

Bringing precision omics to life™

The potential of ‘omics’ to further our understanding of cell biology and disease progression has been discussed for over 30 years, but these technologies have so far failed to translate to a healthcare setting. One of the major challenges has been the lack of reproducible results, making it difficult to distinguish between true discoveries and experimental artifacts. ProtiFi was founded to overcome these challenges: to solve the bottlenecks around sampling, sample preparation and data interpretation in order to accelerate the deployment of omics technologies in real-world clinical applications.



Omics approaches aim to understand the structure and function of living organisms by quantifying and characterizing all biomolecules of a certain type present within biological samples. Genomics, first proposed in the 1980s, has been widely adopted by labs around the world, and has been joined by mass spectrometry-based proteomics, metabolomics, lipidomics and glycomics as researchers aim to further characterize biological

processes and diseases. The piecemeal development of these technologies has led to an incredibly diverse array of methods and techniques, with little consistency between labs. This issue is further compounded by the huge variation in results between – and even within – research groups.

Long Island-based ProtiFi – a spin out from Cold Spring Harbor Laboratory – was created to tackle this issue by

establishing robust, reproducible and accessible technologies that allow omics approaches to be executed in clinical settings. Co-founder and CEO Dr John Wilson explained the company’s ethos: “Our mission is to revolutionize omics research by developing turnkey solutions that improve the reproducibility of, and access to, omics techniques. We’re essentially taking the challenges that exist in omics today – sampling, reproducibility, data analysis and ease of use – and tackling them one at a time to help labs generate meaningful results that will advance humanity’s scientific understanding.”

Sample preparation prior to mass spectrometry analysis is a major hurdle for current approaches and, according to published reports, accounts for 75 percent of the overall variability seen in omics data.¹ This level of variation can make it almost impossible to compare results and gain meaningful insights. ProtiFi set out to eliminate these inconsistencies in sample handling and preparation by creating universal workflows that could be applied to all sample types. John continued: “If you start by using a host of different reagents and workflows, you can’t expect to get the same results. We therefore face a fundamental challenge



Members of the ProtiFi team (NOTE: Photo taken prior to social distancing)

in proteomics: how can you handle the proteins from a brain – which are generally highly hydrophobic – and the water-soluble proteins of blood in a consistent manner? Our answer to this is S-Trap™ sample processing technology, which uses a combination of highly denaturing conditions to provide a universal approach to sample preparation. The S-Trap protocol begins with strong detergent lysis and solubilization of the sample, continues with acidification to pH <1 to further denature proteins and eliminate enzymatic activity, and completes the process with exposure to high concentrations of organic, before the sample is processed enzymatically. This process does not need to change from bone to blood to brain – you can even use it on decalcified bone – and it's also been used to study gut microflora in stool samples. It is truly a universal protocol, and that's the key."

While the entire workflow can be performed manually using S-Trap spin columns, ProtiFi has partnered with Tecan to create an integrated, highly scalable and easy-to-use proteomics workflow using the S-Trap sample preparation system in combination with a Resolvex® A200 automated positive pressure workstation and PIXUL™ multi-sample megasonicator (Active Motif/Matchstick Technologies). "Automation can increase the speed, sensitivity and reproducibility of sample preparation by ensuring the protocol is performed exactly the same every time," John said. "We hold ourselves to a very high quality standard because, in a protocol with 10 to 20 steps, even minor inconsistencies can lead to large cumulative errors. I reached out to Tecan because the company is known as the gold standard for automation, and has a good

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reputation as a collaborative partner, so it was a natural fit. The Tecan team immediately saw the value of automating a workflow that would bring the idea of precision omics to life, and that is exactly what we're now doing in a wonderful collaboration that's bringing these techniques to the masses."

The joint system provides researchers with an automated, standardized and optimized workflow that increases productivity and, crucially, eliminates the need for method development. "I chose the Resolvex A200 for this workflow because it is very intuitive to use. We can provide the system with the standard S-Trap proteomics protocols preinstalled – or users can create custom protocols optimized for unique needs – meaning that all you need to do is select the right protocol and it just works! The system's gas-based positive pressure provides very controlled flow rates, and it can handle everything from water to xylene to hexane, allowing users to perform an extra wash step for pernicious contaminants to guarantee very clean samples for analysis."

Following the success of the S-Trap technology, ProtiFi has also developed Si-Trap™, which is the world's only multi-omics sample processing system. This technology allows researchers to separate and capture multiple classes

of biomolecules – proteins, transcripts, glycans, lipids and metabolites – from a single sample. "The Si-Trap protocol, which can also be processed on the Resolvex A200, allows you to obtain two to five different omics analyses from the same sample – there's nothing left once you've finished. This is where the field needs to go to, for example, discover all the different markers that are prognostic of developing a certain cancer. This will allow far earlier clinical interventions at the outset of disease, truly and finally delivering on the promises of the omics revolution."

1) Piehowski PD, *et al.* Sources of technical variability in quantitative LC-MS proteomics: human brain tissue sample analysis. *Journal of Proteome Research*, 2013, 12(5), 2128-37.

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To find out more about Tecan's Resolvex A200 automated positive pressure workstation, visit www.tecan.com/positive-pressure-processors

To learn more about ProtiFi, go to www.protifi.com