Special Issue

Linking Genomic Changes with Cancer in the NGS Era

Message from the Guest Editor

The developing of the next-generation sequencing (NGS) technology has opened a new era in the identification of disease-causing genetic changes. The "translationability" of the identified changes is complex, and the establishment of a new driver gene/variant constitutes the NGS-based genetic screening bottleneck. This is particularly true in cancer, where only a very small fraction of the 10-20% of the cancers associated with familial aggregation have a known underlying genetic cause. Moreover, the profile of genomic changes of the 80-90% of the cancers arising sporadically is highly heterogeneous, making difficult to distinguish driving, secondary and progression-associated genomic variation.

We appreciate the work highlighting or discarding the identification of new genes/variants as a cause of cancer development or progression. Evidences may include case-control studies, segregation analysis, gene/variant specific gene editing, protein structure analysis, functional studies, or other approaches considered relevant for validation of a gene-disease association.

Guest Editor

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The International Journal of Molecular Sciences (*IJMS*, ISSN 1422-0067) is an open access journal, which was established in 2000. The journal aims to provide a forum for scholarly research on a range of topics, including biochemistry, molecular and cell biology, molecular biophysics, molecular medicine, and all aspects of molecular research in chemistry. *IJMS* publishes both original research and review articles, and regularly publishes special issues to highlight advances at the cutting edge of research. We invite you to read recent articles published in *IJMS* and consider publishing your next paper with us.

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