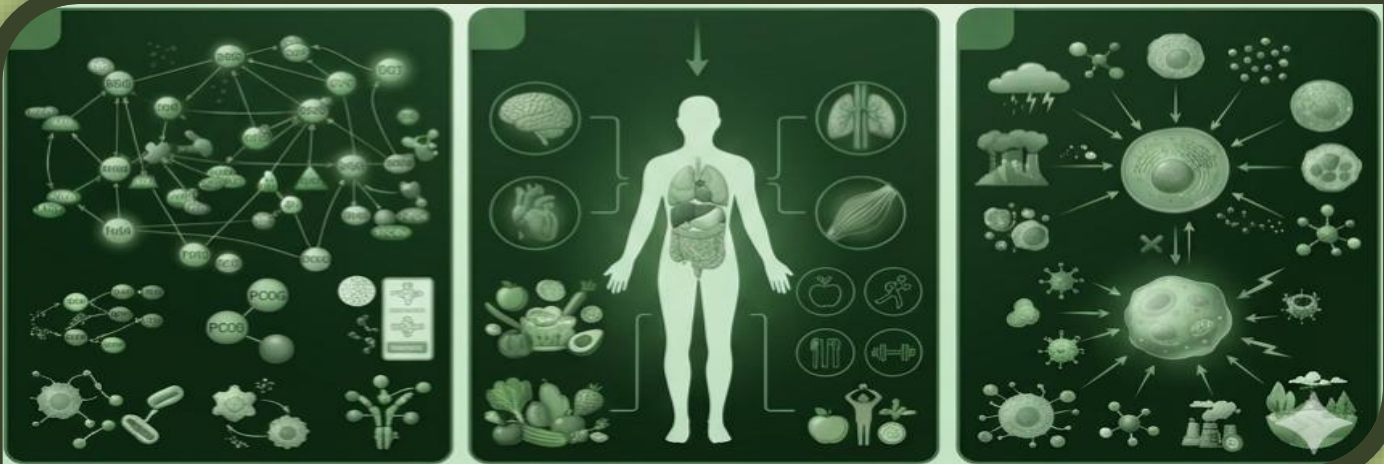


PROTEOMICS SOCIETY, INDIA (PSI)

NEWSLETTER



EDITORS

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Editor's Message



Dear PSI members,

It gives me immense pleasure to welcome you to the latest issue of the PSI Newsletter, which captures another year of exciting developments, scientific achievements, and collaborative initiatives within the proteomics community in India. The Proteomics Society, India (PSI) continues to promote research, education, training, and scientific exchange, bringing together researchers, students, academicians, and professionals working across proteomics and allied disciplines.

A major highlight of the year was the 17th Annual Meeting and Conference of PSI, held at CSIR-CCMB, Hyderabad, from December 18-20, 2025. The meeting provided an excellent platform for researchers from India and abroad to present their latest findings, exchange ideas, discuss emerging technologies, and explore new opportunities for collaboration. The scientific programme reflected the rapid growth and expanding scope of proteomics research.

The Annual Meeting was preceded by PSI Education Day, held at CCMB, Hyderabad, on December 17, 2025. The programme focused on education, training, and capacity building in modern proteomics, offering students and early-career researchers valuable exposure to contemporary technologies, methodologies, and applications.

PSI also continued its outreach through several specialized workshops and scientific programmes across the country. The National Workshop on Mass Spectrometry-Based Proteomics (NWMSB-2026), held at BRIC-ILS, Bhubaneswar, from March 9-11, 2026, provided participants with valuable insights into mass spectrometry-based proteomics and its applications.

Another significant event was OMICS FEST '26: Fostering Next-Generation Multi-Omics Research and Celebrating Proteomics Day, held at BITS Pilani, Hyderabad, on March 17-18, 2026. The event highlighted emerging developments in multi-omics research and the growing importance of integrating proteomics with genomics and other omics approaches.

The National Workshop on Proteomics, Genomics & Bioinformatics (NWPGB-2026), organized at Jai Narain Vyas University, Jodhpur, Rajasthan, from March 23-25, 2026, further strengthened PSI's commitment to interdisciplinary education and skill development. In addition, the Multi-Omics Summit 2026, hosted by Thermo Fisher Scientific in collaboration with PSI on March 13, 2026, provided an important forum for discussing emerging technologies and future directions in multi-omics research.

Together, these initiatives reflect PSI's continued commitment to advancing proteomics through education, innovation, collaboration, and interdisciplinary research. They also demonstrate the enthusiasm and dedication of our members and partners in strengthening the proteomics ecosystem across India.

Looking ahead, we are pleased to announce the 18th Annual Meeting of PSI and International Conference, which is set to take place at BRIC-Institute of Life Sciences (BRIC-ILS), Bhubaneswar. We look forward to another enriching scientific gathering that will provide opportunities to share discoveries, foster collaborations, and explore emerging frontiers in proteomics and multi-omics research.

I sincerely thank all PSI members, organizers, speakers, participants, collaborators, and supporters for their continued contributions and enthusiasm. I encourage everyone to remain actively engaged with PSI activities and initiatives as we continue our collective journey toward scientific excellence.

We hope you enjoy the collation. Your feedback will be much appreciated.

Thank you and Regards,

Dr. Amol R. Suryawanshi

Dr. Niranjana Chakraborty

Dr. Manas Santra

Prof. Renu Deswal

Dr. Alka Rao

Dr. Sandhya Sadashivaiah

Message from President, PSI

Dear Members of the Proteomics Society of India,

Warm greetings to all.

It is a great honour and privilege to address you as President of the Proteomics Society, India (PSI), as we begin a new chapter in the journey of our Society. I extend my warmest greetings to all members of PSI and a special welcome to the **newly elected Council members**. I look forward to working together with the entire PSI community to further strengthen our Society and its role in advancing proteomics research, education, training, and scientific collaboration in India.

The past year has been an exciting and productive one for PSI, marked by a wide range of scientific, educational, and outreach activities. The **17th Annual Meeting and Conference of PSI**, held at CSIR-CCMB, Hyderabad, from December 18–20, 2025, brought together scientists, faculty members, students, young researchers, and industry professionals from India and abroad. The meeting provided an excellent platform for presenting new research, exchanging ideas, discussing emerging technologies, and fostering scientific collaborations. The breadth of the scientific programme reflected the rapidly expanding scope of proteomics and its growing relevance across the life sciences.

The Annual Meeting was preceded by **PSI Education Day**, held at CCMB on December 17, 2025. The emphasis on education, training, and capacity building reflects one of PSI's important responsibilities—to equip young researchers with the knowledge and practical skills needed to engage with the rapidly evolving technologies of modern proteomics.

This commitment to training continued through several programmes across the country. The **National Workshop on Mass Spectrometry-Based Proteomics (NWMSP-2026)**, held at BRIC-ILS, Bhubaneswar, from March 9–11, 2026, provided intensive exposure to high-resolution mass spectrometry-based proteomics through lectures and hands-on sessions. The workshop brought together research scholars, postdoctoral fellows, and faculty members from several institutions and focused on developing practical expertise in contemporary proteomics workflows.

PSI has also continued to expand its engagement with the rapidly emerging field of **multi-omics**. The **India Multi-Omics Summit 2026**, held in New Delhi on March 13, brought together scientists, clinicians, policymakers, industry experts, and technology partners to explore how genomics, proteomics, metabolomics, clinical phenotyping, cohort science, biobanking, and data science can be integrated to advance precision health and innovation. The summit represented an important step towards moving from data generation to meaningful biological and clinical translation.

Our **Proteomics Day** activities further demonstrated the growing reach of PSI. OMICS FEST '26 at BITS Pilani, Hyderabad, on March 17–18, 2026, provided hands-on training in omics data analysis and highlighted the integration of proteomics with genomics and other omics disciplines. Similarly, the Educational and Proteomics Day programme at Alagappa University, Karaikudi, brought together students, research scholars, academicians, and scientists through lectures, practical training, and scientific interaction. These initiatives are important in nurturing scientific curiosity and creating opportunities for young researchers to develop both conceptual understanding and practical skills.

The **National Workshop on Proteomics, Genomics & Bioinformatics (NWPGB-2026)** at Jai Narain Vyas University, Jodhpur, further reinforced the importance of interdisciplinary approaches and computational expertise in contemporary life-science research. Together, these programmes demonstrate the growing geographical and scientific reach of PSI and our collective commitment to building a strong and connected proteomics community.

As we look ahead, the opportunities before proteomics are greater than ever. The field is moving beyond the measurement of protein abundance towards a more comprehensive understanding of **proteoforms, post-translational modifications, protein interactions, spatial organization, structural states, and molecular dynamics**. At the same time, advances in artificial intelligence and computational biology are opening new possibilities for integrating diverse layers of biological information. The interview with Prof. Ruedi Aebersold featured in this issue offers an inspiring perspective on how multi-modal proteomics and AI-driven integration could contribute to a deeper mechanistic understanding of biological systems.

For PSI, this changing landscape presents both an opportunity and a responsibility. We must ensure that the Indian proteomics community remains at the forefront of technological and scientific developments while also addressing the practical needs of researchers—access to advanced platforms, training, data analysis expertise, interdisciplinary collaboration, and opportunities for young investigators. Equally important is the need to strengthen connections between proteomics and the wider communities of biology, medicine, biotechnology, and industry.

I am therefore particularly pleased to announce the **18th Annual Meeting of PSI and International Conference**, to be hosted at **BRIC-Institute of Life Sciences (BRIC-ILS), Bhubaneswar**. I am confident that this meeting will provide an enriching platform for scientific exchange, presentation of new discoveries, interaction among researchers, and the development of new national and international collaborations.

I invite every member of PSI to actively participate in the activities and initiatives of the Society. The strength of PSI lies in its members and in our ability to work together across institutions, disciplines, and generations. Let us bring together **experience and new ideas, established expertise and emerging talent, and technology and biology** to build an even stronger proteomics ecosystem in India.

Together, I am confident that we can further enhance the role of PSI as a platform for scientific excellence, capacity building, collaboration, and innovation, and contribute meaningfully to the advancement of proteomics in India and to the global proteomics community.

With warm regards and best wishes,

Warm regards,

Shantanu Sengupta

President, Proteomics Society, India

Perspectives in Proteomics: Interview of renowned Scientists

Interview - 3 Prof. Ruedi Aebersold

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Thank you for giving me the opportunity for this “Perspectives in Proteomics” interview and for the great questions. Over the years, I had the opportunity to attend several scientific events in India. I have always been impressed with the growth of the proteomics community and the keen interest of students to learn and of established investigators to interact and exchange internationally. I wish the Indian Proteomics Society best success and a bright future.

-Prof. Ruedi Aebersold

- 1. You have been one of the pioneers of modern proteomics, with seminal contributions to quantitative mass spectrometry and systems biology. Looking back, what inspired you to pursue proteomics when the field was still in its infancy?**

When I trained as a PhD student proteomics did not exist and neither did any other “OMIC” discipline. I was trained as a protein chemist in Basel Switzerland. Specifically, I learned how to purify proteins from complex samples and to then determine the amino acid sequence of the isolated proteins by a technique called the Edman degradation. This type of work was tedious and slow. To purify the milligram amounts of a specific protein to a level of homogeneity conducive to sequencing took me several months and to then determine the sequence from overlapping peptides required another few months of work. Naturally, the proteins for which a sequence could be identified at the time were abundant, and easily accessible proteins such as immune globulins, albumin, myoglobulins etc. Actually, no one knew how many types of proteins there were in a cell. As an interesting historical fact, in 1973 Francis Crick published a paper entitled: *Project K: The Complete Solution of E. coli* (Perspectives in Biology and Medicine, 17:pp67-70). In there he wrote: ... “of course it is unlikely that the work will ever be pushed to the point that every possible detail about the cell is known. It does not seem very probable, for example, that all the various proteins of the cell (which may number several thousand) will all have their amino acid sequences and stereochemical structure determined...”. Today, with modern proteomic techniques, at least identification part of Crick’s statement can be accomplished by a PhD student within a day.

I then joined the laboratory of Lee Hood at Caltech as a postdoc. At the time his lab was leading in building automated instruments for the analysis and synthesis of biomolecules, including the protein sequencing instruments based on the Edman degradation that were later commercialized by the company Applied Biosystems. I found myself in the paradoxical situation that the instrument could sequence proteins at much lower amounts than could be purified by the column-based methods of the day. I therefore developed methods to downscale protein purification to the levels required by the sequencing instrument.

Perspectives in Proteomics: Interview of renowned Scientists

I worked out electroblotting methods that allowed us to transfer gel-separated proteins onto suitably treated glass fibre membranes. So all we had to do then was to detect the transblotted bands, cut them out and put them into the sequencing instrument, or to detect the transblotted proteins, digest them on the membrane by a protease, separate the peptides and sequence them. Initially conceived as methods to identify proteins from 1D gels, it was a natural progression to apply it also to proteins separated by 2D electrophoresis. The ability to identify proteins from 2D gel spots connected my work with the grandiose vision of Norman and Leigh Anderson to establish what they called the Human Protein Index (*Taylor, J, et al, (1982) Clin. Chem. 28, 739-49*). The index essentially entailed the separation of proteins in a sample as spots of a 2D gel and the annotation of the spots with the identity of the proteins and other available information. Since we believed at the time that the ensemble of protein spots in a 2D gel represented the whole protein content of a cell, in today's terminology we could call a 2D gel pattern a representation of a proteome. Later, we learned that this assumption was not valid. But nevertheless, the ability to identify most spots in a 2D gel (albeit slowly) was clearly the first attempt to try to grasp the complexities of the proteome.

So, getting into the field of proteomics (which had no name at the time) was less a question of inspiration than of a natural progression from identifying single proteins to identifying ever larger numbers of proteins as the technological capabilities progressed.

2. Your pioneering work on targeted proteomics and data-independent acquisition (DIA), particularly SWATH-MS, has transformed protein quantification. What were the biggest scientific and technological challenges in developing these approaches, and what impact have they had on biomedical research?

The development, primarily by the group of John Yates, of shotgun proteomics, in combination with the technical challenges associated with 2D gel electrophoresis catalysed a rapid transition of proteomics away from 2DE based approaches to approaches based on LC-MS/MS. This greatly accelerated the pace at which proteins could be identified from complex samples. However, shotgun proteomics also left important information about the identified proteins in the wake. Specifically, it was difficult to estimate quantitative changes of specific proteins across samples, and it was (and still remains) difficult to distinguish proteoforms from shotgun MS data. Furthermore, at least in the early days of LC-MS/MS the number of peptides generated by tryptic digestion of a proteome by far exceeded the precursor selection/fragmentation cycles provided by instruments at the time, resulting in stochastic under sampling of the of the peptide population. A consequence of that phenomenon was that if different proteome sample, e.g. protein extract from cells at different states were analysed, and different sets of proteins were identified, the researcher did not know whether proteins identified in one sample, but not the other were truly not present in both samples, or whether they simply had not been sampled by the mass spectrometer from both samples.

Our work in proteomics was always driven by the interest to compare proteome differences between samples and we felt that to achieve that we needed to address three issues. The first was accurate relative or, preferably, absolute quantification of proteins across sample sets. The second was the reproducibility of protein identification as defined by the reproducibility of the list of proteins identified from serial analysis of identical samples.

Perspectives in Proteomics: Interview of renowned Scientists

Reproducibility was an important indicator to determine whether a peptide not detected in a sample was actually absent from it or just not selected for fragmentation. The third issue was the development of statistical tools to assign a probability of correct match between fragment ion spectrum and peptide sequence to minimize the number of false positive identifications. We attempted to address the third challenge by the development of software tools for assigning a probability of true identification to every peptide (*PeptideProphet*) and for assigning a probability of true protein inference, given a set of truly identified peptide (*ProteinProphet*). We attempted to address challenges one and two by eliminating the stochastic sampling process. This was achieved initially by adapting selected reaction monitoring (SRM) to proteomic samples and to automate the analysis of the resulting data. In SRM pre-defined sets of analytes sequentially selected by the mass spectrometer, fragmented, and pre-defined, analyte-specific fragment ions and their intensities are recorded by the instrument. Later this approach was extended via SWATH-MS by making the data acquisition parallel-in-time to address the issue of the limited number of peptides that can be identified in a SRM measurement. Rather than isolating a specific, pre-determined precursor ion for fragmentation, SWATH-MS, now more generally referred to as DIA-MS, isolates packets of different fragment ions and concurrently fragments them, resulting in convoluted fragment ion spectra. The precursor isolation windows are chosen in a way that they collectively cover most of the retention time vs. m/z range populated by peptides in LC-MS/MS maps. The convoluted fragment ion spectra were then resolved to identify multiple peptides from the acquired composite spectra by applying the principles of targeted MS in silico.

The impact of these targeting and parallel-in-time targeting methods were a higher degree of reproducibility of protein maps across samples, a reduction of missing values in cohort studies, and improved quantification of the same peptide across samples. Compared to the early days of these techniques, the last few years have seen rapid advances in instrument performance that has yielded incredible gains in sensitivity, sample throughput and data quality that boosted the performance of proteomic analyses to surprising levels.

3. Your recent work demonstrates how AlphaFold3 can be integrated with experimental techniques such as NMR, cryo-EM, and X-ray crystallography to generate structural ensembles rather than single static models. How do you envision experimentally guided AI reshaping structural biology and proteomics in the coming years?

Anfinsen's finding that proteins are only functional if folded to a specific structure is one of the bedrock tenets of molecular biology. Discussions with David Baker, who at the time had his laboratory in a building next to my laboratory at the University of Washington, made me aware of a fundamental problem with protein structural modelling. David had developed the Rosetta protein modelling suite and he discovered that the tool would frequently predict a small number of possible structures from a particular sequence that had similar scores and could therefore not be further distinguished by the information available to the program. He suggested that even a small number of experimentally determined constraints would be very useful to select the true structure from among the equally possible ones calculated by Rosetta. This motivated us to develop cross-linking/MS methods to determine distance constraints between two cross-linked residues on a folded protein. Eventually, this became a fairly robust technique that gained further in significance in the early days of cryoEM based structure determination of protein complexes. The data generated by the microscope were by themselves frequently insufficient to determine structure.

Perspectives in Proteomics: Interview of renowned Scientists

As for ab-initio modelling of proteins a few experimental distance constraints, determined by XL-MS proved extremely useful to refine cryo-EM structures. Today, the data generated by cryoEM are of a quality that frequently no longer requires orthogonal data. However, as is pointed out in the question above, it is now well known that protein complexes can occur in different structures which generally indicate different functional states. This message, clearly supported by XL-MS data on a wide range of complexes was initially a hard sell. Initially, our papers identifying different structural states of protein complexes for which x-ray diffraction structures were available, were systematically rejected by reviewers on the grounds that some of the cross-links, when projected on the x-ray structure were longer than the length of the fully extended connection between the crosslinked amino acids in the model. The reviewers concluded that such cross links were false positive identification, whereas we argued that they were indeed correct but were derived from the complex in a different structural state compared to state the protein had in the crystal lattice and that was solved by X-ray structure. Eventually, the view of structural heterogeneity became widely accepted, also by the observation in cryoEM studies that protein complexes in a preparation fell into multiple classes.

Now, that AlphaFold is increasingly used to predict structurally/functionally different states of proteins and complexes, I am convinced that experimental data distinguishing these states will again be indispensable to support the modelling efforts. Such data include experimentally identified proteoforms generated by protein modification, processing or allosteric interactors, and cross-linking data. In this regard, data generated by mass spectrometric methods that probe structural variance on a proteome-wide scale such as LiP-MS or thermal profiling are particularly exciting and promising.

4. Throughout your career, you have emphasized that proteins are dynamic molecules. How important is it for future proteomics research to move beyond static protein structures and embrace protein conformational dynamics?

As discussed above, considering proteins as dynamic molecules assuming different states is biologically critically important. It is also a unique opportunity for proteomics to generate functionally important information that is difficult to obtain or infer by other means.

If we look at the proteomic literature a sizable fraction, maybe the majority of papers is focused on generating abundance profiles at ever increasing proteomic depth and sample cohort size. A notable example is the large-scale plasma proteomic analysis from the UK Bio Bank by the O-Link technology. Affinity-based and MS-based methods have been used for such studies, each with characteristic strength and weaknesses. While the results of such studies have proven invaluable, e.g. to identify disease biomarkers or associations between protein abundance and phenotypic traits (pQTL's), it also has to be realized that they only scratch the surface of the richness of information that can, in principle, be generated from proteomic analyses. Specifically, most proteomic profiling studies report the identification and abundance of the canonical protein from the respective coding gene. In principle, current state of MS-based proteomic technology makes it possible to also measure at large scale other properties of proteins, many of which are of great functional significance. These include the detection of sequence proteoforms, PTM's and PTM proteoforms, subcellular protein localization, protein interactions with other proteins, as well as with other types of biomolecules, and, as is alluded to in the question, changes in protein structure that indicate conformational dynamics.

Perspectives in Proteomics: Interview of renowned Scientists

Now, it is obvious that the large-scale generation of such data that collectively reveal not only the identity and abundance of canonical proteins, but also their contextual functional state are expensive and still technically challenging. It is nevertheless interesting to ask how proteomic studies should be structured to maximize the gain of biological or clinical information. Let's assume a scientist is awarded \$ 1mio grant to carry out proteomic analyses on a large clinical cohort of phenotypically well-annotated samples. Should they spend the funds on generating profiles of canonical proteins on as many samples as the budget affords, or should they intelligently select a subset of the available samples and generate multi-layer proteomic data? I am convinced that if the field of proteomics intends to advance from statistical associations towards mechanistic insights into the processes of life, the multi-modal path will prove superior. At this time, this is largely conjecture, because the question asked has not been rigorously tested, although a string of recent publications, also from our group, point in the multi-modal direction. Ultimately, it boils down to the question whether proteins teach us most biology if we consider them as invariant, canonical entities or if we consider them as agents of biological function that dynamically adapt to and shape the state of the cell or organism.

5. Artificial intelligence is rapidly transforming protein science, from structure prediction to proteomics data analysis. How do you see AI complementing experimental proteomics, and where do you think human expertise will continue to play an indispensable role?

As discussed above, AI has already transformed structural proteomics. It also profoundly affected core challenges of MS-based proteomics, including the assignment of sequence and PTM's to fragment ion spectra, protein inference etc. Following-up on the discussion above under question #4, it seems plausible that in proteomics a profound impact will also be achieved by focusing AI on the integration of multiple proteomic modalities generated from aliquots of the same sample set. Given the enormous space generated by the sheer number of proteins in a cell multiplied with the astronomical number of combinatorially possible protein states this is a daunting task. I therefore think that the use of AI towards linking the molecular state of the proteome with the phenotypic state of the system will greatly benefit from using the detailed biochemical and biophysical knowledge contained in millions of research papers published to date. To make the contents of these papers systematically accessible and to mine it by AI is a challenging task by itself.

There is presently an intense discussion about generating AI models of cells or organisms. If such a model is expected to explain or predict how a system mechanistically adapts to external or internal perturbations to generate a new phenotype (e.g. how one or several point mutations in a cell change it from a normal cell into a cancer cell), the generation and integration of multi-model proteomic data, indicating the state change of proteins seems indispensable. It seems to me that for quite some time human expertise will be required to create a suitable conceptual framework for life science research, for asking the right questions, for putting the results from AI in perspective and to devise experiments to test their validity.

6. With rapid advances in single-cell proteomics, spatial proteomics, and multi-omics integration, what scientific discoveries do you believe these technologies will enable over the next decade.

Following up on the answers to the questions above, I believe that single cell proteomics and spatial proteomics are just two of many proteomic modalities. That they are even possible today attests to the rapid technological progress in the field.

Perspectives in Proteomics: Interview of renowned Scientists

Excitingly, other types of proteomic measurements, such as absolute protein quantification, protein turnover rates, modification by any of the hundreds of known PTM's, interactions with other proteins or different types of biomolecules, changes in structure, and more are now also measurable. Each of these data modalities display a different view on the molecular state of a cell or organism. I see the situation analogous to that of tomography, where each two dimensional section displays a particular view of the tomographed systems and where the full three-dimensional state of the system is only becoming apparent by combining the information from all acquired sections from the same object. Transported to proteomics, this suggests that if we are able to generate data on the different data modalities, each one representing a unique, complementary view of the system from aliquots of a sample in a particular state and if we can meaningfully integrate the different modalities, we will gain unprecedented understanding of the molecular basis of living systems.

At present, the complex technological capabilities required for multi-modal proteomic acquisition are dispersed in the community. Many laboratories are highly proficient in the techniques to measure one or several data modalities. There are few, if any, research groups or platforms worldwide capable today of high-quality measurements of the majority or all of the modalities discussed above. In relation to the question of multimodal data integration, several questions therefore need to be resolved. They include i) which data modalities are essential and most informative to gain new insights into the homeostasis and adaptation of biological systems?, ii) how are the data from multimodal measurements of the same sample integrated?, iii) how can we generate a single platform or a network of platforms with the capability of generating high-quality multi-modal data sets from large sample cohorts? If these challenges can be resolved, I expect that the understanding of the molecular basis of life will dramatically increase.

7. *Proteomics is increasingly influencing precision medicine and clinical diagnostics. What scientific, technological, or regulatory challenges must still be overcome before proteomics becomes a routine part of healthcare?*

If we carry the discussion around the questions asked above into the field of precision medicine and clinical diagnostics, first and foremost, technical, conceptual, and logistical challenges discussed above, need to be resolved. In addition and specific to medical questions, success will depend on the quality of samples that were collected around a specific clinical research question, the number of samples collected, and the quality and accessibility of clinical/phenotypic data associated with the samples. In addition, of course, compliance with local patient protection laws and regulations is paramount.

8. *Having served the international proteomics community through your scientific leadership and collaborations, what role do you see organizations such as HUPO and national societies like the Proteomics Society, India (PSI) playing in advancing proteomics worldwide?*

I am very proud of my long-term association with HUPO and the interactions with national societies from numerous regions and countries. Some topics of raised in this interview clearly point to the urgent need for discussion, exchange of know-how and coordination of activities across national boundaries.

This can only happen through national and international organizations. In that regard, I think HUPO and national proteomics societies are absolutely essential for the future of proteomics and the life sciences in general. In recent years, the view that genomics alone is not sufficient to fully explain the full complexity of life has gained broad acceptance, particularly also in the fields of drug development and medicine.

Perspectives in Proteomics: Interview of renowned Scientists

It is anticipated that an in-depth understanding of the molecular processes underlying disease or other phenotypes and the in-depth understanding of the biology of proteins or protein complexes that are targeted by therapeutic agents will be the basis for further advancement in medicine. This in depth understanding will significantly depend on proteomics. It will be incumbent to national and international proteomic societies and at the same time one of their most important and challenging tasks to communicate this message to life scientists outside of proteomics. Societies can therefore also serve as the bodies that define and sharpen the core message the proteomics community wants to convey to the general life science and medical communities. Proteomics, after all is not just about technical advances and knowledge about specific proteins but ultimately about increasing the understanding of biology and medicine.

9. *India has made significant progress in proteomics research over the last decade. What opportunities do you see for Indian scientists to contribute to the next generation of global proteomics research, and what advice would you offer to young investigators in the country?*

I had the opportunity to visit proteomic events in India and to interact with local scientists. In addition, several members of my laboratory visited India numerous times to participate in symposia and to teach in courses. We all have been impressed with the ambition, the energy and the enthusiasm of the Indian proteomics community. We also understand that in India, like in other places, the development of the field is constrained by a wide range of factors including fiscal constraints, lack of understanding of the technology and its incredible capabilities by the medical and life science communities and accessibility to state of the art platforms and laboratories. Based on the arguments made throughout this interview I would advise Indian scientists to consider proteomics as the life science research field with the highest potential to dramatically change our understanding of biological systems. Launching a career in the field will equip them with the opportunity to communicate the enormous present capabilities of proteomics and its future potential to the medical and life science communities, to help the national and international societies thrive, and to enjoy the privilege of making discoveries that shed light on the breathtakingly complex molecular processes that sustain life.

10. *After decades of pioneering discoveries - from quantitative proteomics and systems biology to AI-guided structural biology - what scientific questions excite you the most today, and what legacy would you like to leave for future generations of proteomics researchers?*

A few years ago, I reached the mandatory retirement age that applies in Switzerland where I live and work. This forced me to dissolve my laboratory. I am therefore no longer in the position to lead a research program to directly address exciting questions. Of course I remain interested in proteomics and life science research in general and the greatly increase level of unstructured time allows me to take a step back from daily challenges in research group the contemplate the bigger picture. Of course I remain interested in proteomics and life science research in general and the greatly increase level of unstructured time allows me to take a step back from daily challenges in research group the contemplate the bigger picture.

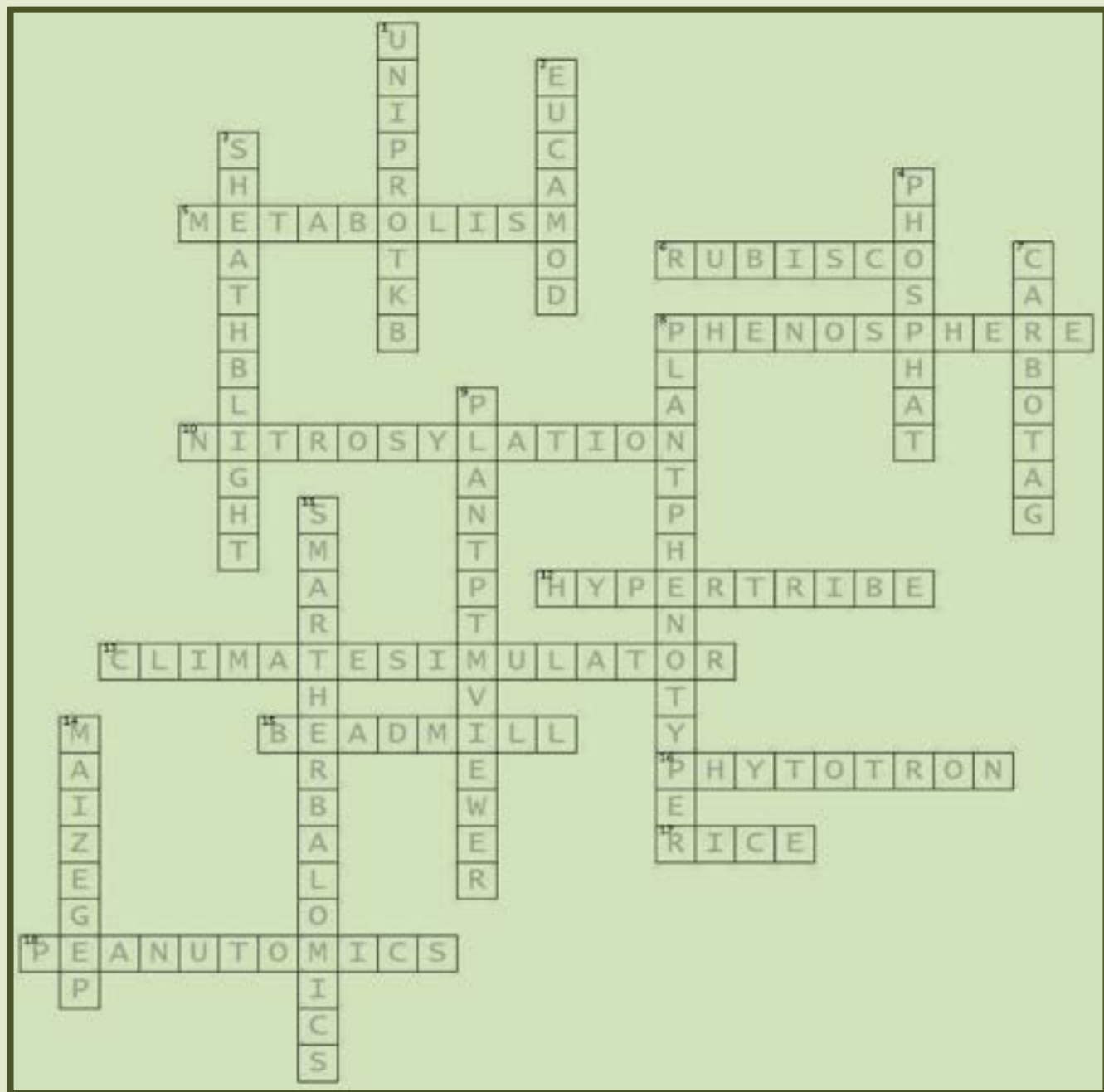
In the discussion above, I tried to indicate what excites me most. It is the question whether and how the incredibly powerful technologies to identify all molecules of a cell, particularly proteins, in their contextual state along with computer science/AI based integration of the data will be sufficient to generate models that can accurately predict how the cell will respond to any perturbation, based on deep mechanistic understanding of the evolved adaptive processes the cell has available to respond to the perturbation.

Perspectives in Proteomics: Interview of renowned Scientists

The legacy I am most proud of is the large number of young scientists who came through the lab, brought their ideas and enthusiasm, grew as scientists and persons and contributed to advancing the field. Many are now scientific leaders in their own right who, I like to think, carry forward some bits and pieces they picked up and cherish the personal connections they made while working in the group.

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PSI Crossword Puzzle 4 - Answer keys



Omics Fest @ BITS Pilani, Hyderabad



OMICS FEST '26 Fosters Next-Generation Multi-Omics Research and Celebrating Proteomics Day

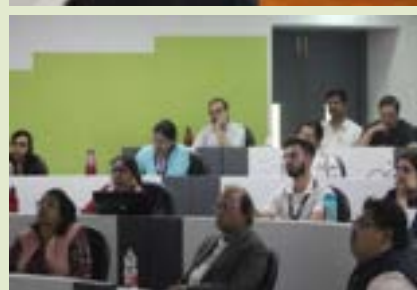
On 17-18th March at BITS Pilani, Hyderabad

Convenor- Dr. Shuvadeep Maity, Dr. A. Sanyal and Dr. S. Ghosh

The department of Biological Sciences At BITS Pilani Hyderabad campus served as a vibrant center for scientific exchange by successfully hosting OMICS FEST '26 on 17–18 March 2026. Organized by Dr. Shuvadeep maity, Dr. Amartya Sanyal, and Dr. Supratim Ghosh, this intensive two- day workshop was conducted with a carefully selected cohort of 20 participants to maximize individual engagement and provide highly effective, personalized hands-on training. Designed to equip passionate graduate students and early-career researchers with the skills required for omics data analysis, the event attracted an enthusiastic and talented group of participants from leading academic institutions across Hyderabad, including Csr-centre For Cellular And Molecular Biology, Osmania University, Maulana Azad National Urdu University, and BITS Pilani.

All logistic support from BITS leadership allowed timely and proficient professional execution of this program. The seamless logistical support provided by the BITS Pilani administration and leadership played a key role in ensuring the timely and professional execution of the program. Their valuable support and guidance are sincerely acknowledged and appreciated. The organizers gratefully acknowledge the generous support of the Proteomics Society of India as the principal sponsor, along with the valuable contributions of Sciex and Genetix, whose support played a crucial role in making this significant academic initiative possible.

The intellectual atmosphere of the workshop was significantly enriched by a distinguished lineup of keynote speakers and highly integrated analytical modules. Santanu Chattopadhyay (Prof. Barry J. Marshall Research Centre for Helicobacter pylori, Asian Healthcare Foundation) captivated the audience with his insights into Using Next-Generation Sequencing to Study Microbial Genomics and Metagenomics. Similarly, Srikanth Rapole (National Centre for Cell Science, Pune) delivered an inspiring masterclass on the Application of Mass Spectrometry-Based Proteomics for Biomarker Discovery in Haematological Malignancies. His session also beautifully complemented the celebration of “Proteomics Day” on 18th March 2026, commemorating the 17th anniversary of the Proteomics Society of India.

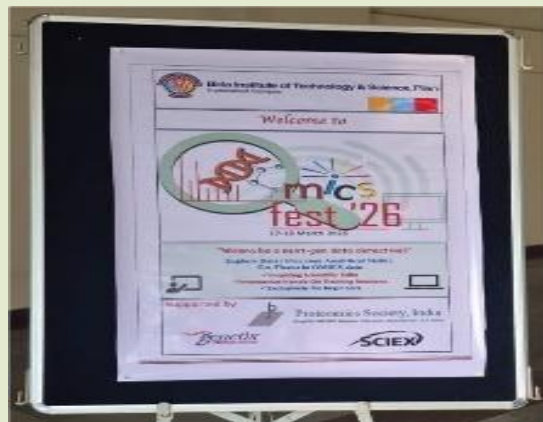


Omics Fest @ BITS Pilani, Hyderabad

In addition, Dr. Dipankar Malakar (Sciex India) provided valuable industry perspectives through a technical session on Sciex High-Throughput DIA Proteomics Data Acquisition and Handling, effectively bridging academic concepts with advanced industrial workflows.

The in-depth workshop sessions for beginners were carefully designed with a progression from basic concepts to real data-based hands-on exercises. The multiple practical modules conducted over the two days by Prof. Amartya and Prof. Shuvadeep were well integrated with the lecture sessions, ensuring a coherent learning experience. These hands-on sessions were highly appreciated by the participants and received exceptional feedback from the 20 selected candidates due to their strong practical utility in building a foundational understanding of complex computational pipelines. The deliberate small-cohort design promoted high engagement through direct mentorship, enabling participants to successfully progress from beginner-level concepts toward independent data analysis and helping them develop the confidence to design experiments and explore the omics field.

Overall, the significant impact of the training strengthened Hyderabad's collaborative scientific ecosystem by empowering a new generation of researchers. The overwhelming success of the workshop also generated a strong demand for expansion, with participants unanimously requesting that future workshops be extended into week-long programs.



Proteomic Day @ Alagappa University, Karaikudi



Educational and Proteomic Day Celebration Advances in Proteomics and Metabolomics On March 16-18, 2026 at Alagappa University, Karaikudi Convenor- Dr. K. Balamurugan

The Department of Biotechnology, Alagappa University, in association with the Aravind Medical Research Foundation, organised a three-day programme titled “Educational Day and Proteomics Day Celebration – Advances in Proteomics and Metabolomics” from 16–18 March 2026. The programme was sponsored by RUSA 2.0 and the Department of Biotechnology, Government of India, and brought together eminent scientists, academicians, research scholars and postgraduate students for lectures, practical training and scientific interaction.

Educational Day – 16 & 17 March 2026

The first two days focused on educational and hands-on sessions designed to strengthen students’ understanding of modern biotechnology and its applications. Dr. Krishnan Venkateswaran, former Chief Scientist, ITC Life Science and Technology, delivered a session on “Proteomics in the FMCG Industry.” He discussed applications of proteomics in food, cosmetics, personalised nutrition and wellness, including the influence of proteins on product characteristics such as texture and shelf life. He also highlighted the emerging role of artificial intelligence in proteomics and industrial innovation.

Dr. K. Balamurugan, Senior Professor and Head, Department of Biotechnology, Alagappa University, conducted theoretical and practical sessions on Real-Time PCR (qPCR). Participants were introduced to PCR and qPCR principles, primers, Ct values, melting temperature, melt curves and fluorescence-based detection. Practical training covered reagent calculations, master-mix preparation, pipetting, sample loading into 96-well plates and precautions to avoid contamination.

Students were taken to the University Science Instrumentation Center (USIC) for hands-on exposure to the RT-PCR instrument. They learned instrument operation, setting of run parameters, real-time monitoring of amplification and interpretation of amplification curves.

Dr. Venkateswaran also delivered a session on “AI for Food: Accelerating and Democratizing Discovery and Innovation,” discussing the use of artificial intelligence in food development, nutrition, ingredients, flavour, taste, sensory properties and rheology.

Proteomics Day – 18 March 2026

Proteomics Day began with an inaugural programme. Dr. K. Balamurugan, Convenor and Life Member of the Proteomics Society, India, delivered the welcome address. Sr. Prof. G. Ravi, Vice-Chancellor, Alagappa University, delivered the Presidential Address; Dr. K. Dharmalingam, Director, Aravind Medical Research Foundation and Life Member of the Proteomics Society, India, delivered the thematic address; and Prof. M. Krishnan, Vice-Chancellor, Central University of Tamil Nadu, participated as Guest of Honour. The inaugural session concluded with a vote of thanks by Dr. S. Karutha Pandian, Honorary Professor, Department of Biotechnology, Alagappa University.



Proteomic Day @ Alagappa University, Karaikudi

Dr. K. Dharmalingam delivered a lecture on “Proteomics: A Comprehensive Introduction,” explaining the fundamentals of proteomics and its importance in understanding biological functions at the protein level. He highlighted integration with transcriptomics, relationships between gene and protein expression, protein isoforms and the potential of serum proteins as biomarkers for disease diagnosis.

A poster presentation session provided research scholars and M.Sc. students an opportunity to present their work. Topics included proteomic analysis in diabetes, extracellular vesicles, maternal infection-associated meningitis, *C. elegans* models of immunity and metabolic dysregulation, natural compounds against lung cancer, antibiofilm activity and host-pathogen interactions.

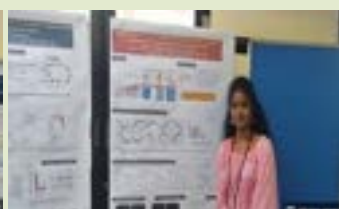
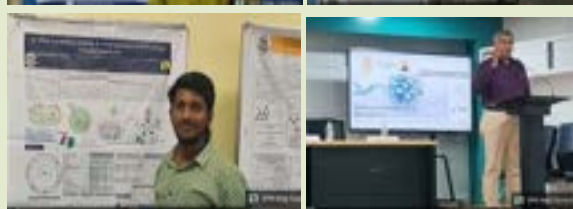
Dr. K. Balamurugan discussed the integration of proteomics with metabolomics and other omics technologies, including LC-MS, GC-MS and NMR-based metabolomics, lipidomics, multi-omics data integration, volatilomics and fluxomics. The session emphasised the transition from discovery-based proteomics towards integrated systems-level approaches with potential clinical applications.

Dr. K. Dharmalingam further presented recent developments in proteomics with special emphasis on Olink proteomics technology and the Proximity Extension Assay (PEA). He explained its use for sensitive multiplexed protein detection and biomarker discovery, including applications in glaucoma, while stressing the importance of experimental design and relevant biological variables.

Dr. K. Emmanuel Rajan, Professor and Head, Department of Animal Science, Bharathidasan University, discussed proteomics in higher animal models. He highlighted applications in biomarker discovery, disease progression, therapeutic evaluation, veterinary science, drug discovery and translational research, along with the use of two-dimensional gel electrophoresis, mass spectrometry and bioinformatics.

Outcome

The three-day programme successfully combined fundamental concepts, emerging technologies, industrial perspectives and hands-on training. Participants gained practical exposure to RT-PCR and a broader understanding of proteomics, metabolomics, multi-omics integration, biomarker discovery, artificial intelligence and translational applications. The poster session encouraged scientific interaction among students, research scholars and senior scientists. The programme concluded with a valedictory address by Dr. K. Balamurugan, who appreciated the active participation of the students and encouraged them to apply the knowledge and practical skills gained during the programme.



Mass Spectrometry-Based Proteomics Workshop @ BRIC-ILS, Bhubaneswar



National Workshop on Mass Spectrometry-Based Proteomics

On March 9-11, 2026 at BRIC-ILS, Bhubaneswar

Convener- Dr. Amol R. Suryawanshi

The BRIC-Institute of Life Sciences (ILS), Bhubaneswar successfully organised the national workshop on mass spectrometry-based proteomics (NWMSP-2026) from March 9-11, 2026, at its advanced mass spectrometry facility. This three-day intensive workshop focused on high-resolution mass spectrometry (HRMS)-based proteomics and its applications in biomedical research.

The workshop was supported by the DBT-SAHAJ program and the Proteomics Society Of India. The workshop commenced with the ceremonial lighting of the lamp by Dr. Arun Bandyopadhyay, Director, Gujarat Biotechnology University, in the presence of distinguished dignitaries. The welcome address was delivered by Dr. Debasis Dash, Director, ILS, who highlighted the importance of proteomics in translational research. The inaugural address was delivered by Dr Amol R. Suryawanshi, the workshop's convener, who outlined the objectives and emphasised the need for hands-on training in advanced proteomics technologies.

The Chief Guest, Dr. Arun Bandyopadhyay, delivered an insightful inaugural lecture on multi-omics approaches for identifying circulating proteins associated with metabolic and inflammatory diseases.

The workshop witnessed enthusiastic participation from more than 20 delegates, including research scholars, postdoctoral fellows, and faculty members from reputed institutes and universities such as KIIT, KIDS, ICMR-RMRC, ICMR-NIRBI, IISER Berhampur, NISER Bhubaneswar, ICMR-NIRRRCH, Rama Devi Women's University, Bhubaneswar, University of Hyderabad (UoH), SOA University, and University of Calcutta, among others.

The scientific program was structured into thematic modules combining lectures and hands-on sessions. Day 1 included lectures on the fundamentals of mass spectrometry and proteomics. A key technical session on Orbitrap-based mass spectrometry and proteomic approaches was delivered by Dr. Venkatesh Chanukuppa, who also led hands-on training on sample preparation, protein extraction, and enzymatic digestion workflows. A special lecture on "Clinical Proteomics: Advantages and Challenges" was delivered by Dr. Saikiran Jajula and Dr. Amol R. Suryawanshi.



Mass Spectrometry-Based Proteomics Workshop @ BRIC-ILS, Bhubaneswar

Day 2 focused on advanced proteomics techniques and data acquisition workflows. Expert lectures were delivered by Dr. Sandipan Ray and Dr. Kaushik Dey. The module on data acquisition and processing using mass spectrometry was conducted by Dr. Venkatesh Chanukuppa, followed by extensive hands-on training sessions covering peptide desalting, instrument calibration, Vanquish Neo Nano-LC operation, and qualitative and quantitative data acquisition. A thematic lecture on “Marine Proteomics: Advantages and Challenges” was delivered by Dr. Somnath Sahoo and Dr. Saikiran Jajula.

The final day (Day 3) focused on proteomics data analysis and interpretation. A dedicated module on data analysis using Proteome Discoverer (PD) software was conducted by Dr. Venkatesh Chanukuppa, which included training on qualitative and quantitative analysis, data visualization, LFQ and statistical analysis, and isobaric labeling (TMT) data analysis. Participants also gained exposure to troubleshooting and maintenance of LC-MS systems. The sessions were further enriched by interactive discussions and a workshop quiz, enhancing participant engagement.

The workshop concluded with a valedictory session, during which participants shared their feedback and experiences. Certificates were distributed to all participants. The concluding remarks were delivered by Dr. Debasis Dash,, ILS, followed by a vote of thanks by Dr. Soma Chattopadhyay, Co-convenor of NWMSP-2026.



Multi-Omics Summit @ New Delhi



Multi-Omics Summit Integrating genomics, proteomics and beyond for precision health and innovation

Organized by Proteomics Society of India | Supported by Thermo Fisher Scientific

On 13 March, 2026 at The Leela Palace, New Delhi

Convenor- Dr. Tushar Maiti

A national conversation on the next era of precision health

The India Multi-Omics Summit 2026 brought together leading scientists, clinicians, policymakers, industry experts and technology partners to discuss how integrated omics can shape the future of precision health in India. Organized by the Proteomics Society of India, supported by Thermo Fisher Scientific, and held with IHW Council as advocacy partner, the summit created a timely platform for cross-disciplinary dialogue and collaboration.

The discussions reflected a clear shift in India's scientific landscape. With strong national momentum in genomics, the next frontier is the integration of genomics with proteomics, metabolomics, clinical phenotyping, cohort science, biobanking and data science. The summit focused on this transition from generating data to translating biological insight into meaningful clinical and public health impact.

Why the summit mattered

- Advanced the conversation from genomics-led discovery to integrated multi-omics translation.
- Created a neutral scientific platform for government, academia, clinicians and industry to engage together.
- Highlighted the need for strong cohorts, biobanks, data infrastructure and cross-institutional collaboration.
- Reinforced proteomics as a critical layer for understanding disease biology, biomarkers and treatment response.

PSI's role in shaping the platform

- PSI brought scientific credibility, community trust and access to leading KOLs across the proteomics ecosystem.
- The Society helped anchor the summit in science, ensuring that the dialogue remained relevant to researchers and clinicians.
- PSI's leadership made the summit a strong example of how professional societies can convene diverse stakeholders around national scientific priorities.



Multi-Omics Summit @ New Delhi

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Thermo Fisher Scientific's contribution

- Thermo Fisher supported the summit by bringing global scientific perspectives, workflow expertise and technology context across genomics, proteomics, mass spectrometry, Olink and data.
- The focus was on enabling an end-to-end multi-omics discussion rather than a product-led conversation.
- The summit also demonstrated how industry can partner with scientific societies to strengthen capacity, collaboration and translational impact.

Voices from the summit

"This is the right time to integrate genomics with proteomics and other omics technologies to advance future discoveries." - **Dr Tushar Maiti**

"Without considering proteomics or metabolomics, our understanding of health and disease will not be complete." - **Dr K. Thangaraj**

"For precision medicine we need molecular data from multiple layers. The genome is only one part of the puzzle." - **Dr Sandra Goetze**

"Proteomics is an important catalyst to drive precision medicine in cardio-kidney metabolic disease." - **Dr Sok Cin Tye**

A collaborative step forward

The India Multi-Omics Summit 2026 marked an important step in building a stronger, more connected omics ecosystem in the country. It brought together the scientific depth of PSI, the healthcare advocacy lens of IHW Council, and Thermo Fisher Scientific's global workflow expertise in service of a larger goal: enabling integrated science for better health outcomes.

The message from the summit was clear. India has the scientific talent, biological diversity, clinical need and collaborative momentum to play a leading role in the multi-omics era. The next step is to continue building partnerships that can translate these conversations into shared infrastructure, research programs, and real-world impact.





National Workshop on Proteomics, Genomics & Bioinformatics

MARCH 23 -25 2026 at Jai Narain Vyas University, Jodhpur, Rajasthan
Organising Secretary - Dr. Sweta Jha

Department of Botany (UGC-Centre for Advanced Studies) at Jai Narain Vyas University, Jodhpur, Rajasthan, organized a three-day **National Workshop on Proteomics, Genomics, and Bioinformatics (NWPGB-2026)** from March 23–25, 2026, as a part of PSI Day celebration, and sponsored by PSI and the PM-USHA. The program, tailored to a specific group of scholars and faculty members, garnered significant interest across India, with over 65 applications received from 7 states, 13 districts and 20 different institutions. A cohort of 45 confirmed participants was chosen belonging to various disciplines including life sciences, genetics and plant breeding, botany, zoology, biochemistry, plant pathology, biotechnology, human system integration etc.

The workshop framework consisted of five technical sessions, including invited lectures, industry talks, hands-on experimental and live demonstrations. Eminent scientists from various esteemed institutions delivered the invited lectures. During the formal inauguration, Prof. Kiran Ambatipudi (IIT Roorkee) provided a detailed account of the national milestone of the PSI Day celebrations. He underscored the significance of such gatherings in the establishment of robust academic research linkages across the nation. The Guest of Honor, Dr. Pankaj Bhardwaj (Director, ICMR-NIIRNCD, Jodhpur), delivered an address that underscored the growing importance of omics platforms in the administration of contemporary epidemiology, offering a clinical and public health perspective.

In the first technical session, Prof. Kiran Ambatipudi delivered an expert lecture on proteomic detection of mastitis to MFG-mediated microbiome and immune modulation. Prof. Shri Ram Yadav (IIT Roorkee) illustrated the genetic regulation of fibrous root system orchestration in plants using omics technologies. In the third technical session, Dr. Jitendra Thakur's (ICGEB, New Delhi) explained the complicated structural architecture of the plant Mediator complex and its role in the transcription apparatus. Dr. Amar Pal Singh (BRIC-NIPGR, New Delhi) presented state-of-the-art bio-imaging frameworks and proteomics techniques that are being used to monitor the tissue-level dynamics of hormone-responsive signaling proteins. Technical Session-V was initiated by an online lecture by Prof. Ashwani Kumar Thakur (IIT Kanpur), which concentrated on the spatial biophysics of seed germination and the structural impact of native seed storage proteins, focusing on amyloid bodies in plants.



Proteomics Workshop @ JNV University, Jodhpur

The hands-on sessions were primarily held in two technical sessions, and led by scientists from different industries. Dr. Durgesh Singh (Bio-Rad Laboratories) delivered the industrial lectures on streaming protein electrophoresis and mastering Western Blotting data, and workflow optimization of qPCR. Participants were engaged in practical runs of SDS-PAGE gel casting, V3 demo lysates, target-specific Western Immunoblotting using TBT protein transfer protocols, and optical band captures on the ChemiDoc fluorescence imaging platform. They were instructed for the operation of automated thermal cyclers, qPCR run setups, real-time data acquisition and analysis. Dr. Brijesh Pandey (Thermo Fisher Scientific) delivered the industrial lecture on exploring the world of proteomics using mass spectrometry.

A comprehensive mass spectrometry masterclass featured a live demonstration of high-throughput liquid chromatography-mass spectrometry (LC-MS/MS) instrumentation, remotely arranged by Thermo. As a part of hands-on bioinformatic exercises, participants were able to identify structural proteins from tandem MS data. An exclusive round-table discussion was also organized, which brought the PSI leadership, eminent scientists, regional faculty, and students together to discuss strategic mentorship, fellowships and collaborative funding opportunities. The milestone event was successfully concluded with an assessment quiz, open feedback session, and formal certificate distribution ceremony. Overall, this National Workshop bridged cutting-edge -omics research with practical applications, acting as a catalyst for advanced scientific training in India, and to keep the next generation of scientists up-to-date with emerging global technologies.



Upcoming events



18th Annual Meeting of Proteomics Society, India

INTERNATIONAL CONFERENCE

INTEGRATIVE PROTEOMICS

HEALTH, DISEASE AND ENVIRONMENT

BRIC Institute of Life Sciences, Bhubaneswar, India

November 11th - 14th, 2026



PSI Education Day
11th November, 2026

International Conference
12th - 14th November, 2026

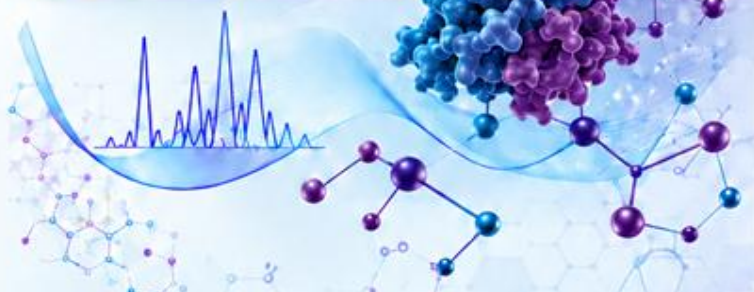
Major Highlights

- ❖ Seven Thematic Sessions
- ❖ Five Plenary Talks
- ❖ Fifteen Keynote Address
- ❖ Twenty Invited Speakers
- ❖ Fifteen Selected Oral Talks
- ❖ Ten PSI Travel Award
- ❖ 100 Poster Presentations
- ❖ Three Best Poster Awards

Registration opens 6th Aug 2026

17th Sep, 2026 is last date for

- PSI Travel Award Application
- Abstract Submission
- Early-bird Registration



Register Now



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visit website

Organizing Committee

Chairman
Dr. Debasis Dash

Convener
Dr. Amol R. Suryawanshi

Co-Conveners
Dr. H. Nanaocha Sharma
Dr. Soma Chattopadhyay
Dr. Gulam H. Syed
Dr. Soumen Chakraborty

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Upcoming events

Forthcoming International conferences and workshops

Sl. no	Conference and workshop Details	Online link
1.	Workshop on Single-Cell & Spatial Genomics Solutions Date: 17 July 2026 Venue: ACTREC, Tata Memorial Centre, Navi Mumbai, Maharashtra	https://ns2.actrec.gov.in/index.php/events/workshop-single-cell-spatial-genomics-solutions
2.	World of Microbiome 2026 Date: 21 August 2026 Venue: Hotel Greenpark, Bengaluru	https://www.womicrobiome.com/
3.	RISE 2026 – Longevity India Conference Date: 6–7 August 2026 Venue: J. N. Tata Auditorium, Indian Institute of Science, Bengaluru	https://www.longevity.iisc.ac.in/rise-2026
4.	Advances in Bioinformatics and Artificial Intelligence (BIOAI-2026) Date: 22–23 August 2026 Venue: Online, India	https://sbbsindia.in/?utm_source=chatgpt.com
5.	Manipal Genetics Update VIII – Multi-omics for Rare Diseases Date: September 18th - 20th 2026 Venue: Luminaire Hall, Fortune Valley View, Manipal	https://conference.manipal.edu/MGU8/
6.	Genomics India Conference (GIC 2026) Date: 2–3 September 2026 Pre-conf workshops: 1 September 2026 Venue: Dr. Babu Rajendra Prasad International Convention Centre, GKVK Campus, Bengaluru	https://genomicsindia.co.in/
7.	International Conference on Recent Trends and Emerging Challenges in the Biotechnology Industry: An Indian Public Health Perspective Dates: 17–19 September 2026 Venue: Koneru Lakshmaiah Edu Foundation, Guntur, Andhra Pradesh	https://liveforlives716.wordpress.com/
8.	VESICON 2026 – Annual International Conference on Extracellular Vesicles and Translational Medicine Date: 5–7 October 2026 Hands-on workshop: 8–9 October 2026 Venue: AIIMS, New Delhi	https://www.vesicon2026.com/
9.	International Conference on Innovations in Biotechnology for Sustainable Developments (IBSD 2026) Date: 22–25 October 2026 Venue: NIT Puducherry,	https://ibsd2026.in/About_NITPU
10.	International Conference on Integrating Biotechnology & Bioengineering for Sustainable Health and Environment (IBSHE 2026) Date: 27–28 October 2026 Venue: Vel Tech, Chennai	https://veltech.edu.in/ibshe/
11.	Frontiers in Animal Biotechnology – FiAB 2026 Date: 5–6 November 2026 Venue: NIAB, Hyderabad	https://fiab.niab.org.in/
12.	ICGCW 2026 – 8th Indian Cancer Genetics Conference & Workshop, Date: November 25–29, 2026 Venue: ACTREC, Tata Memorial Centre, Navi Mumbai, Maharashtra	https://actrec.gov.in/events/icgcw-2026-8th-indian-cancer-genetics-conference-workshop
13.	BAW-2026 – IISER Kolkata Date: 14-17 December, 2026 Venue: IISER, Kolkata, Mohanpur Campus.	https://www.iiserkol.ac.in/~baw/
14.	BIOSPECTRUM 2026– 10th International Conference on Biotechnology & Biological Sciences Dates: 18–20 December 2026 Venue - University of Engineering & Management (UEM), Kolkata	https://biospectrum.org/

Upcoming events

Forthcoming International conferences and workshops

Sl. No	Conference and workshop Details	Online link
	INTERNATIONAL	
15.	HUPO 2026 – 25th Human Proteome Organization World Congress Date: 27 September – 1 October 2026 Venue: Suntec Singapore Convention & Exhibition Centre, singapore	https://2026.hupo.org/
16.	7th European Symposium on Single Cell Proteomics (ESCP 2026) Dates: 1–3 September 2026 Venue: Vienna BioCenter, Vienna, Austria	https://www.apma.at/7thescp/
17.	EuPA XV Annual Congress 2026 – Proteomic Forum Date: 29 th November – 3 rd December 2026 Venue: Congress Centrum Würzburg in Würzburg, Germany	https://proteomic-forum.com/
18.	Nature Conference – Reframing Precision Medicine: Innovation to Implementation Date: 13–15 October 2026 Venue :The Royal Institution, London	https://www.nature.com/naturecareers/event/12858578/reframing-precision-medicine-innovation-to-implementation/
19.	ASMS Asilomar Conference – High-Throughput Mass Spectrometry Date: 9–13 October 2026 Venue : Asilomar Conference Center, Pacific Grove, California, USA	https://www.asms.org/conferences/asilomar-conference/asilomar-conference-homepage_
20.	Harvard PQG Conference 2026 - Integrated Multimodal Genomic & Health Data Date: 29–30 October 2026 Venue: Joseph B. Martin Conference Center Harvard T.H. Chan School of Public Health, Boston, USA	https://hsph.harvard.edu/research/quantitative-genomics/pag-conference/
21.	SUMS-RAS 2026 — Stanford University Mass Spectrometry Symposium Date: 20 th October 2026 Venue: Stanford University / Stanford Health Care, California, USA	https://mass-spec.stanford.edu/education-events/sums-ras/sums-ras-2026_
22.	14th Structural Proteomics Symposium — UCSF Date: 4–6 November 2026 Venue - University of California, San Francisco (UCSF)	https://qbi.ucsf.edu/events/ssp2026
23.	International Network for Clinical Applications of Mass Spectrometry Date: 11–13 December 2026 Venue: Rimini, Italy	https://www.incamsmeeting.org/
24.	Multi-Omics 2026 Date: 6–9 December 2026 Venue: Brisbane Convention Centre, Queensland, Australia	https://www.multiomics2026.org/

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High impact articles published by Indian groups in the field of Proteomics / Metabolomics / Lipidomics

Sl. No.	Publication Details	Online link
1.	Garg, P., Verma, N., Valsan, A., Sarohi, V., Basak, T., Gupta, T., Kaur, P., Ralmilay, S., Singh, S., De, A., Premkumar, M., Taneja, S., Duseja, A., Singh, V., & Bajaj, J. S. (2026). Proteomics: guided Biomarker Discovery, Validation, and Pathway Perturbation in Infection: related Acute Decompensation of Cirrhosis. Clinical Gastroenterology and Hepatology, 24(2) 407–420.e39. <i>Impact factor: 16.2</i>	https://doi.org/10.1016/j.cgh.2025.01.005
2.	Basumatary, T., & Sarma, H. (2026). Soil: applied polystyrene nanoplastics (PSNPs) remain cortically confined but trigger systemic oxidative and metabolic disruption in Zea mays L. seedlings. Science of the Total Environment, 1017, 181485. <i>Impact factor: 12.2</i>	https://doi.org/10.1016/j.scitotenv.2026.181485
3.	Banerjee R, Maheswarappa NB, Varakumar P, Lalthanmawii J, Govindaiah PM, Belore BM, Mohan K (2025). Discrimination of cold: slaughtered versus freshly slaughtered chicken meat using a heat: stable hemoglobin: derived biomarker: Targeted MRM: based quantification and validation. Food Chemistry, 496, 146941. <i>Impact factor: 10.4</i>	https://doi.org/10.1016/j.foodchem.2025.146941
4.	Patil, K. M., Kumar Srivastava, N., Gupta, U., Halawar, S., Kamaiah, J., & Sinha, N. (2026). Metabolic profiling of different developmental stages of Coriandrum sativum L. leaves using ¹H: nuclear magnetic resonance spectroscopy. Food Chemistry, 516, 149232. <i>Impact factor: 10.4</i>	10.1016/j.foodchem.2026.149232
5.	Verma, A. K., Rakwal, P., Rathor, P., Singh, S., Shivanna, B., Kedar, S. C., Gupta, A. K., Birse, N., & Ch, R. (2026). Comprehensive metabolomics reveals defense: driven metabolic reprogramming via withanoid biosynthesis under insect herbivory in Withania somnifera. The Plant Journal, 125, e70771. <i>Impact factor: 10</i>	https://doi.org/10.1111/tpj.70771
6.	Chaudhary, R., Baliyan, S., Khungar, L., Sirohi, P., Singh, S., Mishra, S. K., Rajkumar, M. S., Saini, S. S., Germain, H., Sircar, D., & Chauhan, H. (2026). Overexpression of barley heat stress transcription factor HvHsfA6a provides thermotolerance by modulating transcriptome and metabolome. The Plant Journal, 126, e70895. <i>Impact factor: 10</i>	https://doi.org/10.1111/tpj.70895
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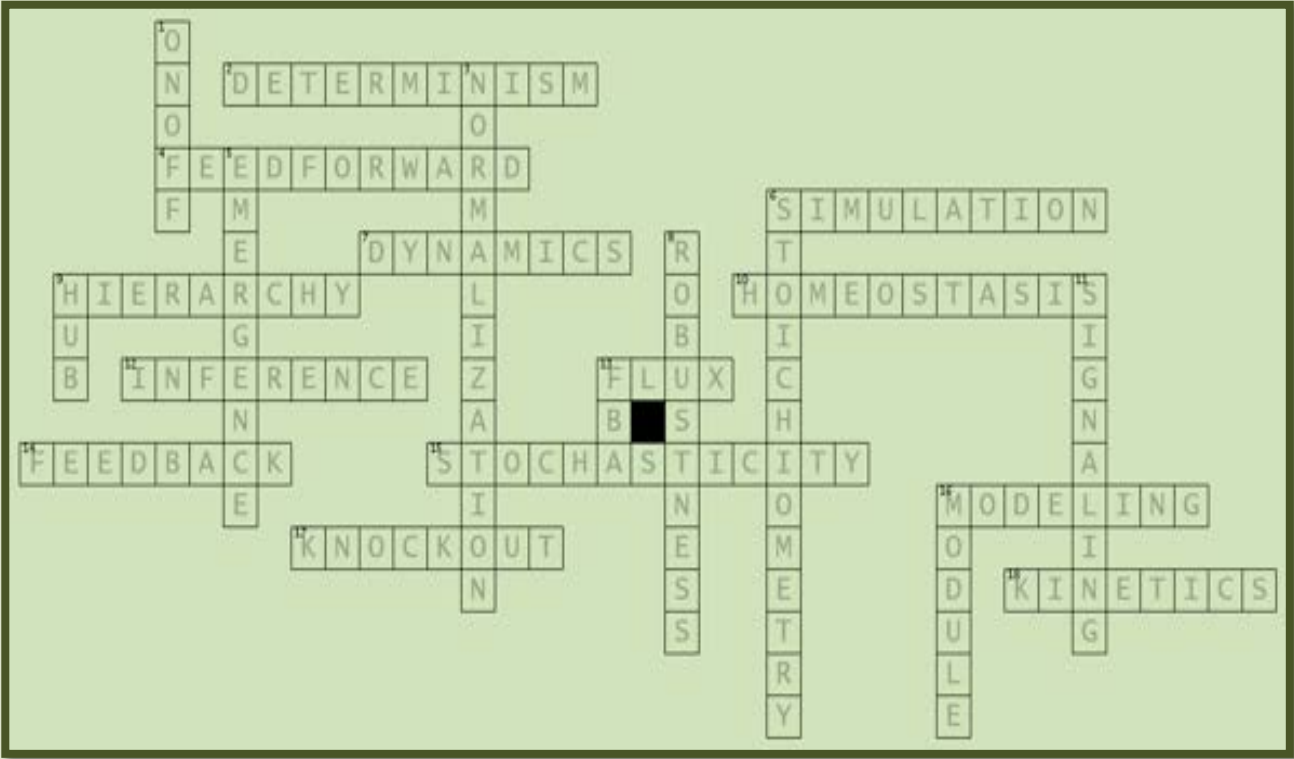
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PSI Crossword Puzzle 3 - Answer keys





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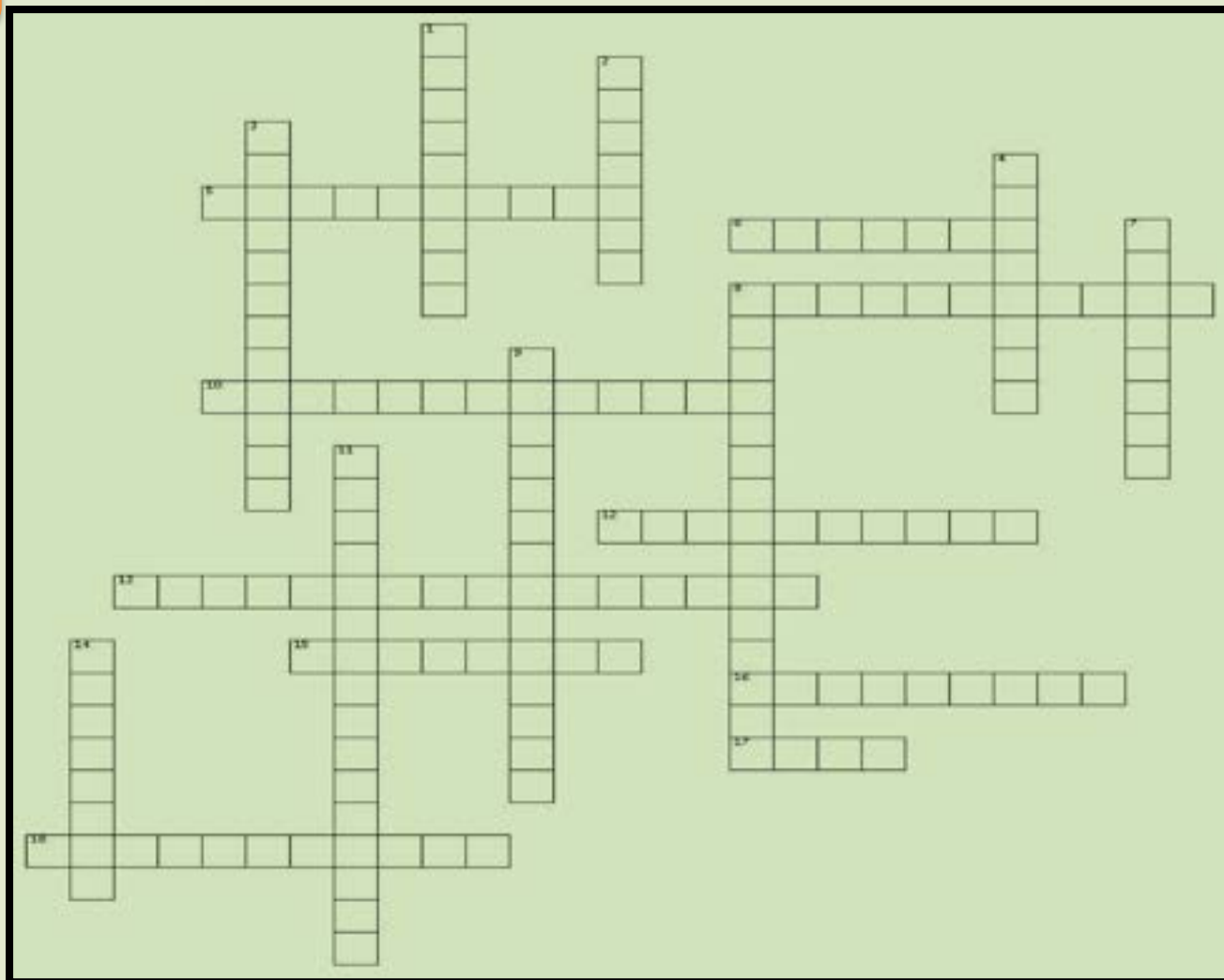


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PSI Crossword Puzzle - 4

Theme: Plant Proteomics



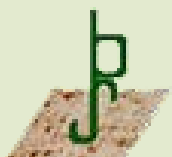
ACROSS

5. Sum of chemical reactions managed by the plant's enzymatic machinery.
6. Protein that dominates leaf proteomes and masks low-abundance proteins
8. Automated high-throughput plant phenotyping facility/platform
10. Nitric oxide-mediated modification affecting target plant proteins under stress.
12. Method to map RNA-binding protein targets using RNA editing
13. designed to mimic natural field conditions indoors
15. homogenizer optimized for plant cell wall disruption
16. Controlled environment facility for plant growth experiments
17. Crop plant with one of the most comprehensive proteome atlases
18. Multi-omics resource for groundnut (peanut) research

DOWN

1. Universal protein sequence and annotation knowledgebase
2. Molecular omics database for Eucalyptus species
3. Major fungal disease of rice often studied in crop proteomics
4. Arabidopsis-focused database of protein phosphorylation sites
7. Live imaging of plant cell walls
8. enabling long-term monitoring of plant development
9. Web-based platform for visualizing post-translational modifications in plant proteins
11. Omics platform focused on herbal/medicinal plants
14. Maize gene expression / omics resource used in crop studies

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The Proteomics Society, India, established in 2009, serves as a vibrant community of proteomics researchers dedicated to fostering knowledge exchange, collaboration, advancing proteomics research by disseminating cutting-edge information, facilitating networking opportunities, offering specialized training, and promoting scientific developments to nurture a robust proteomics culture across India. The Society which is strongly dedicated to education for research in Proteomics.

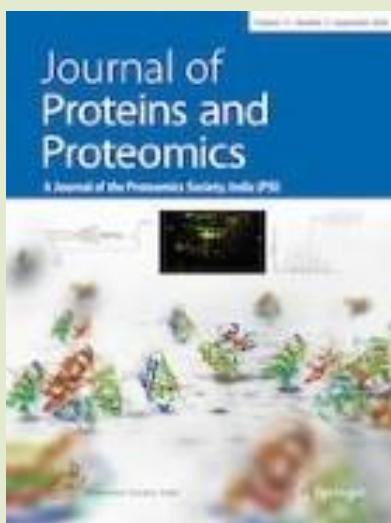
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