

Santosh Bhosale

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Previously, as a scientist, I applied my expertise in proteomics to develop and validate biomarkers for precision medicine. Collaborations with clinicians, mass spectrometry experts and bioinformaticians. Currently, I am leveraging the capabilities of AI and ML tools to accelerate the drug discovery process by collaborating with data engineers and scientists.

Research Proficiency _____

Wet lab

Cell culture work, animal handling and clinical samples, Cell & tissue sample lysis, SDS-PAGE electrophoresis (1D, 2D) and western blotting

High throughput proteomics

Trypsin digestion, immunodepletion of serum &/or plasma samples, label free quantification (DIA and DDA based), isobaric labeling, off-line high pH fractionation, PTMs enrichment, immunoprecipitation experiments and targeted proteomics measurements

Mass spectrometry

OPERATION AND TROUBLESHOOTING OF A RANGE OF INSTRUMENTS LTQ ORBITRAP VELOS PRO, Q EXACTIVE SERIES, ORBITRAP EXPLORIS 480 MASS SPECTROMETER, TSQ VANTAGE (ALL FROM THERMO SCIENTIFIC), TIMSTOF PRO (BRUKER), MALDI-TOF-MS (APPLIED BIOSYSTEM)

Mass spectrometry informatics tools

XCALIBUR, PROTEOME DISCOVERER (THERMO SCIENTIFIC), BRUKER TIMSCONTROL AND COMPASS HYSTAR, MAXQUANT AND PERSEUS, PROGENESIS, SKYLINE, INFERNORDN, FRAGPIPE, SPECTRONAUT (BIOGNOSYS) AND DIA-NN

Chromatography instrumentation

EASY NLC SERIES (THERMO SCIENTIFIC), EVOSEP ONE

Automation platform

SP100 AUTOMATION INSTRUMENT (HAMILTON ROBOT), BIOMEK I-SERIES AUTOMATED WORKSTATION

Language and softwares

R, PYTHON, MACHINE LEARNING, JUPYTER ENVIORNMENT, OMICS DATA, CYTOSCAPE AND INGENUITY PATHWAY ANALYSIS

Data curation

Data validation for output generated by Al and ML model, working in an agile enviornment, database mining, Llama prompt refinement

Employment _____

Product Manager

Pune - India

Innoplexus Consulting Pvt Ltd

January 2025 -> Present

- · Leading an effort to develop biomarker module for omics data
- Data extraction task from external databases (ClinicalTrials.gov, PubChem) using Llama and Gemini models
- Python scripting for automating biocuration
- · Collaboration with data engineers and data scientists

Associate Scientific Manager

Pune - India

INNOPLEXUS CONSULTING PVT LTD

August 2024 -> November 2024

- Data curation for the outputs generated via different modules built to accelerate the drug discovery and development process using AI/ML approach
- · Collaboration with data engineers and data scientists in an agile enviornment

Associate Biomedical Scientist

Los Angeles - USA

February 2023 -> June 2024

CEDARS-SINAI PRECISION BIOMARKER LABORATORIES

- Applied mass spectrometry based proteomics technlogy to study the complexity of proteome
- Lead end-to-end delivery projects related to the proteomics (From SOW to deliverable).
- Supervised technician, cross-team collaboration with bioinformatician, vendors and stakeholders

Postdoctoral Researcher Odense - Denmark

PROTEIN RESEARCH GROUP, DEPARTMENT OF BIOCHEMISTRY AND MOLECULAR BIOLOGY, UNIVERSITY OF SOUTHERN DENMARK

January 2020 -> December 2022

- Development of a post-translational modification (Cysteine, N-linked glycosylated and phospho modified) specific biomarkers discovery platform for the diagnosis of disease
- · Analysis of PTMomics data to identify candidate plasma biomarkers to stratify ovarian cancer patients
- Supervise and work with technician and PhD students
- · Work presentation internally and to the collaborators and, report writing

Postdoctoral Researcher Turku - Finland

University of Turku - Turku Bioscience

November 2018 -> December 2019

- · Serum proteomics measurements to compare the effects of nutrition supplementation in infancy and, child and mother proteome correlation
- Analyzed temporal serum proteomes of celiac disease (CD) developing children
- Conducted the interactomics measurements and data analysis for several trasnscription factors of T cells
- Designed and presented practical courses on proteomics data analysis

Project Assistant Pune - India

NATIONAL CHEMICAL LABORATORY

November 2009 -> December 2011

 Proteomics laboratory work including protein extraction, digestion and cleanup, SDS-PAGE, MS analysis of glycated proteins, oligonulceotides and small molecules

Lecturer Pune - India

JSPMs JSCOPR AFFILIATED TO UNIVERSITY OF PUNE

July 2008 -> November 2009

- · Taught theory and practicals for pharmaceutical biochemistry and pharmaceutical analysis to the bachelor of pharmacy students
- Supervised undergraduate pharmacy students
- · Graded course assignments and examinations

Education

PhD Turku - Finland

UNIVERSITY OF TURKU (TURKU BIOSCIENCE)

2012 -> 2018

- Developed quantitative proteomics methodology for the analysis of human serum samples, including immunoaffinity depletion, protein digestion, isobaric labelling, label free quantification, offline-SCX fractionation, LC-MS/MS and data analysis
- Developed targeted SRM-LC-MS methods to monitor multiple protein targets
- Cellular proteomic analyses of Th17 and iTreg cells from mouse and human
- Teaching experience in proteomics data analysis (presented at a national meeting, 2017)

Master of Pharmacy (Pharmaceutical Chemistry)

Jodhpur - India

RAJASTHAN UNIVERSITY OF HEALTH SCIENCES (LACHOO MEMORIAL COLLEGE OF SCIENCE & TECHNOLOGY)

2005 -> 2008

University of Pune (Sitabai Thite College of Pharmacy)

Shirur - Pune 2001 -> 2005

Awards

Bachelor of Pharmacy

Doctoral dissertation award

Turku - Finland

Awarded with EUR 5000 from Orion Pharma

2018

Doctoral dissertation award

Turku - Finland

AWARDED WITH EUR 5000 FROM THE MAUD KUISTILA MEMORIAL FOUNDATION

Turku - Finland

AWARDED WITH EUR 500 TO ATTEND COMPUTATIONAL PROTEOMICS COURSE AT ETH ZURICH FROM TURKU CENTRE FOR

SYSTEM BIOLOGY

Travel grant

2015

Research grant

Turku - Finland

AWARDED WITH EUR 3500 FROM HOSPITAL DISTRICT OF SOUTHWEST FINLAND & TURKU CITY

Mumbai - India

Secured first position in an oral session (6 minute competition) organized by South Asian Chapter of American

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COLLEGE OF CLINICAL PHARMACOLOGY

Dr. Ashok B. Vaidya prize

Publications

Comparative proteomics analysis of the mouse mini-gut organoid: insights into markers of gluten challenge from celiac disease intestinal biopsies	Front. Mol. Biosci
Moulder R, Bhosale SD, Viiri K, Lahesmaa R	2024
An Inflection Point in High-Throughput Proteomics with Orbitrap Astral: Analysis of	J Proteome Res
Biofluids, Cells, and Tissues	J Proteome Res
HENDRICKS NG, BHOSALE SD, KEOSEYAN AJ, ORTIZ J, STOTLAND A, SEYEDMOHAMMAD S, NGUYEN CDL, BUI JT, MORADIAN A, MOCKUS SM, VAN EYK JE	2024
Serum proteomics of mother-infant dyads carrying HLA-conferred type 1 diabetes risk	iScience
BHOSALE SD, MOULDER R, SUOMI T, RUOHTULA T, HONKANEN J, VIRTANEN SV, ILONEN J, ELO LL, KNIP M, LAHESMAA R	2024
HIC1 interacts with FOXP3 multi protein complex: novel pleiotropic mechanisms to regulate human regulatory T cell differentiation and function	Immunol Lett
Andrabi SBA, Batkulwar K, Bhosale SD, Moulder R, Khan MH, Buchacher T, Khan MM, Arnkil I, Rasool O, Marson A, Kalim UU, Lahesmaa R	2023
Serum APOC1 levels are decreased in young autoantibody positive children who rapidly progress to type 1 diabetes	Sci Rep
Hirvonen MK, Lietzén N, Moulder R, Bhosale SD, Koskenniemi J, Vähä-Mäkilä M, Nurmio M, Orešič M, Ilonen J, Toppari J, Veijola R, Hyöty H, Lähdesmäki H, Knip M, Cheng L, Lahesmaa R	2023
Cardiovascular-related proteomic changes in ECFCs exposed to the serum of COVID-19 patients	Int J Biol Sci
BELTRÁN-CAMACHO L, BHOSALE SD, SÁNCHEZ-MORILLO D, SÁNCHEZ-GOMAR I, ROJAS-TORRES M, ESLAVA-ALCÓN S,	
Martínez-Torija M, Ruiz de Infante MA, Nieto-Martín MD, Rodríguez-Iglesias MA, Moreno JA, Berrocoso E, Larsen MR, Moreno-Luna R, Carmen Durán-Ruiz M	2023
A systematic comparison of FOSL1, FOSL2 and BATF-mediated transcriptional regulation	Nuclaio Acido Dos
during early human Th17 differentiation	Nucleic Acids Res
SHETTY A, TRIPATHI SK, JUNTTILA S, BUCHACHER T, BIRADAR R, BHOSALE SD, ENVALL T, LAIHO A, MOULDER R, RASOOL O, GALANDE S, ELO LL AND LAHESMAA R	2022
Phosphoproteomics: Methods and Challenges	Reference Module in Life Sciences
Kang T, Bhosale S, Edwards A, Larsen MR	2022
HDL proteome remodeling associates with COVID-19 severity	J Clin Lipidol
Souza Junior DR, Silva ARM, Rosa-Fernandes L, Reis LR, Alexandria G, Bhosale SD, Ghilardi FR, Dalçóquio TF,	2021
BERTOLIN AJ, NICOLAU JC, MARINHO CRF, WRENGER C, LARSEN MR, SICILIANO RF, DI MASCIO P, PALMISANO G, RONSEIN GE	
Interactome Networks of FOSL1 and FOSL2 in Human Th17 Cells	ACS Omega
SHETTY A, BHOSALE SD, TRIPATHI SK, BUCHACHER T, BIRADAR R, RASOOL O, MOULDER R, GALANDE S, LAHESMAA R	2021
CIP2A Constrains Th17 Differentiation by Modulating STAT3 Signaling	iScience
Khan MM, Ullah U, Khan MH, Kong L, Moulder R, Välikangas T, Bhosale SD, Komsi E, Rasool O, Chen Z, Elo LL, Westermarck J, Lahesmaa R	2020
Protein interactome of the Cancerous Inhibitor of protein phosphatase 2A (CIP2A) in Th17 cells	Current Research in Immunology
Khan MM, Välikangas T, Khan MH, Moulder R, Ullah U, Bhosale SD, Komsi E, Butt U, Qiao X, Westermarck J, Elo LL & Lahesmaa R	2020
Quantitative Proteomics Reveals the Dynamic Protein Landscape during Initiation of Human Th17 Cell Polarization	iScience
Tripathi SK, Välikangas T, Shetty A, Khan MM, Moulder R, Bhosale SD, Komsi E, Salo V, De Albuquerque RS, Rasool O, Galande S, Elo LL, Lahesmaa R	2019
Serum Proteomic Profiling to Identify Biomarkers of Premature Carotid Atherosclerosis	Sci Rep
BHOSALE SD, MOULDER R, VENÄLÄINEN MS, KOSKINEN JS, PITKÄNEN N, JUONALA M, KÄHÖNEN M, LEHTIMÄKI T, VIIKARI J, ELO LL, GOODLETT DR, LAHESMAA R, RAITAKARI OT	2018
Quantitative proteomic characterization and comparison of T helper 17 and induced	PLos Biol
regulatory T cells	1 LOS DIOI
Mohammad I, Nousiainen K, Bhosale SD, Starskaia I, Moulder R, Rokka A, Cheng F, Mohanasundaram P, Eriksson JE, Goodlett DR, Lähdesmäki H, Chen Z	2018

Analysis of the plasma proteome using iTRAQ and TMT-based Isobaric labeling Mass Spectrom Rev MOULDER R, BHOSALE SD, GOODLETT DR, LAHESMAA R Mass Spectrometry-Based Serum Proteomics for Biomarker Discovery and Validation Methods Mol Biol BHOSALE SD, MOULDER R, KOUVONEN P, LAHESMAA R, GOODLETT DR The progress and potential of proteomic biomarkers for type 1 diabetes in children Expert Rev Proteomics MOULDER R, BHOSALE SD, LAHESMAA R, GOODLETT DR Serum proteomes distinguish children developing type 1 diabetes in a cohort with **HLA-conferred susceptibility** Moulder R, Bhosale SD, Erkkilä T, Laajala E, Salmi J, Nguyen EV, Kallionpää H, Mykkänen J, Vähä-Mäkilä M, Hyöty H, Veijola R, Ilonen J, Simell T, Toppari J, Knip M, Goodlett DR, Lähdesmäki H, Simell O, Lahesmaa R Proteome wide reduction in AGE modification in streptozotocin induced diabetic mice by hydralazine mediated transglycation KESAVAN SK, BHAT S, GOLEGAONKAR SB, JAGADEESHAPRASAD MG, DESHMUKH AB, PATIL HS, BHOSALE SD, SHAIKH ML, THULASIRAM HV, BOPPANA R, KULKARNI MJ Zoom-ln A targeted database search for identification of glycation modifications analyzed by untargeted tandem mass spectrometry BHONSLE HS, KORWAR AM, KESAVAN SK, BHOSALE SD, BANSODE SB, KULKARNI MJ Comparative and chemical proteomic approaches reveal gatifloxacin deregulates

enzymes involved in glucose metabolism

SURESH KK, BHOSALE SD, THULASIRAM HV, KULKARNI MJ

Eur J Mass Spectrom (Chichester)

J Toxicol Sci

2018

Diabetes

2015

Sci Rep

2013

2012

Patent Applications _____

Means and methods for determining risk of type-1 diabetes by serum protein biomarkers

Moulder R, Bhosale SD, Goodlett D, Lähdesmäki H, Simell S, Lahesmaa R

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References

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