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Institute for Systems Biology, ABSciex to collaborate

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Institute for Systems Biology, ABSciex join hands to enhance biomarker profile

Singapore: Institute for Systems Biology (ISB) and AB SCIEX have signed a multi-year agreement to collaborate on the development of methods and technology in proteomics mass spectrometry with the goal to redefine biomarker research and complement genomics through fully comprehensive quantitative proteomics analysis. This will help advance the development of a new approach to medical care.

The objective is to make medical care more personalized and better prevent the onset of diseases in the future through research into P4 medicine underway by scientists at the Institute for Systems Biology, including National Medal of Science award winner Dr Leroy Hood and ISB proteomics research director, Dr Robert Moritz, supported by a collaboration with AB SCIEX's analytical technology.

ISB's concept of P4 medicine promises to provide deep insight into disease mechanisms on the path to develop medical care that is predictive, personalized, preventive and participatory (the four "P"s) - a pioneering vision that requires a combination of analytical tools, workflows, databases, collaborations and computational strategies.

"With breakthroughs in translating research into clinical relevance, P4 medicine is expected to enable the creation of a virtual cloud of billions of data points around each individual as the basis for straightforward predictions about health and disease," said Dr Hood, ISB president and co-founder. In December, he was named a recipient of the National Medal of Science, which is the highest honor the President of the United States can bestow on a scientist, in recognition of visionary work for the advancement of science.

Led by Dr Hood, ISB's groundbreaking research is being accelerated by SWATH acquisition, a data-independent acquisition

(DIA) mass spectrometry workflow that can quantify virtually all detectable peptides and proteins in a complex sample - all in a single analysis.

"Quantifying enormous numbers of protein analytes at the same time is a critical need to accelerate P4 medicine and the democratization of proteomics, a revolution that is akin to the sequencing of the genome and the democratization of DNA," added Dr Hood. "SWATH is a game-changing technique that essentially acts as a protein microarray and is the most reproducible way to generate comprehensive quantitation of the entire proteome. It generates a digital record of the entire proteome that can be mined retrospectively for years to come."

ISB's know-how in systems biology and informatics will support the development of SWATH libraries, similar to its highly regarded SRMAtlas project for the human proteome, pioneered by Rob Moritz and his collaborators, and the proteomes of other clinically-relevant organisms. "With complete proteome-wide libraries, ISB provides the basis to support comprehensive SWATH analysis," said Dr Moritz, director, ISB Proteomics Research.

Committed to an open policy of sharing data and methods, ISB will make the SWATH libraries available to the global scientific community to accelerate the use of SWATH for other biological research. Utilizing the depth in proteomics technology development and underpinned by the extensive proteomics computational resources in data interpretation tools, standards initiatives and database development under the leadership of Dr Moritz, ISB will develop new SWATH technologies and tools to enable the community to quickly adopt comprehensive quantitative proteome analysis.

"Having the proteomics data standardized across laboratories and across samples really enables us to quantitate entire proteomes at a level that hasn't been done before," said Dr Moritz. "We aim to define markers that can predict whether a patient will respond to a certain treatment or not, and applying SWATH will play a big part in taking our advancements to another level. Not only can we now complement the breadth of genomics, but we will have the much-needed libraries and software development going forward to make data-sharing quite easier and standardized."

ISB will be using the AB SCIEX TripleTOF 5600+ System and an Eksigent ekspert nano-LC 400 System as the instrument platforms on which to conduct the protein identification and quantitation. The TripleTOF 5600+ System provides the high speed necessary for SWATH Acquisition. TripleTOF technology combines high speed and high sensitivity with high resolution and accurate mass. ISB also plans to use SelexION technology, a recent advancement in differential ion mobility, in the future to advance its research.