GRK 2576 Guest Lecture

Title: Proteomics and phosphoproteomics approaches to study metabolism

Speaker: Atul Deshmukh, PhD

Group Leader at Novo Nordisk Foundation Center for Basic Metabolic Research, University of Copenhagen, Denmark

Date: **22. May 2024**
Time: **14:00 h CET**
Location: **Oskar Minkowski-Hall & Paul Langerhans-Hall, DDZ**

Zoom:
https://us06web.zoom.us/j/87255482975?pwd=a6uC9Oqq7gLHAm1kTJy55HOPW4byGX.1
Meeting-ID: 872 5548 2975; Kenncode: 451133

Biography

Prof. Dr. Atul Deshmukh received his PhD degree from Karolinska Institute, Stockholm, in December 2009, where he worked on role of insulin and exercise-induced protein signaling in skeletal muscle metabolism. He then pursued postdoctoral research at Max Plank Institute of Biochemistry, Munich, supported by a fellowship from Federation of European Biochemical Societies (FEBS). During his postdoc time, he developed advanced proteomics methods for analyzing muscle proteome and cell culture secretome. Transitioning to the University of Copenhagen in 2014 for his second postdoc, he became an Associate Professor by 2016. In 2019, he became group leader at the Novo Nordisk Foundation Center for Basic Metabolic Research at University of Copenhagen. His group applies state-of-the art proteomics technologies to study how changes in lifestyle affects cellular communication and metabolism. His group specializes in using cutting-edge proteomics to investigate how exercise and diet influence intracellular signaling via protein post-translational modifications and inter-organ communication via secreted proteins. Dr. Deshmukh has been recognized with the Future Leader Award from European Foundation for the Study of Diabetes (EFSD).
For more insight, please read - https://cbmr.ku.dk/research/research-groups/deshmukh-group/

Selected recent publications

Hostrup M, Lemminger AK, Stocks B, Gonzalez-Franquesa A, Larsen JK, Quesada JP, Thomassen M, Weinert BT, Bangsbo J, **Deshmukh AS**. High-intensity interval training remodels the proteome and acetylome of human skeletal muscle. **eLife** 2022 (PMID: **35638262**)

Gonzalez-Franquesa A, Stocks B, Chubanava S, Hattel HB, Moreno-Justicia R, Treebak JT, Zierath JR, **Deshmukh AS,** Mass-spectrometry based proteomics reveals mitochondrial supercomplexome plasticity. **Cell Reports**.2021 (PMID: **34038727**)

Deshmukh AS, Steenberg DE, Hostrup M, Birk JB, Larsen JK, Santos A, Kjøbsted R, Hingst JR, Schéele CC, Murgia M, Kiens B, Richter EA, Mann M and Wojtaszewski JFP , Deep muscle-proteomic analysis of freeze-dried human muscle biopsies reveals fiber type-specific adaptations to exercise training. **Nature Communications**. 2021 (PMID: **33436631**)

Deshmukh AS, Peijs L, Beaudry JL, Jespersen NZ, Nielsen CH, Ma T, Brunner AD, Larsen TJ, Bayarri-Olmos R, Prabhakar BS, Helgstrand C, Severinsen MCK, Holst B, Kjaer A, Tang-Christensen M, Sanfridson A, Garred P, Prive GG, Pedersen BK, Gerhart-Hines Z, Nielsen S, Mann M, and Scheele C. Proteomics-Based Comparative Mapping of the Secretomes of Human Brown and White Adipocytes Reveals EPDR1 as a Novel Batokine. **Cell Metabolism**. 2019. (PMID: **31668873**)

Information on access: please visit https://www.vivid.hhu.de/qualification-program/guest-lectures
Contact: Dr. Nicole Rockel, +49-211-3382-558, vivid@hhu.de

Talk teaser

GRK 2576 vivid Guest lecture with Dr. Atul Deshmukh

Proteomics and phosphoproteomics approaches to study metabolism

Mass spectrometry-based proteomics offers a robust method for studying metabolism. These technologies enable comprehensive analysis of protein dynamics, including changes in intracellular proteins (expression proteomics), secreted proteins (secretomics), and post-translational modifications, as well as specific alterations in cells, and organelles. In the first part of this presentation, I will provide the latest insights into proteomics technology and its application in studying various aspects of metabolism. In the latter part, I will present specific case studies where we have utilized expression proteomics, secretomics, and phosphoproteomics to investigate protein dynamics in tissue and body fluid samples.