Special Issue

Advancing Forensic Genetics Through Massive Parallel Sequencing

Message from the Guest Editor

The field of forensic genetics has experienced significant advancements in the last decade, both in terms of laboratory practices and methods as well as the statistical methods involved in the evaluation of the genetic data. The introduction of massive parallel sequencing (MPS) stands out as one of the most important breakthroughs in the genetic field allowing numerous applications such as typing of dense SNP panels to resolve distant kinship and complex DNA mixtures, SNP microhaplotype typing, sequence-based STR typing and quantifying methylation status to predict age and identify tissue. Sequencing technologies continue to evolve and advance, in particular for low quality and quantity DNA commonly found in forensic grade samples.

This Special Issue aims to gather the most recent research in forensic genetics with a special focus on massive parallel sequencing appliction including, but not limited to, topcis such as forensic investigative genetic genealogy, forensic DNA mixture interpretation, inference of relationships, ancestry estimationa and prediction of age using DNA methylation. The issue will include original research articles, case series, case reports and reviews.

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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