Editorial: *Molecular Endocrinology* Articles in the Spotlight for October 2012

Donald B. DeFranco, Ronald Margolis, and Neil McKenna

Department of Pharmacology and Chemical Biology (D.B.D.), University of Pittsburgh School of Medicine, Pittsburgh, Pennsylvania 15260; National Institute of Diabetes and Digestive and Kidney Disease (R.M.), National Institutes of Health, Bethesda, Maryland 20892-5460; and Department of Molecular and Cellular Biology and Nuclear Receptor Signaling Atlas (N.M.), Baylor College of Medicine, Houston TX 77030

This issue of *Molecular Endocrinology* features four minireviews that highlight recent advances in the application of various forms of "-omics" technology to the study of endocrinology (*i.e.* "endocrinomics").

The term "omics" refers to global, discovery-driven data platforms that generate large data sets from which investigators can glean new hypotheses or validate existing models. The trail was blazed by high-throughput genomic technologies used to generate vast quantities of DNA sequence from a variety of genomes. From there, the omics revolution progressed to encompass: 1) "transcriptomics," which profiles changes in gene expression levels using expression microarrays and RNA-Seq 2) "proteomics," interrogating steady-state cellular protein levels and protein posttranslational modifications using protein arrays, mass spectrometry, and related technologies; 3) chromatin immunoprecipitation (ChIP)-based technologies such as ChIP-Seq and ChIP-chip, which report on transcription factor DNA-binding events ("cistromics") and chromatin modifications ("epigenomics"); and 4) "metabolomics," the identification of specific molecules and metabolites in serum or plasma resulting from changes in the actions of proteins contained within the proteome, using primarily mass spectrometry-based approaches.

To be relevant to the endocrine research community, these large data sets must be understood in terms of molecular functions and roles in disease. Achieving this payoff for the larger community requires that these data sets be publicly deposited, consistently annotated, and then opened for free access to allow researchers to build queries across multiple individual data sets, allowing them to infer system-wide physiological function. These insights help us to appreciate how subtle changes at the molecular level contribute to disease and can reveal new modes for intervention. In this way, the application of multi-omics technologies and concepts, and the subsequent archiving of these data sets, can lead directly to the translation of basic discovery into new understanding of disease.

Rather than focus on specific experimental outcomes of such technology, these minireviews focus on emerging technologies and data analysis tools that were developed, in part, through the efforts of a visionary National Institute of Diabetes and Digestive and Kidney Diseases (NIDDK)-funded consortium, the Nuclear Receptor Signaling Atlas (NURSA, www.nursa.org). *Molecular Endocrinology's* productive relationship with NURSA has been featured in past editorials and we are pleased to provide a view to the future of NURSA and other consortia that will provide the community of endocrinology researchers and practitioners with user-friendly omics data and analytical tools that will advance future hypothesis-driven research and increase our detailed understanding of endocrine physiology and diseases.

Readers are directed to descriptions of the outcomes of nuclear receptor and coregulator proteomics by O'Malley and colleagues and of the applications of next-generation sequencing on analysis of nuclear receptor function spearheaded by Liu. The minireview by Becnel and McKenna focuses mainly on mass spectrometry as a model for current progress and challenges in data analysis, management, sharing and integration in proteomics, and provides some thoughtful discussion of current efforts to develop data standards and mechanisms for data interchange between distinct proteomics data bases. Finally, the research resource by Cartailler and colleagues describes dkCOIN (www.dkcoin.org), a pilot interconnectivity network supported by NIDDK to aggregate high content data sets and reagents derived from multiple research consortia with interests in β-cell biology, nuclear receptors, diabetes, and metabolic disorders. We welcome our readers to the snapshot of endocrinomics that can be made accessible to the scientific community.

Donald B. DeFranco, Ph.D.
Editor-in-Chief, *Molecular Endocrinology*
Ronald Margolis, Ph.D.
Neil McKenna, Ph.D.

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