Integrated Health Research Journal (IHRJ)

The Official Journal of the College of Health and Allied Sciences

RESEARCH ARTICLE

Computational-Aided Drug Discovery Approaches Exploring Therapeutic Potential of Global Health Priority Box Compounds Against *Schistosoma haematobium* Infection

Jonathan Cobbinah[1], William Owusu[1], Abdul-Samad Alhassan[1], Emmanuel Adu Sarpong[1], Nicholas Donkor[1], Pius K. Sam[1], Alberta Serwah Anning[1], George Ghartey-Kwansah[1*]

[1] Department of Biomedical Sciences, School of Allied Health Sciences, University of Cape Coast, Ghana

Correspondence should be addressed to George Ghartey-Kwansah (email: george.ghartey-kwansah@ucc.edu.gh)

Abstract

Background: Urinary schistosomiasis caused by *Schistosoma haematobium* remains a major global health burden, with nearly 800 million people at risk worldwide. The growing concern over reduced praziquantel efficacy underscores the urgent need for alternative therapeutic agents. Advances in computational drug discovery provide an efficient framework for identifying novel antischistosomal candidates targeting parasite-specific proteins.

Objective: This study employed integrative computational drug discovery approaches to evaluate Global Health Priority (GHP) Box compounds for therapeutic potential against *S. haematobium,* focusing on the 23-kDa integral membrane protein (Sh23) as a putative drug target.

Methodology: The Sh23 protein was identified and structurally characterized as a potential therapeutic target. A curated library of 80 GHP Box compounds was subjected to virtual screening with PyRx, yielding 33 top-scoring candidates based on binding affinity. These candidates were further evaluated with ADMET-AI for *in silico* pharmacokinetic and toxicity profiling, with MolSoft for drug-likeness assessment, and with the PASS platform (Way2Drug) for biological activity prediction.

Results: MMV1262756 emerged as the lead compound, demonstrating strong binding affinity to Sh23 protein, low predicted clinical toxicity (0.14), high drug-likeness (0.87), and favorable predicted activity related to urological disorders.

Conclusion: This study identifies MMV1262756 as a promising antischistosomal candidate and highlights the utility of computationally driven drug discovery in accelerating the identification of therapeutic candidate for S. haematobium. The findings support the potential of bioinformatics-guided strategies to address emerging challenges in praziquantel efficacy and advance schistosomiasis control.

Keywords: Schistosomiasis; *Schistosoma haematobium*; Global Health Priority Box Compounds; Molecular Docking; ADMET Profiling; PASS Prediction.

Citation: Cobbinah J, Owusu W, Alhassan A-S, Sarpong EA, Donkor N, Sam PI, Anning AS, Ghartey-Kwansah G. Computational-aided drug discovery approaches exploring therapeutic potential of Global Health Priority Box compounds against *Schistosoma haematobium* infection. Integrated Health Research Journal. 2026;3(2):59-66. https://doi.org/10.47963/ghbf5j40

Received 26th March 2026; **Accepted** 24th July 2026; **Published** 8th September 2026.

Introduction

Schistosomiasis, also known as bilharzia, remains one of the most devastating neglected tropical diseases globally and ranks second only to malaria in parasitic disease burden. More than 250 million people are infected across 78 countries, with an estimated 500,000 deaths annually [1,2]. The disease is caused by trematode parasites of the genus *Schistosoma*, with *Schistosoma haematobium* responsible for approximately two-thirds of cases in Africa, where over

90% of individuals requiring treatment reside [3,4]. Chronic infection with *S. haematobium* is associated with severe urogenital morbidity, including hematuria, bladder fibrosis, hydronephrosis, and increased risk of squamous cell carcinoma of the bladder, underscoring its substantial clinical and socioeconomic impact.

A key determinant of *S. haematobium* survival and pathogenicity is the 23 kDa integral membrane protein (Sh23), a member of the tetraspanin family that is abundantly expressed during the schistosomula stage and localized on the parasite tegument [5]. Sh23 is implicated in host–parasite interactions through its role in maintaining tegumental integrity, parasite adhesion, and modulating host immune responses [6]. Mechanistically, Sh23 participates in membrane organization and signal transduction, facilitating parasite adaptation within the host environment and contributing to immune evasion by masking antigenic epitopes and modulating host inflammatory pathways [7]. Its surface accessibility, stage-specific expression, and functional relevance make Sh23 an attractive yet underexplored molecular target for therapeutic intervention.

Despite decades of control efforts, praziquantel remains the sole widely used antischistosomal drug [8]. However, growing evidence of reduced drug sensitivity, absence of prophylactic activity, limited efficacy against immature parasite stages, and the risk of resistance development highlight critical gaps in current treatment strategies. Furthermore, most existing drug discovery efforts have focused on a narrow range of parasite targets, leaving key tegumental proteins such as Sh23 insufficiently characterized and poorly exploited in therapeutic development. This represents a major unmet need in schistosomiasis research [9].

Recent advances in computational drug discovery offer powerful tools for accelerating the identification of novel antischistosomal agents [10]. Structure-based virtual screening, pharmacokinetic prediction, and machine learning–driven prioritization of compounds have significantly reduced the cost and time associated with early-stage drug development [11]. When combined with curated compound libraries such as the Global Health Priority Box developed by the Medicines for Malaria Venture (MMV), these approaches provide a unique opportunity to systematically explore previously untapped molecular targets in *S. haematobium*.

To date, no comprehensive computational study has systematically evaluated Global Health Priority Box compounds against Sh23 or integrated molecular docking, pharmacokinetic profiling, and biological activity prediction to identify targeted inhibitors of this protein. Moreover, the mechanistic and therapeutic potential of Sh23 as a drug target remains largely unexplored compared with other schistosome proteins. This study addresses these critical gaps by implementing an integrative computational framework that combines structure-based virtual screening and advanced in silico drug discovery approaches to identify and prioritize novel candidate compounds targeting Sh23. By focusing on a biologically relevant yet underutilized tegumental protein, this work provides new mechanistic insights and establishes a rational pipeline for the development of next-generation antischistosomal therapeutics.

Materials and Methods.

Target Protein Retrieval and Validation

The 23 kDa integral membrane protein of *Schistosoma haematobium* (Sh23) was selected as the therapeutic target due to its crucial role in parasite adhesion and survival. The protein sequence (UniProt accession: AF-Q26499-F1) was retrieved from the AlphaFold Protein Structure Database(https://alphafold.ebi.ac.uk/) in PDB format. To further validate the accuracy of the predicted structure of the Sh23 protein, the model was uploaded to the SWISS-MODEL platform for structural validation. SWISS-MODEL is widely used for homology modeling and performs automated alignment of a query protein structure with known experimental templates. After alignment, the analysis showed a 100% sequence identity between the AlphaFold-predicted structure and the closest homologous protein in the SWISS-MODEL database. This perfect match confirmed that the predicted amino acid sequence and folding pattern of Sh23 are consistent with experimentally validated data, thereby reinforcing the reliability of the model.

In addition, the integrity and confidence of the predicted structure were evaluated using the pLDDT score, which was 90.56 for this 23 kDa integral membrane protein from *Schistosoma haematobium* (Sh23). A pLDDT value this high indicates very high confidence, supporting the accuracy and stability of the predicted structure [12].

Protein Preparation

The retrieved Sh23 structure was processed using BIOVIA Discovery Studio. Water molecules were removed, hydrogen atoms were added, bond orders were corrected, and geometry optimization was carried out to ensure structural fidelity [13,14]. The finalized protein model was saved as a PDB file for subsequent molecular docking simulations.

Ligand Preparation

A total of 80 compounds from the Medicines for Malaria Venture (MMV) Global Health Priority (GHP) box were retrieved in SMILES format [15]. The SMILES notations were converted into three-dimensional PDB structures using the NovoPro SMILES-to-PDB converter. The generated structures were imported into BIOVIA Discovery Studio, where conformations were inspected and validated against their two-dimensional representations. Finalized

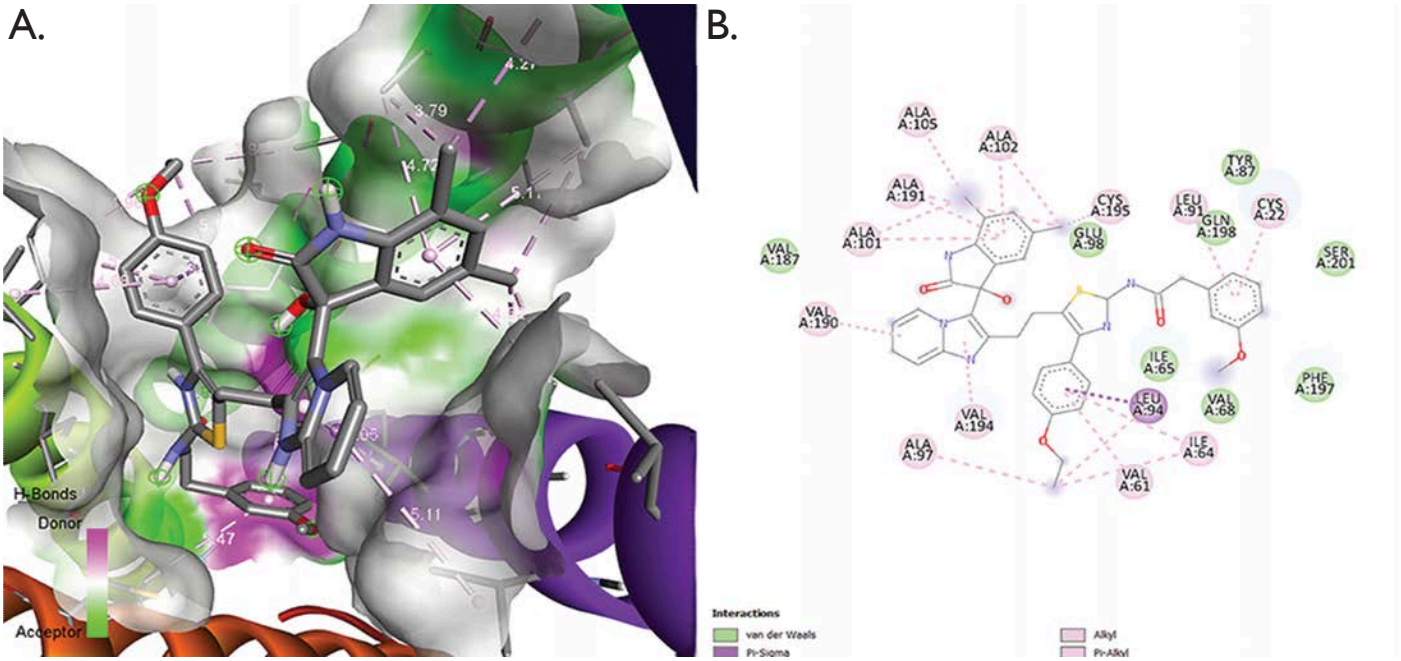

Figure 1: (A) 3D representation of MMV014853 docked to the 23 kDa integral membrane protein, illustrating hydrophobic contacts, π-alkyl interactions, and van der Waals stabilization within the binding pocket. (B) 2D interaction map highlighting key residues involved in ligand binding, including alkyl and π-alkyl interactions and van der Waals contacts.

ligands were stored in a dedicated library for downstream docking experiments.

Binding Pocket Prediction

The putative ligand-binding site of Sh23 was identified before docking simulations to ensure accurate targeting. Residue-level binding pocket analysis predicted an active site spanning residues 107-184, forming a well-defined cavity suitable for small-molecule interactions. No co-crystallized ligand or reference ligand was available for Sh23; therefore, we validated docking using alternative controls ("self-docking" of a template ligand), and the corresponding RMSD < 2.0 Å performed using PyRx (version 0.8, Scripps Research Institute, USA). This site served as the reference for docking grid box construction, ensuring that simulations explored biologically relevant binding regions [13].

Protein-Ligand Docking and Virtual Screening

Docking simulations were performed using PyRx (version 0.8, Scripps Research Institute, USA), which integrates AutoDock Vina for ligand-protein interaction analysis [16]. The docking grid box was centered at X = 11.25 Å, Y = 1.39 Å, and Z = –4.33 Å, with grid dimensions of 49.22 Å × 343.12 Å × 38.3 Å to fully encompass the predicted binding pocket. Exhaustiveness was set to 20 to maximize sampling accuracy. In this study, the docking validation metric is therefore limited to binding scores and interaction profiles.Binding affinity scores (kcal/mol) and RMSD values were used to rank the compounds. Ligands with binding energies ≤ -8.0 kcal/mol were considered high-affinity hits. Protein-ligand interactions were analyzed in detail, with hydrogen bonds, hydrophobic contacts, and electrostatic interactions visualized using BIOVIA Discovery Studio to confirm the stability and orientation of ligand binding.

Compound Characterization

ADMET and Drug-Likeness Profiling

The pharmacokinetic and toxicological profiles of the top 33 compounds were predicted using ADMET-AI (https://admet.ai.greenstonebio.com/) and MolSoft(https://www.molsoft.com/) servers. Submitted SMILES notations were analyzed for molecular descriptors, absorption, distribution, metabolism, excretion, and toxicity (ADMET) properties [17]. Predictions included hERG channel inhibition, mutagenicity, drug-induced liver injury, carcinogenicity, LD50, mitochondrial membrane potential disruption, and skin sensitization. Drug-likeness scores were calculated independently using MolSoft.

Biological Activity Prediction (PASS Analysis)

Biological activity spectra of the shortlisted compounds were predicted using the PASS (https://www.way2drug.com/passonline/predict.php)server. SMILES strings were evaluated for probability scores corresponding to potential pharmacological effects. Only activities relevant to *S. haematobium* infection and associated pathologies were considered for downstream analysis.

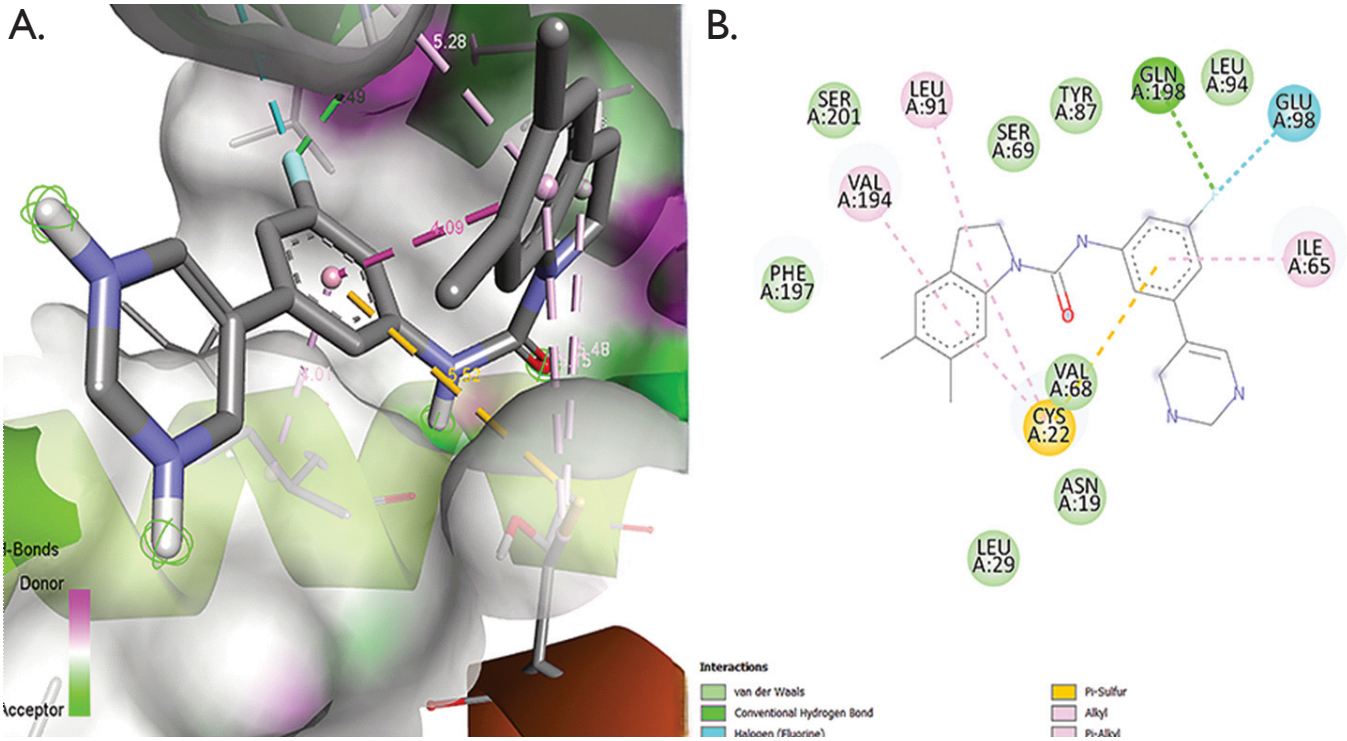

Figure 2: (A) 3D representations of MMV028822 docked to the 23 kDa integral membrane protein (AF-Q26499-F1), showing hydrogen bonding, π–sulfur interaction, and key hydrophobic/van der Waals contacts within the binding pocket. (B) 2D interaction map highlighting key residues involved in ligand binding, including alkyl and π-alkyl interactions and van der Waals contacts.

Similarly, molecular docking revealed that MMV028822 adopted a stable binding conformation within the active site of the 23 kDa integral membrane protein (AF-Q26499-F1), with a binding energy of -8.2 kcal/mol. The compound formed a key hydrogen bond with GLU A:98 and a π–sulfur interaction with CYS A:22, in addition to multiple hydrophobic and van der Waals contacts involving LEU A:29, ASN A:19, VAL A:68, VAL A:194, LEU A:94, PHE A:197, SER A:201, GLN A:198, and TYR A:87. These interactions collectively indicate a well-stabilized binding pose and strong affinity for the target site (Figure 2A–B).

Molecular docking revealed that MMV1262756 adopted a stable binding pose within the active site of the 23 kDa integral membrane protein (AF-Q26499-F1), with a binding energy of –8.2 kcal/mol (Figure 3A–B). The compound engaged in a π-anion interaction with GLU A:133, a π-sigma interaction with VAL A:36, and π–π stacking/T-shaped contacts with PHE A:134 and TRP A:51. Additional hydrophobic interactions with PHE A:40, TYR A:35, ALA A:32, and ILE A:58 contributed to overall complex stabilization and strong target affinity.

Physicochemical and ADMET Profiling

Physicochemical and ADMET profiling provide comprehensive insights into the properties of the studied compounds. Physicochemical profiling evaluates the compounds' physical and chemical characteristics, while ADMET analysis assesses their pharmacokinetic behavior, including absorption, distribution, metabolism, and excretion, as well as their toxicity profiles.

ADMET profiling of the 33 compounds revealed molecular weights (345.38-769.97 g/mol), logP (1.17-6.07), TPSA (37.19-154.73 Å²), and QED scores (0.13-0.74) (Table S2). Oral bioavailability scores ranged from 0.62–0.98, while plasma protein binding spanned 71.37%-100% (Table S3). Toxicity markers varied, with hERG inhibition (0.35-0.99) and clinical toxicity probabilities (0.07-0.82) (Table S4). Among all, MMV028822 and MMV1262756 showed superior drug-likeness alongside favourable pharmacokinetic properties compared with the reference, praziquantel (Table 1 & 2); MMV014853 showed favourable pharmacokinetics but a drug-likeness score below praziquantel.

Praziquantel, used as the reference control, demonstrated an overall favorable safety profile with low probabilities of cardiotoxicity (0.18), clinical toxicity (0.05), mutagenicity (0.06), and carcinogenicity (0.03). However, a relatively high likelihood of skin reactions (0.64) was observed, aligning with its known side effect profile. The compound showed moderate acute safety (LD50 = 2.75) and negligible mitochondrial toxicity (0.01). Despite its established efficacy, praziquantel recorded only a modest drug-likeness score (0.29), underscoring the need for more optimized alternatives (Table 2).

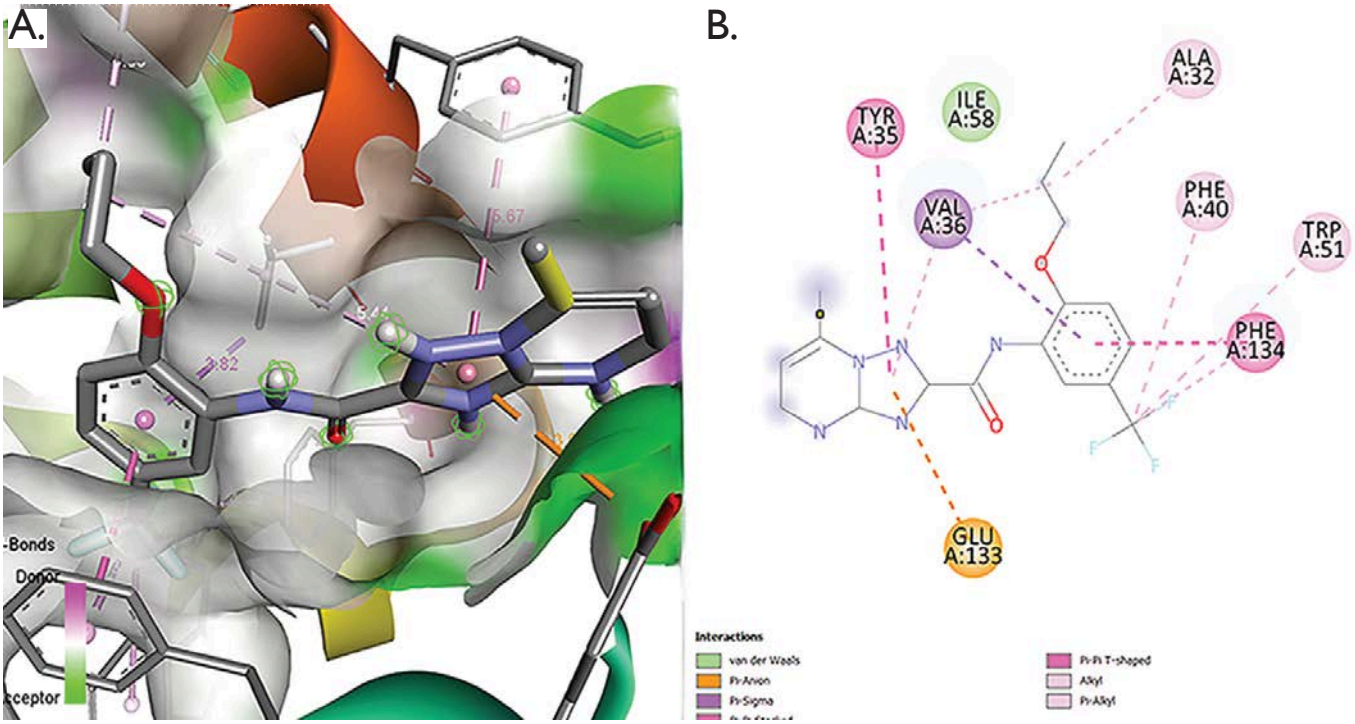

Figure 3: Illustration of the binding interactions of MMV1262756 (−8.2 kcal/mol) within the active site of the 23 kDa membrane protein (AF-Q26499-F1). **(A)** 3D visualization of the docking complex showing the ligand anchored in the binding cavity. **(B)** 2D interaction map depicting hydrogen bonds, π-alkyl contacts, and van der Waals interactions with key residues.

PASS Biological Activity Prediction

PASS provides an activity-spectrum view that helps distinguish which compounds are most likely to modulate biologically relevant functions which is going beyond docking or structural compatibility alone. It also enables fast triage under limited resources, since testing every compound experimentally is costly and time-intensive; PASS helps identify the most promising candidates early for downstream validation. The PASS analysis revealed distinct activity profiles across the evaluated compounds. MMV014853 was predicted as a membrane integrity agonist (Pa = 0.23; Pi = 0.26), suggesting limited therapeutic potential. MMV028822 demonstrated a broader activity spectrum, with predicted roles in urinary incontinence (Pa = 0.16), urologic disorders (Pa = 0.17), and antineurogenic pain (Pa = 0.21). Among the compounds, MMV1262756 emerged as the most promising, showing predicted activities in urologic disorders (Pa = 0.14), urinary incontinence (Pa = 0.13), and interleukin-2 antagonism (Pa = 0.10), with consistently low inactivity scores, highlighting its potential as a viable therapeutic candidate (Table S6).

Discussion

This study explored the potential of targeting the Sh23 tetraspanin protein in *Schistosoma haematobium* using an integrative computational drug discovery approach. These findings contribute significantly to the growing body of research by identifying potential anti-schistosomal

Table1: Predicted Pharmacokinetic Properties (ADME) of lead compounds and Praziquantel.

Compound ID	OR	CEP	Blood-Brain Barrier Penetration	Plasma Protein Binding Rate	CYP3A4 Inhibition	Half Life	Drug Clearance (Hepatocyte)
Praziquantel (control)	0.54	-4.45	0.99	62.60	0.77	0.00	34.40
MMV014853	0.96	-4.67	0.86	84.45	0.37	41.37	35.41
MMV028822	0.96	-4.63	0.93	97.28	0.99	68.79	35.69
MMV1262756	0.98	-4.73	0.89	100.00	0.33	0.00	43.07

Table 2: Predicted Toxicity and drug-likeness profiles of lead compounds and Praziquantel.

Compound ID	hERG Blocking	Clinical Toxicity	Mutagenicity	Carcinogenicity	Acute Toxicity LD50	SR	MMP	DLMS
Praziquantel (control)	0.18	0.05	0.06	0.03	2.75	0.64	0.01	0.29
MMV014853	0.44	0.21	0.45	0.23	2.85	0.26	0.47	0.24
MMV028822	0.73	0.24	0.12	0.12	2.68	0.16	0.46	0.66
MMV1262756	0.60	0.14	0.58	0.38	2.65	0.18	0.31	0.87

Abbreviations: DLMS = Drug-Likeness Model Score; MMP = Mitochondrial Membrane Potential; SR = Skin Reaction.

compounds from the Global Health Priority Box and demonstrating the utility of computational approaches in accelerating drug discovery. The study provides valuable insights into compound efficacy, safety, and pharmacokinetic properties, thereby supporting the development of new therapeutic options for *Schistosoma haematobium* infection. These chronic and often debilitating outcomes underscore the urgent need for improved and diversified therapeutic strategies beyond the current standard of care, which relies primarily on the anthelmintic drug Praziquantel. This study pioneers a computational pipeline for targeting the Sh23 tetraspanin protein in *Schistosoma haematobium,* revealing MMV1262756 as a standout lead from the Global Health Priority (GHP) Box library. The identification of these compounds therefore reflects not only their computational affinity for the Sh23 target but also their origin from a chemically validated library with prior relevance to infectious disease research. By identifying 33 high-affinity ligands through virtual screening and prioritizing three top candidates via docking and ADMET analysis, our findings illuminate Sh23's druggability and underscore the untapped potential of tegumental proteins in antischistosomal drug discovery.

The superior binding profiles of MMV014853, MMV028822, and especially MMV1262756 stem from multifaceted interactions within the Sh23 binding pocket among the leads. MMV1262756 distinguished itself with the most favorable overall profile. It combined strong binding affinity with the highest drug-likeness score (0.87), the lowest predicted clinical toxicity (0.14), and superior PASS-predicted activities in urologic disorders (Pa = 0.14), urinary incontinence (Pa = 0.13), and interleukin-2 antagonism (Pa = 0.10). These predicted pharmacological effects align closely with the immune-mediated pathology of schistosomiasis, in which chronic inflammation, bladder fibrosis, and increased risk of squamous cell carcinoma are driven by dysregulated host immune responses and urogenital tissue damage[19, 20]. In contrast, MMV014853 showed moderate toxicity concerns (higher mutagenicity and carcinogenicity, with a lower drug-likeness score), while MMV028822 offered a balanced but less optimal safety-efficacy ratio. These results directly address praziquantel's shortcomings, which include reduced sensitivity, immature-stage inefficacy, and adverse effects like hepatotoxicity, by proposing Sh23 inhibitors with complementary mechanisms. The PASS-predicted activities (Pa ≈ 0.10–0.21) fall within a low-confidence range, where values below 0.30 generally indicate weak or uncertain biological relevance. As such, these results should be interpreted cautiously as hypothesis-generating rather than definitive evidence of pharmacological activity. Predicted functions, including associations with urologic disorders, likely reflect indirect or symptom-modulating effects related to the pathophysiology of urogenital schistosomiasis rather than direct antiparasitic mechanisms. Similarly, the predicted antagonistic activity of MMV1262756 against interleukin-2 (IL-2) suggests that the compound may possess immunomodulatory properties. However, this prediction is based on computational analysis and remains speculative until confirmed through experimental validation.

Overall, PASS analysis provides limited but complementary insight within the computational framework. While MMV1262756 remains a promising candidate based on its binding affinity and pharmacokinetic profile, PASS predictions should be treated as secondary indicators, with compound prioritization primarily guided by structural and ADMET evidence and validated through further experimental studies.

Unlike praziquantel's tegumental disruption via calcium influx, Sh23 targeting exploits stage-specific vulnerability in schistosomula, potentially enabling prophylaxis against early infections. The GHP Box's proven utility in neglected tropical diseases (NTDs) validates this library as a cost-effective source, consistent with Hernandez, Veale et al.,[21, 22], while Kondapuram et al.,[23] affirm docking's reliability in parasitology. The identification of candidate compounds from an open-access library aligns with global efforts to expand affordable and scalable treatment strategies. Furthermore, while the compounds investigated here are synthetic or semi-synthetic molecules, this partially parallels the rationale underlying certain ethnobotanical practices, where plant-derived therapies are traditionally used to alleviate urinary symptoms and inflammation. Although no direct ethnopharmacological linkage can be

established for these specific compounds, the conceptual overlap underscores the importance of integrating computational findings with traditional knowledge systems in future research.

Currently, praziquantel remains the gold-standard treatment for schistosomiasis, yet its limitations, such as hepatotoxicity, skin reactions, and moderate drug-likeness, underscore the need for alternative therapies [23]. The predicted pharmacological and safety profile of MMV1262756 highlights its potential as a complementary or replacement therapy and supports the call for diversification of the anti-schistosomal drug arsenal. From a mechanistic perspective, targeting the Sh23 protein offers a novel therapeutic approach distinct from the action of praziquantel, which primarily disrupts parasite tegument integrity via calcium influx. In contrast, Sh23 inhibition may interfere with tegumental organization and host–parasite interactions during the schistosomula stage, suggesting potential utility in early infection control and possibly prophylaxis. This is particularly relevant given the limitations of praziquantel, including reduced sensitivity in some settings, lack of efficacy against immature parasite stages, and adverse effects such as hepatotoxicity and skin reactions [24, 25].

In summary, this work presents a streamlined computational pipeline that combines target prioritization, molecular docking, and multi-parameter evaluation to accelerate anti-schistosomal drug discovery. Among the screened ligands, MMV1262756 emerged as the most promising hit, warranting further in vitro and in vivo validation. Beyond *S. haematobium,* this integrative approach can be readily applied to other neglected tropical diseases, leveraging open-access libraries such as the GHP Box to expand therapeutic options [26, 27].

Conclusion

This study highlights the effectiveness of the effectiveness of integrating computational drug discovery approaches in identifying novel therapeutics against *Schistosoma haematobium*. Virtual screening of Global Health Priority (GHP) Box compounds against the Sh23 protein yielded MMV1262756 as the lead candidate, with a strong binding affinity of -8.2 kcal/mol, high drug-likeness score (0.87), and low predicted clinical toxicity (0.14). These attributes position MMV1262756 as a potential candidate to address the limitations of praziquantel. Future in vitro and in vivo studies are warranted to validate its therapeutic potential and advance it toward clinical development.

Acknowledgements

The authors would like to thank all individuals and institutions that contributed to the successful completion of this work. Their support, guidance, and valuable feedback are gratefully acknowledged.

Authors' contributions

GGK and ASA conceptualized and designed the study. JC, WO, ND and EAS collected the data. JC, EAS, WO, A-SA, and PKS analyzed the data. JC, EAS, ND, ASA, and GGK wrote and edited the manuscript. All authors read and approved the final version of the manuscript.

Funding

This research received no specific grant from any funding agency in the public, commercial, or not-for-profit sectors.

Conflict of Interest

The authors declare that there are no conflicts of interest regarding the publication of this paper.

References

1. Anderson RM, Turner HC, Farrell SH, Truscott JE,et al. Studies of the Transmission Dynamics, Mathematical Model Development and the Control of Schistosome Parasites by Mass Drug Administration in Human Communities. Advanced Parasitology. Doi:2016;94:199-246.10.1016/bs.apar.2016.06.003

2. LoVerde PT. Schistosomiasis. Adv Exp Med Biol. 2024;1454:75-105. Doi:10.1016/j.ijpddr.2021.05.002

3. Yamey G, McDade KK, Anderson RM, Bartsch SM, Bottazzi ME, Diemert D, et al. Vaccine value profile for schistosomiasis. Vaccine. 2024:126020. doi:10.1016/j.vaccine.2024.05.068

4. Au MFF, Williams GA, Hui JHL. Status Quo and Future Perspectives of Molecular and Genomic Studies on the Genus Biomphalaria-The Intermediate Snail Host of Schistosoma mansoni. Int J Mol Sci. 2023;24(5). doi:10.3390/ijms24054895.

5. Jafaru S. Antigens of Three Medically Important Schistosoma spp. doi:10.9734/ajriz/2022/v5i330139

6. Mekonnen GG, Tedla BA, Pearson MS, Becker L, Field M, Amoah AS, et al. Characterisation of tetraspanins from *Schistosoma haematobium* and evaluation of their potential as novel diagnostic markers. PLoS neglected tropical diseases. 2022;16(1):e0010151. doi: 10.1371/journal.pntd.0010151.

7. Oettle RC, Dickinson HA, Fitzsimmons CM, Sacko M, Tukahebwa EM, Chalmers IW, et al. Protective human IgE responses are promoted by comparable life-cycle dependent Tegument Allergen-Like expression in *Schistosoma haematobium* and Schistosoma mansoni infection. PLoS Pathog. 2023;19(5):e1011037. doi:10.1371/journal.ppat.1011037.

8. Bergquist R, Utzinger J, Keiser J. Controlling schistosomiasis with praziquantel: How much longer without a viable alternative? Infectious diseases of poverty. 2017;6(1):74. doi:10.1186/s40249-017-0286-2.

9. Soleymani N, Sadr S, Santucciu C, Dianaty S, Lotfalizadeh N, Hajjafari A, et al. Unveiling novel insights in helminth proteomics: Advancements, applications, and implications for parasitology and beyond. Biologics. 2024;4(3):314-44.doi:10.3390/biologics4030020.

10. Neves BJ, Muratov E, Machado RB, Andrade CH, Cravo PVL. Modern approaches to accelerate discovery of new antischistosomal drugs. Expert opinion on drug discovery. 2016;11(6):557-67. doi:10.1080/17460441.2016.1178230.

11. Ruiz DGT, Guevara-Pulido J. Recent advances in drug discovery and development through machine learning: A rational drug design (2000-2024). Revista Facultad de Ciencias Básicas. 2023;19(2):107-23. doi:10.18359/rfcb.7873.

12. Binbay FA, Rathod DC, George AAP, Imhof D. Quality Assessment of Selected Protein Structures Derived from Homology Modeling and AlphaFold. Pharmaceuticals. 2023;16(12):1662.doi:10.3390/ph16121662.

13. Mathur N, Chandra M, Sai S, Santoki KM, Vadhavana NN, Shah S, et al. *in silico* Docking: Protocols for Computational Exploration of Molecular Interactions. In: Podlipnik Č, editor. Unravelling Molecular Docking - From Theory to Practice. Rijeka: IntechOpen; 2024. doi: 10.5772/intechopen.1005527.

14. Ferreira LG, Dos Santos RN, Oliva G, Andricopulo AD. Molecular docking and structure-based drug design strategies. Molecules. 2015;20(7):13384-421. doi:10.3390/molecules200713384.

15. Gentile F, Yaacoub JC, Gleave J, Fernandez M, Ton A-T, Ban F, et al. Artificial intelligence–enabled virtual screening of ultra-large chemical libraries with deep docking. Nature Protocols. 2022;17(3):672-97. doi:10.1038/s41596-021-00659-2.

16. Dallakyan S, Olson AJ. Small-molecule library screening by docking with PyRx. Methods Mol Biol. 2015;1263:243-50. doi:10.1007/978-1-4939-2269-7_19.

17. De Carlo A, Ronchi D, Piastra M, Tosca EM, Magni P. Predicting ADMET Properties from Molecule SMILE: A Bottom-Up Approach Using Attention-Based Graph Neural Networks. Pharmaceutics. 2024;16(6). doi:10.3390/pharmaceutics16060776.

18. Batirel A, Regmi SK, Singh P, Mert A, Konety BR, Kumar R. Urological infections in the developing world: an increasing problem in developed countries. World Journal of Urology. 2020;38(11):2681-91. doi:10.1007/s00345-020-03120-3.

19. Yan-Rong L, Han-Guo X, Zhu-Yun C, Li-Zhen X, Rong-Yan Z. [Diagnosis and treatment of an imported case of schistosomiasis haematobium]. Zhongguo Xue Xi Chong Bing Fang Zhi Za Zhi. 2017;29(1):108-10. doi:10.1371/journal.pntd.0006171.

20. Lo NC, Addiss DG, Hotez PJ, King CH, Stothard JR, Evans DS, et al. A call to strengthen the global strategy against schistosomiasis and soil-transmitted helminthiasis: the time is now. The Lancet Infectious Diseases. 2017;17(2):e64-e9. doi: 10.1016/s1473-3099(16)30535-7

21. Hernandez HW, Soeung M, Zorn KM, Ashoura N, Mottin M, Andrade CH, et al. High Throughput and Computational Repurposing for Neglected Diseases. Pharm Res. 2018;36(2):27.doi:10.1007/s11095-018-2558-3

22. Veale CGL. Unpacking the Pathogen Box-An Open Source Tool for Fighting Neglected Tropical Disease. ChemMedChem. 2019;14(4):386-453. doi:10.1002/cmdc.201800755.

23. Kondapuram SK, Sarvagalla S, Coumar MS. Chapter 22 - Docking-Based Virtual Screening Using PyRx Tool: Autophagy Target Vps34 as a Case Study. In: Coumar MS, editor. Molecular Docking for Computer-Aided Drug Design: Academic Press; 2021. p. 463-77. doi:10.1016/b978-0-12-822312-3.00019-9

24. Balahbib A, El Omari N, Lghazi H, Hatoufi K, El Atki Y, Bouyahya A, et al. Therapeutic challenges of schistosomiasis: mechanisms of action and current limitations. Journal of Parasitic Diseases. 2025;49(3):498-512. doi:10.1007/s12639-025-01785-4.

25. Villamizar-Monsalve MA, López-Abán J, Vicente B, Peláez R, Muro A. Current drug strategies for the treatment and control of schistosomiasis. Expert Opin Pharmacother. 2024;25(4):409-20. doi: 10.1080/14656566.2024.2333372.

26. Midzi N, Bärenbold O, Manangazira P, Phiri I, Mutsaka-Makuvaza MJ, Mhlanga G, et al. Accuracy of different diagnostic techniques for *Schistosoma haematobium* to estimate treatment needs in Zimbabwe: Application of a hierarchical Bayesian egg count model. PLoS Negl Trop Dis. 2020;14(8):e0008451. doi: 10.1080/14656566.2024.2333372.

27. Ogwu MC, Izah SC. Potential Future Trends in Managing Tropical Diseases. In: Ogwu MC, Izah SC, editors. Technological Innovations for Managing Tropical Diseases. Cham: Springer Nature Switzerland; 2025. p. 329-56. doi:10.1007/978-3-031-82622-1_14.