Special Issue

The Increasing Role of Next Generation Sequencing Methods in Mutation Analysis

Message from the Guest Editor

The implementation of next-generation DNA sequencing techniques has revolutionized molecular diagnostics. In the middle of an era where we are moving towards a more simplified workflow of mutation analysis, a lot of issues arise. There is a need for standardized wet lab and in silico analysis methods. In the case of exome and genome sequencing-based diagnosis, we have to deal with incidental findings and also with the evidence-based pharmacogenetic data that might be included in the personal healthcare database of the patient. The classification of detected mutations is also inevitable. Mutation-specific treatment is more and more widespread. Altogether, these improvements open up possibilities not only for personalized genome-based medicine, but also for predictive medicine as well. Molecular genetic diagnostics involves both germline and somatic mutation analysis; therefore, this Special Issue of the journal *Life*, covering the topic "The Increasing Role of Next Generation Sequencing Methods in Mutation Analysis" is open for research papers and reviews from both major fields of genetic testing, i.e., the analysis of inherited disorders and cancers.

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Life (ISSN 2075-1729) is an international, peer-reviewed open access journal that publishes scientific studies related to fundamental themes in life sciences. Some papers are published individually, while others are submitted for inclusion in special issues with guest editors. You are invited to contribute a research article, essay, or a review to be considered for publication.

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