

Rahil Tadjale | Curriculum Vitae

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Education

PhD in Bioinformatics — Institute of Bioinformatics, University of Georgia, Athens, GA 2015 — 2021
(GPA – 4.0)

Master of Science in Bioinformatics — Department of Biological Sciences, 2013 — 2015
Northern Illinois University, DeKalb, IL (GPA – 4.0)

Bachelor of Technology in Biotechnology — Kathmandu University, Dhulikhel, Kavre, Nepal 2007 — 2011
(GPA – 3.65)

Publications

Tadjale R, Uchimiya M, Clendinen CS, Turck C, Borges RM, Edison AS. **PyINETA: A python package for INADEQUATE network analysis**. In Preparation. 2021

Tadjale R, Soleymani S, Priyadarshi A, Venkat A, Yeung W, Kochut K and Kannan N. **GTXplorer: A portal to navigate and visualize the evolutionary information encoded in fold A glycosyltransferases**. 2021
Accepted with minor revisions at Glycobiology.

Tadjale R, Zhou Z, Yeung W, Moremen KW, Li S and Kannan N. **Mapping the glycosyltransferase fold landscape using deep learning**. Under revision at Nature Communications. 2021

Huang LC, **Tadjale R**, Gravel N, Venkat A, Yeung W, Byrne DP, Eysers PA, Kannan N. **KinOrtho: a method for mapping human kinase orthologs across the tree of life and illuminating understudied kinases**. Submitted to BMC Bioinformatics. 2021

Tadjale R, Venkat A, Huang LC, Yeung W, Rasheed K, Edison AS, Moremen KW, Kannan N. **Deep evolutionary analysis reveals the design principles of fold A glycosyltransferases**. eLife, 2020 Apr 1. 2020

Moret N, Liu C, Gyori BM, Bachman JA, Steppi A, **Tadjale R**, Huang LC, Hug C, Berginski M, Gomez SM, Kannan N, Sorger P, NIH Understudied Kinome Consortium. **Exploring the understudied human kinome for research and therapeutic opportunities**. (bioRxiv doi: <https://doi.org/10.1101/2020.04.02.022277>) 2020

Bento AI, **Tadjale R**, Schot C, Bosch T, Mariman R, King AA, Rohani P. **Phylogenetics of pertussis in the vaccine era: transition to re-emergence**. (medRxiv: <https://doi.org/10.1101/19012138>; In preparation) 2020

Beattie NR, Keul ND, Hicks Sirmans TN, McDonald WE, Talmadge TM, **Tadjale R**, Kannan N, Wood ZA. **Conservation of Atypical Allosteric in C. elegans UDP-Glucose Dehydrogenase**. ACS Omega, 2019 Sep 24;4(15):16318-16329. 2019

Florimond C, Cordonnier C, **Tadjale R**, Wel HVD, Kannan N, West CM, Blader IJ. **A Toxoplasma Prolyl Hydroxylase Mediates Oxygen Stress Responses by Regulating Translation Elongation**. mBio, 2019. 10(2) 2019

Kwon A, Scott S, **Tadjale R**, Yeung W, Kochut KJ, Eysers PA, Kannan N. **Tracing the origin and evolution of pseudokinases across the tree of life**. Science Signaling, 2019. 12 (578) 2019

Rahil Taujale	2021
Soares V, Taujale R , Garrett R, da Silva AJR, Borges RM. Extending compound identification for molecular network using the LipidXplorer database independent method: A proof of concept using glycoalkaloids from Solanum pseudoquina A. St.-Hil. Phytochemical Analysis, 2018.	2018
Borges RM, Taujale R , de Souza JS, de Andrade Bezerra T, Silva ELE, Herzog R, Ponce FV, Wolfender JL, Edison AS. Dereplication of plant phenolics using a mass-spectrometry database independent method. Phytochemical Analysis, 2018. 29(6):601-612	2018
Rahman K, Mandalasi M, Zhao P, Sheikh MO, Taujale R , Kim HW, Wel HVD, Matta K, Kannan N, Glushka JN, Wells L, West CM. Characterization of a cytoplasmic glucosyltransferase that extends the core trisaccharide of the Toxoplasma Skp1 E3 ubiquitin ligase subunit. Journal of Biological Chemistry, 2017. 292(45):18644-18659	2017
Hu L, Taujale R , Liu F, Song J, Yin Q, Zhang Y, Guo J, Yin Y. Draft genome sequence of Talaromyces verruculosus ("Penicillium verruculosum") strain TS63-9, a fungus with great potential for industrial production of polysaccharide-degrading enzymes. Journal of Biotechnology, 2016. 219:p.5-6	2016
Taujale R , Yin Y. Glycosyltransferase Family 43 Is Also Found in Early Eukaryotes and Has Three Subfamilies in Charophycean Green Algae. PloS One, 2015. 10(5)	2015
Ekstrom A, Taujale R , McGinn N, Yin Y. PlantCAZyme: a database for plant carbohydrate-active enzymes. Database: The Journal of Biological Databases and Curation, 2014.	2014

Published Abstracts

Taujale R , Soleymani S, Priyadarshi A, Yeung W, Kochut KJ, Kannan N. The GTXplorer portal to access, navigate and mine evolutionary relationships of fold A glycosyltransferases. Glycobiology 30 (12), 1117-1118	2020
Taujale R , Huang LC, Venkat A, Yeung W, Edison AS, Moremen KW, Kannan N. Understanding the sequence-structure-function relationships through a comprehensive evolutionary analysis of GT-A fold glycosyltransferases. Glycobiology 29(12).	2019
Bifarin OO, Panagos C, Taujale R , Edison AS. UDP-Glycosyl or Glucuronosyl transferases in Caenorhabditis elegans: Insights into Roles in Xenobiotics Detoxification. Glycobiology 28(12).	2018
Taujale R , Edison AS, Kannan N. An evolutionary systems approach to investigate sequence-structure-function relationships in Glycosyltransferases. Glycobiology 26(12).	2016
Parajuli R, Shrestha N, Priyadarshani P, Taujale R , Adhikari S. Production, characterization and optimization of wine from Nephrolepsis cordifolia. 7th National Conference of Food Science & Technology. pp.283-299 ref.7	2014

Awards

3 Minute Thesis Competition Winner , 2017 UGA Institute of Bioinformatics Symposium: Parsing the Microbiome, University of Georgia	2017
Glycoscience Training Program Fellowship , Complex Carbohydrate Research Center, University of Georgia	2016

Sidney A. Mittler Award for Outstanding graduate student, Department of Biological Sciences, Northern Illinois University

2015

Conferences/ Workshops

2019 Annual Meeting of the Society for Glycobiology, Phoenix, AZ - Oral and Poster talks	November 2-5, 2019
Trees in the Desert 2019: A workshop on ultra-large phylogenetic trees, Tucson, AZ - Part of a working group to discuss current approaches and issues in building large phylogenies	April 12-14, 2019
RevBayes: Bayesian Inference of Phylogeny, NIMBioS Accelerated Tutorial, University of Tennessee, Knoxville - Discussion group for implementation of Bayesian methods towards phylogenetic inference	August 7-11, 2017
21 st International C. elegans conference, University of California, Los Angeles - Poster talk	June 21-25, 2017
2016 Annual Meeting of the Society for Glycobiology, New Orleans, LA - Poster talk	November 19-22, 2016

Community Involvement

Organizing Committee Member , Institute of Bioinformatics Spring Retreat 2018	April 2018
Treasurer , Nepalese Student Association	October 2016 — October 2018
Member , Biotechnology Society of Nepal	June 2009 — present
Vice President , Kathmandu University Biotechnology Creatives	August 2008 — August 2009

Experience

Sr. Bioinformatics Scientist — Cognizant Technology Solutions	May 2021 — present
Graduate Research Assistant — Evolutionary Systems Biology Lab (Kannan) and Small Molecules in Biology (Edison) labs, University of Georgia	August 2015 — May 2021
Research Assistant — Bioinformatics and Evolutionary Genomics Lab (Yin lab), Northern Illinois University	July 2014 — August 2015
Teaching Assistant — Northern Illinois University General Biology (BIOS 105)	Fall 2013 — Summer 2014

Projects

GT fold prediction using deep learning , University of Georgia (Dissertation project)	2019 — 2021
An evolutionary systems approach to investigate sequence-structure-function relationships in Glycosyltransferases , University of Georgia (Dissertation project)	2016 — 2019

An integrative pipeline for the processing, analysis and visualization of 1D NMR data, University of Georgia	2016 — 2019
Detailed study of the evolution of Plant CAZymes in <i>Klebsormidium flaccidum</i>, a recently sequenced charophytic green algae, Northern Illinois University (Research Assistant)	2014 — 2015
Prediction of 3D structure and study of functional motifs for Arabidopsis CslA protein, Northern Illinois University (Research Assistant)	2013 — 2014
An Integrative Evolutionary Analysis of Xylan Biosynthesis-related Glycosyltransferase Family 43, Northern Illinois University (Master's thesis)	2013 — 2014

Skills

Cloud computing, High Performance Computing, Workflow automation, Machine Learning

Programming languages — Perl, Python, MATLAB, MySQL, PHP, R, Bash scripting

Sequence alignment tools — BLAST, HMMER, MEGA, MAFFT, Muscle, T-coffee

Phylogenetic analysis tools — IQTree, RaxML, PhyML, FastTree, Mr. Bayes, RevBayes

Next Generation Sequencing assembly and analysis tools — Velvet-oases, Trinity, Tuxedo suite, STAR, DESeq

Protein structure visualization and handling tools — PyMol, Chimera, AutoDock tools

Protein structure prediction, modelling and comparison tools — I-TASSER, Modeller, Rosetta, TM-Align

Languages

English (Proficient) Nepali (Proficient)

Newari (Proficient) Hindi (Competent)

Major Courses

Graduate School at UGA:

Statistical Inference for Bioinformatics, Algorithms for Computational Biology, Applied Genome Analysis, Glycobiology, Glycochemistry

Graduate School at NIU:

Programming for Bioinformatics, Databases, Recombinant DNA Techniques Laboratory, Biostatistics

Undergraduate:

Bioinformatics, Proteomics & Genomics, Protein Engineering, Quantitative Analysis, Instrumental Analysis