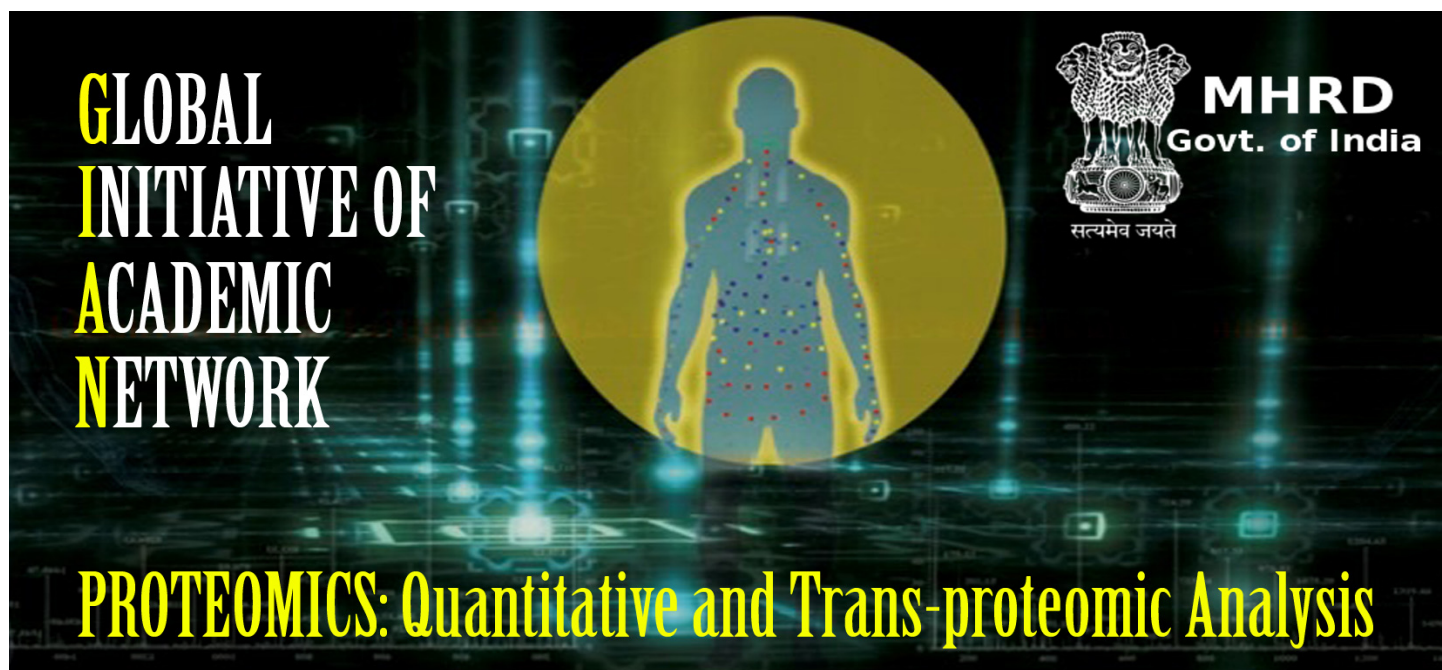


# PROTEOMICS: Quantitative and Trans-proteomic Analysis



## Overview

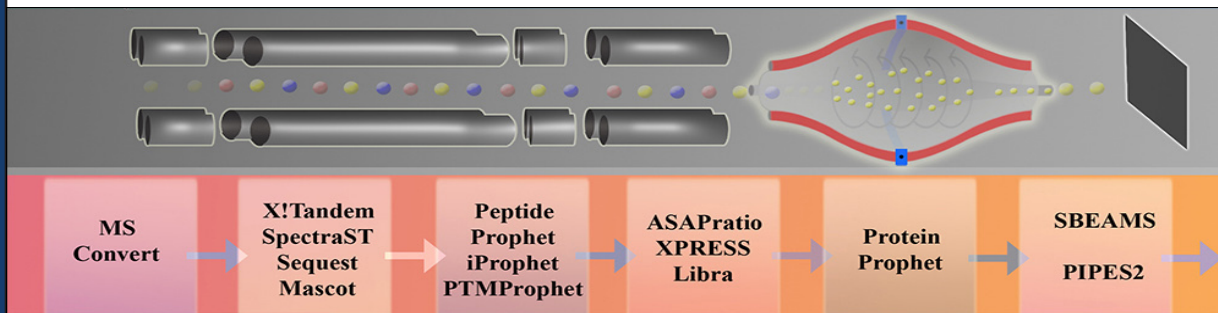
Proteomics is study of protein complements of a given cell at a given time, including the set of all protein isoforms and modifications. Emerging proteomics technologies capable of rapid and accurate screening of thousands of proteins are found to be very effective for the multidisciplinary research and these high-throughput technological approaches have propelled their implication in almost all areas of modern life-science research. Various high-throughput integrated proteomics technologies capable of fast and accurate screening of thousands of biomolecules are found to be very effective for studying disease pathobiology and identification of next-generation biomarkers and potential drug/ vaccine targets, and therefore considered as valuable tools for multidisciplinary research. Proteomic technologies are rapidly evolving and new technological platforms are coming forward regularly with versatile novel applications; therefore, there is need to keep-up the pace with latest developments in field. In this proteomics course, distinguished faculty scientists involved in advanced proteomics research will deliver lectures and provide training to the students and young researchers. The overall course will be comprised of 10 days enduring lectures and practical courses with a focus on cutting-edge quantitative and targeted proteomic technologies and trans-proteomic pipeline platform.

# GIAN-PROTEOMICS COURSE

## Modules, Dates and participants

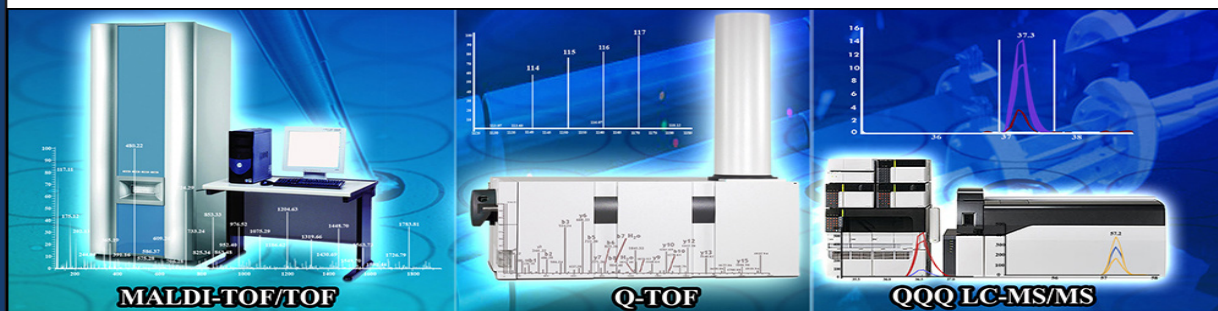
### Module: Trans-proteomic pipeline (Dr. Robert Moritz)

Proteomics overview: Why Trans-proteomic pipeline? PeptideProphet for statistical validation, InterProphet and PTMProphet, An overview of XPress, ASAPRatio and Libra for TPP, Kojak - Protein Cross-linking, SRM and SWATH targeted proteomics, Whole Proteome Resources – PeptideAtlas, SWATH analysis of Modifications, Advanced analysis of proteomics data, Advanced SWATH Resources



### Module: Quantitative & Targeted proteomics (Drs. Srivastava, Srikanth, Kulkarni)

Basics of mass spectrometry and Label-free proteomic techniques, MALDI-TOF/TOF for the PMF and MS/MS analysis, Quantitative proteomics using iTRAQ, iTRAQ protocol & applications, PTM studies using Mass Spectrometry, Case studies: studying glycosylation and phosphorylation using MS, Targeted proteomics applications for glycomics, Application of quantitative proteomics, Metabolomics using LC-MS & GC-MS, Multi-Omics and Systems medicine



**Duration: Ten days: 10 to 19 December 2015**

**No. of participants for the course will be limited to fifty**

## You should attend If.....

This course is designed for last yrs of Bachelor's/ M.Tech / M.Sc / PhD students of Life science, Biology, Medicine (with special interest), who are likely to be benefited by learning the fundamental aspects of proteomics and the latest technology. Faculty members and Research Associates are also welcome. This is an excellent opportunity for the participants to learn details of fast growing field in life science.

## Fees

The participation fees for taking the course are as follows:

Participants from abroad : US \$250

Industry/ Research Organizations: INR 5000

Academic Institutions: INR 1000

The above fee include all instructional materials, laboratory equipment usage charges, free internet facility. The participants will be provided with accommodation on payment basis. Participants should bring their own laptop for data analysis.

# The Faculty

## Dr. Sanjeeva Srivastava, Course Coordinator



Dr. Srivastava is Associate Professor and Group Leader of Proteomics Laboratory at the Indian Institute of Technology Bombay India. Dr. Srivastava is recipient of several awards including the National Young Scientist Award (Canada), Young Scientist Awards (India) and the Apple Research Technology Support Award (UK). Recently he was awarded the excellence in Teaching Award – 2014 at IIT Bombay. His group has developed E-learning resources such as Virtual Laboratory as a community resource and is collaborating actively both across India and internationally to advance this knowledge frontier for the benefit of global health.

## Dr. Robert Moritz, Invited International Scientist



Dr. Moritz, is the Professor and Director of Proteomics Research at ISB. He has designed and implemented a number of technologies such as TPP, PeptideAtlas, SRMATlas, currently used in many proteomics laboratories across the globe. He is continuing that work at ISB by expanding the ISB proteomics centre into a national facility with online tools for data analysis. Recently he was appointed as Vice-president of Human Proteome Organization (HUPO).

## Dr. Mahesh Kulkarni, Invited National Scientist



Dr. Mahesh Kulkarni is scientist at CSIR-National Chemical Laboratory Pune. He obtained his Ph.D. from University of Agricultural Sciences Bangalore. He was post-doctoral fellow at CCMB, Hyderabad and Genome Institute of Singapore. His area of research is chemical proteomics, mass spectrometry, diabetes and aging.

## Dr. Srikanth Rapole, Invited National Scientist



Dr. Srikanth is working as a scientist at NCCS, Pune. His main research interest is to quantitatively identify the protein signatures involved in human diseases, including cancer, using mass spectrometry-based proteomic approaches. In addition, his group is also working to identify and quantify key metabolites and lipids associated with human diseases using mass spectrometry and bioinformatics. He has received best paper award from CSIR in physical sciences. Recently, he received the DBT-Rapid grant for young investigators award.

## Course Coordinators

### Dr. Sanjeeva Srivastava

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### Dr. Robert Moritz

Professor  
Institute for Systems Biology, USA  
Vice President President, Human  
Proeome Organization (HUPO)

### Dr. Mahesh Kulkarni

Scientist  
National Chemical Laboratory, Pune  
India

### Dr. Srikanth Rapole

Scientist  
National Center For Cell Sciences,  
Pune  
India