



OPEN ACCESS

EDITED AND REVIEWED BY
Maxim B Freidin,
Queen Mary University of London,
United Kingdom

*CORRESPONDENCE
Arivusudar Everad John,
arivusudar.m@gmail.com

SPECIALTY SECTION
This article was submitted to Human
and Medical Genomics,
a section of the journal
Frontiers in Genetics

RECEIVED 01 September 2022
ACCEPTED 08 September 2022
PUBLISHED 10 October 2022

CITATION
Everad John A (2022), Editorial: Multi-
omics studies and applications in
precision medicine.
Front. Genet. 13:1034283.
doi: 10.3389/fgene.2022.1034283

COPYRIGHT
© 2022 Everad John. This is an open-
access article distributed under the
terms of the [Creative Commons
Attribution License \(CC BY\)](https://creativecommons.org/licenses/by/4.0/). The use,
distribution or reproduction in other
forums is permitted, provided the
original author(s) and the copyright
owner(s) are credited and that the
original publication in this journal is
cited, in accordance with accepted
academic practice. No use, distribution
or reproduction is permitted which does
not comply with these terms.

Editorial: Multi-omics studies and applications in precision medicine

Arivusudar Everad John*

Mazumdar Shaw Medical Centre, Bengaluru, India

KEYWORDS

multi-omics, precision medicine, metabolomics, phosphoproteomics, transcriptomics

Editorial on the Research Topic

[Multi-omics studies and applications in precision medicine](#)

In the recent years multi-omics has emerged as a vital approach in discovery studies. With advent of high throughput technologies, it has become feasible for scientists across the globe to perform large scale experiments. Instead of looking at few molecules, Omics studies unleashes the potential of looking at the entire repertoire of genome, transcriptome, epigenome, proteome metabolome or microbiome. Such studies lead to novel discoveries and aids in providing a holistic view of the biological systems. For instance, [Zhi-e et al.](#) have applied metabolomics and transcriptomics to delineate the hepatotoxicity in mice models. Using two different approaches, they could pinpoint and emphasize the toxicity associated with the use of Aristolochic Acid I. [Mohd et al.](#) employed a phosphoproteomics analysis to decipher the role of a crucial tyrosine kinase CAMKK2 in gastric cancer. They have delineated the entire pathway of CAMKK2 and this study could provide potential novel targets for targeted therapy in gastric cancer.

In the current Omics era, scientists have gone a step further where the publicly available datasets are used to derive deeper insights into the biological problem. In this issue, two groups have actually done a deep dive into the freely available omics

datasets to derive meaningful insights of the problem of interest. [Kunpeng et al.](#) used TCGA datasets to perform a pan-cancer analysis of the role of 4EBP1 (Eukaryotic translation initiation factor 4E binding protein 1) and its prognostic significance. Similarly, [Shizhe et al.](#) used TCGA datasets to develop a prognostic model for prognosis of hepatocellular carcinoma. In summary, multi-omics approaches can be proven useful and serves as a treasure trove in the field of biomarkers.

Author contributions

The author confirms being the sole contributor of this work and has approved it for publication.

Conflict of interest

The author declares that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

Publisher's note

All claims expressed in this article are solely those of the authors and do not necessarily represent those of their affiliated organizations, or those of the publisher, the editors and the reviewers. Any product that may be evaluated in this article, or claim that may be made by its manufacturer, is not guaranteed or endorsed by the publisher.