Editorial

I would like to welcome you to Volume 5, Issue 3 of *Human Genomics*. As discussed in Issue 2, we have introduced the open-access opportunity for papers published in the *Journal*. Our instructions to authors have been revised to reflect this change and to include other modifications that will improve the submission process. The instructions to authors can be found at the end of this issue on p. 208.

Our submission rate has increased and our publication rate is constant to the point that our Impact Factor will be provided by ISI by the summer of 2011.

We have a new addition to our Editorial Board. I therefore welcome and introduce to you, Samir Zakhari, who is Director of the Division of Metabolism and Health Effects of the National Institute on Alcohol Abuse and Alcoholism at the National Institutes of Health, USA.

In this issue, we start with the *Research Highlights*. Webb, Smith and Cotton then describe the difficulties associated with finding SNPs and related phenotypic data in world wide web resources using simple, uncomplicated search terms and they also provide a suggested solution. This is followed by the Filocamo and Morrone *Review* of the molecular basis and laboratory testing of lysosomal storage disorders, a group of more than 50 different inherited metabolic diseases. In the *Update on Gene Completions and Annotations* section, Smathers and Petersen review the human fatty acid-binding protein (FABP) family, a member to the superfamily of intracellular lipid-binding proteins. In this paper, the evolutionary divergences and functions of the FABPs are discussed. In Issue 5.2, Wright and Bruford provided an excellent *Review* on the nomenclature of non-coding RNAs (pp. 90-98). In the *Software Review* section of the current issue, Agirre and Eyras discuss databases and resources available for non-coding RNAs (sRNAs). They look at the main issues related to the integration and annotation of sRNA datasets. In the *Genome Databases* section, Valerio discusses toxicology models and databases as Critical Path toolkits for predicting toxicities early in drug development. Finally, Cassiman reviews the second edition of a book entitled 'Molecular Diagnostics' published by Elsevier (Academic Press) in 2010 and edited by George Patrinos and Wilhelm Ansorge.

Vasilis Vasiliou
Editor, Human Genomics
University of Colorado,
Denver, CO, USA