Who will be the next Face of Mass Spectrometry? Nominate a member who exemplifies diversity of ASMS (nationality, ethnicity, age, etc.) and path to a career in mass spectrometry.

FACES OF MASS SPECTROMETRY / Pratik Jagtap

Anne Brenner and J.D. Brookbank are science writers at Technica Editorial Services.

November 2025

Exploring New Avenues

Pratik Jagtap's interest in mass spectrometry developed over the course of his career. He was introduced to mass spectrometry while pursuing his PhD at the Center for Cellular and Molecular Biology in Hyderabad, India. After earning his PhD degree, Pratik worked as a post-doctoral researcher at the Max-Planck Institute for Developmental Biology in Tübingen, Germany, and then at the University of Michigan in Ann Arbor. He then moved to Minneapolis to accept a position at the Minnesota Supercomputing Institute at the University of Minnesota as a computational proteomics consultant. He then managed the mass spectrometry core facility at the university, before taking on his current role as the co-lead of the Galaxy-P project with Professor Timothy Griffin.

The Galaxy-P project is a platform dedicated to the development of software tools and workflows that can be used for performing multi-omics analysis, including mass spectrometry–based proteomics. Pratik explains that Galaxy-P is a user-friendly resource for sharing open-source software tools and workflows with academic researchers. The Galaxy Training Network provides free step-by-step guides and online training video tutorials. Since the project's inception in 2012, the Galaxy-P team has published more than sixty manuscripts, developed twenty-two tutorials, and cultivated a robust network of users.

Pratik has attended ASMS conferences for almost two decades. Since 2007, he has presented more than sixty posters and delivered six oral presentations. Pratik notes that these experiences with ASMS have been extremely rewarding, providing high-quality feedback, which has allowed him to take his work to the next level. Furthermore, Pratik highly recommends that young scientists in the field attend ASMS conferences to help instill a greater perspective and confidence in presenting their work.

Did your focus on mass spec begin before or after your PhD studies in India?

My interest in mass spectrometry began during my PhD in India and developed as I proceeded forward in my career. As part of my PhD, I was working on identifying proteins that are isolated after 2D SDS-PAGE from Antarctic bacteria. I used Edman sequencing and peptide mass fingerprinting as methods for proteomics analysis. Later, I used peptide mass fingerprinting during my post-doctoral research in Germany and tandem mass spectrometry in the United States.

How did you arrive at your current position at the University of Minnesota?

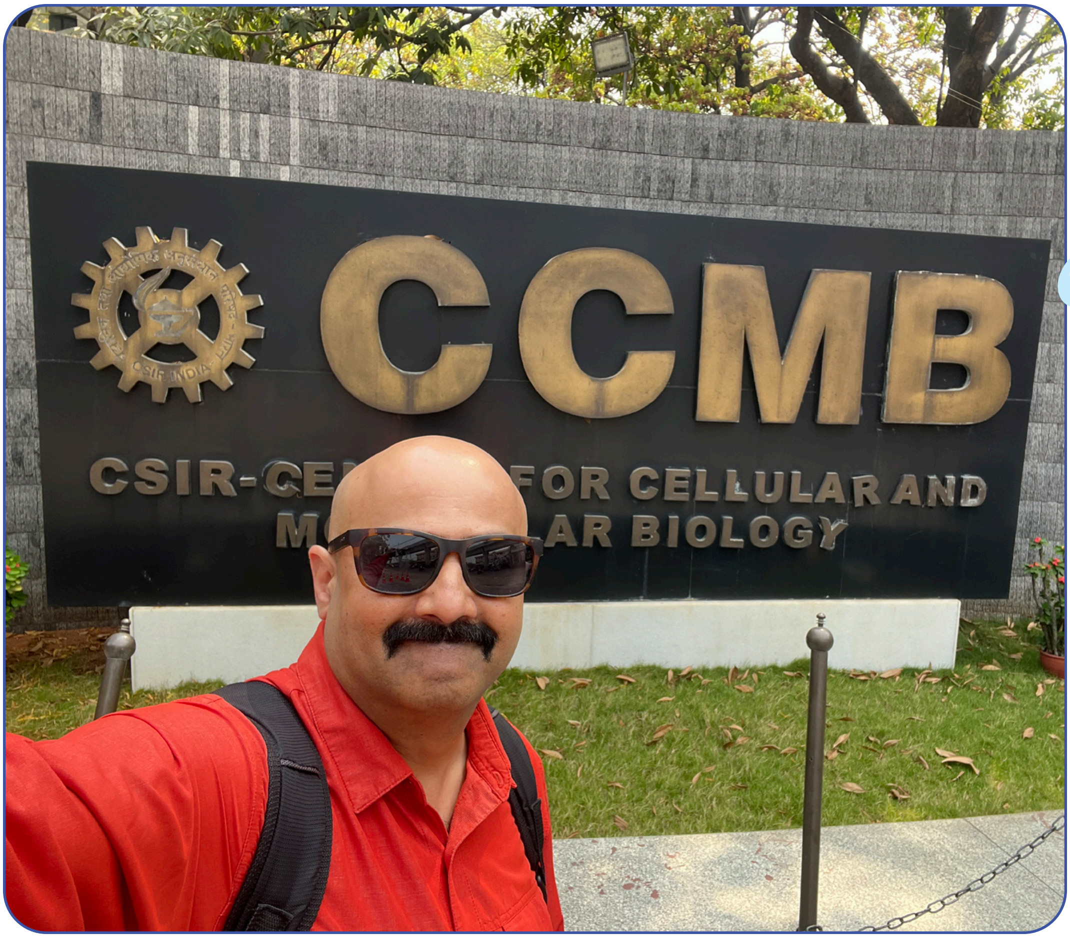
I completed both my bachelor's and master's degrees in microbiology in Pune, India. During my PhD, I was at the Center for Cellular and Molecular Biology in Hyderabad. After my PhD in 2000, I worked as a proteomics project manager in Bio-Rad Laboratories in India. After that, I had two stints as a post-doctoral researcher at the Max-Planck Institute for Developmental Biology and at the University of Michigan. Next, I joined the Minnesota Supercomputing Institute as a computational proteomics consultant in 2008 and then as manager of the scientific consulting group at the University of Minnesota in Minneapolis. There I managed the mass spectrometry core facility from 2013 to 2016. My current position is as co-lead on the Galaxy-P project at the University of Minnesota. It has been quite a journey, filled with interesting anecdotes every step of the way.

When did you first begin to focus on proteomics?

When I first started my career, proteomics was just emerging as a powerful tool for functional genomics analysis. During my PhD, I ran quite a few SDS-PAGE gels and 2D SDS-PAGE with the intention of detecting phosphoproteins during cold-adaptation in Antarctic bacteria. Given my background in microbiology, I was closely following the field of microbial genomics.

What are some of the applications of your research that you consider important?

As the co-director of the Proteogenomics Shared Resource, I work with the Masonic Cancer Center studying bioinformatic analysis and biological interpretation of multi-omics studies.



> If you are interested in progressing in your research, you should not be afraid to reach out to experts in the field. You never know where it might lead you!

This photograph is from February 2025 while visiting my alma mater, Center for Cellular and Molecular Biology in Hyderabad, India. (Photo courtesy of Pratik Jagtap)

One important aspect of the research is that the proteogenomics workflows developed by Galaxy-P are used in cancer research. Many researchers use our clinical metaproteomic workflows to detect microbial proteins associated with disease conditions from clinical samples. The Galaxy-P team also develops analytical workflows in the fields of quantitative proteomics, metaproteomics, and immunopeptidomics research. The metaproteomics workflows are used in both clinical research and environmental research.

How has presenting posters and oral presentations at ASMS events helped you grow and learn as a scientist?

The ASMS conferences have played a crucial role in guiding me through this journey. For example, any ongoing research project starts with writing an abstract for the ASMS conference, then working toward creating a presentation. Presenting at the ASMS conference serves as an important milestone in getting your work published. This is due to the high quality of feedback you might receive from experts in the field at the conference. Knowing this, beginners can start to overcome some of their anxieties and gain confidence in their budding ideas. When you attend the ASMS conference, you might meet a specialist in your field who has published multiple manuscripts and has years of experience—yet they are still a human being who started off the same way as everyone else did. It just goes to show: If you are interested in progressing in your research, you should not be afraid to reach out to experts in the field. You never know where it might lead you!

I have benefited immensely from attending ASMS events because it allows me to network with top proteomics researchers in the field and meet young researchers presenting their work. I have been presenting posters at ASMS since 2007 and as part of the Galaxy-P team and the Metaproteomics Initiative, I have presented evening workshops there for many years. As research developments advance, ASMS conferences can be a useful resource to explore new methods and applications in your specialty. I highly recommend attending ASMS events to anyone who is new to the field, because it offers opportunities and perspective early in your career.

Tell us about your involvement in the US Human Proteome Organization and the Association of Biomolecular Resource Facilities?

I served as a chairperson of the Proteomics Research Group and ABRF Informatics Proteomics Research Group. This included working on many emerging research areas such as meta proteomics, data independent acquisition, and promoting cloud computing environments for proteomics data analysis. I have also chaired the US-HUPO Education and Outreach Committee and have had the opportunity to interact with some brilliant young minds in promoting proteomics research. In addition, I am an active member of the executive board and scientific committee of the Metaproteomics Initiative, an international consortium involved in promoting metaproteomics research.

> Keep your mind open to new avenues in your research field of interest and strive to achieve the best results with the resources at your disposal. You may surprise yourself with the progress you make as the field develops.

This photograph is from February 2025 after a biking in the city of Pune, India. (Photo courtesy of Pratik Jagtap)

Has your work in academia included any mentoring?

Over the years, I have mentored undergraduate students, PhD students, and post-doctoral researchers. Many of the undergraduate students have been lead authors on publications under my guidance, and some have ended up joining our lab on a full-time basis. It is satisfying to see how these students have gone on to develop in their careers. Some have taken jobs in industry, while others have transitioned into PhD research and careers in academia. It is rewarding to see them learning, mastering, and using the tricks of the trade in mass spectrometry–based proteomics data analysis.

Can you tell us about your work on the Galaxy-P project?

Galaxy-P was started in 2012 as an NSF-funded bioinformatics project which focuses on developing software tools and workflows for multi-omics analysis, including mass spectrometry–based proteomics. The Galaxy-P platform is a resource to share software tools and workflows with academic researchers. Multiple researchers have used our clinical metaproteomic workflows in cancer research to detect microbial proteins associated with disease conditions from clinical samples. These workflows are helpful for detecting proteins that are responsible for the initiation or progression of cancer. We use the platform often for research and analysis here at the University of Minnesota, and many others benefit from it because it is both user-friendly and easy to access. The Galaxy Training Network is a way to disseminate information to researchers who are interested in using these workflows. Since its inception, the Galaxy-P project team has published over sixty manuscripts and generated twenty-two educational tutorials.

What are your interests outside the lab?

I have been playing cricket in a local Minnesota league since 2009. In India, cricket has a religious following—it is as big as American football, or basketball is in the United States. When I came to Minnesota, I gave up on cricket, but before long, I realized that there are multiple cricket leagues here during the summer. In fact, I think I have ended up playing more cricket as an adult than I did as a child. My children Pramit and Meer, aged twenty-one and fourteen respectively, also play cricket; following an interest and passion that runs in the family. Biking is another hobby I developed while growing up in Wai, India which has stayed with me. I love to bike indoors during Minnesotan winters and outdoors in the summer (Figure 2). During the pandemic, my wife Gouri and I took advantage of the biking trails near our home in Maple Grove. That hobby has stuck with us, and it helps us stay fit and enjoy the outdoors. When I visit India, I still love renting a bicycle and going for early morning bicycle rides. It is the best way to explore as well as interact with locals and capture memories through photography. While visiting new cities during ASMS and other conferences, I enjoy exploring the location by biking or walking around the city. Thanks to ASMS, I have visited some fascinating cities in North America, such as Salt Lake City, Denver, and Vancouver.

What advice would you give to young people who are interested in entering the science field?

As I mentioned before, if high-quality research interests you, do not hesitate to seek guidance from senior researchers in the field. Reach out, network, and ask questions. It is also important to keep an eye on new and emerging fields. Mass spectrometry is a field that is rapidly evolving. Finally, keep your mind open to new avenues in your research field of interest, and strive to achieve the best results with the resources at your disposal. You may surprise yourself with the progress you make as the field develops.