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Using Genomics to Understand Venom Evolution

Guest Editors:

Dr. Mark J. Margres

Department of Integrative
Biology, University of South
Florida, Tampa, FL 33620, USA

Dr. Jason L. Strickland

Department of Biology, University
of South Alabama, Mobile, AL
36688, USA

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Message from the Guest Editors

Venoms are complex cocktails of peptides, proteins, and/or organic molecules that have multiple origins across the animal tree of life. Animal venoms have emerged as a model system for understanding the genotype–phenotype relationship in polygenic traits because of their genetic tractability, contributions to fitness, and exceptionally high evolutionary rates. Although venoms are commonly investigated using transcriptomics and proteomics, genomic information is required to understand the processes and mechanisms that underlie venoms’ multiple origins, as well as the mechanisms producing the exceptional degree of variation known in these systems. The aim of this Special Issue is to publish genomics-based research to further our understanding of venom evolution using data generated through whole-genome sequencing, sequence capture, RAD-seq, BAC clones, Sanger sequencing, and other genomic approaches. This issue is expected to publish original research articles, reviews, and short communications in the broad area of venom genomics (but will not include studies solely relying on transcriptomes or proteomes).



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Prof. Dr. Jay Fox

Department of Microbiology,
University of Virginia,
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Toxins Editorial Office
MDPI, St. Alban-Anlage 66
4052 Basel, Switzerland

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