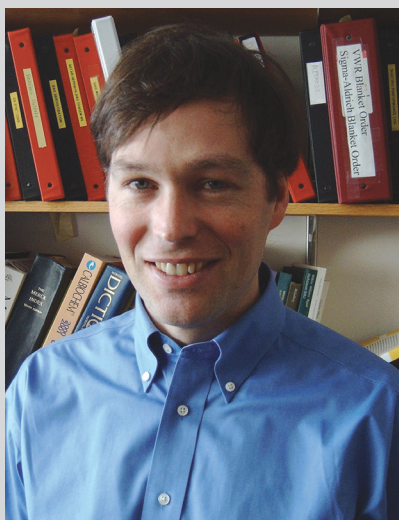


THE END OF SILOS AGILENT HELPS RESEARCHERS GATHER MULTI-OMICS DATA



Joseph Zaia, Ph.D.

Associate Director, Center for Biomedical
Mass Spectrometry
Professor of Biochemistry
Boston University School of Medicine

Biology is complicated, and the more you look, the more complicated it gets.

That hasn't deterred Joseph Zaia.

Zaia is the Associate Director of the Center for Biomedical Mass Spectrometry at the Boston University School of Medicine. His research combines what have traditionally been separate specialties: proteomics, glycomics, and glycoproteomics.

"To fully understand the biology, we need to connect these different data silos," Zaia says.

Not an easy task, given the variables involved. Consider glycosylation alone. This endoplasmic reticulum and Golgi apparatus-directed, site-specific protein glycosylation process serves various biological functions.

"The challenge is that the glycosylation at any protein site is heterogeneous by nature," Zaia says. "Every site might have 50 variants, just to use an arbitrary number. If you have 10 different sites, you can imagine how now you have an extremely complicated molecule."

Zaia and his team have been using Agilent technology, including the 6550 iFunnel Q-TOF and the 6560 Ion Mobility Q-TOF LC/MS systems, to decipher these diverse structures.

He believes the analytical methods they have developed and the mass spectral data they are producing will be invaluable to understanding normal and disease-related cellular growth.

It's groundbreaking work, and Zaia credits the Agilent 6560 in particular with increasing the reach of his investigations:

"With a standard LC/MS system you're going to get a certain level of detail, but the 6560 adds a whole new dimension—ion mobility—and that will have applications in understanding glycan structure and in mining the glycoproteome," he says.

"In biotherapeutics, for example, scientists need to characterize low-abundance structures to see if they are within acceptable limits. The 6560 provides a way to get analytical data very quickly to make sure the levels of nonhuman glycosylation are, or are not, acceptable."



Agilent Technologies

"That's one of the reasons we like the HILIC-C18 HPLC-chip from Agilent. The chip allows us to produce high-quality LC/MS data on glycoproteins to facilitate that whole problem of characterizing protein glycosylation. It is in fact a big step in that direction."

Those data are vital because drug companies (and government agencies such as the U.S. Food and Drug Administration) depend on accurate, detailed analyses to ensure safety and efficacy.

"The FDA acknowledges the power of analytical chemistry," Zaia says, "so if the chemistry is good enough, a biosimilar, for example, won't have to go through expensive clinical trials."

He believes that glycosylation needs the same level of attention that nucleic acids or proteins have received.

"Right now you can go the National Center for Biotechnology Information, NCBI, and you can get all kinds of tools for genetic information and protein sequence information. Ultimately, glycosylation information needs to be represented at the same level of importance," he says.

The chip (available as a custom order) is particularly useful, Zaia says, for eliminating steps.

"Now we can enrich our glycoproteins and analyze them without having to handle the sample at all. That's a big benefit because a lot of the variability comes from sample handling. I see it as a winner. It really works. You get really robust data," he says.

"We use the chip to characterize influenza glycosylation from the point of view of comparing how glycosylation changes as influenza evolves. The ultimate need is to have really high-quality proteomics, glycomics, and glycoproteomics all at once. We are doing pretty well at that using Agilent technology."

Related Information

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