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PROTEOMICS SOCIETY INDIA (PSI)

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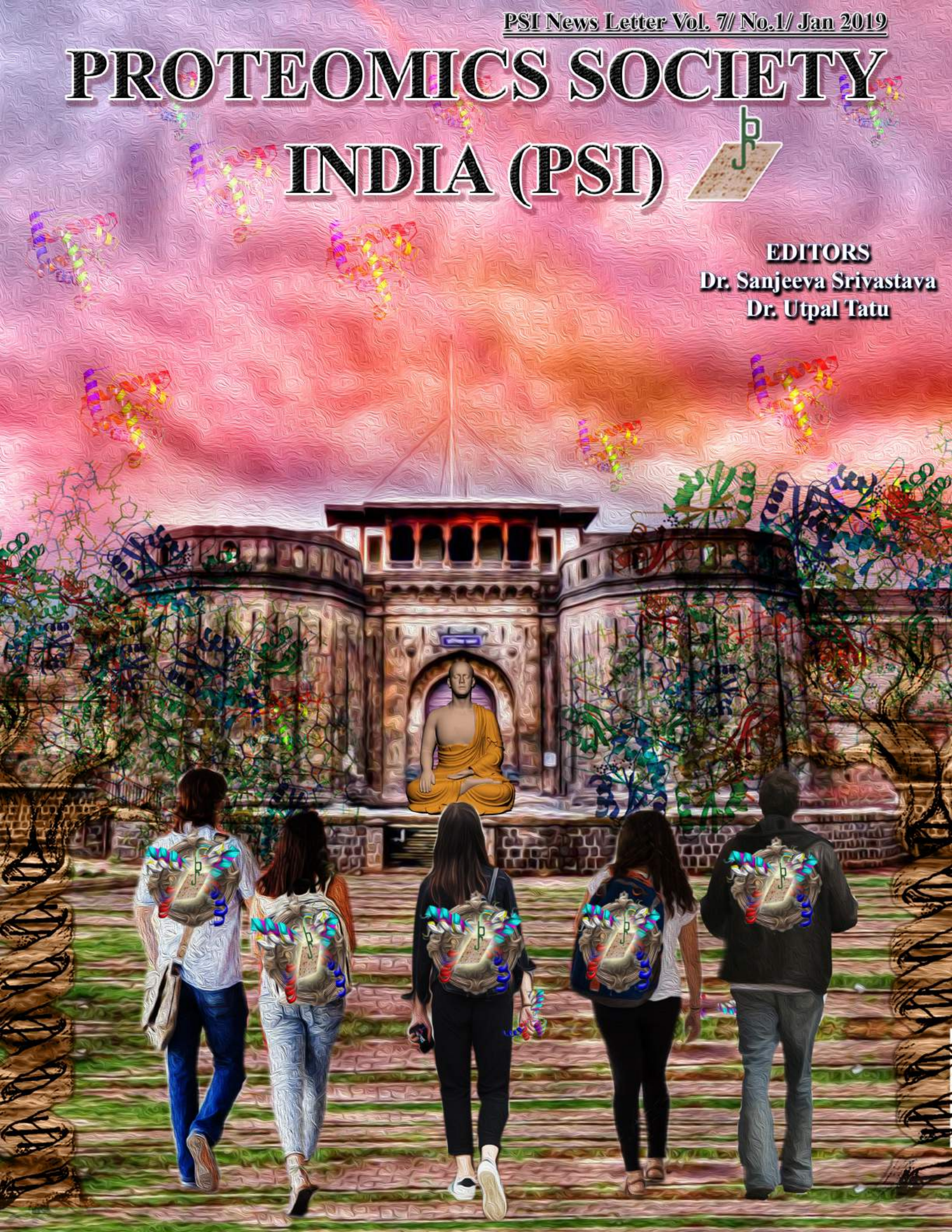

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EDITOR'S MESSAGE

Dear members of the Proteomics Society of India,

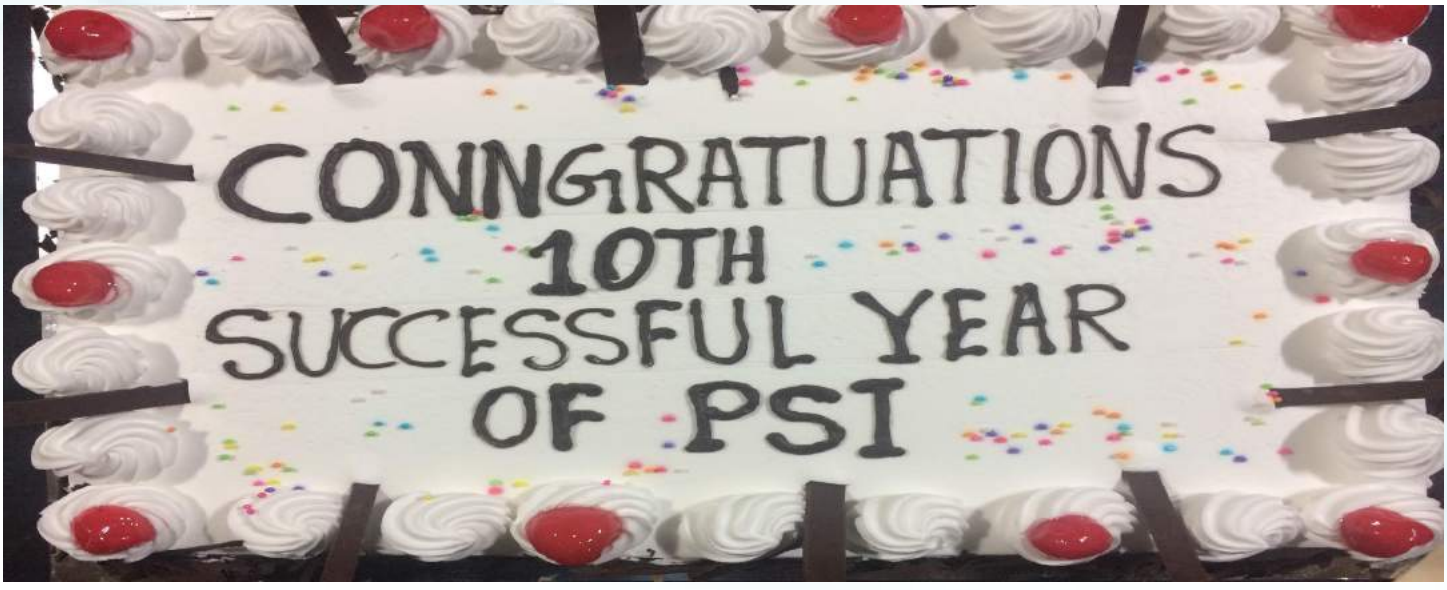
Welcome to the 1st Edition of the Proteomic Society of India newsletter in 2019. First let me wish you all a very happy, healthy and proteomic productive new year! It is a pleasure for me to share with you that the Proteomics Society of India has completed 10 successful years of function . All of our executive committee members we have worked sincerely and consistently to promote proteomic education and technologies in various parts of the country during the last ten years and impact of it all is beginning to be felt.

We have recently concluded the 10th annual meeting of PSI, held at National Centre for Cell Science Pune which was elegantly organized by Dr. Srikanth Rapole and team. It was attended by hundreds of participants and inspiring speakers from India and abroad.

I am happy to share with you that, in addition to organizing meetings at national levels, the Proteomics Society of India has successfully conducted two AOHUPO meetings in the last decade. In the coming few years, we are also hoping to bring to India, the world HUPO Congress. We hope that the international advisory board of HUPO, will honor our desire to make this vision a reality in organizing this important event in India.

I also have some exciting news for the student community in India. As you may already know, this year the HUPO congress is going to be held in Adelaide Australia. In partnership with AOHUPO as well a HUPO, we are trying to explore some highly concessional registration fee for limited number of students from India to attend the HUPO conference in Adelaide, Australia later this year. Please stay tuned for further details on this wonderful opportunity to listen to the best speakers in the field of proteomics from across the world.

With warm regards,
Utpal Tatu



10th Annual Meeting of the Proteomics Society, India(PSI)

The International Conference on Proteomics for Cell Biology and Molecular Medicine along with 10th Annual meeting of the Proteomics Society, India (PSI) (ICPCBMM - PSI 2018) was held at National Centre for Cell Science (NCCS), Pune, India from 12-14 December 2018. The ICPCBMM - PSI 2018 aimed at bringing together renowned national and international researchers working in the areas of proteomics, metabolomics and cell biology under one umbrella to exchange scientific ideas and foster future collaborations. This conference hosted a mixed scientific crowd of around 250 young, intermediate and experienced researchers (faculties from different Universities, medical colleges and research institutes, post-doctoral researchers and PhD scholars) from India and abroad. The themes of this conference included proteomics in cell biology,interaction proteomics, cancer proteogenomics, systems biology and bioinformatics, clinical proteomics; metabolomics and disease markers, plant and animal proteomics, proteomics and metabolomics for infectious diseases,PTMs and splice variants, recent advances in proteomics applications and lastly, proteomics in molecular medicine. All these themes were covered across the three days International Conference with 61 talks from scientific leaders in proteomics and metabolomics research from India and abroad.

PSI 2018
CPCBMM
International Conference on Proteomics for Cell Biology and Molecular Medicine

The Chief Guest Maj. Gen. Madhuri-Kanitkar, Dean, Armed Forces Medical College, Pune, inaugurated the ICPCBMM - PSI 2018 conference in the presence of Dr. Gopal C. Kundu, Director In-Charge, NCCS Pune, Dr. John Yates, The Scripps Research Institute, California, USA, Dr. UtpalTatu, President, PSI, Dr. Srikanth Rapole, Convener, PSI-2018. As PSI 2018 was the 10th anniversary of the Proteomics Society, India, the founder president of PSI, Dr. Ravi Sirdeshmukh, the past president of PSI, Dr. SurekhaZingde and the present president of PSI, Dr. UtpalTatu were felicitated for their contributions in bringing the Proteomics Society, India in the global platform.Dr. Srikanth Rapole, Convenor, ICPCBMM – PSI 2018, concluded the conference inauguration with a vote of thanks.The scientific program of this conference comprised of plenary lectures, Invited lectures, Short lectures, Poster sessions and other opportunities of interactions amongst the participants.Meritorious research work of seven young scientists and research scholars were selected for short oral presentations, thereby providing them with an opportunity to present their work in front of a large global proteomics community. Similarly, 105 young researchers were provided the platform to present their scientific work through poster presentations.

The Conference started with a plenary talk on "Understanding the Molecular Defect in Cystic Fibrosis" by Dr. John Yates from The Scripps Research Institute, California, USA in the first session entitled Proteomics for Cell Biology.This session included three more talks from senior proteomics science leaders from India namely, Dr. Rakesh Mishra (CCMB, Hyderabad), Dr. UtpalTatu (IISc, Bangalore) and Dr. Shantanu Sengupta (IGIB, New Delhi). The second session was on Interaction Proteomicsand had two plenary talks. Dr. Akhilesh Pandey, from Mayo Clinic, USA talked on "Dissecting Bcr-Abl and downstream signalling through interaction proteomics and PTM analysisand Dr. Philip Andrews from University of Michigan Medical School, USA spoke on "Protean proteins: Probing protein structures and interactions with CXL-MS". This session had subsequent talks by Dr. Sanjeeva Srivastava (IIT Bombay, Mumbai), Dr. Ramesh Ummanni (IICT, Hyderabad), Dr. Samir Maji (IIT Bombay, Mumbai) and Dr. RakhiDhawan (AFMC, Pune). Cancer Proteogenomicswas the third session which had the plenary talk by Dr. D. R. Mani from the Broad Institute of MIT and Harvard, USA who talked on "Multi-Cancer proteogenomic tumor analysis in the cloud". This session had subsequent talks on the area of cancer proteogenomics by Dr. Karsten Krug(the Broad Institute of MIT and Harvard, USA), Dr. Bing Zhang (Baylor College of Medicine, USA), Dr. Karl Clauser (the Broad Institute of MIT and Harvard, USA), Dr. Debasis Dash (IGIB, New Delhi) and Dr. Pratik Jagtap (University of Minnesota,




USA). The fourth session of the day was themed on Systems Biology and Bioinformatics and started with a plenary talk by Dr. David Fenyo from NYU Langone Medical Centre, USA followed by a couple of talks from the Indian experts from this field. The first day of the conference concluded with a Gala Dinner for all the participants and invited guests.

The second day of the conference initiated by plenary talk entitled " Developing and delivering advanced protein biomarker tests for an era of precision medicine" by Dr. Stephen Pennington from School of Medical Conway Institute, Dublin, Ireland on the session themed on Clinical Proteomics. Another plenary talk for this session was from Dr. Jennifer Van Eyk, Cedars-Sinai Medical Center, USA who talked on "Moving towards proteomic-centric individualized medicine". This session constituted a few more talks from the Indian experts in clinical proteomics like Dr. Arun Bandyopadhyay (IICB, Kolkata), Dr. Srikanth Rapole (NCCS, Pune), Dr. Kalpana Bhargava (DIPAD, New Delhi) and Dr. SwastiRaychaudhuri (CCMB, Hyderabad).





The next session was on Metabolomics and Disease Markers, which started with a plenary talk by Dr. Arun Sreekumar from Baylor College of Medicine, USA who talked on "AADAT: a novel metabolic enzyme in aggressive breast cancers with tumor intrinsic and paracrine medicine". This followed by talks from Dr. PutluriNagireddy (Baylor College of Medicine, USA), Dr. Siddhesh Kamat (IISER, Pune), Dr. S. Prabhakar (IICT, Hyderabad) and Dr. S. Venketesh (SSSIHL, Anantapur) who gave the concluding talk for this session. The seventh session entitled Proteomics and Metabolomics for Infectious Diseases commenced with the talk by Dr. Vladimir Havlicek from Institute of Microbiology, Czech Republic who talked on "Multimodal imaging and microbial metabolomics on track of infectious diseases". Dr. DhanasekaranShanmugam (NCL, Pune), Dr. M. V. Jagannadham (CCMB, Hyderabad), Dr. Sheetal Gandotra (IGIB, New Delhi) and Dr. Raju Mukherjee (IISER, Tirupati) were the other speakers for this session. Further, the last session of second day was on the theme of Plant and Animal Proteomicsand started with the talk from Dr. Niranjan Chakraborty (NIPGR, New Delhi) who spoke on "Mitochondrial antioxidant defence system and dehydration tolerance in crops". This session had other talks from experienced scientists like Dr. Ashok Giri (NCL, Pune), Dr. Subhra Chakraborty (NIPGR, New Delhi), Dr. Sharmila Chattopadhyay (IICB, Kolkata), Dr. Ashok Mohanty (NDRI, Karnal) and Dr. Sudarshan Kumar (NDRI, Karnal). After the talks, Dr. UtpalTatu, President, PSI arranged for a cake cutting ceremony to mark the celebration of 10th anniversary of PSI. Senior member of PSI, Dr. M. A. Vijayalakhsmi cut the cake for this ceremony, following which the GB meeting of PSI was conducted. The second day was concluded by cultural program followed by dinner.




The third day of the conference commenced with the session on PTMs and Splice Variants, which started with the plenary talk by Dr. Chunaram Choudhary from University of Copenhagen, Denmark who talked on "The global scope and kinetics of CPB/p300-regulated acetylation". Dr. Ravi Sirdeshmukh (IOB, Bangalore), Dr. Mahesh Kulkarni (NCL, Pune), Dr. Tushar Maiti (RCB, Faridabad) and

Dr. Alka Rao (IMTECH, Chandigarh) were other speakers for this session. Next session was the tenth session of the conference themed on Recent Advances in Proteomics Applications that started with plenary talk by Dr. Richard Vachet from University of Massachusetts, USA who spoke on "Covalent labelling and mass spectrometry for studying protein-protein and protein-ligand interactions". This session followed by talks from Dr. M. A. Vijayalakshmi (VIT, Vellore), Dr. Ashis K. Mukherjee (Tezpur University, Tezpur), Dr. Christie Hunter (SCIEX, USA), Dr. Amit Bhattacharya (Premas Life Sciences, New Delhi), Dr. Amit Singh (Merck Life Sciences, Pune) and Dr. Kaushik K. Dey (St. Jude Children's Research Hospital, USA). Since this session was on recent advances in proteomics applications, it involved many talks from companies with advanced proteomics basedproducts. The eleventh and the last session for this international conference was on the theme of Proteomics in Molecular Medicine. Dr. Harsha Gowda from QIMR Berghofer Medical Research Institute, Australia was the first speaker for this session who talked on "Characterization of molecular mechanisms that confer erlotinib resistance in head and neck squamous cell carcinoma using genomic and proteomic approaches". This session comprised with talks from other expert scientists in this field like Dr. Suman Thakur (CCMB, Hyderabad), Dr. Suman Kundu (Delhi University, New Delhi), Dr. Soumen Kanti Manna (SINP, Kolkata), Dr. Saravanan Kumar (ThermoFisher Scientific, Bangalore) and Dr. Pragyan Acharya (AIIMS, New Delhi).

After the completion of the scientific sessions, the valedictory function took place that marked the successful completion of the three day long ICPCBMM – PSI 2018 Conference. Various awards like best poster awards for poster presentation and PSI travel awards were awarded to selected participants. The venue for 11th PSI meeting, PSI 2019 was announced to be at NDRI, Karnal and Dr. Ashok Mohanty, Convener of PSI 2019 took this platform to invite the proteomics community from India and abroad for the upcoming PSI 2019. Dr. Stephen Pennington who is the President elect, HUPO, invited all for the HUPO 2019 meeting to be held at Adelaide, Australia from September 15-18, 2019. The convener of this conference, Dr. Srikanth Rapole, officially concluded the ICPCBMM – PSI 2018 with a vote of thanks. On behalf of organising committee, Dr. Srikanth Rapole thanked all the eminent speakers, session chairs, all the participants, industry partners and media partners for making this conference successful.

Dr. Srikanth Rapole,
Convener, ICPCBMM – PSI 2018
National Centre for Cell Science
Pune-411007, MH, India

Report on Education day during 10th Annual Meeting of the Proteomics Society, India (PSI) at NCCS, Pune.

Every year, proteomics society,India, organises education day as a pre-conference event during their annual meetings.This is a welcome initiative undertaken by PSI to generate interest in students, researchers and clinicians as well as to make them aware about recent the emerging advanced trends in proteomics and metabolomics approaches. This programme was also helpful to established scientists who wish to integrate these techniques to answer the questions which werepreviously unanswerable by routine methods.This year, education day program was enthusiastically arranged at National Centre for Cell Science (NCCS), Pune during10th Annual Meeting of the Proteomics Society, India (PSI) on 11th December 2018 with the theme of "Current Trends in Proteomics and Metabolomics". More than 100 participants took part in the event and major chunk of the candidates comprised of the clinicians from the Armed forces Medical College, Pune.

The programme commenced with the welcome address by Dr. Srikanth Rapole, convenor PSI 2018 who greeted all the participants and briefed them about the theme of the programme. This was followed by the inaugural messages by Dr. Gopal Kundu, Director In-Charge, National Centre for Cell Science (NCCS), Puneand Dr. UtpalTatu, President, PSI who briefedabout the importance of such initiative for young researchers. The programme was coordinated by Dr. Amol Suryawanshi, Institute of Life Sciences (ILS), Bhubane shwar and Dr. M. V. Jagannadham, CSIR- Centre for Cellular and Molecular Biology, Hyderabad.



The programme was divided into five sessions in which renowned Scientists from various prestigious institutes and universities delivered invited presentations. The first session was themed around Mass spectroscopy based Proteomics. Dr. M. V. Jagannadham from CSIR- Centre for Cellular and Molecular Biology, Hyderabad delivered first lecture of the session on Mass Spectrometry basics and applications. The second lecture of the session was delivered by the Dr. Amol Suryawanshi from Institute of Life Sciences (ILS), Bhubaneshwar on Quantitative proteomics approaches and its applications. The final lecture of first session was given by Dr Mahesh Kulkarni from CSIR-National chemical laboratory, Pune on targeted quantification of glycated peptides of albumin in diabetes.





The topic of second session was clinical proteomics. Dr. K. Dharmalingam from Aravind Medical Research Foundation, Madurai elaborated on Selected Reaction Monitoring for the clinical assay development. The second lecture of the session was conducted by Dr. Suman Thakur from CSIR- Centre for Cellular and Molecular Biology, Hyderabad. He explained protein quantitation by using stable isotope labelling with amino acids in cell culture (SILAC) and isobaric tags for relative and absolute quantitation (iTRAQ) approaches. The session was concluded with participants' group photo.

The third session was focussed on Metabolomics and its Applications. The session commenced with the lecture by Dr PutluriNagireddy from Baylor College of Medicine, Houston, Texas, USA. Dr. Nagireddy explained the basics of metabolomics approach as well as elaborated on how the methodology can be used to understand the metabolic adaptations in bladder cancer. The next lecture of the session was delivered by Dr. Arun Sreekumar from the same institute. Dr. Sreekumar nicelyelaborated on breast cancer metabolomics, flux analysis and its importance in understanding the dynamic metabolic scenario under altered pathophysiology.





The penultimate session of the programme was centered on topic "Applied proteomics". The first lecture of the session was given by Dr. Philip C Andrews from Department of Biological Chemistry, University of Michigan, AnnArbor, MI, USA. Dr. Andrews described about how chemical CID-cleavable cross linkers can be used to study the structural aspect of proteins in solution by using Mass spectroscopy. The next lecture was delivered by Dr. Niranjan Chakraborty from National Institute of Plant Genome Research, New Delhi. Dr. Chakraborty explained how a plant responds to various environmental stresses by altering the protein composition in plant organelles. The third lecture of the session was presented by Dr. Ramesh Ummanni from CSIR-Indian Institute of Chemical Technology, Hyderabad. Dr. Ummanni described reverse phase protein array (RPPA) as a high throughput proteomic platform for discovery, validation and clinical application. The final lecture of the session was given by the Dr. GeetanjaliSachdeva from ICMR-National Institute for Research in Reproductive Health, Mumbai. Dr. Sachdeva elaborated on differential expression analysis of cellular proteome under various pathophysiological conditions and their implication for translational research.

The final session of the Education Day programme was comprised of a lecture on "Getting Published in the Digital Age" by Taylor and Francis. The lecture provided guidance for manuscript writing for an academic journal, care to be taken while submitting the manuscript for publication, peer review process and answering reviewers comments etc. The lecture also covered issues such as plagiarism, conflict of interest and publishing ethics.

The programme was concluded with vote of thanks proposed by Dr. Srikanth Rapole, Convenor PSI 2018. Dr Srikanth also acknowledged all the speakers, coordinators, PSI EC members and participants for their contribution in making Education day a big success.

Dr. Ravindra Taware, PSI 2018 conference organising team member &
Dr. Srikanth Rapole, Convenor PSI 2018,
National Centre for Cell Science,
S.P. Pune University Campus, Ganeshkhind,Pune-411007.

NCCS

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National Centre for Cell ScienceIndo-U.S. Science & Technology Forum

Indo–US Bilateral Workshop on Understanding Cell Biology through Proteomics and Metabolomics

The principal challenge of cell biology is to reveal the mechanisms underpinning the fundamental processes in cell function. To characterize these processes and to reveal their underlying mechanisms, one needs to evaluate the composition, localization and molecular phenotypes viz. proteins and metabolites. During the last decade, proteomics and metabolomics approaches have demonstrated a significant impact on various aspects of cell biology research. High-throughput proteomics and metabolomics technologies capable of fast and accurate screening of thousands of protein and metabolites are found to be very effective for understanding disease mechanisms and therefore considered as valuable tools for cell biology research. However, these technologies are rapidly advancing with new applications in cell biology and there is a need for frequent updates to keep pace with fields.

A two-day Indo–US Bilateral Workshop on Understanding Cell Biology through Proteomics and Metabolomics was held at National Centre for Cell Science (NCCS), Pune, India from 10-11 December 2018. This meeting was coordinated by Dr. Srikanth Rapole (NCCS, Pune, India),Dr. John Yates (The Scripps Research Institute, La Jolla, California, USA), Dr. Shantanu Sengupta (IGIB, New Delhi), and Dr. Arun Sreekumar (Baylor College of Medicine, Houston, USA). This workshop was attended by various experienced principal investigators from India and USA working in the field of proteomics and metabolomics.In this bilateral workshop, supported by IUSSTF, the intention was to discuss how modern MS-based proteomics and metabolomics technologies can be leveraged to explore various areas of cell biology. Moreover, the researchers from the two countries came together on a common platform to discuss the know-how of high-throughput proteomics and metabolomics technologies and their applications in basic and translational research.





The workshop initiated with a welcome note by Dr. Arvind Sahu, Acting Director, NCCS, Pune who thanked all the delegates for attending this bilateral workshop towards fruitful scientific sessions and future collaborations. The coordinators Dr. Srikanth Rapole,Dr. John Yates, Dr. Shantanu Sengupta and Dr. Arun Sreekumar further briefed the participants about the necessity behind organizing this bilateral Indo–US workshop. Further, all the participant principal investigators introduced themselves to other participants briefly.This Indo-US workshop brought together 36 proteomics and metabolomics investigators from the United States and India, where they presented their ongoing proteomics and metabolomics projects. A wide range of topics were discussed that mainly focused on the themes of proteomics for cell biology, translational research, metabolomics for disease markers and interaction proteomics. This resulted in an effective exchange of ideas between diverse groups using proteomics and metabolomics tools. The workshop also emphasized advancements in proteomic and metabolomic technologies for translational research.Different aspects of basic as well as applied proteomics and metabolomics research such as amino acid modifications to study newly synthesized proteins and protein-protein interactions, database searches for tissue specific proteins/peptides and for chimeric peptides in various cancers, proteomics derived markers for diagnostics, metabolomics derived markers for diagnostics, integrative OMICS analysis to understand glioblastoma, diabetes, stress and immunity against pathogens in plants, proteomics for identifying important protein regulators for specific biological queries was discussed during the meeting.

The first session was themed on Proteomics for Cell Biology that started with the talk by Dr. John Yates who spoke on "PALM (Pulse AzidohomoalanineLabeling in Mammals) analysis for global analysis of newly synthesized proteins in animal models of disease". Dr.UtpalTatu (IISc, Bangalore), Dr. Arvind Sahu (NCCS, Pune), Dr. Ravi Sirdeshmukh (IOB & MSCTR, Bangalore), Dr.Subhra Chakraborty (NIPGR, New Delhi), Dr. M. Balasubramanyam (MDRF, Chennai), Dr.Debasis Dash (IGIB, New Delhi) and Dr. Sharmila Bapat (NCCS, Pune) were the other speakers of the first session who shared their research on the application of proteomics in the field of cell biology. The next session was eventually an extension of the first session and was also themed on Proteomics for Cell Biology. This session commenced with the talk from Dr.Philip Andrews who spoke on the insights into protein structures and interactions from crosslinking mass spectrometry. The second session gradually progressed with talks from Dr.GeetanjaliSachdeva (NIRRH, Mumbai), Dr. Anjali Shiras (NCCS, Pune), Dr. Mahesh Kulkarni (NCL, Pune), Dr. Girdhari Lal (NCCS, Pune) and Dr. Amol Suryawanshi (ILS, Bhubaneswar) followed by dinner.

The second day commenced with talks on the theme Proteomics for Translational Research, the secondsession. Dr. Akhilesh Pandey from Mayo Clinic, Minnesota, USA was the first speaker for this session who conveyed to the participants, how the use of Proteomics for Microbial Diagnosticscould be an emerging concept. Dr. Jennifer Van Eyk from Cedars-Sinai, California, USA further spoke on the topic of "Defining S-nitrosylation in heart disease and its impact on GSK-3β". This followed by talks from Indian counterparts Dr. Abhijit Chakrabarti (SINP, Kolkata), Dr. Arun Bandyopadhyay (IICB, Kolkata), Dr. Srikanth Rapole (NCCS, Pune), Dr.Niranjan Chakraborty (NIPGR, New Delhi), Dr. Gopal C. Kundu (NCCS, Pune) and Dr. Suman Thakur (CCMB, Hyderabad). The third session was entitled Metabolomics for Disease Markers and was started with a talk by Dr. Arun Sreekumar from Baylor College of Medicine, Texas, USAwho talked on "Metabolic detours in Cancer: Biological, Biomarkers and Therapeutic Implications". The talk by Dr.PutluriNagireddy from Baylor College of Medicine, Texas, USA discussed about the utilization of metabolomics approach to study metabolic dysregulation and the role of AOX1 in bladder cancer progression. Dr. Shantanu Sengupta (IGIB, New Delhi), Dr. Koel Chaudhury (IIT-KGP, Kharagpur), Dr. Ranjan Nanda (ICGEB, New Delhi), Dr. H. V. Thulasiram (NCL, Pune) and Dr.SiddheshKamat (IISER, Pune) were the other speakers who discussed about metabolomics research in health and diseases. This was followed by lunch and networking.The next session, i.e. the fourth session was on the theme of New Strategies for Interaction Proteomicswhere the first talk was by Dr. Richard Vachet from University Massachusetts, Amherst, USA talked on "Covalent labelling and mass spectrometry for studying Protein-Protein and Protein-Ligand Interactions". This session further progressed with talks from other distinguished experts in the field of interaction proteomics like Dr. Ramesh Ummanni (IICT, Hyderabad), Dr. Manas Santra (NCCS, Pune), Prof.SukeshBhaumik (Southern Illinois University School of Medicine, USA), Dr. Prasad Kulkarni (ARI, Pune) and Dr. Krishnan Venkataraman (VIT, Vellore).

With an aim at fostering and strengthening bilateral ties, a panel discussion was also held, where all the participants discussed the possibilities of sabbatical training for academic scientists, post-doctoral fellowship opportunities, and training programs for PhD students which can help advancing the proteomic and metabolomic science in India.This panel discussion was moderated by Dr. Ravi Sirdeshmukh, Dr. John Yates, Dr.SurekhaZingde and Dr. Arun Sreekumar. This was followed by vote of thanks by the coordinators which officially concluded this Indo – US Workshop. Networking and dinner was arranged for all the participants after the panel discussion session.

Mr. Khushman Taunk, PSI 2018 conference organising team member &
Dr. Srikanth Rapole, Indian Coordinator IUSSTF workshop, Convenor PSI-2018
National Centre for Cell Science, Pune-411007

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Proteomics is the study of entire protein complement of an organism. Advancements in proteomics have been phenomenal over the last decade with several promising high-throughput technologies emerging at the forefront of various applications. Owing to the rapid advancements in state-of-the-art proteomics technologies, continuous expansion of our scientific understanding, and challenges associated with omics research, it has become essential to keep up with current trends and advances in proteomics research. In this light, we conducted three workshops at IIT Bombay, where eminent scientists and researchers from India and abroad had shared their knowledge and expertise to train the participants and familiarize them to the vast applications of proteomics.

Basics and Advanced Proteomics Approaches (December 3 to 14, 2018)

The DST supported programme was specially designed for Scientists/Technologists who are actively involved in research and development activities. The overall goal of the programme was to develop an educational training program on diverse proteomic technologies and offer hands-on training on the cutting edge proteomics technology to benefit the scientists in their research skill enhancement and keeping them abreast with the last technological advancements in the field of science. 25 scientists were selected for this program.

Cancer Proteogenomics Workshop (December 6 to 11, 2018)

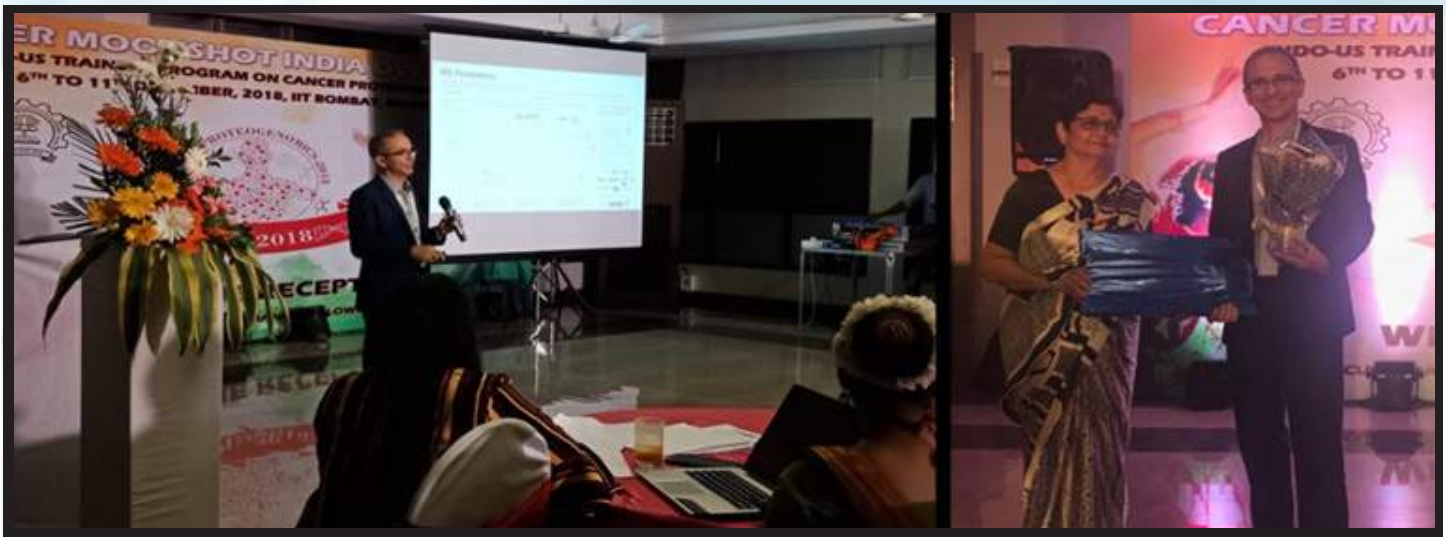
This training program utilized advanced genomic & proteomic technologies and their data from high-quality human biospecimens to identify potentially actionable therapeutic molecular targets. This IUSSTF funded training program was a collaborative effort by experts in the fields of proteomics and proteogenomics in cancer research from the Broad Institute of MIT and Harvard (Convener, USA: D. R. Mani) and Indian Institute of Technology Bombay (Convener, India: Sanjeeva Srivastava). The program comprised interactive lectures with case studies, hands-on sessions and demonstrations on proteogenomics aimed at accelerated understanding of cancer. 200+ participants attended this training program.

Cancer proteogenomics workshop, Group photograph

Cancer Moonshot India Program – December 7, 2018

The Cancer Moonshot aims to accelerate cancer research to make effective therapies available to more patients, while also improving early and accurate detection.
https://www.cancer.gov/research/key-initiatives/moonshot-cancer-initiative

Similar to the Cancer Moonshot project of USA, to expedite cancer diagnosis and treatment, we have initiated the Cancer Moonshot India project. India has now become the 12th country to join the International Cancer Proteogenome Consortium (ICPC) of the National Cancer Institute (NCI), U.S. The Indian Institute of Technology Bombay (IITB) aims to study proteomics and the Tata Memorial Hospital (TMH), Mumbai, aims to study the genomics of three cancers, breast, cervix and oral. Dr. Henry Rodriguez, Director, NCI Office of Cancer Clinical Proteomics Research inaugrated this event and delivered a speech to the gathering, which included distniguished clinicians from ACTREC, TMC and KEM hospitals; key industry leaders; and scienitsists working in genomics and proteomics area.



Dr. Henry Rodriguez addressed audience and provided updates on ICPC and Cancer Moonshot(left); Felicitation by Dr. Surekha Zingade(right)

Enchanting dance performances by Faizal Kahan and his group

A memorable cultural performance byRanjana Phadke and her Kathak group

Trans-Proteomic Pipeline (December 12 to 14, 2018)

The TPP workshop was scheduled from 12th to 14th December 2018. This advanced mass spectrometry data analysis workshop was supported by IUSSTF joint virtual center grant and conducted by Institute for Systems Biology scientists.

A reflection document of this event could be found on:
http://www.bio.iitb.ac.in/~sanjeeva/cpg2018/

Journal of Proteins and Proteomics (JPP) "Springs" to the International Stage

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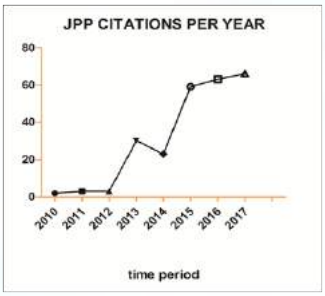
To members of Proteomics Society, India (PSI) and to the community of researchers engaged in research in Protein Science and Proteomics, JPP is no stranger. The journal, one of its kind in India committed to nurture and disseminate research findings in areas related to protein science and proteomics, have been in existence since 2010 published by an Indian publisher (Serials Publications). Quietly but steadily it created a niche for itself in the Indian Scientific community. It has published issues on time and as per pre-announced schedule over the years with remarkable consistency, both regular and special issues. It has held hands with organizers of several scientific conferences and symposiums and published conference proceedings as well. The journal published a range of articles – original research articles, reviews, mini reviews, communications, technical notes, methods papers, profiles of scientists, intellectual property rights related papers, opinions, brief history, so on and so forth. By publishing abstracts of conference proceedings it has often show-cased the diversity and width of ongoing research in India. While it promoted publications put forth by talented, young researchers, it has published articles from established researchers with equal enthusiasm. The icing on the cake has been the fact that publication has been totally free in the journal and PDFs were always available freely on the journal website. The journal only promoted academic charity by way of subscriptions from supportive individuals and institutions to help with the cost of printing. Some of the best institutes of India had subscribed the journal. In addition, the journal has always received industry support to keep it going while authors enjoyed publishing and reading articles free of any cost.

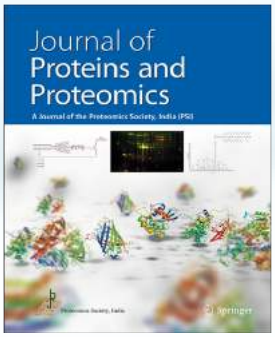
Dedicated and generous researchers helped the journal by serving as Editorial Board Members, National and International Advisors and Reviewers. There are numerous colleagues, friends and well wishers who stood by as the journal huffed and puffed to take root. One landmark that brought life and popularity to the journal was its association with PSI, which adopted the journal in Jan 2016. From 2014, however, the proximity between JPP and PSI took shape and both surged ahead with purpose and dream in their steps to serve the scientific community to the best of ability. JPP, born in 2010, served as a younger brother to PSI, born in 2009 and both walks the path together now. Together, the scientific community is being better served.

While PSI celebrated a decade of its existence in December 2018 in its Annual Meeting in NCCS, Pune, JPP completed nine years of its own sojourn. In its nine years the journal achieved as much as it could. It is a peer reviewed (single blind) journal and stands out in the era of predatory journals. It published key research findings that led to growing citations in Google Scholar and now in Web of Science. The growth in citations over the years is evident in the adjacent graph.



Our calculations reveal a projected impact factor of ~1.2 for the journal. It has enjoyed a NAAS rating of 4.55 and featured in UGC list as well for a while. It has been indexed in several international databases like Index Copernicus International, DOAJ, CAS, SJIF, UI Factor, Indian Science Abstracts, Genamics Based Journal Seek, Research Bible, CAP International (UK) and WorldCat. Established scientists adorn the Editorial Board of the journal as well.

Having established a strong platform in India, time was ripe for the journal to go global. With the help of PSI, the journal achieved this distinction as well. It "springs" to the international stage this year, with Springer Nature as its official publisher. This has been yet another landmark for the journal. Springer Nature, the acclaimed international publisher, needs no introduction and with them on board, the journal has ambitious plan to reach great heights. The first issue with Springer Nature will be published in January 2019. All preparations are in place and the journal is open to article submissions. The weblink of the journal is: https://www.springer.com/biomed/journal/42485



Springer to publish the *Journal of Proteins and Proteomics* – A Journal of the Proteomics Society (India) – from January 2019

Articles are currently being accepted for the journal

Journal of Proteins and Proteomics

The cover page of the journal in its association with Springer is shown here:

Springer handles submissions, reviews, decisions on articles and related activities through a user friendly Editorial Manager. The journal has an extended Editorial Board now and includes some of the biggest names in Proteomics research. Some of the accepted articles in the ambit of Springer are already online. The USP of the journal is as follows:

- Unique platform for amalgamation of classical protein science and modern proteomics
- No Publication Charges
- Colored Figures free
- Easy submission (User friendly Editorial Manager for authors for submission and follow-up)
- High visibiliy
- Scope of the journal wide – all areas related to Protein Science and Proteomics
- Theoretical, Computational and Experimental investigations published
- World- wide circulation through the largest publication house (Springer Nature)
- Articles of the journal increasingly cited in Google Scholar and Web of Science
- An accomplished Editorial Board
- Manuscripts reviewed carefully with suggestions for improvements for value addition
- Fast turnaround time with online availability of articles immediately upon acceptance
- Free access to Articles of the journal for members of Proteomics Society, India

The journal looks forward to articles from all PSI members. The journal articles will be available freely for PSI members through PSI website. Together we will scale great heights and the journal is our pride.

CSIR- Institute of Genomics and Integrative Biology

MRM Consortium: A PSI initiative

Shalini Pradhan, Shantanu Sengupta
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In the last decade, there has been a tremendous thrust in identification of potential protein biomarkers for various diseases. Most of the markers that are currently used has been the product of hypothesis based approaches. Current clinical assays suffer from many difficulties including a lack of specificity, interfering substances, misleading results at extreme concentrations, and poor inter-platform concordance.With the advent of high resolution mass spectrometers, there has been a shiftin the strategy towards hypothesis free approach, where proteins that are differentially expressed in cases and controls are identified at a global scale from biological fluids. Clinical proteomics can fill the gap left by the existing menu of clinical assays by providing a more complete survey of proteins in clinically relevant samples.

The current protocols involving biomarker discovery entails an unbiased proteomics (Discovery phase)study, which results inidentification of several proteins (sometimes up to 100)as candidate leads, but unfortunately, the majority of these have no clinical utility. These, then are validated in the second phase using large number of samples usually by ELISA or other such techniques. However, performing ELISA for multiple proteins in large number of samples is often cumbersome and costly. This can be overcome by exploiting the sensitivity and specificity of targeted MS usingmultiple-reaction monitoring (MRM) where multiple proteins can be quantified by multiplexing.MRM has demonstrated to have high reproducibility within and across laboratories and instrument platforms. Using MRM-MS is thus far less cumbersome and cost effective. This is especially relevant for screening multiple proteins as a part of verification step. So, MRM-MS can be used to develop diagnostic or predictive tests that if successfully developed and are analytically perfect, would have potential use and would improve patient outcomes and diminish the cost of healthcare. This indeed can also be used for routine checkups to assess disease risk of an individual. This technology can aid in regular health checks which in turn can help a person to understand their health needs, values and concerns, and help identify some potential health risk factors where healthy improvements can be made. Further, disease specific panels can be created that will have better predictive accuracy.

Keeping this in view, the Proteomics Society, India (PSI) has formed a consortium, the objective of which is to develop MRM assays for clinically relevant proteins. Members of the consortia will have the opportunity to develop MRM assays for proteins relevant to their field of research, which can then be validated across platforms. This initiative of PSI, first of its kind, will help create disease panels specific for Indian population.

Involvement of bacterial vesicles in antibiotic resistance

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Emergence of bacterial strains, resistant to one or more than one therapeutically resistant antibiotic, poses a serious challenge to the prospect of chemotherapy. In the US alone, about 2 million people are known to be infected by antibiotic-resistant bacteria and about 23000 people are killed by antibiotic-resistant infections every year. While discovery of new antibiotics that could kill or suppress the growth of resistant bacteria is the need of the hour, it also appears equally important to look into the various mechanisms used by bacteria to defy antibiotics. It is well-known that resistant organisms generally bypass the growth-inhibitory or bactericidal effect of antibiotics by chemical inactivation of the drug, alteration of the intracellular target of antibiotics, alteration of the cellular permeability and energy-mediated efflux of the antibiotic from the cell. Deletion of a particular gene was found to be associated with INH-resistant of some strains of some strains of Mycobacterium tuberculosis. Some recent reports underscore involvement of some nanosized (20-250 nm in diameter) bacterial vesicles in the antibiotic resistance. These outer membrane vesicles (OMV) are bag-like structures continuously released predominantly by gram-negative bacteria in the culture medium as well as inside the host tissues. They are indispensible for growth and survival of bacteria as evident from the fact that so far it has not been possible to isolate a vesicle non-producing bacterial strain. They are involved in secretion, cell-to cell communication, acquisition of nutrients, quorum sensing and pathogenesis of bacteria [1]. Possible mechanisms underlying their role in antibiotic-resistance of bacteria were discussed earlier [2]. A recent study provides further evidence of the vesicle-mediated resistance of bacteria to some therapeutically-useful antibiotics [3].

The organism chosen for this study was Acenetobacter baumanni, a gram-negative. pleomorphic, nosocomial pathogen, notorious for its ability to acquire genes that confer resistance to multiple antibiotics. During august 2012 to November 2013, altogether 71 strains were collected from a tertiary care hospital in the capital of Assam, one of the seven states in north-east India. The antibiotic-resistant profiles of the isolates were obtained. One antibiotic-resistant and one antibiotic-sensitive strains were chosen for further studies.

Vesicles produced by the multiple-antibiotic resistant strains were found to be of bigger size compared to the vesicles obtained from the antibiotic-sensitive strain. It was also observed that the vesicles protected the organism from the growth-inhibitory effect of polymixin-B, a peptide antibiotic. Indole and some indole derivatives were shown to inhibit vesicle formation in Pseudomonas in an earlier study [4]. In the present investigation, studies with ethyl-2-(3-indolyl)-4-methyl-thiazole-5-corboxylate, an indole derivative known to have a suppressive effect on the production of bacterial vesicles, revealed that the inhibitor might help sensitize the bacteria to the effect of antibiotics. Thus the inhibitor might have a dual beneficial effect in the clinical management of pathogenic bacteria. Maturation and degradation of RNA is dependent on efficacy of a group of enzymes, occurring in the form of a complex called degradosome. The present investigation for the first time reported that some of the members of this protein complex in A.boumanni (RNase E, Dna K) are packaged into the vesicles produced by the organism. The implication of this observation is not definitely known. However, it was postulated by the investigators that the enzymes could be transported through the OMVs to elicit maturation and degradation of host RNA. Comparison of the proteomic profiles of the vesicles, produced by the antibiotic-sensitive and multiple-antibiotic-resistant strains, revealed the presence of higher number of resistant-conferring proteins in the vesicles obtained from the resistant strains. This investigation once again indicates involvement of bacterial vesicles in antibiotic-resistance. Studies involving the inhibitor of vesicle production promises future application of the inhibitor in counteracting the resistance-promoting effect of antibiotics.

References

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[3] Agarwal B, Karthikeyan R, Gayathri P, Ramesh Babu B, Ahmed G, Jagannadham MV (2018) Studies on the mechanism of multidrug resistance of Acinetobacter baumannii by proteomic analysis of the outer membrane vesicles of the bacterium. Journal of Proteins and Proteomicshttps://doi.org/10.1007/s42485-018-0001-4

[4] Tashiro Y, Toyofuku M, Nakajima-Kambe T, Uchiyama H, Nomura N (2010) Bicyclic compounds repress membrane vesicle production and Pseudomonas quinolone signal synthesis in Pseudomonas aeruginosa.FEMS Microbiol Lett 304 : 123-130

Noninvasive fluid of animal origin act as a potential source for the diagnostic purpose of normal physiology vis a vis pathological condition

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Description

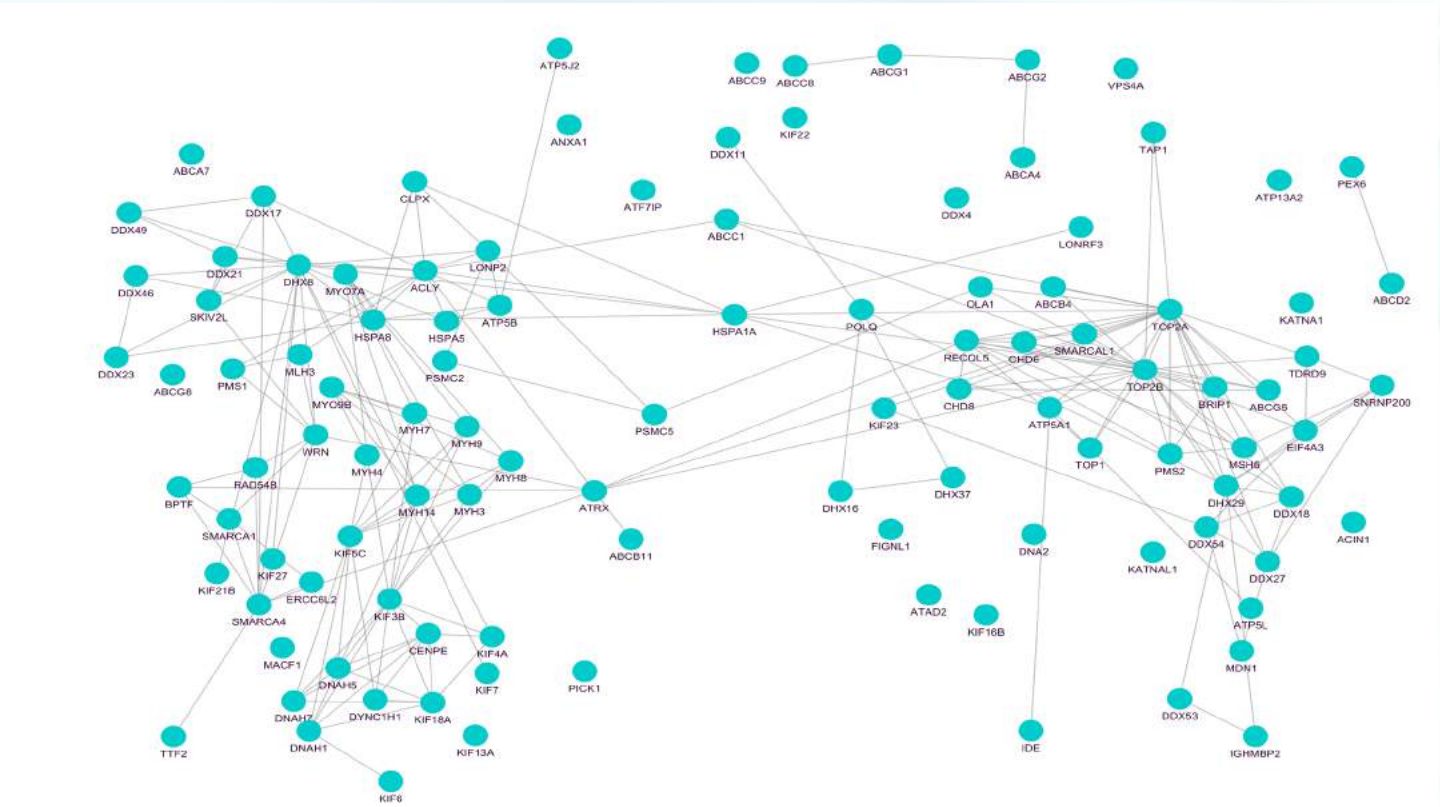
Excretory non-invasive biological fluids such as urine, saliva, milk, tear, mucus, stool, and sweat are significantly important for the maintenance of homeostasis in normal physiological conditions. The qualitative and quantitative alterations in the endogenous peptidome/proteome composition of such fluids recapitulate the events in the body and are very useful for diagnostic purpose. Thus, it can be utilized as an excellent source for the discovery of biomarkers associated with general health and disease status. On the other hand, it will allow speeding up the drug development process, and that is the reason, the pharmaceutical companies are getting extensively involved for the identification and validation of proteinaceous biological markers of diseases. In that path, the foremost thrust within the field of clinical proteomics is the profiling of such endogenous peptides/proteins. The urine and saliva are two outstanding sources that can be utilized for this purpose and in fact, in the case of human and mouse, abundant literature is available. On contrary, limited information is available in relevance to the animal science.

To augment the knowledge, our group previously performed the comprehensive proteome profiling of the healthy cow urine and surprisingly identified the presence of 1564 proteins with not much effort and fractionation (Bathla et al., 2015). Now, we are in the process of carrying out the deep profiling of the urine proteome using high fractionation technique and long gradient to catalog the presence of maximum proteins. Recently, we also reported the label-free quantitative (LFQ) analysis for the discovery of pregnancy-specific proteins and identified 195 significant hits ($p>0.01$). This is the first report uncovered the hidden proteins that can prove to be act as prominent biomarkers for the determination of early pregnancy diagnosis in cow urine. In case of farm animals this type of useful assay is not available till date (Rawat et al., 2016). In a separate study of endogenous peptide determination, we were able to identify 2977, 1389, and 1611 peptides specific to pregnancy, lactation, and heifer respectively, with high confidence (1% FDR). The presence of a huge number of peptides depicts their specific role in respective stages (data not published yet).

Along with this, currently, we are at the stage of completing the comprehensive cataloging of saliva proteome and discovered 5683 proteins with high confidence at 1% FDR. Interestingly, the 60% of the same saliva proteome was found to be common upon comparison with the plasma proteome database. Furthermore, we unravel the microbiota of the cow saliva and performed the metaproteomics analysis of unique peptides by filtering out the razor peptides (here it defines the common peptide specific to Bos taurus proteome). Fascinatingly, the results showed the presence of approximately 125 species of the bacteria present in the saliva and among them, majority of the class identified as proteobacteria (data not published yet). In addition, our currently published work on the estrus cycle specific comparison of the proteome reported the identification of total 275, 371, 304 and 565 proteins with ≥2 peptides during proestrus, estrus, metestrus, and diestrus stages, respectively. Among the identified proteins 31, 62, 32 and 104 proteins were found specific to proestrus, estrus, metestrus and diestrus stage of the estrous cycle (Shashikumar et al., 2018). The presence of diverse proteins

defines the stage-specific changes in the proteome profile for the maintenance of oral health. For example, cleansing of the oral cavity, lubrication, digestion, tooth mineralization, antiviral and antibacterial activities and so on. In essence, using the high-resolution mass spectrometer, we are continuously working on unrevealing the unique peptides/proteins in the biological fluids of farm animal to apprehend the functions.Caption Figure

Figure 1. Protein-Protein interaction network for ATP catabolic process with MCODE score 40. All the



proteins used in the network were identified with 1% FDR and proteins were shown as node and connections were depicted as edges.

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Rawat P, Bathla S, Baithalu R, Yadav ML, Kumar S, Ali SA, Tiwari A, Lotfan M, Naru J, Jena M, Behere P. Identification of potential protein biomarkers for early detection of pregnancy in cow urine using 2D DIGE and label free quantitation. Clinical proteomics. 2016 Dec;13(1):15.

Shashikumar NG, Baithalu RK, Bathla S, Ali SA, Rawat P, Kumaresan A, Kumar S, Maharana BR, Singh G, Kumar DP, Singh SK. Global proteomic analysis of water buffalo (Bubalus bubalis) saliva at different stages of estrous cycle using high throughput mass spectrometry. Theriogenology. 2018 Apr 1;110:52-60.

PSI-10th Annual Conference Award Winners

Name:Abinaya R
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Biography: Abinaya graduated with Bachelor and Master Degree in Biotechnology from SASTRA University,Thanjavur and VIT University, Vellore, respectively. She moved toProf. SandhyaVisweswariah's laboratory in IISc, Bangalore, as a JRF to work on the characterization of mycobacterial adenylyl cyclases. Currently she is pursuing her PhD at Dr. SiddheshKamat's laboratory in Department of Biology at IISER,Pune.

Functional annotation oforphan enzymes by chemoproteomics and metabolomics

Abinaya R, KaveriVaidya and Siddhesh S Kamat

The advent of genome sequencing technologies has made a large number of genomesequences available in public databases. These genome sequences have revealed that allprokaryotic and eukaryotic organisms, including humans, possess a large number ofuncharacterized enzymes, and in turn unexplored biological pathways. This finding belies the historical notion that our knowledge of cellmetabolism is nearly complete and further underscores the vast landscape of unannotatedbiochemical pathways operating in our cells and tissues. Thus, the functional annotation ofuncharacterized enzymatic pathways represents a grand challenge for researchers in the postgenomicera. We leverage a well-established chemical proteomicsstrategy, termed activity-based protein profiling (ABPP)to address this problem. ABPPuses a small molecule chemical probe to label enzyme active sites in a mechanism-based manner followed by detection, enrichment and identification of the enzymeof interest either using gel platforms or mass spectrometry (A). Currently chemical probes are available for severalclasses of enzymes like serine hydrolases, metalloproteases, cysteine proteases, kinases, tyrosine phosphatases, glycosidases, histone deacetylases etc. Another approach we take towards achieving our goal is untargeted metabolomics. Comparing the metabolome of wild type with that of knock down or overexpression systems will allow us to find the differentially changing substrates (or products) of unannotated enzymes(B). Both these approaches in tandem bypass the need to purify the enzyme and allow performing high throughput screens that enable studying enzymes in their native state

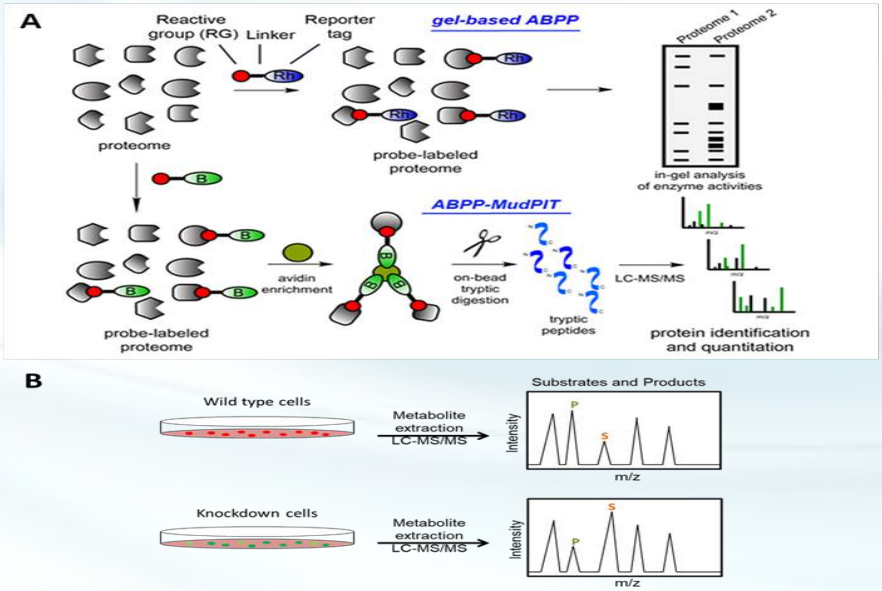

Figure:(A) Schematic representation of ABPP. Proteome labeled either by fluorophore-conjugated probe or biotin-conjugated probe to analyze by different platforms like in-gel fluorescence or LC-MS/MS, respectively.

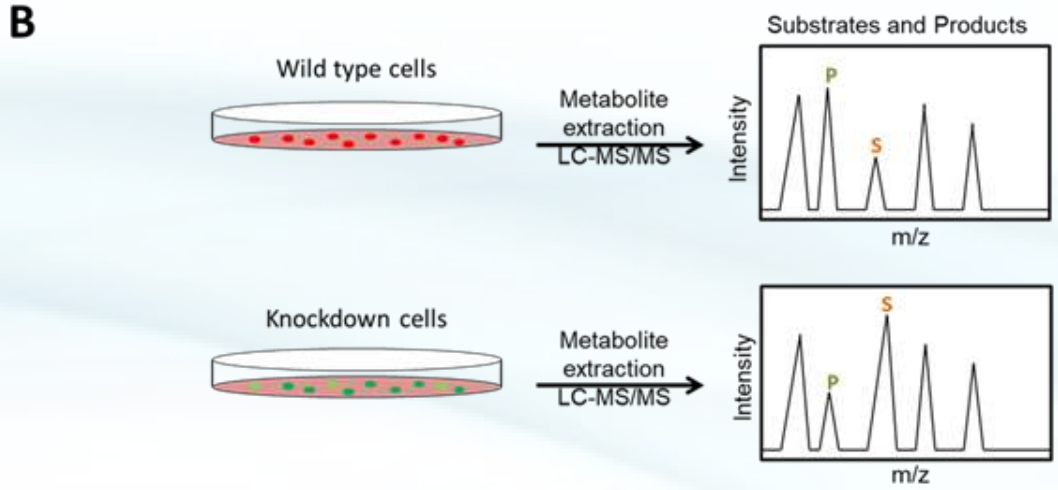

Figure:(B) Schematic representation of untargeted metabolomics. Comparative metabolomics analysis of wild type and knockdown cells for the discovery of substrates (S) and products (P) of an enzyme

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Biography: I am doing doctoral work (CSIR-SRF fellow) under the guidance of Dr. Srikanth Rapole and Dr. Manas Kumar Santra.I did my M.Sc. from Banaras Hindu University in Molecular and Human Genetics and B.Sc. from Bareilly College, Bareilly.I am working to decipher the role of F-box protein FBXO31 in DNA damage repair and response.

Summary of research work:

F-box protein FBXO31, a substrate-recognizing subunit of SCF E3 ligase, acts as a dedicated DNA damage checkpoint protein. It helps to arrest the cells at the G1 and M phases of the cell cycle through two independent pathways under genotoxic stresses. Following genotoxic stress, FBXO31 interacts with and mediates the degradation of MDM2 in p53-positive cells and cyclin D1 to facilitate the cell cycle arrest at the G1 and M phase. Further study revealed that FBXO31 depleted cells are lethal following exposure to genotoxic stress indicating the possibility of active participation of FBXO31 in DNA damage repair. Therefore, in this study, we performed mass spectrometry to identify the genotoxic stress specific interacting partners of FBXO31. From mass spectrometry data, we identifiedγH2AX and RAD51 as interacting partners of FBXO31 under DNA damage condition. We confirmed their interaction with FBXO31 under DNA damage condition by individual co-immunoprecipitation. γH2AX and RAD51 play crucial role in double stand DNA damage repair. Interestingly, we discovered that FBXO31 degrade the levels of RAD51 and γH2AX under unstressed condition but not under stressed condition. Our data suggests that FBXO31 may be involved in regulation of RAD51 and γH2AX distinctly under normal and DNA damaged condition. This study will help to better understand DNA repair regime as well as can be useful to design future therapeutic approaches.

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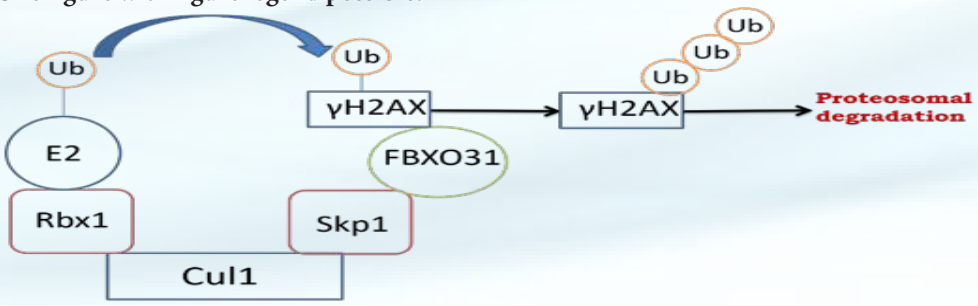

Figure showing FBXO31 facilitating degradation of γH2AX under unstressed condition through SCF complex.

Name: Shivani Sachin Gayakwad
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Biography: Shivani is a microbiologist aspiring for PhD and currently working in Pharmacology department at RAIFR. She is working in proteomics and metabolomics field in order to decipher the molecular mode of action of Ayurvedic plants. Her work focuses on validating the concepts of Ayurveda by using modern sciences.

Summary of research work:

The LC-MS based bottom-up proteomic approach has proved great applicability in characterization at the organismal proteome level. In this study, an immune response of an Ayurvedic formulation was traced through proteomics profiling by delayed type hypersensitivity (DTH) model in Albino Wistar rats. The study groups were composed of disease control, Levamisole as standard immunomodulatory drug, and Ayurvedic formulation (AYUSH PJ7) at 250mg/kg, 500mg/kg, and 1000mg/kg body weight administered by oral route. The blood samples were collected after 21 days of treatment and were centrifuged to obtain serum. The proteins extracted from serum were digested in-solution and subjected to mass spectrometric analysis. The comparison among above mentioned five groups yielded 20 significant proteins. Licocortin/ annexin that inhibit inflammation, Alpha/beta hydrolases, Tumor necrosis factor receptor member CD267 which regulates the humoral immunity, and V - ATPases subunit H were few significant proteins. Gene Ontology bioinformatics tools were searched to identify the location and function of differential proteins that were related to various biological processes, mainly response to stimulus, biological regulation, developmental process, cellular component organization or biogenesis, and cellular process. Pathways obtained in common to all samples were majorly related to immunomodulatory activity such as Wnt pathway which induces phagocytosis, Rho GEF and Ras GTP pathway which regulates cell homeostasis and related functions, Cadherin signaling pathway, Integrin signaling pathway, Collagen lamina, and Actin signaling pathways act as important sensors and transmitters of the extracellular signals and thereby crosstalk's with immunomodulatory pathways like Wnt/β-catenin signaling.

Names of Proteins	Disease Control	500 mg/kg	1000 mg/kg	Levamisole
Lipocortin I	3.99E+04	1.71E+04	5.64E+04	4.11E+04
Matrilin 2	1.23E+04	9.51E+03	1.75E+04	1.45E+04
Similar to RIKEN cDNA	3.68E+04	2.56E+04	3.35E+04	8.42E+04
Tyrosine-protein kinase	2.62E+04	3.03E+04	7.42E+04	6.89E+04
Coiled-coil domain-containing 92	1.23E+04	1.44E+04	2.50E+04	3.96E+04
Calmodulin-regulated spectrin-associated protein 2	3.51E+04	4.02E+04	9.86E+04	3.49E+04
Voltage-dependent R-type calcium channel subunit alpha	8.12E+03	2.82E+04	2.37E+04	1.10E+04
Serum albumin	6.21E+04	2.98E+04	5.40E+04	2.61E+04
Krueppel-like factor 6	5.48E+04	1.14E+05	1.36E+05	8.69E+04

Figure: Heatmap of differentially expressed proteins in control, treatment and standard groups.

Name: GayathreeKarthikkeyan

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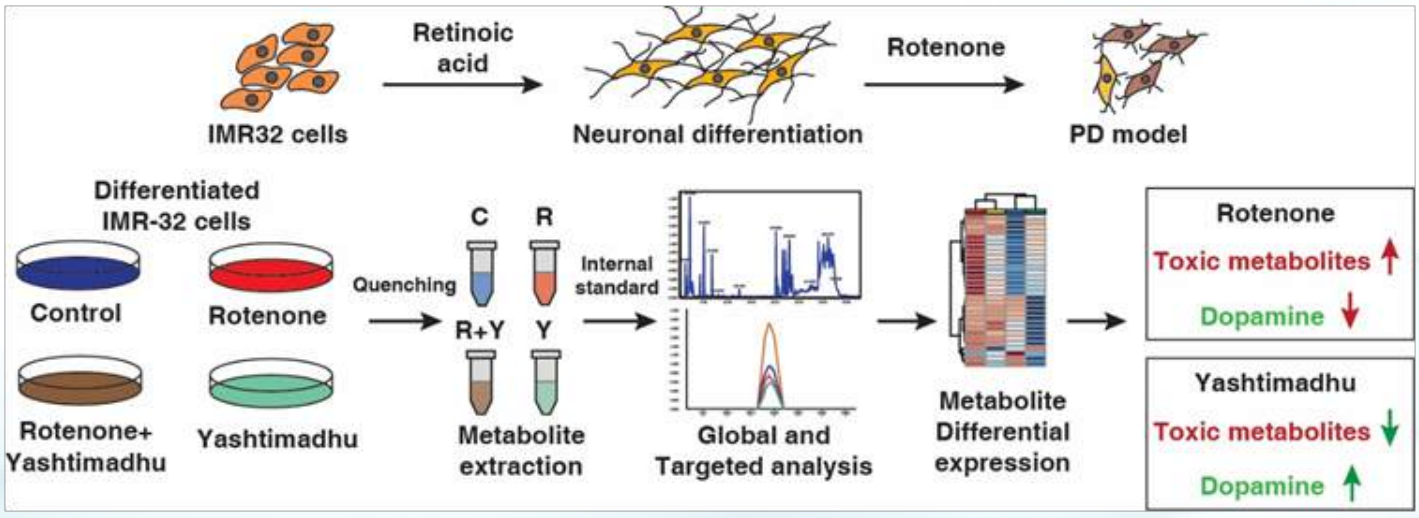
keshav@yenepoya.edu.in

Biography: GayathreeKarthikkeyan, a CSIR-NET Senior Research Fellow is a member of Dr. Keshava Prasad's laboratory at CSBMM atYenepoya .She completed her B.Tech from Anna University in 2012 and M.Tech in Biotechnology from SASTRAUniversity in 2014. She joined the Dr. Prasad'slaboratory in 2017, to work towards understanding the molecular networks involved in neuroprotective effects of Traditional Indian Medicine formulations, as guided by Dr. Prasad and Dr. Prashant Kumar Modi. Apart from conventional molecular techniques, she is trained heavily in handling QTRAP-6500 mass spectrometry facility at CSBMM and in global and targeted metabolomics platform developed at the center. Her Ph.D. dissertation features identifying molecular networks which bring about neuroprotective efficacy of Yashtimadhu (Glycyrrhizaglabra) in Parkinson's disease model using proteomic, metabolomic,andphosphoproteomicapproach.
Summary of your research work:

Parkinson's disease (PD) is a progressive neurodegenerative and motor-function disorder, due to the selective loss of dopaminergic neurons from the Substantia nigra. Current treatment modalities lead to several complications with prolonged usage. Exploration of sustainable-management options for PD is a need of the hour. Yashtimadhu (Glycyrrhizaglabra), is classified as a neuroprotectant and a memory-enhancer in Indian traditional medicine system, however, molecular understanding on its neuroprotective mechanism in PD is limited. We used mass spectrometry-based metabolomic to decipher the molecular pathways or targets associated in its neuroprotective function. We confirmed its neuroprotective function in cell culture-model of PD, using biochemical and molecular approaches. We also identified 560 differentially abundant features associated with neuroprotection among the total of 2,570 features by LC-MS/MS global metabolomic analysis on QTRAP-6500 MS. These differentially abundant metabolites were found to be enriched inthe citric acid cycle, oxidative phosphorylation, and glycolysis and, dopamine pathways. Multiple reaction monitoring (MRM)-based targeted analysis showed increased accumulation of toxic metabolites and a stark decrease in dopamine in the PD model, while treatment with Yashtimadhu rescued dopamine levels and reduced build-up of toxic metabolites. Our results provide prospective insights into molecular underpinnings and potential molecular targets associated with neuroprotection conferred by Yashtimadhu, which will provide novel opportunities for interventions.

Schematic representation



Poster title: "Metabolite landscape involved in neuroprotective functions of Yashtimadhu (Glycyrrhizaglabra) in rotenone-induced Parkinson's disease model".
Rotenone-induced PD model was generated using IMR-32 cells. Metabolite extraction was followed by global and targeted metabolomics using QTRAP-6500, which revealed a decrease in dopamine and increase in the accumulation of toxic metabolites with rotenone treatment, which was found to be countered by Yashtimadhu treatment.

Name: Rahul Chakraborty

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Contact: 9711737099

Biography: Rahul obtained his undergraduate degree in Microbiology from Asutosh College, University of Calcutta and his Master's degree in Biotechnology from department of Biotechnology, University of Calcutta, Kolkata. Later after qualifying CSIR-UGC NET he has joined as a PhD student in CSIR-Institute of Genomics and Integrative Biology.

Summary of research work:

One carbon metabolism (OCM) involves transfer of a single carbon unit in the form of methyl group. In OCM, dietary Methionine is converted to S-adenosyl methionine (SAM) by S-adenosyl methionine synthase.SAM is converted to S-adenosylhomocysteine (SAH) which is further hydrolyzed to homocysteine and adenosine by the action of SAH hydrolase. The homocysteine thus formed is re-methylate to form methionine or undergoestranssulfuration for the biosynthesis of cysteine and glutathione. Among different metabolites which are part of OCM, excess levels of SAH, homocysteine and cysteine has been shown to be toxic in different model organisms. All three of these toxic metabolites are also associated with various diseases (Cardiovascular diseases, Neurodegenerative diseases,osteoporosisetc). However it is still unclear if the mechanism of toxicity for metabolites overlap and does cell responds to these toxic metabolites in the similar way. This study is focused on in-depth comparison of the toxicity of cysteine, homocysteine and SAH using the eukaryotic model system Saccharomyces cerevisiae. Excessive Cysteine,Homocysteine and SAH cause ribosomal protein up-regulation and metabolite alteration (aminoacids) in the cells.Ncl1(tRNA methyl transferase) is necessary for survival in thiol toxicity. So we are basically focusing on the role of Ncl1 in thiol toxicity.

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Institute: Regional Centre for Biotechnology (RCB)
Contact: amitkdey@rcb.res.in

Biography: M.Sc. in Biochemistry from Universityof Calcutta, M. Tech in Biotechnology from Jadavpur University, PhD in Biochemistry with Dr. Rukhsana Chowdhury from Indian Institute of Chemical Biology (IICB-CSIR). Presentlypost-doctoral research associate at RCB with Dr. Dinakar Salunke and Dr. Tushar Kanti Maiti.

Summary of research work:

Human pregnancy induces physiological, hormonal, and immunological transient changes in a highly controlled and coordinated manner. Disruption of the delicate balance of these biological processes leads to adverse pregnancy outcome like, preterm birth. Saliva is a significant contributor to maternal and fetal health. Around 27% of whole saliva proteins were overlapped with plasma proteins that may be reflective of the various patho-physiological and biological changes. Our study aims to understand the temporal expression of proteins in saliva at different stages of pregnancy in healthy term birth using high throughput mass spectrometry-based proteomics. Maternal saliva with three periods of gestation (POG), < 14, 18-20, and 26-28 weeks and plasma with four POG, < 14, 18-20, 26-28, and 37-40 (delivery) weeks respectivelywere obtained from singleton pregnant women underwent term labour (delivered within 37 to 40 weeks). Differential proteome of saliva (N=20) across the pregnancy was profiled by label free quantitative LC-MS/MS methodology. We identified 730 proteins (FDR<1%) in saliva of which 93 were differentially modulated ($p<0.05$) and grouped into three distinctive clusters. Each cluster had unique temporal trajectory expression profile signatures. Neutrophil degranulation, platelet regulation, antimicrobial activity and carbohydrate metabolism are the major pathways where most of the differentially regulated proteins are belonging to. Interestingly, protein-protein interaction module and network analysis identified 'hub' proteins which enriched to significant pathways allied to pregnancy progression. In addition, targeted mass spectrometry-based quantification (MRM) of 'hub' proteins in a separate subset of saliva samples and plasma samples strengthen our discovery data and provide a systemic signature of these proteins in pregnancy.

Name: Chanukuppa Venkatesh

Institute: National Centre for Cell Science, Pune

Contact: Phone no: 8007951660, Email: venkatesh.ch53@gmail.com

Biography: I'm doing my PhD under the guidance of Dr. Srikanth Rapole at proteomics laboratory, NCCS, Pune. My research work mainly focuses on identification of diagnostic and therapeutic protein markers for multiple myeloma cancer, using high throughput mass spectrometry based proteomic approaches and molecular biology tools.

Summary of research work:

Multipronged proteomic analysis of multiple myeloma towards new targets and chemoresistance markers

Multiple myeloma (MM) is a heterogeneous disease and accounts for 14% of all hematological malignancies. The major challenge remains the identification of better diagnostic and therapeutic markers. In this work, we used MM serum, bone marrow interstitial fluid (BMIF), BM mono nuclear cells and respected controls for identification of diagnostic and therapeutic biomarkers. Our quantitative proteomic analysis of serum and BMIF resulted in identification of 116 and 184 differentially expressed proteins respectively and out of these a panel of 8 proteins which were identified in both serum and BMIF were proposed as diagnostic markers. Furthermore, proteomic analysis of BM MNCs yielded a total of 222 differentially expressed proteins. Based on the literature, we selected two proteins viz. MZB1 and VDAC3 which were subjected to functional studies. Knock down of MZB1 and over expression of VDAC3 proteins in the RPMI 8226 cell line proves that these proteins could be better targets for MM. As chemoresistance is a major hurdle for the treatment of MM, we established the RPMI 8226 resistance cell line towards bortezomib and performed quantitative proteomics experiments. A total of 130 proteins were commonly identified from both approaches, out of those Exportin 1(XPO1) selected for the functional analysis. Further, knock down of the XPO1 protein resensitized the RPMI 8226R cell line towards bortezomib drug, suggesting that it could be a potential chemoresistance target for MM.

One figure with figure legend:

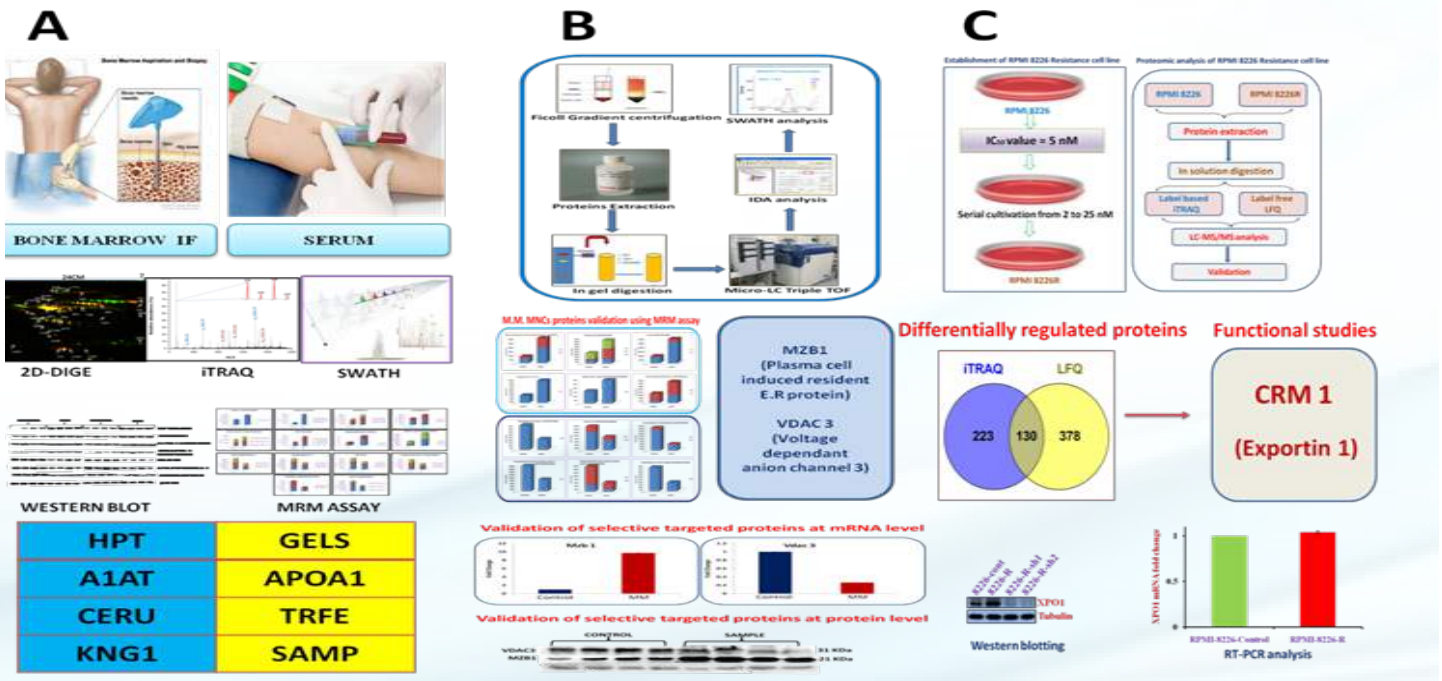


Figure: Identification and validation of potential targets for MM. A) Identification and validation of potential targets using serum and BMIF, B) Identification and validation of potential targets for MM using BM MNCs. C) Identification and validation of Chemoresistance markers using RPMI 8226 (MM) cell line towards bortezomib.

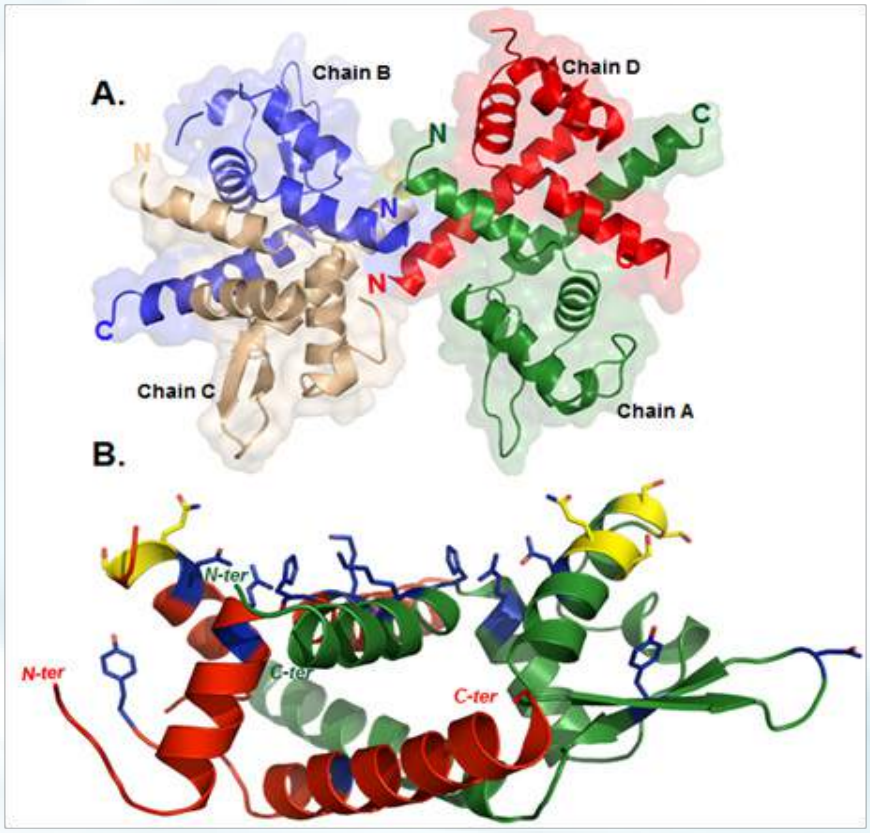
Name: Ashwani Kumar

Institute: National Centre for Cell Science
Contact: Phone no. 020-25708238, Mobile no. 7875730636

Biography: Currently, I am working as PhD student at NCCS, Pune, India under the guidance of Dr. Shekhar C. Mande. My work focuses on structural and functional characterizations of redox sensing proteins in dormancy state of Mycobacterium tuberculosis.Ihave donemy M.Sc. from IIT-Bombay and B.Sc. from BHU, Varanasi.

Summary of research work:

Mycobacterium tuberculosis(Mtb), the causative agent of tuberculosis, exists in dormant or latent stages in a majority of infected people.The dormant formsare non-replicative, metabolically inactive anddrugresistant and residein lung alveoli, entrapped in macrophages.Inside host, the dormant bacteriumadapts to a number of immune responsessuch as hypoxia, low pH, nitric oxide (NO), and nutrient starvation.It is crucial step to understand the mechanism of evading the host-induced stressesby mycobacteria duringthe dormant state. During the dormancy, hypoxia is one of such stress response experienced by Mtb. Rv0081 is a transcriptional regulator expressed during hypoxia andacts as a regulatory hub in the dormant state ofMtb infection. However, the structure of this crucial transcriptional regulator was not yet known. We successfully crystallized the Rv0081 protein and solved its structure at 3.3Å. Our analysis indicates that Rv0081 belongs to ArsR/SmtB family of transcription repressors. Furthermore, we identified the crucial residues in Rv0081 needed for specific recognition of self-regulatory elements in rv0081-rv0088 operon. Overall, our analysis provides the novel insights on the structure and function relationship of Rv0081 protein during the hypoxia condition of Mtb infection.



Crystal structure of the Rv0081 at 3.3 Å: (A) Incrystal latticeAsymmetric unit shows four identical chains shown in different colored and the overall structure is typical of the ArsR/SmtB family of transcriptional repressors.(B) In consistent with our biochemical analysis, this structure shows an extensive monomer-monomer interface that suggests the dimeric nature of Rv0081 in in vivo state.Crucial residues in DNA binding (base binding-S48, S49, S52, Q53),and (PO4 back interacting-K15, H19 R22 Q54, N71 and Y75) highlighted are yellow and blue respectively.

11th Annual Meeting of Proteomic Society of India, 2019 and International Conference on Proteomics for System Integrated Bio-Omics, One Health and Food Safety

Invitation

Dear peers, colleagues and friends,
Warm welcome to the annual meeting of PSI-2019 !

On behalf of the PSI, it is my pleasure to invite all of the great scientists, academicians, young researchers, and industry partners to participate in the annual meeting and international conference. It gives me immense pleasure to invite you for the 11th "Annual Meeting of Proteomic Society of India (PSI), and International Conference on Proteomics for System Integrated Bio-Omics, One Health and Food Safety" at NDRI, Karnal, Haryana, India. This is the special event for PSI and NDRI as well for hosting 11th annual meeting of this society. The event is proposed to be held in late November to early December 2019. Exact date of the event will be decided soon.

In the era of high through muti-omics technologies, it is an essential requirement to gather all researchers throughout the world to share and exchange the current knowledge under one umbrella. So this gathering presents the ideal platform and provides the opportunity for fostering the knowledge and future collaborations. The proposed areas which will be covered for this conference are one health and productivity, omics work flows & mass spectrometry update, cellular and molecular proteomics, model/unique organism proteomics, proteomics, bioinformatics and big data analysis, clinical and disease proteomics in human, animal and plant, post translational modifications (PTM) and applications, metabolomics, integrative bio-omics and systems biology, translational proteomics in human, animal and plant, biomarker discovery, targeted proteomics and entrepreneurship, proteomics and mass spectrometry applications in food safety and health, proteogenomics, structural proteomics and drug targets.

Along with the international conference, the schedule for the event is also enriched with education day and pre / post conference workshop, lead talks, poster presentations, young researcher oral presentations and many more opportunities, especially for the interaction with young mind to experience colleagues. In this occasion we might be able to listen the recognized international and national level scientists, academicians and industry experts who are involved in proteomics research in the proposed areas.. Proteomic Society of India is a dynamic society which has grown rapidly in a short span of time and with active cooperation of its active members, it is going to make the ensuing highly scientific and unique in many aspects.

For the first time, the 11th PSI meeting and international conference will be organized at ICAR-National Dairy Research Institute, Karnal (Haryana) which is a deemed university under Indian Council of Agricultural Research (ICAR) and a research institute of eminence in the area of Animal and Dairy Science. Karnal is located 125 kilometers north of Delhi on national highway no. 1 towards Chandigarh. ICAR-NDRI is in existence since 1923 which initially started from its currently located Southern Regional Station at Bangalore in the name of Imperial Institute of Animal Husbandry and Dairying. Subsequently it was renamed to its current name in 1947. In the year 1955, NDRI headquarter was shifted from Bangalore to Karnal, Haryana and was accorded deemed university status in 1989. The institute covers an area of more than 1000 areas of beautiful land scaping and is involved in research and teaching in contemporary areas of biological sciences involving Animals, Science, Dairy Technology and Engineering. ICAR-NDRI, Karnal has excellent infrastructure in terms of conducting meetings and seminars with availability of two auditoriums namely D. Sunderesan auditorium (900 capacity) and N. N. Dastur auditorium (160 capacity). Apart it has many small seminar rooms for holding small scale meetings. It has well furnished hostels and guest houses for hosting the guests. NDRI has a vibrant student community. It has also beautiful domesticated livestock more than 2000 cattle and buffaloes with availability of delicious dairy products.

Karnal is a historical town of Mahabharata era which was the capital of kind Karna and nearby area includes Kurukshetra which is a pilgrimage town.

I am sure with the active participation of students, faculties, scientists and industry personnel; the 11th annual meeting of PSI 2019 is going to be a successful event.

I welcome you all.

With greetings from
Ashok K. Mohanty,
Principal Scientist,
Animal Biotechnology Centre, NDRI, Karnal
Email: ashokmohanty1@gmailcom; Phone: 91-184-2259538 (Office)

The 18th Human Proteome Organization World Congress - HUPO 2019, Adelaide, Australia

The 18th Human Proteome Organization World Congress - HUPO 2019 will be hosted by the Australasian Proteomics Society (APS) in the beautiful 'City of Churches', Adelaide. HUPO 2019 will focus on "Advancing Global Health Through Proteome Innovation" and will bring together world-leading experts and the next generation of early career scientists to promote how proteomics is advancing our knowledge of human and planetary health. HUPO 2019 will both celebrate what has been achieved and look forward to future advances and discoveries that will revolutionize global health.
The Australasian Proteomics Society (APS) has started to design a fantastic program for the HUPO 2019 in Adelaide and have confirmed already a number of plenary speakers:

- Prof Rudi Aebersold
- Prof Yu-Ju Chen
- Prof Fuchu He
- Prof Albert Heck
- Prof. Kathryn Lilley
- Prof Mathias Uhlen

With plenary lectures from outstanding speakers and over 30 parallel sessions - including 6 HPP sessions, the 2nd Australasian Glycoscience Symposium, Plant and Food Proteomics sessions - the program will offer opportunities for fruitful discussions.Other Themes include:

- Health and Disease
- Biological Applications of The Proteome
- Beyond the Proteome
- Our Human Environment
- Enabling Technologies

The Organizing Committee of the HUPO 2019 consists of the committee members of the Australasian Proteomics Society (APS) plus a number of prominent Australian Proteomics Scientists:
HUPO 2019 Organizing Committee
Prof. Stuart Cordwell (Co-Chair, APS President)
Prof. Peter Hoffmann (Co-Chair and LOC Chair, APS Vice President))
Prof. Anthony Purcell (APS Treasurer)
Prof. Mark Molloy (APS Secretary)
Prof. Marc Wilkins (APS Committee)
Dr. Michelle Colgrave (APS Committee)
Dr. Morten Thaysen-Andersen (APS Committee)
Dr. Andrew Webb (APS Committee)
Additional HUPO 2019 Organizing Committee
Prof. Mark Baker (HPP)
A/Prof. Michelle Hill (HUPO EC Secretary)
A/Prof. Vera Ignjatovic (HPP)
Dr. Ed Nice (HPP and social event committee)
Prof. Nicolle Packer (Glycoscience)
Prof. Paul Haynes (Plant and Food Proteome)
Prof. Gavin Reid (Multi-omics)

Visit the conference website www.hupo2019.org for more details.
We look forward to welcoming you to Adelaide in 2019 for an unforgettable HUPO World Congress.

Upcoming Proteomics Courses/ Workshops

February 5th to 7th, 2019

For more information contact Prof. Sanjeeva Srivastava: sanjeeva@iitb.ac.in

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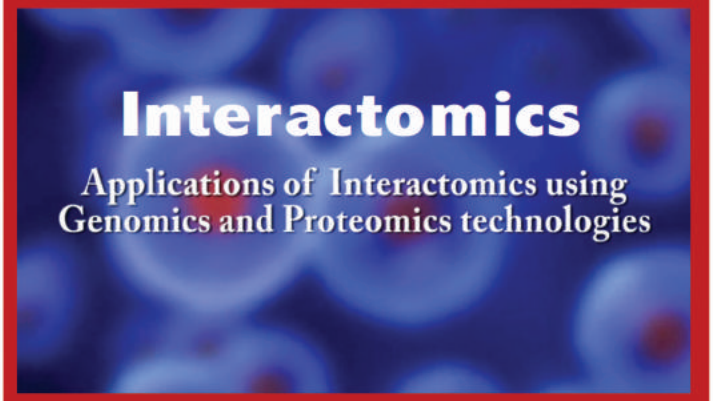

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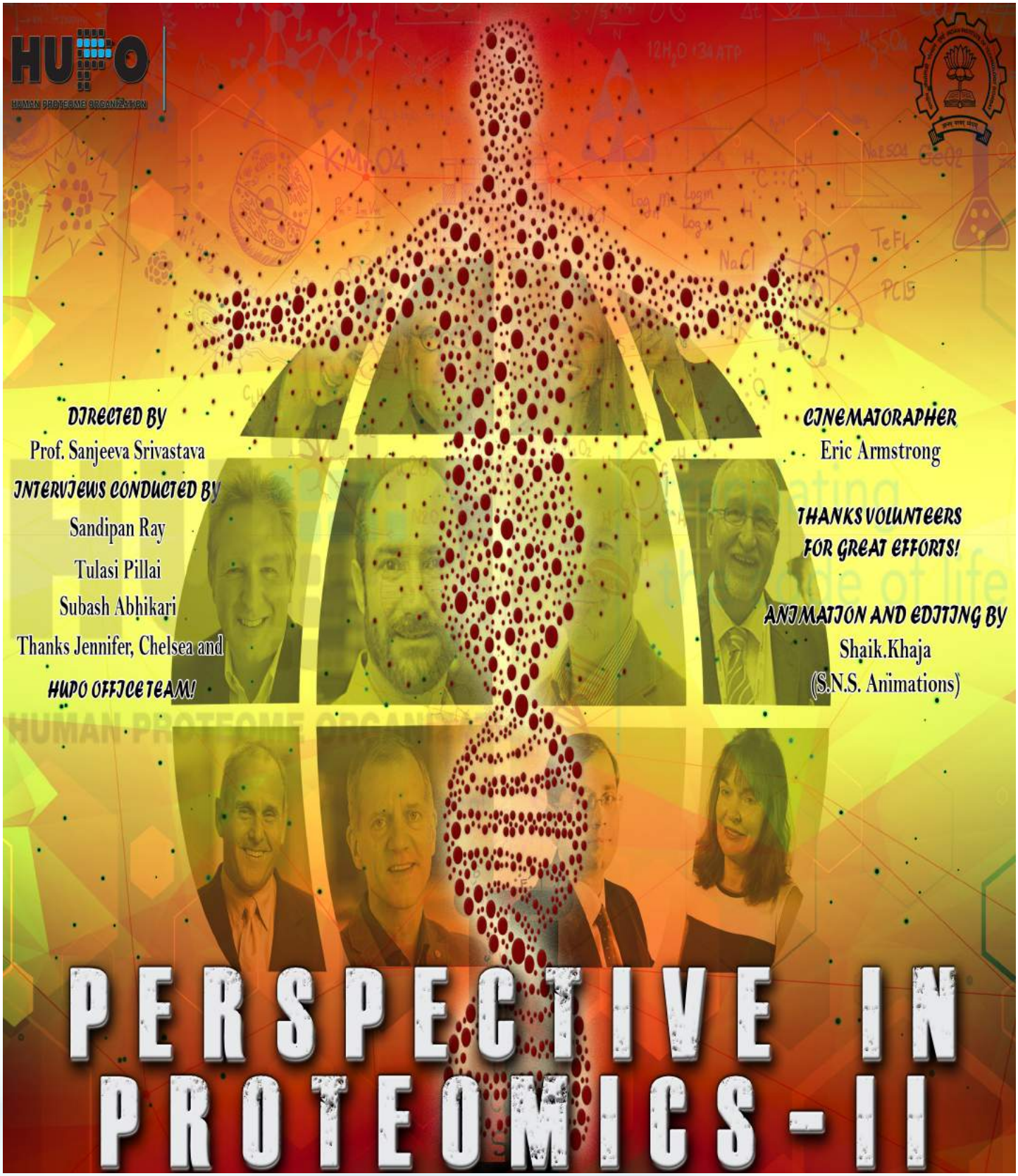
OPEN FOR ENROLLMENT

February 25th, April 19th, 8 Week Course

Exam Date:- Apr 27th, 2019



A video project titled "**Perspective in Proteomics: Part-II**" was directed by Dr. Sanjeeva Srivastava at the Human Proteome Organization World Congress in Orlando, Florida. Stay tuned to watch the videos of proteomics experts every month.