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Chemical Genomics – CALBIOsummit 2002 April 21,22,23

(BW Healthwire)—April 18, 2002—Xencor’s President and CEO, Dr. Bassil Dahiyat Chairs Panel at CALBIOsummit 2002

Monrovia, CA – April 18, 2002 – Xencor, a drug discovery company focused on chemical genomics and protein optimization, today announced that Bassil Dahiyat, Ph.D., President and CEO, will chair the "Chemical Genomics-Linking Drug Activity with Protein Function" panel at the 10th annual CALBIOsummit in San Diego, CA, April 22 from 1:45pm-3:15pm. The panel will discuss the use of small molecule drugs as probes to find new targets and to understand and predict compound effects in the body.

“Chemical genomics is a rapidly emerging drug discovery approach, as understanding proteins and predicting the way in which they interact with chemical compounds in the body is imperative to the advancement of drug discovery,” stated Dr. Dahiyat. “New technologies are driving the field of chemical genomics, allowing scientists to analyze libraries of expressed proteins on a genome-wide scale for protein-small molecule and protein-protein interactions. Chemical genomics provides scientists with the ability to validate gene functions and potential drug candidates in one step, bridging the gap between genetic breakthroughs and medical advances.” In addition to Dr. Dahiyat, other panelists include John Kozarich, Ph.D., President and CEO, ActivX and Les Browne, Ph.D., COO, Iconix Pharmaceuticals.

Using its ProCode™ technology, Xencor can quickly analyze libraries of expressed proteins from humans, animals, plants and microbes for protein-small molecule and protein-protein interactions, critical in assessing protein function. This proprietary technology uniquely combines protein expression in a wide range of native cell types, including human cells, with the ease of DNA detection to deliver enormous improvements in speed and sensitivity over protein detection methods such as mass spectrometry and 2-D gels.

ActivX Biosciences, Inc., is a pioneer in the field of activity-based proteomics, the identification and analysis of active proteins. ActivX technology includes novel chemistry integrated into a high-throughput platform to rapidly interrogate the activities of proteins in all ranges of abundance in any biological sample, a process it has termed chemoproteomics. ActivX is using its technology and next generation proteomics approach to bridge the gap generated by standard genomics and proteomics techniques.

Iconix Pharmaceuticals develops integrated technologies that allow life science researchers to discover drug candidates for novel therapeutic targets and predict the potential efficacy, toxicity and other side effects of drug candidates at the earliest stages of drug discovery. Iconix also maintains internal drug discovery and development programs based on novel targets resulting from genomic studies.

Xencor’s ProCode™ Technology

ProCode™ is a chemical genomics tool that enables the use of small molecule compounds as the starting point for target identification and side effect profiling. ProCode™ creates cDNA expression libraries of soluble DNA-protein complexes, where each expressed protein is linked to its corresponding cDNA. ProCode™ libraries can incorporate any cDNA library and are rapidly created and screened in a pooled format. Thus, by panning for protein binding to a compound of interest and amplifying the tethered DNA, one can carry out repeated rounds of screening to isolate genes encoding proteins that interact with compounds of interest.

The direct linkage of expressed proteins (function) to DNA (genotype) eliminates the need for laborious detection and purification technologies such as mass spectrometry and 2-D gels. ProCode™ technology provides the sensitivity of DNA amplification and detection, a billion-fold improvement over existing methods and a feature that greatly simplifies miniaturization and high throughput automation.

Xencor’s Protein Design Automation™ Technology

Protein Design Automation uses three-dimensional structure information to optimize protein sequences. A structural model of a protein is computationally determined from public database information or created by modeling from homologous proteins. A structural region for design is selected based on the protein properties to be optimized. Because the amino acid sequence of

the protein is defined by the structures of the amino acid side chains, the PDA™ technology is then used to accurately model the atomic interactions among the side chains to screen for the best sequence of amino acids for this protein structure. The optimal sequence for the design region is determined, as well as from thousands to millions of other nearly optimal sequences.

Highly efficient computational search methods allow the screening of over 1080 sequences, exploiting protein diversity unreachable by non-computational methods. Following this in silico pre-screen, the predicted sequences are then experimentally tested in vitro, either singly or as small libraries, for improved performance. By testing only those sequences that are compatible with the protein structure, the PDA technology eliminates deleterious changes that are created by directed evolution, creating focused libraries that require far less effort and cost to screen for optimized proteins.

Xencor, a privately held company, is focused on using its cutting edge chemical genomics and protein optimization technologies to accelerate the discovery of therapeutic proteins and novel compounds. With its proprietary ProCode™ and Protein Design Automation™ (PDA™) technologies, Xencor scientists can rapidly determine the interactions and functions of a cell's entire protein complement, identify proteins of interest, and then optimize key properties of these proteins to fit commercial applications. The use of these technologies alone or in combination will accelerate the compound identification and development programs of Xencor's strategic partners in the pharmaceutical, biotechnology, agricultural and chemical industries. Xencor is headquartered in Monrovia, California.