



Advances in Nanopore Sequencing Technology: Methodological Issues and Application

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Message from the Guest Editors

In recent years, third generation sequencing is transforming the standard way of conceiving genomic analyses. What was considered impossible only a few years ago in terms of throughput, potential, ease of use and costs, today is becoming achievable.

In 2012, the first long-read nanopore-based sequencer was released, overcoming the main limits of short-reads sequences generation and offering a revolutionizing approach finalized to have a profound, positive impact on society. NS allows an easier characterization of genomic regions that are difficult to be studied; it is the only approach able to perform the direct RNA sequencing and to detect the epigenetic base modifications without preliminary DNA or RNA treatment.

The present Special Issue aims to debate the most recent advances in NS technology, focusing on its methodological benefits and applications. Contributions (research and review articles), addressing the NS performance in various “-omic” sciences: genomics, epigenomics and transcriptomics are welcome, with particular interest in NS aiming to allow the analysis of anything, by anyone, anywhere.





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Message from the Editor-in-Chief

As the world of science becomes ever more specialized, researchers may lose themselves in the deep forest of the ever increasing number of subfields being created. This open access journal Applied Sciences has been started to link these subfields, so researchers can cut through the forest and see the surrounding, or quite distant fields and subfields to help develop his/her own research even further with the aid of this multi-dimensional network.

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