



**toxins**



*Special Issue Reprint*

## **Identification and Functional Characterization of Novel Venom Components**

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Throughout most of the 20th century, the toxinological literature consisted largely of pharmacological and functional characterizations of crude venoms and venom constituents, often constituents that could not be identified unambiguously. The advent of amino acid composition analysis in the 1950s enabled the first forays into physical characterizations of purified toxins, though these remained few in number until the 1970s. Then, the tryptic and chymotryptic cleavage of venom proteins coupled with manual Edman degradation began to provide the first complete sequences, particularly of three-finger toxins. Polyacrylamide gel electrophoresis and improved resins for liquid chromatography permitted improved purification and better gross structural characterization of venom components. The early 1980s witnessed the advent of automated Edman degradation, and entire sequences of longer proteins began to be reported in the literature. Then, the molecular biology revolution enabled the generation of cDNA sequences of more and larger proteins, followed by mass-spectrometry-based proteomics and quantitative high-throughput DNA sequencing and genomics. Today, we face an unprecedented situation in which our capacity to generate sequence/structural data has completely overwhelmed our capacity to functionally characterize venom constituents. This Special Issue of *Toxins* includes 11 publications addressing the discovery and functional characterization of novel venom constituents of vertebrate and invertebrate venoms.



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