Bioanalysis Rising Star Award 2019: announcing our finalists!

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Over the past 9 years, *Bioanalysis* and Bioanalysis Zone have been proud to host the Bioanalysis Rising Star Award (formerly the New Investigator Award), to recognize and showcase the most promising early-career scientists in our community. The time has now come for you to select your winner for the Bioanalysis Rising Star Award 2019.

We are delighted to present our judges' selection of finalists (in alphabetical order):

- Justin Mak (Stanford Healthcare; CA, USA);
- Kruthika Sundaram (Viapath Analytics; London, UK);
- Lee Andrews (Syneos Health; NC, USA);
- Sebastien Boridy (Charles River; Montreal, Canada);
- Xiaoyu Wang (Nanjing University; Jiangsu Sheng, China);
- Zhiyu Li (WuXi AppTec; Shanghai, China).

To view the finalists' profiles and short interviews, please visit www.bioanalysis-zone.com. The 2019 Award is being held in association with Waters Corporation (MA, USA), with the winner receiving a US \$1000 prize and a year's subscription to *Bioanalysis*. The winner will be announced and presented with the award at the European Bioanalysis Forum Open Meeting taking place in Barcelona (Spain) in November this year, where they will also present their work.

Justin Mak
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Supporting comments

I am delighted to support Justin Mak's nomination for the Bioanalysis Rising Star Award. Justin is a bright, self-motivated and independent researcher who consistently seeks out ways to push clinical metabolomics testing to the next level. His work focuses on new methods for screening, diagnosis and monitoring patients with inborn errors of metabolism. Justin has developed, validated and implemented process improvements for a number of small-molecule assays including methylmalonic acid [1] and carnitine, as well as a novel LC-MS/MS method for quantitative amino acid analysis [2], and its expansion to additional analytes (e.g., sulfocysteine and guanidinoacetate) and classes of compounds (arylglycines and acylcarnitines). He is now focusing on novel methods for targeted and untargeted broad-scale metabolomics testing using LC-QTOF-MS, representing a paradigm shift for our field. His innovations include designing and optimizing chromatographic methods to capture all clinically relevant compounds from the most polar to nonpolar, and developing rigorous procedures for sample preparation, quality control and statistical analysis appropriate for clinical testing. Along

the way, he has independently reached out to industry and academic leaders in analytical hardware, software and statistical methods, and is an invaluable resource and mentor to our entire team.

Nominated by: Tina Cowan, Stanford Healthcare (CA, USA); tcowan@stanfordhealthcare.org

Describe the main highlights of your bioanalytical work

The main focus of my work has been to improve patient care by developing and implementing novel, rapid and underivatized LC–MS assays that assess metabolic health.

It is known that matrix effects diminish assay accuracy and sensitivity, both of which are unacceptable for patient testing. Rather than using laborious and slow extraction methods, such as solid-phase extraction, my approach has been to fully leverage the principles of chromatography. For example, serum methylmalonic acid samples are traditionally processed by solid-phase extraction and derivatized, totaling 4–6 h. I was able to minimize sample preparation using ultrafiltration, a 15 min process, while maintaining assay precision, accuracy and sensitivity by developing a chromatographic method that consistently excluded matrix effects [1].

Second, I have implemented a 14.5 min, underivatized amino acid method [2]. While derivatization kits are available, result turnaround is slower and these methods cannot baseline separate clinically significant isobars or isomers, such as alloisoleucine from isoleucine and leucine.

At last, I am validating a newly developed chromatographic method that may supplant the traditional reverse-phase and HILIC methods used in clinical metabolomics. In conjunction, I have programmed the necessary data analysis tools in Python and R.

Kruthika Sundaram
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Supporting comments

Sundaram has been with us in Viapath Analytics, responsible for R&D Immunology, for 3 years now. Her expertise is exploring the pathogenesis of immune disorders to identify potential drug targets and biomarkers, using a variety of cellular and molecular techniques. She has extensive experience in assay development. She and her team have introduced new assays that have led to the expansion of diagnostic tests offered by our department. Her persistence during budget cuts has been impressive and she consistently works on improving existing methods to save us time and money. She is an excellent team player, exemplified by the guidance she provides for the PhD students in her team. She is highly collaborative and never hesitates to seek and provide help where necessary. She always takes the initiative to gather and share knowledge on relevant cutting-edge technologies like NextGen sequencing data analysis and multicolor flow cytometry through departmental presentations. She was awarded the learning and development funding from Viapath for two consecutive years, to present her work at international conferences and she actively publishes. She is a great asset to the company and the bioanalysis community. I give her my highest recommendation for the BRSA award.

Supporting comments: Mohammad AA Ibrahim, Viapath at King's College Hospital (London, UK)

Nominated by: Srividya Sundararaman, Xencor (CA, USA); svidya.sraman@gmail.com

Describe the main highlights of your bioanalytical work

I am an immunology expert interested in translational research. In my doctoral dissertation, I identified transcription factor IκBζ as a potential therapeutic target for allergic asthma with RS-LPS and Anakinra as treatment choices. I also evaluated ways of tackling challenges associated with antibody specificity and sensitivity while using immunohistochemistry to explore protein expression in tissue samples.

In my current position as the R&D Immunology manager in Viapath Analytics, my team and I have designed and standardized four novel assays as tools for use in diagnosis of immune disorders including common variable immunodeficiency (CVID), and rheumatoid arthritis. We introduced exome sequencing as a diagnostic test for primary immunodeficiencies, a cell-based assay to detect the presence of anti-GMCSF autoantibodies in patient sera and a plate-based assay to quantify NFκB pathway activation as an indicator of disease severity in patients. We also identified CXCL13 as a potential biomarker for CVID and rheumatoid arthritis and blood subsets of T follicular helper cells as classifiers of heterogeneous CVID phenotype.

I have published five peer-reviewed papers, presented ten posters and given four oral presentations in international conferences like American Association of Immunologists, American Thoracic Society and European Society of Immunodeficiencies.

Lee Andrews
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Supporting comments

Lee has a passion for bioanalysis unlike anyone you will ever meet. In the few years that he has been at Syneos Health, he has been involved with many different facets of bioanalysis in our lab. He has been involved with large molecule PK, ADA and NAB method development, method validation and sample analysis. He is an innovative thought leader when it comes to troubleshooting and the development of difficult assay challenges. He takes on every challenge with enthusiasm and a 'no fail' mentality that is contagious and

motivating to others in the team.

Lee has spent time in our small molecule discovery group as well as playing an active role in the critical reagent characterization process. Lee also leads our immunogenicity data handling initiative from the lab perspective. He has spent countless hours with our LIMS programmer and other Business Technology representatives to automate the generation of custom reports for more efficient and error-free data tables.

Lee oversees a small team of about five individuals, and they all share a similar passion. This proves his leadership ability and is proof that he will continue to advance in the bioanalysis field based on his scientific, innovative and managerial skill set.

Nominated by: Kevin Andrew Carleton, Syneos Health (NC, USA); kevin.carleton@syneoshealth.com

Describe the main highlights of your bioanalytical work

I function as a Bioanalytical Principal Investigator and a leader for Ligand Binding method development. In the course of my job, I designed a hybrid Immunoassay format that uses a SPEAD clean-up step followed by a standard bridging format for detection. This hybrid format allowed for the assay to overcome matrix effects that caused analytical variance, and therefore, a high percent of false positives, and to maintain a high degree of drug tolerance (50 ng/ml ADA in the presence of 500 ug/ml of drug [or 1:10000 ratio ADA:drug]).

I designed and developed a series of protocols in SMP that allow for the automatic evaluation of ADA and NAB data. This has since been implemented by my entire site, and the company is expanding it to other lab locations due to the efficiency it produces in the collection, evaluation and reporting of ADA/NAB data.

Sebastien Boridy
Charles River Laboratories (Montreal, Canada)
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Supporting comments

Sebastien leads the immunogenicity group at the Montreal Charles River facility. Over the past 2–3 years, he has been actively involved in the AAPS community by providing feedback on our practices and experience with various immunogenicity programs. His contribution was even highlighted by people from the immunogenicity community. Indeed, he has been highlighted as an active member of the AAPS community and was asked to be one of the key experts for a discussion on pre-existing antibodies. He also gave

a presentation at the AAPS conference on the same subject, which was well received. From a mentoring perspective, he has also been involved in giving courses at McGill to undergraduate students in order to expose them to the field of immunogenicity in the context of drug development. He also recently mentored a master's student, who completed at the end of 2018 her degree (her project was on the development of nAb bioassays).

Sebastien also worked in harmonizing the activities in the immunogenicity group at the Montreal site and also across the Charles River organization. He maintains a positive environment for his employees and encourages their participation in various initiatives in the immunogenicity field (participation to workshops, conferences, presentation of posters, etc). This contributes in developing the group and increasing the knowledge of the

employees. He also shares his expertise whenever needed with his staff, members of the immunogenicity community as well as with his colleagues from the other Charles River Laboratory sites. For example, he helped two of the smaller Charles River Laboratory sites to build their lab and develop their immunogenicity services.

Sebastien is starting to be recognized in the immunogenicity field as being a key player with good ideas. I see that he definitely has potential to continue this growth as he will become more and more involved in the immunogenicity scientific community.

Nominated by: Marie-Soleil Piche, Charles River Laboratories (Montreal, Canada); marie-soleil.piche@crl.com

Describe the main highlights of your bioanalytical work

- Part of AAPS working groups and active member;
- Mentoring of Master's students (one student recently graduated following completion of her project in my laboratory);
- Teaching courses at McGill University. These courses are specifically aimed at teaching undergraduate students what immunogenicity means in drug development;
- Participation/presentation at AAPS, CHI immunogenicity summit and WRIB;
- Lead for the immunogenicity group at Charles River Montreal (team of 11 scientists).

Xiaoyu Wang
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Supporting comments

Xiaoyu is a PhD candidate in my research group in the Department of Biomedical Engineering at Nanjing University. I have been working closely with him for 4.5 years. His work is focused on the development of high performance nanozymes for bioanalytical applications. In the past several years, his research work greatly promoted the development of nanozyme bioanalysis. Xiaoyu developed a straightforward and predictive activity descriptor for guiding the search for highly active peroxidase mimics, which provided the basic research for nanozyme bioanalysis. This interesting work was published by *Nature Communications*, which attracted great attention after publication and was highlighted by Phys.org. Besides this project, he also developed nanozyme sensors and sensor arrays for versatile analytes from bioactive small molecules to proteins and even cells. Some of these results have been published in *Analytical Chemistry* and *Theranostics*. He has won numerous prestigious awards, such as 'The National Scholarship for Graduate Students' and '2018 Baxter China Young Investigator Awards' because of his academic achievements. Overall, Xiaoyu is a creative and collaborative researcher and I am confident in his potential for future success. Therefore, I most strongly and enthusiastically support his application for this prestigious Bioanalysis Rising Star Award.

Nominated by: Hui Wei, Nanjing University (China); weihui@nju.edu.cn

Describe the main highlights of your bioanalytical work

During my first bioanalytical study, I developed a ratiometric electrochemical biosensor for ascorbic acid detection. The obtained ratiometric response can substantially overcome intrinsic systematic errors of traditional electrochemical sensors and thus improve the reproducibility and robustness.

Subsequently, the main focus of my work has been evolved to developing bioanalytical assays with peroxidase-like nanozymes. Currently, the search for peroxidase-like nanozymes mainly relies on trial-and-error strategies. The rational strategies for designing effective nanozymes with peroxidase-like activity will promote nanozymes' application for bioanalysis. I demonstrated that the efficacy of e_g occupancy to predict and identify the peroxidase-like activity of perovskite oxide nanomaterials. According to the descriptor of e_g occupancy, LaNiO_3 was identified as the most active peroxidase mimic. Further, I constructed biosensors for some important biomolecules (e.g., H_2O_2 , glucose and sarcosine) by using the peroxidase-mimicking LaNiO_3 as natural enzyme's alternatives.

Previous 'one-to-one' nanozyme biosensors are generally based on the preselected bioligands for specific recognition, which may not be available for the emerging analytes. To detect emerging analytes without preselected bioligands, I constructed nanozyme sensor arrays for detection and fingerprint identification of bioactive molecules,

proteins and cells. Moreover, I developed nanozyme sensor arrays for tracking patterns to follow real-time biologically related events.

Zhiyu Li
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Supporting comments

Zhiyu Li has continuously shown strong technical capabilities, outstanding innovative mind, constant drive for excellence, as well as strong leadership since joining our DMPK department at Lab Testing Division in WuXi AppTec in August 2016 as a Principle Scientist I.

As the head of our new capability building team, Zhiyu has led her team in the development several new bioanalytical platforms, including the LC–MS-based large molecule analysis platform. This platform has been applied in more than 300 projects and has led a new trend among competitors. Zhiyu has been heavily involved with cross-functional and cross-division collaboration in WuXi AppTec. Zhiyu and her team has transferred new platforms to the Toxicology and GLP Bioanalysis department. And she has comanaged the collaboration between our department and the Clinical Diagnostics department. Zhiyu has given presentations at multiple national and international conferences and participated in the bioanalytical community. Because of her excellent work, she was quickly promoted to the position of Principle Scientist II and Associate Director.

Overall, Zhiyu has made multiple scientific advances that have significant impact in WuXi AppTec as well as in the bioanalytical community. I strongly support her in the competition for the Bioanalysis Rising Star Award.

Nominated by: Yi Tao, WuXi AppTec (Shanghai, China)

Describe the main highlights of your bioanalytical work

Since joining WuXi AppTec in August 2016, I am responsible for developing analytical methods for challenging projects, introducing new technologies and building new capabilities for the non-GLP bioanalysis unit in the DMPK department of the Lab Testing Division.

I have had the opportunity to develop and validate the first LC–MS-based large molecule bioanalysis platform in China, which had been used in more than 300 projects thus far. Moreover, I have set up the first dry plasma spot assay platform for pharmacokinetics in the world, which is quite useful for the sampling of water- or enzyme-unstable compounds. Third, I have developed a new type of chromatography, mobile sorbent affinity chromatography, by introducing a third phase, the analyte sequestering transport phase, into the traditionally two phase liquid chromatography system, in which only the target analyte elutes first within a short time, while all the nonanalytes are retained.

Thus far during my first bioanalytical job, I have published two peer-reviewed papers, supported the application of one patent and presented five posters at international conferences such as Clinical & Pharmaceutical Solutions through Analysis, International Society for the Study of Xenobiotic and American Society of Mass Spectrometry.

Disclaimer

The opinions expressed in this interview are those of the interviewees and do not necessarily reflect the views of Future Science Group.

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