

Editor's Introduction to This Issue

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The theme of this issue's review articles is epigenomics – one of the hot topics in genome sciences. Recent publications by the Encyclopedia of DNA Elements (ENCODE) Consortium have sparked interest in this field. Dr. Jung Kyoong Choi, KAIST, Korea, reviews the results of the ENCODE project on the chromatin environment in regulatory elements. Dr. Jae-Bum Bae, National Institute of Health, Korea, reviews the status quo of several international collaborative projects on human epigenomics. We plan to invite more reviews on epigenomics in upcoming issues as well. One of the original articles by Dr. Kyu Bum Kwack's group, Cha University, Korea, reports a diplotype analysis on the association between polymorphisms and clearance of hepatitis B virus. This new type of analysis has the potential to detect novel signals. In addition, we have four special articles from four groups that report different analysis viewpoints of the same exome dataset of Korean leukemia

patients. In the application notes section of this issue, one may find useful resources, such as a phylogenomic database and an siRNA processing tool. Dr. Yong-Hwan Lee's group, Seoul National University, Korea, reports a comprehensive database on the evolutionary relationships among a ubiquitous molecular chaperone family. Dr. Hyun Seok Kim's group, University of Texas Southwestern Medical Center, USA, describes a simple and yet extremely convenient and powerful tool for processing cell-based assay data.

As of last fall, *Genomics & Informatics* has been available in PubMed Central (PMC) and PubMed. Since then, we are now observing a dramatic increase in access to our articles around the world. However, it is premature to assess the increase in impact factor.

I hope you enjoy this year's first issue of *Genomics & Informatics*. Your continued support is greatly appreciated.

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