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Source Attribution Using Forensic Genomics

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Deadline for manuscript
submissions:

closed (20 October 2021)

Message from the Guest Editor

In this Special Issue of *Genes*, we examine the recent advances in source attribution of biological material in the field of forensic genomics. Analysis of single nucleotide (SNP) and short tandem repetitive (STR) polymorphisms is the gold standard for human identification. These procedures have evolved considerably since their inception due, in part, to the rapid application of massively parallel sequencing, dense SNP arrays, and the bioinformatic analysis of these data for research and casework. Laboratories are now better able to resolve DNA mixtures using sequence-level data, are capable of predicting outwardly visible characteristics for investigative leads and can map unidentified remains to a country or region of origin with unprecedented accuracy. I am humbled to guest edit this Special Issue and hope that you enjoy reading about the recent benchtop and computational advances to source attribution in the field of forensic genomics.



mdpi.com/si/78483

Special Issue



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Message from the Editor-in-Chief

Genes are central to our understanding of biology, and modern advances such as genomics and genome editing have maintained genetics as a vibrant, diverse and fastmoving field. There is a need for good quality, open access journals in this area, and the *Genes* team aims to provide expert manuscript handling, serious peer review, and rapid publication across the whole discipline of genetics. Starting in 2010, the journal is now well established and recognised.

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