

Special Issue

Isotope-Guided Analytical Strategies for Assessing Metabolic Networks in Cancer

Message from the Guest Editors

The reprogramming of the cancer metabolism is central to the process of malignant transformation. Stable isotope-guided analysis, whether targeted or untargeted, has enabled fundamental discoveries in the cancer metabolism. Hypothesis-driven approaches that interpret targeted metabolite ^{13}C , ^{15}N , ^{18}O or ^2H labeling patterns have uncovered key nutrient dependencies in tumor and immune cells, revealed metabolic reprogramming driven by oncogenic mutations, and led to the identification of unique metabolic adaptations that enable the continuity of energy generation, while fostering enhanced biosynthetic pathways. In contrast, unsupervised isotope-tracing metabolomics can measure metabolome-wide shifts in pathways, which is discovery-based and hypothesis-generating without a defined model. This issue will cover how advances in stable isotope and computational flux methodologies have yielded new insights into metabolic networks within the tumor niche, and then detail how emerging flux methods at the cutting-edge of isotope flux analysis are being applied to examine compartmental and spatial metabolic interactions within tumors.

Guest Editors

Dr. Irwin J. Kurland

Prof. Dr. Henri Brunengraber

Dr. Alison E. Ringel

Dr. Yunping Qiu

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Metabolites
Editorial Office
MDPI, Grosspeteranlage 5
4052 Basel, Switzerland
Tel: +41 61 683 77 34
metabolites@mdpi.com

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About the Journal

Message from the Editor-in-Chief

The metabolome is the result of the combined effects of genetic and environmental influences on metabolic processes. Metabolomic studies can provide a global view of metabolism and thereby improve our understanding of the underlying biology. Advances in metabolomic technologies have shown utility for elucidating mechanisms which underlie fundamental biological processes including disease pathology. *Metabolites* is proud to be part of the development of metabolomics and we look forward to working with many of you to publish high quality metabolomic studies.

Editor-in-Chief

Dr. Amedeo Lonardo

Internal Medicine, Ospedale Civile di Baggiovara, Azienda Ospedaliero-Universitaria, 41126 Modena, Italy

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