

Curriculum Vitae
Bhanwar Lal Puniya, Ph.D.
Research Assistant Professor
Department of Biochemistry, University of Nebraska-Lincoln, NE 68503
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EDUCATION

Ph.D. in Biotechnology	<i>Savitribai Phule Pune University, Pune, India</i>	2010 – 2015
M.Sc. in Microbiology	<i>University of Rajasthan, Jaipur, India</i>	2005 – 2007
B.Sc.	<i>University of Bikaner, Bikaner, India</i>	2001 – 2005

PROFESSIONAL APPOINTMENTS

Research Assistant Professor	05/2020 - Present
<i>Department of Biochemistry, University of Nebraska-Lincoln, NE, USA</i>	
Postdoctoral Research Associate	07/2015 – 04/2020
<i>Department of Biochemistry, University of Nebraska-Lincoln, NE, USA</i>	
Senior Research Fellow (Ph.D. Candidate)	03/2011 – 09/2014
<i>CSIR-Institute of Genomics and Integrative Biology, Delhi, India</i>	
Junior Research Fellow (Ph.D. Candidate)	03/2009 – 03/2011
<i>CSIR-Institute of Genomics and Integrative Biology, Delhi, India</i>	
Lecturer of Biotechnology	07/2008 – 02/2009
<i>Seth Motilal P.G. College, Jhunjhunu, India</i>	

PUBLICATIONS

Google Scholar Profile: <https://scholar.google.com/citations?hl=en&user=tXybjcAAAAI>

Published (26 full-length peer-reviewed articles and 5 conference abstracts)

- [31] Niarakis, Anna, et al. Drug-Target identification in COVID-19 disease mechanisms using computational systems biology approaches, *Front. Immunol.* 2023 (Accepted for publication)
- [30] Bessell B, Loecker J, Zhao Z, Aghamiri SS, Mohanty S, Amin R, Helikar T, **Puniya BL***. COMO: a pipeline for multi-omics data integration in metabolic modeling and drug discovery. *Brief Bioinform.* 2023 Sep 22;24(6):bbad387. doi: 10.1093/bib/bbad387. (*Corresponding author)
- [29] **Puniya BL***, Dräger A. Advancements in computational modelling of biological systems: seventh annual SysMod meeting, *Bioinformatics*, Volume 39, Issue 9, September 2023, btad539, <https://doi.org/10.1093/bioinformatics/btad539> (*Corresponding author)

- [28] Puniya BL, Bessell B, Zhao Z, Loecker J, Aghamiri SS, Mohanty S, Amin R, Helikar T. A computational pipeline for drug discovery in immunometabolism against autoimmune diseases. *J Immunol* 1 May 2023; 210 (1_Supplement): 85.15. <https://doi.org/10.4049/jimmunol.210.Supp.85.15> (conference abstract)
- [27] Aghamiri SS, Puniya BL, Amin R, Murry DJ, Helikar T. Identification of Novel Immunosuppressive Drug Targets for Liver Transplantation Using Genome-Scale Metabolic Modeling. *J Immunol* 1 May 2023; 210 (1_Supplement): 173.43. <https://doi.org/10.4049/jimmunol.210.Supp.173.43> (conference abstract)
- [26] Amin R, Aghamiri SS, **Puniya BL**, Helikar T. A multiscale mechanistic model of human dendritic cells for in-silico investigation of immune responses and novel therapeutics discovery. *J Immunol* 1 May 2023; 210 (1_Supplement): 221.22. <https://doi.org/10.4049/jimmunol.210.Supp.221.22> (conference abstract)
- [25] Aghamiri SS, **Puniya BL**, Amin R, Helikar T. A multiscale mechanistic model of human dendritic cells for in-silico investigation of immune responses and novel therapeutics discovery. *Front. Immunol.* 2023, 10:14:1112985.
- [24] Yue Y, **Puniya BL**, Helikar T, Girardo B, Hinrichs SH, Larson MA. Arginine Catabolism and Polyamine Biosynthesis Pathway Disparities within Francisella tularensis Subpopulations. *Front. Microbiol.* 2022, 13:890856
- [23] Fan R, Thomas S, You M, Li Z, Bessell B, **Puniya BL**, Helikar T, Liu Z, Chung S. Fish Oil Intake During Gestation and Lactation Attenuated STZ-Induced Diabetes in Male Offspring via Activation of Brown Fat and Modulating Oxylipin Profile. *Current Developments in Nutrition*. 2022 Jun;6(Supplement_1):640-. (conference abstract)
- [22] Mobeen A, **Puniya BL**, Ramachandran S. A computational approach to investigate constitutive activation of NF-κB. *Proteins*. 2022 May 27. doi: 10.1002/prot.26388. Epub ahead of print. PMID: 35620856.
- [21] Yook JS, You M, Kim J, Toney AM, Fan R, **Puniya BL**, Helikar T, Vaulont S, Deschemin JC, Okla M, Xie L, Ghosh M, Rouault T, Lee J, Chung S. Essential role of systemic iron mobilization and redistribution for adaptive thermogenesis through HIF2α/hepcidin axis. *Proc. Natl. Acad. Sci. USA*, 2021 Oct 5;118(40).
- [20] Ostaszewski, M, et al. COVID19 Disease Map, a computational knowledge repository of virus–host interaction mechanisms. *Mol. Syst. Biol.*, 2021 Oct;17(10):e10387.
- [19] Wertheim KY, **Puniya BL**, La Fleur A, Shah AR, Barberis M, Helikar T. A multi-approach and multi-scale platform to model CD4+ T cells responding to infections. *PLoS Comput. Biol.* 2021 Aug 3;17(8):e1009209.
- [18] Vieira D da S, Polveiro RC, Butler TJ, Hackett TA, Braga CP, **Puniya BL**, et al. An in silico, structural, and biological analysis of lactoferrin of different mammals. *Int. J. Biol. Macromol.* 187:119–26, 2021.
- [17] Moore R, **Puniya BL***, Robert Powers, Chittibabu Guda, Kenneth W Bayles, David Berkowitz, Helikar T. Integrative network analysis of transcriptomics data reveals potential drug targets for acute radiation syndrome. *Sci. Rep.* 11, 5585, 2021. (*co-first author)
- [16] **Puniya BL**, Amin R, Lichter B, Moore R, Ciurej A, Townsend S, Shah AR, Barberis M, Helikar T. Integrative computational approach identifies new targets in CD4+ T cell-mediated immune disorders. *npj Syst. Biol. Appl.* 7, 4 2021.
- [15] Larson MA, Abdalhamid B, **Puniya BL**, Helikar T, Kelley DW, Iwen PC Differences in Blood-derived *Francisella tularensis* Type B Strains from Clinical Cases of Tularemia. *Microorganisms*, 8 (10), 1515, 2020.

- [14] Lampe AT, Puniya BL, Pannier AK, Helikar T, Brown DM Combined TLR4 and TLR9 agonists induce distinct phenotypic changes in innate immunity in vitro and in vivo. *Cell. Immunol.* 104149, 2020.
- [13] Pentzien T, **Puniya BL**, Helikar T, Matache MT. Identification of biologically essential nodes via determinative power in logical models of cellular processes. *Front. Physiol.* 9:1185, 2018.
- [12] **Puniya BL**, Todd RG, Mohammed A, Deborah MB, Barberis M, Helikar T. A mechanistic computational model reveals that plasticity of CD4+ T cell differentiation is a function of cytokine composition and dosage. *Front. Physiol.* 9:878, 2018
- [11] Sharma J, Mittal I, Pramanik A, Singh N, Dube N, Sharma S, **Puniya BL**, Raghunandanan MV, Mobeen A, Ramachandran S. T2DiACoD: A gene atlas of type 2 diabetes mellitus associated complex disorders. *Sci. Rep.* 7: 6892, 2017
- [10] Perez VM, **Puniya BL**, Helikar T, DiRusso C C, Black, PN. Computational modeling of human fatty acid transport protein 2. *The FASEB Journal*, 31(1 Supplement), 630-20, 2017. ([Conference Abstract](#))
- [9] **Puniya BL**, Kulshreshtha D, Mittal I, Mobeen A, and Ramachandran S. Integration of metabolic modeling with gene co-expression reveals transcriptionally programmed reactions explaining robustness in *Mycobacterium tuberculosis*. *Sci. Rep.* 6: 23440, 2016
- [8] **Puniya BL**, Allen L, Hochfelder C, Majumder M, & Helikar T. Systems perturbation analysis of a large scale signal transduction model reveals potentially influential candidates for cancer therapeutics. *Front. Bioeng. Biotechnol.* 4, 2016
- [7] Yadav VK, Mandal RS, **Puniya BL**, Kumar R, Dey S, Yadav S. Structural and binding studies of N-terminally truncated form of cystatin S (SAP-1 protein) with heparin". *Chem. Biol. and Drug. Des.*, 2014
- [6] Gupta P, **Puniya B**, Barun S, Asthana M, Kumar A. Isolation and characterization of endophytes from different plants: effects on growth of *Pennisetum typhoides*. *Biosci, Biotechnol Res Asia*. 2014, 11(1):223-34.
- [5] Kalra S, **Puniya BL**, Kulshreshtha D, Kumar S, Kaur J, Ramachandran S, Singh K. De novo transcriptome sequencing reveals important molecular networks and metabolic pathways of the plant, *Chlorophytum borivilianum*. *PLoS ONE* 8(12): e83336, 2013.
- [4] Yadav VK, Mandal RS, **Puniya BL**, Singh S, Yadav S. Studies on the interaction of SAP-1 (an N-terminal truncated from cystatin S) with its binding partners by CD-spectroscopic and molecular docking methods. *J Biomol. Struct. Dyn.* 2013.
- [3] **Puniya BL**, Kulshreshtha D, Verma SP, Kumar S, and Ramachandran S. Integrated gene co-expression network analysis in the growth phase of *Mycobacterium tuberculosis* reveals new potential drug targets. *Mol. BioSyst.*, 9, 2798-2815, 2013.
- [2] Kumar S, **Puniya BL**, Parween S, Nahar P, and Ramachandran S. Identification of novel adhesins of *M. tuberculosis* H37Rv using integrated approach of multiple computational algorithms and experimental analysis. *PLoS ONE*, 8(7):e69790, 2013.
- [1] Ramachandran S, Chaudhuri R, Verma SP, Shah AR, Paul C, Chakraborty S, **Puniya BL**, Mandal RS. Biological data modelling and scripting in R. *Systems and Computational Biology - Bioinformatics and Computational Modeling*, Ning-Sun Yang (Ed.), ISBN: 978-953-307-875-5, InTech, 2011. ([Book Chapter](#))
- In press, under review, and to be submitted.**
- [2] Amin R, Aghamiri SS, **Puniya BL**, Helikar T. A comprehensive logic-based model of the human immune system to study the dynamics responses to mono- and coinfections. ([In Preparation](#))
- [1] Musilova J, Vafeck Z, **Puniya BL**, Helikar T, Sedlar K. The Augusta Python package: From RNA-Seq to Boolean Models through Gene Regulatory Networks (Under revision for *Computational and Structural Biotechnology*)

RESEARCH SUPPORT

Submitted/Pending

Title: PIPP Phase II: Theme 3: The Host as the Universe. Immune Digital Twins for Pandemic Prevention and Preparedness
Proposed period: 05/2024 – 04/2031
Source: National Science Foundation
Role: Co-Investigator
Funding amount: \$18 M

Currently active

Title: Digital Twin Innovation Hub
Proposed period: 08/01/2022–07/31/2027
Source: Grand Challenges Catalyst Competition - Catalyst Awards
Role: Co-Investigator
Funding amount: \$5,039,652

Completed

Title: Computational tools for drug discovery in immune cells
Dates: 01/08/2021 – 07/31/2022
Source: Jane Robertsson Layman Fund
Role: PI (Project director)
Funding: \$10,000

AWARDS, HONORS, AND FELLOWSHIPS

Layman Award, 2021-2022 Layman Seed Awards competition, the University of Nebraska Foundation
F1000 Poster Award, *Intelligent Systems for Molecular Biology (ISMB)-2018*, Chicago, USA, 2018
Best poster award at SysMod COSI, ISMB-2018, Chicago, USA, 2018
Travel grant, *Whole Cell Modeling Summer School- 2017*, Centre for Genomic Regulation, Barcelona, Spain, 2017
Honorable mention (poster), *Open-Source Computer Aided Translational Medicine (OSCAT)*, CSIR-Institute of Microbial Technology, Chandigarh, India, 2012
CSIR-Senior Research Fellowship, *Council of Scientific and Industrial Research*, Government of India, 2011 - 2014
CSIR-Junior Research Fellowship, *Council of Scientific and Industrial Research*, Government of India, 2009 - 2011

CERTIFICATIONS

Joint CSIR-UGC National Eligibility Test (NET), India	Dec 2008; Jun 2008 ; Dec 2007; Jun 2006
Graduate Aptitude Test in Engineering (GATE), India	2007

INVITED TALKS

- [11] Closing Remarks and poster awards , *SysMod COSI, ISMB-2022 Conference*, Madison, WI, July 11, 2022
- [10] Systems biology and its applications in biomedical research, Brno University of Technology, Brno, Czechia (Virtual), Mar 02, 2022
- [9] Metabolic drug repurposing for autoimmune diseases, SysMod COSI, ISMB ECCB, (Virtual), July 29, 2021
- [8] Systems biology and its applications in biomedical research, Amity Institute of Biotechnology, Amity University, Noida, India (Virtual), Mar 06, 2021.
- [7] Modulating CD4+ T cell response using systems approaches, College of Arts and Science, Texas A&M University-San Antonio, TX, USA (Virtual), Feb 09, 2021
- [6] Knowledge discovery using integrative computational modeling of biological systems. Department of Immunology, St. Jude Children's Research Hospital, Memphis, TN, USA, Nov 05, 2019
- [5] An integrative computational modeling approach to identify repurposable metabolic drug targets in CD4+ T cells. *Great Lake Bioinformatics Conference -2019*, University of Wisconsin Madison, Madison, WI, USA, May 22, 2019
- [4] Multi-scale systems modeling of the regulation of CD4+ T-cell differentiation. Nebraska Center for Virology, University of Nebraska-Lincoln, Sep 1, 2017
- [3] Systems modeling of interplay among extracellular cytokines regulating phenotypic plasticity of CD4+ T-cell differentiation. *International Conference on Systems Biology*, VirginiaTech, Blacksburg, VA, USA, Aug 07, 2017
- [2] Systems perturbation analysis of signal transduction to prioritize cancer therapeutic targets. *Molecular Mechanism of Disease seminar series*, Department of Biochemistry, University of Nebraska-Lincoln, NE, USA, Sep 15, 2016
- [1] Systems perturbation analysis of signal transduction to prioritize cancer therapeutic targets. *Complex Biosystems seminar series*, Department of Biochemistry, University of Nebraska-Lincoln, NE, USA, Mar 10, 2016

POSTER PRESENTATIONS

- [9] A computational pipeline for drug discovery in immunometabolism against autoimmune diseases, *Immunology2023™*, May 12, 2023, Washington, DC.
- [8] Metabolic drug repurposing for autoimmune diseases, SysMod COSI, ISMB ECCB, Jul 29, 2021 (Virtual).
- [7] An integrative computational modeling approach to identify repurposable metabolic drug targets in CD4+ T cells. *Great Lakes Bioinformatics Conference (GLBIO)*, 2019, Madison, WI, USA
- [6] Systems modeling of phenotypic plasticity of CD4+ T cell differentiation. *Intelligent Systems for Molecular Biology (ISMB)*, 2018, Chicago, USA
- [5] Systems modeling of interplay among extracellular cytokines regulating phenotypic plasticity of CD4+ T-cell differentiation. *International Conference on Systems Biology (ICSB)*, 2017, VirginiaTech, Blacksburg, USA
- [4] Systems perturbation analysis of signal transduction to prioritize cancer therapeutic targets. *Intelligent Systems for Molecular Biology (ISMB)*, 2016, Orlando, Florida, USA
- [3] Investigating gene co-expression modules in optimally growing *Mycobacterium tuberculosis*. *Kolkata International School Cum Conference on Systems Biology (KOLSYSBIO)*, 2013, Kolkata, India

[2] Analyzing highly co-expressed sub-network modules across multiple strains of *Mycobacterium tuberculosis*. *Open-Source Computer Aided Translational Medicine (OSCAT)*, 2012, Chandigarh, India

[1] Exploring critical genes and pathways by analyzing co-expression networks in *Mycobacterium tuberculosis*. *Genomeet*, 2012, Delhi, India

SUPERVISING AND MENTORING

Mentored/Supervised researchers (at the University of Nebraska-Lincoln)

[23] Dennis Startsev (Undergraduate)	2023 – present
[22] Astha Mishra (Contractor, modeler)	2022 – present
[21] Achilles Gasper Rasquinha (Computer science master student)	2021- 2022
[20] Sara Aghamiri (Senior reseracher)	2021 – present
[19] Jana Musilova (visiting PhD student from Technical University of Brno, Czech Republic)	2021 – 2022
[18] Ronit Gandhi (3rd year undergraduate student majoring in biochemistry and mathematics, INBRE student):	2021
[17] Josh Loecker (first year PhD student in Biochemistry)	2021 – present
[16] Sabyasachi Mohanty (Undergraduate from Amity University, Noida, India)	2021 – present
[15] Brandt Bessell (Research Assistant)	2020 – 2022
[14] Di Wu (Ph.D. Candidate)	2020
[13] Savannah Hargens (Undergraduate)	2020
[12] Samuel Streeter (Undergraduate)	2020
[11] Hana McMahon-Cole (Undergraduate)	2020
[10] Robert B. Moore (Research Assistant):	2017 – present
[9] Dielson da Silva Vieira (Visiting Ph.D. student from UNESP, Brazil)	2019-2020
[8] Aimee Kessel (Ph.D. Student)	2017 – 2019
[7] Mihir Samdarshi , (Visiting Student from Loyola Marymount University)	2018
[6] Sydney Townsend (Biochemistry UG student)	2017 – 2018
[5] Bailee Lichter (Biochemistry UCARE student)	2017 – 2019
[4] Alicia Johnson , (Ph.D. student)	2017
[3] Joshua Floth (Ph.D. student)	2016
[2] Alex Ciurej (Biochemistry UCARE Student)	2015 – 2016
[1] Vincent Perez (Ph.D. student)	2015 - 2019

Thesis Supervision (at the University of Nebraska-Lincoln)

[1] Thesis title: Characterization of metabolic networks in differentiated Cd4+ T cells. Student: Bailee Lichter (Biochemistry Honors); Thesis submitted on March 12, 2018

[2] Thesis title: Creating differentiated t cell-specific metabolic models using microarray expression data. Student: Alex Ciurej (Biochemistry Honors); Thesis submitted on March 13, 2017

Mentor for Google Summer of Code 2016 and 2017

Organization: Computational Biology@ University of Nebraska-Lincoln, NE, USA

TEACHING

Teacher (Spring Semester) 2016 - 2021

Department of Biochemistry, University of Nebraska-Lincoln, USA

Modules: Metabolic modeling; kinetics modeling

Course BIOC 439/839: Dynamics of Biochemical and Biological Networks

Lecturer 2008 -2009

Biotechnology Department, Seth Motilal PG College, Jhunjhunu, Rajasthan, India.

Subjects: Genetics, molecular biology and bioinformatics

Classes: Bachelor of Science and Master of Science

PROFESSIONAL SERVICES

Executive Chairperson, SysMod CoSI, International Society for Computational Biology

2022 – Present

Coordinator, SysMod CoSI, International Society for Computational Biology

2022 – Present

Track chair, SysMod CoSI, ISMB-2023 conference

2023

Moderator, SysMod CoSI, ISMB-2022 conference, Madison, WI

2022

Track chair, SysMod CoSI, ISMB-2022 conference, Madison, WI

2022

Academic Editor, Computational and Mathematical Methods

2023 – Present

Academic Editor, PLoS One

2022 – Present

Editorial Board Member, BMC Research Notes

2021 – Present

Review Editor, Frontiers in Immunology

2022 - Present

Review Editor, Frontiers in Bioinformatics

2021 – Present

Guest Editor, Bioengineering (MDPI)

2020

Topic Editor, Bioengineering (MDPI)

2020 – Present

Review Editor, Frontiers in Physiology; Frontiers in Genetics

2019 – 2021

Reviewer, Nature Scientific Reports; Bioengineering; Diagnostics; Metabolites; International Journal of Molecular sciences; Mathematics; Cells

2015 – Present

Research Proposal Evaluator, UCARE at University of Nebraska-Lincoln

2019

Poster Judge, Spring Research Fair at University of Nebraska-Lincoln

Apr 15, 2019

Science Project Judge, Southeast Regional Science Fair sponsored by the Nebraska Junior Academy of Science (NJAS)

Mar 29, 2019

Instructor, WSC Computational Systems Biology for Complex Human Disease (Virtual) Dec 13-17, 2021

Instructor, EMBL-EBI Mathematics of Life training course (Virtual)

Sept 27 - Oct 01, 2021

Instructor, Computational Systems Biology for Complex Human Disease (Virtual)

Dec 07-11, 2020

CONFERENCES AND WORKSHOPS

[19] Immunology2023™, Washington, DC, May 11-15, 2023

[18] ISMB-2022 Coneference, Madison, WI, July 10-14, 2022

[17] WSC Computational Systems Biology for Complex Human Disease (Virtual) 13-17 December 2021.

[16] EMBL-EBI Mathematics of Life training course, September 27 - October 01, 2021 (virtula).

[15] ISMB/ECCB - 2021, Lyon, France, July 25 -30, 2021 (Virtual).

[14] Computational Systems Biology for Complex Human Disease (Virtual Course), December 07-11, 2020

- [13] AAI 2020 Advanced Course in Immunology, July 26 – 31, 2020
- [12] ISMB – 2020, International Society of Computational Biology, Virtual Conference, July 13 – 16, 2020
- [11] EUvsVirus Hackathon, project: Disease Maps and text mining for drug prediction, April 24 – 26, 2020.
- [10] GLBIO-2019, International Society of Computational Biology
University of Wisconsin, Madison, WI, USA, May 19 – 22, 2019
- [9] ISMB-2018, International Society of Computational Biology
Chicago, IL, USA, July 06 – 10, 2018
- [8] Whole Cell Modeling Summer School
Centre for Genomic Regulation, Barcelona, Spain, September 04 – 07, 2017
- [7] International Conference on Systems Biology (ICSB)
VirginiaTech, Blacksburg, VA, USA, August 06 – 12, 2017
- [6] ISMB-2016, International Society of Computational Biology
Orlando, FL, USA, July 08 – 12, 2016
- [5] KOLSYSBIO
Bose Institute and S N Saha institute of Nuclear Physics, Kolkata, India, December 29, 2012 – January 03, 2013
- [4] Open Source Computer Aided Translational Medicine (OSCAT)
CSIR-Institute of Microbial Technology, Chandigarh, India, February 22 – 25, 2012
- [3] Genomeet
CSIR-Institute of Genomics and Integrative Biology, Delhi, India, December 30, 2011 – January 01, 2012
- [2] International Next Generation Sequencing Data Analysis Workshop
Persistent Systems Ltd., Pune, India, October 19 – 22, 2011
- [1] Connect 2 Decode (C2D)
Summer Research Program, Open Source Drug Discovery, CSIR, Delhi, India (Contributed as volunteer), April 9 – 11, 2010

SCIENTIFIC SKILLS

Computer Platforms:	Linux/Unix, Microsoft Windows and Mac OS X
Programming/scripting Languages:	R, MATLAB, Python
Microarray data analysis:	Data acquisition, Data analysis, data integration
Next Generation Sequencing Analysis:	DNA-Seq, RNA-Seq, single cell RNA-seq
Metabolomics/Lipidomics data analysis:	PCA, PLS, PLS-DA, Post hoc analysis
Proteomics data analysis:	Expression analysis, Post hoc analysis
Biological Systems Modeling and Analysis:	Logic-based Boolean modeling, Metabolic reconstruction and analysis, ODE based modeling, Gene co-expression
Functional analysis:	Annotation, Functions, Pathways
Data mining:	-Omics data, text data
Algorithm development:	-Omics data integration, Drug discovery in metabolism
Machine learning:	Data preprocessing, Regression, Classification, Clustering, natural language processing, dimensionality reduction

Deep learning:	Artificial neural networks
Statistical Analysis:	Data normalization, Statistical tests
Phylogenetic Analysis:	Sequence Alignment, Sequence Similarity Search, phylogenetic tree construction
Structural Bioinformatics:	Protein structure modeling, molecular docking analysis
Microbiology:	Culture media preparation, isolation of microorganisms
Molecular Biology:	DNA purification, Gel Extraction, Gel Electrophoresis, PCR