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Viral Diagnostics Using Next-Generation Sequencing

Guest Editor:

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Deadline for manuscript submissions:

closed (31 July 2019)

Message from the Guest Editor

Diagnostic virology is undergoing a revolution due to technological developments, especially in the area of Next-Generation Sequencing. The rapid production of large amounts of sequence data combined with in-depth bioinformatic analyses enable new insights into the identity, abundance, genome organization, and molecular epidemiology of viral agents in clinical samples. We are calling for articles for a Special Issue on "Viral Diagnostics Using Next-Generation Sequencing" that will consist of either original research articles and short-communications on the detection, identification, enrichment, genomic characterization, resistance profiling, and bioinformatic applications related to the diagnostic of viruses; or examine the current state of the field through review articles. We also welcome comparative methodological approaches of wet or dry laboratory aspects of viral diagnostics using NGS, demonstrating the superiority of specific approaches in terms of turnover time, costs, ease of implementation, and biological information generated for applications in the clinical routine setting.

Dr. Alban Ramette *Guest Editor*













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Message from the Editor-in-Chief

Genes is central to our understanding of biology, and modern advances such as genomics and genome editing have maintained genetics as a vibrant, diverse and fast-moving 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. Why not consider *Genes* for your next genetics paper?

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