NOVEMBER / DECEMBER 2022 # 108

the Analytical Scientist®

2022 Analytical Data Management Survey

Effective data management and access has never been a bigger focus in scientific R&D than it is today.

We asked* those responsible for analytical data to share their experience with analytical data management.

>92% of scientists

- use multiple techniques
- collect data on numerous instruments
- process data using diverse software

Analytical data is managed and stored in a multitude of systems

80% Microsoft applications

70% Instrument software

34% In-house software

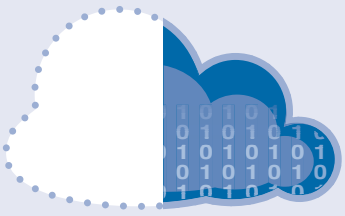
24% LIMS

13% ELNs

68% say data is hard to access and share

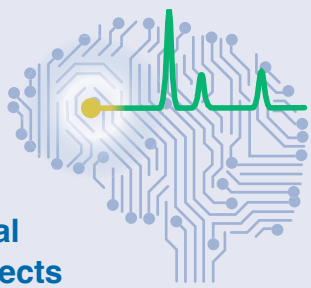
9/10 need analytical data on a daily basis to make decisions

~50%



feel that cloud-based data management is important

Only **6%** are using analytical data in AI /ML projects



70% want more investment in data management technologies

*A market research survey was conducted in 2022 in partnership with The Analytical Scientist. Survey participants: 41% academia/non-profit, 45% industry, 11% government, 3% other.

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Will You Play Upon This HPLC?

Are new analytical "instruments" becoming more like smart phones?

If you were to hand me a guitar, I'd happily pluck the strings and make some noise, but I couldn't command them to any utterance of harmony – as Shakespeare put it. Similarly, I could push a few buttons on a HPLC – perhaps even get it to run – but extracting information is another matter entirely. But the first time I used an iPhone, I quickly figured out how to make calls, browse the internet, and stream a movie. And that's why HPLC systems (and not iPhones) are referred to as "instruments" – a true master can extract a magnum opus, and there's a certain level of expertise required to use them at all. But for how long?

I recently asked a number of people from our 2022 Power List for an opinion with which the rest of the field might disagree. Michael Marty, Associate Professor, Department of Chemistry and Biochemistry, University of Arizona, USA, discussed the offense often caused when analytical instruments are referred to as machines. "My controversial opinion is that I don't really care," he said. "I'd be confused if you called a guitar a machine, but I wouldn't correct you for calling an HPLC a machine." I wondered whether Michael's point is reflective of a wider trend. Namely, are analytical "instruments" becoming less like guitars and more like iPhones – "smart devices" that any novice can pick up and play? And if so, where does that leave the analytical scientist?

Admittedly, this trend is not new – and there are certain advantages to opening up analytical techniques to many more researchers, with sensors and portable devices. But there's a big gap between the cutting edge and the truly accessible – and this middle ground must not become an open but confused playing field.

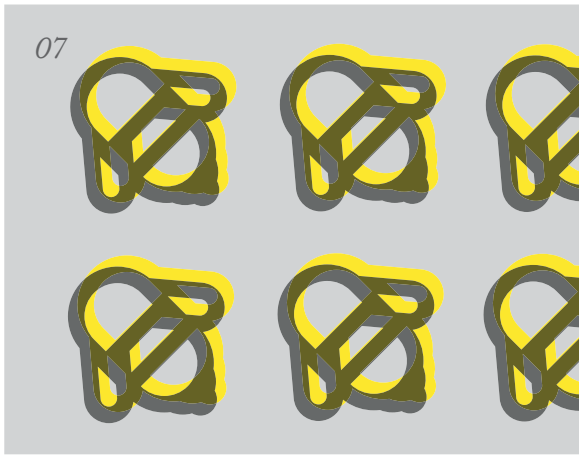
Education is key. But as Gert Desmet and Deirdre Cabooter discuss on page 12, some universities are in danger of focusing too heavily on chromatography application at the expense of chromatography fundamentals. Could this leave students ill-equipped to tackle new problems, to adopt the latest tools and techniques, or to become instrument innovators in their own right?

If this year's Innovation Awards (page 16) are anything to go by, the cutting (or bleeding) edge will always deliver exciting but, almost by definition, less mature instruments and technologies. Will the next generation of analytical scientists have the skills and knowledge to apply – and, perhaps more importantly, critically assess – these new tools?

One thing's for certain, I couldn't command any of this year's Innovation Award winners to any utterance of harmony – so we are firmly in instrument territory!

James Strachan
Editor

Contents



On The Cover

It's the return of our annual Innovation Awards. See who made the cut on page 16

Upfront

In My View

Feature

Core Topics

Sitting Down With

the Analytical Scientist

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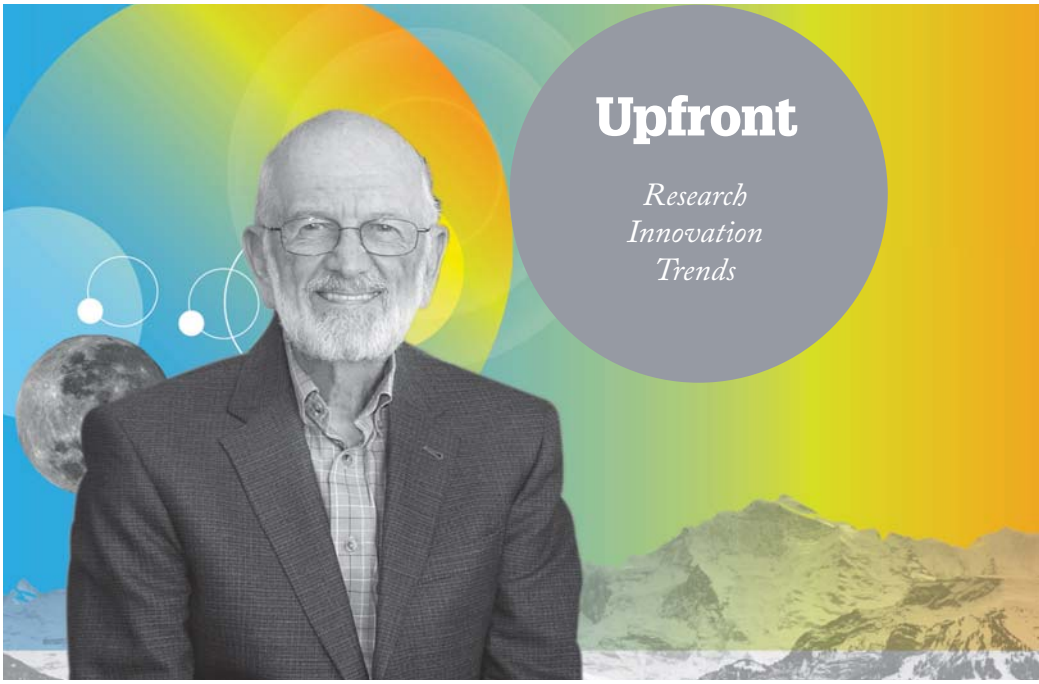

Life On the Margin

Have we identified the chemistry behind the origins of life?

Graham Cooks recently made one of the most important discoveries of his long and illustrious career: water isn't wet – at least not everywhere. Let's take a step back – a big step back to the beginning of life itself. Scientists have theorized that life on Earth began in the oceans and involved amino acids delivered to earth by meteorites. But to form peptides, the chemistry requires the loss of a water molecule – which is unlikely in, well, water.

Cooks and his Purdue colleagues generated aqueous droplets containing two amino acids using nano-electrospray ionization, which they monitored with mass spec. On the margins, where the water droplets meet the atmosphere, they found incredibly rapid peptide-forming reactions taking place – a hundred to a million times faster than the same chemicals reacting in bulk solution. The researchers were able to demonstrate, for the first time, that simple amino acids spontaneously form peptides, the building blocks of life, in droplets of water (1,2).

The speed of the reactions means that catalysts are unnecessary and could explain how life arose from abiotic chemistry. Understanding exactly how this process works has been the goal of years of scientific research – and may now inform the search for life on other planets.

"This is a dramatic discovery – essentially the chemistry behind the origin of life," says Cooks, who also hints at major implications for the chemistry field as a whole. "It could be that all of prebiotic major biochemistry, including making peptides, proteins, and ligand nucleotide RNA is microdroplet chemistry," he says. "I think that accelerated reactions in microdroplets will become a very significant field of science."

References

1. *D Holden et al., PNAS, 119, 42 (2022). DOI: 10.1073/pnas.2212642119*
2. *Purdue University (2022). Available at: https://bit.ly/3AqHWqP*

Speedy Dilute-and-Shoot

Liquid chromatography-tandem mass spectrometry assay rapidly quantifies cannabis metabolites in human urine

With cannabis one of the most commonly used psychoactive substances, researchers are constantly looking for new testing methods. In a recent study, researchers from the University of Rochester Medical Center, New York, USA, have developed a liquid chromatography-tandem mass spectrometry assay that quantifies cannabis metabolites THC-COOH and THC-COO in human urine.

The assay uses a direct "dilute-and-shoot" approach – in which urine samples are diluted 10 times before being directly injected onto the liquid chromatography and mass spectrometer – to simplify the sample preparation process and improve overall throughput. The turnaround time was five minutes, a significant improvement over existing dilute-and-shoot assays that typically take 20 minutes.

"This method can be easily implemented and has great potential to be routinely performed in any high-throughput clinical laboratory setting," the authors wrote (1).

Reference

1. *BL Young, YV Zhang, J Chromatogr B Analyt Technol Biomed Life Sci, 1211, 123495 (2022). DOI: 10.1016/j.jchromb.2022.123495.*

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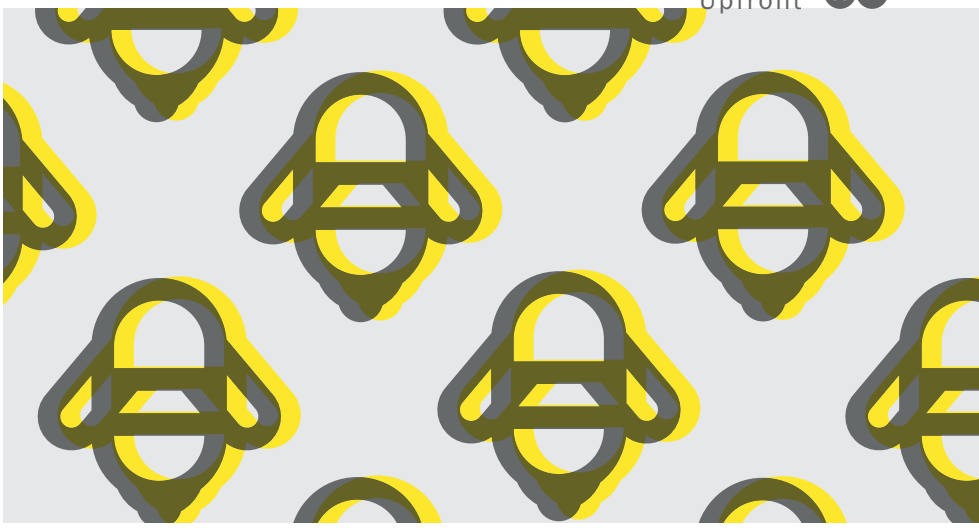
To Bee or Not to Bee

How proteomics is helping reveal the mechanism of mite resistance in honey bees



The European honey bee is susceptible to a mite with a rather frightening name: Varroa destructor. On the other hand, Eastern honey bees and African honey bees are naturally resistant to this parasite. But why? And given the crucial role that honey bees play in both ecosystem stability and human food production, can we intervene?

An international team from China, Ethiopia, and the US decided to dig into the biology at play, exposing half of each species to mites and then used tandem mass spectrometry to gather proteome profiles, identifying almost 2,000 proteins in the process. When comparing bee cohorts, the researchers found variation between those they had exposed to the mites and those they had not (1). And the two resistant bee species showed a significant increase of those proteins involved in immune responses and detoxification.

The authors plan to further examine the specific proteins involved and ultimately hope that beekeepers will be able to use this information to breed naturally resistant bees.

Reference

1. *Y Fang et al., Mol Cell Proteom, 21 (2022). DOI: 10.1016/j.mcpro.2022.100257*

Four Become One: Simplifying mRNA Analysis

A collaboration between Tosoh and Axolabs simplifies lipid nanoparticle mRNA vaccine analysis – condensing several techniques into a single method

With Stephan Seiffert and Jonas Wege

Why is there so much excitement about mRNA and lipid nanoparticles?

Jonas Wege, Application Specialist at Tosoh Bioscience: I don't think there's much doubt that the COVID-19 pandemic showed how powerful mRNA therapeutics can be. Moreover, they are versatile, easy to adapt – once you have an established platform – and relatively cost effective to produce. All of these aspects are essential when handling a pandemic. Compared with alternative approaches, I also think mRNA and LNPs are easy to manage. Of course, there are some challenges with the use of lipid nanoparticles (LNPs) – especially regarding quality control and characterization of the particles – but these are the challenges we sought to address with this collaboration.

Stephan Seiffert, Team Leader at Axolabs: I'll add that the success of the two vaccines from BioNTech and Moderna led to an explosion of the field! Most pharma companies have invested heavily in mRNA technology and many have invested in manufacturing capabilities for mRNAs and LNP production. The pandemic has spurred additional research into new LNP formulations (including new proprietary lipids – the major building blocks of LNPs) and into using mRNA as a therapeutic modality for other illnesses, such as cancer.

For those who don't live and breathe mRNA therapeutics, I should also add a little detail around the importance of LNPs. mRNA is a fairly volatile molecule and needs to be stabilized by a carrier system to be effectively administered to patients. LNPs serve as stabilizing vehicles that enable the transport of mRNA into the cells and the cytoplasm. Without a delivery vehicle, the mRNA (the active pharmaceutical ingredient) cannot cross the cell membrane and would be ineffective because of rapid degradation.

What methods are typically used to analyze mRNA and LNPs?

Jonas: There are a plethora of methods used to fully characterize an LNP mixture. The first method is visual inspection – observing the sample, making sure there is no visible debris! Another fairly common technique is dynamic light scattering (DLS), which is used to determine particle size and polydispersity.

Other techniques are used to assess lipid concentration, drug concentration, and drug encapsulation efficiency. Essentially, we need to know how well the mRNA has been incorporated into the LNPs – how much free mRNA might be in the mixture and how many empty LNPs might be present.

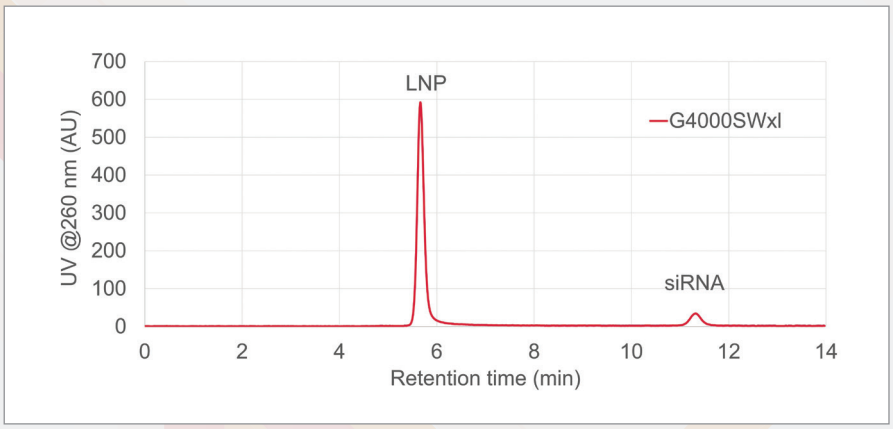
Overall, there are six or seven different analytical techniques that are used to fully characterize an LNP mixture.

Stephan: In addition to the techniques Jonas mentioned, differential scanning calorimetry (DSC) is used to study the stability of LNPs. High-performance liquid chromatography (HPLC) with a charged aerosol detector (CAD) or multi-angle light scattering (MALS) detection are also commonly used to study the LNP forming lipids and their composition and relationship to each other. LC-mass spectrometry (LC-MS) can also be used to study various analytical properties of mRNA molecules, such as five-prime cap and poly(A) tail.

What are the limitations with these methods?

Jonas: In my opinion, the biggest disadvantage is the sheer number of different techniques required to fully characterize LNPs – and we wanted to address this limitation with the collaboration. These methods can be very time consuming – and it's clear that people in manufacturing and quality control would benefit from the ability to determine more characteristics of LNPs using fewer methods, thus streamlining lab processes.

Stephan: Currently, the size and polydispersity of the mRNA poly(A) tail can only be reliably quantified up to a certain length. Furthermore, because of the large size of intact mRNA, electrospray ionization-mass spectrometry (ESI-MS) is not a suitable option for its detection. To allow characterization, the mRNA must be broken



down into smaller fragments – which, once again, takes time and is not particularly easy. And as with any chromatographic technique, resolution can always be an issue.

As Jonas mentioned, mRNA analytics can be time consuming and may require automated procedures, which are usually difficult to implement. In the past, it has also been difficult to distinguish filled LNP particles from empty particles, which can be associated with safety concerns.

All of these challenges informed the objectives of the collaboration between Tosoh and Axolabs!

And how are Tosoh and Axolabs working together?

Stephan: In short, Axolabs provided Tosoh with LNPs for studies using its new size exclusion chromatography-MALS detector. And new columns developed at Tosoh were tested at Axolabs to evaluate their potential for current analytical challenges in mRNA and LNP analysis.

Jonas: As mentioned earlier, our overall goal was to develop a simple method that condensed numerous analytical techniques into one method. Indeed, we've been working very closely together on a more standardized approach to characterize LNPs – so Axolab's LNPs have been essential!

Using our SEC-MALS detector, we were able to measure particle size, dispersity index, lipid concentration, drug concentration, and drug encapsulation efficiency. Previously, we would have needed at least four different techniques to get these measurements – now, we're able to get all this data from a single injection on an SEC column. Not only is this much simpler, but it is also less time consuming; the analysis takes about an hour or so, including the calibration of the detector.

What impact could these new methods have on mRNA therapy development?

Stephan: Critical quality attributes of mRNA molecules can now be assessed rapidly and efficiently, which will enable safer medication in the long run (side effects become less likely with increased purity). Moreover, a stable and reliable method that allows quick analysis and characterization of an established product will really help in quality control, potentially helping companies ramp up productivity – and thereby saving money.

What expertise did Tosoh and Axolabs bring to the project – and why was collaboration so important?

Stephan: Axolabs has over 20 years of experience in the field of oligo-nucleotide research and development, allowing us to build on an unparalleled knowledge base. On the other hand, Tosoh is a renowned supplier of columns for chromatography – and there is an undeniably strong need for columns with consistent quality in the field of biopharmaceutical analytics! Tosoh also brings SEC-MALS technology and long-standing expertise in the field of SEC chromatography for a wide range of applications for large molecules and formulations.

In short, much like Axolabs, Tosoh is known for innovation and is open to exploring new fields!

Jonas: At Tosoh, we did not have ready access to LNPs – and it was very important for us to find the right specialist partner; specifically, we needed a reliable company that could supply high-quality LNPs. To cut a long story short, we recognized that Axolabs – an expert in LNPs – was such a partner!

Collaboration is always important, but I believe it is vital in this specific area of research. In such a specialized area, no single one company can be expected to have answers to all the questions. Joining forces with other renowned experts is a fantastic way of producing relevant data that ultimately helps the whole field move forward.

Working with Axolabs, we've been able to show that our SEC-MALS detector not only streamlines lab processes, but also offers improved sensitivity and increased versatility. Notably, we did not find any similar methods in existing literature, so I think it's safe to describe our approach to characterizing LNPs as innovative!

Stephan Seiffert studied Chemistry in Regensburg, Germany, and joined Alnylam Europe 2004 as a scientist in the Analytics group. He is now team leader at Axolabs, responsible for 12 employees, in non-regulated analytics. He has more than 18 years extensive experience with high-performance liquid chromatography (HPLC) and mass spectrometry (MS), as well as various techniques that support the characterization of oligonucleotides, including mRNA.

Jonas Wege graduated from Karlsruhe Institute of Technology, Karlsruhe, Germany, with a major in biotechnology and biopharmaceutical process engineering. Today, he works as an Application Specialist at Tosoh Bioscience, Griesheim, Germany. His work includes application development for process resins, HPLC columns and Tosoh's instruments – as well as technical support.

In My View

Experts from across the world share a single strongly held opinion or key idea.

Out with the Old, In with the New

How can we change the way we communicate to build public trust, dispel stereotypes, and encourage more young people to choose science?

By Mimi den Uijl, PhD Candidate, University of Amsterdam, Amsterdam, The Netherlands

Communicating our science is vitally important – and how we communicate it is even more so. Currently, the scientific community often favors "traditional" approaches to communication – such as presentations and posters – and does not use the full potential of the tools unleashed by the digital revolution.

For academia to stay connected to the science performed in industry, we need to explore new methods of science communication – including infographics, videos, or even podcasts. Thankfully, conferences are now creating more and more room for this kind of communication through video contests, pitch competitions, or even open assignments in which candidates are free to share their science in their own way – the HPLC Separation Science Slam being a good example.

Unfortunately, few students actually commit to these assignments. Should we conclude from this that the new generation of scientists isn't ready for change? I don't think so – for multiple reasons. Early-career scientists are encouraged by their supervisors to present their work in posters or presentations and often have limited knowledge of the possibilities inherent in these new forms of communication. It also takes a considerable amount of time to prepare both a poster and a pitch or video, and supervisors may perceive this effort as "duplicated" or even "wasted." Simply put, the current generation of students has not been encouraged to use new communication methods.

In my 10 years at university, I was never challenged to think outside the box when it came to communicating science within the field. Implementing new approaches to communication in undergraduate courses could stimulate creativity, which could lead to more scientific innovation down the line.

In March 2020, we all experienced a seismic shift in science communication due to the COVID-19 pandemic. With the bulk of science communication migrating online, new methods suddenly became more accepted. Online platforms such as LinkedIn started to play a bigger role in connecting scientists with colleagues in the field. Fast forward to 2022 and we can still see the evidence of this sudden shift – and of researchers' subsequent realization that new methods of communication desperately need a place in the scientific world.

Despite these positive outcomes, the COVID-19 pandemic also increased the public's distrust in science – which could be attributed to (among other things) the communication from academia to the public. With minimal interaction, scientists are often perceived as living in an "ivory tower" and lacking humanity. Science needs to be fun. It needs to be engaging. And, most importantly, it needs to be accessible. If the public – especially its youngest members – are on Instagram, TikTok, or YouTube, then scientists also need to be on those platforms.

Unfortunately, I believe the way we communicate science to the public has also resulted in stereotyping. Many people picture scientists as old, white, and male. It reduces diversity in all layers, from aspiring students to full professors, because the "ideal" scientist is always portrayed in a certain way. The resulting feeling of "not belonging" may be one reason young people overlook science as a potential career path.

Furthermore, I believe current students

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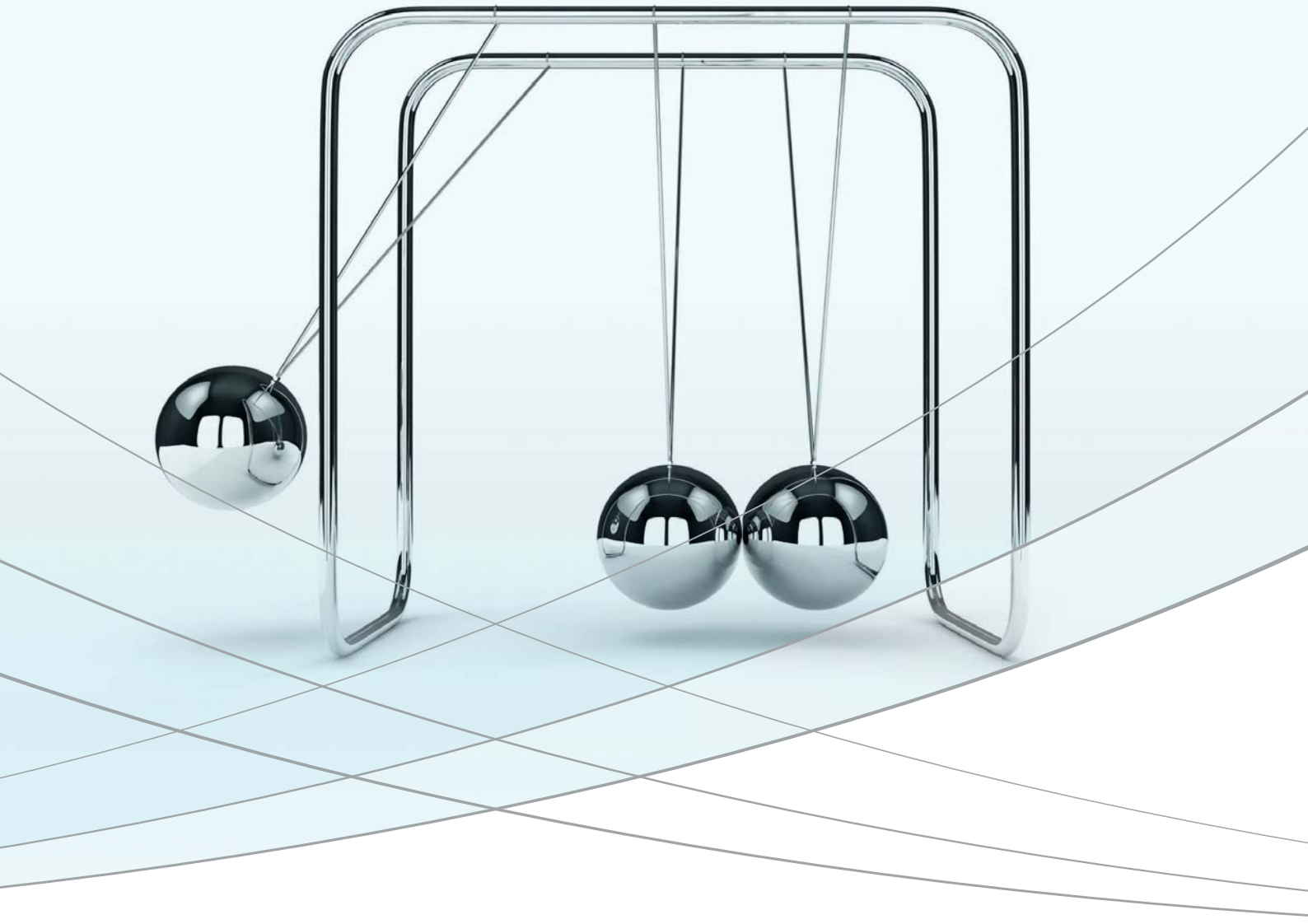

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are under the impression that science studies offer a poor career outlook. When I was a high school student, we used to say that with a bachelor's in law or economics we could "still become anything" and not limit our future options. In retrospect, I could not agree less. Where is the logic in that? And why could you not still "be anything" if you were to pursue chemistry or physics? I truly believe there is a disconnect between what people think "science" is and its real-world impacts. By better communicating science and showing its influence on our society, students will hopefully become aware of the countless possibilities it offers.

Because the world is not equally exposed to role models from all fields, we as scientists have a duty to spread our stories to the public. Communication is a crucial part of being a scientist and, in my opinion, we should enhance people's skills in that arena at every level of their education.

During my PhD, I began looking for new ways to communicate my science. I discussed many of the problems described here with my dear colleagues Noor Abdulhussain and Lotte Schreuders. The outcome? We decided to create an Instagram channel about our life at university – Sisters in Science NL. Our slogan eventually became, "If you can see it, you can be it."

One thing led to another. Since then, we have appeared on national television twice, on the radio once, performed in a theater show, and shared our story about finding a fast, fun, exciting, and creative way to communicate science in a variety of interviews and podcasts. With Sisters in Science, we hope to make an impact on three different levels. First, by making ourselves visible to the public, we hope to break the vicious cycle of scientist stereotyping. Second, we aim to show the current generation of students that they can become scientists, even if they don't initially feel that they belong in the scientific world. Finally, we hope to show future generations that they too can be scientists. Academia is a privileged place – a locked door to which many feel they do not hold a key. With our initiative, we hope to remove these barriers.

When we started Sisters in Science, we were unsure of the scientific community's reaction. However, in December 2021 we were granted the Diversity Initiative Award by the Dutch Research Council – a clear indication that what we are doing benefits science as a whole. Still not convinced? Think about this: a brilliant scientist may perform fantastic research, publish important papers, or even win a Nobel prize – but a brilliant science communicator may inspire thousands of children, motivate many early-career scientists, and generate an army of change-makers.

Curious Minds

Curiosity drives learning – but how can separation scientists translate this into effective teaching strategies?

By Gert Desmet, Full Professor, Vrije Universiteit Brussel, and Deirdre Cabooter, Professor, University of Leuven, Belgium

There's a common saying: "Involve me and I will learn." But the truth is that it can be difficult to leverage student curiosity prior to the PhD level. In BSc or MSc stages, we often don't have the time to set up intriguing lab work for all the different classes we teach in separation science. And chromatography instruments are expensive – so in our basic courses we are limited to one instrument for every 5 to 10 students. That hampers hands-on involvement, which in effect means there's no outlet for student curiosity.

In our experience, basic courses such as general analytical chemistry are perceived as boring by many first-year students. It gets better when we start teaching actual chromatography, which is where the coursework becomes more obviously applied – but that comes later. In the meantime, if you're faced with the challenge of first-year analytical chemistry, you can try to make it more interesting by giving examples of how the concepts you are explaining and the experimental tools you are demonstrating are used in real life. The idea is to continually make a link to current challenges and provide glimpses of the future so that students understand why analytical chemistry techniques are necessary and how they are actually applied. This helps bring home to the students that their future careers rely on a firm understanding of the basics.

But even that is a passive way of learning. If we really want students to be curiosity-driven, we must allow them to explore things themselves. Give them a problem and let them develop solutions independently. Unfortunately, for chromatography this is only possible at the PhD level, where the number of instruments roughly matches the number of students. Another issue that compromises undergraduate courses in analytical chemistry is that chromatography

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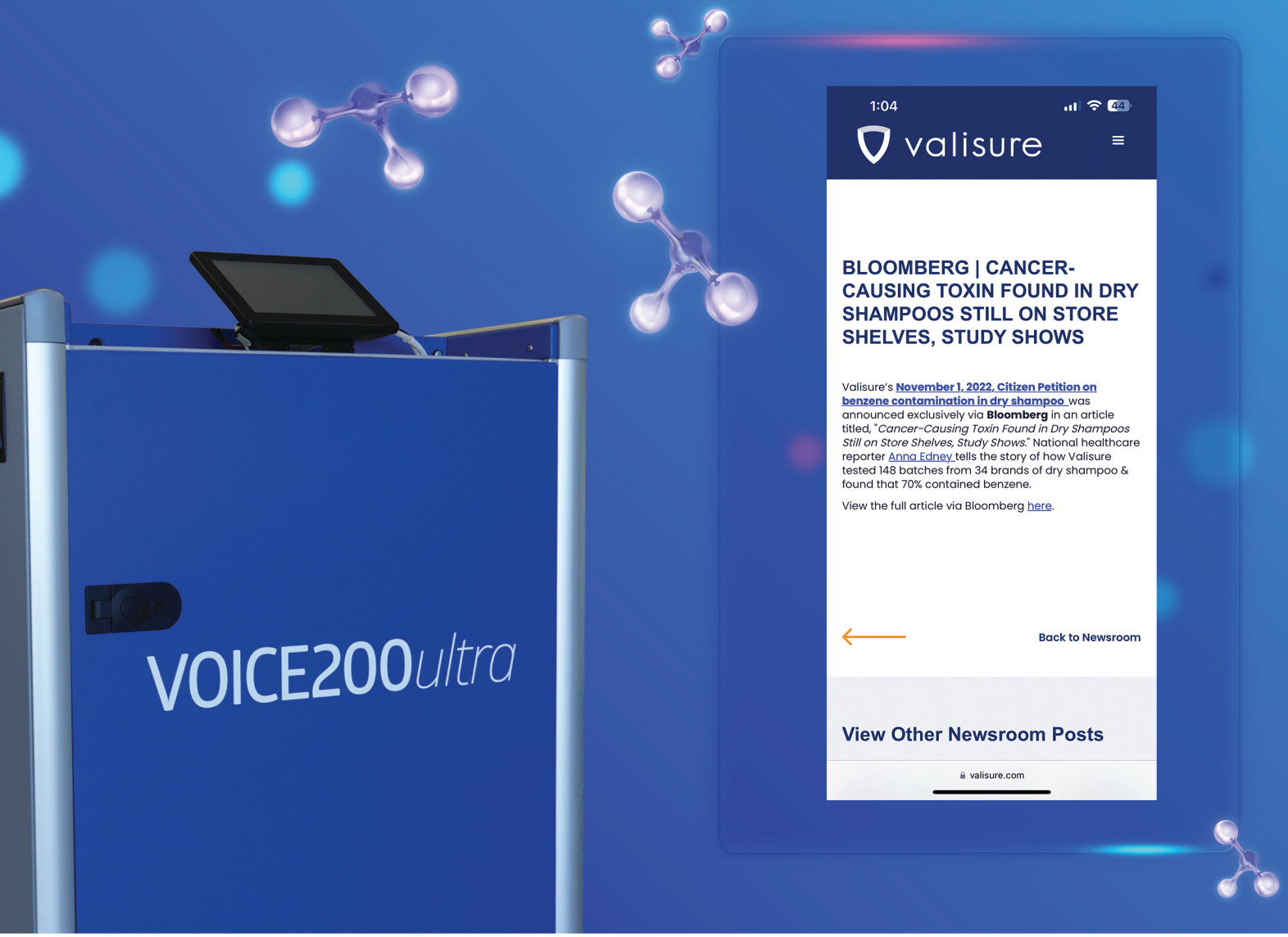

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"We should focus on teaching students the basics so that they are well equipped to later address real-world applications."

is increasingly taught as just one of many chemical analysis methods; dedicated separation science courses hardly exist anymore. This is probably a consequence of funding patterns – it is now easier to get grant money for applied research than for fundamental research, so basic research groups have transformed into applied research groups. That's why we have departments for toxicology or biopharmaceutical analysis, for example, instead of pure analytical chemistry departments.

You see the same pattern in pharmacy departments; here, too, separation sciences are downplayed in favor of biotechnology, especially since the onset of the pandemic. The real shame is that the time stolen from separation sciences is often given to the development of soft skills, such as presentation techniques. In our view, it's a mistake to put resources into developing these skills at the cost of ending up deficient in key fundamentals. People can always pick up soft skills later, or have already acquired them during high school, but making up for missed opportunities to acquire fundamental techniques is not so easy.

We should focus on teaching students the basics so that they are well-equipped to later address real-world applications. We should be sending them into the world with a reliable skillset; instead, we're just teaching them selected ways chromatography is used. Their fundamental instruction is curtailed and the result is that they might never really understand the technology. Unfortunately, this reflects a general trend to simplify undergraduate courses – in the engineering faculty, for example, "difficult" subjects, such as mathematics, have been decreasing in size over the past 20 years. The more challenging subjects in pharmacy courses also have been dropped. Bluntly, it's also about the money – universities are partly funded according to the number of degrees they issue, so they are under pressure to record high pass rates. The more difficult modules, which require more investment from students, are simply not compatible with this driver and in some faculties this has led to a reduction of the number of hours devoted to the "hard" courses.

Given the constraints that now apply to today's science courses and restrict teaching, it is even more essential to develop ways to motivate students. How might we do this? We believe it is vital to be enthusiastic. Try to show students not only the real-world applications of what you're teaching, but also your passion for the techniques and their applied impact. Do that and you can drag your students with you! Above all, don't be the kind of teacher that just sits at the front of the class and reads out of a course handbook – be animated, driven, and passionate! It makes a huge difference. That's also important for postgraduate students, by the way – they, too, may need encouragement and motivation.

It's true that some students are more difficult to motivate than others – for example, those who are just doing the course because their parents want them to get a degree! Naturally, it's easier to teach ambitious, self-driven students who have the will to grapple with the harder topics. Nevertheless, one motivation tactic that may help with even reluctant learners is to emphasize that industry values the skills taught in separation science and that separation scientists will have many job opportunities to choose from.

We can also remind them that a good understanding of the basics is essential to any career in separation science. Without this, you cannot maximize process efficiency, something many students do not appreciate. Standard questions asked during a PhD defense may include, "Why did you pick this flow rate, or this gradient, or this column?" Usually, the students haven't even considered these questions; they copied what the PhD student working on the project before them was doing, and have little understanding of what is happening at the methodological level. This unquestioning approach – this lack of curiosity – is a consequence of failure to achieve an understanding of the basics. It's such a pity!

But it's not only a lack of curiosity, it's also a lack of competitive drive – a lack of desire to be the best. This can manifest itself in mental laziness; for example, people put a new kind of column into an existing system without thinking through the compatibility issues and then not understand why they don't get the promised separation performance. Again, it's so important to understand the basics. If you don't, things can go horribly wrong; in the best case, wasting valuable time, and in the worst case, failing to detect dangerous impurities.

Overall, to motivate students – including those who may be a little less ambitious or curiosity-driven than we would like – we ourselves must set a good example. Just ensuring you are always the first one to arrive in the morning can make a difference. In other words, the general has to be in the front line! In addition, exposing students to conferences and industry can be tremendously helpful – it gives them context and shows them that their work is worth the effort.

Students need experience-based learning mediated by enthusiastic teachers and backed up with examples of real-world applications. Above all, we must persuade them of the importance of understanding the key fundamental principles of separation science!

Supporting Chromatography Everywhere – Even Mars

DataApex founder and general manager Jan Hrubý explains how a combination of serendipity and a spike of post-communist innovation led to the birth of company that spent 30 years perfecting data acquisition, processing, and instrument control software to give us Clarity

Tell us about the genesis of DataApex…

I was born and raised in communist Czechoslovakia, which was occupied by the Soviet army until I turned four. My great love and hobby since childhood was electronics and later computers, which I eventually studied at university in the 1980s – though I never actually saw a computer with my own eyes the whole time! Immediately after the fall of communism in 1989, my friends and I started thinking about starting a business.

But I suppose it was my then mother-in-law who was really responsible for founding DataApex. She was an excellent scientist, but her instrumentation was limited. In the early 1990s, she asked me if I could build a better integrator for her – in other words, a tool for measuring and evaluating chromatograms.

Sometimes things come together at the right time in the right place. My best friend – an excellent programmer – was studying for his PhD at the University of Science and Technology, Czech Republic, and his friend was writing his thesis on modern integration algorithms at the same time. So, a decision was made, and six months later we handed over to my mother-in-law the first working version of the PC software, including our own A/D converter.

What challenges did you face starting a software company from scratch in those times?

There were many challenges; where should I start? First, a computer in the early 1990s cost about 10–20 monthly salaries; we couldn't afford to buy one, so we took turns using one at the university. Second, A/D converter parts were also pricey (for us), so we had to visit the electronic bazaars in Munich to drive down the cost. Third, because private business was forbidden in Czechoslovakia for 40 years until 1989, we didn't have many mentors to learn from. The list is long but, fortunately, we were young and full of optimism about the freedom we had gained, so we embraced all the challenges!

Tell us about your chromatography software, Clarity, and the company culture…

I can say with some satisfaction that Clarity is a mature product after thirty years of development. The current generation – our third iteration – speaks six languages, runs over 1,000 chromatography instruments across almost every manufacturer around the world, and is sold in more than 100 countries.

Though we are a single product company, we have several variants of Clarity that cover the needs of diverse customers; we have simple and affordable software for legacy chromatographs (it is often impossible to find original software), an educational version for universities, and more sophisticated solutions for tightly regulated markets and GC/LC-MS instruments, for instance. But all variants share one thing in common: they are reliable and easy to use.

And because we're a single product company, all staff are united by a singular focus, which results in a family-like atmosphere and a level of dedication that is otherwise hard to cultivate. As a result, our customers are often surprised by how quickly our support team reacts – sometimes they ask if our support colleagues get any sleep. (Yes, they do!).

Finally, our chromatography instrument manufacturer partners know and trust that we are – and want to continue to be – an independent and vendor-neutral company.

Where can people find out more?

Our company policy is very open and virtually all information is available on our website (dataapex.com). We post all news on social media, especially on LinkedIn, and there are dozens of short tutorial videos and brief video tips and tricks available on YouTube, for example. We have an extensive network of trained distributors all over the world. We also offer demos or free trial versions.

What are your hopes for the field – and for DataApex?

I long for a unified communication interface for all analytical instruments that is independent of manufacturers and available to all – as well as a uniform analytical data format for easy exchange and sharing among software platforms. Everyone in the industry is calling for both – but, for many reasons (some obvious and some unclear), neither are forthcoming.

Finally (and mainly), I dream of delivering Clarity to a lab on Mars!

the Analytical Scientist

INNOVATION AWARDS

INNOVATION ABOUND!

Introducing the best analytical technology, software, and instruments of 2022

15

LUCIDITY GC-FID

With changeable column cartridges, Lucidity aims to bring GC-FID to the masses

Produced by Lucidity Systems

One of the biggest pains with conventional gas chromatography (GC) instruments is installing and removing columns. The Lucidity GC-FID (flame ionization detection) aims to make installing and removing standard GC columns like changing a video game cartridge, while also eliminating potential user error that can lead to small leaks or incorrect positioning of the column ends, which affects results.

Potential impact

With the Lucidity GC-FID's small size and changeable column cartridges, Lucidity hopes GC-FID – which has been used in many chemical and industrial applications – will become an option for many more labs.

What the judges say…

"Interesting premise, may be impactful!"

THERMO SCIENTIFIC µPAC NEO HPLC COLUMN

Bringing improved column-to-column reproducibility and better protein identification to proteomics

Produced by Thermo Fisher Scientific

The Thermo Scientific µPAC Neo HPLC Column promises strong separation performance over a wide range of flow rates. And due to the way they're fabricated, µPAC columns should avoid sample-related column failure and be able to withstand more sample injections without losing performance – delivering column-to-column consistency and extended column lifetime relative to packed-bed column alternatives.

Potential impact

Proteomics researchers are demanding ever-greater sample coverage and improved protein identification to advance their research. At the same time, such studies require multiple columns, which makes consistent performance key. With its separation capabilities, column-to-column reproducibility, and simplified cross-column data processing, Thermo Fisher Scientific is confident the µPAC Neo HPLC Column will enable laboratories to identify a greater number of proteins and peptides in their proteomics experiments.

What the judges say…

"Rarely do we see such a step change in analytical performance as what the µPAC Neo HPLC columns deliver. This product substantially enhances separation performance and reproducibility, democratizing high performance proteomic separations across the research community."

14

13

HYDROINERT

A GC-MS source optimized for hydrogen carrier gas

Produced by Agilent Technologies, Inc.

Due to the global helium shortage and concerns over sustainability, many organizations are looking for an alternative carrier gas, such as hydrogen, which is relatively low cost and renewable. Traditionally, the problem with hydrogen for GC-MS and GC-MS/MS analyses is hydrogenation. But the HydroInert source improves chromatographic efficiencies with hydrogen, allowing labs to achieve faster separations with better peaks and reduced spectral anomalies.

Potential impact

With its spectral fidelity, even for compounds highly susceptible to hydrogenation, and high-boiler peak shape, especially for PAHs, Agilent hopes the HydroInert source – alongside their 5977C GC/MSD system – will open the door for more organizations to make the switch away from helium to hydrogen.

What the judges say…

"This innovation focuses on long term sustainability – the finite and dwindling supply of helium gas!"

12

CHROMATOF SYNC

Full peak finding statistical software for GC-MS sample sets

Produced by LECO Corporation

ChromaTOF Sync is a data processing tool designed to address the lack of tools for non-targeted discovery work for GC-MS sample sets. Sync adds statistical analysis capabilities to ChromaTOF's deconvolution algorithms, enabling full peak finding for sets of samples.

Potential impact

Non-targeted discovery is used to figure out what you didn't know was in your sample – and then identify it. ChromaTOF Sync is designed to speed up this process with software that understands data inputs, highlights statistically significant similarities and differences, and processes and sorts sets of data faster than a human researcher could. The idea is to give laboratories directions and leads to pursue – freeing up resources for the identification and explanation of unknown targets.

What the judges say…

"This nice software looks to help improve deconvolution for GC-MS – a vital part of the metabolomics pipeline for identification of unknown small molecules."

11

OMNITRAP

A novel linear ion trap for multidimensional multiple-stage tandem MS

Produced by Fasmatech

The Omnitrap is a novel linear ion trap designed to support multidimensional multiple-stage tandem ion processing workflows for in-depth, top-down characterization of proteins and DNA molecules. The enhanced performance is enabled by dynamically incorporating the entire range of ion activation methods into a single platform.

Potential impact

The Omnitrap is currently used for in-depth characterization of intact antibodies. And due to its ability to perform fast electron-based activation reactions on liquid chromatographic time-scales, may be deployed in bottom-up proteomics and in other application areas involving the analysis of low charge state ions, such as metabolomics, lipidomics, glycomics, and so on.

What the judges say…

"This could be very helpful and expand access to complex proteomics experiments."

ZENO SWATH DIA

This mass spec-based tool aids researchers in the discovery of potential clinical biomarkers and new therapies

Produced by SCIEX

By combining the ZenoTOF 7600 system with the new Zeno SWATH Data Independent Acquisition (DIA), researchers can detect and quantify up to double the number of cell and plasma proteins. Sample loads can start at 10 ng with runtimes shortened to ~5 mins, allowing large-scale biomarker studies to run as routine projects in a matter of weeks, without compromising the depth of proteome coverage.

Potential impact

According to SCIEX, Zeno SWATH DIA helps researchers discover potential biomarkers for diagnostic tests and new therapy targets, as well as aiding in the development of next-generation therapies such as gene-editing by allowing researchers to characterize off-target effects with greater sensitivity and reliability.

What the judges say…

"SWATH has excited the proteomics field and this latest addition from SCIEX looks to improve proteomics workflows."

10

TOTAL CORRELATION MASS SPECTROMETRY

MS/MS data for every precursor ion in a complex sample without the need for separation

Produced by Verdel Instruments

Total Correlation Mass Spectrometry (TOC-MS) is a new approach to MS that enables true data independent analysis (DIA) by providing MS/MS data for every precursor ion in a complex sample. This approach eliminates the need to separate analytes prior to fragmentation, removing the dependency on chromatography and quadrupole isolation, thus increasing the speed of analysis.

Potential impact

Verdel believes that any sector working with complex samples stands to benefit. For example, in the lipidomics field, TOC-MS enables the precise identification of the head group and fatty acid chains, and the location of the double bonds, meaning that multiple lipids can be detected and analyzed simultaneously; in short, a detailed lipidome profile using a single analytical technique. Other fields could include proteomics, wastewater based epidemiology, defense/security, and the pharmaceutical and biotechnology industries.

What the judges say…

"A novel approach to data independent analysis within MS/MS. This is essential for metabolite identification and especially lipids."

8

INLUX SEM RAMAN INTERFACE

A universal solution for in situ scanning electron microscope Raman analysis

Produced by Renishaw PLC

The Renishaw inLux scanning electron microscope (SEM) Raman interface can be added to a range of SEM microscopes and allows users to collect Raman spectra that can produce detailed chemical images whilst simultaneously imaging in the SEM. With the inLux interface, users can collect spectra from single points, multiple points, or generate 2D and 3D confocal Raman images to correlate to SEM micrographs. Overall, the system can analyze areas larger than 0.5 mm in each axis and features encoded position control down to 50 nm.

Potential impact

The inLux SEM Raman interface aims to help researchers expand their SEM analysis and produce richer data. The addition of chemical information to complement SEM images opens up a range of applications – from industrial contamination identification to academic research – and increases the power of both Raman and SEM.

What the judges say…

"Interesting coupling of imaging modalities – could be impactful!"

7

THERMO SCIENTIFIC ORBITRAP ASCEND TRIBRID

Thermo builds upon the Tribrid platform with a new mass spectrometer designed for challenging analytes

Produced by Thermo Fisher Scientific

The Thermo Scientific Orbitrap Ascend Tribrid mass spectrometer builds upon the Tribrid architecture to enable single-cell sensitivity for proteomics and metabolomics while also analyzing macromolecules – all on the one platform. New features include: an extended mass range of up to 16,000 m/z, two ion routing multipoles allowing users to analyze more samples at lower concentrations, and a new "Auto-Ready" ion source.

Potential impact

The Orbitrap Ascend Tribrid mass spectrometer aims to overcome many of the challenges associated with multiplexed proteomics and native protein characterization, such as insufficient sample throughput, a lack of sensitivity for single and rare cell populations, and a scan range insufficient to detect macromolecules.

What the judges say…

"This system promises to deliver a multitude of scientific discoveries for researchers looking to push the boundaries of chemical analysis in a wide range of applications."

"This mass spectrometer builds upon the proven Tribrid platform, which has improved metabolomics workflows. One to look out for!"

6

AUTOMATED TOTAL NITROSAMINES ANALYSER

A system to rapidly analyze a sample's total (carcinogenic) nitrosamine content

Produced by Ellutia

Nitrosamines are carcinogenic compounds that can be found and formed in many products, and their presence has been a particular issue in the pharmaceutical industry of late. Traditional approaches to the analysis, such as by mass spec, have been challenged by the low detection levels required. Ellutia's system combines chemical reaction targeting of nitrosamine compounds with a highly selective and sensitive detector to give a single result for the total nitrosamine content.

Potential impact

This system helps alleviate the nitrosamine bottleneck in the pharma industry by rapidly screening almost any sample type for nitrosamine content. Because both volatile and non-volatile nitrosamines are measured concurrently, only positive samples need passing to more time-consuming speciated analysis. And though the current focus of nitrosamine analysis is on the pharmaceutical industry, other sectors, such as medical materials or implants, may be affected in the future.

What the judges say…

"There is a need to measure nitrosamine compounds in pharmaceuticals as they are potentially carcinogenic. This fills this gap nicely."

"Important technology for the safety of pharmaceuticals – and possibly more in the future – while yielding a reduction of analysis costs."

RNA 9000 PURITY AND INTEGRITY KIT

Addressing key analytical challenges in the characterization of RNA-based therapeutics

Produced by SCIEX

This RNA 9000 Purity and Integrity Kit integrates with the BioPhase 8800 system and PA 800 Plus system to overcome traditional issues of low resolution and poor transferability in RNA analysis. Kits are applicable from 50 to 9,000 bases and can be used for final product quality control to assess quality and length post nanoparticle or viral vector encapsulation, as well as during early-stage development immediately following IVT (in-vitro transcription) to ensure the integrity and size of mRNA payloads.

5

Potential impact

RNA integrity and purity analysis is critical to the efficacy of RNA-based therapeutics and vaccines, but scientists have faced poor resolution, method transferability issues, and the need for multiple methods and platforms. The RNA 9000 Purity and Integrity Kit aims to overcome these issues, and thus help accelerate RNA-based medicine development.

What the judges say…

"RNA-based therapeutics represent an incredibly important tool for public health – as the recent pandemic has exposed – and this kit offers a reliable workflow for addressing key analytical challenges in the characterization of these compounds"

"Innovations like this are needed to push mRNA therapeutics forward."

4

HAVOC

An automated mass spectrometry-based sensory system for volatile organic compounds

Produced by Plasmion GmbH

Many labs have struggled with in-line process control of volatile organic compounds (VOCs) due to instrument and sample preparation costs. HaVoc is an automated "lab-in-a-box" mass spec- and sensor-based system that can detect VOCs at trace analysis detection limits, in real time, and without the need for trained personnel.

Potential impact

The HaVoc system enables MS-based gas analyses in various fields, such as emission monitoring, forensics, medical and breath analysis, pharmaceuticals, fragrances and cosmetics, food, and even aroma sensing.

What the judges say…

"Low-temperature plasma-based ionization sources have long been limited to academic demonstrations due to lack of commercial options. This product brings easy to use, direct analysis of volatile analytes within reach, and the ability to ionize and directly detect/identify compounds has the potential to open up numerous new spaces to analytical exploration that have previously been inaccessible."

"A new system that allows real-time gas monitoring using MS with very low detection limits. It could be very important from a safety perspective in, for example, the chemical industry."

3

MALDI-8030

A benchtop MALDI with the power of larger, more expensive instruments

Produced by Shimadzu Corporation

Shimadzu's benchtop MALDI has a number of key features. The dual-polarity ion source and the WideBore ion optics enable low-level detection of proteins, peptides and polymers, among other analytes, in either positive or negative ion mode; the Fast-MS is designed to accelerate the time-to-results turnover; TrueClean performs automated UV laser self-cleaning of the ion optics; and the absence of desiccant and use of an oil-free diaphragm pump aims to reduce maintenance costs.

Potential impact

The MALDI-8030 is a benchtop instrument that Shimadzu are confident performs similarly to larger, more expensive MALDI-TOF models. It could be used in academic, QC, and other high-demand applications – especially given the integrated barcode scanner that automates workflows.

What the judges say…

"The MALDI-8030 Benchtop MALDI-TOF is a big step toward making mass spectrometry analysis available for the applications where it is needed most. This compact and capable system that is easy to use and suitable for regulated environments opens up possibilities for delivering high quality results with faster turnaround times for researchers that have traditionally had to settle for less."

2

THERMO SCIENTIFIC DIRECT MASS TECHNOLOGY

Thermo's Direct Mass Technology mode enables simultaneous charge detection for previously unmeasurable analytes

Produced by Thermo Fisher Scientific

The Thermo Scientific Direct Mass Technology mode equips Thermo Scientific Q Exactive UHMR Hybrid Quadrupole-Orbitrap mass spectrometers with charge detection, making direct mass determination of thousands of individual ions in a single spectrum possible. Users can now decipher protein complexes, biotherapeutics, and viral particles that are too complex to resolve using ensemble methods.

Potential impact

The main aim of Thermo's Direct Mass Technology is to open up new areas of investigation – from resolving heavily modified proteoforms to revealing small changes in large antibody-drug conjugate complexes. With accurate mass determination, scientists will be able to examine small changes to large molecules – post-translational modifications, for example.

What the judges say…

"The Thermo Scientific Direct Mass Technology mode of operation represents an ingenious solution to a long-standing analytical challenge of characterizing large biomolecules. This advancement promises to deliver enhanced understanding of structure and interaction mechanisms for proteins and protein complexes essential to biological processes and biotherapeutic development."

1

IMSCOPE QT

A unique combination of microscopy and high resolution accurate mass mass spectrometry imaging in one system

Produced by Shimadzu Corporation

The iMScope QT is a unique fusion of two analytical techniques: an optical microscope with a MALDI high resolution accurate mass (HRAM) spectrometer. Mass spectrometry imaging (MSI) and chromatography coupled HRMS workflows can be exchanged, and the MALDI source can be replaced by other ionization sources, such as ESI, APCI or PESI. Overall, the iMScope QT aims to make MSI more accessible to a broad range of applications by shortening timescales and improving precision.

Potential impact

The main challenges in MSI are high spatial resolution at high acquisition speed and accuracy. Traditionally, acquiring MSI data can take many hours, depending on sample size and resolution – a significant resource burden in terms of chemicals and energy consumption that reduces sample throughput and can negatively affect data quality. Shimadzu's aim was to develop a system that can acquire high resolution images (50 px/s) with maximum overlay accuracy of MS and histological images – to bring high-end MSI to researchers in various fields, such as clinical, pharma, or food.

What the judges say…

"This technique allows microscopy to be combined with high-resolution MS imaging with different ionization sources, while reducing its footprint (resources, chemical, energy)."

"Really nice application where mass spec images can be overlaid properly with histology and light microscope images."

the Analytical Scientist

THE INNOVATORS

Showcasing the products and companies making a difference in 2022

BRING THE LAB ANYWHERE WITH THE VOCUS EIGER

Comprehensive, fast, and sensitive VOC analysis for mobile applications – the Vocus Eiger is the ideal combination of performance and size, offering robust, sensitive, real-time chemical ionization time-of-flight mass spectrometry on the go

The Vocus Eiger is the most robust solution for direct trace gas analysis – perfect for demanding applications where mobility is crucial. A rugged, compact design offers reliability in any environment and is easily installed in mobile labs or smaller vehicles. TOFWERK's trusted chemical ionization time-of-flight mass spectrometry platform enables ultra-sensitive, fast, and simultaneous quantification for 1,000s of VOCs, reported in real time. Straightforward, remote operation allows users to operate and view their data completely online, from anywhere. Unparalleled speed and sensitivity at low parts-per-trillion limits of detection provides a superior solution to conventional technologies that operate with slower time resolutions, limited compound coverage, and inadequate sensitivity.

The flexible Eiger is well suited for a diverse and lengthy list of applications: ambient air analysis, regulatory monitoring, cleanroom AMC monitoring, breath analysis, food and flavor analysis, and more.

The Vocus Eiger sits in the middle of TOFWERK's CI-TOF portfolio, offering the perfect blend between smaller monitoring instruments and high-performance, research grade instruments – delivering excellent performance for both research and monitoring interests.

Learn more at www.tofwerk.com/products/vocus/.

TOFWERK – INNOVATIVE SOLUTIONS FOR CHEMICAL ANALYSIS

Time-of-flight mass spectrometers for applications that demand exceptional speed and sensitivity

TOFWERK is making the world a cleaner place through innovative solutions for chemical analysis. Their scientists and engineers design, manufacture, and optimize high-performance mass spectrometers for use in a diverse variety of applications, including ambient air monitoring, breath analysis, food and flavor analysis, geological science, and material science. Used by researchers and industrial customers around the world, TOFWERK time-of-flight mass spectrometers offer unmatched speed and sensitivity with compact, robust construction for use in any environment.

Visit www.tofwerk.com to learn more.

NEXT GENERATION GC-MS IS HERE TODAY

Delivering high performance GC-MS to redefine your workflows on tandem quadrupole and high-resolution mass spectrometers

Atmospheric Pressure Gas Chromatography (APGC™) is a mass spectrometry (MS) ionization technique similar to atmospheric pressure chemical ionization (APCI). In contrast to electron ionization (EI), a common ionization mode used for gas chromatography (GC) coupled with mass spectrometry (MS), APGC is considered a soft ionization technique, meaning in-source fragmentation of analytes is very low. APGC offers some key advantages including:

- increased selectivity
- increased sensitivity
- simpler GC injection techniques
- streamlined sample preparation
- unrestricted use of nitrogen as a safe and sustainable carrier gas

Background

Waters commercialized APGC over a decade ago, coupling the technology to both tandem/triple quadrupole (TQ) and quadrupole time of flight (QTof) MS systems. The launch of the Waters' Xevo™ TQ-S system (2010) saw the introduction of StepWave™ ion optics, which when combined with APGC, allowed the system to sample greater volumes of gas – with game-changing sensitivity. The continuing development of TQ technology with the Xevo TQ-XS and Xevo TQ Absolute has resulted in an even greater level of sensitivity for GC applications when APGC technology is used. The benefits of this increased sensitivity not only allow for lower achievable limits, but also lower on-column sample volumes, which can reduce the amount of maintenance required for the GC inlet, column, and ion source.

How does APGC work?

APGC is a chemical ionization technique, where a corona pin situated within an ionization chamber creates a nitrogen plasma, which reacts with any analytes or reagent gases present in the region. There are two primary mechanisms of ionization that can occur: charge transfer and protonation. Choosing between these ionization mechanisms is achieved by altering source conditions. And mixed mode, combining charge transfer and protonation, is also possible.

What applications is APGC used for?

With multiple reaction monitoring (MRM), APGC is suitable for a variety of targeted GC-MS/MS applications, which include the identification and quantitation of:

- dioxins, furans, and dioxin like PCBs
- pesticides and persistent organic pollutants
- semi-volatile compounds (SVOCs)

As well as targeted analysis, APGC can also be coupled to QTof and ion-mobility-enabled MS technologies to provide a powerful tool for non-targeted analysis.

APGC technology offers laboratories a powerful alternative to EI technology, enabling low limits of detection and confident compound identification and confirmation, while reducing laboratory costs (from reduced GC system maintenance and the ability to use nitrogen as an alternative carrier gas).

Learn more at www.waters.com/NextGenGCMS

ACD/MS STRUCTURE ID – RAPID IDENTIFICATION OF UNKNOWNS WORKFLOW

Our most advanced multi-technique, vendor agnostic mass spectroscopy software for structure characterization and rapid identification of unknowns

With MS Structure ID you get a simple, replicable workflow for quickly generating and narrowing down structural candidates. With it you can:

Import

Import, extract, and interpret all MS data from all major instrument vendors in one software platform. Detect all key components, extract relevant peaks, and visualize all GC/MS or LC/UV/MSn data together in one interface.

Identify

Identify and characterize components for seamless structure identification. Componentize data and automatically search PubChem for accurate mass and molecular formula matches to increase the number of identified compounds. Compare experimental and candidate mass spectra directly via mirrored plots.

Integrate

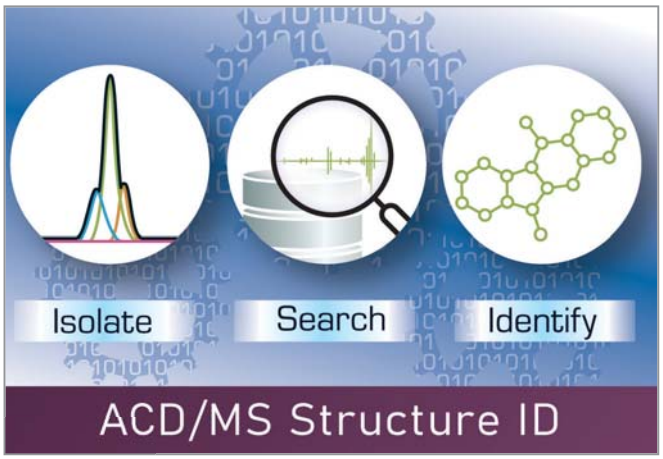
Streamline results interpretation by compiling and analyzing data in a single environment. Add fragments to include and/or exclude lists to further narrow down candidate structures creating more manageable lists. Create a database from experimental data to increase the number of compounds identifiable. Use the AutoAssignment tool to rank structures based on the Assignment Score between generated fragments and the MSn spectrum, and determine the best structural match for experimental data.

Inform

Complete databasing capabilities with simplified collaboration and reporting. Generate readily accessible and comprehensive reports including analytical interpretations and structure assignments. Effortlessly communicate and collaborate on projects.

MS Structure ID provides the tools for a fast and efficient way to import, extract and interpret MS data – allowing you to search for a wide range of potential structures, curate a reasonable and relevant list of candidates, and identify the most likely structure for a chromatographic peak.

Learn more at www.acdlabs.com/MSStructureID



STREAMLINE YOUR WORKFLOW WITH GENIUS XE

Take control of your lab's nitrogen gas needs with PEAK Scientific's in-house, on-demand nitrogen generator

It's always important to be looking at ways to make labs more independent, streamlined, and efficient. That's why PEAK Scientific developed the Genius XE – a cutting-edge nitrogen generator, designed to incorporate advanced technology and robust engineering. The Genius XE offers stress-free nitrogen gas generation in the lab at the press of a button – providing a premium, standalone nitrogen solution for high performance LC-MS.

Inspired by the success of PEAK's best-selling Genius line of nitrogen gas generators for LC-MS, Genius XE Nitrogen is a cutting-edge evolution combining advanced technology with refined and robust engineering. And with an in-house gas generator, PEAK can remove the reliance that many labs have on gas cylinders or dewars and provide them with a sustainable source of gas for their instruments.

PEAK have introduced a number of innovations into the Genius XE, including Multi-Stage Purification™, which can be broken down into five different stages:

- A Triplex Particulate Filter with three sequential stages of micro-particulate and coalescing filtration ensures the nitrogen is as clean and high-purity as possible from a generator.
- The AirMax™ air intake maximizes air flow into and around the integrated compressors which, combined with first-stage filtration, allows compressors to operate at full efficiency.
- Genius XE employs two-stage moisture removal. This unique reheat technology and proprietary lock-and-drain moisture removal ensures your application is extra protected against any risk of moisture in the gas stream, delivering ultra-dry nitrogen gas into your instrument.
- A custom advanced polymer hollow fiber nitrogen membrane technology, developed in collaboration with a world leading nitrogen membrane manufacturer, ensures a consistently high purity of nitrogen gas from Genius XE, even at high flow rates.
- Genius XE's Multi-Stage Purification™ includes NMHC Capture. This proprietary non-methane hydrocarbon (NMHC) filtration stage is designed to remove ambient long-chain hydrocarbons (down to <1ppm), which can cause spectral interference in some analytical results, depending on the method. The innovative design has been optimized for efficiency, performance and service life.

Genius XE Nitrogen generators are the next evolution in PEAK's Genius line, engineered to exceptionally high specification using proven and precision designed components, developed and refined over years of experience in manufacturing nitrogen generators for the laboratory.

Genius XE has been designed to ensure the lab has a constant, consistent nitrogen gas supply – there is no concern that gas will run out as the gas is produced through compressed air on-demand in the lab. The Genius XE, therefore, is a more sustainable option for labs who are looking to make greener choices and reduce their impact on the environment.

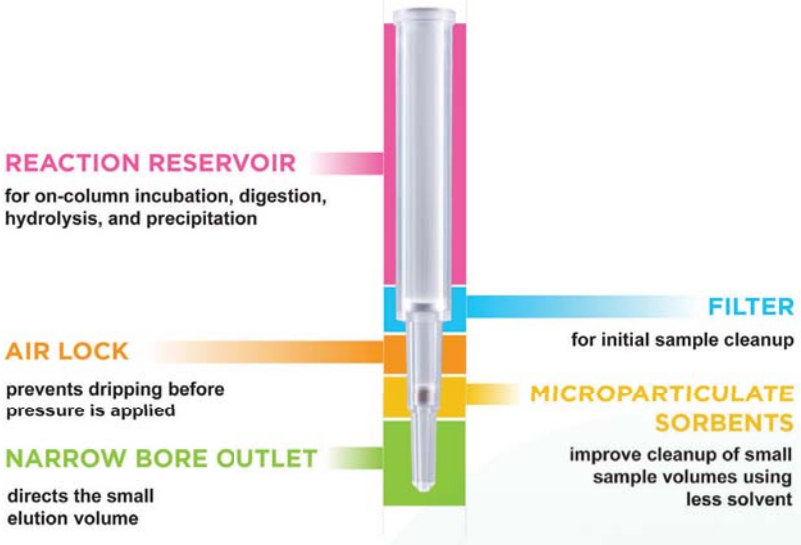
NBE™: A REVOLUTION IN SPE COLUMN DESIGN

Tecan NBE™ columns' dual chamber design consolidates steps – saving time and resources

Tecan Narrow Bore Extraction™ (NBE™) columns feature a unique dual chamber design that combines a reaction vessel with an SPE column all in one revolutionary format. By utilizing a novel pocket seal airlock and filter, the top reaction vessel is separated from the microparticulate sorbents in the SPE chamber until positive pressure is applied. This provides the ability to integrate pre-SPE digestion or incubation steps into your SPE workflow without having to re-pipette samples or change labware prior to extraction. The pocket seal airlock also enables drip-free operation until positive pressure is applied, making the NBE column ideal for automated applications and scaling of workflows.

The innovations included in Tecan NBE format columns are empowering the consolidation of workflow steps to deliver faster, more efficient processes. Additionally, like all Tecan SPE solutions, NBE columns deliver the improved reproducibility, higher sensitivity, and lower solvent and reagent consumption that today's labs are looking for, alongside the game-changing addition of unparalleled efficiency gains in more complex workflows. If you're looking to scale sample prep, automate processes, eliminate bottlenecks, or improve workflow efficiency, the Tecan NBE SPE columns are a must-consider innovative option for your lab.

Learn more at https://www.tecan.com/Biopharma-SPE



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OUR PURPOSE AND VISION

Scaling healthcare innovation globally

At Tecan, we are driven to improve people's lives and health. We do this by empowering our customers to scale healthcare innovation globally, from life science to the clinic. We collaborate with our customers in healthcare and the life sciences, from early-stage innovation through project implementation and beyond. We deliver the products, services, and solutions that make lab processes and medical procedures precise, reproducible, and compliant. This leads to scalable outcomes that are further reaching and ever more valuable to humankind.

Everything we do is guided by our values:

- *Ambition.* We push the boundaries of possibility. Through continuous innovation and support, we empower our teams, customers, and partners to achieve their personal and professional potential and reach their research and business goals.
- *Highest standards.* Customers choose us because we consistently deliver the highest standards in every market we serve. We lead our business with courage, curiosity, respect, and brutal honesty.
- *Trust.* We have earned our reputation through honest actions and responsible leadership. Our employees, customers, shareholders, and partners know that their success is our top priority.


Agilent
Agilent
6475 LC/TQ

AGILENT 6475 TRIPLE QUADRUPOLE LC/MS

Intelligence that powers ultimate productivity

The next evolution of our trusted LC/TQ platform is designed to address daily productivity demands in the lab and help meet your efficiency goals. With integrated system intelligence, the new Agilent 6475 triple quadrupole LC/MS provides a pathway to increase your sample throughput, without having to add more instruments and lab personnel or extend lab hours.

Sophisticated, yet easy-to-use onboard intelligence provides immediate validation of results to both improve speed of analysis and predict when maintenance is needed, reducing downtime. Time-saving automation software lets you schedule tuning and calibration in advance, which means when you walk in the lab the 6475 LC/TQ is ready to run samples. And proven, ultra-rugged quadrupole technology ensures instrument reliability for peace of mind and lower cost of ownership.

Tweaking and fine-tuning your LC/MS to optimize performance is challenging and time consuming. An innovative tuning algorithm in the 6475 triple quadrupole LC/MS takes the guesswork out of achieving peak performance. Smart procedures utilize artificial techniques to evaluate many parameters simultaneously, resulting in faster start-up time and greater consistency.

Unexpected instrument issues and the resulting downtime is extremely disruptive – especially if you don't know the source of the problem. The 6475 triple quadrupole LC/MS monitors its own vitals, giving you a real-time overview of the system's health. And to help you pinpoint where and when issues may arise, key operational areas are tracked and monitored as part of early maintenance feedback.

You can ensure confidence and throughput with Intelligent Reflex, which uses reflexive reinjection logic to check that results are immediately trustworthy and within operational limits. And cross-contamination is prevented with Carryover Detection, which inserts additional blanks to ensure the next sample is unaffected by the previous sample. The above Cal. Range workflow detects if a sample is outside the calibration range and can reinject the sample with less volume. Lastly, Fast Screening processes samples with incredible speed. For example, if a target analyte is detected with a screening method (short LC gradient), an analytical method (standard gradient) is run on that sample automatically; if the target isn't detected, the system proceeds to the next sample.

These latest innovations included in the 6475 triple quadrupole LC/MS will empower your lab to meet increasing sample throughput and productivity demands.

Learn more at www.agilent.com/chem/6475

AUTOMATED TOTAL NITROSAMINE ANALYSER

The Automated Total Nitrosamine Analyser takes a totally unique approach to analyzing Nitrosamine content of almost any sample down to ppb levels

Nitrosamines are carcinogenic compounds found across a wide range of industries. In recent years this has been a particular issue for the pharmaceutical industry, with several high-profile product recalls due to the presence of nitrosamines in medication. Off the back of these cases, regulatory bodies have required pharmaceutical companies to conduct risk assessments and monitor their products, ingredients, and processes for their potential to introduce nitrosamine content.

Historically, this has been performed using mass spectrometry coupled to a GC or HPLC system. This has, however, proved very inefficient for pharmaceutical companies due to the sheer volume of samples and sample types, the often complex sample preparation required, the extremely low detection limits required, and the potential for false positives. The Automated Total Nitrosamine Analyser helps alleviate many of these pain points, allowing users to automatically screen up to 10 samples an hour for total nitrosamine content – which means only positive samples need passing on for further speciated analysis.

Some sample types, such as medicated shampoos, can be analyzed directly with no additional sample prep required, while others, such as tablets, require an initial extraction into a solvent. Samples are placed into a vial with the reagent and then loaded onto the autosampler. The system uses a unique in-vial chemical reaction to target any nitrosamines in the sample. This reaction breaks off the NO group from the nitrosamines, which is then sampled from the headspace of the vial and detected using the 800 Series TEA chemiluminescence detector. This gives a single result for the total nitrosamine content present down to 1 ppb levels. This approach also significantly reduces the chance of false positives because of the selectivity and sensitivity for nitrosamine compounds.

The nitrosamine issue is not going away anytime soon, likely becoming a more significant problem across many other industries as their presence is detected. So, with an ever-growing number of samples, the need for a system that can rapidly screen for total nitrosamine content is clear. The Automated Total Nitrosamine Analyser has already been recognised, winning the Automation Award at Lab Innovations 2022 and looks set to revolutionize the world of nitrosamine analysis.

For further info, please visit https://www.ellutia.com/ATNA

AGILENT 5977C GC/MSD

Discover the possibilities when your lab runs at peak efficiency

The never-ending pressure to improve operating costs by increasing sample throughput and decreasing sample turnaround time is exhausting. Meeting these goals is even more challenging because of unplanned downtime – things break, staff turnover is high, regulations change, and new application needs arise all the time. Not only does downtime slow your progress, but it's expensive. You find yourself constantly feeling like you need to keep up – but it doesn't have to be that way. Meet the Agilent 5977C GC/MSD. Coupled with new technologies that drive maximum productivity in your lab, the 5977C is designed to provide robust, day-in, day-out performance so you can focus your time on things that add value to your lab.

The Agilent JetClean self-cleaning ion source maximizes instrument uptime and sample throughput by greatly reducing or even eliminating the need for manual ion source cleaning, resulting in an additional one to two days per month to perform analyses.

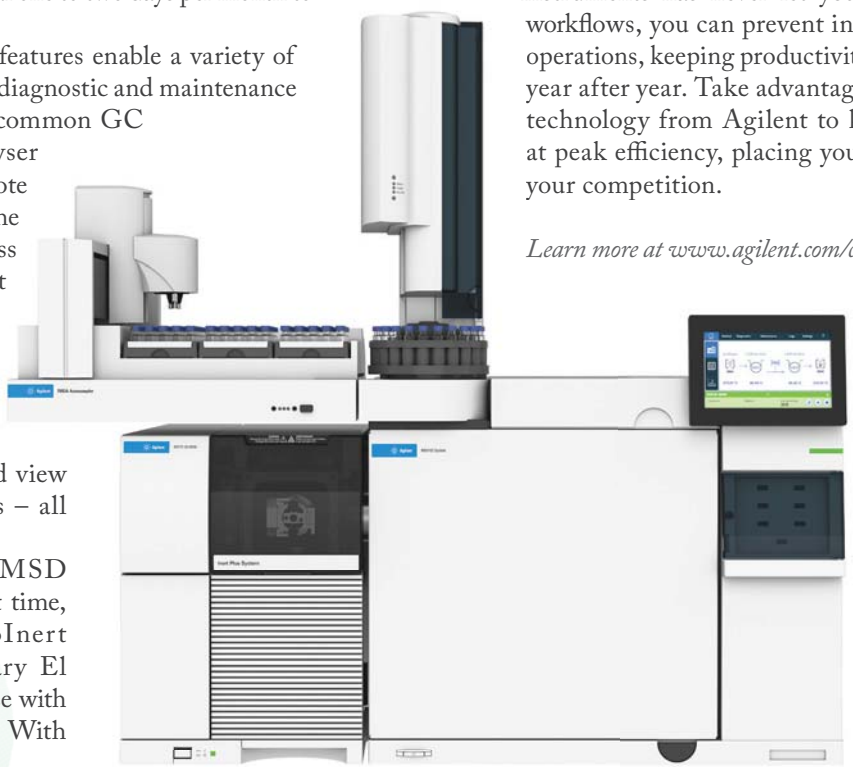
The self-aware GC features enable a variety of useful and convenient diagnostic and maintenance options that prevent common GC problems. The browser interface provides remote connectivity through the lab network and access to features without the need for a data system. Users can view instrument status, run diagnostics, check maintenance logs, and view helpful service videos – all from a mobile device.

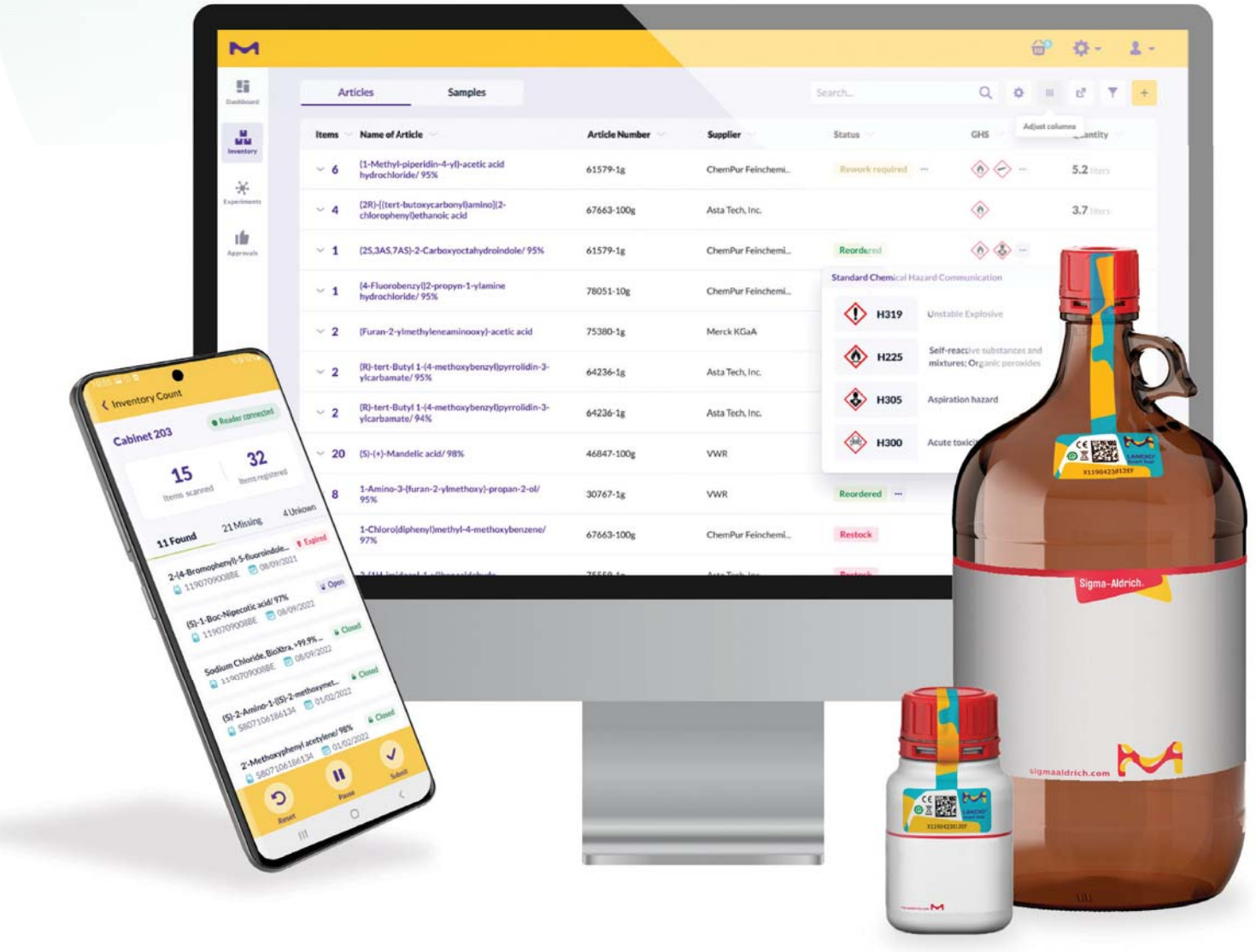
The 5977C GC/MSD introduces for the first time, the Agilent HydroInert source a revolutionary El source optimized for use with hydrogen carrier gas. With helium being a finite and dwindling resource with an inefficient production, it is expensive, and availability is a concern. Hydrogen is a low cost, renewable gas that is the best alternative to helium. The novel HydroInert source improves chromatographic efficiencies with hydrogen, allowing labs to achieve faster separations with better peaks and reduced spectral anomalies while maximizing return on investment with hydrogen gas.

The 5977C GC/MSD has also been developed with resource conservation and reducing carbon footprint in mind. By emphasizing accountability, consistency, and transparency (ACT) around manufacturing, energy and water use, packaging, and end-of-life, scientists and procurement specialists can easily choose more sustainable products.

You've trusted Agilent GC/MS solutions for decades. Their proven legacy of leadership, innovation, and high-performance instruments has never let you down. With Agilent workflows, you can prevent interruptions to your lab operations, keeping productivity and profitability high year after year. Take advantage of the latest GC/MS technology from Agilent to keep your lab running at peak efficiency, placing you comfortably ahead of your competition.

Learn more at www.agilent.com/chem/5977c

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ChemPur Feinchemi...
Rework required
5.2 liters
[2R]-[(tert-butoxycarbonyl)amino][2-chlorophenyl]ethanoic acid
67663-100g
Asta Tech, Inc.
3.7 liters
[2S,3AS,7AS]-2-Carboxyoctahydroindole/ 95%
61579-1g
ChemPur Feinchemi...
Reordered
[4-Fluorobenzyl]2-propyn-1-ylamine hydrochloride/ 95%
78051-10g
ChemPur Feinchemi...
Standard Chemical Hazard Communication
H319
Unstable Explosive
H225
Self-reactive substances and mixtures; Organic peroxides
H305
Aspiration hazard
H300
Acute toxicity
[Furan-2-ylmethyleneaminooxy)-acetic acid
75380-1g
Merck KGaA
[R)-tert-Butyl 1-(4-methoxybenzyl)pyrrolidin-3-ylcarbamate/ 95%
64236-1g
Asta Tech, Inc.
[R)-tert-Butyl 1-(4-methoxybenzyl)pyrrolidin-3-ylcarbamate/ 94%
64236-1g
Asta Tech, Inc.
[S)-(+)-Mandelic acid/ 98%
46847-100g
VWR
1-Amino-3-(furan-2-ylmethoxy)-propan-2-ol/ 95%
30767-1g
VWR
Reordered
1-Chloro[diphenyl]methyl-4-methoxybenzene/ 97%
67663-100g
ChemPur Feinchemi...
Restock
Inventory Count
Cabinet 203
Reader connected
15
Items scanned
32
Items registered
11 Found
21 Missing
4 Unknown
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LANEXO® SYSTEM: SMARTER INVENTORY MANAGEMENT

Track your lab's inventory – what was used, by whom, when, and for what – with just a few taps of a smartphone

Say goodbye to Excel and paper inventories

With its mobile app and radiofrequency identification (RFID) labels, the LANEXO® System captures and stores all consumables data in a secure cloud with just a few taps of a smartphone. Excel and paper become obsolete, and managing your stocks across multiple sites becomes easier. And remote access to real-time digital data on consumables – SDS, owner, opening/expiry dates, location, usage, disposal information – gives you the complete traceability you need for audit readiness.

A more sustainable laboratory

This fully 21 CFR Part 11-compliant solution captures digital data on chemicals from RFID labels placed on bottles, providing a real-time picture of your storage locations and stock/usage levels. The LANEXO® System also reduces the time you spend on repetitive, error-prone manual processes; automates expiry date monitoring and root cause analysis with inventory control; and manages stocks based on the "first-in/first-out" principle. Fewer chemicals expire or go unused – and your lab becomes more sustainable.

Regulatory compliance and audit readiness made easy

With the LANEXO® System, consumables documentation is automatically traceable, as are storage compliance checks such as GHS codes and identity checks of experimental workflows, for full 21 CFR Part 11 compliance. And any actions performed in the app –such as adjustments of consumable volumes, or what was used by whom, when, and for what – are captured in the audit trail and can be easily exported. Each consumable in the system is matched to a time-stamped audit report that documents its lifecycle from receipt to disposal.

A safer lab with lower operational risk

Rapid electronic access to safety data sheets (SDS) helps lab staff store and handle consumables safely. Automatic calculation of expiration dates helps prevent the inadvertent use of expired chemicals in experiments. And real-time alert notifications warn when two incompatible chemicals are stored together.

An intuitive, easy-to-implement solution

With the LANEXO® Web and Mobile Apps' highly intuitive user interfaces, you can register, store and relocate consumables with just a few taps of a phone. You also won't have to worry about running out of chemicals again: set up Restock Rules that alert you when you're running low on a consumable, and then you can reorder it either automatically or manually. Finally, the LANEXO® System is easy to set up and integrate into existing workstreams, thanks to API integration into ELN, ERP and LIMS. Training takes less than a day before you're up and running.

For further info, please visit www.lanexosystem.com

AGILENT 7000E AND 7010C TRIPLE QUADRUPOLE GC/MS INSTRUMENTS

Unparalleled sensitivity and robust day-to-day performance powered by intelligence

Labs across the world are under increased pressure to improve operating costs and increase sample throughput. To meet these challenges, the next evolution of the Agilent GC/TQ platform is built to help you exceed your productivity goals. With integrated system intelligence, the Agilent 7000E and 7010C triple quadrupole GC/MS instruments provide a pathway to robust, day-in and day-out performance with unparalleled sensitivity.

The latest Agilent GC/TQ instruments are powered by a new, smarter core that enables new tune and diagnostic capabilities. Among these enhancements is SWARM autotune. This tune algorithm uses a technique called particle swarm optimization, which utilizes the intelligence of a swarm – much like a flock of birds – to converge on the best parameters. It employs the high speed and precision of the hardware to test many settings simultaneously and converge on the ideal system settings for optimal performance. Additional intelligent features, like diagnostic tune, function to gather as much information as possible about the GC/TQ system and organize it into a very detailed system report for a quick diagnosis to get your instrument up and running when you need it.

HydroInert, compatible with the 7000E GC/TQ, is a revolutionary ion source optimized for use with hydrogen carrier gas. With helium being a finite resource, it can get expensive to procure. Hydrogen is a low cost, renewable gas and is the best alternative to helium. The novel HydroInert source improves chromatographic efficiencies with hydrogen, allowing labs to achieve faster separations with better peaks and reduced spectral anomalies while maximizing return on investment with hydrogen gas.

Users can also take advantage of new acquisition modes for improved confidence to identify what is truly there. With up to 10 confirmatory transitions for Triggered MRM and the ability to perform retrospective analyses with simultaneous dMRM/scan data, labs now have more tools for compound identification with reduced risk of false positives.

When it comes to identifying leaks in your GC column and other connections, the next evolution in the MassHunter Acquisition software helps get your GC/TQ system up and ready for analysis quicker by improving upon the way users perform leak tests. The 7000E and 7010C both contain new functionality to assist in identifying the source of these leaks or monitoring the amount of leak over time.

These latest innovations included in the 7000E and 7010C triple quadrupole GC/MS will empower your lab to meet increasing sample throughput and productivity demands.

Learn more at www.agilent.com/chem/7000e
www.agilent.com/chem/7010c


Intuvo
9000 GC System
High Efficiency System

APGC: A Better Future with Nitrogen

Atmospheric pressure ionization gas chromatography mass spectrometry can help solve the increasing difficulties of economically sourcing helium by opening the door to the use of nitrogen carrier gas with uncompromised performance

By Frank Dorman, Douglas Stevens, and Rhys Jones

Helium is an inert gas that is obtained from natural gas well sources where helium recovery infrastructure is installed. Over several decades, helium has evolved to be the GC carrier gas of choice because of its availability and good chromatographic performance. This has most notably been the case for GC-MS using electron ionization (EI) and instruments have been optimized for its use. But helium is non-renewable; its availability is linked to petroleum production and therefore to the vagaries of that troubled market. Additionally, helium is under high demand in a number of areas including medical diagnostics, which often take a priority over chromatographic use. As a consequence, the global helium infrastructure is facing great challenges, including geopolitical influence, natural events, dwindling sources, and technical issues at extraction facilities.

In short, helium availability is severely impacted, which ultimately means increasing costs and increasingly a lack of availability for end users.

The increasing pressure of the helium shortage has led many to consider other options. We have seen increased use of hydrogen and nitrogen as alternative carrier gases. Hydrogen's optimum linear velocity is greater than helium, which can increase sample throughput through decreased analysis times. However, its combustible nature and general safety concerns have hampered its adoption. Additionally, hydrogen is a reducing gas and often results in chemical changes of fragmentation ions which can negatively impact operation in mass spectrometry. And finally, the use of hydrogen can cause discrimination and other issues related to its reactivity in the injection port of the GC as well.

Nitrogen has been described as a "slow gas" because its optimum linear velocity is lower than helium, and is often overlooked as a helium alternative, due to historic issues which are no longer limitations. In GC-MS applications, many commercial systems have evolved to using helium and electron ionization which occurs in vacuum. For successful operation, high vacuum must be maintained, and instruments and vacuum pumps have been optimized for helium gas operation for most manufacturers. This leads to an issue when they might consider nitrogen as a possible replacement gas as a result of helium supply concerns.

But when we utilize atmospheric pressure ionization for ion formation, the downsides of nitrogen disappear. In atmospheric pressure gas chromatography (APGC) – where we are dealing with a high-pressure environment for ionization – the presence or absence of nitrogen as the GC carrier gas makes no difference to either sensitivity or noise. Additionally, the atmospheric chemical ionization process already utilizes nitrogen for the initial formation of charged species. Therefore, use of nitrogen as the carrier gas actually simplifies the system because we are only introducing nitrogen from an additional source through the column, effectively removing helium from the equation altogether.

The game-changer

Although the coupling of GC and MS with atmospheric pressure ionization (API) appeared in published papers as early as the 1970s, the commercial interest in coupling GC with an atmospheric pressure ion source has only expanded in the last decade. The need to preserve highly diagnostic molecular ions for some applications has made "soft" ionization (which causes less fragmentation) more desirable than "hard" ionization techniques that can extensively fragment molecules but are, nevertheless, the expectation with traditional GC-MS. The crux of the matter is that reduced fragmentation yields higher sensitivity and specificity, simplifying precursor ion selection for targeted MS/MS applications using MRM acquisitions.

At Waters, we promote APGC as an

ion source for multiple models of mass spectrometer. Options exist for highly sensitive GC-MS/MS performance as well as high-resolution and even ion mobility separations. Furthermore, it is straightforward to swap between APGC-MS and UPLC-MS in a matter of minutes. For this, no venting is required, and LC-MS and GC-MS can be performed using the same mass spectrometer. Finally, it's worth noting that APGC analysis are not flow-rate limited as is the case for most EI-based GC-MS systems. This allows for a wider range of compatibility for GC column flow and carrier gas type.

These new systems provide us with a range of unique, data-rich experimental capabilities, giving analytical platforms a greater reach than ever before. Using APGC, we can harness a combination of sensitivity, mass accuracy, resolution, and ion mobility to give levels of selectivity that will thoroughly characterize samples and yield data at an entirely different and exciting level.

In short, APGC is robust, sensitive, and very well suited to the identification and determination of a wide variety of compounds. With APGC, unlike EI, the molecular ion is typically well preserved, resulting in higher sensitivity and selectivity. Then, of course, there is the cost. The ability to use nitrogen as the carrier gas has an immediate impact on costs and this alone is a big driver for adopting APGC. If you're not concerned about cost (congratulations), you probably are worried about the volatility of the helium supply chain; the supply-and-demand equation is certainly tipped heavily toward demand. We've seen suppliers limiting the volumes of helium sold to any one laboratory, making it increasingly important for labs to have alternative options to ensure effective and agile responses to supply chain interruptions.

Jumping on the API bandwagon

We are now beginning to see other manufacturers looking to API techniques and, although they are a little less mature than ours, we anticipate rapid growth over the next decade. Due to the combination of positive performance characteristics of APGC we fully expect the rapid growth in use of the technique across the coming decade.

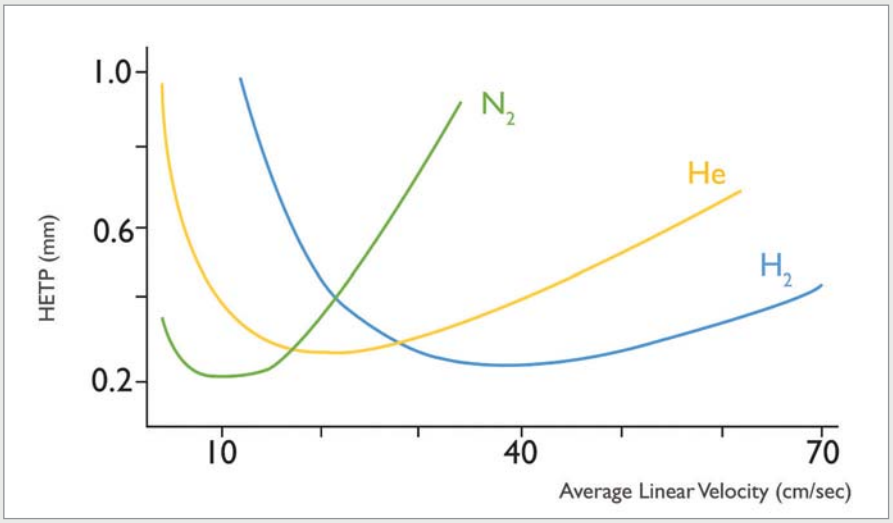

Figure 1: van Deemter curves for the three common GC carrier gasses.

We can find a good analogy for APGC in the LC-MS world, which began using electrospray ionization to the point where, with MS/MS in particular, it became the gold standard for small molecule analysis. Why? Because ESI delivered high sensitivity and specificity for MS/MS. APGC looks set to follow the same path – and the helium issue will simply act as a catalyst. Overall, APGC-MS/MS offers an affordable, well-suited alternative to GC-MS/MS with electron ionization for the determination of organic compounds at ultra-trace levels.

There will be some inertia to overcome – as with any new technique! There is an inherent resistance to change but, as APGC continues to be incorporated in published methodologies, we will see increasing adoption in more applications and more laboratories. Moving from EI to API is a big step change – and moving away from tradition involves a strong belief in the technique and a willingness to invest in retraining and in new or modified instrumentation. Luckily for us, the latter two are low bars, whereas leaving decades of experience with EI to support the "new kid on the block" requires a somewhat higher leap of faith! Much of people's understanding of any given process is also directly related to the limitations of the original technique, and this understanding is often slower to change than the techniques themselves.

Final thoughts

The APGC system is a significant step up in terms of analytical performance relative to what we can currently achieve with EI systems. It represents a change in technology that aims to alleviate some of the biggest challenges the field currently faces. And, specifically with respect to helium shortages, APGC offers a simple plug-and-play solution for swapping to nitrogen – an affordable, renewable alternative that delivers results without any analytical compromise. We truly believe it is a game-changer – and we hope users will, too.

Frank Dorman is Senior Principal Market Development Manager, Global Food & Environmental; Douglas Stevens is Principal Scientist, Global Scientific Operations; and Rhys Jones is Principal Consulting Research Scientist, Mass Spectrometry Research; all at Waters Corporation, (Milford, MA, USA, for Frank and Doug; and Wilmslow, UK, for Rhys.)

APPLICATION SPOTLIGHT:

Aromatic Analysis

An understanding of whiskey aroma profiles can lead to a better understanding of different whiskey products, but comparing various similar but complex chromatograms can be complicated and time-consuming. ChromaTOF® Sync takes the challenge out of the comparison by compiling and aligning analyte information across the entire sample set, highlighting statistically significant similarities and differences.

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Core Topic
Mass Spec

Proteomics-based long Covid test. Advances in our understanding of how to manage COVID-19, plus mutations to the virus, have – fortunately – reduced the chances of a hospitalization. But the prospect of developing "long Covid" remains a worry given how little we know about the condition. Now, researchers from University College London have developed a proteomics- and machine-learning-based blood test, taken at the time of infection, that can predict a patient's chances of developing long Covid.

"Our study shows that even mild or asymptomatic COVID-19 disrupts the profile of proteins in our blood plasma," said lead author Gaby Captur in the press release. "This means that even mild COVID-19 affects normal biological processes in a dramatic way, up to at least six weeks after infection."

Speedy spectrometry. Mass spec imaging has faced ongoing technical challenges – particularly finding the balance between spatial resolution and throughput without compromising one for the other. Researchers from The Netherlands have devised a new, continuous-acquisition method to combat these constraints by combining a secondary ion mass MS microscope with a Timepix3 detector. The method, aptly termed fast mass spectroscopy, achieves 2–3 orders of magnitude higher throughput than any microprobe-mode MSI whilst retaining high spatial resolving power. Gigapixel images of fingerprints and rat tissue were collected in just 33.3 minutes.

Life on Europa? NASA has published details of their Ocean World's Life Surveyor (OWLS), which in the future could be used to land on and sample ice from the surfaces of Europa and Enceladus. How are they planning to detect the organic molecules produced by potential alien life? Capillary electrophoresis coupled with MS (CE-MS). And if that wasn't enough CE-MS for you, Agilent has signed a co-marketing agreement with CMP Scientific to "provide an integrated CE-MS solution to life science and pharmaceutical industry."

Jonathan Sweedler on single-cell metabolomics. What is currently possible with state-of-the-art single-cell metabolomics? That is the question last year's Power Lister winner Jonathan Sweedler – plus an international team of collaborators – set out to answer. And, in addition to technical developments to increase sensitivity and reliability of identification and quantification, the authors hope metabolic information will soon be integrated with protein and gene expression data to complement the information available from metabolomics studies.

IN OTHER NEWS

Continuing with COVID-19 (and proteomics), two researchers from Boston University School of Medicine highlight use of mass spec to profile SARS-CoV-2 proteome from nasopharyngeal swab samples.

Researchers combine two-dimensional gas chromatography–mass spectrometry/olfactometry and human sensory evaluation to understand how that "new car smell" decays over time.

Drift tube ion mobility spectrometry–mass spectrometry (DTIMS-MS) paired with solid phase extraction platform enables rapid screening of urine samples for opioids, with marked improvements on traditional methods.

Novel miniature mass spectrometer with continuous atmospheric pressure interface offers robust, repeatable, and rapid MS analysis.

Essential Mass Spec

This year's Top 40 Under 40 Power Listers discuss challenges – and future opportunities – in mass spec

Bram Heijs: In the last decade, mass spectrometry (MS) has become far more widely available. Manufacturers and vendors are making it increasingly simple to operate and maintain analytical equipment – to the point where someone with no MS background can run experiments and process the data. These trends are replicated in the mass spectrometry imaging (MSI) field. The relative simplicity of the equipment makes it an attractive method to experts from other scientific disciplines, who often lack the required expertise needed to fully interpret the multifaceted data.

I truly believe that, to make analytical sciences more accessible to the larger scientific community, we must inject more effort into education. A more altruistic outlook is needed in the current competitive academic and scientific environment to enable peers to actively work together, sharing knowledge and expertise.

With the rate at which MSI is currently developing, there is also no doubt that incredible new advances will be unveiled in the near future. About 10 years ago, routine measurements were performed at 100 µm spatial resolution. Now, state-of-the-art technology performs measurements at subcellular spatial resolution to enable the analysis of individual cells. It is a no-brainer that the future has single-organelle imaging in store – in fact, modern mass spectrometers can already analyze the molecular content of isolated single organelles! In addition to the ongoing push for spatial resolution, spatial molecular identification and annotation tools will likely become more commonplace, which should see the end of "putative identifications" commonly seen in MSI-based work.

Shane Ellis: Agreed; MSI has progressed rapidly in the last decade. Though often used in isolation, MSI can also be used in combination with other imaging modalities, such as optical and fluorescence microscopy, spatial transcriptomics, and even in vivo techniques such as MRI. The struggle we now face is merging different imaging modalities and interpreting the data to acquire the most information out of both.

Our work focuses heavily on lipid imaging. We can already generate rich MSI datasets that show the distribution of hundreds of lipid species throughout tissues, but we know that a large fraction of the lipidome is not detected. Conventional MSI methods also cannot resolve the precise molecular structures of lipids – although we and others are addressing this through the development of various isomer-resolved MSI techniques. These challenges limit our ability to properly understand the biological origins and precise metabolic pathways that give rise to the altered lipid distributions observed with MS. New technologies and data analysis are needed to fully extract the vast amount of metabolic data contained in MSI datasets.

In the future, I believe MSI will be increasingly integrated with other imaging modalities – including multiplexed immunohistochemistry using MSI – and its capabilities for single cell analysis and subcellular resolution using soft desorption/ionization techniques will rapidly develop. I also believe that MSI-based tissue classification will become prevalent in clinical diagnostics and complement conventional histopathology.

Ying Zhu: On a related note, I envision that single-cell MS will undergo rapid progress and transform biomedical research and drug discovery. The essential requirement of single-cell analysis is to analyze a large number of cells, so the analytical procedures must be robust and high-throughput. We will see fascinating developments in microfluidic sample preparation, high throughput liquid chromatography, and highly sensitive MS.

Laura Sanchez: I think we need better standardization protocols for imaging mass spectrometry and reporting data acquisition and processing – because it is often difficult to even consider reanalyzing someone else's data. Additionally, the unavailability of data and standard spectra is often a major bottleneck. I believe that data availability and reporting standards should be a priority so that we can best leverage the advances taking place in data science and our MS datasets can be mined to the fullest extent!

Boniek Gontijo: I work with high-resolution Fourier-transform ion cyclotron resonance mass spectrometry (FT-ICR MS) and the biggest challenge we face is the shortage of helium, which is essential for magnetic resonance. New developments to produce cryogen-free superconducting magnetic systems feasible for MS are urgent for FT-ICR MS to continue delivering ultra-high mass accuracy and vital resolving power in the analysis of complex mixtures.

Daniel DeBord: I believe that the lack of analytical scientists with experience and training in advanced MS techniques is hindering the growth of academic and industrial organizations. It is very difficult to find candidates with the necessary skills to succeed at developing and using analytical instrumentation. The educational pipeline produces a fixed number of graduates each year – but the demand for these individuals continues to grow year after year across the field. Many positions remain unfilled, with human capital the "limiting reactant" for the speed at which research and development proceed.

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Polymer Analysis: Conquering the Gummy Bear

Christian Dauwe, Head of R&D at AppliChrom GmbH, discusses the challenges of a particularly complex sample in the food industry – and explains how KNAUER's AZURA HPLC system and AppliChrom's new LC columns can help

Why is polymer analysis important?

Polymers are widespread compounds found in both natural and synthetic products – synthetic polymers mainly come from the petrochemical industry. One example of a seemingly simple product partially made of biopolymers? Gummy bears!

What are the main challenges of polymer analysis?

Polymer analysis tends to be complex because, in most cases, polymers are not simply made up of uniform long molecules, but a mixture of molecules with different molecular weights and functionalities. Increasing the complexity further, polymers are often mixed with many other small molecules, including sugars, acids, vitamins, and colors. Gummy candy is a good example of this complexity, comprising sugars (sometimes maltodextrin), small amounts of flavoring, (bio-)polymers to keep the structure of the product, and packaging – which can impact the final consumed product.

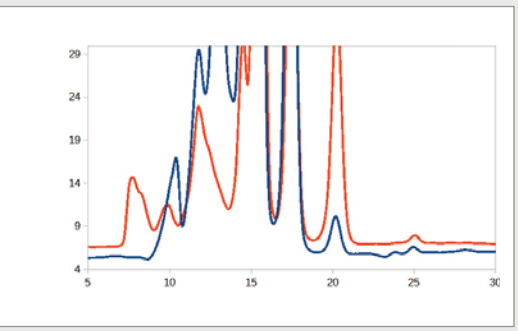


Figure 1. Sugar chromatogram comparison of two different gummy candy suppliers. The chromatogram can be seen as a fingerprint for the different gummy candy brands.

And what is the best way to analyze gummy bears?

In our experience, gel permeation chromatography (GPC), size exclusion chromatography (SEC) and ion exchange chromatography are among the most successful, easy, and reproducible approaches to analyze complex food matrices. In Figure 1, we show separations of two different gummy candy suppliers – for sugars and maltodextrin – to illustrate. The second figure demonstrates a quality check for the ingredient maltodextrin.

However, the main challenge with these separation modes is the type of solvents used, which tend to be organic and apolar solvents or salty solvents. The instruments need to be built to withstand these conditions.

For the past 13 years, AppliChrom has relied on KNAUER equipment – not only for HPLC, but also for GPC/SEC separation methods. Why? Because of its excellent stability and longevity with aqueous salty solvents and organic solvents, such as CHCl3, THF, Acetone, DMSO, NMP, DMF, DMAc.

You also mentioned the analysis of packaging materials. Can you give us an example?

Sure. GPC is suitable for the analysis of the plastic material used to pack the gummy candy and the glue that is used to seal the package. The packaging should contain no small molecular residues. For quality testing of the glue, GPC can be used to ensure the activity measured by the content of small molecules. We used two AppliChrom StyDiViBe columns (1500A for 100–120 000 Da; 10E5 Multipore for 100–1 Mio Da) at 20 °C, under THF elution conditions and refractive index detection with a KNAUER AZURA HPLC system. The result of the quality test showed no toxic residues from the glue or packaging in the final product.

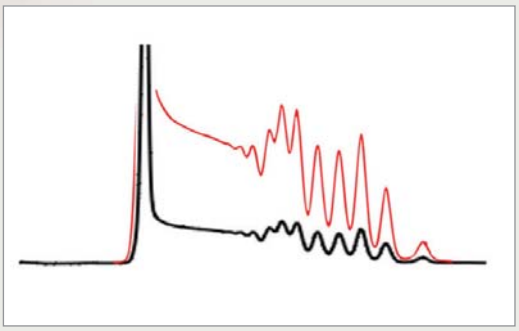


Figure 2: Combined ligand exchange and SEC analysis of raw materials, e.g. maltodextrin from monomer (Dp1) to Dp12. The red and black chromatograms show two different concentrations of maltodextrin solution. The red chromatogram is 10 times more concentrated, showing that the higher molecular peaks are real signals.

How does Applichrom support the polymer and food industries?

New analytical challenges always represent the beginning of a journey. For example, a user might start with a GPC/SEC separation, but soon they have to cover extra fields in HPLC. AppliChrom, in partnership with KNAUER, can offer complete solutions – equipment, material, methods, and expertise – to cover the whole range of applications, with effective communication and cooperation.

For more information, visit www.knauer.net and www.applichrom.de

Core Topic
Chromatography

My GC×GC Story

Join me on a comprehensive trip down a two-dimensional memory lane – and reflect on the legacy bequeathed by John Phillips

By Philip Marriott, Professor in the School of Chemistry, Monash University, Melbourne, Australia

John B. Phillips – in collaboration with Zaiyou Liu – is recognized as the inventor and "father" of comprehensive two-dimensional gas chromatography (GC×GC). His untimely passing in 1999 meant that he never witnessed GC×GC flourish into a new force in ultra-high-resolution GC analysis. Though not widely published, his research spanned multiplex GC, thermal desorption and on-column modulation, and fast GC with thermal modulation – and can be seen as a precursor to what was to come. His spirit of innovation was evidently invested in his former students, such as Janusz Pawliszyn – the inventor of solid-phase microextraction – who studied on-column photochemistry in glass GC columns with John.

I am not sure how many chromatographers got their inspiration to commence GC×GC from hearing John Phillips "wax lyrical" and extol the virtues of this new operating mode he had started working on – but I did. My student Russell Kinghorn and I had been researching the benefits of a longitudinal modulation cryogenic system (LMCS) – an idea I had at the ISCC meeting in Riva Del Garda in May 1994 while listening to Hans Gerd Janssen discuss large volume injection. (But that is another story.) The essence of the LMCS is a cryogenic region encapsulated in a small "shuttle" device that oscillates back-and-forth around a capillary column. The idea was that it would/should allow trapping and rapid re-mobilization of a migrating chromatographic band – a theory we were able to demonstrate.

John had been invited to a chromatography meeting in Sydney, and I was organizing a satellite meeting in Melbourne – the Victorian Separation Science Symposium (1997). This was a good chance to snaffle the speakers who were visiting Sydney. John was eloquent, and very upbeat about this new GC×GC technique. And why wouldn't he be?! Today – perfectly vindicated – GC×GC has spawned a whole new area of advanced capability in GC analysis. The technique was critically dependent on the process of transferring narrow "cuts" from a first (1D) to a second (2D) column – and to do so with an incredible efficiency, delivering an extremely sharp band to the 2D column. Russell and I must have had the same idea, at the same time; "Surely our LMCS could work as an effective modulator for GC×GC" – we whispered as John spoke. So we dropped everything, and focused on developing the concept of a cryogenic modulator for GC×GC. The rest, as they say, is history – our cryogenic process has proved to be a great enabling modulation mode for GC×GC.

But at that time, John reminded me that we had met before. At Pacifichem in Hawaii, in 1985, when I was at the National University of Singapore. We met at my poster on chemical interconversion processes in GC – research that we are still doing today, but now using GC×GC. A story within a story!

Cryogenic devices and GC×GC modulation

John lived long enough to see his vision taken up by a select group of researchers, but their enthusiasm did not translate into major chromatography companies running with the idea. Tools for doing GC×GC were largely in-house devices or the sweeper interface that Zoex championed. Our cryogenic concept apparently spawned a similar device – the dual jet cryo-system

at the heart of the LECO GC×GC commercial system. And with the hardware sorted out, LECO was then charged with developing software control and data presentation/reduction for GC×GC. So at last, GC researchers and industrial users could access a package that offered the full suite of hardware and software required for many research and industrial applications.

How did LECO commence their journey in GC×GC? It is hard to know the inner workings and discussions within a commercial entity, but LECO had already commercialized fast GC-TOFMS technology. And I recall that at the Wintergreen ISCC (1997) meeting there was some excitement about TOFMS for very high throughput GC-MS analysis – and some of us realized that such capability was almost perfectly suited to the acquisition rate demanded of GC×GC. Most users had to be satisfied with FID and other GC detectors – not all correctly engineered for peaks 0.1 s wide. We knew samples were much more complex than a 1D GC analysis suggested – we could see all those extra peaks staring right at us in the GC×GC result! But that also posed a universal and highly unsatisfactory problem: we couldn't identify those same peaks. All a sceptical observer had to ask was, "What are all those peaks – are they real?" And given that our answer was, "We don't actually know," it was easy to dismiss the value of GC×GC. MS had to be a priority.

Putting TOFMS to work for GC×GC

A couple of years later at the Park City ISCC meeting (1999), a few presentations really put GC×GC in the spotlight – but where was MS? A few of us – René Vreuls, Jan Beens, and I – had a serious discussion with Rick Parry (at that time LECO's Separation Science Product Manager) to beseech LECO to move into GC×GC, based on using their TOFMS technology. We knew such technology would help GC×GC users step up to the next level.

To be honest, I'm not sure if Rick took this idea to LECO or if the company was already deep in discussions regarding GC×GC technology; perhaps all we did was confirm our commitment to GC×GC with TOFMS, giving "extra ammo" for Rick to transmit to LECO. Irrespective, early researchers adapted TOFMS to various modulators as bespoke hyphenated systems; later, LECO adopted GC×GC with TOFMS – much to the delight of our close-knit community.

So, John Phillips' earlier demonstration of separation of complex petrochemical and atmospherics samples truly was a beacon illuminating the path towards super-high resolution GC×GC.

Then, Don Patterson's very compelling study of contaminants in human adipose tissue was presented at Wintergreen ISCC in 1997 for trace dioxins following the factory explosion at Seveso. He required the absolute best separation and sensitivity of analysis, and this allowed translation to sampling less of the adipose tissue that was needed to provide a positive screen for exposure. If I recall, he said that it was easier to convince someone to part with a 1 g fat sample than to request upwards of 20 g to achieve the necessary detection limits…

Fast forward – GC×GC today

For many in the GC community, simply seeing a 2D chromatogram plot is sufficient to clearly demonstrate the capabilities of GC×GC – enough to ask, "How do I get a piece of this action?!" And the fact that GC×GC is based firmly on principles of GC means that it can be easily understood in terms of operation and design. There is no "jiggery pokery" required to make it work; apply the technique correctly and it will reward the analyst with both separation and sensitivity.

However, tools to correctly report the hundreds of peaks in our analyses both reliably and precisely are crucial. Getting baselines correct, assigning modulated peaks of a given component to that compound, and being able to do this over a series of replicates or a long time-series analytical study, requires the software engineer to ensure the tools process data correctly. But I would say that the final GC×GC result is clearly better than the significant uncertainty that accompanies a poorly resolved 1D GC result.

There is no reason why every sample that is analysed by 1D GC cannot or should not be applied to GC×GC methodology. All the information available to a 1D GC analysis is still available in GC×GC, but the latter will almost assuredly provide information or details that were not available or evident using a 1D GC method! In other words, the risk/reward equation firmly favors the reward side.

The killer application?

Many analysts are asked – with respect to a new or alternative technique – "What are the killer applications?" This question was especially pertinent for capillary electrophoresis, which was promoted as an alternative to (or at least could be applied to) many applications suited to HPLC. But I don't think there was one killer application that demanded the community to move from packed to capillary GC analysis; instead, it just happened as a natural progression in technical capability. Put simply, capillary GC offered much better resolution in a similar time. And so it is with GC×GC. Although the nuances of the technique and the extent of training, familiarization, and method development are acknowledged, better sample characterization is its own reward.

I'd say every lab dealing with volatiles needs GC×GC at the heart of its capabilities – as prior screening of samples or a process using GC×GC allows the analyst to delegate samples to 1D GC, GC-MS, and so on, as the specific analysis demands.

In fact, GC×GC offers a unique generic capability that simply has no analogy in 1D GC. And that's the opportunity to use clustering of compounds in the 2D separation space to simplify data processing, sample-to-sample comparisons, and process interpretation for sample analysis. This might be a "killer capability," rather than a single application. With the ability to essentially "see" all the important compounds in most samples – especially for non-target applications – the analyst is free to apply whatever interpretation they require to their data, "without let or hindrance."

Thus, GC×GC has spread its wings. Though certainly not lacking in imagination, I doubt John would have guessed – or dared dream – of the legacy that he bequeathed to the GC community.

Defying Uncertainty in Gene Therapy

How new mass spectrometry-based technology is allowing researchers to characterize proteins and gene editing off-target effects with greater sensitivity and reliability

By Hugo Gagnon, Chief Scientific Officer, PhenoSwitch Bioscience & Director, Allumiqs, Canada

A new era of medicine

Recent advances in gene therapy – such as CRISPR/Cas9-based tools – are allowing researchers to introduce or modify genes with unprecedented feasibility. These technologies are hugely exciting from a therapeutic standpoint, particularly in addressing rare and chronic diseases. The ability to potentially heal lethal diseases based on genetic variants, such as muscular dystrophy, cystic fibrosis, and Huntington's disease, explains the hype around these technologies. In addition, the versatility of gene therapy approaches seems endless.

Diabetes, a chronic disease affecting over 400 million people globally according to the WHO, is another prime example of how potential therapies could be life-changing – I would know, I am diabetic myself. To think that we might be able to not just treat but cure all genetic-based diabetes with a single injection is incredible! The potential to save and change millions of lives is right at our fingertips. Although this is exciting at an individual level, it also helps solve issues at a societal level – in terms of time, resources, and cost. Solving long-term problems like these would be truly groundbreaking.

Analytical challenges

One downside of gene editing approaches is the risk of unwanted or unexpected changes at the protein level – so-called off-target effects. Ensuring the correct change in the genome does not automatically mean the results on the expression level are as expected. Cell networks are extremely complex and changing one variable can unexpectedly affect other parts or proteins. Developers must ensure their gene editing therapies do not introduce harmful off-target effects, which is why we need reliable and highly sensitive analytical methods.

Compared to traditional therapies based on small molecules, the analytical requirements for gene therapy applications are significantly more complex. Small molecules benefit from a very defined structure and purification processes built over decades. Newer therapies based on proteins often expressed in well-established cell lines already have increased complexity because they do not have a single defined structure, and the development processes and related analytical technologies are more sophisticated.

Gene therapies take this one step further. For instance, therapies or vaccines based on viral vectors consist of several proteins from the virus, contain the included gene, and are produced in a variety of different cell lines – which can impact impurities and post-translational modifications of the viral proteins. Production yields are also significantly lower for these types of therapies, which means that existing analytical setups need to be adapted.

The latest analytical techniques detecting changes made to DNA or its transcribed products – the messenger RNA (mRNA) – are suitable even with minimal sample amounts. However, these techniques cannot determine the outcome on a protein-level: the phenotype. For instance, a desired gene modification could be successful on the gene level but also result in an unanticipated disturbance of protein interactions. Understanding the effects beyond genomics is a necessity for safe gene therapies.

The most common assays for protein-level verification involve immuno-based techniques, such as Western blot and ELISA, which require antibodies that may be difficult to obtain, of low quality, or too costly to produce at scale. And most importantly, how can we ensure that no other proteins

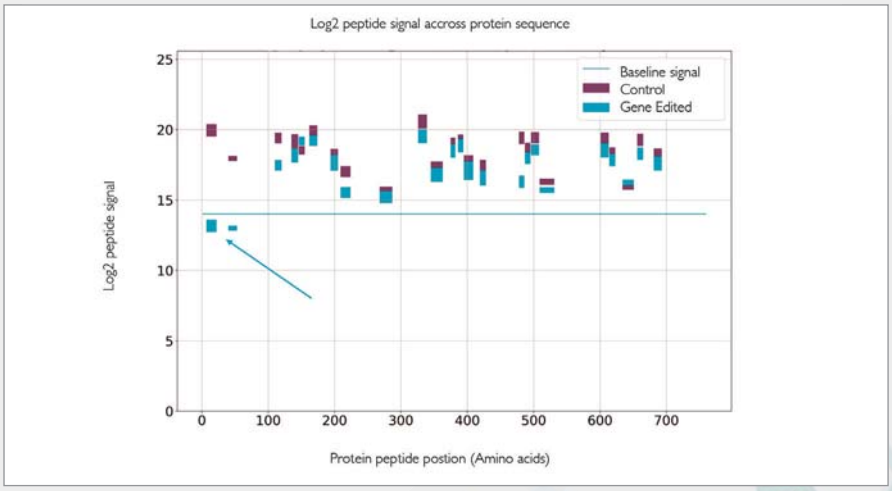


Figure 1: An example of insertion-deletion (INDEL) errors induced by gene editing detected by bottom-up proteomics using SWATH DIA. In this gene editing example, the expectation is that all peptides in the gene-edited samples (blue) are below the detection level. However, compared to the control (purple), only two peptides at the N-terminus of the protein (blue arrow) were silenced based on a shift in the initiation of the protein transcription. Bar thickness represents standard deviation of the peptides.

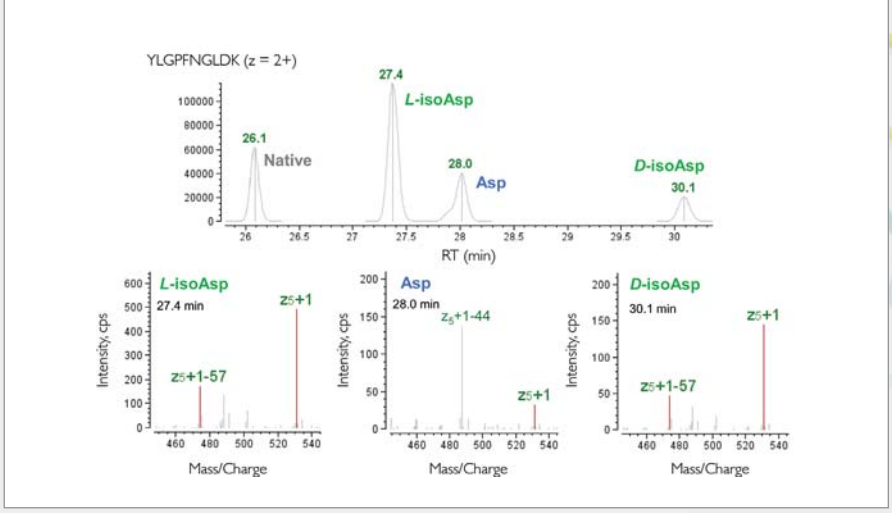


Figure 2: Differentiation between iso-aspartate (isoAsp) and aspartate (Asp) with EAD from a deamidated peptide of the capsid of adeno-associated virus (AAV). The fragment ions of z5-44 and z-57 are diagnostic for Asp and isoAsp, respectively.

were affected in case of a gene editing approach? Liquid chromatography coupled to mass spectrometry (LC-MS) is a critical key technology – its versatility and sensitivity enables product characterization and the ability to investigate changes, such as off-target effects.

Understanding gene editing by state-of-the-art proteomics

The latest developments in mass spectrometry allow us to tackle these challenges with confidence. Researchers are increasingly looking to understand and quantify gene editing induced changes across the entire proteome. The emergence of data independent acquisition (DIA) – an LC-MS/MS workflow that capitalizes on the speed and selectivity gains achieved with modern accurate mass spectrometry instrumentation – allows researchers to identify vast numbers of proteins more reproducibly than with conventional data-dependent acquisition (DDA) methods, while allowing for quantitative analysis from the same set of data (FIGURE 1).

Now, SCIEX has combined the speed and selectivity of DIA on the ZenoTOF 7600 system with significant sensitivity gains through the Zeno trap, which enables the identification of previously undetectable proteins with better protein sequence coverage, painting an even clearer and fuller picture of how gene editing affects other parts of the proteome. SWATH DIA provides the selectivity needed for such complex samples through its data-independent nature, ensuring accurate detection of as many relevant changes as possible. Partnering this technology with the enhancement of MS/MS spectral quality in terms of signal-to-noise results in Zeno SWATH DIA, which is key for detecting and quantifying the low-abundance changes in samples of low amounts.

Additional benefits for gene therapy applications

However, it does not stop there. Another key technology, unique to the ZenoTOF 7600 system, is electron activated dissociation (EAD). EAD is a newly developed dissociation approach that uses tunable electron energy, ranging from electron capture dissociation (ECD) to hot ECD and electron impact excitation of ions from organics (EIEIO), a mode comparable to electron impact (EI) dissociation. These modes can be used to produce varied fragmentation patterns for a wide range of modalities, including peptides. The technology offers more structural specificity compared with traditionally used collision-induced dissociation (CID) and can close gaps from existing electron-transfer dissociation (ETD) or ECD with charge-state independent efficiency.

So, what does this mean for gene therapy application? This technology can enable single amino acid resolution for MS/MS spectral matches – something that CID struggles to achieve in the case of longer, difficult-to-fragment peptides and fragile modifications, such as glycosylations, phosphorylations, and sulfations. It can also identify isobaric amino acids, such as leucine versus isoleucine or aspartate versus iso-aspartate derived from deamidation through descriptive signature fragment ions (see figure 2).

Understanding peptide sequence and modifications, including their localizations, with certainty can greatly enhance biomarker ID and protein characterization work, which ultimately enables more streamlined development of new therapies. Liabilities, such as deamidations that could affect the uptake of viral vectors into the target cells for instance, can be understood and addressed early, removing guesswork from the equation.

Just as critical as obtaining the data for all analytical questions we seek to answer is the ability to process the raw data information in a streamlined, yet flexible manner. Although SCIEX provides access to the raw data, Biologics Explorer software is what allows us to really take full benefit from the extremely rich datasets. And that is vital! You can have the best MS system in the world producing the best data, but if the data cannot be converted into answers, it is essentially pointless. Having access to a capable software suite – the complete package – is very important.

What will the future bring?

Like any new field in medicine, drawbacks and failures are to be expected. We are still very much in a learning phase, as is the regulatory environment and the adoption of new technologies. And issues in clinical phases are usually linked to a lack of understanding of the therapeutic products. However, these modalities have the ability to truly make a difference – targeting what used to be undruggable targets and helping to cure diseases that were thought to be terminal. Very detailed characterization of these highly impactful medicines is absolutely necessary. Cutting corners in terms of product understanding is not an option; and with the ZenoTOF 7600 system offering Zeno SWATH DIA and Zeno EAD technology, we are well equipped to tackle analytical challenges. I am truly excited for the future of gene therapy and gene editing.

Analysis of mRNA Coupled to EGFP by RP and IEX

Oligonucleotides are not only important in genetic and forensic testing and research, but also pharmaceutical applications. To monitor the temporal and dimensional spreading of oligonucleotides or proteins, they can be coupled to enhanced green fluorescent protein, which has a molecular weight of 26.9 kDa and improved spectral characteristics.

mRNA coupled to EGFP can be analyzed by ion pairing reversed phase (IP-RP) or ion exchange chromatography (IEX). Due to the analyte's high molecular weight and the accompanying high hydrophobicity, a widepore column at pH 7 and 80 °C is the ideal choice in IP-RP. The bioinert coated column YMC-Accura Triart Bio C4 with 300 Å provides excellent peak shapes and recoveries.

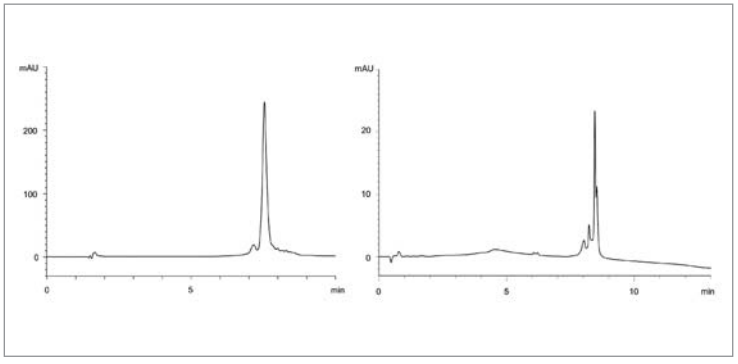


Fig.: IP-RP (left) and IEX (right) analysis of EGFP mRNA (996nt).

The strong anion exchanger BioPro IEX QF is the perfect choice in IEX. The non-porous exchange column has quaternary amine residue functionality. It offers high efficiencies, exceptionally high resolution at low operating pressures independent of the analyte's molecular weight.

Full method details can be accessed here:
https://ymc.eu/d/brDok

Quantification of Phthalates in CE and RoHS Compliance Testing

The requirements for a CE mark now include the requirements for RoHS compliance, which consists of the disclosure of 4 phthalates: Bis(2-Ethylhexyl) phthalate (DEHP), Benzyl butyl phthalate (BBP), di-n-butyl phthalate (DBP), Diisobutyl phthalate (DIBP). A quantification method is defined in IEC 62321- 8 by a TD (Thermal Desorption)-GC-MS technique. The CDS 6150 Pyroprobe is a multi-function thermal sample injection system for GC-MS, meeting and exceeding the RoHS phthalates testing requirements.

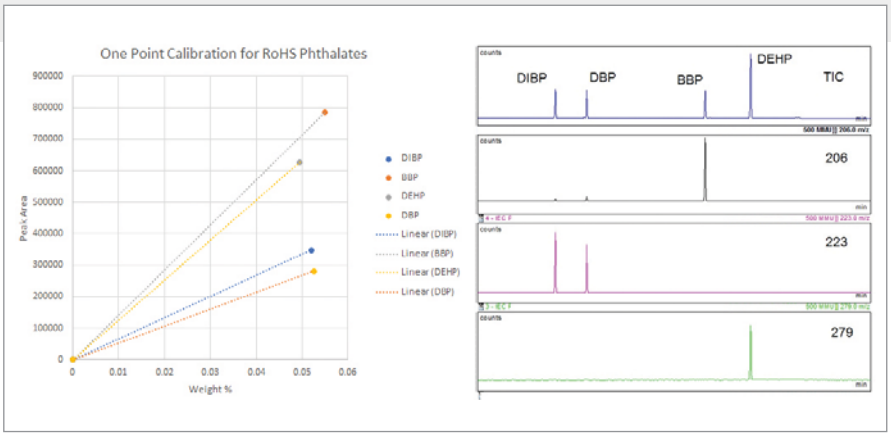
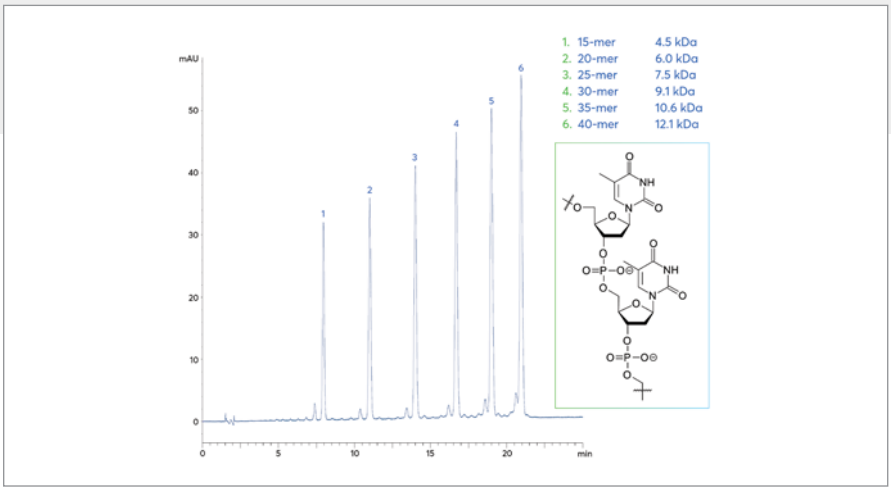


Figure 1: Single point calibration and Chromatograms (TIC and EICs) for the four phthalates.

Table 1 shows the RSD (n=8) averaged at 3.2 percent, four times better than the method requirement, with MDLs all below 25 ppm, four times better than the method requirement.

Phthalate	*Area RSD*	*MDL*
DIBP	3.2%	21.7ppm
DBP	2.3%	21.0ppm
BBP	4.3%	21.0ppm
DEHP	2.9%	14.7ppm

Table 1: Area RSDs and MDLs of Regulated Phthalates.



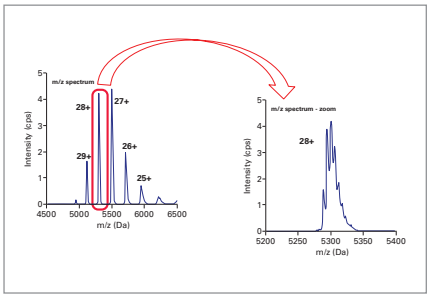
Ion-Pair Reversed-Phase Analysis of an Oligonucleotide Ladder Standard with Avantor® ACE® Oligo

Oligonucleotides are short lengths of DNA/RNA that are increasingly being used as therapeutic agents for the treatment of genetic disorders and cancers. With oligonucleotide treatments, it is possible to synthesise a single-strand of DNA/RNA with a complementary sequence to a disease-causing gene. Once this therapeutic DNA sequence has bound to the target gene in the body, the gene is deactivated. This method of treatment is known as antisense therapy. Currently, over 100 oligonucleotide-based therapies are in the clinical pipeline with many more in the pre-clinical development stage.

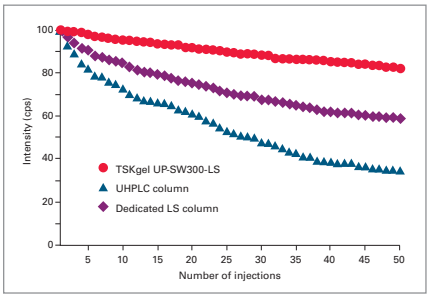
Several impurities can be produced during the oligonucleotide synthesis (e.g. failure sequences), due to a less than 100 percent efficient process, and these need to be removed from the desired product. This purification process can be performed using ion-pair reversed-phase HPLC (RPLC).

Download the technical note at: https://uk.vwr.com/assetsvc/asset/en_GB/id/31027837/contents/ion-pair-reversed-phase-analysis-of-an-oligonucleotide-ladder-standard.pdf

Selecting the Optimal Column for Native SEC-MS of Monoclonal Antibodies



A Mass spectrum of mAb sample



B Ionization efficiency

Characterization of monoclonal antibodies (mAbs) is essential for product safety and efficacy. Size exclusion chromatography (SEC) coupled with mass spectrometry (MS) is increasingly used to identify the accurate molecular mass of mAbs and their impurities. However, traditional SEC generates high particle shedding, which decreases ionization efficiency over time. To avoid shedding for MS and multi-angle light scattering (MALS) applications, Tosoh Bioscience developed TSKgel® UP-SW3000-LS U/HPLC size-exclusion columns. In this application note, the column was coupled with an MS instrument for the analysis of a mAb standard. Data demonstrate that the TSKgel UP-SW3000-LS column surpasses competitive UHPLC columns and a dedicated low shedding column for SEC of proteins in terms of particle shedding observed by MS. Moreover, the column helps maintain ionization efficiency in the electrospray ionization (ESI) source >90% compared to the initial injection over >50 injections, thus increasing data quality and reducing ion source cleanings.

Read the full application note here: bit.ly/SEC-MS-of-mabs

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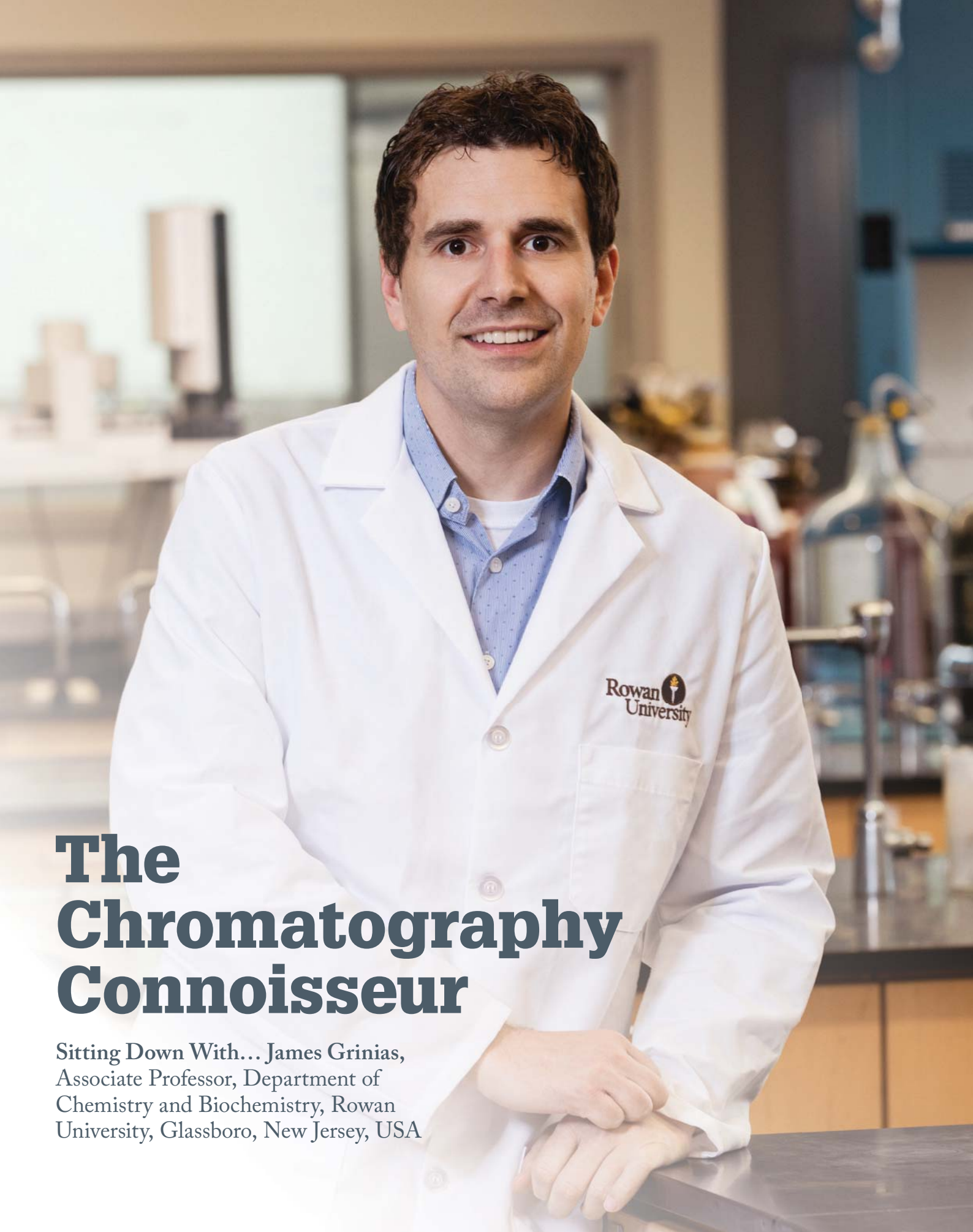

The Chromatography Connoisseur

Sitting Down With… James Grinias, Associate Professor, Department of Chemistry and Biochemistry, Rowan University, Glassboro, New Jersey, USA

Did you always want to be a scientist?

Growing up, I always imagined myself pursuing a career in medicine. I loved chemistry and figured I would choose it as my undergraduate major and then attend medical school. However, it soon dawned on me that I was likely too squeamish to follow my original plan! Luckily, my first advisor (Heather Holmes, Associate Professor at Eastern Michigan University) provided me with an opportunity to pursue chromatography research early in my undergraduate career and everything fell into place.

What do you credit most for your success in the early part of your career?

When I started university, I was told that seeking out good mentors is critical to success. Throughout the educational pipeline, I had research advisors who were passionate about chromatography and taught me a lot about the field. They quickly became great collaborators and friends, providing me with a strong network of trusted colleagues in the field. My wife – one of the group members – has been extremely supportive and is a great chromatographer to discuss new ideas with! Finally, I must acknowledge the amazing students I have worked with over the years who are driving our field forward.

Can you tell us a bit about your research?

My doctoral and postdoctoral advisors (James Jorgenson and Robert Kennedy) are well-known for pushing the limits of the field and, after working with them on various capillary and microfluidic liquid chromatography (LC) projects, I started thinking about the possibility of shrinking instrument components.

My goal was to not only enhance chromatographic performance by matching the scale of these smaller columns, but also achieve a fully portable LC instrument. Milton Lee, a professor at Brigham Young University, had similar aspirations and was in the process of commercializing new, miniaturized LC technology. When my independent career began, I called him to see if he would be interested in collaborating, which marked the beginning of a longstanding and successful partnership!

The most exciting thing about a fully portable instrument is the limitless ways it can be employed. Although our research has focused on pharmaceutical and clinical applications, we have also dabbled in beer characterization that can be used in breweries – and we were able to transport the whole instrument to public-facing demonstrations! More broadly, others working on miniaturized separation instruments are continuously coming up with creative ways of sending chromatographic instruments into space, which fascinates me.

What needs to happen before a compact LC system is available for clinical use?

I know that it is likely a few years away but, for point-of-care environments, simplicity and speed are key. It's not just the instrument that must be robust and simple to operate; sample preparation is vital for accurate examination of clinical samples. Thankfully, we have recently received funding to overcome some of these challenges – so hopefully we will be able to report more progress soon!

Do you have any predictions for your field over the next five to 10 years?

As a field, we continue to strive for "greener" analytical methodologies that reduce energy consumption and the use of toxic solvents. Within LC, multiple compact instruments have been commercialized that reduce solvent usage 100- to 1,000-fold compared with standard benchtop instruments. Though many consider capillary LC columns "less robust," modern advances have brought them closer to the technology with which a typical HPLC user may be familiar. HPLC is frequently the preferred choice for routine analysis, so I believe scientists could scale down their systems for a greener approach. Although changes are often met with resistance because of the need for revalidation, the reduction in solvent and power consumption from using these compact instruments would be worthwhile. Continued improvements in column quality and instrument performance will hopefully help this vision become a reality.

"Within analytical science, there has been a shift away from training in the fundamentals of instrument design."

What are your biggest fears for analytical science?

Within analytical science, there has been a shift away from training in the fundamentals of instrument design. Effective experimental design, data acquisition, and data analysis all rely on an understanding of the core molecular properties that different instruments measure. I fear that it may become more difficult to bridge the gap between the engineers who design instruments and the scientists from a range of disciplines who use them. There is a balance between breadth and depth that educators must consider. Analytical chemists familiar with chemistry, statistics, electrical engineering, and computer programming will be crucial to the future of our field!

Do you have any personal missions for the next 10 years?

I would love to see a compact LC system used in a clinical setting, providing real-time patient data to healthcare professionals.

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