Special Issue

Using Genomics to Understand Venom Evolution

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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About the Journal

Message from the Editor-in-Chief

Toxinology is an incredibly diverse area of study, ranging from field surveys of environmental toxins to the study of toxin action at the molecular level. The editorial board and staff of *Toxins* are dedicated to providing a timely, peer-reviewed outlet for exciting, innovative primary research articles and concise, informative reviews from investigators in the myriad of disciplines contributing to our knowledge on toxins. We are committed to meeting the needs of the toxin research community by offering useful and timely reviews of all manuscripts submitted. Please consider *Toxins* when submitting your work for publication.

Editor-in-Chief

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