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special issue

Tomorrow's PIs

Genome Technology's special year-end issue profiling rising young investigators

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primer

A special issue for special scientists

You're a busy person. If you're like most of our readers, you probably spend your day scrambling from one meeting to the next, squeezing in experiments and data analysis whenever you can, and after your long, hard day, you finally go home — where you catch up on all of your work e-mail. Sound familiar?

In a field where speed is essential — you need results *now*, you have to release your data immediately, and there's always a grant application or project presentation looming — it's a rare thing indeed to step back and actually take a moment to appreciate what you and your colleagues have accomplished.

It's that rare moment we offer to you with this issue of *Genome Technology*, aimed at celebrating the accomplishments of a select group of researchers in this community. In the past several months, readers have asked me for more profiles of up-and-coming scientists. So when we decided to add a bonus tenth issue to our calendar, choosing the theme was simple: who would be the PIs of tomorrow's labs? Who are the rising stars people should be watching right now?

We tapped today's leading PIs to find out, and they had no shortage of names to share with us. The tough part was narrowing the field to the 30 most promising scientists whose profiles you will find on the following pages. Our criteria were simple: they had to be involved in the disciplines that comprise systems biology, and could be no more than five years into their first faculty or equivalent post.

In what has been perhaps the most fun issue we've ever put together, the *GT* staff got to spend hours talking with these bright researchers not only about what they're doing today, but also about where they see the field going in the years to come (we did get mocked soundly, though, for my own favorite question: "If you were to one day win the Nobel Prize, what accomplishment would you like that to be for?"). What we found was that these scientists are already fluent in some key attributes: if you read the profiles carefully, you'll notice a theme of highly collaborative people who understand the importance of networking and surrounding themselves with other very smart people.

I'd like to thank all of the current lab heads who recommended people for inclusion in this issue, and also *GT* reporter Matt Dublin for heading up this project. And though we keep our editorial and advertising departments completely separate, I will take a moment to thank our advertisers, whose contributions for this issue have allowed us to give travel stipend honoraria to our profiled investigators.

You'll notice that this issue doesn't look like a typical *Genome Technology*. With different content comes a different designer, and GenomeWeb's own Elena Coronado has done an outstanding job in giving our bonus issue a very special look. We'll be back to our usual designers, the talented folks at Three Bears, with our next issue.

Finally, for those of you who thought we'd forgotten about the cartoon caption contest we offered earlier this year, don't miss the Blunt End. We held results till now since so many entries were plays on the PI/postdoc dynamic. Check out p. 50 for the winning caption and our honorable mention.

Meredith W. Salisbury

proteomics

alexeynesvizhskii

From Physics to Proteins

Armed with a PhD in physics and a desire to apply his technology savvy, Alexey Nesvizhskii is shaping a career around seeking out the more interesting questions in science. This drive led him to bring his expertise to proteomics, specifically in the development of computational tools to parse out the seemingly endless stream of data generated by mass spectrometry-based technologies.

"This is a really active field," he says, "and when you have an active field [in which] people are developing new technologies, new chemistries, new ways of generating data — they end up with data and no really good way to analyze it. That's where I come in."

Title: *Assistant Professor of Pathology, University of Michigan*

Education: *PhD, Physics, University of Washington, 2001*

Recommended by: *Phil Andrews, Steven Carr*

Nesvizhskii dove into this proteomic imbroglio first as a postdoc and later as a research scientist in Ruedi Aebersold's lab at the Institute of Systems Biology. There, he worked to develop algorithms and computational tools for processing and validating proteomic data, as well as for mining and integrating information derived from proteomics, genomics, and metabolomics. He's continued to extend these approaches at his current post in the University of Michigan's pathology department. "Probably most applications are going to be disease-related," he says, "but the methods can be applied in general to proteomic data generated from model or human systems."

In his current work, Nesvizhskii says that identifying post-translational modifications from mass spec-based data is an increasingly salient problem, especially considering his new clinical post and the relevance of phosphorylation and glycosylation to cancer. His aim instead is "to go beyond this typical proteomics-based approach, where you collect data and compare it by searching across databases to identify peptides and proteins."

Looking ahead

Nesvizhskii sees the field moving toward more targeted analyses, by which researchers may evaluate data they've accumulated to seek out interesting trends that will dictate strategies taken at the experimental level. He notes that earlier researchers were more interested in exploring the proteome and seeing what could be identified using mass spec. "In the last five years, we've realized that there are a lot of challenges in terms of the dynamic range," and that getting down to the level of biologically or disease-relevant proteins is the current challenge.

Publications of note

Nesvizhskii, along with co-investigators at ISB, pioneered a method designed to increase the amount of information that can be extracted from MS/MS datasets. The method picks up spectra where conventional sequence database searching falls short, with the result that iterative searches can pave the way to new insights drawn from existing datasets. The paper, entitled "Dynamic spectrum assessment and iterative computational analysis of shotgun proteomic data," published in *Cellular Proteomics* earlier this year.

Last year, Nesvizhskii co-authored a paper with Ruedi Aebersold reviewing the difficulties of interpreting shotgun proteomic data. This kind of data is "peptide-centric," the authors wrote in *Molecular and Cellular Proteomics*, leading to problems in determining the true nature of proteins in a sample. Aebersold and Nesvizhskii also touched on the state of protein sequence databases, and the need for a common computational infrastructure to integrate proteomic and transcriptional data.

How to succeed in science

"If you're a computational scientist like me, the key is to be really interdisciplinary, to know as much as you can about biology so you can speak the same language [as biologists], and, at the same time, to know as much as you can about technology so that you can suggest ways to design experiments," Nesvizhskii says. *— JC*