors. Bioinformation, 2010; 4(8): 357-365.
6. Theo Tasoulis, Geoffrey K. Isbister. A Review and Database of Snake Venom Proteomes. Toxins, 2017; 9(9): 290.
7. Anandie le Roux, Stephanus J. Cloete, Jacobus P. Petzer, An´el Petzer. In vitro inhibition of snake venom toxins by varespladib, marimastat, nafamostat and dimercaprol. Toxicon, 2025; 268: 108626.

8. Battu Ganga Rao, Dodda L N Rajeswari, Devarakonda Ramadevi, Battu Heera. Phytochemical and pharmacological studies on wrightia tinctoria. World journal of pharmacy and Pharmaceutical sciences, 2018; 7(4): 562-585.
9. Hanwell MD, Curtis DE, Lonie DC, Vandermeersch T, Zurek E, Hutchison GR. Avogadro: an advanced semantic chemical editor, visualization, and analysis platform. J Cheminform, 2012; 4: 17.
10. Morris GM, Huey R, Lindstrom W, Sanner MF, Belew RK, Goodsell DS, Olson AJ. Autodock4 and AutoDock Tools4: automated docking with selective receptor flexiblity. J. Computational Chemistry, 2009; 30(16): 2785–2791.
11. Lukas Polak, Petr Skoda, Kamila Riedlova, Radoslav Krivak, Marian Novotny, David Hoksza. PrankWeb 4: a modular web server for protein–ligand binding site prediction and downstream analysis. Nucleic Acids Research, 2025; 53(W1): W466–W471.
12. Philipp Schake, Sarah Naomi Bolz, Katja Linnemann, Michael Schroeder. PLIP 2025: introducing protein–protein interactions to the protein–ligand interaction profiler. Nucleic Acids Research, 2025; 53: W463–W465.
13. Lipinski C.A. Lead and drug-likeness compounds: the rule of five revolution. Drug Discov Today Technol, 2004; 1(4): 337–341.
14. Antoine Daina, Olivier Michielin, Vincent Zoete. SwissADME: a free web tool to evaluate pharmacokinetics, drug-likeness and medicinal chemistry friendliness of small molecules. Sci. Rep, 2017; 7: 42717.