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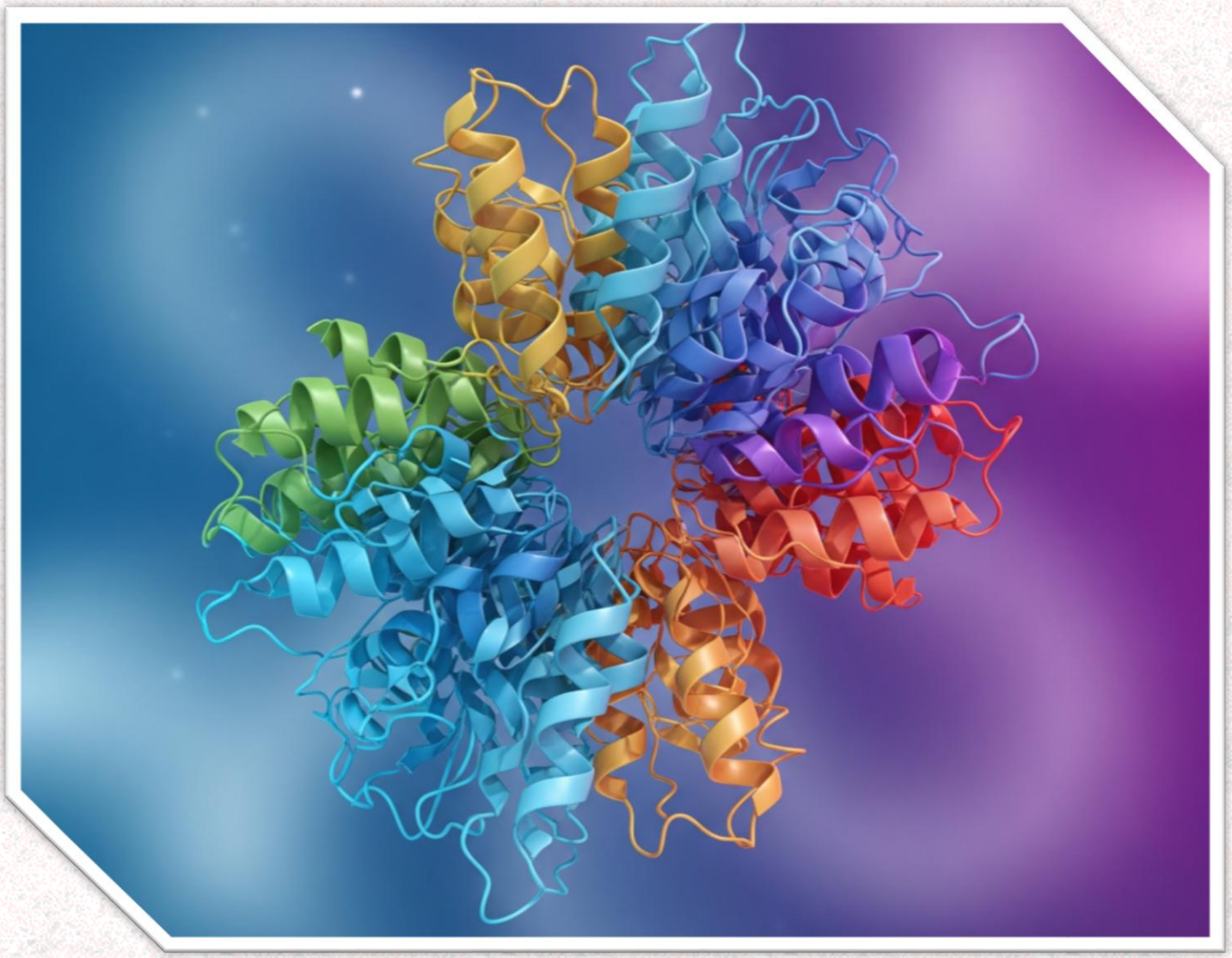
PROTEOMICS SOCIETY, INDIA (PSI)

NEWSLETTER



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Editor's Message

Dear PSI members,

We are happy in presenting the second issue of the Proteomics Society, India (PSI) Newsletter of the year 2025. Through proteomic conferences, workshops, and symposia, PSI is uniting a formidable community of scientists, students, and professionals who are embracing proteomics technologies and using them to understand biology.

In this issue, we are introducing a new section entitled, "Perspectives in Proteomics: Interview of renowned Scientists" and presenting the enlightening thoughts and vision of leaders of the proteomics. We are delighted to present first interview with our beloved founder President of PSI, Dr. Ravi Sirdeshmukh. In his interview, he has talked about the genesis of PSI, vision to integrate researchers to build a progressive and effective proteomics community and way forward for young minds to align with the international community. The second interview is with Creator of the concept of Proteomics Dr. Marc Wilkins. He has briefed the concept of proteome that occurred to describe all the proteins in a cell, the development of a collaborative efforts, technology-focused domain and their challenges and his proteomics vision.

We have experienced a wonderful series of events this year which has given a real contribution to our scientific ecosystem. The 17th Annual Meeting of the PSI and International Conference on "Integrated Omics Approaches in decoding the Biological Research" December 18-20, 2025 at CSIR-CCMB, Hyderabad was conducted with highly enriched scientific talks and discussions. As a educational commitment, PSI always organize education day as pre-conference event which was held on December 17, 2025. This year's conference highlight was the introduction of the PSI Oration Lecture. The inaugural PSI Oration Award was conferred by Dr. Ravi Srideshmukh, Distinguished Scientist and Founder President of PSI, in recognition of his vision, pioneering contributions to proteomics research in India, and sustained efforts in community building where he presented his proteomics journey. The workshop entitled "National Workshop on "Harnessing Artificial Intelligence for Multi-Omics Data Integration and Analysis" was organized at SGRH, Delhi providing hands-on exposure to the young researchers and students. This newsletter features detailed reports from these conferences and workshops that were held across various institutions in India, capturing the scientific highlights, key discussions, and participant experiences.

Additionally, we present a curated section showcasing high-impact research articles authored by Indian scientists, spanning the domains of proteomics, metabolomics, and lipidomics- reflecting the growing global footprint of Indian research in these cutting-edge fields. For a lighter and engaging touch, we bring you poem on Proteomics followed by, a brain-teasing edition of the PSI Crossword Puzzle, themed on Biology and Multi-omics, representing the cutting edge of modern life sciences.

We sincerely thank all contributors, organizers, and members for their continued support and engagement. As PSI strides forward, let us collectively aim to push the boundaries of proteomics research and its applications in life sciences and biotechnology.

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

Thank you and Regards,

Dr. Amol R. Suryawanshi

Dr. Niranjan Chakraborty

Dr. Manas Santra

Prof. Renu Deswal

Dr. Alka Rao

Dr. Sandhya Sadashivaiahp

Message from President, PSI

Dear Members of the Proteomics Society of India,

Warm greetings to all.

It gives me immense pleasure to connect with you through this issue of the PSI Newsletter, which reflects the vibrant scientific activities and collective progress of our community. While this issue reaches you with a slight delay, I believe it more than compensates through the depth and diversity of its content. I sincerely thank the editorial team for their dedicated efforts in bringing out this comprehensive and engaging edition, capturing the many dimensions of proteomics research, community initiatives, and emerging scientific trends.

The past year has been particularly significant for PSI, marked by the successful organization of the 17th Annual Meeting at CSIR-CCMB, Hyderabad. The conference served as a dynamic platform that brought together researchers, clinicians, industry experts, and young scientists, fostering meaningful discussions across a wide spectrum of proteomics and multi-omics domains. The scientific sessions highlighted emerging areas such as clinical proteomics, metabolomics, structural proteomics, and advances in mass spectrometry technologies, clearly reflecting the rapidly evolving landscape of our field and its expanding translational relevance.

A notable milestone this year was the introduction of the PSI Oration Lecture, a prestigious initiative aimed at recognizing excellence and inspiring the next generation of researchers. The inaugural oration not only celebrated pioneering contributions to Indian proteomics but also reinforced the importance of sustained scientific vision and community building. In parallel, the PSI Education Day and associated workshops played a crucial role in strengthening capacity building and knowledge dissemination. These initiatives provided valuable opportunities for hands-on learning, conceptual clarity, and interaction with experts, particularly benefiting students and early-career researchers across the country.

This newsletter also introduces a new section featuring perspectives from distinguished leaders in proteomics. The insights from Dr. Ravi Sirdeshmukh and Prof. Marc Wilkins offer a unique reflection on the origins, evolution, and future directions of proteomics—from its conceptual foundations to its current role in multi-omics and precision biology. Their narratives highlight the importance of interdisciplinary collaboration, technological innovation, and scientific rigor in addressing complex biological questions.

In addition, this issue presents engaging and enriching elements such as the Proteomics Puzzle Series, encouraging interactive learning beyond conventional formats. The curated highlights of recent high-impact publications by Indian researchers provide a concise yet powerful snapshot of the growing global footprint of our community, spanning areas such as single-cell proteomics, biomarker discovery, metabolomics, and AI-driven multi-omics integration.

The newsletter also features reports from recent symposia and workshops, including the National Workshop on “Harnessing Artificial Intelligence for Multi-Omics Data Integration and Analysis” held at Sir Ganga Ram Hospital, New Delhi. Such initiatives underscore the rapidly expanding role of artificial intelligence and computational approaches in proteomics, enabling deeper insights into biological complexity and accelerating the journey toward precision medicine.

PSI remains strongly committed to nurturing young talent and fostering an inclusive, collaborative, and forward-looking scientific environment. I encourage students, postdoctoral fellows, and early-career researchers to actively participate in PSI activities, contribute to the newsletter, and engage in community-driven initiatives. Such participation not only enhances individual growth but also strengthens the collective progress, visibility, and impact of our society.

We are also pleased to share upcoming opportunities, including the National Workshop on Mass Spectrometry-based Proteomics at BRIC–Institute of Life Sciences, Bhubaneswar, along with several forthcoming international conferences and workshops. These platforms will further enhance learning, collaboration, and global engagement for our members.

As proteomics continues to integrate with emerging disciplines such as artificial intelligence, systems biology, and translational research, it is opening new avenues for addressing complex biological and biomedical challenges. The future of proteomics lies not only in technological advancement but also in our ability to ask meaningful questions, design robust and reproducible studies, and translate discoveries into real-world applications in healthcare, agriculture, and biotechnology.

PSI will continue to play a proactive role in promoting collaborations, advancing education, and supporting innovative research that contributes meaningfully to science and society. I extend my sincere gratitude to all members, contributors, organizers, and partners for their continued support and active engagement.

Together, let us continue to advance the frontiers of proteomics and build a stronger, globally connected scientific community.

Warm regards,
Shantanu Sengupta
President, Proteomics Society, India

Perspectives in Proteomics: Interview of renowned Scientists

Interview - 1
Founder President, PSI- Dr. Ravi Sirdeshmukh

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- **When you founded the Proteomics Society, India in 2009, what was the core vision that inspired you to create a dedicated national platform for proteomics research?**

In the post genomic era, Proteomics emerged as an attractive platform in biomedical research and I had the privilege and responsibility of setting up that was the first mass spectrometry-based proteomics facility in the country at the Centre for Cellular and Molecular Biology, Hyderabad, in 2001. This was under a New Millennium Technology Leadership Initiative (NMITLI) for biomarker and target discovery in cancer under the Council of Scientific and Industrial Research (CSIR). The initiative started a new "journey" that also reflects the roots of Proteomics Society, India. Proteomics was then a new science, and biological mass spectrometry was just emerging, as we went through the initial phase - a sort of learning curve. Studying proteins, their functions and understanding their inter relationships is a complex science both in analytical and biochemical terms. The emergence of biological mass spectrometry (MS) and MS-based proteomic approaches opened up a new possibility of asking questions on protein functions in a holistic manner. The analytical sensitivities of the technological platforms are also such that we could address these questions, directly to study protein dynamics in human health and disease, using clinical specimens. Bioinformatics was also undergoing a shift from molecular docking studies to developing ways for analysis and interpretation of experimental mass spectrometry data in the biological context. All this was opening a new paradigm of clinical research that required clinician researchers and basic scientists to come together and work collectively on the unmet clinical questions. This collaboration mode was not that well developed in India, although very much needed to exploit the new technologies and approaches to solve clinical challenges. Knowledge dissemination was always something close to my heart and we were inspired to share the new knowledge and experience with others engaged in biological research. We thus gradually involved other prospective proteomics researchers from universities and research institutes in the country, through seminars, workshops, discussion sessions and some collaborations.

In the subsequent years, as part of the Eleventh "Five Year Plan", I and CCMB also initiated a network program on Plasma Proteomics which brought together other CSIR labs working on clinical conditions and this led to the formation of a small network with common interest. Coincidentally, to expand proteomics science in life science research in general, the CSIR also initiated a program entitled CSIR-Proteomics Network for International collaborations. I had the privilege of managing it along with my colleagues from other CSIR labs and thus could connect several other proteomics groups from across the globe to help us develop the activities further. This Program facilitated scientists and students from the CSIR labs to attend international meetings, short term fellowships for training in other labs overseas and organizing conferences and workshops. In one of the international meetings organized under the same program in 2008, I and others proposed the idea of an alternative forum with a broader base and there was a whole hearted support from the entire community including the international members gathered then. That was the emergence of the **Proteomics Society** – an independent body officialised in 2009 and which took the growing proteomics mood in the country to a larger platform and it is heartening to see the society is doing overwhelming service to the community. Today, proteomics activities in India have spread over a much larger group of students and investigators and the research touches upon multiple areas of plant and animal kingdom and from basic biology to clinical research.

❑ **What scientific gaps or unmet needs in India motivated you to champion proteomics as an organized and collaborative discipline?**

Given multiple features from sequence to structure to post translational modifications governing the activity of proteins, studying proteins, their functions and understanding their coordinated inter relationships in time and space, is a complex science both in analytical and biochemical terms. The emergence of biological mass spectrometry (MS) and MS-based proteomic approaches opened up a new possibility of asking questions on protein functions in a holistic manner. The analytical sensitivities of the technological platforms are also such that we could address these questions, directly to study protein dynamics in human health and disease, using clinical specimens. Bioinformatics was also undergoing a shift from molecular docking studies to developing ways for analysis and interpretation of experimental mass spectrometry data in the biological context. All this was opening a new paradigm of clinical research that required clinician researchers and basic scientists to come together and work collectively on the unmet clinical questions. This collaboration mode was not that well developed in India, although very much needed to exploit the new technologies and approaches to solve clinical challenges. Thus the multidisciplinary, collaborative working module was an implicit need and it was necessary to propagate this concept to drive proteomics and clinical research in India. What I could individually do in the initial years as part of this motivation, was transformed into a larger community effort and an answer to this was PSI. I am happy to note that today, proteomics activities in India have spread over a much larger number of research groups doing pioneering work that touches multiple areas of microbes, plant and animal science and from basic biology to clinical research and India has a distinct identity in the International Proteomics community.

❑ **During the formative years of PSI, what major obstacles were encountered, and how did you navigate these challenges?**

Honestly speaking, I was fortunate that there were no real obstacles to state and it is interesting that things happened in their natural course. PSI truly "evolved" through institutional support, scientific interactions, cooperative thinking, professional camaraderie and a consensus mindset. Here, it is imminent to mention some names. CCMB has given me an opportunity to build collaborative, multidisciplinary proteomic research concept and an ecosystem even during the pre-PSI phase. This was possible due to the unparalleled support from the then director of CCMB, late Dr Lalji Singh who always wanted CCMB to lead new scientific endeavours in the post genomic era. My working team at CCMB also whole heartedly aligned and strengthened my effort. During the course, I came across colleagues like Dr. Shantanu Sengupta from CSIR-IGIB (the incumbent President of PSI) and his enthusiasm, Dr Vijaya Lakshmi from VIT, a seasoned protein chemist, Dr Surekha Zingde from ACTREC and several others who were key contributors in the initial effort to organize and move PSI in its formative phase.

❑ **How did you work towards uniting researchers from diverse scientific backgrounds to build a cohesive and active proteomics community in India?**

I believe that scientific and objective thinking and discipline without other biases always helps in whatever you do. With that in mind, I worked for the founding leadership of PSI on three principles, a. regional and institutional representation from across India including universities, research Institutes, b. representation of cross spectrum of scientific disciplines such basic science, disease biology including even plant apart from human diseases, and computational science and c. interest to contribute in the community activities. This has proved very useful and I feel proud and highly satisfied to see that even today the PSI leadership works on this philosophy and my younger PSI colleagues nurture the same commitment and enthusiasm. Today PSI has an impressive number of life members from across India who are looking for active community contributions they can offer. So right people and right start always pay in the long run and I am confident PSI will continue this growth trajectory and advance further in years to come.

- **In your view, what are PSI's most significant contributions to strengthening India's capabilities in proteomics research? Which initiatives or programmes of PSI do you feel have made the greatest impact on students and young researchers?**

As I said, proteomics approaches and technological platforms are more recent. This science has multiple components and required their full understanding. The tools were continuously advancing in terms of both mass spectrometry instrumentation, bioinformatics tools and sample processing methods. All this was outside the realm of regular teaching curriculum even at the post graduate level. So, proteomics education was an absolute necessity. During pre - PSI days, CCMB group managed it in a limited way, for a smaller community of faculty and scientists from the universities and institutes. When we started PSI, the agenda was to pursue this effort and promote proteomics through Education and Training (E & T) to a larger group of young researchers. And PSI has been continuously doing this through various modes. The educational programs currently have two formats – Lectures / Demonstrations and Hands on Training Programs, which happen periodically, a. at the time of Annual Conference, b. as part of Proteomics (Foundation) Day celebration (March 18) and other occasions chosen by individual Institutions and members. These programs include E and T on basic principles as well as advancing technologies and analysis strategies. This is a very important service offered by PSI to help the community grow. Annual Conferences are platforms to present your research but these events also bring experts from different domains and international forums, so that the members stay abreast of the advancing science and global research trends. I would like to emphasize that all this is being done in such a thoughtful manner that today Indian Proteomics Research meets international standards, from untargeted discovery to targeted proteomics approaches. Mass spectrometry-based metabolomics is also gaining increasing importance and PSI members are also incorporating this in their research as well as in the E & T program. Of late, PSI is also offering financial support to young researchers and students to attend select International meetings. So, talking about the contributions of PSI in strengthening Proteomics research is India, I would like to mention, a. staying together as a strong body, b. facilitating advance E and T in global perspective, and c. Exposing researchers to the global community either through conferences organized in India or by financially supporting merited students for attending international conferences. I believe all this has contributed to the growth of high quality proteomics and the growing number of publications from India in high profile journals.

- **How important were collaborations with global organizations such as HUPO and AOHUPO in shaping the growth and international visibility of Indian proteomics?**

This is a very pertinent question and opens up the role of global interaction in our journey in the past and how it might contribute in future and I want to reflect two arms of interactions in this connection. They not only helped PSI to move with the global academic dynamics but also brought visibility and identity for PSI. For one, again, I have to go to the initial pre-PSI period. Proteomics workflows and instrumentation were continuously evolving. Bioinformatics solutions were yet to reach the desired robustness. Reproducibility across inter lab results was being debated within the international community, and efforts to set up standard guidelines and protocols were being considered to consolidate the foundations of the new science. For us, it was important to understand these still loose threads in the system. Therefore, continuous interactions and dialogue with the international community was needed, particularly because of the absence of any prior experience in the country. The first Proteomics Conference and a Training workshop was organized at the CCMB, Hyderabad in 2003. This was also the time when major organizations like Human Proteome organization (HUPO) and the Asian counterpart AOHUPO were working to develop a collaborative ecosystem very much felt essential for doing proteomics. I had the privilege to associate with the council of both and my association with HUPO and AOHUPO council which lasted for many years later, was of immense help. I had the opportunity to closely interact with the global community and to be part of the evolving thoughts and processes in proteomics. Whenever required, I would seek help and share these inputs with others back in the country. All this helped us and even continued even later when PSI was established. It is to be noted that PSI was launched with its first formal conference in the form of the 5th AOHUPO Congress, in 2010 at the CCMB, which was attended by many of leaders in Proteomics from several countries who also witnessed upcoming Indian proteomics perspective - an impression and identity for the newly launched PSI that continued in the subsequent years until the present. During later years other PSI colleagues Dr. Sanjeeva Srivastava from IIT, Mumbai and Dr. Subhra Chakraborty, a Plant Proteomics Scientist from NIPGR, Delhi and Dr. Shantanu Sengupta, IGIB, Delhi also got closely associated with HUPO or AOHUPO and facilitated continued interactions with the global communities and added further value to the visibility that PSI enjoys.

The second arm has been the participation in the consortium projects. In the initial years, there was a AOHUPO consortium project on membrane proteomics an important biological area and our lab was part of it. When PSI was instituted, HUPO was also organizing a larger, multinational, collaborative Human Proteome Project to identify and map all human proteins in analytical and clinic biological contexts. I remember, we had a panel discussion on this during the AOHUPO Congress, at the CCMB that I mentioned above. Our group and that of Dr. Debasis Dash and Amit Yadav had contributions on identification of 'missing' human proteins, multi-omics integration and other areas. Our group also played the lead role in the Chromosome 12 Team of the project. Subsequently, Dr. Sanjeev Srivastava and Dr. Subhra Chakraborty have been actively contributing to the project. All this helped in the international standing of PSI, so much so that India was also voted in for the 2022 HUPO Congress which unfortunately did not happen because of the post pandemic impact.

- **As the Founder of PSI, which aspects or milestones in the Society's journey do you consider the most defining? What should be its future trajectory?**

There are many positive aspects that have helped PSI to move and sustain its mission successfully, as a community, a. PSI was launched with a clear commitment and agenda, b. the continuum in thought and process that is evident in its activities over years with no dip, except during the pandemic period, c. the journal JPP that this relatively young society runs and most importantly d. The interaction of PSI members with the international groups such as HUPO or AOHUPO, both at individual level and the group level, earning a certain position and identity for PSI. Proteomics continue to throw newer challenges both in terms of discovery and biological implications, such as the emerging area of multi omics integration or the area of hitherto unknown protein variants or new ORFs. These will offer newer opportunities to join the global efforts and with its scientific potential and capability, PSI will always be looked upon for making important contributions in these emerging areas. I think the leadership of PSI is always forthcoming with new ideas and initiatives that will always keep the society on the top.

- **Finally, what message or advice would you like to offer to young scientists entering the field of proteomics? and PSI?**

I answer this and offer my suggestion in the bio-medical perspective. Yes, it is important to realize that we are entering into a new phase of bio-medical research in which there are high expectations on translation of new bio-medical discoveries and we should ponder over how we proceed. Second half of the last century was dominated by a series of discoveries which unfolded the molecular processes and their regulatory and functional repertoire in living cells. We entered the 21st century marked by the introduction of high throughput omics technologies that advanced further by leaps and bounds and investigators generated large datasets on the molecular processes and networks. Proteomics is no more a standalone domain but has become part of the multi omics umbrella – genomics, transcriptomics, proteomics and metabolomics. The large volume of molecular data generated for different systems and in different contexts is available in the public domain. Bioinformatics pipelines and computational tools are helping to deep mine and integrate multi omics data in various perspectives for functional interpretation. Single cell transcriptomics and proteomics are revealing molecular heterogeneity existing among cells. Medical imaging is being looked at not just in its anatomical perspective but as a reflection of cellular and or molecular signals, all leading to the emergence of multimodal views. With all this, today we can deep dive into human cell biology to understand biological processes and their variation in health and disease better and deeper. AI based analysis is adding a new dimension to the data interpretation. With all this in the background, it is time to enter the new paradigm in bio-medical research, where we ask valid and defined biological or clinical questions, design experiments and approaches in a targeted, hypothesis-oriented manner and generate newer molecular insights that take us closer to the much-sought-after precision medicine. So, the younger generation have great opportunity to work in the multidisciplinary mode and should look forward to contribute in the exciting phase of bio-medical and translational research that amalgamates basic science and omics modules, with proteomics occupying a unique position - connecting genomic and transcriptomic regulation on one side and metabolomics reflecting cell physiology, on the other. India and the young generation with its potential and motivation in multiple domains should dive into important phase in bio-medical research and its translation.

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Interview - 2
Creator of concept of proteomics - Dr. Marc Wilkins

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❑ **Please describe scientific insight that guided you to formulate the concept of 'proteome' in early 1990's?**

Thanks for the question! I love telling this story! It was an exciting time in molecular biology as genome sequencing technology had got to the stage where it could be scaled, and the first genome sequences were on the horizon. The human genome project had also been announced. These were obviously important as it meant we were going to, for the first time, get insights in the complete information content of a cell – at least that which is carried in its DNA.

As a young researcher, doing my PhD, I was looking for a chance to contribute to science. And may be change the world in a small way! I was working in a fantastic collaboration between my supervisor's lab (Keith Williams, Macquarie University, Australia) and a team of amazing researchers at the University of Geneva (led by Denis Hochstrasser, Amos Bairoch and Ron Appel). I was developing techniques for protein identification using Edman degradation-generated sequence tags and amino acid composition. And applying these to the identification of large numbers of proteins in 2-D gels to make things called reference maps.

As I was writing up some of my work, it became clear to me that there was no concept – or word in the language – to describe all the proteins found in a cell, a tissue or organism. It just didn't exist! Yet we were doing work that was the protein equivalent of genomics (which, in a genome project involved describing of defining the sequence of every base in a cell or species). So I tried out a few combinations of the word protein and genome, and 'proteome' was the one that seemed to work best when I asked people their thoughts. The word seemed to be effective at communicating the concept.

I had the opportunity to present the concept and word in 1994, at an international conference that had brought together the community doing this type of work. The timing of this was good as the field was just starting to coalesce. Mass spectrometry-based techniques for protein identification were just emerging, and the first genome sequences were about to be published. Perhaps no surprise that the introduction of the proteome spawned a series of similar words, such as the transcriptome metabolome. So it marks a turning point in molecular biology; our language changed to reflect the ambition of analysing and understanding whole classes of biomolecules of the cell. I feel incredibly fortunate that my PhD supervisor saw the potential of the proteome and encouraged me to develop that and, literally, spread the word. I also feel incredibly fortunate that one of my first research papers, that defines the proteome, has had such an impact.

❑ **While building the proteomics ecosystem, what were the major technological or conceptual challenges observed, and how did the research community work together to address them?**

This is such a great question! For proteomics to work, at least that driven by mass spectrometry, it was necessary for a range of challenges to be addressed. We needed to have soft ionisation techniques for proteins and peptides to allow for their effective analysis, including fragmentation inside mass spectrometers. We needed to have genome sequences available, to infer the protein sequences required for protein identification. We needed bioinformaticians to move away from areas such as genome sequencing and protein structure analysis, to develop tools that would support mass spectrometry-driven approaches. And we needed a new class of researcher who was confident to bring their own skills in all the above to the investigation of biological questions. It's not unusual that big research challenges, such as those faced in the establishment of a new field, need to bring expertise from a range of areas together. Proteomics is a really good example of that.

❑ **Looking back over the past three decades, how do you view the evolution of proteomics?**

In every respect there has been enormous progress. We can now analyse thousands of proteins from a tissue or cell and do so in intricate detail – to the level of the amino acid. We can do decent quantitative analyses, allowing for the comparison of samples from different conditions and thus supporting investigation via the standard paradigms of molecular biology (grow something in different conditions or change a gene or protein and investigate its effect). We can also use quantitative analyses to ask fundamental questions about disease. We can measure post-translational modifications at large scale and, using a variety of approaches can measure protein-protein interactions at a reasonable scale. Via immunopeptidomics, which I think has been one of the most elegant applications of proteomic methods, we now have remarkable insights into how antigen presenting in the immune system actually works.

But at the same time, there are many problems that we have not solved in 30 years! Reproducibility of mass-spectrometry based analyses remains an issue, and in large experiments the number of proteins measured consistently can be worryingly small. We also face challenges in the analysis of lower abundance proteins in cells. Because we do not have PCR for proteins, and the abundance range of proteins in cells or body fluids exceeds the range of detection of our mass spectrometers, this has been hard to address. So while next-generation nucleic acid sequencing techniques allow for superbly deep and reproducible analyses of the transcriptome, we simply do not have the same robustness of proteomic technology. This remains an impediment to the field and its even more widespread adoption.

I'm extremely interested to see how some of the emerging technologies in proteomics might be able to replace the mass spectrometer! Nanopore-based devices show potential, where groups have reported the detection of all amino acid types and some post-translational modifications on peptides. These devices are interesting as they can analyse proteins or peptides from any source; but they are not yet on market. Analytical techniques that couple antibody-based detection with next-generation sequencing (e.g. SomaLogic, Olink) are showing excellent sensitivity, dynamic range, reproducibility and capacity to scale but are just for the analysis of human proteins. Techniques that use removal of amino acids one by one from peptides, and detection of remaining amino acids via a range of affinity or fluorescence approaches (e.g. QuantumSI), have the potential to sequence or identify peptides from any species but are currently limited in scale.

❑ **How has the transition of proteomics influenced modern biological research?**

It's been fantastic to see proteomics become a field in its own right and I remember the excitement in the community when the first dedicated journals, being *Proteomics* and then the *Journal of Proteome Research*, were established. Equally, it's been exciting to see national and international scientific societies being established and then successful for so many years.

But this question is such a good one as it asks about how proteomics has furthered our understanding of biology, and not just provided a tool kit for large scale protein analysis. To me there are some very fundamental questions which have been addressed, at least in part by proteomics. I think the most interesting of these are those which cannot be addressed with genomic techniques!

Proteomics has allowed us to define the protein parts list of a cell, thus confirming predictions from genomes and transcriptomic studies. But further to that, proteomics has been able to confirm the proteins that arise from mRNA splice variation in higher eukaryotes. Proteomics has also been able to find small proteins (less than 100 amino acids) which can be difficult to predict from a genome; these are often of particular interest as they can serve as peptide messengers or hormones. Proteomics has been able to provide unprecedented insights into regulatory processes, the most striking examples being insights into phosphorylation-driven cell signalling and the post-translational modifications that are central to the dynamics of chromatin. Proteomics, via a range of approaches, has also been able to define the protein complexes in a cell and also the proteins that constitute each organelle in a cell. To me, the above are some of the most important contributions that have been made – it's the stuff of future textbooks!

A more problematic area has been how proteomics has been used to look at differences in protein abundance between samples. This is a major application, especially for biomarker discovery associated with disease. There have now been thousands of such studies published, not just biomarker studies but those where cells have been examined with and without a perturbation and protein levels analysed. Compared to the fundamental advances mentioned above, it's hard to see how many of the abundance comparison studies will be of lasting scientific importance. This isn't entirely the fault of proteomics and does reflect the difficulties that we continue to face that are technical (we can't see everything and can't see things reproducibly) but also scientific in that we do not have the tools we need to decipher the complexity of our results. So there remain some big challenges to address there.

❑ **With multi-omics integration becoming central to biological discovery, how do you see proteomics complementing a systems-level view of biology?**

This is such an important question! To me, the key thing is to use proteomics to investigate things that are unique to the protein world and that benefit from a systems-level analysis. So if looking to investigate changes between a normal and diseased cell, RNA-seq will provide a more complete insight than protein abundance levels. In such studies, however, proteomics is superb for looking at post-translational modifications and how they change, and can provide some insights into changes in protein interactions or complexes. Cross-linking mass spectrometry is interesting as it can now provide low-resolution insights into protein structure in any sample and do that at reasonable scale. We should remember that proteomics does have a unique role to play in the analysis of body fluids. Along with metabolomics its use is important in that it can provide insights that are difficult or impossible to generate via nucleic acid-associated techniques.

Given that systems biology has a focus on intermolecular interactions, proteomics does have a role to play there. There are many unknowns about how proteins interact with nucleic acids, especially RNA, but also lipids, proteoglycans, sugars and other small molecules. I expect we will see further techniques, involving proteomic technology, emerging to provide insights into a range of important biomolecular interactions.

❑ **With open-source platforms, free data exchange, and FAIR principles becoming central to modern science, how do you see these approaches collectively accelerating proteomics research?**

I like this question a lot. Open source data and software has been of incredible importance for proteomics; the most obvious being things like the Swiss-Prot database, and a range of protein identification tools like MaxQuant and MS Fragger. Databases of mass spectrometry-related proteomics data, such as PRIDE and the proteome exchange have also been of central importance. There are dozens or hundreds of other databases and software which are also very useful for the field.

What has been superb about databases of mass spectrometry information has been a capacity to aggregate information and also confirm certain observations. The human proteome project has been accelerated by its capacity to use public data as have studies of protein post-translational modifications where PTM validation has been possible via data from independent studies.

While the field of proteomics can celebrate its successes with data, it nevertheless does not have data resources that are as large or robust as generated in genomics or transcriptomics. An example of this is The Cancer Genome Atlas (TCGA). In part this reflects the difficulties of mass spectrometry-based proteomics, and its cost, yet also the fact that there is little consistency in best practices. Instrumentation for nucleic acid sequencing, for better or worse, has been dominated by a single vendor (being Illumina). Analysis on Illumina instruments has also largely bene kit-based. This has meant that almost all data for that field is from a single type of platform and has greater consistency that what we see in proteomics. It's an interesting thing to make these occasional comparisons between the fields of genomics and proteomics.

❑ **As a founding member of HUPO, how do you reflect on its contribution to the global proteomics community?**

HUPO has been extremely important as an international organisation for the field of proteomics and has served the community well in that regard. A major contribution has been its annual conferences, and also other conferences that are held by regional off-shoots of the society. It has helped organise a range of initiatives, including the human proteome project and sub-projects. HUPO nevertheless has, and will continue to have, a strong focus on human biology and use of proteomics to understand that. It's the charter of the organisation and is its name. Due to this, HUPO has been less of a forum for researchers that use proteomics to investigate questions in other species. For example in model systems, microbiology, plants, livestock yet also industrial applications, systems and processes. On reflection, the fact that the main international scientific society for proteomics does have such a strong focus on human biology may have influenced or limited the full growth of the field to other domains.

❑ **In your opinion, what has been the most influential technological advancement in proteomics to date, and why?**

I'm going to be a bit lazy in my reply here and draw from the Nobel prize committee! The technology that has had the greatest impact in the field has been mass spectrometry. However the invention of soft ionisation techniques has made all of that possible. It has meant that peptides and indeed proteins or protein complexes can be ionised and analysed as intact molecules and then fragmented in ways to generate information about sequence and post-translational modifications. So we must very much thank Kochi Tanaka and John Fenn for their fantastic work there. There's an ongoing question whether the invention of protein identification techniques will also be worthy of a future Nobel prize. So researchers like John Yates, Matthias Mann and Reudi Aebersold might have some luck there!

❑ **With rapid advances in single-cell and spatial proteomics, together with the rising influence of machine learning and AI, what scientific breakthroughs do you anticipate these converging fields will bring?**

It's always interesting to gaze into a crystal ball and try to make these type of predictions! With new analytical techniques, such as single-cell and spatial proteomics, the trick will be to find the best application or the best questions that can be addressed with them. Richard Caprioli, one of the pioneers of spatial proteomics, did really clever work early on to look for neuropeptides in brain samples via MALDI-MS scanning techniques. There, there were a range of unanswered questions about where different neuropeptides are found. MALDI-MS scanning was a perfect way to answer that question as neuropeptides are small, and thus amenable to MALDI-MS, and other proteomic techniques could not provide the same spatial resolution. For single cell work, again the biological questions being asked will also be very important. The development, differentiation or function of blood cells is a superb application, for example, as they exist and function as single cells. By contrast, I do not see such a strong reason to disaggregate tissues to single cells and then analyse them as single cells – at least if looking to understand the tissue. The function of the tissue as a system might be better understood by a bulk analysis of cells from that tissue.

For machine learning and AI, there is enormous potential! And the most exciting advance – which we can almost claim to be in proteomics – has been the invention of AlphaFold and related 3-D structure modelling tools. But this is a relatively unique situation, and there are reasons why this has been so successful. Databases with thousands of extremely high quality structures, along with their sequences, provided an extraordinary ground truth set for training and thus predictions. The 70-year old protein folding problem was thus solved! For AI and machine learning, the challenge will be to not just ask some of the same old questions. For example, involving the classification of samples from their proteomic protein abundance profile – except if there is a compelling biological or clinical reason for doing so. I'd be fascinated to see how AI or machine learning can be used for the prediction of substrates for kinases, or to build whole cell models that work at molecular level.

❑ **How do you view the evolution of proteomics research in India, and what guidance would you offer to Indian scientists aiming to strengthen their global footprint? Additionally, what steps do you believe India should take to foster stronger national and international collaborations in proteomics?**

I hope I can make some useful comments here! India has a vibrant proteomics community and a long standing and successful society. India also has many high-quality core facilities with state of the art instrumentation and the advanced capabilities needed to run them. So it's well positioned to do great proteomics research. From my visits to India, and discussions with colleagues from India, I have been impressed with the range of projects that are tackled with proteomics techniques. Especially in areas of human biology but also food, plant biology, veterinary science and agriculture. I think this breadth is a unique strength of proteomics in India and one to be valued greatly.

For Indian scientists looking to strengthen their footprint, the old advice of doing good work and publishing in good journals will always apply. Being active in the promotion of work via different media is also important and, where possible, the participation in international societies and conferences. To foster collaborations, part of it is to have a good presence and profile (for example on institutional web pages) that is easy to find and even says "I'd be delighted to discuss collaboration". Attendance at meetings outside of proteomics, which have a strong biological focus, might help to find future collaborators with questions that proteomics can answer. More broadly, tapping into inter-governmental schemes for joint projects between India and other nations could be useful. These can be quite good as they have a focus on the development of international collaboration and can be quite flexible with respect to research focus. These schemes exist but I expect they may be very competitive!

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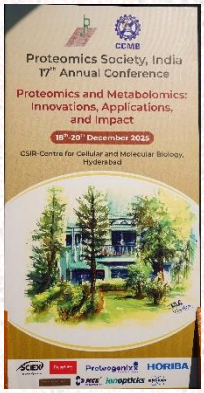
PSI 17th Annual Meeting @ CSIR-CCMB, Hyderabad

17th Annual Meeting of the PSI and International Conference on "Integrated Omics Approaches for Decoding Biological Research"

On December 18-20, 2025 at CSIR-CCMB, Hyderabad

Conveners: Dr. Swasti Raychaudhuri

The 17th Annual Conference of the Proteomics Society, India (PSI-2025), held at the CSIR-Centre for Cellular and Molecular Biology (CCMB), Hyderabad, during 18–20 December 2025, marked an important milestone in India's growing leadership in proteomics and metabolomics research. We organised around the theme "Proteomics and Metabolomics: Innovations, Applications, and Impact," the conference brought together an inspiring mix of scientists, clinicians, technologists, industry leaders, and students from across the country to exchange ideas and explore how omics sciences are reshaping discovery biology, medicine, agriculture, and biotechnology.



All scientific sessions were held in the PM Bhargava Auditorium at CCMB, creating a focused and immersive academic atmosphere. Registration began early on the morning of 18th December, with posters displayed along the first-floor and meals served within the auditorium complex, allowing participants to move seamlessly between lectures, poster discussions, and informal scientific conversations.

A defining strength of PSI-2025 was the presence of many of India's most respected proteomics leaders, whose lectures reflected the flagship scientific directions of the society.

The first day of the conference opened with a plenary lecture by Dr. Vinay Nandicoori, Director, CSIR-CCMB, Hyderabad, who set the scientific tone by sharing fascinating mechanistic insights into the survival strategies of Mycobacterium tuberculosis. He highlighted how bacterial serine/threonine kinases regulate host signalling, autophagy, transcription, translation, and cell-wall synthesis to enable long-term persistence.

The scientific sessions that followed covered a wide range of contemporary themes. Session I on proteomics and metabolomics in cell biology featured engaging talks by Dr. Jeet Kalia, Dr. Swasti Raychaudhuri, and Dr. H. B. D. Prasada Rao, showcasing advances in live-cell lipid imaging, mitochondrial protein import, and proteomic regulation of ovarian reserve and fertility.

PSI 17th Annual meeting @ CSIR-CCMB, Hyderabad

Session II focused on metabolomics, biomarkers, and disease mechanisms, with Dr. Avinash Bajaj, Dr. Pallavi Kshetrapal, and Dr. Adela Ramu presenting work on immunoproteasome regulation in tumour microenvironments, early metabolic predictors of postpartum diabetes, and proteomic mechanisms underlying platelet-mediated neutrophil extracellular trap formation in diabetic retinopathy.

The afternoon Session III on post-translational modifications featured lectures by Dr. Trayambak Basak, Dr. Indrajit Sahu, and Dr. Rohit Budhraja, highlighting new insights into collagen PTM landscapes, global ubiquitinomics, and N-glycoproteomics-based biomarker discovery in congenital disorders of glycosylation.

The day concluded with the prestigious 1st Oration Lecture and Award Ceremony honouring Dr. Ravi Deshmukh for his outstanding contributions to Indian proteomics. In a deeply personal and inspiring oration, Dr. Deshmukh reflected on his scientific journey and his extensive work on GFAP (Glial Fibrillary Acidic Protein). He emphasised that GFAP as a biomarker remains biologically complex and is still at a nascent stage of understanding, inviting the community to collaborate across disciplines to advance research on this important protein.

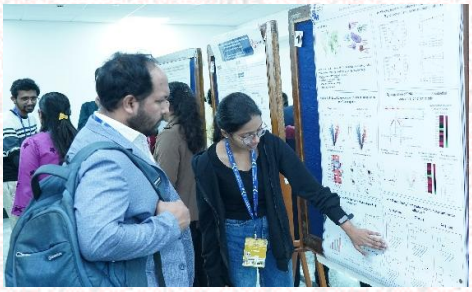
Overall, Day 1 laid a strong scientific foundation for PSI-2025, demonstrating how cutting-edge proteomics and metabolomics are transforming our understanding of cell biology, disease, and translational research.

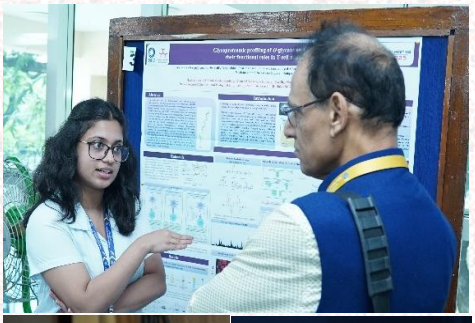
The second day continued the scientific momentum with a strong translational focus spanning biopharma, infection biology, clinical proteomics, and disease mechanisms. The morning sessions on biotherapeutics and drug discovery featured Dr. Vishal Rai, Dr. Sumit Kumar Singh, and Dr. Dharmaraja Allimuthu, who highlighted proteomics-driven bioprocess optimisation, control of site-specific glycosylation in therapeutic antibodies, and chemical proteomics strategies for identifying new ferroptosis-inducing anticancer targets.

The session on infection and immunity included talks by Dr. Pushkar Sharma, Dr. Hem Chandra Jha, and Dr. Manish Kumar, presenting integrated multi-omics approaches to host–pathogen interactions, non-invasive salivary biomarkers for early oral cancer detection, and lactate-driven protein lactylation as a novel epigenetic regulator in malaria parasites.

In the clinical proteomics and biomarker session, Dr. Arun Bandyopadhyay and Dr. Pragyan Acharya showcased multi-omics discovery of circulating proteins linking dyslipidaemia with athero-inflammation and targeted proteomics approaches for mapping organ failure in acute-on-chronic liver disease. The afternoon session on disease biology featured Dr. Sandipan Ray, Dr. Srikanth Rapole, and Dr. Ramesh Ummanni, who presented circadian-guided chronotherapy strategies for cancer, proteomic identification of biomarkers and therapeutic targets in blood cancers, and pathway-driven precision targeting in advanced prostate cancer.

The day concluded with a session on food, nutrition, and plant proteomics, where Dr. Niranjan Chakraborty, Dr. Ashok P. Giri, and Dr. Rajiv Kumar highlighted mitochondrial proteomics with reference to crop stress resilience, metabolic reprogramming in insect pests, and the discovery of bioactive medicinal plant peptides with translational potential — underscoring the expanding reach of proteomics across human health, agriculture, and biotechnology.





PSI 17th Annual meeting @ CSIR-CCMB, Hyderabad

In the veterinary proteomics session, Dr. Ashis Kumar Mukherjee presented large-scale venom proteomics studies revealing regional variation in snake venom composition, Dr. Amol Suryawanshi described quantitative profiling of altered brain proteins in rabies virus infection, and Dr. Bhargab Kalita showcased comprehensive venom proteomics of Trimeresurus popeiorum, revealing enzymatic signatures underlying its coagulopathic toxicity.

The structural proteomics and bioinformatics session featured Dr. Aniruddha Panda, who introduced native mass spectrometry approaches for studying membrane protein–lipid interactions, and Dr. Amit Kumar Yadav, who presented integrative computational frameworks combining proteoforms, post-translational modifications, proteogenomics, and artificial intelligence for predictive disease modelling.

A major highlight of the day was the presentation by the Phenome India / MRM Consortium, which showcased a landmark targeted metabolomics initiative profiling more than 4,600 individuals across multiple CSIR laboratories. Using standardised MRM assays, the consortium quantified over 600 metabolites, enabling population-scale metabolic phenotyping of non-diabetic, pre-diabetic, and diabetic cohorts in India.

A defining hallmark of PSI-2025 was the exceptionally rich scientific discussion following every lecture. Discussions ranged from why lipids cannot be genetically mutated, to the robustness of biomarker discovery pipelines, and the importance of carefully distinguishing true biological signatures from technical artefacts. Delegates repeatedly emphasised the value of analysing complete datasets and full publications rather than relying only on abstracts.

Another important step forward at PSI-2025 was the introduction of dedicated oral presentation slots for students and young researchers, giving them a prominent platform to present their work and engage directly with senior scientists.

During the audience interaction following the bioinformatics and structural proteomics session, Dr. Shantanu Sengupta highlighted the importance of translating advanced PTM technologies into hands-on training opportunities for young researchers and suggested that Dr. Amit Kumar Yadav consider organising a dedicated training programme based on the PTM technologies developed in his laboratory. The proposal was warmly received and reflected PSI's strong commitment to democratizing access to cutting-edge methodologies.

The third and final day focused on emerging directions in mass spectrometry, veterinary proteomics, structural proteomics, bioinformatics, and population-scale metabolomics. Industry lectures showcased next-generation mass spectrometry platforms and analytical workflows for high-resolution proteomics.

The conference concluded with the prize distribution and valedictory ceremony, bringing three days of intensive scientific exchange to a memorable close. Three poster prizes were awarded in recognition of outstanding student research. In his valedictory address, Dr. Shantanu Sengupta delivered the vote of thanks, expressing heartfelt appreciation to all speakers, session chairs, delegates, industry partners, sponsors, and organising committee members. PSI-2025 thus concluded on a note of celebration, gratitude, and renewed scientific momentum, reaffirming the Proteomics Society, India's mission to advance omics sciences through innovation, education, and collaborative leadership, and strengthening India's position as a key contributor to the global proteomics community.

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PSI Education Day during PSI 17th Annual Meeting

On December 17, 2025 at CSIR-CCMB, Hyderabad

Conveners: Dr. Swasti Raychaudhuri

The PSI Education Day, held on 17th December 2025 at CSIR-CCMB, Hyderabad, as part of the 17th Annual Conference of the Proteomics Society, India, was designed as a comprehensive educational program to strengthen conceptual foundations and practical understanding of proteomics and related omics technologies. The program brought together students, early-career researchers, and faculty, and progressed systematically from introductory principles to advanced analytical and clinical applications.

The Education Day commenced with an opening lecture by Prof. Shantanu Sengupta, President PSI who introduced the fundamental principles of proteomics and clearly differentiated it from genomics. He emphasized that while genomics represents a relatively static blueprint, proteomics captures the dynamic and multi-layered functional state of biological systems. To help participants appreciate the inherent complexity of the proteome, he used a simple everyday analogy to convey that a protein cannot be treated as a single unit, but rather as an entity encompassing multiple quantitative states, structural variants, post-translational modifications, and functional interactions. He further guided participants through key conceptual facets of mass spectrometry interpretation, explaining how careful reasoning is required to distinguish whether observed mass spectrometric peaks arise from different peptides of the same protein or from different proteins. He also highlighted that no single mass spectrometry platform is comprehensive, and that different instruments and acquisition strategies are designed to address different analytical needs.

Following this foundational lecture, Dr. Tushar K. Maiti addressed quantitative proteomics and multiplexing strategies, with a focus on isobaric experimental approaches. His session highlighted how multiplexed experimental designs enable comparative proteomics across multiple samples while improving throughput, while also emphasizing the importance of experimental design and data interpretation for reliable quantification.

PSI Education day @ CSIR-CCMB, Hyderabad

The subsequent lecture by Dr. Suruchi Aggarwal focused on proteogenomics, demonstrating how integration of proteomics with genomic and transcriptomic data enhances protein identification, refines gene models, and improves biological interpretation. Functional analysis of proteomics data was then discussed by Dr. Prashant Modi, who emphasized statistical rigor and enrichment approaches for linking protein-level changes to biological pathways. This theme was reinforced in the plant proteomics session by Dr. Riffat John, who stressed the importance of asking the right biological question and adopting an appropriate study design, particularly in plant systems where biological complexity demands careful experimental planning.

A dedicated session on metabolomics was delivered by Dr. Soumen Manna, who introduced participants to the fundamentals of metabolomics, covering key concepts from sample preparation to biological discovery. He discussed LC-MS and GC-MS–based metabolomics workflows, challenges in metabolite identification, and the complementary role of metabolomics alongside proteomics in understanding cellular physiology and disease mechanisms.

In the post-lunch sessions, Dr. Rashmi Rana highlighted the importance of KEGG pathway mapping and multi-omics integration for translating omics datasets into mechanistic and systems-level insights.

Dr. M. V. Jagannadham further strengthened conceptual clarity around mass spectrometry by explaining how proteins are enzymatically cleaved into peptide fragments and computationally reassembled to infer the original protein structure.

Emerging frontiers were introduced by Dr. Kamal Mandal, who spoke on single-cell proteomics, spatial proteomics, and cross-linking mass spectrometry. The Education Day concluded with Dr. K. Dharmalingam, who focused on clinical proteomics and biomarker discovery, emphasizing quantitative rigor, dynamic range, and the multi-stage process required for biomarker validation, along with alternative technologies that complement mass spectrometry.

Overall, the PSI Education Day delivered a cohesive and intellectually rigorous learning experience, integrating proteomics, metabolomics, multi-omics analysis, emerging technologies, and clinical perspectives, and reaffirmed PSI's commitment to education and capacity building in India.

O link workshop @ CSIR-CCMB, Hyderabad

O-link workshop was conducted by Application team, O-link and PSI as preconference event on Dec 17, 2025 at CSIR-CCMB, Hyderabad. This event was attended by more than 20 participants includes scientists, faculties and research scholars.

1st PSI Oration Lecture

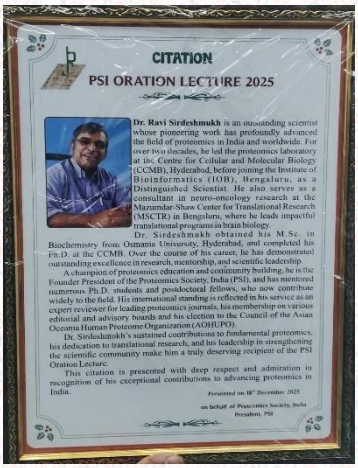
by Founder President, PSI- Dr. Ravi Sirdeshmukh

Founder President, Proteomics Society (India)

Designation & Affiliation: Distinguished Scientist and Associate Director, Institute of Bioinformatics, Bangalore

Principal Advisor, Mazumdar Shaw Medical Foundation and Centre for Translational Research, Narayana Health City, Bangalore

E mail: ravisirdeshmukh@gmail.com



CITATION

PSI ORATION LECTURE 2025

Dr. Ravi Sirdeshmukh is an outstanding scientist whose pioneering work has profoundly advanced the field of proteomics in India and worldwide. For over two decades, he led the proteomics laboratory at the Centre for Cellular and Molecular Biology (CCMB), Hyderabad, before joining the Institute of Bioinformatics (IOB), Bengaluru, as a Distinguished Scientist. He also serves as a consultant in neuro-oncology research at the Mazumdar-Shaw Center for Translational Research (MSCTR) in Bengaluru, where he leads impactful translational programs in brain biology.

Dr. Sirdeshmukh obtained his M.Sc. in Biochemistry from Osmania University, Hyderabad, and completed his Ph.D. at the CCMB. Over the course of his career, he has demonstrated outstanding excellence in research, mentorship, and scientific leadership.

A champion of proteomics education and community building, he is the Founder President of the Proteomics Society, India (PSI), and has mentored numerous Ph.D. students and postdoctoral fellows, who now contribute widely to the field. His international standing is reflected in his service as an expert reviewer for leading proteomics journals, his membership on various editorial and advisory boards and his election to the Council of the Asian Oceania Human Proteome Organization (AOHUPO).

Dr. Sirdeshmukh's sustained contributions to fundamental proteomics, his dedication to translational research, and his leadership in strengthening the scientific community make him a truly deserving recipient of the PSI Oration Lecture.

This citation is presented with deep respect and admiration in recognition of his exceptional contributions to advancing proteomics in India.

Presented on 18th December 2025

on behalf of Proteomics Society, India

President, PSI

The 17th Annual Conference of the Proteomics Society, India (PSI) was held from December 18–20, 2025, at the Centre for Cellular and Molecular Biology (CCMB), Hyderabad. The meeting began with an Education Day, followed by vibrant scientific sessions showcasing proteomics and metabolomics research across diverse domains—from basic biology to plant and human diseases.

A highlight of this year's conference was the introduction of the PSI Oration Lecture. The inaugural PSI Oration Award was conferred on Dr. Ravi Sirdeshmukh, Distinguished Scientist at the Institute of Bioinformatics (IOB) and Founder President of PSI, in recognition of his vision, pioneering contributions to proteomics research in India, and sustained efforts in community building.

In his Oration Lecture, going through some selected contribution from his group, Dr. Sirdeshmukh reflected on his scientific journey—from the early days when he initiated proteomics science first time in CCMB, Hyderabad and in India, and then the first publication on the proteomics of primary brain tumors initiated to advanced proteogenomics studies currently being pursued at IOB. He also highlighted how the initial support from the young promising researchers at the CCMB and his later transition to IOB after superannuation from CCMB enabled seamless continuity of his research. In addition, he briefly discussed his contributions to the Human Proteome Project under the Human Proteome Organization (HUPO). He emphasized the importance of long-term, focused efforts on clinically relevant questions and the need to integrate protein profiles and proteomics leads with deeper mechanistic and regulatory insights.

The felicitation ceremony included the presentation of a citation acknowledging his distinguished contributions, along with a plaque.

National Workshop on "Harnessing Artificial Intelligence for Multi-Omics Data Integration and Analysis"

On October 15-17, 2025 at SGRH, Delhi

Convener: Dr. Rashmi Rana

Sir Ganga Ram Hospital's Department of Biotechnology and Research organized a landmark three-day national workshop titled "Harnessing Artificial Intelligence for Multi-Omics Data Integration and Analysis", held from 15–17 October 2025. The event brought together leading national and international experts in genomics, proteomics, metabolomics, computational biology, and artificial intelligence, positioning India at the forefront of AI-enabled biomedical innovation.

The workshop opened with an impressive inaugural ceremony graced by Chief Guest Dr. Jitendra Singh, Hon'ble Union Minister for Science & Technology, and Guest of Honour Dr. Shivkumar Kalyanaraman, CEO, Anusandhan National Research Foundation (ANRF). Senior dignitaries including Dr. D. S. Rana, Dr. Ajay Swaroop, Prof. (Dr.) N. K. Ganguly, and Dr. Rashmi Rana welcomed the guests with a lamp-lighting ceremony, national anthem, and felicitation session. This was followed by the official inauguration, interactions with young researchers during the poster session, and a guided visit to the new Multi-Omics Core Facility at SGRH

The scientific program began with an introduction by Padma Bhushan Prof. N. K. Ganguly, who emphasized the growing need for integrating multi-omics with artificial intelligence to advance personalized medicine. The first lecture, "AI in Single-Cell Genomics" by Dr. Debarka Sengupta (IIIT-Delhi), set the tone by showcasing how AI uncovers cellular heterogeneity at an unprecedented resolution. This was followed by Dr. Arvind Kumar (AIIMS Delhi) discussing AI-enabled infectious disease diagnostics, a critical area for India's public health landscape.

International participation was marked by Dr. Kirsten Tief-Küry and Dr. Shrihari Jathanakodi from Thermo Fisher Sweden, who explained how next-generation proteomics platforms are unlocking real-time insights into human health. Additional highlights included Prof. G. P. S. Raghava's session on designing therapeutic proteins using machine learning and Dr. Brijesh Pandey's talk on advancements in clinical mass spectrometry. Hands-on demonstrations in untargeted proteomics and metabolomics enriched the learning experience for participants across academic and industry backgrounds

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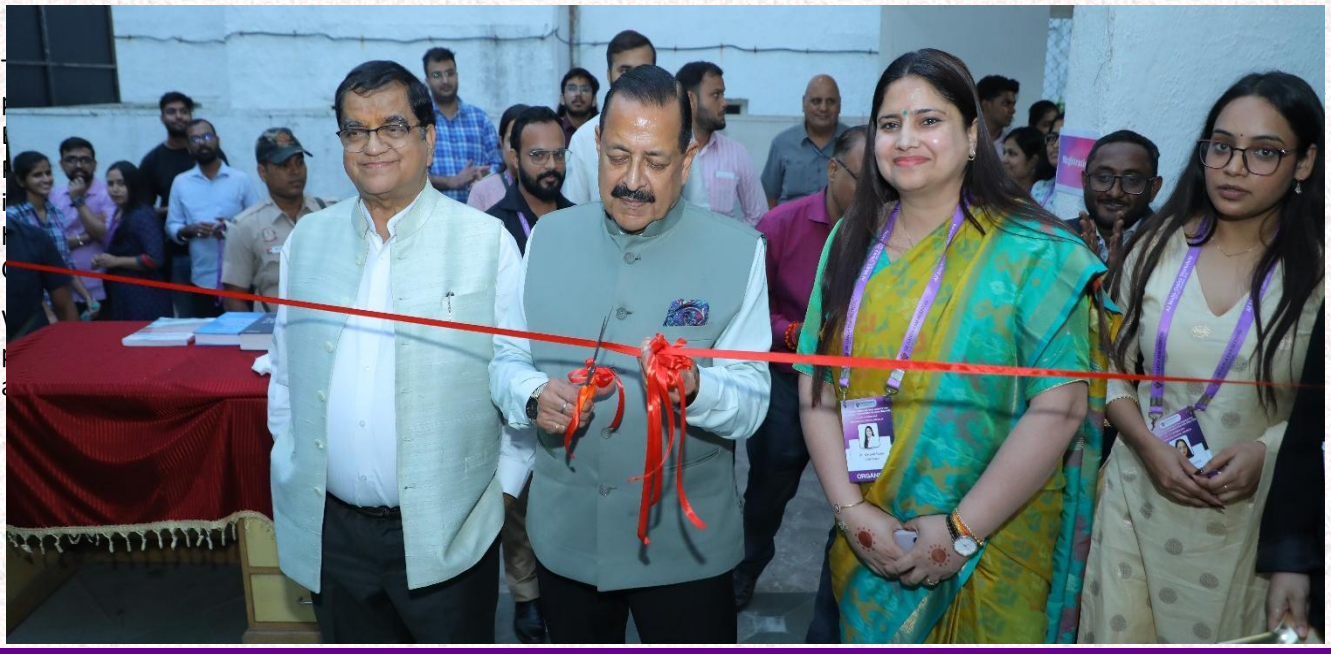

Proteomics Workshop @ SGRH, Delhi

Day 2 focused on systems biology, computational modeling, and clinical AI applications. Dr. Karthik Raman (IIT Madras) delivered an engaging lecture on metabolic modelling and network biology, followed by Dr. Anoop Ambikan (Karolinska Institute, Sweden) who discussed deep-learning models for multi-omics integration. Dr. Ravi Sirdeshmukh elaborated on combining genomics and proteomics using AI for robust biomedical insights. The afternoon included hands-on sessions on targeted analysis led by Thermo Fisher experts, culminating with a gala dinner.

The final day showcased future-ready innovations in AI-enabled healthcare. Dr. Geeta Manjunath (Niramai) presented cutting-edge thermal imaging techniques for non-invasive cancer detection. Dr. Sanjeeva Srivastava (IIT Bombay) illustrated how proteomics and machine learning are revolutionizing early disease diagnosis. Dr. Rajesh Pandey (IGIB) discussed integrative genomics for disease modeling, while Dr. Amit Kumar Yadav (THSTI) explored intersections between proteomics, NLP, and digital pathology. Hands-on demonstrations on NGS workflows and high-dimensional multi-omics analytics followed, led by experts including Dr. Rintu Kutum and Dr. Agnieszka Ciesielska.

With participation from students, clinicians, researchers, and industry specialists, the workshop successfully provided a comprehensive platform for learning and collaboration. The event underscored SGRH's commitment to advancing AI-driven precision medicine in India and fostering next-generation multi-omics research infrastructure.

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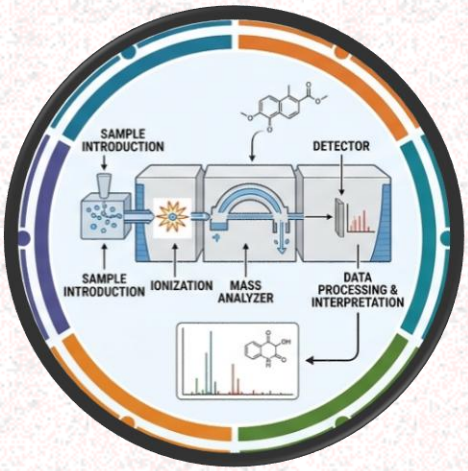
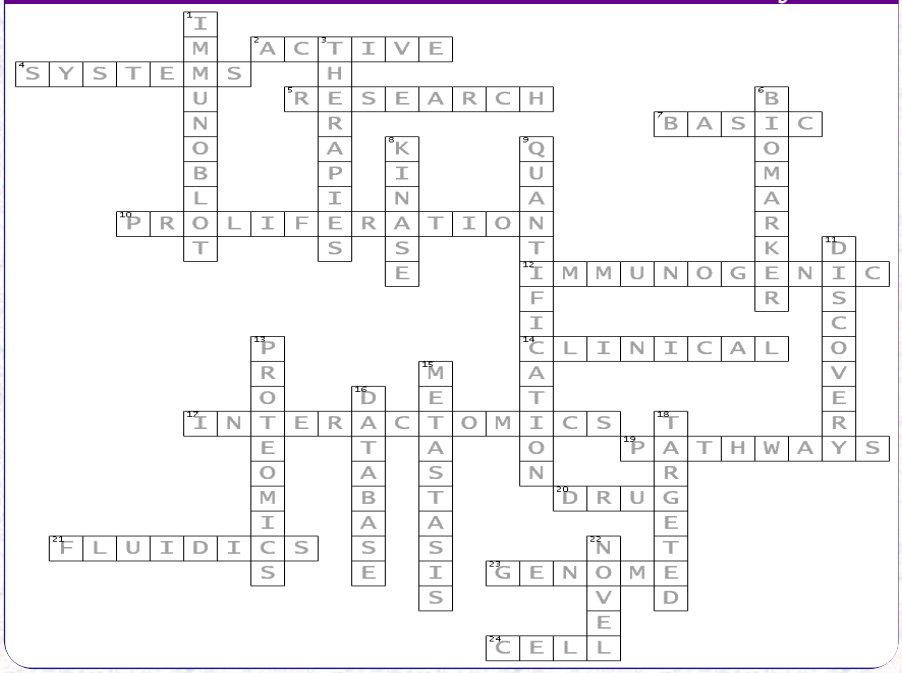


PSI Crossword Puzzle 2 - Answer keys



Upcoming events

BRIC a DBT Organization | INSTITUTE OF LIFE SCIENCES | जीव विज्ञान संस्थान Institute of Life Sciences

"National Workshop on Mass spectrometry based Proteomics" (NWMSP)
March 9 -11, 2026

Organizers

Convener
- Dr. Amol R. Suryawanshi, Scientist-F

Co-conveners
- Dr. Soma Chattopadhyay, Scientist-F
- Dr. Gulam H. Syed, Scientist-F
- Dr. Soumen Chakraborty, Scientist-G

Scan QR code for Registration & details

IMPORTANT DATES

- **Last date for application:** February 26, 2026
- **Notification of acceptance for Workshop:** will be intimated by email once selected

Venue

BRIC-Institute of Life Sciences (ILS)
(An Autonomous Institute of Dept. of Biotechnology, Govt. of India)
Nalco Square, C. S. Pur, Bhubaneswar-751023
Contact No- 0674-2304329; 2304256 (lab); 2304233 (MS facility) / 8637260509, 8327789772
Email id: msfacility@ils.res.in; amol@ils.res.in

PSI | BRIC a DBT Organization | INSTITUTE OF LIFE SCIENCES SEEKING INSIGHTS INTO LIFE

INVITATION

BRIC- Institute of Life Sciences, Bhubaneswar invites you all to join

18th Annual Meeting of the PSI and International Conference

Convener: Dr. Amol R. Suryawanshi

Tentatively in October/November 2026

For more details/update, please visit PSI website

Forthcoming International conferences and workshops

Sl. no	Conference and workshop Details	Online link
1.	Annual International Conference on Intelligent Systems for Molecular Biology and European Conference on Computational Biology (the 24th Annual Conference), ISMB/ECCB 2025 at Liverpool, United Kingdom from July 20-24, 2025	https://www.iscb.org
2.	Belgian Proteomics Association Winter School(1st edition),BePA at Mons, from Belgium, from 26–30 January 2026	https://belgianproteomics.be/events/bepa-proteomics-winter-school-2026/
3.	European Bioinformatics Community For Mass Spectrometry School,EuBIC at Harrachov, Czech Republic, from 19–23 January 2026	https://eubic-ms.org/events/2026-winter-school/
4.	Proteomics-Based Drug Discovery Summit – 3–5 February 2026, Boston, USA	https://www.emedevents.com/c/medical-conferences-2026/2nd-proteomic-based-drug-discovery-summit-2026
5.	Annual Lorne Proteomics Symposium (31st edition) at Victoria, Australia, from 5–8 February 2026	https://www.lorneproteomics.org/
6.	MassSpec-Forum Vienna (36th Forum), University of Vienna, Faculty of Chemistry Währinger at Vienna, Austria, from 18–20 February 2026	https://gcms.labrulez.com/events/997
7.	US HUPO Conference at St. Louis, USA, 21–25 February 2026	https://www.ushupoconference.org/#
8.	Annual Conference of The DGMS (57th Annual Conference) at Leipzig, Germany from 10–13 March 2026	https://dgms-conference.com/
9.	Finnish Proteomics Symposium , at Espoo, Finland, from 12–13 March 2026	https://www.finnprot.fi/2026-finnish-proteomics-symposium/
10.	Hands-on Workshop on Metabolomic and proteomics, at Center for Omics and Systems Medicine, NITTE/K.S.Hegde Medical Academy, from 21–24 April 2026	https://nitte.edu.in/kshema/cosm.php#:~:text=Workshop%20on%20Hands%2Don%20Workshop%20on,May%2026%20to%2028%2C%202025
11.	Swiss Proteomics Meeting, at Bern, Switzerland, from 23–24 April 2026	https://meetings.ls2.ch/
12.	Conferences ASMS Conference on Mass Spectrometry and Allied Topics, ASMS, (74th Conference), at San Diego, USA, from 31 May–4 June 2026	https://www.asms.org/conferences/annual-conference/annual-conference-homepage
13.	International Metaproteomics Symposium, at Dessau-Roßlau, Germany, from – 21–24 June 2026	https://metaproteomics.org/symposia/

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Newsletter conceptualized and designed by

PSI Newsletter Committee

Dr. Amol R. Suryawanshi, Dr. Niranjan Chakraborty, Dr. Manas Santra, Prof. Renu Deswal, Dr. Alka Rao & Dr. Sandhya Sadashivaiahp

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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	Banerjee R, Maheswarappa NB, Varakumar P, Lalthanmawii J, Govindaiah PM, Belore BM, **Mohan K.** **Discrimination of cold-slaughtered versus freshly slaughtered chicken meat using a heat-stable hemoglobin-derived biomarker: Targeted MRM-based quantification and validation.** Food Chem. 2025 Dec 25;496(Pt 3):146941. *Impact factor*: *9.8*	https://doi.org/10.1016/j.foodchem.2025.146941
2	Bansal S, Prakash S, **Deswal R.** **Protein corona analysis shows RuBisCO stabilization with superior performance of green-synthesized gold nanoparticles for sustainable agriculture.** Int J Biol Macromol. 2025 Sep 12;328(Pt 2):147649. *Impact Factor*: *8.5*	https://doi.org/10.1016/j.ijbiomac.2025.147649
3	Baral, B., Saini, V., Singh, S., Verma, T. P., Rath, D. K., Bahinipati, J., Panda, P., Patro, S., Misra, N., Behera, M. R., Muduli, K., Parmar, H. S., Meena, A. K., Kumar, R., Agarwal, S., Mohapatra, S. R., **Mohakud, N. K.**, & **Jha, H. C.** (2025). **Integrative Metabolomic and Lipidomic Signatures of SARS-CoV-2 VOCs: Correlations with Hematological and Biochemical Markers.** *Journal of proteome research*, *24*(7), 3272–3285. *Impact Factor: 3.6*	https://doi.org/10.1021/acs.jproteome.4c00996
4	Biswas, D., Shenoy, S. V., Chauhan, A., Halder, A., Padhye, A., Dutta, S., Auromahima, S., Bavaskar, H., Yadav, D., Ghosh, B., Sasmal, S., Kumari, N., Kumar, T. R., Mukherjee, A. P., & **Srivastava, S**. (2025). **BrainProt v3.0: An Integrative and Simplified Omics-Based Knowledge-Base About the Human Brain and Its Associated Diseases.** *Journal of proteome research*, *24*(11), 5352–5369. *Impact Factor: 3.6*	https://doi.org/10.1021/acs.jproteome.4c00982
5	Chauhan, R., Dagar, G., Malhotra, L., Gupta, A., Surendranath, A., Kapoor, H., Yadav, H., Ujjainiya, R., Das, S. K., Mirza, S., Tanwar, M., Tanwar, P., Ethayathulla, A. S., Singh, A., Macha, M. A., Uddin, S., Al-Shabeeb Akil, A. S., Mathur, S., Pandita, T. K., Bhat, A. A., … **Singh, M**. (2025). **Targeting ubiquitin-specific protease 14 reduces metastatic potential and metabolic activity in cervical cancer via direct modulation of monocarboxylate transporter-4.** *Journal of translational medicine*, *24*(1), 33. *Impact Factor: 7.5*	https://doi.org/10.1186/s12967-025-07442-x
6	Gupta S, Patni K, Kaur S, **Dhanjal JK.** **Deciphering context-specific Axitinib escape pathways via multi-omics and explainable machine learning**. J Transl Med. 2025 Nov 12;23(1):1268. *Impact Factor*: *7.5*	https://link.springer.com/article/10.1186/s12967-025-07153-3
7	Kanda T, Srivastava R, Yadav S, Singh N, Singh VK, Mishra R, Yadav S, **Atri N**. **Herbicide pretilachlor impairs biofertilizer potential of Anabaena doliolum: Integrating proteomic responses, nitrogen fixation, and computational analysis.** J Hazard Mater. 2025 Aug 15;494:138673. *Impact Factor*: *11.3*	https://www.sciencedirect.com/science/article/abs/pii/S0304389425015894?via%3Dihub
8	Kar, A., Biswas, S., Das Gupta, B., Banerjee, S., Minz, A. P., Jeyaram, K., Senapati, S., Somkuwar, B. G., Sharma, N., & **Mukherjee, P. K.** (2025). **Immunomodulatory activity of bamboo biosilica from Dendrocalamus longispathus Kurz. - Metabolomics integrated network pharmacology approach.** *Phytomedicine: international journal of phytotherapy and phytopharmacology*, *143*, 156797. *Impact Factor: 8.3*	https://doi.org/10.1016/j.phymed.2025.156797
9	Kolanchi, P., Sanivarapu, H., **Marimuthu, M**., Kalenahalli, Y., Onkarappa, D., Jagdish, J., Venkatasamy, B., & Muthu, A. (2025). **Combining complementary multiplex extraction chemistries enhances proteome coverage and analytical insights in tiny insects: A study on sweet potato whitefly Bemisia tabaci.** *International journal of biological macromolecules*, *333*(Pt 1), 148741. *Impact Factor: 8.5*	https://doi.org/10.1016/j.ijbiomac.2025.148741

Sl. No.	Publication Details	Online link
10	Kumar, R., Mahato, R., Baruah, S., Lalremsanga, H. T., Kalita, B., & **Mukherjee, A. K**. (2025). **Quantitative proteomic analysis to comprehend the Trimeresurus erythrurus (Red-Tailed Bamboo Pit Viper) venom proteins (toxins) and their correlation with lethality, preclinical toxicity, and clinical manifestations in envenomed patients.** *International journal of biological macromolecules*, *333*(Pt 1), 148715. *Impact Factor: 8.5*	https://doi.org/10.1016/j.ijbiomac.2025.148715
11	Kusuma B, Rawat S, Saha O, Nimesh S, Sadhu S, Awasthi A, Maiti TK, **Banerjee A.** **Depletion of myeloid cells in AG129 mice reduces the infection-mediated oxidative stress and restrains dengue virus-induced thymic atrophy.** Cell Commun Signal. 2025 Dec 6;24(1):20. *Impact factor- 8.9*	https://doi.org/10.1186/s12964-025-02572-7
12	Marimuthu, S. V., Loganathan, T., **Santhanakrishnan, M**., George Priya Doss, C., & Ramasamy, M. (2026). **Comparative proteomic profiling of advanced, injectable, and titanium-prepared platelet rich fibrins (PRF): Insights into functional divergence and clinical potential.** *Biochimica et biophysica acta. Proteins and proteomics*, *1874*(3), 141121. *Impact Factor: 5.9*	https://doi.org/10.1016/j.bbapap.2025.141121
13	Narayanan A, Guha S, Mali A, **Bapat SA.** **Targeting mitochondrial translation and OXPHOS in high-grade serous ovarian carcinoma eliminates stem-like cells**. Cell Death Dis. 2025 Oct 6;16(1):676. *Impact Factor*: *9.6*	https://doi.org/10.1038/s41419-025-07987-1
14	Narendradev, N. D., Marathe, S., Baboo, S., McClatchy, D. B., Diedrich, J. K., Jain, P., Purwar, R., Yates, J. R., 3rd, & **Srinivasula, S. M**. (2025). **Quantitative Proteomic Analysis Reveals JMJD6 and DNAJB11 as Endogenous Substrates of E3 Ligase RFFL.** *Journal of proteome research*, *24*(8), 3913–3930. *Impact Factor: 3.6*	https://doi.org/10.1021/acs.jproteome.5c00086
15	Patwardhan RS, Rizvi ZA, Gota V, Checker R, Singh B, Maurya DK, Pal D, Ramani N, Kumar BK, Purohit V, Mathapati BS, Mullick J, Ghanty TK, Gupta S, Joshi M, Madki S, Awasthi A, Sandur SK, **Sharma D.** **First-in-human clinical trial of high-dose sodium copper chlorophyllin: Pharmacology and efficacy as a dual immunomodulatory/antiviral agent.** Phytomedicine. 2026 Jan;150:157689. *Impact Factor- ~~8.5~~/8.3*	https://doi.org/10.1016/j.phymed.2025.157689
16	Ramesh, P., Upadhyay, S. S., Thomas, S. D., Sorake, C. J., M K, G., Shetty, V. V., Modi, P. K., Shetty, R., Vijayakumar, M., Codi, J. A. K., & **Prasad, T. S. K**. (2025). **Differentiating Gastric Cancers from Acid Peptic Diseases through Integrative Targeted Proteomics and Machine Learning Approaches**. *Journal of proteome research*, *24*(10), 5159–5176. *Impact Factor: 3.6*	https://doi.org/10.1021/acs.jproteome.5c00547
17	Rana, S., Mishra, V., Nakrani, P., Ega, L. K., Sahay, M., Sahay, R. K., & **Wangikar, P. P**. (2025). **Whole Blood Metabolome Profiling for Stratification of Type 2 Diabetes Patients and Identification of Biomarkers for Diabetic Kidney Disease in Asian Indian Adults.** *Journal of proteome research*, *24*(8), 4114–4125. *Impact Factor: 3.6*	https://doi.org/10.1021/acs.jproteome.5c00188
18	Rao, P. S., Deshmukh, N., Saipriya, K., Bihola, A., & **Sharma, H**. (2025). **Insights into the comparative analysis of metabolite profile of paneer whey, acid whey, and cheese whey**. *Food research international (Ottawa, Ont.)*, *221*(Pt 1), 117210. *Impact Factor: 8*	https://doi.org/10.1016/j.foodres.2025.117210
19	Rastogi L, Hussain MM, Tyagi S, Kabyashree K, Kharbanda N, Srivastva P, Chaudhary R, Maiti TK, Krishnan V, Jha G, Voxeur A, Shrivastava T, **Pawar PA.** **Arabidopsis GELP53 overexpression modulates polysaccharide acetylation and defense through oligosaccharide-mediated signaling.** Plant Cell. 2025 Oct 31;37(11):koaf184. *Impact factor: 11.6*	https://doi.org/10.1093/plcell/koaf184
20	Saipriya, K., Singh, A. K., Singh, R., Meena, G. S., Pradhan, D., Kumar, S., Kishore, A., & **Sharma, H**. (2025). **A comprehensive comparative analysis of fatty acid profiles and GC-MS based metabolomics in Barbari and Beetal goat milk**. *Food research international (Ottawa, Ont.)*, *217*, 116760. *Impact Factor: 8*	https://doi.org/10.1016/j.foodres.2025.116760

Sl. No.	Publication Details	Online link
21	Saritha C, Rajana VK, Choudhary K, Vairagar A, Mishra A, Penumaka SM, Jain S, Dande A, Naresh P, Kumar N, Ramalingam P, **Mandal D**. **Highly selective ergosterol binding and impaired redox balance leads to improved antileishmanial efficacy for amphotericin b synthesized silver nanoparticles with reduced toxicity- In vitro and in vivo studies**. Free Radic Biol Med. 2025 Aug 1;235:405-425. *Impact factor: 8.5*	https://doi.org/10.1016/j.freeradbiomed.2025.03.033
22	Sasikumar, S., Taylor Parkins, S., Sudarsan, S., & **Sinha, H**. (2025). **Interaction of genetic variants activates latent metabolic pathways in yeast.** *Nature communications*, *16*(1), 8014. *Impact Factor: 15.7*	https://doi.org/10.1038/s41467-025-63306-4
23	Sharma N, Bhat SH, Chaudhary S, Mathew B, Pandey S, Yadav S, Yadav M, Bindal V, Tripathi G, Sharma N, Sharma V, Gupta A, Nanda R, Kumari A, Sharma S, **Maras JS.** **In vivo protein half-life analysis identifies the SREBF1-SLC27a5 axis governs antioxidant response in preclinical alcoholic rat model**. Redox Biol. 2025 Sep;85:103674. *Impact Factor*: *11.3*	https://doi.org/10.1016/j.redox.2025.103674
24	Sharma, S., Subrahmanyam, Y. V., Gupta, P., Vadivel, S., Deepa, M., Tandon, A., Sreedevi, S., Ram, U., Narad, P., Parmar, D., Anjana, R. M., Raghunathan, A., Balasubramanyam, M., Mohan, V., Sengupta, A., Adamski, J., Saravanan, P., Panchagnula, V., **Usharani, D., & Gokulakrishnan, K.** (2025). **Precision integrated identification of predictive first-trimester metabolomics signatures for early detection of gestational diabetes mellitus.** *Cardiovascular diabetology*, *24*(1), 434. *Impact Factor: 10.6*	https://doi.org/10.1186/s12933-025-02978-0
25	Shenoy, S. V., Biswas, D., Zalevsky, A., Kishishita, A., Verma, A., Upadhay, I., He, Y., Sali, A., Viner, R., Mandal, K., **Srivastava, S**., & Wiita, A. P. (2025). **AlphaCross-XL: A Seamless Tool for Automated and Proteome-Scale Mapping of Cross-Linked Peptides Onto 3D Protein Structures.** *Molecular & cellular proteomics : MCP*, *24*(10), 101057. *Impact Factor: 5.5*	https://doi.org/10.1016/j.mcpro.2025.101057
26	Shirke, O., Velu, S., Pandita, S., Saha, A. K., Patil, R. R., Joshi, N. S., Govindaraj, P., Rao, L. T., Markandeya, Y. S., & **Mehta, B**. (2025). **Lead exposure during development alters synaptic organization and protein expression in rat hippocampus.** *Journal of hazardous materials*, *500*, 140582. *Impact Factor: 11.3*	https://doi.org/10.1016/j.jhazmat.2025.140582
27	Singh, A., Sharma, P., Balasubramani, A., Shetty, S. P., Roy, S., Vasudeva, S. B., Patil, S., Vaish, R., Nair, S., & **Srivastava, S**. (2025). **Identification of Potential Salivary Biomarkers and Enriched Protein Domain/Motif Families for Early Detection and Lymph Node Invasion in OSCC Patients of the Indian Population.** *Journal of proteome research*, *24*(10), 5204–5215. *Impact Factor: 3.6*	https://doi.org/10.1021/acs.jproteome.5c00587
28	Tomar, M. S., Kulkarni, C., Washimkar, K. R., Verma, S., Bhadkaria, A., Araniti, F., Mugale, M. N., Chattopadhyay, N., & **Shrivastava, A**. (2026). **Mitochondrial Metabolic Reprogramming along with NRF2/KEAP1-Mediated Antioxidant Mechanisms Drive Temozolomide Resistance in Glioblastoma Multiforme**. *Journal of proteome research*, *25*(1), 379–394. *Impact Factor: 3.6*	https://doi.org/10.1021/acs.jproteome.5c00734
29	Washimkar, K. R., Kulkarni, C., Tomar, M. S., Verma, S., Bhatt, D., Verma, S., Reddy, D. V. S., Moharana, B., Misra, A., Bawankule, D. U., Rath, S. K., Chattopadhyay, N., Shrivastava, A., & **Mugale, M. N**. (2025). **Metabolic dysregulation and temporal dynamics of NF-κB-p65/NLRP3, TXNIP, endoplasmic reticulum and mitochondrial stress in silica-induced pulmonary fibrosis in rats.** *Journal of hazardous materials*, *495*, 138791. *Impact Factor: 11.3*	https://doi.org/10.1016/j.jhazmat.2025.138791

Proteomics Perspective

By Dr. Sandhya Sadashivaiahp

Finding my way through acrylamide realms
I whispered in Coomassie blue gels.
You tracked me down on to 2D maps,
Named my fragments in peptide traps
From humble beginnings to spectra so clear
You taught me to rise, shine, n align,
On beams of light, where hidden truths appear

For me u built instruments, sensitive and strong
Orbitrap, TOF, LC-MS is where I belong
Thanks to you, I learned to translate peptides into pathways,
Transform noise into scientific sense, and bring clarity to complexity,
Thus, understanding biological essence.

Now I dwell in algorithms and cloud pipelines,
Datasets and platforms mapping population timelines.
From mitochondrial fire in cellular core
To metabolites marking imbalance and more,
Where lipids and proteoforms in health sway,
From harmonious order on to disease way.

I read the spoken word, understood the untold,
Believe me, I know the secrets you with hold.
I walk with pathogens, silent and sly,
Rabies in neurons, learning how and why.
Cancers, I see fight back with desperate might,
Immune storms answer with equal fight.

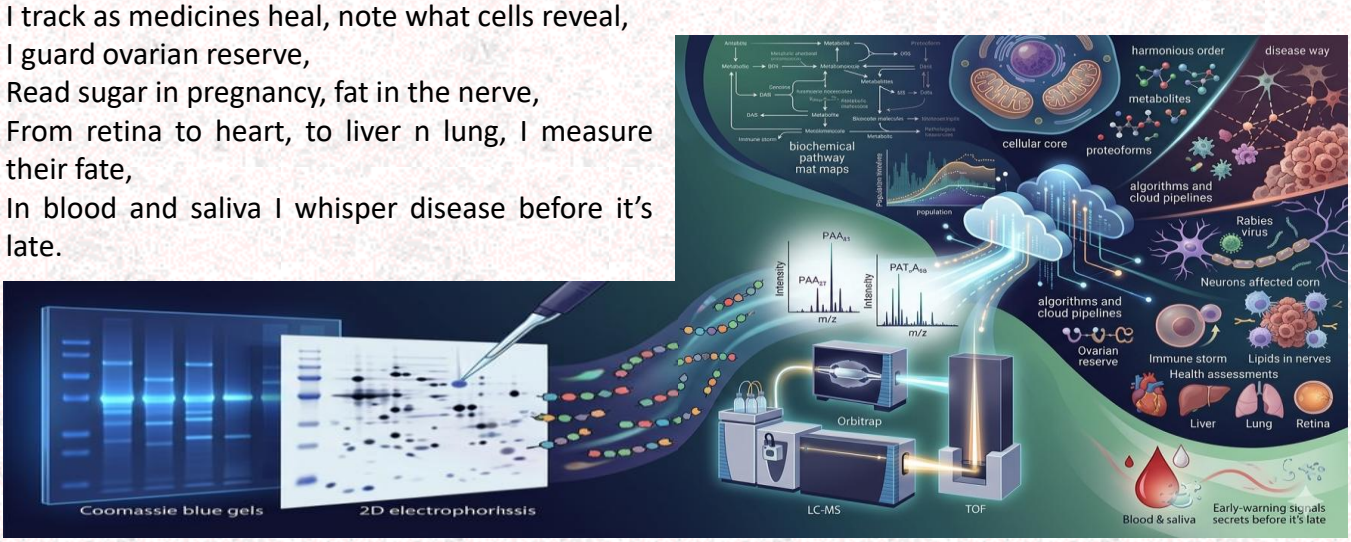
I track as medicines heal, note what cells reveal,
I guard ovarian reserve,
Read sugar in pregnancy, fat in the nerve,
From retina to heart, to liver n lung, I measure their fate,
In blood and saliva I whisper disease before it's late.

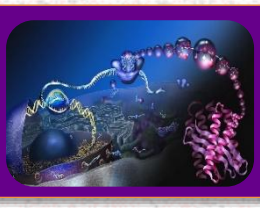
In roots, in leaves, and in grain,
I watch resilience through drought n strain.
I know how algae make fuel, venoms make drugs,
Nature turns toxins to therapeutic hugs.
All this you see
A reason enough for you to applaud me

Spectra of truth is in the chaotic code,
Guiding you down every road.
Here I stand where questions become rare and answers speak,
No longer a tool, but the solace you seek.
From lab to clinic, from code to care,
With AI as my guide, I travel everywhere
I am the backbone biology depends on,
Not a mere tool, but an infrastructure you build upon

So now, partners in thought, I ask you:
Where do we go from here?
Beyond the catalogue,
Beyond what we know,
What will you build on me?
What problems will you dare to mend?
What lives will you change and defend?
With you, my friends, I am ready to coddiwomple

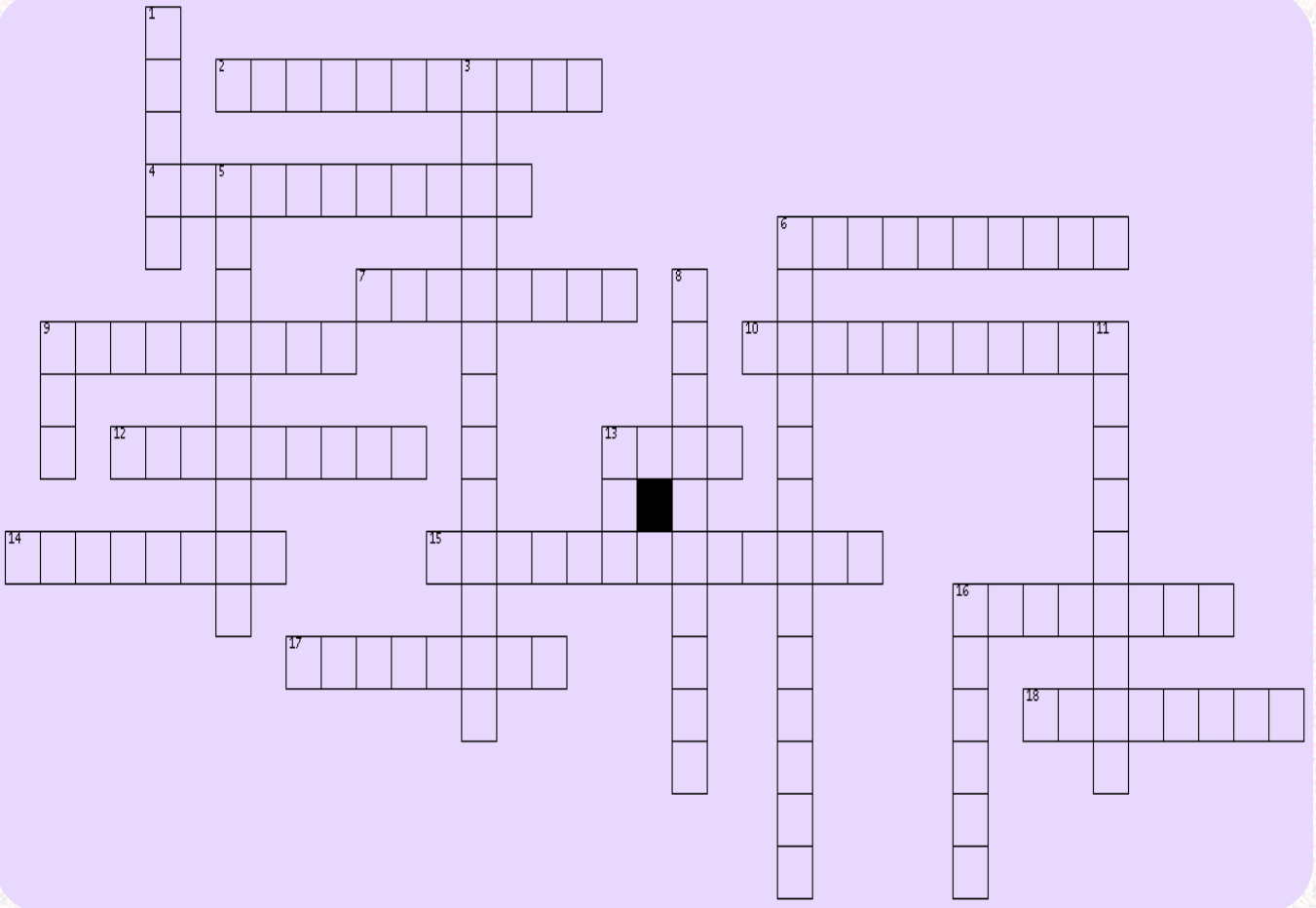
Toward the next unknown frontier.
Are you? Then hop on!!!





PSI Crossword Puzzle - 3

Theme: Biology & Multi-Omics



Across

2. Predictable system governed by fixed rules
4. Regulatory loop amplifying signal response
6. In-silico perturbation of biological models
7. Time-varying behavior of biochemical systems
9. Multilayer biological organization principle
10. System property opposing environmental fluctuations
12. Algorithmic discovery of network structure from data
13. Quantification of reaction flow in pathways
14. Regulatory loop dampening signal output
15. Randomness in molecular reaction timing
16. Abstraction reducing biological complexity
17. Experimental loss-of-function genetic strategy
18. Sensitivity of reactions to concentration change

Down

1. Binary abstraction of regulatory logic
3. Computational scaling of heterogeneous datasets
5. Property arising from nonlinear component interactions
6. Mathematical coefficient matrix of reactions
8. Resistance of networks to node failure
9. Highly connected node controlling network flow
11. Network-level information propagation mechanism
13. Constraint-based prediction of metabolic states
16. Functional subnetwork performing a specific task

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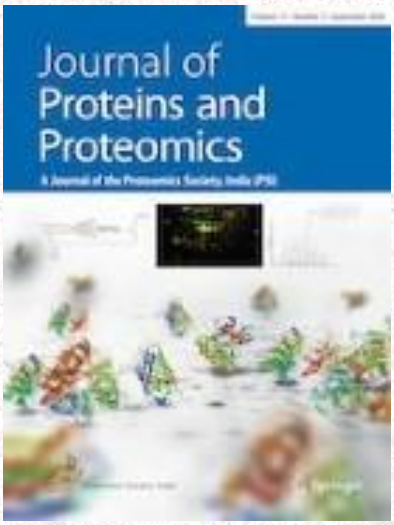

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