



International Journal of Veterinary Sciences and Animal Husbandry



ISSN: 2456-2912

NAAS Rating (2026): 4.61

VET 2026; 11(1): 80-87

© 2026 VET

www.veterinarypaper.com

Received: 08-10-2025

Accepted: 18-11-2025

Silamparasan M

Pharmaceutical Division,
Institute of Veterinary
Preventive Medicine, Ranipet,
Tamil Nadu, India

Babu Prasath N

Department of Veterinary
Pathology, Veterinary College &
Research Institute, Tirunelveli,
Tamil Nadu, India

Ramamoorthy M

Veterinary Dispensary,
Athangudi, Sivaganga, Tamil
Nadu, India

Corresponding Author:

Silamparasan M

Pharmaceutical Division,
Institute of Veterinary
Preventive Medicine, Ranipet,
Tamil Nadu, India

Homology modeling and docking analysis of phytochemicals of *Catharanthus roseus* and *Vernonia amygdalina* against *Ancylostoma caninum* metalloprotease-2

Silamparasan M, Babu Prasath N and Ramamoorthy M

DOI: <https://www.doi.org/10.22271/veterinary.2026.v11.i1b.2923>

Abstract

The available anthelmintic medications are ineffective against many helminths of veterinary importance and controlling such resistant parasites is challenging. In this study, we focused *Ancylostoma caninum*'s anthelmintic resistance and targeted its metalloprotease-2 (Ac-MTP-2). *A. caninum* is a canine hookworm that infects dogs, cats, and also humans. The phytochemicals of common plants, *Catharanthus roseus* (Periwinkle) and *Vernonia amygdalina* (Bitter leaf) were evaluated for their anthelmintic potential against Ac-MTP-2. The application of Computer-aided drug discovery fastens the traditional drug discovery process and facilitates the prompt finding of newer lead molecules. The docking study performed showed that ajmalicine (-9.4 kcal/mol), serpentine (-9.2 kcal/mol), raubasins (-9.12 kcal/mol), vernolide (-8.09 kcal/mol), and hydroxyvernolide (-8.04 kcal/mol) had the lowest binding of all the molecules. The present study suggests a few promising *in silico* anthelmintic actions of a few phytochemicals. The ability of these compounds to act as an anthelmintic drug is to be evaluated further by *in vitro* and *in vivo* studies.

Keywords: Anthelmintic resistance, Homology modelling, Molecular docking, Metalloprotease, Phytochemicals

Introduction

The economically important canine hookworm, *Ancylostoma caninum* Ercolani, 1859 is a parasite of veterinary and public health problems, especially in developing countries that causes ancylostomiasis in many mammals (Lee *et al.*, 2022; Bowman, *et al.*, 2010) [10, 3]. The adult *A. caninum* also infects humans and causes eosinophilic enteritis (Tsuji, 2020; Prociv and Croese, 1996) [18, 15]. The anthelmintic drugs Albendazole, fenbendazole, febantel, moxidectin, ivermectin, pyrantel pamoate, and milbemycin oxime are that have been approved for the treatment of *A. caninum* infection (Aziz *et al.*, 2020; Reinemeyer, 2016) [1, 16]. The occurrence of multiple drug resistance to benzimidazoles, macrocyclic lactones, and pyrantel in *A. caninum* was shown (Jimenez *et al.*, 2019) [8]. The reports of multiple anthelmintic drug-resistant are numerous (Castro *et al.*, 2023; Leutenegger *et al.*, 2023; Venkatesan, *et al.*, 2023; Marsh and Lakritz, 2023) [4, 11, 13, 19].

The direct life cycle having *A. caninum* secreted/excreted many proteins, during their establishment in the host. The excretory/secretory proteins of the helminths participate in a variety of functions including host penetration, tissue invasion, immune evasion, reproduction, and feeding (Williamson *et al.*, 2006; Haffner *et al.*, 1998; Karanu *et al.*, 1993) [21, 7, 9]. These proteins are important antigens for the development of new therapeutic or vaccine targets. Adult *A. caninum* secrete a unique metalloprotease that resembles astacin called Ac-MTP-2 which is identified only in hookworms. Ac-MTP-2 is localized in the oesophageal gland and uterus of the parasite and is found involved in the parasite attachment and digestion of the mucosa of the gastrointestinal tract, nourishment, and reproduction. The role of the Ac-MTP-2 is suggestive of the possibility of them being therapeutic or vaccine candidate (Feng *et al.*

2007) [5]. Many drugs were developed either directly or indirectly from plants, making plants a key source of new pharmacologically active molecules (Veeresham, 2012) [12]. The various tools of computer-aided drug design (CADD) facilitate the identification of newer lead from a great number of phytochemicals available in commonly available plants. In the present study, the phytochemicals of *Catharanthus roseus* (Periwinkle) and *Vernonia amygdalina* (Bitter leaf) were explored for their *in silico* anthelmintic potential against *Ancylostoma caninum* by molecular docking.

Materials and Methods

Homology modelling and preparation of the three-

dimensional structure of *Ancylostoma caninum* protein for docking: The amino acid sequence of *A. caninum* acstatin-like metalloprotease 2 (Ac-MTP-2) (Accession number: ABG49116.1) was obtained from NCBI. The three-dimensional model of Ac-MTP-2 (Figure-01) was built in server SWISS-MODEL using *Ancylostoma caninum* metalloendopeptidase with a sequence identity of 77.68% as a template. The built model was refined in a web server GalaxyRefine. The refined model was then validated in the SAVESv6.0 server. The validated model was then prepared in AutoDock Tools 1.5.6 by the addition of polar hydrogens, Kollman charges, and AD4-type atoms. The protein models were visualized in UCSF Chimera 1.16.

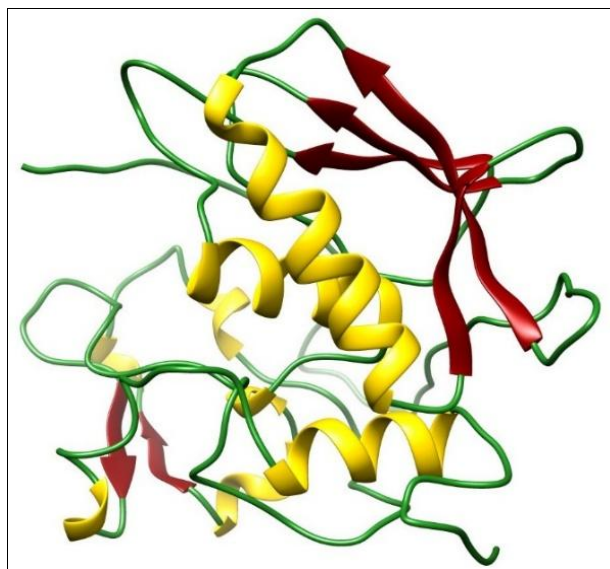


Fig 1: Three-dimensional model of *Ancylostoma caninum* metalloprotease-2 homology-modeled in SWISS-MODEL server. Alpha-helices are depicted in yellow color, beta sheets in dark red color, and loops in dark green color.

Selection and preparation of ligands for molecular docking:

The phytochemicals of *Catharanthus roseus* and

Vernonia amygdalina obtained through a literature search are given in Table 1.

Table 1: Phytochemicals present in *Catharanthus roseus* and *Vernonia amygdalina*

Plant names	Phytochemicals
<i>Catharanthus roseus</i> ²⁵ (Periwinkle)	Vindesin, Vindeline tabersonine, Vinblastine, Vincristine, Raubasin, Reserpine, Vincamine, Catharanthine, Vineamine, Ajmalicine, Vinene, Vinca leukoblastine, Vintsine, Leurosine, Vinomine, Vinoxine, Ibogaine, Vindolidine, Vindoline, Vindolicine, Yohimbine, Lochnerine, Serpentine, Tabersonine, Harhammericine, Echitovenine, Tricin, Vingramine, Methylvingramine
<i>Vernonia amygdalina</i> ²⁶ (Bitter leaf)	Vernodalinalol, Vernolepin, Vernomygdin, Hydroxyvernolide, Vernolide, Vernodalol, 11, 13 - Dihydrovernodalinal, Vernodalinal, Vernomenin, Epiverodalol, Vernonioside

The evaluation of the physicochemical properties, druglikeness (Lipinski, Veber, and Egan rules), lipophilicity, solubility, gastrointestinal absorption, and bioavailability score of the ligands are important before it is selected as a drug molecule. The canonical SMILES of the obtained phytochemicals (ligands) were available in the PubChem server and were submitted to the Swiss ADME server to select the ligands for docking. *In silico* toxicity of the ligands was predicted in the ProTox-II server. The three-dimensional structure of the ligands was obtained from the PubChem server. The selected phytochemicals (ligands) were prepared in AutoDock Tools 1.5.6 for docking.

In silico molecular docking and analysis of the docking results

The docking of the prepared Ac-MTP-2 and ligands were carried out in AutoDock tools 1.5.6 to know the active site

where the ligands are binding to the protein. Using AutoGrid4 and AutoDock4, the grid box was set around the entire protein to perform blind docking. The dimension of the grid box was 126 x 92 x 126 with a spacing of 0.414 angstroms. The docking was carried out using the Lamarckian genetic algorithm to find the best binding pose of the ligands within the protein. The pose with the lowest binding energy is considered the best pose. The docking results were analyzed in AutoDock Tools 1.5.6, and Biovia discovery studio to view the amino acids of the protein interacting with the ligands. The active site of the protein was predicted in the Computed Atlas of Surface Topography of Proteins (CASTp) server to compare the residues of the protein interacting with the ligands.

Results and Discussion

The quality of the modeled and refined three-dimensional Ac-

MTP-2 protein model was validated in SAVES v6.0 server based on the ERRAT score and Ramachandran plot. The ERRAT score for good-quality protein should be more than 50. The overall quality factor (ERRAT score) of the Ac-MTP-2 protein model was 93.66 (Figure 2a). The Ramachandran

plot was obtained from PROCHECK which showed that 91% of residues were present in the most favored region and none of the residues were present in the disallowed regions (Figure 2b). This shows the higher quality of the modeled protein.

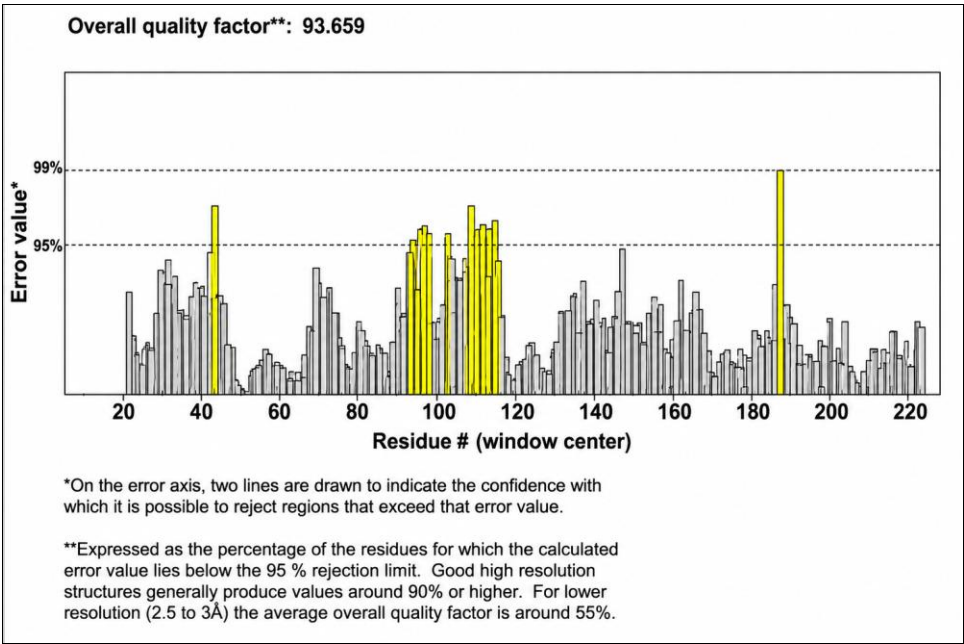


Fig 2a: ERRAT server showing the overall quality factor of *Ancylostoma caninum* metalloprotease-2

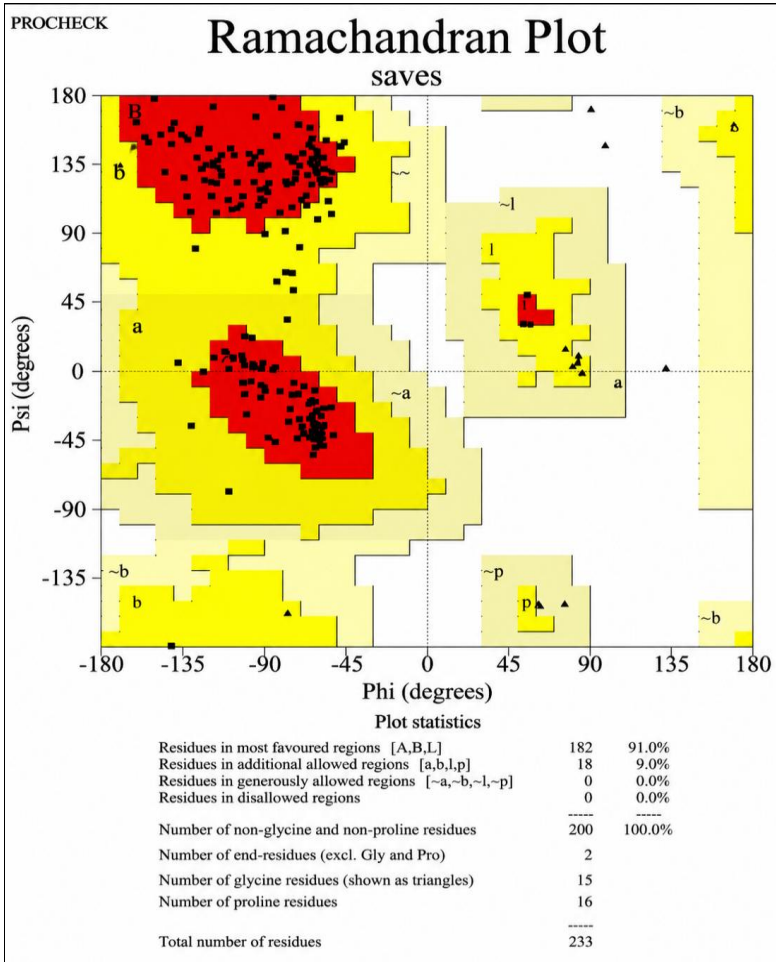


Fig 2b: The Ramachandran plot shows the percentage of residues in the most favored, favored, and disallowed regions.

The area, volume, and residues of the largest active site of the protein predicted in the CASTp server are given in Table-2, Figure-3.

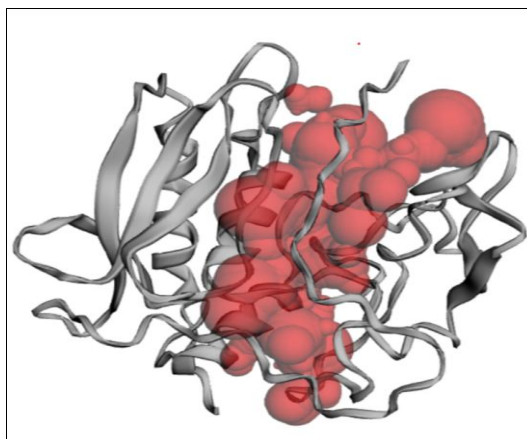


Fig 3: The largest active site of the Ac-MTP-2 predicted in the CAST-p server

Table 2: Area ($\text{\AA}^2$), volume ($\text{\AA}^3$), and residues that form the active site of Ac-MTP-2 predicted in the CASTp server

Area $\text{\AA}^2$	Volume $\text{\AA}^3$	Residues
1320.137	806.506	2 LYS, 3 TYR, 4 PHE, 5 VAL, 6 LEU, 7 CYS, 8 PHE, 9 CYS, 10 ALA, 11 PHE, 12 PHE, 13 VAL, 14 VAL, 21 ASP, 22 LEU, 23 PRO, 24 ARG, 25 ASN, 26 PRO, 27 LEU, 87 GLY, 88 GLU, 89 GLY, 90 THR, 91 GLY, 92 ALA, 93 VAL, 94 VAL, 96 LYS, 97 PRO, 102 ILE, 104 LEU, 106 GLU, 110 ILE, 111 LEU, 112 ASN, 113 ASP, 117 ALA, 118 PRO, 121 GLN, 122 THR, 125 LYS, 128 GLY, 129 LEU, 130 PRO, 131 PRO, 132 GLU, 134 ILE, 135 ARG, 136 PRO, 137 GLU, 150 GLU, 151 LYS, 152 GLY, 153 TYR, 155 ALA, 156 PHE, 158 ALA, 160 SER, 161 SER, 162 VAL, 163 LYS, 164 PRO, 165 ASP, 166 PRO, 167 TYR, 175 SER, 176 ILE, 177 MET, 178 HIS, 179 TYR, 180 LYS, 182 ASP, 183 ALA, 184 PHE, 185 ALA, 186 LYS, 187 PRO, 188 GLY, 189 THR, 204 GLY, 206 GLN, 213 ASP, 216 LYS, 220 LYS

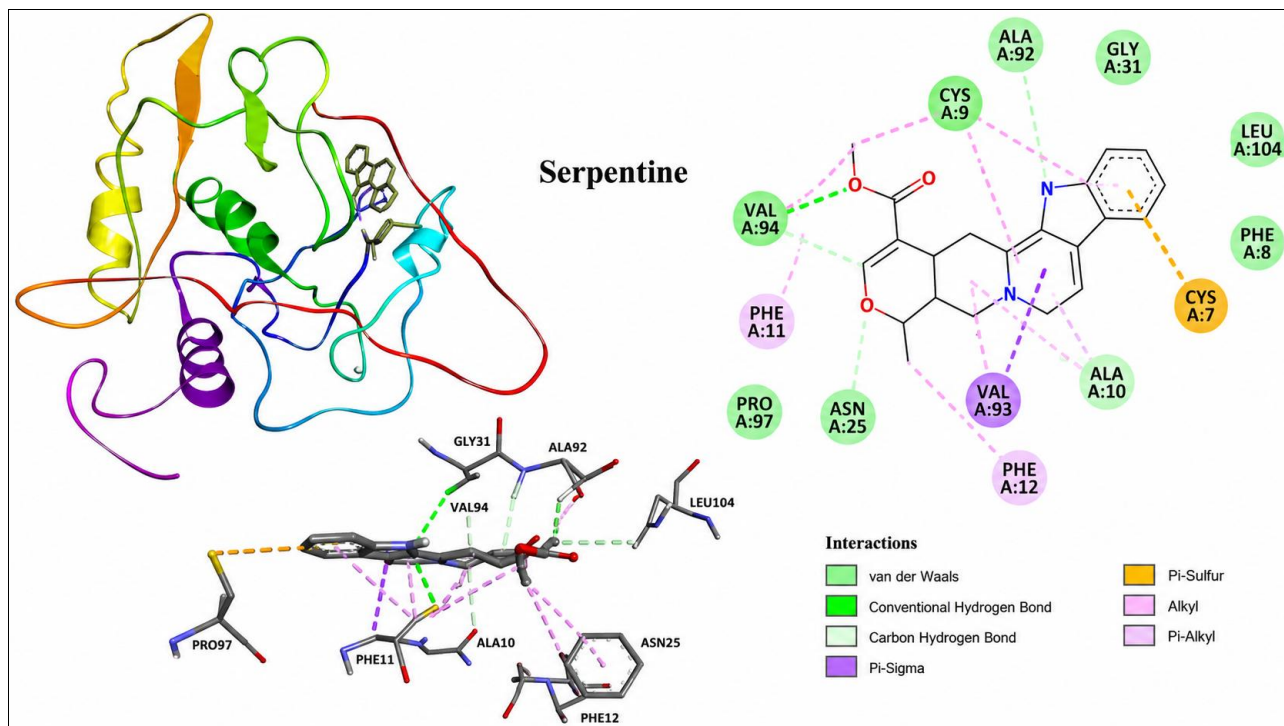
In the SwissADME web server, forty ligands from two commonly available plants, *Catharanthus roseus*, and *Vernonia amygdalina* were evaluated for their pharmacokinetic and pharmacodynamic properties. The evaluation of the drug likeness of the compounds before proceeding with the clinical trials would save money and time for the researchers. The properties of the newer ligands are compared with the already existing drugs in the webserver to predict the compounds that are likely to thrive in all phases of clinical trials. To know the drug likeness of the compounds, Lipinski, Veber, and Egan rules that involve molecular weight, lipophilicity, number of hydrogen bond acceptors and donors, number of rotatable bonds, and topological polar

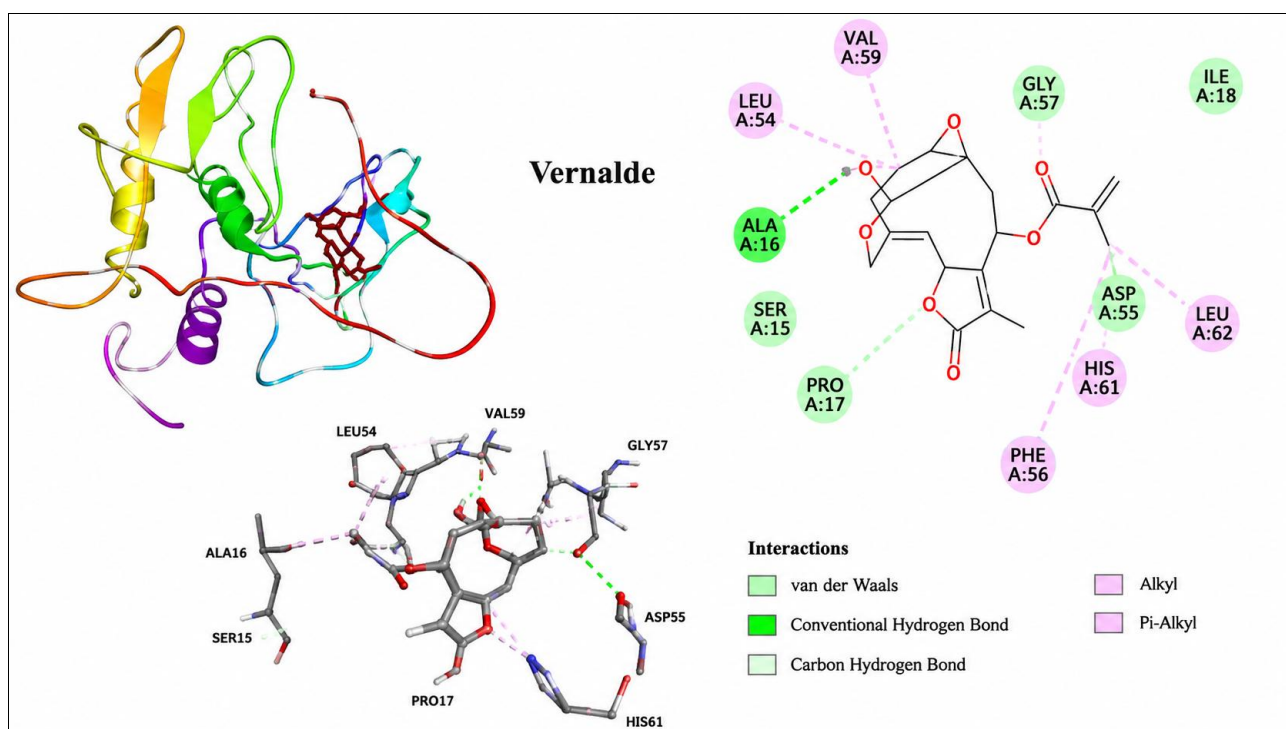
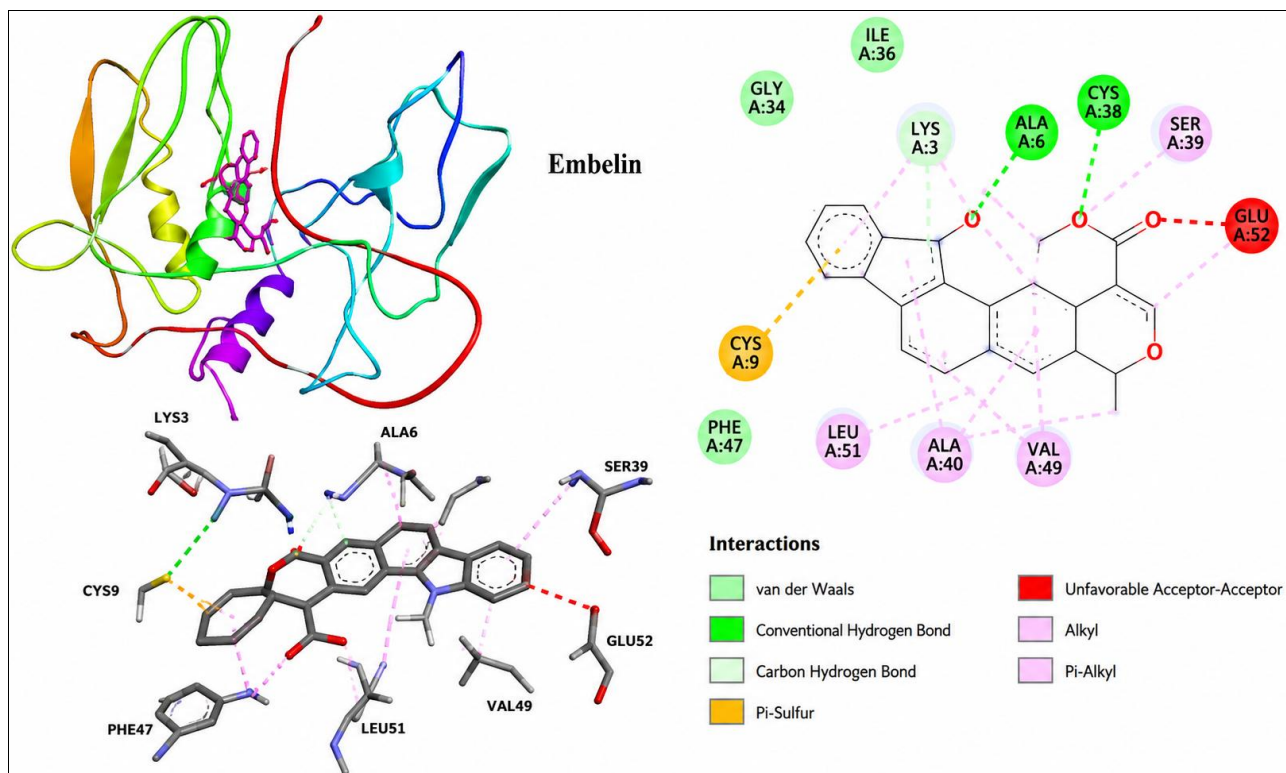
surface area are considered (Lipinski *et al.* 1997) ^[12]. A total of 24 ligands obeyed all three (Lipinski, Veber, and Egan) rules without any violations. All 24 ligands had high gastrointestinal absorption and a bioavailability score of 0.55. The lipophilicity of the compounds contributes to their absorption, distribution, metabolism, and excretion. Lipophilicity is given by LogP and should be between 0 and 5 (Berger *et al.* 2022) ^[2], and in the present study lipophilicity ranged from 0.66. All these compounds were in moderately soluble, soluble, and very soluble classes. These 24 compounds were selected for further docking study. The ADME property of 24 ligands selected for the docking study is given in Table 3.

Table 3: PubChem CID, lipophilicity, solubility, GI absorption, druglikeness, and bioavailability score of the phytochemicals of *Catharanthus roseus* and *Vernonia amygdalina* are given

Ligands	PubChem CID	Lipophilicity	Solubility	GI absorption	Druglikeness			Bioavailability score
					Lipinski	Veber	Egan	
11,13- dihydrovernodalin	23786372	1.75	Soluble	High	Yes	Yes	Yes	0.55
Ajmalicine	441975	2.67	Soluble	High	Yes	Yes	Yes	0.55
Catharanthine	5458190	3.14	Soluble	High	Yes	Yes	Yes	0.55
Echitovenine	443402	2.77	Soluble	High	Yes	Yes	Yes	0.55
Horhammericine	443358	1.60	Soluble	High	Yes	Yes	Yes	0.55
Hydroxyvernolide	5281472	0.66	Very Soluble	High	Yes	Yes	Yes	0.55
Ibogaïne	197060	3.56	Moderately Soluble	High	Yes	Yes	Yes	0.55
Lochnerine	6436184	2.54	Soluble	High	Yes	Yes	Yes	0.55
Raubasin	251561	2.67	Soluble	High	Yes	Yes	Yes	0.55
Serpentine	73391	2.09	Moderately Soluble	High	Yes	Yes	Yes	0.55
Tabersonine	20485	2.98	Moderately Soluble	High	Yes	Yes	Yes	0.55
Tricin	5281702	2.15	Moderately Soluble	High	Yes	Yes	Yes	0.55
Vernodalin	179375	1.47	Very Soluble	High	Yes	Yes	Yes	0.55
Vernodalinalol		0.88	Very Soluble	High	Yes	Yes	Yes	0.55
Vernodalol	442318	1.58	Soluble	High	Yes	Yes	Yes	0.55
Vernolepin	442322	1.25	Very Soluble	High	Yes	Yes	Yes	0.55
Vernolide	5281508	1.52	Soluble	High	Yes	Yes	Yes	0.55
Vernomenin	442324	1.47	Soluble	High	Yes	Yes	Yes	0.55
Vernomygdin	5281509	1.57	Soluble	High	Yes	Yes	Yes	0.55
Vincamine	15376	2.61	Soluble	High	Yes	Yes	Yes	0.55
Vindolidine	261578	1.83	Soluble	High	Yes	Yes	Yes	0.55
Vindoline	260535	1.87	Soluble	High	Yes	Yes	Yes	0.55
Vinoxine	101650351	2.14	Soluble	High	Yes	Yes	Yes	0.55
Yohimbine	8969	2.46	Soluble	High	Yes	Yes	Yes	0.55

ligands with a binding energy of -8.04 and -8.09 kcal/mol, respectively. The selected ligands interacted with the predicted active site residues. The interaction of the selected five ligands with *Ancylostoma caninum* metalloprotease-2 analyzed in Biovia discovery studio is given in Figure 4.





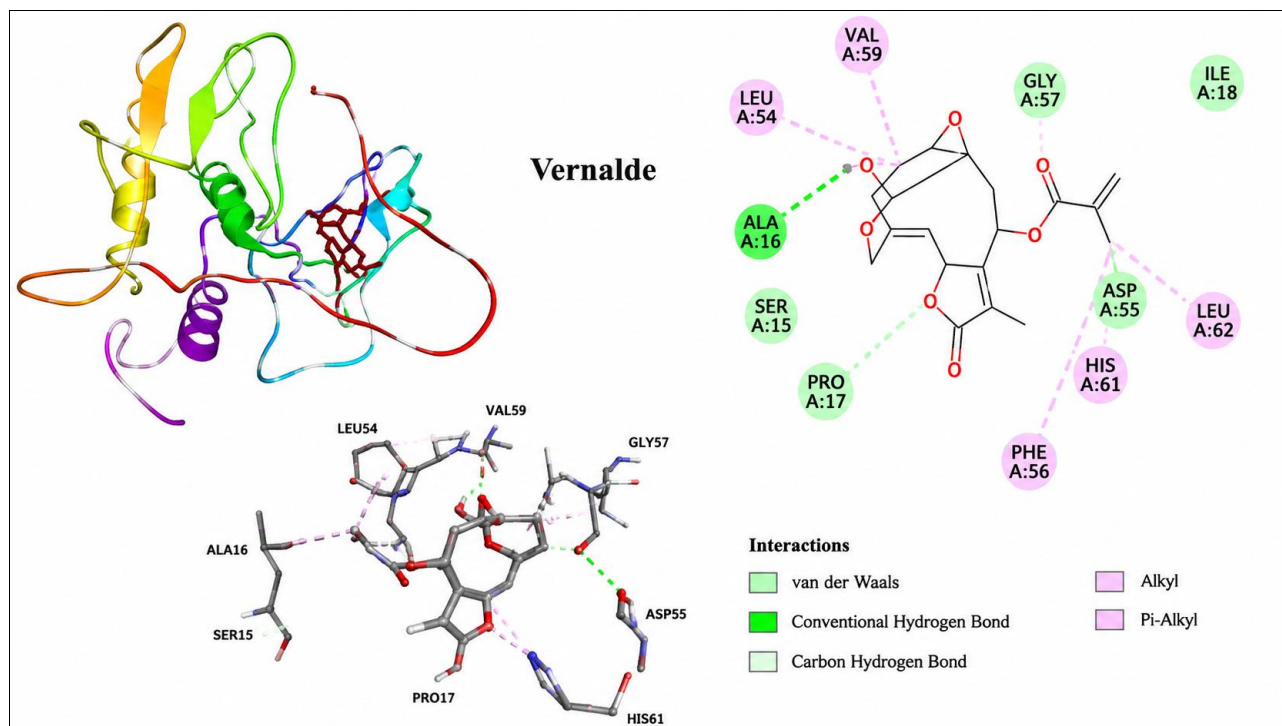


Fig 4: Protein-ligand complex, 3D and 2D images of the interaction of the ajmalicine, serpentine, raubasin, vernolide, and hydroxyvernolide with *Ancylostoma caninum* metalloprotease-2 are shown

Serpentine formed two hydrogen bonds with 9 CYS and 94 VAL of distance 2.59 and 2.10 Å, respectively, raubasin formed two hydrogen bonds with 92 ALA and 94 VAL of distance 2.41 and 2.28 Å, respectively, vernolide formed one hydrogen bond with 10 ALA of length 1.90 Å, hydroxyvernolide formed one hydrogen bond with 2 LYS with length of 2.17 Å whereas ajmalicine did not form any hydrogen bond. 6 LEU, 8 PHE, 9 CYS, 11 PHE, 134 ILE, 152 GLY, 153 TYR, 155 ALA, and 156 PHE interacted with ajmalicine through various interactions and 7 CYS, 13 VAL, 131 PRO, 158 ALA are the pocket atoms. Raubasin interacted with 7 CYS, 9 CYS, 10 ALA, 11 PHE, 12 PHE, 25 ASN, and

93 VAL whereas 8 PHE, 91 GLY, and 125 LYS are the pocket atoms. Serpentine interacted with 7 CYS, 10 ALA, 11 PHE, 12 PHE, 25 ASN, and 93 VAL whereas 8 PHE, 91 GLY, 92 ALA, 97 PRO, and 104 LEU are the pocket atoms. 4 PHE, 185 ALA, and 187 PRO interacted with hydroxyvernolide and the pocket atoms are 1 MET, 3 TYR, 150 GLU, 153 TYR, 180 LYS, 184 PHE, 186 LYS, 188 GLY, and 189 THR. 11 PHE, 12 PHE, 22 LEU, 93 VAL, 94 VAL interacted with vernolide and 25 ASN, 97 PRO, and 160 SER are the pocket atoms. The binding energy and the residues of the Ac-MTP-2 interacting with the ligands are given in Table 4.

Table 4: Binding energy and residues of the protein interacting with the selected ligands are given

Ligand names	Binding energy	Interacting residues
Ajmalicine	-9.4	6 LEU, 7 CYS, 8 PHE, 9 CYS, 10 ALA, 11 PHE, 12 PHE, 13 VAL, 131 PRO, 134 ILE, 152 GLY, 153 TYR, 154 GLU, 155 ALA, 156 PHE, 158 ALA, 179 TYR
Serpentine	-9.2	7 CYS, 8 PHE, 9 CYS, 10 ALA, 11 PHE, 12 PHE, 25 ASN, 90 THR, 91 GLY, 92 ALA, 93 VAL, 94 VAL, 97 PRO, 104 LEU
Raubasin	-9.12	7 CYS, 8 PHE, 9 CYS, 10 ALA, 11 PHE, 12 PHE, 25 ASN, 90 THR, 91 GLY, 92 ALA, 93 VAL, 94 VAL, 125 LYS
Vernolide	-8.09	10 ALA, 11 PHE, 12 PHE, 22 LEU, 23 PRO, 24 ARG, 25 ASN, 26 PRO, 93 VAL, 94 VAL, 95 GLY, 97 PRO, 160 SER
Hydroxyvernolide	-8.04	1 MET, 2 LYS, 3 TYR, 4 PHE, 150 GLU, 153 TYR, 180 LYS, 182 ASP, 183 ALA, 184 PHE, 185 ALA, 186 LYS, 187 PRO, 188 GLY, 189 THR

Ajmalicine and serpentine had good enzyme inhibitory activity against the cysteine protease, cruzain of *Trypanosoma cruzi* with a binding energy of -9.59 and -9.28 kcal/mol, respectively (Souza *et al.* 2022) [17] and in the present study, ajmalicine and serpentine had -9.4 and -9.2 kcal/mol binding energy against Ac-MTP-2. Yohimbine was identified as a novel inhibitor of NS2B-NS3 protease with a binding energy of -7.18 kcal/mol by the *in-silico* docking study performed in a study (Girija *et al.* 2019) [6]. However, in our study, yohimbine had a binding energy of -7.81 kcal/mol against Ac-MTP-2 which was comparatively higher than the other few ligands. The present study demonstrates the *in silico* anthelmintic activity of ajmalicine, raubasin, serpentine,

hydroxyvernolide, and vernolide against a metalloprotease of *Ancylostoma caninum* (Ac-MTP-2). The selected ligands should be tested *in vitro* and *in vivo* for their anthelmintic activity and toxic properties against *A. caninum*. The successful development of lead compounds into drugs treats infected dogs in addition to human infections.

Conclusion

Gastrointestinal parasites are responsible for various diseases and lead to tremendous economic losses in the livestock industry. In addition to the diseases caused by them, anthelmintic resistance is a severe problem. The parasites alter their genetic makeup to protect themselves from the

available drugs. Therefore, there is a need for the identification of newer drug molecules against different drug targets. The present study identified a few phytochemicals with promising *in silico* activity against a metalloprotease, Ac-MTP-2. We suggest further evaluation of these phytochemicals *in vitro* against *Ancylostoma caninum* for their anthelmintic property.

Conflict of Interest

Not available.

Financial Support

Not available.

References

1. Aziz PR, Marodia S, Meena S. Hookworm infection in a dog: a case report. *Haryana Veterinarian*. 2020;59(2):283-284.
2. Berger TA, Berger BK, Kogelman K. Supercritical fluid chromatography for chiral analysis and semi-preparative purification. Hoboken (NJ): Wiley; 2022.
3. Bowman DD, Montgomery SP, Zajac AM, Eberhard ML, Kazacos KR. Hookworms of dogs and cats as agents of cutaneous larva migrans. *Trends in Parasitology*. 2010;26(4):162-167.
4. Castro PDJ, Durrenre K, Durrenre S, Giannechini LS, Collins J, Dunn K, Kaplan RM. Multiple anthelmintic drug resistance in hookworms (*Ancylostoma caninum*) in a Labrador breeding and training kennel in Georgia, USA. *Journal of the American Veterinary Medical Association*. 2023;261(3):342-347.
5. Feng J, Zhan B, Liu Y, Liu S, Williamson A, Goud G, Loukas A, Hotez P. Molecular cloning and characterization of Ac-MTP-2, an astacin-like metalloprotease released by adult *Ancylostoma caninum*. *Molecular and Biochemical Parasitology*. 2007;152(2):132-138.
6. Girija R, Aruna S, Sangeetha R. In silico docking analysis of yohimbine alkaloids from *Catharanthus roseus* against dengue fever. *Asian Journal of Pharmaceutical and Clinical Research*. 2019;12(5):344-345.
7. Haffner A, Guilavogui AZ, Tischendorf FW, Brattig NW. *Onchocerca volvulus*: microfilariae secrete elastinolytic and males non-elastinolytic matrix-degrading serine and metalloproteases. *Experimental Parasitology*. 1998;90(1):26-33.
8. Jimenez Castro PD, Howell SB, Schaefer JJ, Avramenko RW, Gilleard JS, Kaplan RM. Multiple drug resistance in the canine hookworm *Ancylostoma caninum*: an emerging threat? *Parasites & Vectors*. 2019;12(1):576-590.
9. Karanu FN, Rurangirwa FR, McGuire TC, Jasmer DP. *Haemonchus contortus*: identification of proteases with diverse characteristics in adult worm excretory-secretory products. *Experimental Parasitology*. 1993;77(3):362-371.
10. Lee MF, Cadogan P, Eytle S, Walochnik J, Lindo J. Molecular evidence of intestinal exposure to *Ancylostoma caninum* among humans in Jamaica. 2022.
11. Leutenegger CM, Lozoya CE, Tereski J, Savard C, Ogeer J, Lallier R. Emergence of *Ancylostoma caninum* parasites with the benzimidazole resistance F167Y polymorphism in the US dog population. *International Journal for Parasitology: Drugs and Drug Resistance*. 2023;21:131-140.
12. Lipinski CA, Lombardo F, Dominy BW, Feeney PJ. Experimental and computational approaches to estimate solubility and permeability in drug discovery and development settings. *Advanced Drug Delivery Reviews*. 1997;23(1-3):3-25.
13. Marsh AE, Lakritz J. Reflecting on the past and fast-forwarding to present-day anthelmintic-resistant *Ancylostoma caninum*: a critical issue we neglected to forecast. *International Journal for Parasitology: Drugs and Drug Resistance*. 2023;22:30-36.
14. Morosetti A, Horvath H, Chen R, Redman E, Dunn K. Molecular evidence of widespread benzimidazole drug resistance in *Ancylostoma caninum* from domestic dogs throughout the USA and discovery of a novel β -tubulin benzimidazole resistance mutation. *PLoS Pathogens*. 2023;19(3):e1011146.
15. Prociv P, Croese J. Human enteric infection with *Ancylostoma caninum*: hookworms reappraised in the light of a “new” zoonosis. *Acta Tropica*. 1996;62(1):23-44.
16. Reinemeyer CR. Formulations and clinical uses of pyrimidine compounds in domestic animals. In: Pyrantel parasiticide therapy in humans and domestic animals. London: Academic Press; 2016. p.67-107.
17. Souza JL, Lima FCA, Cruz JV, Reis Almeida T, Silva CBB. In silico study of alkaloids derived from *Catharanthus roseus* in the active site of *Trypanosoma cruzi* by molecular docking. *Research, Society and Development*. 2022;11(5):e23711528114.
18. Tsuji N. Schistosomiasis and hookworm infection in humans: disease burden, pathobiology, and anthelmintic vaccines. *Parasitology International*. 2020;75:102051.
19. Veeresham C. Natural products derived from plants as a source of drugs. *Journal of Advanced Pharmaceutical Technology and Research*. 2012;3(4):200-201.
20. Venkatesan A, Jimenez Castro PD, Morosetti A, Horvath H, Chen R, Redman E, et al. Molecular evidence of widespread benzimidazole drug resistance in *Ancylostoma caninum* from domestic dogs throughout the USA and discovery of a novel β -tubulin benzimidazole resistance mutation. *PLoS Pathogens*. 2023;19(3):e1011146.
21. Williamson AL, Lustigman S, Oksov Y, Deumic V, Plieskatt J, Mendez S, et al. *Ancylostoma caninum* MTP-1, an astacin-like metalloprotease secreted by infective hookworm larvae, is involved in tissue migration. *Infection and Immunity*. 2006;74(2):961-967.

How to Cite This Article

Silamparasan M, Babu Prasath N, Ramamoorthy M. Homology modeling and docking analysis of phytochemicals of *Catharanthus roseus* and *Vernonia amygdalina* against *Ancylostoma caninum* metalloprotease-2. *International Journal of Veterinary Sciences and Animal Husbandry*. 2026; 11(1): 80-87.

Creative Commons (CC) License

This is an open-access journal, and articles are distributed under the terms of the Creative Commons Attribution-Non Commercial-Share Alike 4.0 International (CC BY-NC-SA 4.0) License, which allows others to remix, tweak, and build upon the work non-commercially, as long as appropriate credit is given and the new creations are licensed under the identical terms.