Dedicated to

Maa and Baba

List of Publications

Sections of the work presented in this thesis are reported in the following publications

- Saha, D. and Nath Jha, A. Computational multi-target approach to target essential enzymes of Leishmania donovani using comparative molecular dynamic simulations and MMPBSA analysis. *Phytochemical Analysis*, 34(7):842-854, 2023
- Saha, D., Borah, N. J. and Jha, A. N. Molecular scaffold recognition of drug molecules against essential genes of Leishmania donovani using biocomputing approach. *South African Journal of Botany*, 162:52-63, 2023
- Saha, D. and Jha, A. N. Integrated subtractive genomics and structure-based approach to unravel the therapeutic drug target of Leishmania species. *Archives of Microbiology*, 206(10):1-17, 2024

Other Publications

- Quraishi, S., Saha, D., Kumari, K., Jha, A. N. and Roy, A. S. Non-covalent binding interaction of bioactive coumarin esculetin with calf thymus DNA and yeast transfer RNA: A detailed investigation to decipher the binding affinities, binding location, interacting forces and structural alterations at a molecular level. *International Journal of Biological Macromolecules*, 257,128568, 2024.
- Rather, M. A., Saha, D., Bhuyan, S., Jha, A. N. and Mandal, M. Quorum quenching: A drug discovery approach against Pseudomonas aeruginosa. *Microbiological Research*, 127173, 2022.

Conference Proceeding

 Saha, D. and Jha, A. N. Multi-target approach on Leishmania donovani and finding out potent inhibitors for essential enzymes. In *Proceedings of the XXXVIII Symposium of Bioinformatics and Computer-Aided Drug Discovery pp*, 2022.

Book Chapter

 Saha, D., Khataniar, A., Singh, A. K. and Jha, A. N. Review of methods for encapsulation of nutraceutical compounds. In *Nutraceuticals* (pp. 127-156). Academic Press, 2023.

Declaration

I, hereby, declare that the thesis entitled, "Study on Genomic Sequences and Proteins of *Leishmania donovani* by Sequence and Structure-Based Approach" has been submitted to the Department of Molecular Biology and Biotechnology, Tezpur University under the School of Sciences in partial fulfillment for the award of the degree of Doctor of Philosophy in Molecular Biology and Biotechnology. The work reported in this thesis is original and was carried out by me during my tenure as a PhD student at the Department of Molecular Biology and Biotechnology, Napaam. This thesis work has not been previously considered for the award of any degree, diploma, associateship, membership or similar title of any university or institution or organization.

Date: 6/01/2025 Place: Tezpur, Assam

Debanjan Sala (Debanjan Saha)

(Debanjan Saha) Registration No: TZ203872 of 2022 Enrollment No: MBP19111 Department of MBBT School of Sciences, Tezpur University, Assam



TEZPUR UNIVERSITY

Certificate of the Supervisor

This is to certify that the thesis entitled, "Study on Genomic Sequences and Proteins of Leishmania donovani by Sequence and Structure-Based Approach", submitted to the School of Sciences, Tezpur University in partial fulfillment for the award of the degree of Doctor of Philosophy in Molecular Biology and Biotechnology is a record of research work carried out by Mr. Debanjan Saha under my supervision and guidance.

All help received by him from various sources have been duly acknowledged. No part of this thesis has been submitted elsewhere for award of any other degree.

Date: 6th Jan, 2025 Place: Tezpur

Signature of Supervisor

Dr. Anupam Nath Jha Designation: Associate Professor School: Sciences Affiliation: Tezpur University Dr. Anupam Nath Jha

Associate Professor Dept. of Molecular Biology & Biotechnology Tezpur University, Tezpur-784028

Acknowledgement

Firstly, I would like to express my sincere gratitude to my PhD. supervisor, **Dr. Anupam Nath Jha** for his continuous support throughout my Ph.D. study and related research. His suggestions, scientific discussions and guidance during my tenure helped me in all the time of PhD work and writing of this thesis. Besides my advisor, I would also like to thank the rest of my doctoral committee: **Dr. Suman Dasgupta** and **Dr. Aditya Kumar** for their encouragement and suggestions which were valuable for carrying out my work. Their insightful comments have widened up my research from various perspectives. I extend my sincere thanks to **Dr. Atanu Singha Roy & Sana Quraishi** (NIT Meghalaya) for the insightful scientific discussions & collaborative work. I would like to thank Tezpur University for its infrastructure and allowing me to pursue my research work. Also, I would like to acknowledge the financial support provided by University Grant Commission and Tezpur University (for project and institutional fellowship, respectively). I am grateful to the Head of Department, all the faculty members, research scholars, non-teaching staff, all seniors, juniors and project students of the MBBT department for helping me throughout my Ph.D. tenure.

I also thank my fellow lab mates & alumni: Sapna Di, Nikita Di, Zaved Da, Upasana, Sibasree, Nayan, Aroop, Afreen and Shiba for their motivation. Also, their active participation in the discussions and presentations stimulated the scientific knowledge within me.

In particular, I am immensely grateful to **Ajit** who has been throughout all the phases of my PhD and personal life. His support and suggestions in times is a priceless effort that helped me in dealing with the queries. I would also like to thank my fellow doctoral student **Tapas** for their cooperation and he has been constantly there throughout my tenure. He kept me going and helped me in achieving my dreams. My heartfelt thanks to **Muzamil Bhaiya**, **Shuvam**, **Upalabdha**, **Babli**, **Archana Di**, **Susmita**, **Ankita**, **Priyanjana**, **Tamal**, **Kunal Da**, **Gitashree**, **Akash**, **Deepshikha** and all my batchmates for their care and support.

My heartfelt thanks to my friend, **Amit Kumar Chaudhary** for their care and support & making my stay at TU memorable. I thank my friends **Mahari, Jyotirmoy and Hirak** whose

presence and moral support led to an easy and memorable stay on the campus. I am highly grateful to my fellow wishers **Rohan** and **Gurgi** who always provided me the motivation in successfully completing my PhD tenure. I am deeply grateful to **Anupama Di** and **Pranjana** for their unwavering support during and beyond my teaching tenure.

Lastly, I would acknowledge with gratitude, the support, love and care of my family throughout my life. I am grateful to my parents, "**Basudev Saha (baba)** and **Kanika Saha (maa)**" who always stood by me throughout the difficult and steady times and their belief which motivated me in fulfilling my dreams. I am thankful to **Dr. Manirupa Saha** and **Dr. Arun Kumar Saha**, for being there and continuously supporting me through PhD hardship.

Last but not the least, I would like to thank especially my family members, Late Gandeswari Saha (Grandmother), Mrs. Minati Rani Saha (Aunt) and Mrs. Jharna Saha (Sister), Debosmita Saha (Sister), Mrs. Mani Saha (Aunt), Mr. Ashim Kumar Saha (Uncle), Mrs. Pulaka Saha (Aunt), Mr. Babul Saha (Brother-in-law) for their love, moral support, always standing by my side, encouraging me to pursue my goals, and above all, the Almighty God for his never-ending blessings on me.

(Debanjan Saha)

LIST OF TABLES

Table No.	Caption	Page No.
Table 1.1	Chemotherapeutic drugs for leishmaniasis treatment	7
Table 1.2	Vaccination strategies investigated for combatting Leishmania	14
Table 3.1	List of available L. donovani structures on PDB database	69
Table 3.2	ADMET screening of inhibitors	71
Table 3.3	Ligands that passed PASS analysis	72
Table 3.4	PASS analysis for inhibitors	73
Table 3.5	Docking result of APRT and DHODH with top molecules	74
Table 3.6	RMSD result of APRT and DHODH docking complexes with co-crystal APRT and DHODH structures	75
Table 3.7	Docking result of APRT and DHODH with inhibitors which cleared PASS analysis	75
Table 3.8	Number of non-bonded interactions involved between proteins (APRT and DHODH) with compounds and inhibitors during the course of simulation time	85
Table 3.9	Average MMPBSA energy term for the binding of compounds with APRT and DHODH	88
Table 4.1	Drug targets of Leishmania donovani with UniProt ID	108-109
Table 4.2	Essential genes of Leishmania donovani with their respective UniProt ID	109-111
Table 4.3	List of essential protein present on essential pathway of <i>L</i> . <i>donovani</i> .	111
Table 4.4	Details of modelled structures for PK and SDM protein	112
Table 4.5	PASS analysis, docking result of both proteins with 10 molecules and its common uses	114
Table 4.6	The number of non-bonded contacts between proteins (PK and SDM) and selected molecules	121
Table 4.7	Average MMPBSA energy (kJ/mol) for the binding of PK and SDM with selected ligands	124
Table 5.1	Details of reference proteome of 5 Leishmania species	141
Table 5.2	Druggability test of proteins	144
Table 5.3	List of selected protein targets	145
Table 5.4	Ramachandran plot analysis of all five proteins	145

Table 5.5	List of GDH proteins obtained from Alphafold method	146
Table 5.6	Percentage identity and RMSD of the GDH protein among five different Leishmania species	146
Table 5.7	Ligand-binding active sites of the GDH protein based on CASTp predictions	148
Table 5.8	Docking score between selected ligands and GDH of various Leishmania species	149
Table 5.9	Numbers of interactions between GDH proteins and ligands during the course of simulation	159
Table 5.10	MM/PBSA analysis of the bound complexes	160

LIST OF FIGURES

Figure No.	Caption	Page No.
Figure 1.1	Endemic status of CL 2022 taken from WHO	4
Figure 1.2	Endemic status of VL 2022 taken from WHO	4
Figure 1.3	Distribution of Leishmaniasis in Indian subcontinent	5
	Diagrammatic representation of force field interactions:	
Figure 2.1	covalent bonds are shown with bold solid lines, while non-	46
	bonded interactions are depicted with light dashed lines	
E	Visualization of periodic boundary conditions in two	10
Figure 2.2	dimensions	49
E	Schematic diagram to show the multi-target approach on	(5
Figure 3.1	two enzymes of Leishmania donovani	65
E: 2.2	3D structure of <i>Leishmania donovani</i> (a) APRT and (b)	
Figure 3.2	DHODH protein	66
	Docked structure of APRT with Lig_1(a), Lig_2(b),	
Figure 3.3	Lig_3(c), Lig_4 (d) and Lig_5 interactions. The interactions	76
Figure 5.5	present are van der Waals bonds (cyan), H-bonds	70
	(green), π - σ bonds (purple), and alkyl bonds (pink)	
	Docked structure of DHODH with Lig_1(a), Lig_2(b),	
Figure 3.4	Lig_3(c), Lig_4 (d) and Lig_5 interactions. The interactions	77
Figure 5.4	present are van der Waals bonds (cyan), H-bonds	//
	(green), π - σ bonds (purple), and alkyl bonds (pink)	
	Short simulation of 20ns of APRT protein with four ligands	
Figure 3.5	and with one inhibitor, respectively. (a), (b) and (c)	79
	represents RMSD, RMSF and Rg plot of APRT protein	
	Short simulation of 20ns of DHODH protein with four	
Figure 3.6	ligands and with one inhibitor, respectively. (a), (b) and (c)	80
	represents RMSD, RMSF and Rg plot of DHODH protein	
Figure 2.7	RMSD plot of APRT(a) and DHODH(b) in the presence	81
Figure 3.7	and absence of compounds and inhibitor	01

Eiguno 2.9	RMSF plot of APRT(a) and DHODH(b) in the presence	82	
Figure 3.8	and absence of compounds and inhibitor		
Figure 3.9	Rg plot of APRT(a) and DHODH(b) in the presence and	83	
	absence of compounds and inhibitor		
Figure 3.10	H-bond plot of APRT(a) and DHODH(b) in the presence	01	
	and absence of compounds and inhibitor	84	
	2D visualization of APRT with Lig_2 (a,b) and Lig_3 (c,d)		
F ' 2 11 1	at 0 ns and 100 ns of simulation. The compounds remained	96	
Figure 3.11.1	bound to APRT throughout the simulation time with stable	86	
	interactions		
	2D visualization of DHODH with Lig_2 (a,b) and Lig_3		
	(c,d) at 0 ns and 100 ns of simulation. The compounds		
Figure 3.11.2	remained bound to DHODH throughout the simulation	87	
	time with stable interactions		
	Graphs showing per residue decomposition of energy of		
Figure 3.12.1	APRT(a,b,c) with Lig_2, Lig_3 and inhibitor complexes	90	
Ei	Graphs showing per residue decomposition of energy of	01	
Figure 3.12.2	DHODH(a,b,c) with Lig_2, Lig_3 and inhibitor complexes	91	
E ¹	Systematic diagram for identifying possible inhibitors	105	
Figure 4.1	against PK and SDM drug targets	105	
	Docked structure of PK with Lig_1(a), Lig_2(b), Lig_3(c)		
	and SDM with Lig_1(d), Lig_2(e) and Lig_3(f)		
Figure 4.2	interactions. The interactions present are van der Waals	115	
	bonds (cyan), H-bonds (green), π - σ bonds (purple), and		
	alkyl bonds (pink)		
Eigung 4 2 1	Representation of PK with Lig_1, Lig_2 and Lig_3 at 0 ns,	117	
Figure 4.3.1	50 ns and 100 ns of MD simulation		
Eigung 4.2.2	Representation of SDM with Lig_1, Lig_2 and Lig_3 at 0	117	
Figure 4.3.2	ns, 50 ns and 100 ns of MD simulation	117	
Figure 4.4	RMSD plot of PK-apo, SDM-apo and complexes with	110	
Figure 4.4	selected ligands	118	
Figure 4.5	RMSF plot of PK-apo, SDM-apo and complexes with	119	
Figure 4.5	selected ligands	119	

Figure 4.6	Radius of gyration plot of PK-apo, SDM-apo and complexes with selected ligands	119
Figure 4.7	Hydrogen bond interaction plot of PK and SDM with selected ligands	120
Figure 4.8.1	2D visualization of PK using Lig_1(a,b), Lig_2(c,d), and Lig_3(e,f) at simulation times of 0 ns and 100 ns. van der Waals (cyans), H-bond (green), pi-sigma (purple), and alkyl interactions are all present (pink)	122
Figure 4.8.2	2D visualization of SDM using Lig_1(a,b), Lig_2(c,d), and Lig_3(e,f) at simulation times of 0 ns and 100 ns. van der Waals (cyans), H-bond (green), pi-sigma (purple), and alkyl interactions are all present (pink)	123
Figure 5.1	Illustration depicting the subtractive genomic and structure-based methodologies for identifying drug targets in Leishmania species	137
Figure 5.2	Multiple Sequence Alignment of GDH proteins	143
Figure 5.3	Phylogenetic tree of GDH proteins	144
Figure 5.4	3D structure of five GDH Leishmania species	147
Figure 5.5	2D structure of three ligands	149
Figure 5.6	Docked structure of bithionol with GDH of <i>L. donovani</i> (a), <i>L. braziliensis</i> (b), <i>L. infantum</i> (c), <i>L. major</i> (d) and <i>L. mexicana</i> (e). The interactions present are van der Waals bonds (cyan), H-bonds (green), π - σ bonds (purple), and alkyl bonds (pink).	150
Figure 5.7	Docked structure of GW5074 with GDH of <i>L. donovani</i> (a), <i>L. braziliensis</i> (b), <i>L. infantum</i> (c), <i>L. major</i> (d) and <i>L. mexicana</i> (e). The interactions present are van der Waals bonds (cyan), H-bonds.	151
Figure 5.8	Comparison of average Root Mean Square Deviation (RMSD) of Glutamate dehydrogenase of <i>L. donovani</i> , <i>L. braziliensis</i> and <i>L. infantum</i>	153

Figure 5.9	Comparison of average Root Mean Square Fluctuations		
	(RMSF) of Glutamate dehydrogenase of L. donovani, L.	154	
	braziliensis and L. infantum		
Figure 5.10	Comparison of average Radius of Gyration (Rg) of		
	Glutamate dehydrogenase of L. donovani, L. braziliensis	155	
	and L. infantum		
Figure 5.11	Comparison of average number of Hydrogen bonds of		
	Glutamate dehydrogenase of L. donovani, L. braziliensis	156	
	and L. infantum		
	Interaction profile of GDH protein with Lig1. (A) GDH of	157	
	L. braziliensis (3D visualization); (B) GDH of L.		
F' 5121	braziliensis (2D visualization); (C) GDH of L. donovani		
Figure 5.12.1	(3D visualization); (D) GDH of L. donovani (2D		
	visualization); (E) GDH of L. infantum (3D visualization);		
	(F) GDH of <i>L. infantum</i> (2D visualization)		
Figure 5.12.2	Interaction profile of GDH protein with Lig2. (A) GDH of		
	L. braziliensis (3D visualization); (B) GDH of L.	158	
	braziliensis (2D visualization); (C) GDH of L. donovani		
	(3D visualization); (D) GDH of L. donovani (2D		
	visualization); (E) GDH of L. infantum (3D visualization);		
	(F) GDH of <i>L. infantum</i> (2D visualization)		

List of Abbreviation

2D	Two dimensional
3D	Three dimensional
Ag ₂ O	Silver oxide
AmB	Amphotericin B
AAH	Adenine aminohydrolase
Ade	Adenine,
Ado	Adenosine
ADMET	Absorption, Distribution, Metabolism, Excretion and Toxicity
ADSL	Adenylsosuccinate Lyase
ADSS	Adenylosuccinate syntheatse
AMBER	Assisted Model Building with Energy Refinement
AML	Acute Myeloid Leukaemia
AMP	Adenosine Monophosphate
AMPDA	AMP deaminase
APRT	Adenine phosphoribosyltransferase
ATB	Automated Topology Builder
BCG	Bacillus Calmette-Guérin
BLAST	Basic Local Alignment Search Tool
COM	Centre of Mass
CL	Cutaneous Leishmaniasis
CHARMM	Chemistry at Harvard Macromolecular Mechanics
DNA	Deoxyribonucleic acid
DHODH	Dihydroorotate dehydrogenase
FDA	Food and Drug Administration
FFT	Fast Fourier transform
GDH	Glutamate dehydrogenase
GLOII	Glyoxalase II
GAPDH	Glyceraldehyde-3-phosphate dehydrogenase
GMP	Guanosine Monophosphate
GMPS	Guanosine monophosphate synthetase
GROMACS	GROningen MAchine for Chemical Simulations
GROMOS	GROningen MOlecular Simulation
GR	glutathione reductase
GUI	Graphical User Interface
LMT	Leishmania miltefosine transporter
UniProt	Universal Protein Resource

IL	Interluekin
(IFN)-γ	Interferon
IDRI	Infectious Disease Research Institute
KEGG	Kyoto Encyclopedia of Genes and Genomes
LGA	Lamarckian genetic algorithm
MDR	Multidrug-resistant
MD	Molecular Dynamics
MCL	Mucocutaneous leishmaniasis
MLR	Multiple Linear Regression
MMPBSA	Molecular Mechanics Poisson-Boltzmann Surface Area
MSA	Multiple Sequence Alignment
NVBDCP	National Vector Borne Disease Control Programme
NAMD	Nanoscale Molecular Dynamics
NCBI	National Center for Biotechnology Information
NMR	Nuclear Magnetic Resonance
NTDs	Neglected Tropical Diseases
PME	Particle mesh Ewald
PASS	Prediction of Activity Spectra for Substances
РК	Pyridoxal kinase
PCA	Principal Component Analysis
PDB	Protein Data Bank
PIN	Protein Interaction Network
PME	Particle Mesh Ewald
QSAR	Quantitative Structure Activity Relationship
RCSB	Research Collaboratory for Structural Bioinformatics
RMSD	Root Mean Square Deviation
RMSF	Root mean square fluctuation
RNA	Ribonucleic acid
SCOP	Structural Classification of Proteins
SDM	Sterol alpha-14 demethylase
SLN	Solid lipid nanoparticles
SMILES	Simplified Molecular Input Line Entry System
SPC	Single Point Charge
TB	Tuberculosis
TNF- α	tumor- necrosis factor-α
TiO ₂	Titanium dioxide
VL	Visceral Leishmaniasis
VS	Virtual Screening
WHO	World Health Organization
XMP	Xanthine Monophosphate
XPRT	Xanthine phosphoribosyltransferase