Santosh **Bhosale**

POSTDOCTORAL RESEARCHER

University of Southern Denmark, Odense, Denmark

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I do mass spectrometry based proteomics research, including discovery and validation of protein biomarkers in clinical samples. Collaborations with clinicians, mass spectrometry experts and bioinformaticians.

Research Proficiency

Wet lab

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

Proteomics

Trypsin digestion, immunodepletion of serum &/or plasma samples, label free quantification, isobaric labeling, off-line high pH fractionation, PTMs enrichment and immunoprecipitation experiments

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), SYNAPT HDMS (Waters), API QSTAR Pulsar (AB SCIEX)

Mass spectrometry informatics tools

Xcalibur, Proteome Discoverer (Thermo Scientific), Bruker timsControl and Compass HyStar 5.1, MaxQuant and Perseus, Progenesis, Skyline, InfernoRDN, FragPipe and Spectronaut (Biognosys), DIA-INN

Chromatography instrumentation

Easy nLC series (Thermo Scientific)

Language and softwares

R, Python (Basics), Machine learning (Basics), Jupyter enviornment, Cytoscape and Ingenuity Pathway Analysis

Employment

Postdoctoral Researcher *Odense - Denmark*

Protein Research Group, Department of Biochemistry and Molecular Biology, University of Southern Denmark *January 2020 –> Present*

- Development of a post-translational modification (Cysteine, N-linked glycosylated and phospho modified) specific biomarkers discovery platform
- Analysis of PTMomics data to identify candidate plasma biomarkers to stratify ovarian cancer patients

Postdoctoral Researcher *Turku - Finland*

University of Turku - Turku Bioscience *November 2018 –> December 2019*

- Analyzed temporal serum proteomes of celiac disease (CD) developing children
- Conducted the interactomics measurements and data analysis for serveral trasnscription factors of T cells

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

Bachelor of Pharmacy
Shirur - Pune

University of Pune (Sitabai Thite College of Pharmacy)
2001 –> 2005

Awards

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
2018

Travel grant
Turku - Finland

Awarded with EUR 500 to attend computational proteomics course at ETH Zurich from Turku centre for system biology
2015

Research grant
Turku - Finland

Awarded with EUR 3500 from Hospital District of Southwest Finland & Turku City
2014

Dr. Ashok B. Vaidya prize
Mumbai - India

Secured first position in an oral session (6 minute competition) organized by South Asian Chapter of American College of Clinical Pharmacology
2009

Publications

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 regulatory T cells
PLos Biol

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
2018

Mass Spectrometry-Based Serum Proteomics for Biomarker Discovery and Validation

Methods Mol Biol

BHOSALE SD, MOULDER R, KOUVONEN P, LAHESMAA R, GOODLETT DR

2017

The progress and potential of proteomic biomarkers for type 1 diabetes in children

Expert Rev Proteomics

MOULDER R, BHOSALE SD, LAHESMAA R, GOODLETT DR

2017

Serum proteomes distinguish children developing type 1 diabetes in a cohort with HLA-conferred susceptibility

Diabetes

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

2015

Proteome wide reduction in AGE modification in streptozotocin induced diabetic mice by hydralazine mediated transglycation

Sci Rep

KESAVAN SK, BHAT S, GOLEGAONKAR SB, JAGADEESHAPRASAD MG, DESHMUKH AB, PATIL HS, BHOSALE SD, SHAIKH ML, THULASIRAM HV, BOPPANA R, KULKARNI MJ

2013

Zoom-ln A targeted database search for identification of glycation modifications analyzed by untargeted tandem mass spectrometry

Eur J Mass Spectrom (Chichester)

BHONSLE HS, KORWAR AM, KESAVAN SK, BHOSALE SD, BANSODE SB, KULKARNI MJ

2012

Comparative and chemical proteomic approaches reveal gatifloxacin deregulates enzymes involved in glucose metabolism

J Toxicol Sci

SURESH KK, BHOSALE SD, THULASIRAM HV, KULKARNI MJ

2011

Patent Applications

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

Europe & USA

MOULDER R, BHOSALE SD, GOODLETT D, LÄHDESMÄKI H, SIMELL S, LAHESMAA R

References

Riitta Lahesmaa, M.D., Ph. D.

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PROFESSOR OF BIOCHEMISTRY & MICROBIOLOGY AND DIRECTOR GENOME BC PROTEOME CENTRE AT UNIVERSITY OF VICTORIA, VICTORIA, BRITISH COLUMBIA, CANADA

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PRINCIPAL SCIENTIST, BIOCHEMICAL SCIENCES DIVISION, CSIR-NATIONAL CHEMICAL LABORATORY, PUNE, INDIA