



## Welcome to the *Phenomics* Journal

Li Jin<sup>1,2,3</sup>

© International Human Phenome Institutes (Shanghai) 2021, corrected publication 2022

The term ‘phenomics’, first coined by Dr. Steven A. Garan in 1996, describes the measurement of phenomes. The phenome is a set of measurable traits, including the physical, chemical and biological traits of individuals and populations, that result from the complex interactions of genes, epigenetics, symbiotic microorganisms, diet and environmental exposures. The high-throughput approaches implied by the term ‘deep phenotyping’ have attracted much attention in the fields of functional genomics, pharmaceutical science, biomedical engineering, phylogenetics and disease genomics in humans and model organisms.

With the emerging interest in phenomic research across many fields, massive efforts based on high-efficiency integrated phenotyping facilities and international collaborative projects have been deployed to systematically study phenotypes. This will further our understanding of the functional underpinnings of human health, biotechnology, agriculture and other areas of life sciences. The number of publications on phenomics has increased rapidly since 2011 in the areas of human genetics, epidemiology, plant biology, etc. It is expected that the number of publications on phenomics will grow continuously with the increasing efforts made to better understand gene function and environmental responses. However, phenomics-related papers are mainly published in broad-based biological journals. Thus, there is an urgent need for the publication forum of *Phenomics*, which will specifically serve this scientific community.

*Phenomics* is dedicated to publishing the finest articles and communicating scientific process in the field of phenomics. The interdisciplinary nature of this topic stretches across

both fundamental and applied research in the life sciences. It focuses on the study of phenomes at all level (including the proteome and metabolome at the molecular level, cell features at the cellular level, and all kinds of organs at the organismal level), the mechanisms underlying genomic architecture and regulatory networks, the relationships among phenotypes and disease risks and the intervention responses, providing a prerequisite understanding of the health and disease states of mammals. The journal considers articles, reviews, commentaries, brief communications, and correspondences, and it intends to publish online every 2 months. For more information, please visit the journal website: <https://www.springer.com/journal/43657>.

The topics of interests to *Phenomics* include but are not limited to high-throughput phenotyping and technological innovations; linking the genome to the phenome with models, algorithms, databases, etc.; exploring the relationships between phenotypes and understanding phenotypic variation and responses to the environment; phenotypic research and its precise application in clinical disease, treatment, prevention and control; phenome-related multiomics studies, novel data fusion approaches and integrated analysis; and phenome-related model organism research, interdisciplinary multiscale research, etc. *Phenomics* has established an international editorial board of leading scientists covering the various areas of its scope, and it strives to achieve a fair peer review process.

We are sincerely grateful for your help in launching *Phenomics*. We would like to invite you to join our editorial board and contribute your manuscript to the journal, marking a new era of phenomics.

✉ Li Jin  
lijin@fudan.edu.cn

<sup>1</sup> School of Life Sciences & Human Phenome Institute, Fudan University, Shanghai 200438, China

<sup>2</sup> Shanghai Medical College, Fudan University, Shanghai 200032, China

<sup>3</sup> International Human Phenome Institutes (Shanghai), Shanghai 200433, China

Li Jin  
Editor-in-Chief, *Phenomics*

**Publisher's Note** Springer Nature remains neutral with regard to jurisdictional claims in published maps and institutional affiliations.